Interactome analysis of NS1 protein encoded by influenza A H7N9 virus reveals an inhibitory role of NS1 in host mRNA maturation

Supporting Information

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Table S-1-1. List of proteins identified in immunoprecipitation product of control vector (Replicate 1)

	Gene name	Accession number	M.W. (kDa)	Protein probability	No. of unique peptide	No. of unique spectra	No. of total spectra	Percentage of total spectra	Sequence coverage	Peptide sequence	Best peptide probability	Mascot			No. of spectra			Calculated +1H peptide mass (AMU)	Peptide index	
												ion score	identity score	delta ion score	+2H	+3H	+4H		start	stop
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	PDK1	PDK1_HUMAN	49.2	100.0%	3	3	5	0.01%	8.5%	AIYDFTDTVIR	99.7%	57.2	25	50.2	2	0	0	1313.67	134	144
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	PDK1	PDK1_HUMAN	49.2	100.0%	3	3	5	0.01%	8.5%	AVPLAGFGYGLPISR	99.7%	70.8	25	66.7	2	0	0	1517.85	349	363
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	PDK1	PDK1_HUMAN	49.2	100.0%	3	3	5	0.01%	8.5%	LYAQYFQGDLK	99.7%	69.1	25	60.6	1	0	0	1345.68	364	374
10 kDa heat shock protein, mitochondrial	HSPE1	CH10_HUMAN	10.9	100.0%	3	3	6	0.01%	25.5%	GGEIQPVSVK	99.7%	49.5	25	37.5	2	0	0	1013.56	57	66
10 kDa heat shock protein, mitochondrial	HSPE1	CH10_HUMAN	10.9	100.0%	3	3	6	0.01%	25.5%	GKGGEIQPVSVK	99.7%	48.7	25	39.7	2	0	0	1198.68	55	66
10 kDa heat shock protein, mitochondrial	HSPE1	CH10_HUMAN	10.9	100.0%	3	3	6	0.01%	25.5%	VLQATVVAVGSGSK	99.7%	103	25	103	2	0	0	1315.76	41	54
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	59	0.06%	30.0%	AFIPAIDSFGFETDLR	99.7%	76.2	25	76.2	3	0	0	1798.90	873	888
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	59	0.06%	30.0%	DSIVQGFQWGTR	99.7%	69.5	25	68.2	1	0	0	1393.69	764	775
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	59	0.06%	30.0%	EGPLCDELIR	99.7%	46.7	25	41.4	2	0	0	1201.59	776	785
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	59	0.06%	30.0%	FFDDPMLLELAK	99.7%	69.6	25	64.7	6	0	0	1438.73	952	963
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	59	0.06%	30.0%	GGGQIIPTAR	98.6%	33.3	25	25.6	6	0	0	969.55	804	813
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	59	0.06%	30.0%	GLSEDVSISK	99.7%	52.9	25	37.3	1	0	0	1034.54	942	951
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	59	0.06%	30.0%	GNEEAQIFRPLK	99.7%	48.5	25	36.5	3	0	0	1401.75	570	581
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	59	0.06%	30.0%	IAVEPVNPSELPK	99.7%	66.3	25	60.1	3	0	0	1392.77	590	602
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	59	0.06%	30.0%	ILAQVVGDVDTSLPR	99.7%	92.2	25	85.8	2	0	0	1582.88	380	394
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	59	0.06%	30.0%	ILDAVVAQEPLHR	99.7%	48.6	25	47.9	2	2	0	1460.82	791	803
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	59	0.06%	30.0%	ITMIAEPLEK	99.7%	48.2	25	44.6	4	0	0	1144.63	685	694
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	59	0.06%	30.0%	IYADTFGDINYQEFAK	99.7%	111	25	108	2	0	0	1894.89	326	341
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	59	0.06%	30.0%	KGLSEDVSISK	97.4%	30.5	25	23	1	0	0	1162.63	941	951
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	59	0.06%	30.0%	LGEFFQTK	99.7%	63.4	25	51	2	0	0	969.50	714	721
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	59	0.06%	30.0%	SFVEFILEPLYK	99.7%	59.5	25	49.2	3	0	0	1484.80	368	379
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	59	0.06%	30.0%	STPVTVVLPDTK	99.7%	67	25	58.1	3	0	0	1256.71	183	194
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	59	0.06%	30.0%	TLDELGIHLTK	99.7%	59.1	25	58.6	1	0	0	1239.69	395	405
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	59	0.06%	30.0%	VADPVVTFCETVVETSSLK	99.7%	62.5	25	57	2	0	0	2081.05	655	673
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	59	0.06%	30.0%	VLGENYTLEDEEDSQICTVGR	99.7%	84.8	25	84.8	1	0	0	2427.10	509	529
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	59	0.06%	30.0%	VLSGTIHAGQPVK	99.7%	87.3	25	82.2	3	0	0	1306.75	496	508
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	59	0.06%	30.0%	VPAGNWVLIEGVDQPIVK	99.7%	49.4	25	49.4	1	0	0	1934.07	544	561
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	59	0.06%	30.0%	VVYSAFLMATPR	95.2%	28	25	18.4	1	0	0	1354.72	815	826
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	59	0.06%	30.0%	YDWDLLAAR	99.7%	63.5	25	56.3	2	0	0	1122.56	722	730
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	59	0.06%	30.0%	YHIEVNR	99.0%	34.9	25	15.3	2	0	0	930.48	537	543
14-3-3 protein beta/alpha	YWHAB	1433B_HUMAN	28.1	100.0%	3	3	4	0.00%	25.6%	AVTEQGHELSNEER	99.7%	64.9	25	59.2	2	0	0	1598.74	30	43
14-3-3 protein beta/alpha	YWHAB	1433B_HUMAN	28.1	100.0%	3	3	4	0.00%	25.6%	DSTLIMQLLR	97.9%	31.5	25	18.1	1	0	0	1205.66	215	224
14-3-3 protein beta/alpha	YWHAB	1433B_HUMAN	28.1	100.0%	3	3	4	0.00%	25.6%	EMQPTHPIR	99.7%	40.2	25	31.6	1	0	0	1108.56	161	169
14-3-3 protein beta/alpha	YWHAB	1433B_HUMAN	28.1	100.0%	3	3	4	0.00%	25.6%	QTTVSNSQQAYQEAFEISK	99.7%	49.8	25	49.8	1	0	0	2159.03	141	159
14-3-3 protein beta/alpha	YWHAB	1433B_HUMAN	28.1	100.0%	3	3	4	0.00%	25.6%	YLSEVASGDNK	99.7%	55.1	25	44.5	1	0	0	1182.56	130	140
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	8	9	15	0.02%	35.3%	DSTLIMQLLR	97.9%	31.5	25	18.1	1	0	0	1205.66	216	225
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	8	9	15	0.02%	35.3%	EAAENSLVAYK	99.7%	67	25	62.2	2	0	0	1194.60	143	153
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	8	9	15	0.02%	35.3%	HLIPAANTGESK	99.7%	47.7	25	36.8	2	0	0	1237.65	107	118
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	8	9	15	0.02%	35.3%	IISSIEQKEENK	99.7%	69.6	25	61.7	2	0	0	1417.75	62	73
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	8	9	15	0.02%	35.3%	LICCDILDVLDK	99.7%	72.6	25	67.8	2	0	0	1476.74	95	106
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	8	9	15	0.02%	35.3%	QMVETELK	99.7%	43	25	26.4	2	0	0	993.49	87	94
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	8	9	15	0.02%	35.3%	VAGMDVELTVEER	99.7%	93.7	25	83.1	2	0	0	1463.70	30	42
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	8	9	15	0.02%	35.3%	YLAEFATGNDR	99.7%	54.5	25	49.3	2	0	0	1256.59	131	141
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	8	9	15	0.02%	35.3%	YLAEFATGNDRK	99.6%	39.3	25	29	1	0	0	1384.69	131	142
14-3-3 protein eta	YWHAH	1433F_HUMAN	28.2	100.0%	3	3	5	0.01%	18.7%	AVTELNEPLSNEDR	99.7%	47.7	25	44.7	1	0	0	1586.77	29	42

14-3-3 protein eta	YWHAH	1433F_HUMAN	28.2	100.0%	3	3	5	0.01%	18.7%	DSTLIMQLLR	97.9%	31.5	25	18.1	1	0	0	1205.66	218	227
14-3-3 protein eta	YWHAH	1433F_HUMAN	28.2	100.0%	3	3	5	0.01%	18.7%	NSVVEASEAAYK	99.7%	59.1	25	39.3	2	0	0	1267.62	144	155
14-3-3 protein eta	YWHAH	1433F_HUMAN	28.2	100.0%	3	3	5	0.01%	18.7%	YLAEVASGEK	99.1%	35.2	25	25	2	0	0	1066.54	133	142
14-3-3 protein gamma	YWHAG	1433G_HUMAN	28.3	99.8%	2	2	6	0.01%	13.8%	AYSEAHEISK	99.7%	42.3	25	42.3	4	0	0	1134.54	153	162
14-3-3 protein gamma	YWHAG	1433G_HUMAN	28.3	99.8%	2	2	6	0.01%	13.8%	DSTLIMQLLR	97.9%	31.5	25	18.1	1	0	0	1205.66	218	227
14-3-3 protein gamma	YWHAG	1433G_HUMAN	28.3	99.8%	2	2	6	0.01%	13.8%	NVTELNEPLSNEER	99.7%	83.8	25	82.2	2	0	0	1643.79	29	42
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	4	4	8	0.01%	22.0%	AVTEQGAELSNEER	99.7%	112	25	100	4	0	0	1532.72	28	41
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	4	4	8	0.01%	22.0%	DSTLIMQLLR	97.9%	31.5	25	18.1	1	0	0	1205.66	213	222
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	4	4	8	0.01%	22.0%	EMQPTHPIR	99.7%	40.2	25	31.6	1	0	0	1108.56	159	167
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	4	4	8	0.01%	22.0%	YDDMATCMK	98.0%	31.8	25	31.8	1	0	0	1134.43	19	27
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	4	4	8	0.01%	22.0%	YLAEVACGDDR	99.7%	45.5	25	45.5	1	0	0	1268.56	128	138
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	4	4	8	0.01%	22.0%	YLAEVACGDDRK	99.7%	50.2	25	45.4	2	0	0	1396.65	128	139
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	7	7	12	0.01%	34.3%	DICNDVLSLLEK	99.4%	37.2	25	33.5	2	0	0	1418.72	92	103
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	7	7	12	0.01%	34.3%	DSTLIMQLLR	97.9%	31.5	25	18.1	1	0	0	1205.66	213	222
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	7	7	12	0.01%	34.3%	EMQPTHPIR	99.7%	40.2	25	31.6	1	0	0	1108.56	159	167
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	7	7	12	0.01%	34.3%	GIVDQSQQAYQEAFEISK	99.7%	78	25	78	2	0	0	2040.99	140	157
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	7	7	12	0.01%	34.3%	SVTEQGAELSNEER	99.7%	99.1	25	94.5	3	0	0	1548.71	28	41
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	7	7	12	0.01%	34.3%	YDDMAACMK	99.7%	41.2	25	33.6	1	0	0	1120.41	19	27
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	7	7	12	0.01%	34.3%	YLAEVAAGDDKK	99.7%	68	25	56.1	2	0	0	1279.65	128	139
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	9	9	12	0.01%	18.3%	AGQVFLEELGNHK	99.7%	96.4	25	90.4	1	0	0	1441.74	205	217
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	9	9	12	0.01%	18.3%	AIFTGYYGK	99.7%	40.7	25	32.5	2	0	0	1019.52	392	400
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	9	9	12	0.01%	18.3%	APGAEEYAQQDVLK	99.6%	39	25	39	1	0	0	1518.74	262	275
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	9	9	12	0.01%	18.3%	APGAEEYAQQDVLKK	98.6%	26.3	25	24.9	0	1	0	1646.84	262	276
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	9	9	12	0.01%	18.3%	GAFSEEYKR	99.7%	57.5	25	45.3	1	0	0	1086.52	94	102
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	9	9	12	0.01%	18.3%	GEEVGELSR	99.5%	38.4	25	4.59	2	0	0	975.47	361	369
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	9	9	12	0.01%	18.3%	GGSRGEEVGELSR	99.7%	50.5	25	42.3	1	0	0	1332.65	357	369
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	9	9	12	0.01%	18.3%	LDCAQLK	98.6%	33.3	25	14.5	1	0	0	847.43	156	162
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	9	9	12	0.01%	18.3%	RPPGVLHCTTK	98.5%	26.1	25	16.5	0	2	0	1265.68	245	255
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	13	15	41	0.04%	38.0%	ADHDFVVQEDFMK	99.7%	50.8	25	50.8	2	0	0	1596.70	357	369
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	13	15	41	0.04%	38.0%	ALQSVGQIVGEVLK	99.7%	89.4	25	89.4	6	0	0	1440.84	49	62
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	13	15	41	0.04%	38.0%	AVASQLDCNFLK	99.7%	72.9	25	62.7	4	0	0	1365.68	186	197
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	13	15	41	0.04%	38.0%	EVIELPLTNPELFQR	99.7%	73.7	25	70.1	3	0	0	1797.97	147	161
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	13	15	41	0.04%	38.0%	FSEGTSADR	99.4%	37.2	25	27.3	2	0	0	969.43	243	251
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	13	15	41	0.04%	38.0%	FSEGTSADREIQR	95.9%	28.6	25	22.4	1	0	0	1495.71	243	255
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	13	15	41	0.04%	38.0%	HGEIDYEAIVK	99.7%	78.2	25	70.7	4	0	0	1273.64	323	333
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	13	15	41	0.04%	38.0%	IHAGPITK	98.4%	32.8	25	28.4	3	0	0	836.50	315	322
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	13	15	41	0.04%	38.0%	KIHIDLPNEQAR	99.7%	45.9	25	45.9	0	2	0	1433.79	298	309
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	13	15	41	0.04%	38.0%	LLEHKEIDGR	99.7%	45.8	25	45.2	1	0	0	1209.66	16	25
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	13	15	41	0.04%	38.0%	NVCTEAGMFAIR	99.7%	76.9	25	68.9	6	0	0	1384.63	345	356
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	13	15	41	0.04%	38.0%	VALDMTTLTIMR	99.7%	90.1	25	90.1	1	0	0	1364.73	98	109
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	13	15	41	0.04%	38.0%	VVSSSIVDKYIGESAR	99.7%	103	25	103	2	4	0	1709.91	198	213
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	20	39	0.04%	50.0%	AICTEAGLMALR	99.7%	60.3	25	52.1	2	0	0	1321.66	397	408
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	20	39	0.04%	50.0%	AVANQTSATFLR	99.7%	79.7	25	69.1	5	0	0	1278.68	238	249
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	20	39	0.04%	50.0%	DDLSGADIK	99.7%	43.4	25	33.5	2	0	0	933.45	388	396
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	20	39	0.04%	50.0%	GVILYGPPGTGK	99.7%	54	25	0	4	0	0	1158.65	221	232
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	20	39	0.04%	50.0%	IETLDPALIRPGR	99.7%	48.3	25	43.5	0	2	0	1450.84	334	346
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	20	39	0.04%	50.0%	IFQIHTSR	99.7%	41.9	25	27.4	2	0	0	1001.55	364	371
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	20	39	0.04%	50.0%	KIEFPLPDEK	99.7%	51.5	25	35.9	2	0	0	1215.66	350	359
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	20	39	0.04%	50.0%	KQEGTPEGLYL	99.7%	42.5	25	34.7	2	0	0	1234.63	430	440
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	20	39	0.04%	50.0%	KYEPPVPTR	99.1%	35.5	25	26	3	0	0	1086.59	24	32
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	20	39	0.04%	50.0%	LPLVTPHTQCR	99.7%	55.3	25	46.1	2	0	0	1321.70	49	59

26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	20	39	0.04%	50.0%	MTLADDVTLDDLIMAK	99.7%	75.6	25	75.6	3	0	0	1780.87	372	387
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	20	39	0.04%	50.0%	NQEQMKPLEEKQEEER	99.7%	41.3	25	41.3	0	3	0	2044.96	81	96
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	20	39	0.04%	50.0%	SKENVLYK	98.0%	31.8	25	19	1	0	0	980.54	422	429
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	20	39	0.04%	50.0%	TMLELLNQLDGFDSR	99.7%	117	25	108	4	0	0	1751.86	308	322
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	20	39	0.04%	50.0%	VAEEHAPSIVFIDEIDAIGTK	99.7%	68	25	65.2	0	2	0	2254.16	273	293
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	20	39	0.04%	50.0%	VAEEHAPSIVFIDEIDAIGTKR	99.7%	57.5	25	57.5	0	2	0	2410.26	273	294
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	20	39	0.04%	50.0%	VHAVIGVLMDDTDPLVTVMK	99.5%	30.2	25	25.9	0	1	0	2153.13	156	175
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	20	39	0.04%	50.0%	VIMATNR	99.4%	37.1	25	32.2	3	0	0	804.44	327	333
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	20	39	0.04%	50.0%	VVGSELIQK	99.7%	55.1	25	42.4	1	0	0	972.57	250	258
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	50	0.05%	52.6%	AMEVDERPTEQYSDIGGLDK	99.7%	55.1	25	55.1	0	2	0	2269.03	174	193
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	50	0.05%	52.6%	APSIIFIDELDAIGTK	99.7%	64.6	25	64.6	2	0	0	1702.93	279	294
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	50	0.05%	52.6%	AVCVEAGMIALR	99.7%	77.8	25	74.6	2	0	0	1289.67	398	409
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	50	0.05%	52.6%	CTDDFNGAQCK	99.7%	54.1	25	52.9	2	0	0	1315.50	387	397
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	50	0.05%	52.6%	DSYLILETLPTEYDSR	99.7%	84.9	25	82.3	2	0	0	1914.93	156	171
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	50	0.05%	52.6%	EKFENLGIQPPK	99.7%	45.1	25	40.1	2	0	0	1399.76	210	221
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	50	0.05%	52.6%	FENLGIQPPK	99.7%	58	25	34.6	2	0	0	1142.62	212	221
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	50	0.05%	52.6%	GVLMYGPPGTGK	99.7%	78	25	72.2	4	0	0	1192.60	222	233
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	50	0.05%	52.6%	IMQIHSR	99.6%	39.9	25	26.4	2	0	0	884.48	365	371
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	50	0.05%	52.6%	KMNVSPDVNYEELAR	99.7%	54.2	25	45.4	0	4	0	1780.85	372	386
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	50	0.05%	52.6%	LAGPQLVQMFIGDGAK	99.7%	80.4	25	80.4	4	0	0	1644.88	251	266
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	50	0.05%	52.6%	LLDSEIK	98.8%	34.2	25	13.1	2	0	0	817.47	47	53
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	50	0.05%	52.6%	MSTEEIIQR	99.7%	66.1	25	43.9	4	0	0	1106.55	36	44
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	50	0.05%	52.6%	QIQELVEAIVLPMNHK	99.7%	33.7	25	33.7	0	1	0	1862.02	194	209
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	50	0.05%	52.6%	QTYFLPVIGLVDAEK	99.7%	80.8	25	60	4	0	0	1692.92	130	144
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	50	0.05%	52.6%	TMLELLNQLDGFQPNTQVK	99.7%	73.2	25	73.2	2	0	0	2189.13	309	327
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	50	0.05%	52.6%	VDILDPALLR	99.7%	63	25	48.7	4	0	0	1124.67	335	344
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	50	0.05%	52.6%	VIAATNRVDILDPALLR	99.7%	85	25	85	1	2	0	1850.09	328	344
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	50	0.05%	52.6%	VTHELQAMKDK	99.7%	58.7	25	51.3	2	0	0	1299.67	62	72
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	38	0.04%	40.4%	ADTLDPALLRPGR	99.7%	44.9	25	42.4	2	0	0	1394.78	314	326
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	38	0.04%	40.4%	AVAHHTTAAFIR	99.7%	56.2	25	52.8	2	2	0	1294.70	218	229
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	38	0.04%	40.4%	EAVELPLTHFELYK	99.7%	50	25	47.1	2	0	0	1688.89	179	192
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	38	0.04%	40.4%	EFLHAQEEVKR	99.7%	54.2	25	34.3	2	1	0	1385.72	71	81
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	38	0.04%	40.4%	ELLKPNASVALHK	99.7%	40.5	25	40.5	0	2	0	1419.83	122	134
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	38	0.04%	40.4%	ENAPAIIFIDEIDAIATK	99.7%	86.5	25	85.7	2	0	0	1944.03	256	273
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	38	0.04%	40.4%	FDAQTGADREVQR	99.7%	49.2	25	40.2	2	1	0	1492.71	275	287
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	38	0.04%	40.4%	GVLMYGPPGCGK	99.7%	54.9	25	54.6	4	0	0	1235.59	201	212
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	38	0.04%	40.4%	ILLELLNQMDGFDQNVNVK	99.7%	109	25	109	4	2	0	2219.14	288	306
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	38	0.04%	40.4%	ILSTIDR	98.5%	33	25	15.9	1	0	0	817.48	115	121
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	38	0.04%	40.4%	KDEQEHEFYK	94.9%	21.7	25	21.7	0	1	0	1352.61	409	418
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	38	0.04%	40.4%	LIFSTITSK	99.7%	48.8	25	44.7	2	0	0	1009.59	343	351
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	38	0.04%	40.4%	RFDAQTGADR	98.4%	32.7	25	12	2	0	0	1136.54	274	283
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	38	0.04%	40.4%	RLIFSTITSK	99.7%	41.3	25	34.5	2	0	0	1165.69	342	351
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	38	0.04%	40.4%	VIMATNR	99.4%	37.1	25	32.2	3	0	0	804.44	307	313
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	38	0.04%	40.4%	VVGSEFVQK	99.7%	76.4	25	64	2	0	0	992.54	230	238
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	56	0.06%	61.9%	ACLIFFDEIDAIGGAR	99.7%	82.7	25	81.1	1	0	0	1767.87	269	284
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	56	0.06%	61.9%	ALDEGDIALLK	99.7%	74.1	25	60.7	2	0	0	1157.64	24	34
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	56	0.06%	61.9%	DIRFELLAR	99.7%	45	25	31.9	2	0	0	1132.65	367	375
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	56	0.06%	61.9%	ESDTGLAPPALWDLAADK	95.2%	28	25	26.1	1	0	0	1869.92	67	84
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	56	0.06%	61.9%	FDDGAGGDNEVQR	99.7%	85.6	25	85.6	3	0	0	1379.58	285	297
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	56	0.06%	61.9%	FVNLGIEPPK	99.7%	52.4	25	25.7	5	0	0	1113.63	201	210
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	56	0.06%	61.9%	FVVDLSDQVAPTDIEEGMR	99.7%	101	25	86.9	4	0	0	2121.02	121	139

26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	56	0.06%	61.9%	GVLLFGPPGTGK	99.7%	77.5	25	72.3	2	0	0	1142.66	211	222
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	56	0.06%	61.9%	IATEKDFLEAVNK	99.7%	68	25	60	2	2	0	1477.79	403	415
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	56	0.06%	61.9%	IEFSLPDLEGR	99.7%	44	25	37.4	2	0	0	1275.66	341	351
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	56	0.06%	61.9%	IINADSEDPK	99.7%	62.2	25	51.1	2	0	0	1101.54	101	110
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	56	0.06%	61.9%	IINADSEDPKYIINVK	99.7%	96.1	25	93.4	2	1	0	1831.98	101	116
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	56	0.06%	61.9%	KINELTGIK	99.7%	45.9	25	29.1	2	0	0	1015.61	58	66
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	56	0.06%	61.9%	LCPNSTGAEIR	99.7%	51.1	25	37.2	2	0	0	1217.59	376	386
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	56	0.06%	61.9%	LREVVETPLLHPER	99.7%	42.5	25	41.7	0	2	0	1687.95	187	200
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	56	0.06%	61.9%	PDYLGADQRK	99.7%	46	25	34.9	2	0	0	1162.59	2	11
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	56	0.06%	61.9%	QTLQSEQPLQVAR	99.7%	75.8	25	68.1	2	0	0	1497.80	85	97
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	56	0.06%	61.9%	QVEDDIQQLLK	99.7%	78	25	66.9	2	0	0	1328.71	47	57
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	56	0.06%	61.9%	SVCTEAGMFAIR	99.7%	61.2	25	61.2	4	0	0	1357.62	387	398
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	56	0.06%	61.9%	TDACFIR	99.7%	50.8	25	37.8	2	0	0	882.41	233	239
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	56	0.06%	61.9%	TMLELINQLDGFDPR	99.7%	79.2	25	76.3	4	0	0	1777.88	298	312
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	56	0.06%	61.9%	TYGQSTYSR	99.7%	49.1	25	31.2	2	0	0	1062.49	35	43
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	56	0.06%	61.9%	VIGSELVQK	99.7%	43.1	25	26.4	1	0	0	972.57	240	248
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	56	0.06%	51.0%	AVAHHTDCTFIR	99.7%	60	25	48.2	2	2	0	1427.68	202	213
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	56	0.06%	51.0%	EELQLLQEQGSYVGEVVR	99.7%	87.7	25	87.7	1	0	0	2076.06	61	78
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	56	0.06%	51.0%	ELFVMAR	99.3%	36.5	25	22.9	3	0	0	881.46	233	239
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	56	0.06%	51.0%	FVVDVDKNIDINDVTPNCR	98.9%	27.3	25	27.3	0	1	0	2233.09	95	113
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	56	0.06%	51.0%	GVCTEAGMYALR	99.7%	68.3	25	65.1	4	0	0	1327.61	361	372
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	56	0.06%	51.0%	GVLLYGPPGTGK	99.7%	54	25	0	4	0	0	1158.65	185	196
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	56	0.06%	51.0%	IAELMPGASGAEVK	99.7%	70.9	25	57.7	4	0	0	1388.71	347	360
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	56	0.06%	51.0%	IDILDSALLRPGR	99.7%	53.6	25	50.8	2	2	0	1438.84	298	310
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	56	0.06%	51.0%	IEELQLIVNDK	99.7%	101	25	87.1	2	0	0	1313.73	28	38
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	56	0.06%	51.0%	LEGGSGGDSEVQR	99.7%	68.6	25	68	7	0	0	1290.59	259	271
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	56	0.06%	51.0%	NDSYTLHK	97.1%	30.1	25	30	1	0	0	977.47	118	125
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	56	0.06%	51.0%	QYYLSK	99.7%	41.4	25	18.8	1	0	0	801.41	22	27
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	56	0.06%	51.0%	TMLELLNQLDGFEATK	99.7%	131	25	129	4	0	0	1838.92	272	287
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	56	0.06%	51.0%	VALRNDSYTLHK	99.7%	54.2	25	39.5	1	2	0	1416.76	114	125
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	56	0.06%	51.0%	VDPLVSLMMVEK	99.7%	80	25	73.3	2	0	0	1360.72	131	142
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	56	0.06%	51.0%	VIMATNR	99.4%	37.1	25	32.2	3	0	0	804.44	291	297
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	56	0.06%	51.0%	VPDSTYEMIGGLDK	99.7%	93.4	25	93.4	4	0	0	1540.72	143	156
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	56	0.06%	51.0%	VSGSELVQK	99.7%	75.9	25	43.2	4	0	0	946.52	214	222
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	30.6%	AAVESLGFILFR	99.7%	84.6	25	84.5	6	0	0	1322.75	617	628
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	30.6%	DNLEWLAR	99.7%	45.2	25	36.2	2	0	0	1016.52	388	395
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	30.6%	DTSEDIEELVEPVAAHGPK	99.7%	77	25	72.9	1	2	0	2035.98	916	934
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	30.6%	EAINLLEPMTNDPVNYVR	99.7%	97.8	25	95.2	4	0	0	2104.04	667	684
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	30.6%	EALQLMATYLPK	99.7%	59	25	53.6	4	0	0	1377.74	418	429
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	30.6%	FTATASLGVIHK	97.4%	24.1	25	24.1	0	1	0	1244.70	402	413
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	30.6%	GLAVGIALVMYGR	99.7%	73.2	25	73.2	2	0	0	1335.75	547	559
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	30.6%	HGGSLGLGLAAMGTAR	99.7%	37.8	25	37.3	0	1	0	1484.76	475	490
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	30.6%	LCMSLMQNK	97.8%	31.4	25	27.2	1	0	0	1156.52	183	191
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	30.6%	LLHVAVSDVNDDVRR	99.7%	46.7	25	46.7	0	1	0	1707.91	602	616
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	30.6%	MEEADALIESLCR	99.7%	107	25	104	4	0	0	1536.70	560	572
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	30.6%	NNNTDLMILK	99.7%	43	25	33.2	2	0	0	1175.61	345	354
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	30.6%	QCVENADLPEGEK	99.7%	56.1	25	51.3	1	0	0	1488.66	111	123
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	30.6%	QDVYDLLK	99.7%	76.8	25	43.3	2	0	0	993.53	491	498
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	30.6%	QFAALVASK	99.7%	66.1	25	45.8	2	0	0	934.54	58	66
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	30.6%	SNCKPSTFAYPAPLEVPK	99.5%	30.2	25	26.6	0	1	0	2006.01	804	821
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	30.6%	TILESNDVPGMLAYSLK	99.7%	106	25	102	2	0	0	1850.96	166	182

26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	30.6%	TPEASPEPK	99.4%	37.2	25	36.1	2	0	0	955.47	311	319
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	30.6%	TPEQCPSVVSLLSESYNPHVR	99.7%	47.5	25	47.5	0	2	0	2399.17	629	649
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	30.6%	VINDKHDDVMAK	99.7%	62.4	25	55.6	2	0	0	1384.69	716	727
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	30.6%	VSTAVLSITAK	99.7%	93.7	25	90.2	2	0	0	1089.65	828	838
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	30.6%	YGAAMALGICCAGTGNK	99.7%	116	25	100	2	0	0	1714.77	650	666
26S proteasome non-ATPase regulatory subunit 10	PSMD10	PSD10_HUMAN	24.4	100.0%	3	3	6	0.01%	21.2%	ASTNIQDTEGNTPLHLACDEERVEEAK	99.7%	73.5	25	64.6	0	2	0	3027.40	163	189
26S proteasome non-ATPase regulatory subunit 10	PSMD10	PSD10_HUMAN	24.4	100.0%	3	3	6	0.01%	21.2%	LEELKESILADK	99.7%	62.9	25	52.3	2	0	0	1387.77	19	30
26S proteasome non-ATPase regulatory subunit 10	PSMD10	PSD10_HUMAN	24.4	100.0%	3	3	6	0.01%	21.2%	MIHILLYYK	99.7%	50.5	25	35.9	2	0	0	1193.68	154	162
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	7	7	10	0.01%	19.2%	EQSILELGSLLAK	99.7%	62.7	25	62.7	2	0	0	1400.80	47	59
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	7	7	10	0.01%	19.2%	IMLNTPEDVQALVSGK	99.7%	51.6	25	51.6	1	0	0	1714.90	259	274
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	7	7	10	0.01%	19.2%	LVSLYFDTKR	97.3%	30.5	25	23.4	1	0	0	1241.69	133	142
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	7	7	10	0.01%	19.2%	LYDNLLEQNLIR	99.7%	64.9	25	60.2	2	0	0	1503.82	326	337
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	7	7	10	0.01%	19.2%	TTANAIYCPPK	99.7%	49.7	25	43	1	0	0	1235.61	195	205
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	7	7	10	0.01%	19.2%	VQIEHISSLIK	99.7%	48.1	25	42.5	2	0	0	1266.74	345	355
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	7	7	10	0.01%	19.2%	VVDSLYNK	98.9%	34.3	25	31.2	1	0	0	937.50	410	417
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	12	14	23	0.02%	35.4%	DLPVSEQQER	99.7%	53.5	25	53.5	2	0	0	1200.59	187	196
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	12	14	23	0.02%	35.4%	FLGCVDIKDLPVSEQQER	99.7%	51.1	25	51.1	0	1	0	2133.06	179	196
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	12	14	23	0.02%	35.4%	GSIDEVDKR	99.2%	36.1	25	26.7	2	0	0	1018.52	322	330
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	12	14	23	0.02%	35.4%	ITVNEVELLVMK	99.7%	91.9	25	91.9	2	0	0	1387.79	302	313
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	12	14	23	0.02%	35.4%	LNIGDLQVTK	99.7%	66.6	25	53.5	2	0	0	1100.63	123	132
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	12	14	23	0.02%	35.4%	LYENFISEFEHR	99.7%	48.5	25	40.1	1	1	0	1583.75	59	70
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	12	14	23	0.02%	35.4%	QLTFEEIAK	99.1%	35.5	25	29.2	1	0	0	1078.58	290	298
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	12	14	23	0.02%	35.4%	QMTDPNVALTFLEK	99.7%	53.3	25	45.8	4	0	0	1606.81	86	99
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	12	14	23	0.02%	35.4%	SSDEAVILCK	99.7%	59.9	25	37	1	0	0	1121.55	106	115
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	12	14	23	0.02%	35.4%	TAWGQQPDLAANEAQLLR	99.7%	92.7	25	91.9	2	0	0	1982.01	253	270
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	12	14	23	0.02%	35.4%	VLDLQQIK	99.7%	60.6	25	42	2	0	0	956.58	340	347
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	12	14	23	0.02%	35.4%	YYQTIGNHASYYK	99.7%	61.8	25	61.8	2	0	0	1607.75	162	174
26S proteasome non-ATPase regulatory subunit 14	PSMD14	PSDE_HUMAN	34.6	100.0%	3	4	8	0.01%	11.6%	AVAVVVDPIQSVK	99.7%	87.4	25	86.6	3	0	0	1324.78	140	152
26S proteasome non-ATPase regulatory subunit 14	PSMD14	PSDE_HUMAN	34.6	100.0%	3	4	8	0.01%	11.6%	AVEEEDKMTPEQLAIK	99.7%	65.3	25	65.3	3	0	0	1830.92	258	273
26S proteasome non-ATPase regulatory subunit 14	PSMD14	PSDE_HUMAN	34.6	100.0%	3	4	8	0.01%	11.6%	VVIDAFR	99.4%	37.2	25	32.1	2	0	0	819.47	155	161
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	APVQPQQSPAAAPGGTDEKPSGK	99.7%	62.5	25	62.5	0	2	0	2218.11	9	31
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	AVPLALALISVSNPR	99.7%	68.7	25	68.7	3	3	0	1520.92	689	703
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	CALGVFR	99.1%	35.6	25	30.2	2	0	0	822.43	251	257
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	DKAPVQPQQSPAAAPGGTDEKPSGK	99.7%	59.7	25	57.8	0	1	0	2461.23	7	31
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	DPNNLFMVR	98.9%	34.4	25	27.4	2	0	0	1105.55	755	763
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	DTSLYRPALEELRR	98.7%	26.7	25	26.7	0	2	0	1718.92	67	80
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	EDVLTLLLPVMGDSK	99.7%	106	25	84.8	5	0	0	1629.88	495	509
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	ELDIMEPK	99.3%	36.6	25	10.7	3	0	0	990.48	336	343
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	EPLLTLVK	98.5%	33.2	25	33.2	1	0	0	912.58	182	189
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	EWQELDDAEK	99.7%	49.3	25	37.9	1	0	0	1262.55	169	178
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	FAADIISVLAMTMSGER	99.7%	74.5	25	69.3	6	0	0	1843.89	121	137
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	FGGSGSQVDSAR	99.7%	113	25	100	5	0	0	1167.54	358	369
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	GTLTLCPYHSDR	99.7%	61.5	25	58.1	2	0	0	1419.67	774	785
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	LAQGLTHLGK	99.7%	53.7	25	51.1	2	0	0	1037.61	764	773
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	LGSIFGLGLAYAGSNR	99.7%	91.6	25	90.4	2	2	0	1595.85	479	494
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	LLTDDGNKWLYK	99.7%	44.4	25	43.7	2	0	0	1465.77	390	401
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	LNILDTLSK	99.7%	50.5	25	26.6	2	0	0	1016.60	704	712
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	LVGSQEELASWGHEYVR	99.7%	54.8	25	54.8	0	2	0	1959.96	144	160
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	QMAFMLGR	99.0%	34.7	25	23.9	2	0	0	953.47	293	300
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	SETELKDTYAR	99.7%	37	25	37	0	2	0	1312.64	546	556
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	SFANTLVDVCAYAGSGNVLK	99.7%	92.1	25	88	2	0	0	2086.03	589	608

26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	SSTTSMTSVPKPLK	99.7%	65.9	25	51.5	4	0	0	1463.78	84	97
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	TITGFQTHTTPVLLAHGER	99.7%	40.8	25	40.8	0	1	0	2079.10	861	879
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	VGQAVDVVGQAGKPK	99.7%	99.7	25	88.8	6	0	0	1452.82	846	860
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	WLPLGLGLNHLGK	99.7%	46.7	25	46.7	2	0	0	1417.83	557	569
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	YGEPTLR	99.3%	36.7	25	35.1	2	0	0	835.43	681	687
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	33	73	0.07%	36.7%	YLYSSEDYIK	99.7%	43.8	25	36.1	2	0	0	1280.60	432	441
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	31	55	0.06%	46.3%	AIQLEYSEAR	99.7%	71.4	25	66.3	2	0	0	1179.60	297	306
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	31	55	0.06%	46.3%	AIQLEYSEARR	95.4%	28.2	25	18.9	1	0	0	1335.70	297	307
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	31	55	0.06%	46.3%	AIRDGVIEASINHEK	99.7%	42.4	25	37.1	0	2	0	1651.88	441	455
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	31	55	0.06%	46.3%	APQHTAVGFK	99.7%	41.3	25	34	2	0	0	1055.56	316	325
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	31	55	0.06%	46.3%	AVQGFFTSNNATR	99.7%	91.1	25	86.6	2	0	0	1412.69	116	128
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	31	55	0.06%	46.3%	CYYYHAR	95.1%	28	25	28	1	0	0	1032.44	210	216
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	31	55	0.06%	46.3%	DGVIEASINHEK	99.7%	54	25	38.3	2	0	0	1311.65	444	455
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	31	55	0.06%	46.3%	DLESAEERR	99.3%	36.2	25	28.2	1	0	0	1104.53	504	512
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	31	55	0.06%	46.3%	ELDTVTLEDIKEHVK	99.7%	67	25	55.8	2	2	0	1768.93	66	80
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	31	55	0.06%	46.3%	EMIDIYSTR	99.7%	54	25	38.2	3	0	0	1143.54	462	470
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	31	55	0.06%	46.3%	EPQLAFHQR	99.7%	71.6	25	56.1	2	0	0	1125.58	471	479
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	31	55	0.06%	46.3%	EQQDLEFAK	99.7%	50.1	25	47.3	1	0	0	1107.53	515	523
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	31	55	0.06%	46.3%	EREQQDLEFAK	99.7%	44.6	25	32.3	1	0	0	1392.68	513	523
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	31	55	0.06%	46.3%	FNQVLDQFGEK	99.7%	65.4	25	42.9	3	0	0	1324.65	375	385
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	31	55	0.06%	46.3%	HDADGQATLLNLLLR	99.7%	66.6	25	66.6	2	0	0	1649.90	242	256
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	31	55	0.06%	46.3%	ISDDLMQK	99.7%	45.9	25	32.5	4	0	0	949.47	187	194
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	31	55	0.06%	46.3%	ISFCLDIHNMSVK	99.7%	51.7	25	51.7	1	0	0	1563.77	480	492
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	31	55	0.06%	46.3%	ISLADIAQK	99.7%	66.6	25	29.2	2	0	0	958.56	417	425
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	31	55	0.06%	46.3%	LQLDSPEDAEFIVAK	99.7%	85.7	25	75	2	0	0	1674.86	426	440
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	31	55	0.06%	46.3%	MISLSYSR	99.4%	37.4	25	35.9	2	0	0	956.49	409	416
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	31	55	0.06%	46.3%	NYLHYSLYDQAEK	99.7%	77	25	62.3	2	2	0	1643.77	257	269
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	31	55	0.06%	46.3%	SLMPYFLLTQAVR	99.7%	88.9	25	75.5	4	0	0	1538.84	356	368
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	31	55	0.06%	46.3%	SVFPEQANNNEWAR	99.7%	74.9	25	74.3	2	0	0	1661.77	274	287
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	31	55	0.06%	46.3%	VYEFLDKLDVVR	99.7%	85.9	25	81.1	2	2	0	1495.82	217	228
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	31	55	0.06%	46.3%	YLYYTGR	96.3%	29.2	25	11.7	1	0	0	935.46	288	294
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	7	10	25	0.03%	25.5%	AAAASAAEAGIATTGTEDSDDALLK	99.7%	120	25	120	2	2	0	2320.12	238	262
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	7	10	25	0.03%	25.5%	IIAFVGSPVEDNEKDLVK	99.7%	78	25	70.1	2	4	0	1973.06	109	126
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	7	10	25	0.03%	25.5%	ITFCTGIR	99.7%	47.6	25	38.5	4	0	0	967.50	84	91
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	7	10	25	0.03%	25.5%	LQAQQDAVNIVCHSK	99.7%	81.3	25	81.3	2	3	0	1710.86	26	40
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	7	10	25	0.03%	25.5%	LTAFVNTLNGK	99.7%	68.3	25	39.6	2	0	0	1177.66	153	163
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	7	10	25	0.03%	25.5%	NAMGSLASQATK	99.7%	81.9	25	70.3	2	0	0	1194.58	354	365
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	7	10	25	0.03%	25.5%	VSMEEQR	99.7%	44.5	25	34.2	2	0	0	878.40	222	228
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	18	23	40	0.04%	49.9%	DNNMAPYYEALCK	99.7%	59.6	25	59.6	2	0	0	1604.67	47	59
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	18	23	40	0.04%	49.9%	DWLFAPHYR	97.9%	31.4	25	25.2	1	0	0	1204.59	285	293
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	18	23	40	0.04%	49.9%	FLLSLPEHR	99.7%	52.6	25	46	2	0	0	1111.63	24	32
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	18	23	40	0.04%	49.9%	GAEILEVLHSLPAVR	99.7%	93.6	25	93.2	2	0	0	1603.92	243	257
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	18	23	40	0.04%	49.9%	GDAAVRDELMAAVR	99.7%	47.8	25	42.9	2	4	0	1489.74	33	46
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	18	23	40	0.04%	49.9%	IDKVNEIVETNRPDSK	99.7%	37.7	25	37.7	0	2	0	1856.97	347	362
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	18	23	40	0.04%	49.9%	IGLFYMDNDLITR	99.7%	95.7	25	94.5	4	0	0	1570.79	147	159
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	18	23	40	0.04%	49.9%	IHAYSQLLESYR	99.7%	60.9	25	48.8	2	2	0	1479.76	301	312
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	18	23	40	0.04%	49.9%	KGDLLLNR	99.7%	47.7	25	34.9	2	0	0	928.56	372	379
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	18	23	40	0.04%	49.9%	LDEELEDAEK	99.7%	61.3	25	59	1	0	0	1190.54	84	93
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	18	23	40	0.04%	49.9%	LDIVFYLLR	99.7%	65.7	25	43.7	2	0	0	1151.68	138	146
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	18	23	40	0.04%	49.9%	NLGESEIR	95.0%	27.9	25	19.3	1	0	0	917.47	94	101
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	18	23	40	0.04%	49.9%	PLENLEEEGLPK	99.7%	75	25	74.3	2	0	0	1367.71	2	13

26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	18	23	40	0.04%	49.9%	QYLFSLYECR	99.7%	59.3	25	51	2	0	0	1378.65	258	267
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	18	23	40	0.04%	49.9%	SLDWQIDVDLLNK	99.7%	44	25	17.6	2	0	0	1558.81	60	72
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	18	23	40	0.04%	49.9%	SLIEEGGDWDRR	98.6%	33.3	25	33.3	1	0	0	1432.68	166	177
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	18	23	40	0.04%	49.9%	VNEIVETNRPDSK	99.7%	61.1	25	45.1	2	0	0	1500.77	350	362
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	18	23	40	0.04%	49.9%	VYQGLYCVAIR	99.7%	75.7	25	75.7	2	0	0	1341.70	182	192
26S proteasome non-ATPase regulatory subunit 7	PSMD7	PSMD7_HUMAN	37.0	99.8%	2	2	2	0.00%	6.5%	ITNQVHGLK	96.2%	29	25	28.4	1	0	0	1009.58	191	199
26S proteasome non-ATPase regulatory subunit 7	PSMD7	PSMD7_HUMAN	37.0	99.8%	2	2	2	0.00%	6.5%	SVVALHNLINNK	99.7%	42.5	25	35.4	1	0	0	1321.76	268	279
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	5	6	11	0.01%	14.3%	DIQTNVYIK	99.6%	38.9	25	29.5	4	0	0	1093.59	219	227
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	5	6	11	0.01%	14.3%	ILFFNTPK	98.4%	32.6	25	21.2	1	0	0	979.56	290	297
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	5	6	11	0.01%	14.3%	ILFTEATR	99.7%	46.6	25	29.5	2	0	0	950.53	282	289
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	5	6	11	0.01%	14.3%	LVLLELNFLPTTGTK	99.7%	62.1	25	62.1	2	0	0	1658.97	121	135
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	5	6	11	0.01%	14.3%	VAEFHTELER	98.6%	26.3	25	20.8	1	1	0	1230.61	205	214
28S ribosomal protein S10, mitochondrial	MRPS10	RT10_HUMAN	23.0	100.0%	3	3	5	0.01%	18.9%	AVLDSYEYFAVLAAK	99.7%	76.7	25	76.3	2	0	0	1659.86	86	100
28S ribosomal protein S10, mitochondrial	MRPS10	RT10_HUMAN	23.0	100.0%	3	3	5	0.01%	18.9%	FTLLQSVHIYK	99.1%	35.6	25	31.2	2	0	0	1348.76	118	128
28S ribosomal protein S10, mitochondrial	MRPS10	RT10_HUMAN	23.0	100.0%	3	3	5	0.01%	18.9%	NLPEGVAMEVTK	99.7%	41.3	25	31.5	1	0	0	1287.66	163	174
28S ribosomal protein S11, mitochondrial	MRPS11	RT11_HUMAN	20.6	100.0%	4	5	7	0.01%	22.2%	FSIYPPIPGEESSLR	99.7%	40	25	40	1	0	0	1691.86	60	74
28S ribosomal protein S11, mitochondrial	MRPS11	RT11_HUMAN	20.6	100.0%	4	5	7	0.01%	22.2%	GTGIAAQTAGIAAAAR	99.7%	95.1	25	89.5	2	0	0	1399.77	123	138
28S ribosomal protein S11, mitochondrial	MRPS11	RT11_HUMAN	20.6	100.0%	4	5	7	0.01%	22.2%	KFEEIPIAHIK	99.7%	41.1	25	41.1	0	1	0	1324.76	79	89
28S ribosomal protein S11, mitochondrial	MRPS11	RT11_HUMAN	20.6	100.0%	4	5	7	0.01%	22.2%	KGTGIAAQTAGIAAAAR	99.7%	122	25	122	2	1	0	1527.86	122	138
28S ribosomal protein S12, mitochondrial	MRPS12	RT12_HUMAN	15.2	99.8%	2	2	6	0.01%	14.5%	GVVLCTFTR	99.7%	51.9	25	33.7	4	0	0	1052.56	60	68
28S ribosomal protein S12, mitochondrial	MRPS12	RT12_HUMAN	15.2	99.8%	2	2	6	0.01%	14.5%	LGPTEGRPQLK	99.2%	35.7	25	25.8	2	0	0	1195.68	49	59
28S ribosomal protein S14, mitochondrial	MRPS14	RT14_HUMAN	15.1	99.8%	2	3	9	0.01%	18.8%	ILQDVADEEIAALPR	99.7%	67.1	25	56.5	4	0	0	1652.89	66	80
28S ribosomal protein S14, mitochondrial	MRPS14	RT14_HUMAN	15.1	99.8%	2	3	9	0.01%	18.8%	MAYEYADER	99.7%	56.6	25	56.6	5	0	0	1163.47	43	51
28S ribosomal protein S15, mitochondrial	MRPS15	RT15_HUMAN	29.8	100.0%	6	6	14	0.01%	22.2%	DYQNVPGIEK	97.8%	31.2	25	24.5	1	0	0	1162.57	75	84
28S ribosomal protein S15, mitochondrial	MRPS15	RT15_HUMAN	29.8	100.0%	6	6	14	0.01%	22.2%	IVANPEDTR	99.7%	46.8	25	39.3	3	0	0	1014.52	115	123
28S ribosomal protein S15, mitochondrial	MRPS15	RT15_HUMAN	29.8	100.0%	6	6	14	0.01%	22.2%	LDDDPPPSTLLK	99.7%	51.3	25	49.8	2	0	0	1310.68	63	74
28S ribosomal protein S15, mitochondrial	MRPS15	RT15_HUMAN	29.8	100.0%	6	6	14	0.01%	22.2%	NTNYDVFEK	99.7%	45.9	25	33.9	2	0	0	1129.52	172	180
28S ribosomal protein S15, mitochondrial	MRPS15	RT15_HUMAN	29.8	100.0%	6	6	14	0.01%	22.2%	SYEEHLEK	99.1%	35.4	25	23.8	2	0	0	1034.48	138	145
28S ribosomal protein S15, mitochondrial	MRPS15	RT15_HUMAN	29.8	100.0%	6	6	14	0.01%	22.2%	YLLMSIDQR	99.7%	60.3	25	41.5	4	0	0	1138.59	155	163
28S ribosomal protein S16, mitochondrial	MRPS16	RT16_HUMAN	15.3	100.0%	3	4	8	0.01%	26.3%	AREVLLASQK	99.7%	48.3	25	31.2	2	0	0	1114.66	115	124
28S ribosomal protein S16, mitochondrial	MRPS16	RT16_HUMAN	15.3	100.0%	3	4	8	0.01%	26.3%	FVEQLGSYDPLPNSHGEK	99.7%	53	25	51.6	2	2	0	2016.97	47	64
28S ribosomal protein S16, mitochondrial	MRPS16	RT16_HUMAN	15.3	100.0%	3	4	8	0.01%	26.3%	LVALNLDR	99.7%	61.4	25	47.7	2	0	0	913.55	65	72
28S ribosomal protein S17, mitochondrial	MRPS17	RT17_HUMAN	14.5	99.8%	2	2	3	0.00%	15.4%	HELAEIVFK	99.7%	41.9	25	41.9	2	0	0	1085.60	79	87
28S ribosomal protein S17, mitochondrial	MRPS17	RT17_HUMAN	14.5	99.8%	2	2	3	0.00%	15.4%	NLEELNISSAQ	99.7%	71	25	55.5	1	0	0	1217.60	120	130
28S ribosomal protein S18a, mitochondrial	MRPS18A	RT18A_HUMAN	22.2	100.0%	2	2	4	0.00%	12.8%	ESPNPPNPSGQCPICR	99.7%	56.9	25	56.9	2	0	0	1809.80	59	74
28S ribosomal protein S18a, mitochondrial	MRPS18A	RT18A_HUMAN	22.2	100.0%	2	2	4	0.00%	12.8%	MPVGSPLLR	97.6%	31	25	27.4	2	0	0	969.56	174	182
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	5	6	10	0.01%	30.2%	APSEEDSLSSVPISPYKDEPWK	99.7%	64	25	64	0	1	0	2461.18	36	57
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	5	6	10	0.01%	30.2%	LYQGHLQEESGPPPESMPK	99.7%	42.8	25	37.5	0	3	0	2124.01	219	237
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	5	6	10	0.01%	30.2%	TPAEASSTGQTGPQSAL	99.7%	60.2	25	60.2	2	0	0	1602.76	242	258
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	5	6	10	0.01%	30.2%	VVGNPCPICR	99.7%	64.9	25	60.6	2	0	0	1171.57	100	109
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	5	6	10	0.01%	30.2%	YLESEEYQER	99.7%	58.9	25	58.9	2	0	0	1345.59	58	67
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	8	9	14	0.01%	23.6%	DCGEYAHTR	98.9%	34.2	25	33.4	2	0	0	1108.45	161	169
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	8	9	14	0.01%	23.6%	FMEPYIFGSR	99.7%	51	25	43.7	3	0	0	1246.59	101	110
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	8	9	14	0.01%	23.6%	GGMLTNAR	96.1%	28.9	25	13.4	1	0	0	819.41	173	180
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	8	9	14	0.01%	23.6%	GIILFISR	99.7%	57.7	25	47.4	2	0	0	918.58	140	147
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	8	9	14	0.01%	23.6%	HSDFFNVK	99.7%	48.6	25	38.2	2	0	0	993.48	69	76
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	8	9	14	0.01%	23.6%	LFQTAITR	99.7%	62	25	47.1	2	0	0	949.55	252	259
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	8	9	14	0.01%	23.6%	LLFGPTVR	99.7%	41.2	25	23.6	1	0	0	902.55	181	188
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	8	9	14	0.01%	23.6%	QFSYLIENMAR	99.7%	69.6	25	60.6	1	0	0	1387.67	150	160
28S ribosomal protein S21, mitochondrial	MRPS21	RT21_HUMAN	10.7	100.0%	3	6	16	0.02%	39.1%	ILTMDGLIEDIK	99.7%	52	25	43.2	4	0	0	1360.74	29	40
28S ribosomal protein S21, mitochondrial	MRPS21	RT21_HUMAN	10.7	100.0%	3	6	16	0.02%	39.1%	IYNMEMAR	99.7%	52.2	25	39.6	5	0	0	1027.47	63	70

28S ribosomal protein S21, mitochondrial	MRPS21	RT21_HUMAN	10.7	100.0%	3	6	16	0.02%	39.1%	TVMVQEGNVESAYR	99.7%	114	25	108	7	0	0	1582.75	11	24
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	14	24	0.02%	32.2%	DQAAEGINLIK	99.7%	67.7	25	58	2	0	0	1171.63	319	329
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	14	24	0.02%	32.2%	IDGLLIDQIQR	99.7%	81.4	25	65.9	2	0	0	1283.73	281	291
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	14	24	0.02%	32.2%	ILTPIIFKEENLR	99.7%	54.9	25	54.9	2	2	0	1585.93	204	216
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	14	24	0.02%	32.2%	KIDGLLIDQIQR	99.7%	83	25	78	2	1	0	1411.83	280	291
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	14	24	0.02%	32.2%	LMTQAQLEEATR	99.7%	100	25	84.7	4	0	0	1390.70	105	116
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	14	24	0.02%	32.2%	MIQVYFPK	99.7%	46	25	45	2	0	0	1025.55	192	199
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	14	24	0.02%	32.2%	MTGLNLQK	99.3%	36.6	25	14	1	0	0	904.49	82	89
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	14	24	0.02%	32.2%	TFKPAIQELKPPTYK	98.9%	27.2	25	27.2	0	1	0	1760.99	90	104
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	14	24	0.02%	32.2%	VPINDVLAEDK	99.7%	46	25	41.5	2	0	0	1212.65	136	146
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	14	24	0.02%	32.2%	YFGGMVWYFVNNK	99.7%	55.2	25	55.2	1	0	0	1624.76	267	279
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	14	24	0.02%	32.2%	YVFTDISYSIPHR	99.7%	65.7	25	65.7	2	0	0	1597.80	156	168
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	4	5	10	0.01%	23.7%	AFDLFNPNFK	99.7%	80.9	25	74	2	0	0	1212.60	84	93
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	4	5	10	0.01%	23.7%	ALLAEGVILR	99.7%	69.7	25	45.2	2	0	0	1054.66	124	133
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	4	5	10	0.01%	23.7%	LETVGSIFSR	99.7%	73.6	25	59.9	2	0	0	1108.60	6	15
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	4	5	10	0.01%	23.7%	LGETDEEKLFVETGK	99.7%	64.8	25	63.9	2	2	0	1694.85	109	123
28S ribosomal protein S24, mitochondrial	MRPS24	RT24_HUMAN	19.0	100.0%	3	3	4	0.00%	10.8%	LHLQTVPSK	99.7%	59	25	48.3	2	0	0	1022.60	153	161
28S ribosomal protein S24, mitochondrial	MRPS24	RT24_HUMAN	19.0	100.0%	3	3	4	0.00%	10.8%	TVEDVFLR	99.7%	45.8	25	34.5	1	0	0	978.53	86	93
28S ribosomal protein S24, mitochondrial	MRPS24	RT24_HUMAN	19.0	100.0%	3	3	4	0.00%	10.8%	TVEDVFLRK	99.3%	36.6	25	26	1	0	0	1106.62	86	94
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	6	8	15	0.02%	37.6%	FVFFNIPQIQYK	99.4%	37.3	25	37.3	2	0	0	1543.83	47	58
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	6	8	15	0.02%	37.6%	NMTPSPFLR	97.1%	30.2	25	6.28	1	0	0	1062.54	69	77
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	6	8	15	0.02%	37.6%	NPWVQIMMFK	99.7%	43.1	25	43.1	3	0	0	1325.64	59	68
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	6	8	15	0.02%	37.6%	TLQYLSQGNVVFK	99.7%	75.1	25	60.1	2	0	0	1496.81	12	24
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	6	8	15	0.02%	37.6%	TLQYLSQGNVVFKDSVK	99.7%	65.2	25	63.6	2	1	0	1926.03	12	28
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	6	8	15	0.02%	37.6%	VMTVNYNTHGELGEGAR	99.7%	34.3	25	34	0	4	0	1847.87	29	45
28S ribosomal protein S26, mitochondrial	MRPS26	RT26_HUMAN	24.2	100.0%	5	7	11	0.01%	23.4%	EGLVVRPQR	99.2%	36.2	25	22.3	1	0	0	1053.62	194	202
28S ribosomal protein S26, mitochondrial	MRPS26	RT26_HUMAN	24.2	100.0%	5	7	11	0.01%	23.4%	EVLQLQEEVK	99.7%	55.4	25	41.3	2	0	0	1214.66	156	165
28S ribosomal protein S26, mitochondrial	MRPS26	RT26_HUMAN	24.2	100.0%	5	7	11	0.01%	23.4%	KAEEVQAWAQR	99.7%	47.4	25	34.8	2	2	0	1315.68	142	152
28S ribosomal protein S26, mitochondrial	MRPS26	RT26_HUMAN	24.2	100.0%	5	7	11	0.01%	23.4%	MEFVSEVQR	99.7%	54.2	25	49.6	3	0	0	1124.54	72	80
28S ribosomal protein S26, mitochondrial	MRPS26	RT26_HUMAN	24.2	100.0%	5	7	11	0.01%	23.4%	VEAALDSRK	96.2%	29	25	22.8	1	0	0	988.54	177	185
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	9	9	28	0.03%	22.9%	EALDVLGAVLK	99.7%	91.2	25	87.8	4	0	0	1127.67	278	288
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	9	9	28	0.03%	22.9%	IESEGLLSLTTQLVK	99.7%	109	25	109	4	0	0	1630.93	347	361
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	9	9	28	0.03%	22.9%	KLPVSSLTISR	99.7%	54.5	25	47.3	3	0	0	1200.73	64	74
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	9	9	28	0.03%	22.9%	LIDNISSR	99.2%	35.9	25	1.32	4	0	0	917.51	75	82
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	9	9	28	0.03%	22.9%	LPQYLER	99.7%	40.9	25	28.9	1	0	0	918.50	327	333
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	9	9	28	0.03%	22.9%	LVEQLDIEETEQSK	99.7%	81.4	25	81.4	2	0	0	1660.83	313	326
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	9	9	28	0.03%	22.9%	NFGASLLLPGLK	99.7%	59	25	51.3	4	0	0	1229.73	203	214
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	9	9	28	0.03%	22.9%	VAASPEDIK	99.7%	41.6	25	37.7	4	0	0	929.49	266	274
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	9	9	28	0.03%	22.9%	VELQQGLR	99.4%	37	25	24	2	0	0	942.54	234	241
28S ribosomal protein S28, mitochondrial	MRPS28	RT28_HUMAN	20.8	100.0%	3	4	13	0.01%	15.5%	AGGFASALER	99.7%	59.2	25	43.5	4	0	0	978.50	49	58
28S ribosomal protein S28, mitochondrial	MRPS28	RT28_HUMAN	20.8	100.0%	3	4	13	0.01%	15.5%	LLDLELTSR	99.7%	66.7	25	58.7	4	0	0	1059.60	144	152
28S ribosomal protein S28, mitochondrial	MRPS28	RT28_HUMAN	20.8	100.0%	3	4	13	0.01%	15.5%	NVESFASMLR	99.7%	65.2	25	57.2	5	0	0	1169.56	76	85
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	7	8	18	0.02%	20.9%	ELLFLSNANPSLLER	99.7%	97.3	25	96.2	2	0	0	1715.93	379	393
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	7	8	18	0.02%	20.9%	FDQPLEASTWLK	99.7%	87.6	25	68.9	2	0	0	1434.73	178	189
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	7	8	18	0.02%	20.9%	GSPLGEVVEQGITR	99.7%	90.1	25	85.1	4	0	0	1441.76	219	232
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	7	8	18	0.02%	20.9%	KAYLPQELLGK	99.7%	63.8	25	63.8	2	0	0	1259.74	321	331
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	7	8	18	0.02%	20.9%	NATDAVGIVLK	99.7%	69.9	25	63.3	2	0	0	1100.63	235	245
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	7	8	18	0.02%	20.9%	NTSFAYPAIR	99.7%	63.1	25	54.5	2	0	0	1139.58	114	123
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	7	8	18	0.02%	20.9%	TFSEACLMVR	99.7%	57.2	25	57.2	4	0	0	1213.57	93	102
28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	5	7	13	0.01%	17.7%	EAPETDTSPSLWDVEFAK	99.7%	68.4	25	68.4	2	0	0	2021.93	267	284
28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	5	7	13	0.01%	17.7%	IQFDEGYDNYPGQEK	99.7%	79.8	25	79.8	2	0	0	1802.79	226	240

28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	5	7	13	0.01%	17.7%	ISFSNIISDMK	99.7%	78.7	25	68.7	4	0	0	1254.64	199	209
28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	5	7	13	0.01%	17.7%	LNIFDMMAVTK	99.7%	51	25	42.9	1	0	0	1282.65	256	266
28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	5	7	13	0.01%	17.7%	SELLSQLQQHEEESR	99.7%	70	25	63.8	2	2	0	1812.87	175	189
28S ribosomal protein S33, mitochondrial	MRPS33	RT33_HUMAN	12.6	99.8%	2	2	5	0.01%	19.8%	LFGEVTRPTNSK	99.7%	58.7	25	49.8	3	0	0	1348.72	18	29
28S ribosomal protein S33, mitochondrial	MRPS33	RT33_HUMAN	12.6	99.8%	2	2	5	0.01%	19.8%	LFSELPLAK	98.7%	33.7	25	14.9	2	0	0	1017.60	36	44
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	5	6	11	0.01%	23.4%	AMIIAER	98.1%	32	25	11.7	2	0	0	819.44	172	178
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	5	6	11	0.01%	23.4%	LLQLLGR	99.7%	45.3	25	13.7	2	0	0	812.54	64	70
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	5	6	11	0.01%	23.4%	LPLFGLGR	99.7%	45.5	25	38	2	0	0	872.54	71	78
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	5	6	11	0.01%	23.4%	NGDTSTEEPMLNVQR	99.7%	68.4	25	66	4	0	0	1690.77	181	195
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	5	6	11	0.01%	23.4%	VRPDYTAQNLDHGK	97.8%	31.3	25	31.3	1	0	0	1613.80	100	113
28S ribosomal protein S35, mitochondrial	MRPS35	RT35_HUMAN	36.8	100.0%	3	3	5	0.01%	11.5%	EGNLELLK	99.3%	36.8	25	20.8	1	0	0	915.51	100	107
28S ribosomal protein S35, mitochondrial	MRPS35	RT35_HUMAN	36.8	100.0%	3	3	5	0.01%	11.5%	NILETLLQMK	99.7%	80.2	25	67.3	2	0	0	1202.68	261	270
28S ribosomal protein S35, mitochondrial	MRPS35	RT35_HUMAN	36.8	100.0%	3	3	5	0.01%	11.5%	SVVSLKNEEENENSISQYK	99.7%	40.3	25	40.3	0	2	0	2197.06	295	313
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	7	10	18	0.02%	18.8%	GAAGFSIGK	99.5%	38.5	25	21.5	2	0	0	807.44	252	260
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	7	10	18	0.02%	18.8%	GALAETGAGAK	99.7%	54	25	35.3	2	0	0	945.50	101	111
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	7	10	18	0.02%	18.8%	LTADELWK	99.7%	47.6	25	41.5	2	0	0	975.51	93	100
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	7	10	18	0.02%	18.8%	NGAVQTIAQR	99.7%	74.4	25	64	2	0	0	1057.57	151	160
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	7	10	18	0.02%	18.8%	VSGSINMLSLTQGLFR	99.7%	93.6	25	90.9	4	0	0	1722.92	336	351
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	7	10	18	0.02%	18.8%	YEDHTIFHDISLR	99.7%	38.8	25	38.8	1	2	0	1645.80	285	297
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	7	10	18	0.02%	18.8%	YGFLWPGLNVPLMK	99.7%	50	25	50	3	0	0	1650.87	137	150
28S ribosomal protein S6, mitochondrial	MRPS6	RT06_HUMAN	14.2	100.0%	3	3	5	0.01%	22.4%	AMQRPETAATLK	99.7%	45.2	25	32.6	2	0	0	1316.70	12	23
28S ribosomal protein S6, mitochondrial	MRPS6	RT06_HUMAN	14.2	100.0%	3	3	5	0.01%	22.4%	DLENLGER	98.9%	34.3	25	21.2	2	0	0	945.46	38	45
28S ribosomal protein S6, mitochondrial	MRPS6	RT06_HUMAN	14.2	100.0%	3	3	5	0.01%	22.4%	TIEALMDR	96.7%	29.6	25	22.8	1	0	0	964.48	25	32
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	5	5	9	0.01%	26.0%	LLEAFHNQGPVIK	99.7%	58.3	25	55.9	2	0	0	1465.82	209	221
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	5	5	9	0.01%	26.0%	NCEPMIGLVPILK	99.6%	39.6	25	32.8	1	0	0	1499.80	151	163
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	5	5	9	0.01%	26.0%	NPYTIFHQALK	99.7%	42.4	25	38	1	0	0	1331.71	140	150
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	5	5	9	0.01%	26.0%	TSSVFEDPVISK	99.7%	50.1	25	45.6	4	0	0	1308.67	82	93
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	5	5	9	0.01%	26.0%	YHAASAEEQATIER	99.7%	66.1	25	54.8	1	0	0	1575.74	126	139
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	6	6	11	0.01%	19.4%	AIAYLFPSGLFEK	99.7%	60.3	25	58.1	3	0	0	1455.79	107	119
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	6	6	11	0.01%	19.4%	ALCSFVTEDEVEWMR	99.7%	49.5	25	49.5	1	0	0	1887.83	351	365
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	6	6	11	0.01%	19.4%	HDVTCTVSGGGR	99.7%	59.2	25	56.6	2	0	0	1245.56	326	337
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	6	6	11	0.01%	19.4%	LLTSQCGAAEEEFVQR	99.7%	94.8	25	94.8	2	0	0	1837.88	228	243
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	6	6	11	0.01%	19.4%	LSDLDYMQFIR	99.7%	58.9	25	52.4	2	0	0	1416.68	213	223
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	6	6	11	0.01%	19.4%	QIEEFNIGKR	99.5%	38.4	25	25.5	1	0	0	1233.66	77	86
2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	GCAT	KBL_HUMAN	45.3	99.8%	2	2	8	0.01%	8.4%	ALGGASGGYTTGPGPLVSLLR	99.7%	65.6	25	65.3	4	0	0	1944.06	266	286
2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	GCAT	KBL_HUMAN	45.3	99.8%	2	2	8	0.01%	8.4%	GIFVIGFSYPVVPK	99.7%	48.2	25	48.2	4	0	0	1522.87	370	383
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	COQ5	COQ5_HUMAN	37.1	100.0%	6	6	10	0.01%	23.2%	AQQNLSWEEIAK	99.5%	38	25	38	1	0	0	1416.71	142	153
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	COQ5	COQ5_HUMAN	37.1	100.0%	6	6	10	0.01%	23.2%	EYQNEEDSLGGSR	99.7%	78	25	76.3	2	0	0	1483.63	154	166
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	COQ5	COQ5_HUMAN	37.1	100.0%	6	6	10	0.01%	23.2%	FLCLEFSQVNNPLISR	99.7%	42.8	25	42.8	2	0	0	1937.00	242	257
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	COQ5	COQ5_HUMAN	37.1	100.0%	6	6	10	0.01%	23.2%	FLNYVQSQHQR	99.7%	40	25	37.8	1	0	0	1419.71	124	134
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	COQ5	COQ5_HUMAN	37.1	100.0%	6	6	10	0.01%	23.2%	NVTHIDQALQEAHR	99.7%	51.8	25	51.8	0	2	0	1631.82	221	234
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	COQ5	COQ5_HUMAN	37.1	100.0%	6	6	10	0.01%	23.2%	VYQVFESVAK	99.7%	61.8	25	55.3	2	0	0	1169.62	68	77
2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	BCKDHA	ODBA_HUMAN	50.5	99.8%	2	2	3	0.00%	6.7%	AVAENQPFLIEAMTYR	99.7%	61.2	25	61.2	2	0	0	1852.93	317	332
2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	BCKDHA	ODBA_HUMAN	50.5	99.8%	2	2	3	0.00%	6.7%	VDGNDVFAVYNATK	99.7%	78.5	25	78.5	1	0	0	1512.73	298	311
2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	BCKDHB	ODBB_HUMAN	43.1	100.0%	3	3	5	0.01%	9.2%	LGVSCEVIDLR	99.7%	77.2	25	61	2	0	0	1260.66	295	305
2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	BCKDHB	ODBB_HUMAN	43.1	100.0%	3	3	5	0.01%	9.2%	SGDLFNCGSLTIR	99.7%	72.1	25	70.6	2	0	0	1439.69	171	183
2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	BCKDHB	ODBB_HUMAN	43.1	100.0%	3	3	5	0.01%	9.2%	TIIPWDVDTICK	97.5%	30.8	25	22.8	1	0	0	1460.75	306	317
39S ribosomal protein L1, mitochondrial	MRPL1	RM01_HUMAN	36.9	99.8%	2	2	3	0.00%	6.8%	FQILDFTSPK	99.7%	49	25	37.1	2	0	0	1195.64	109	118
39S ribosomal protein L1, mitochondrial	MRPL1	RM01_HUMAN	36.9	99.8%	2	2	3	0.00%	6.8%	VAVFTENASEVK	99.7%	75.3	25	60	1	0	0	1293.67	157	168
39S ribosomal protein L10, mitochondrial	MRPL10	RM10_HUMAN	29.3	100.0%	3	4	5	0.01%	12.6%	EIAAVFQDNR	99.7%	61.5	25	58.9	2	0	0	1162.59	85	94
39S ribosomal protein L10, mitochondrial	MRPL10	RM10_HUMAN	29.3	100.0%	3	4	5	0.01%	12.6%	MIAVCQNVALSAEDK	99.7%	64.8	25	64.8	2	0	0	1648.80	95	109

39S ribosomal protein L10, mitochondrial	MRPL10	RM10_HUMAN	29.3	100.0%	3	4	5	0.01%	12.6%	QGFINYSK	97.2%	30.3	25	23.5	1	0	0	956.48	189	196
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	6	7	20	0.02%	41.7%	AGLAMPGPPLGPVLGQR	99.7%	54.4	25	47.8	5	0	0	1630.91	26	42
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	6	7	20	0.02%	41.7%	AQDEAFALQDVPLSSVVR	99.6%	39	25	39	1	0	0	1945.00	125	142
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	6	7	20	0.02%	41.7%	DLSSEELAAFQK	99.7%	62.8	25	52.4	4	0	0	1337.66	158	169
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	6	7	20	0.02%	41.7%	EADLAAQEEAAKK	99.7%	45	25	38	3	0	0	1373.69	180	192
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	6	7	20	0.02%	41.7%	GVSINQFCK	99.7%	45.1	25	37.2	3	0	0	1052.52	43	51
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	6	7	20	0.02%	41.7%	IGQPTVSYFLK	99.5%	38.6	25	38.6	4	0	0	1252.69	82	92
39S ribosomal protein L12, mitochondrial	MRPL12	RM12_HUMAN	21.3	100.0%	3	3	6	0.01%	16.2%	KLVESLPQEIK	99.7%	53.8	25	47.8	2	0	0	1283.76	163	173
39S ribosomal protein L12, mitochondrial	MRPL12	RM12_HUMAN	21.3	100.0%	3	3	6	0.01%	16.2%	LTEAKPVDK	99.7%	43.2	25	42.1	2	0	0	1000.57	134	142
39S ribosomal protein L12, mitochondrial	MRPL12	RM12_HUMAN	21.3	100.0%	3	3	6	0.01%	16.2%	NYIQGINLVQAK	99.7%	71.3	25	62.8	2	0	0	1360.76	151	162
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	5	5	10	0.01%	28.1%	APQQWATFAR	99.7%	59.6	25	51.3	2	0	0	1175.60	7	16
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	5	5	10	0.01%	28.1%	LAAMASIR	99.7%	56.2	25	40	2	0	0	848.47	31	38
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	5	5	10	0.01%	28.1%	LAIYGMLPK	99.1%	35.3	25	25.6	2	0	0	1021.58	106	114
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	5	5	10	0.01%	28.1%	NLVEELPQPR	99.7%	55.4	25	51.8	2	0	0	1194.65	140	149
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	5	5	10	0.01%	28.1%	VYSSHTGYPGGFR	99.7%	66.4	25	66.4	2	0	0	1427.67	76	88
39S ribosomal protein L14, mitochondrial	MRPL14	RM14_HUMAN	15.9	100.0%	4	5	12	0.01%	37.2%	ALIVGHCMPGPR	97.6%	31	25	31	2	0	0	1323.67	84	95
39S ribosomal protein L14, mitochondrial	MRPL14	RM14_HUMAN	15.9	100.0%	4	5	12	0.01%	37.2%	FDSNNVVLIEDNGNPVGTR	99.7%	63	25	63	2	0	0	2060.00	100	118
39S ribosomal protein L14, mitochondrial	MRPL14	RM14_HUMAN	15.9	100.0%	4	5	12	0.01%	37.2%	VLAIAQNFV	99.0%	35.1	25	27.7	2	0	0	974.57	137	145
39S ribosomal protein L14, mitochondrial	MRPL14	RM14_HUMAN	15.9	100.0%	4	5	12	0.01%	37.2%	VVDNSALGNSPYHR	99.7%	72.1	25	72.1	4	2	0	1528.75	40	53
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	6	7	14	0.01%	24.7%	GVTIQPLKR	96.8%	29.8	25	23	2	0	0	1011.63	126	134
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	6	7	14	0.01%	24.7%	GYLADPAKFPEAR	99.7%	44.9	25	38.9	2	2	0	1434.74	221	233
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	6	7	14	0.01%	24.7%	ILKPTDENLLK	99.3%	36.5	25	29.3	2	0	0	1283.76	282	292
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	6	7	14	0.01%	24.7%	LGFEGGQTPFYIR	99.7%	76.5	25	68	2	0	0	1484.75	65	77
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	6	7	14	0.01%	24.7%	NGGVVTTAFYDPR	99.7%	50	25	47.9	2	0	0	1396.69	170	182
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	6	7	14	0.01%	24.7%	SLDIVCKPVPFFLR	99.7%	42.1	25	42.1	0	2	0	1690.94	183	196
39S ribosomal protein L16, mitochondrial	MRPL16	RM16_HUMAN	28.5	100.0%	3	3	5	0.01%	12.7%	GAIDHYVTPVK	99.7%	57.5	25	43	2	0	0	1199.64	145	155
39S ribosomal protein L16, mitochondrial	MRPL16	RM16_HUMAN	28.5	100.0%	3	3	5	0.01%	12.7%	KVLSPYDLTHK	98.1%	25.2	25	22.6	0	1	0	1300.73	228	238
39S ribosomal protein L16, mitochondrial	MRPL16	RM16_HUMAN	28.5	100.0%	3	3	5	0.01%	12.7%	VPAPFKPITR	99.7%	52.4	25	39.3	2	0	0	1125.68	124	133
39S ribosomal protein L18, mitochondrial	MRPL18	RM18_HUMAN	20.6	100.0%	4	4	8	0.01%	24.4%	LQSAMTEGGVVLREPQR	98.2%	25.5	25	23.8	0	2	0	1886.98	161	177
39S ribosomal protein L18, mitochondrial	MRPL18	RM18_HUMAN	20.6	100.0%	4	4	8	0.01%	24.4%	NLELLSVAR	99.7%	46.5	25	17.4	2	0	0	1014.59	55	63
39S ribosomal protein L18, mitochondrial	MRPL18	RM18_HUMAN	20.6	100.0%	4	4	8	0.01%	24.4%	NVVACESIGR	99.7%	50.2	25	42.1	2	0	0	1104.55	121	130
39S ribosomal protein L18, mitochondrial	MRPL18	RM18_HUMAN	20.6	100.0%	4	4	8	0.01%	24.4%	VVVSASTR	99.5%	38.1	25	31	2	0	0	818.47	101	108
39S ribosomal protein L19, mitochondrial	MRPL19	RM19_HUMAN	33.5	100.0%	5	5	8	0.01%	16.8%	FLSPEFIPR	99.6%	39.1	25	35.8	2	0	0	1105.60	75	83
39S ribosomal protein L19, mitochondrial	MRPL19	RM19_HUMAN	33.5	100.0%	5	5	8	0.01%	16.8%	GLGATFILR	99.7%	61.5	25	59.5	2	0	0	947.57	144	152
39S ribosomal protein L19, mitochondrial	MRPL19	RM19_HUMAN	33.5	100.0%	5	5	8	0.01%	16.8%	ISQFLGICIQR	99.7%	58.3	25	56.7	1	0	0	1334.73	130	140
39S ribosomal protein L19, mitochondrial	MRPL19	RM19_HUMAN	33.5	100.0%	5	5	8	0.01%	16.8%	LDDSLLYLR	99.7%	65.3	25	50.9	1	0	0	1107.60	183	191
39S ribosomal protein L19, mitochondrial	MRPL19	RM19_HUMAN	33.5	100.0%	5	5	8	0.01%	16.8%	VTTADPYASGK	99.7%	53.2	25	47.9	2	0	0	1109.55	119	129
39S ribosomal protein L2, mitochondrial	MRPL2	RM02_HUMAN	33.3	99.8%	2	2	4	0.00%	7.2%	AAGTCGVLLR	99.7%	79.2	25	64	2	0	0	1017.55	209	218
39S ribosomal protein L2, mitochondrial	MRPL2	RM02_HUMAN	33.3	99.8%	2	2	4	0.00%	7.2%	SADIALVAGGSR	99.7%	70.9	25	60.5	2	0	0	1116.60	136	147
39S ribosomal protein L20, mitochondrial	MRPL20	RM20_HUMAN	17.4	100.0%	2	2	3	0.00%	14.8%	ITAASQEHGLK	97.7%	31.2	25	25.3	1	0	0	1154.62	72	82
39S ribosomal protein L20, mitochondrial	MRPL20	RM20_HUMAN	17.4	100.0%	2	2	3	0.00%	14.8%	VLADLAIYEPK	99.7%	74.1	25	60.9	2	0	0	1231.69	101	111
39S ribosomal protein L21, mitochondrial	MRPL21	RM21_HUMAN	22.8	100.0%	3	3	8	0.01%	15.6%	IVTTPQTVLR	97.7%	31.2	25	23.4	3	0	0	1127.68	185	194
39S ribosomal protein L21, mitochondrial	MRPL21	RM21_HUMAN	22.8	100.0%	3	3	8	0.01%	15.6%	LFAVVHFASR	99.7%	53.4	25	41.1	4	0	0	1146.64	95	104
39S ribosomal protein L21, mitochondrial	MRPL21	RM21_HUMAN	22.8	100.0%	3	3	8	0.01%	15.6%	VNEMIVTGQYGR	99.5%	38.1	25	29.7	1	0	0	1382.67	83	94
39S ribosomal protein L22, mitochondrial	MRPL22	RM22_HUMAN	23.6	100.0%	5	5	11	0.01%	25.2%	EVLLEAQDMAVR	99.7%	78.8	25	61.9	2	0	0	1389.70	113	124
39S ribosomal protein L22, mitochondrial	MRPL22	RM22_HUMAN	23.6	100.0%	5	5	11	0.01%	25.2%	EYIQQLR	97.8%	31.3	25	0	2	0	0	949.51	192	198
39S ribosomal protein L22, mitochondrial	MRPL22	RM22_HUMAN	23.6	100.0%	5	5	11	0.01%	25.2%	LVEGPPPPPEPPK	99.7%	51.1	25	50.3	2	0	0	1353.74	172	184
39S ribosomal protein L22, mitochondrial	MRPL22	RM22_HUMAN	23.6	100.0%	5	5	11	0.01%	25.2%	SNLYIAESTSGR	99.7%	89.9	25	89.9	4	0	0	1297.64	132	143
39S ribosomal protein L22, mitochondrial	MRPL22	RM22_HUMAN	23.6	100.0%	5	5	11	0.01%	25.2%	VYCHYFVK	97.5%	30.7	25	20.4	1	0	0	1115.53	164	171
39S ribosomal protein L24, mitochondrial	MRPL24	RM24_HUMAN	24.9	100.0%	5	6	7	0.01%	25.9%	ADGIVPETWIDGPK	97.3%	30.4	25	28.2	1	0	0	1497.76	162	175
39S ribosomal protein L24, mitochondrial	MRPL24	RM24_HUMAN	24.9	100.0%	5	6	7	0.01%	25.9%	GTMIPSEAPLLHR	99.4%	37.7	25	28.8	1	2	0	1437.75	106	118

39S ribosomal protein L24, mitochondrial	MRPL24	RM24_HUMAN	24.9	100.0%	5	6	7	0.01%	25.9%	IIPKPEFPR	94.7%	27.6	25	27.4	1	0	0	1096.65	153	161
39S ribosomal protein L24, mitochondrial	MRPL24	RM24_HUMAN	24.9	100.0%	5	6	7	0.01%	25.9%	KPTEIEWR	95.6%	28.6	25.2	23.4	1	0	0	1058.56	129	136
39S ribosomal protein L24, mitochondrial	MRPL24	RM24_HUMAN	24.9	100.0%	5	6	7	0.01%	25.9%	YGMSPPGSVADK	99.1%	35.5	25	31	1	0	0	1208.56	21	32
39S ribosomal protein L27, mitochondrial	MRPL27	RM27_HUMAN	16.1	99.8%	2	2	5	0.01%	14.2%	CLYALEEGIVR	99.7%	81.8	25	73.3	2	0	0	1322.68	88	98
39S ribosomal protein L27, mitochondrial	MRPL27	RM27_HUMAN	16.1	99.8%	2	2	5	0.01%	14.2%	NTEAVDLITR	99.7%	67.8	25	55.1	3	0	0	1131.60	110	119
39S ribosomal protein L28, mitochondrial	MRPL28	RM28_HUMAN	30.2	100.0%	3	3	3	0.00%	10.5%	AAIYDKYK	97.0%	29.9	25	21.4	1	0	0	971.52	185	192
39S ribosomal protein L28, mitochondrial	MRPL28	RM28_HUMAN	30.2	100.0%	3	3	3	0.00%	10.5%	EFYSEILDKK	98.4%	32.7	25	21	1	0	0	1271.65	113	122
39S ribosomal protein L28, mitochondrial	MRPL28	RM28_HUMAN	30.2	100.0%	3	3	3	0.00%	10.5%	VWKPQLFER	97.8%	24.7	25	21.5	0	1	0	1202.67	104	112
39S ribosomal protein L3, mitochondrial	MRPL3	RM03_HUMAN	38.6	99.8%	2	2	3	0.00%	6.0%	MATLSVGGK	98.0%	31.6	25	19.7	2	0	0	879.46	142	150
39S ribosomal protein L3, mitochondrial	MRPL3	RM03_HUMAN	38.6	99.8%	2	2	3	0.00%	6.0%	RPGAVATGDIGR	97.6%	30.9	25	27.8	1	0	0	1169.64	239	250
39S ribosomal protein L33, mitochondrial	MRPL33	RM33_HUMAN	7.6	99.8%	2	3	4	0.00%	38.5%	LTLLHYDPVVK	99.7%	43.3	25	40	2	0	0	1297.75	41	51
39S ribosomal protein L33, mitochondrial	MRPL33	RM33_HUMAN	7.6	99.8%	2	3	4	0.00%	38.5%	MVSEAGTGFCFNTK	99.7%	68.2	25	68.2	2	0	0	1564.68	20	33
39S ribosomal protein L34, mitochondrial	MRPL34	RM34_HUMAN	10.2	99.8%	2	2	3	0.00%	23.9%	GNEYQPSNIK	99.7%	49.2	25	38	2	0	0	1149.55	50	59
39S ribosomal protein L34, mitochondrial	MRPL34	RM34_HUMAN	10.2	99.8%	2	2	3	0.00%	23.9%	LSTPAGVQVILR	98.9%	34.2	25	34.2	1	0	0	1253.76	70	81
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	5	5	8	0.01%	16.3%	ESLLLQVR	99.7%	54.6	25	31.6	2	0	0	957.57	216	223
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	5	5	8	0.01%	16.3%	ETYCPVIVDNLIQLCK	99.7%	52.8	25	52.8	1	0	0	1964.98	174	189
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	5	5	8	0.01%	16.3%	MILFAFGSALAQAR	99.7%	101	25	98.4	2	0	0	1495.81	313	326
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	5	5	8	0.01%	16.3%	VLEQPVVVQSVGTDGR	98.9%	34.5	25	34.5	1	0	0	1682.91	335	350
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	5	5	8	0.01%	16.3%	VYEIPGLEPITFAGK	99.7%	68.6	25	64.1	2	0	0	1633.88	49	63
39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	5	5	8	0.01%	14.2%	DLFHGATFVPR	99.7%	46.1	25	41	2	0	0	1259.65	160	170
39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	5	5	8	0.01%	14.2%	LAEYYGLYR	99.7%	57.4	25	49	2	0	0	1147.58	151	159
39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	5	5	8	0.01%	14.2%	LAFLLFK	99.1%	35.5	25	30.6	2	0	0	851.54	268	274
39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	5	5	8	0.01%	14.2%	TASVPLDAVR	95.4%	28.2	25	21.8	1	0	0	1028.57	127	136
39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	5	5	8	0.01%	14.2%	VAEGQVTCPYLPPFPAR	99.7%	50.4	25	46.3	1	0	0	1901.96	245	261
39S ribosomal protein L39, mitochondrial	MRPL39	RM39_HUMAN	38.7	100.0%	4	4	6	0.01%	13.9%	AFKDEYMVNLVR	96.1%	28.9	25	26.6	1	0	0	1484.76	157	168
39S ribosomal protein L39, mitochondrial	MRPL39	RM39_HUMAN	38.7	100.0%	4	4	6	0.01%	13.9%	DAHALIYK	94.5%	27.5	25	21	1	0	0	930.50	205	212
39S ribosomal protein L39, mitochondrial	MRPL39	RM39_HUMAN	38.7	100.0%	4	4	6	0.01%	13.9%	DLPFETLEVEAK	99.7%	63.9	25	57.9	2	0	0	1390.71	213	224
39S ribosomal protein L39, mitochondrial	MRPL39	RM39_HUMAN	38.7	100.0%	4	4	6	0.01%	13.9%	IGDFIDVSEGPLIPR	99.7%	70.9	25	69.2	2	0	0	1627.87	257	271
39S ribosomal protein L4, mitochondrial	MRPL4	RM04_HUMAN	34.9	100.0%	3	4	7	0.01%	15.1%	ATENPEQVASEGLPEPVLR	99.7%	94.7	25	81.9	2	0	0	2036.03	31	49
39S ribosomal protein L4, mitochondrial	MRPL4	RM04_HUMAN	34.9	100.0%	3	4	7	0.01%	15.1%	GPTSYYYMLPMK	99.7%	49.4	25	35.6	1	0	0	1450.67	157	168
39S ribosomal protein L4, mitochondrial	MRPL4	RM04_HUMAN	34.9	100.0%	3	4	7	0.01%	15.1%	VGLADLHPDVFATAPR	99.7%	46.8	25	46.7	2	2	0	1678.89	77	92
39S ribosomal protein L40, mitochondrial	MRPL40	RM40_HUMAN	24.5	100.0%	3	3	4	0.00%	16.5%	ATQELIPIEDFITPLK	99.3%	36.4	25	33.4	1	0	0	1828.01	78	93
39S ribosomal protein L40, mitochondrial	MRPL40	RM40_HUMAN	24.5	100.0%	3	3	4	0.00%	16.5%	DPNLFPFEK	95.6%	28.4	25	27.3	1	0	0	1106.55	165	173
39S ribosomal protein L40, mitochondrial	MRPL40	RM40_HUMAN	24.5	100.0%	3	3	4	0.00%	16.5%	VYTQVEFKR	99.7%	60	25	55	2	0	0	1169.63	198	206
39S ribosomal protein L41, mitochondrial	MRPL41	RM41_HUMAN	15.4	100.0%	3	3	7	0.01%	19.7%	GIGFLTSGWR	99.7%	55.3	25	47.2	4	0	0	1093.58	40	49
39S ribosomal protein L41, mitochondrial	MRPL41	RM41_HUMAN	15.4	100.0%	3	3	7	0.01%	19.7%	LFQLYPR	98.5%	33	25	32.7	1	0	0	936.53	127	133
39S ribosomal protein L41, mitochondrial	MRPL41	RM41_HUMAN	15.4	100.0%	3	3	7	0.01%	19.7%	YGFEPTQEGK	99.7%	41.3	25	32.5	2	0	0	1155.53	117	126
39S ribosomal protein L43, mitochondrial	MRPL43	RM43_HUMAN	23.4	100.0%	3	3	5	0.01%	14.0%	FLASVLHNGLGR	99.7%	59.7	25	54.8	2	0	0	1283.72	10	21
39S ribosomal protein L43, mitochondrial	MRPL43	RM43_HUMAN	23.4	100.0%	3	3	5	0.01%	14.0%	SVEEISTLVQK	99.7%	57.6	25	44.1	1	0	0	1232.67	93	103
39S ribosomal protein L43, mitochondrial	MRPL43	RM43_HUMAN	23.4	100.0%	3	3	5	0.01%	14.0%	YVQQLQR	99.7%	40.8	25	31.1	2	0	0	934.51	22	28
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	6	6	10	0.01%	18.1%	EAVLLNLK	96.9%	29.9	25	23.4	1	0	0	899.56	113	120
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	6	6	10	0.01%	18.1%	IINPMGLLVEELK	99.7%	53.8	25	53.2	2	0	0	1468.84	234	246
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	6	6	10	0.01%	18.1%	KLYGFTENR	99.6%	39.2	25	35.5	2	0	0	1127.58	303	311
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	6	6	10	0.01%	18.1%	LIAEGPGETVLVAEEEAAR	99.7%	105	25	105	2	0	0	1954.01	280	298
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	6	6	10	0.01%	18.1%	LQENFSLDLLK	99.7%	62.7	25	41.8	2	0	0	1319.72	79	89
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	6	6	10	0.01%	18.1%	LYGFTENR	99.2%	35.8	25	33.9	1	0	0	999.49	304	311
39S ribosomal protein L45, mitochondrial	MRPL45	RM45_HUMAN	35.4	99.9%	2	2	2	0.00%	5.2%	IKDFPEK	94.7%	27.7	25	4.48	1	0	0	876.48	134	140
39S ribosomal protein L45, mitochondrial	MRPL45	RM45_HUMAN	35.4	99.9%	2	2	2	0.00%	5.2%	IKDYDANFK	98.2%	32.1	25	31	1	0	0	1113.56	125	133
39S ribosomal protein L46, mitochondrial	MRPL46	RM46_HUMAN	31.7	100.0%	4	4	9	0.01%	15.4%	ALLLTGDFSQAGNK	99.7%	102	25	97.6	3	0	0	1434.76	236	249
39S ribosomal protein L46, mitochondrial	MRPL46	RM46_HUMAN	31.7	100.0%	4	4	9	0.01%	15.4%	NLVLLVR	98.4%	32.7	25	15	2	0	0	826.55	156	162
39S ribosomal protein L46, mitochondrial	MRPL46	RM46_HUMAN	31.7	100.0%	4	4	9	0.01%	15.4%	SLYSDHELR	99.4%	37.7	25	9.33	2	0	0	1119.54	82	90

39S ribosomal protein L46, mitochondrial	MRPL46	RM46_HUMAN	31.7	100.0%	4	4	9	0.01%	15.4%	TLATLSENNMEAK	99.7%	47.5	25	42.2	2	0	0	1437.69	191	203
39S ribosomal protein L47, mitochondrial	MRPL47	RM47_HUMAN	29.5	100.0%	3	3	6	0.01%	9.2%	NMLLTLEQEAK	99.7%	55.2	25	32.8	2	0	0	1289.68	110	120
39S ribosomal protein L47, mitochondrial	MRPL47	RM47_HUMAN	29.5	100.0%	3	3	6	0.01%	9.2%	NMLLTLEQEAKR	99.7%	40.1	25	28.6	2	0	0	1461.77	110	121
39S ribosomal protein L47, mitochondrial	MRPL47	RM47_HUMAN	29.5	100.0%	3	3	6	0.01%	9.2%	SGAAWTCQQLR	99.7%	55.6	25	48.3	2	0	0	1277.61	81	91
39S ribosomal protein L48, mitochondrial	MRPL48	RM48_HUMAN	23.9	100.0%	4	5	10	0.01%	21.7%	ARPELEELLAK	99.7%	49.2	25	32.4	2	0	0	1268.72	200	210
39S ribosomal protein L48, mitochondrial	MRPL48	RM48_HUMAN	23.9	100.0%	4	5	10	0.01%	21.7%	MLLDSVLTTHER	99.7%	78.5	25	66.4	4	0	0	1414.74	144	155
39S ribosomal protein L48, mitochondrial	MRPL48	RM48_HUMAN	23.9	100.0%	4	5	10	0.01%	21.7%	TIEVLQLQDQGSK	99.7%	89.6	25	84.8	2	0	0	1458.78	131	143
39S ribosomal protein L48, mitochondrial	MRPL48	RM48_HUMAN	23.9	100.0%	4	5	10	0.01%	21.7%	VEESYAMPTK	99.7%	49.3	25	41.2	2	0	0	1170.53	121	130
39S ribosomal protein L53, mitochondrial	MRPL53	RM53_HUMAN	12.1	99.9%	2	2	4	0.00%	20.5%	STNLNCSVIADVR	99.7%	70.9	25	61.6	2	0	0	1448.72	44	56
39S ribosomal protein L53, mitochondrial	MRPL53	RM53_HUMAN	12.1	99.9%	2	2	4	0.00%	20.5%	TFLQTVSSEK	98.2%	32.2	25	32.2	2	0	0	1139.59	32	41
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	5	5	9	0.01%	19.9%	ENLELILTQSVENVGVR	99.7%	65.3	25	64.2	2	0	0	1913.03	92	108
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	5	5	9	0.01%	19.9%	LLPQGLAVYASPENK	99.7%	55.1	25	48.4	2	0	0	1599.87	123	137
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	5	5	9	0.01%	19.9%	LLPQGLAVYASPENKK	99.7%	48.8	25	47.1	2	0	0	1727.97	123	138
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	5	5	9	0.01%	19.9%	LPEEPITR	99.7%	49.8	25	37	1	0	0	954.53	208	215
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	5	5	9	0.01%	19.9%	VPMSVVNFEKPK	98.6%	33.4	25	26.9	2	0	0	1390.74	233	244
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	6	7	12	0.01%	39.5%	GGIVGMTLPIAR	99.7%	61.3	25	46.9	2	0	0	1200.68	173	184
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	6	7	12	0.01%	39.5%	GLVAVITGGASGLGLATAER	99.7%	120	25	120	2	1	0	1813.02	10	29
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	6	7	12	0.01%	39.5%	GVIINTASVAAFEGQVGQAAYSASK	99.7%	46.7	25	46.7	0	1	0	2439.25	148	172
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	6	7	12	0.01%	39.5%	LVAGEMGQNEPDQGGQR	99.7%	104	25	104	2	0	0	1785.82	131	147
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	6	7	12	0.01%	39.5%	VDVAVNCAGIAVASK	99.7%	91.3	25	90.6	2	0	0	1473.77	85	99
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	6	7	12	0.01%	39.5%	VLDVNLMGTFNVIR	99.7%	73.9	25	57.1	2	0	0	1590.87	117	130
3-ketoacyl-CoA thiolase, mitochondrial	ACAA2	THIM_HUMAN	41.9	100.0%	2	2	4	0.00%	5.5%	DFTATDLSEFAAK	99.7%	104	25	99.8	2	0	0	1415.67	26	38
3-ketoacyl-CoA thiolase, mitochondrial	ACAA2	THIM_HUMAN	41.9	100.0%	2	2	4	0.00%	5.5%	ETPALTINR	99.7%	53.5	25	50.3	2	0	0	1014.56	82	90
3-keto-steroid reductase	HSD17B7	DHB7_HUMAN	38.2	99.8%	2	2	4	0.00%	6.2%	ALFFGLFSR	99.7%	47.4	25	39.6	2	0	0	1057.58	103	111
3-keto-steroid reductase	HSD17B7	DHB7_HUMAN	38.2	99.8%	2	2	4	0.00%	6.2%	YATDLLSVALNR	99.7%	61.7	25	57.4	2	0	0	1335.73	198	209
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	5	6	25	0.03%	29.7%	AEAGAGSATEFQFR	99.7%	90.2	25	84.1	5	0	0	1441.67	140	153
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	5	6	25	0.03%	29.7%	DYLHLPPEIVPATLR	99.4%	37.3	25	30.6	2	0	0	1733.96	81	95
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	5	6	25	0.03%	29.7%	GYVKEQFAWR	99.7%	46.5	25	38.4	4	0	0	1283.65	56	65
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	5	6	25	0.03%	29.7%	IAIYELLFK	99.7%	64.4	25	64.4	6	0	0	1109.66	9	17
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	5	6	25	0.03%	29.7%	KAEAGAGSATEFQFR	99.7%	111	25	108	4	4	0	1569.77	139	153
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	51	0.05%	53.8%	CPFTGNVSIR	99.7%	67.3	25	52.6	11	0	0	1150.57	60	69
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	51	0.05%	53.8%	DVQIGDIVTVGECRPLSK	99.7%	89.7	25	82.7	4	3	0	1986.03	119	136
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	51	0.05%	53.8%	DYLHYIR	98.7%	33.6	25	27.8	3	0	0	979.50	91	97
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	51	0.05%	53.8%	EAIEGTYIDK	99.7%	60.5	25	45.9	2	0	0	1138.56	49	58
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	51	0.05%	53.8%	EAIEGTYIDKK	99.7%	53.3	25	37.2	7	1	0	1266.66	49	59
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	51	0.05%	53.8%	ILSGVVTK	99.7%	43	25	22.7	3	0	0	816.52	72	79
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	51	0.05%	53.8%	KCPFTGNVSIR	99.7%	43.7	25	40.5	2	0	0	1278.66	59	69
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	51	0.05%	53.8%	NMSVHLSPCFR	99.7%	46.8	25	46.8	4	2	0	1347.63	108	118
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	51	0.05%	53.8%	QPTIFQNK	99.6%	39.2	25	33.1	3	0	0	975.53	13	20
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	51	0.05%	53.8%	RDYLHYIR	99.5%	37.9	25	16.4	1	0	0	1135.60	90	97
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	51	0.05%	53.8%	RVLLGETGK	97.4%	30.6	25	16.8	2	0	0	972.58	22	30
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	51	0.05%	53.8%	VLLGETGK	99.6%	39.5	25	26.8	1	0	0	816.48	23	30
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	51	0.05%	53.8%	VLLGETGKEK	99.7%	50.9	25	28.8	2	0	0	1073.62	23	32
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	7	8	28	0.03%	57.6%	ESQAKDVIEEYFK	99.7%	68.3	25	61.9	2	0	0	1585.77	117	129
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	7	8	28	0.03%	57.6%	KVVGCSCVVVK	99.7%	66.4	25	60.2	4	0	0	1234.66	102	112
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	7	8	28	0.03%	57.6%	LGEWVGLCK	99.7%	61.3	25	53.7	8	0	0	1061.55	85	93
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	7	8	28	0.03%	57.6%	LVEALCAEHQINLIK	99.7%	69.7	25	63.9	4	2	0	1750.95	64	78
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	7	8	28	0.03%	57.6%	QAHLCVLASNCDEPMYVK	99.7%	42.1	25	42.1	0	2	0	2150.97	46	63
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	7	8	28	0.03%	57.6%	TALIHDGLAR	99.7%	53.3	25	43.2	4	0	0	1066.60	24	33
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	7	8	28	0.03%	57.6%	VVGCSCVVVK	99.7%	61.6	25	49.8	2	0	0	1106.57	103	112
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	9	10	29	0.03%	50.3%	FRLILIESR	98.2%	32.3	25	30.1	1	0	0	1146.70	113	121

40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	9	10	29	0.03%	50.3%	FVTGNKILR	99.1%	35.3	25	34.9	1	0	0	1047.63	65	73
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	9	10	29	0.03%	50.3%	GLAPDLPEDLYHLIK	99.0%	34.7	25	33.2	1	0	0	1693.92	79	93
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	9	10	29	0.03%	50.3%	GLTPSQIGVILR	99.7%	76	25	61.4	4	0	0	1253.76	44	55
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	9	10	29	0.03%	50.3%	KGLTPSQIGVILR	99.7%	82.1	25	82.1	4	0	0	1381.85	43	55
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	9	10	29	0.03%	50.3%	LILIESR	99.7%	47.4	25	27.5	4	0	0	843.53	115	121
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	9	10	29	0.03%	50.3%	LTSDDVKEQIYK	99.7%	85.9	25	84.7	9	2	0	1438.74	28	39
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	9	10	29	0.03%	50.3%	VLPPNWKYESSTASALVA	99.5%	37.8	25	37.8	1	0	0	1933.01	134	151
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	9	10	29	0.03%	50.3%	YESSTASALVA	99.6%	39.5	25	37.3	2	0	0	1098.53	141	151
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	51	0.05%	41.7%	ADRDESSPYAAMLAAQDVAQR	99.7%	51.8	25	51.8	0	4	0	2281.05	64	84
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	51	0.05%	41.7%	CKELGITALHIK	99.7%	72.8	25	66	2	1	0	1382.78	85	96
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	51	0.05%	41.7%	DESSPYAAMLAAQDVAQR	99.7%	79	25	66.8	3	0	0	1938.89	67	84
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	51	0.05%	41.7%	ELGITALHIK	99.7%	63.3	25	54.3	4	0	0	1094.66	87	96
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	51	0.05%	41.7%	IEDVTPIPSDSTR	99.7%	77.6	25	72.7	3	0	0	1429.72	129	141
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	51	0.05%	41.7%	IEDVTPIPSDSTRR	99.7%	39.4	25	33.4	4	4	0	1585.82	129	142
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	51	0.05%	41.7%	IGRIEDVTPIPSDSTR	99.7%	67.5	25	65.4	2	2	0	1755.92	126	141
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	51	0.05%	41.7%	TKTPGPGAQSALR	99.7%	66.3	25	62.9	4	3	0	1283.71	105	117
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	51	0.05%	41.7%	TPGPGAQSALR	99.7%	75.5	25	70.2	15	0	0	1054.56	107	117
40S ribosomal protein S15	RPS15	RS15_HUMAN	17.0	100.0%	3	7	19	0.02%	22.1%	DMIILPEMVGSMVGVYNGK	99.7%	101	25	49.8	7	0	0	2085.01	82	100
40S ribosomal protein S15	RPS15	RS15_HUMAN	17.0	100.0%	3	7	19	0.02%	22.1%	EAPPMEKPEVVK	99.7%	51.4	25	46.6	4	2	0	1353.71	66	77
40S ribosomal protein S15	RPS15	RS15_HUMAN	17.0	100.0%	3	7	19	0.02%	22.1%	KEAPPMEKPEVVK	99.7%	50	25	46.5	2	4	0	1497.80	65	77
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	10	13	31	0.03%	60.0%	DLEKWQNNLLPSR	95.7%	28.5	25	20.2	1	0	0	1612.84	85	97
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	10	13	31	0.03%	60.0%	FDVQLKDLEK	99.7%	58	25	17.7	4	2	0	1234.67	79	88
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	10	13	31	0.03%	60.0%	FLTVMMK	99.7%	42.5	25	21.3	5	0	0	869.46	37	43
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	10	13	31	0.03%	60.0%	HGYIGEFEIIDDHR	99.7%	45.9	25	45.9	0	2	0	1700.80	44	57
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	10	13	31	0.03%	60.0%	IVVNLTGR	99.7%	50.9	25	32.3	2	0	0	871.54	61	68
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	10	13	31	0.03%	60.0%	LNKCGVISPR	99.7%	41.2	25	37.5	2	0	0	1143.63	69	78
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	10	13	31	0.03%	60.0%	MNVLADALK	99.7%	68.7	25	55.6	7	0	0	974.53	4	12
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	10	13	31	0.03%	60.0%	QVLIRPCSK	99.1%	35.2	25	23	2	0	0	1100.62	24	32
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	10	13	31	0.03%	60.0%	VRMNVLADALK	97.6%	24.3	25	13.8	0	2	0	1245.70	2	12
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	10	13	31	0.03%	60.0%	WQNNLLPSR	99.7%	43.7	25	37.2	2	0	0	1127.60	89	97
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	18	73	0.07%	60.3%	ALVAYYQK	99.7%	48.7	25	43.7	7	0	0	955.52	91	98
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	18	73	0.07%	60.3%	EIKDILIQYDR	99.7%	71.7	25	63	7	8	0	1405.77	107	117
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	18	73	0.07%	60.3%	FAGVDIRVR	99.7%	53	25	32.5	2	0	0	1032.59	63	71
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	18	73	0.07%	60.3%	GGGHVAQIYAIR	99.7%	48.8	25	38.7	4	1	0	1241.68	74	85
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	18	73	0.07%	60.3%	GPLQSVQVFGR	99.7%	80.9	25	62.8	4	0	0	1187.65	5	15
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	18	73	0.07%	60.3%	GPLQSVQVFGRK	99.5%	38.1	25	36.6	2	0	0	1315.75	5	16
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	18	73	0.07%	60.3%	LLEPVLLLGK	99.7%	45.6	25	45.6	8	0	0	1094.72	51	60
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	18	73	0.07%	60.3%	LLEPVLLLGKER	99.7%	74.3	25	74.3	4	0	0	1379.86	51	62
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	18	73	0.07%	60.3%	PSKGPLQSVQVFGR	99.7%	78	25	78	4	4	0	1499.83	2	15
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	18	73	0.07%	60.3%	TLLVADPR	99.6%	39.2	25	19	3	0	0	884.52	118	125
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	18	73	0.07%	60.3%	TLLVADPRR	99.7%	50.3	25	39.5	4	0	0	1040.62	118	126
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	18	73	0.07%	60.3%	VNGRPLEMIEPR	99.7%	44.5	25	44.5	4	7	0	1410.75	34	45
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	9	12	26	0.03%	47.4%	IAGYVTHLMK	99.7%	50.8	25	40.6	7	0	0	1132.62	50	59
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	9	12	26	0.03%	47.4%	IAGYVTHLMKR	98.8%	27	25	24.7	0	1	0	1304.71	50	60
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	9	12	26	0.03%	47.4%	LGNDFHTNK	99.7%	41.5	25	34.2	2	0	0	1045.51	24	32
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	9	12	26	0.03%	47.4%	LGNDFHTNKR	99.7%	42.7	25	30.9	2	2	0	1201.61	24	33
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	9	12	26	0.03%	47.4%	LLDFGSLSNLQVTQPTVGMNFK	99.7%	52.5	25	52.5	2	2	0	2425.24	108	129
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	9	12	26	0.03%	47.4%	RVCEEIAIIPSK	99.7%	49.6	25	38.1	1	0	0	1414.77	33	44
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	9	12	26	0.03%	47.4%	VCEEIAIIPSK	99.7%	62.6	25	32.5	2	0	0	1258.67	34	44
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	9	12	26	0.03%	47.4%	VCEEIAIIPSKK	99.7%	64.6	25	52	3	0	0	1386.77	34	45
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	9	12	26	0.03%	47.4%	VIIEKYYTR	99.7%	62.8	25	55	2	0	0	1184.67	15	23

40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	20	23	71	0.07%	69.1%	ADIDLTKR	99.7%	60	25	41.6	2	0	0	931.52	48	55
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	20	23	71	0.07%	69.1%	AGELTEDEVER	99.7%	79.3	25	75.3	4	0	0	1247.58	56	66
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	20	23	71	0.07%	69.1%	DGKYSQVLANGLDNK	99.7%	47.9	25	46.4	1	0	0	1621.82	92	106
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	20	23	71	0.07%	69.1%	FQHILR	95.4%	28.2	25	9.26	1	0	0	813.47	9	14
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	20	23	71	0.07%	69.1%	HFWGLR	94.9%	27.8	25	19.8	1	0	0	815.43	125	130
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	20	23	71	0.07%	69.1%	IAFAITAIK	99.7%	73.1	25	61.5	4	0	0	947.59	26	34
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	20	23	71	0.07%	69.1%	IAFAITAIKGVGR	99.5%	38.7	25	38.7	1	0	0	1316.81	26	38
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	20	23	71	0.07%	69.1%	IPDWFLNR	99.7%	46.1	25	32.3	11	0	0	1060.56	79	86
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	20	23	71	0.07%	69.1%	KADIDLTK	99.7%	41.6	25	28	5	0	0	903.51	47	54
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	20	23	71	0.07%	69.1%	KIAFAITAIK	99.7%	42.3	25	42.3	2	0	0	1075.69	25	34
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	20	23	71	0.07%	69.1%	LREDLER	96.2%	29	25	5.18	1	0	0	930.50	107	113
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	20	23	71	0.07%	69.1%	QYKIPDWFLNR	95.5%	22.2	25	19.5	0	1	0	1479.77	76	86
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	20	23	71	0.07%	69.1%	RAGELTEDEVER	99.7%	58	25	50.1	4	2	0	1403.68	55	66
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	20	23	71	0.07%	69.1%	RYAHVVLR	97.2%	30.3	25	20	1	0	0	1013.60	39	46
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	20	23	71	0.07%	69.1%	VITIMQNPR	99.7%	54.4	25	45.8	13	0	0	1087.59	67	75
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	20	23	71	0.07%	69.1%	VLNTNIDGR	99.7%	63.9	25	52.5	10	0	0	1001.54	15	23
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	20	23	71	0.07%	69.1%	YAHVVLR	96.9%	29.8	25	20.5	1	0	0	857.50	40	46
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	20	23	71	0.07%	69.1%	YAHVVLRK	94.5%	27.5	25	24.2	1	0	0	985.59	40	47
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	20	23	71	0.07%	69.1%	YSQVLANGLDNK	99.7%	89.1	25	82	2	0	0	1321.67	95	106
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	20	23	71	0.07%	69.1%	YSQVLANGLDNKLR	99.7%	56	25	50.2	2	1	0	1590.86	95	108
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	19	0.02%	55.9%	ALAAFLKK	98.9%	34.6	25	28.8	1	0	0	861.56	17	24
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	19	0.02%	55.9%	DLDRIAGQVAAANK	99.7%	47.2	25	47.2	2	1	0	1441.78	130	143
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	19	0.02%	55.9%	DVNQQEFVR	99.7%	61	25	46.7	3	0	0	1134.55	8	16
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	19	0.02%	55.9%	ELAPYDENWFYTR	99.7%	65.5	25	65.5	2	0	0	1703.77	44	56
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	19	0.02%	55.9%	GGAGVGSMTK	95.0%	27.9	25	24.5	1	0	0	864.42	68	77
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	19	0.02%	55.9%	IAGQVAAANK	99.7%	53.3	25	43.9	2	0	0	942.54	134	143
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	19	0.02%	55.9%	LKVPEWVDTVK	98.5%	33	25	22.3	1	0	0	1313.75	28	38
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	19	0.02%	55.9%	PGVTVKDVNQQEFVR	99.7%	61.9	25	61.9	2	0	0	1715.91	2	16
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	19	0.02%	55.9%	RVLQALEGLK	99.1%	35.4	25	18.6	2	0	0	1126.69	102	111
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	19	0.02%	55.9%	VLQALEGLK	99.7%	52	25	37.5	2	0	0	970.59	103	111
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	14	22	85	0.09%	45.7%	AEDKEWMPVTK	99.7%	61.6	25	43	6	3	0	1333.65	55	65
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	14	22	85	0.09%	45.7%	AFVAIGDYNGHVGLGVK	99.7%	84.7	25	78.3	7	1	0	1716.91	126	142
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	14	22	85	0.09%	45.7%	ATFDAISK	99.7%	46.2	25	27.5	4	0	0	852.45	239	246
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	14	22	85	0.09%	45.7%	GCTATLGNFAK	99.7%	64.1	25	53.9	3	0	0	1139.55	228	238
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	14	22	85	0.09%	45.7%	GTGIVSAPVPK	99.7%	44.7	25	44.7	6	0	0	1025.60	201	211
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	14	22	85	0.09%	45.7%	GTGIVSAPVPKK	97.4%	30.5	25	22.2	2	0	0	1153.69	201	212
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	14	22	85	0.09%	45.7%	IGKPHTVPCK	98.4%	32.6	25	21.2	1	0	0	1136.62	174	183
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	14	22	85	0.09%	45.7%	KLLMMAGIDDCYTSAR	99.7%	95.9	25	95.9	7	8	0	1844.87	212	227
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	14	22	85	0.09%	45.7%	LLMMAGIDDCYTSAR	99.7%	104	25	101	8	0	0	1716.78	213	227
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	14	22	85	0.09%	45.7%	LSIVPVRR	99.7%	43.6	25	31.5	5	0	0	939.61	160	167
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	14	22	85	0.09%	45.7%	SLEEIYLFSLPIK	99.7%	93.7	25	92.2	4	0	0	1551.87	77	89
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	14	22	85	0.09%	45.7%	SPYQEFTDHLVK	99.7%	63	25	59	8	5	0	1463.72	264	275
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	14	22	85	0.09%	45.7%	TYSYLTPDLWK	99.7%	64.7	25	62.6	5	0	0	1386.69	247	257
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	14	22	85	0.09%	45.7%	TYSYLTPDLWKETVFTK	99.7%	83.8	25	83.8	2	0	0	2092.06	247	263
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	4	7	15	0.02%	28.6%	DTGKTPVEPEVAIHR	99.7%	59.8	25	59.8	2	2	0	1648.87	5	19
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	4	7	15	0.02%	28.6%	LIDLHSPSEIVK	99.7%	46.4	25	36.2	4	1	0	1350.76	88	99
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	4	7	15	0.02%	28.6%	TPVEPEVAIHR	99.7%	68.5	25	62.7	2	2	0	1247.67	9	19
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	4	7	15	0.02%	28.6%	VCADLIR	99.6%	39.1	25	20.3	2	0	0	846.45	35	41
40S ribosomal protein S21	RPS21	RS21_HUMAN	9.1	99.8%	2	2	4	0.00%	22.9%	MGESDDSILR	99.7%	54	25	50.7	2	0	0	1138.50	62	71
40S ribosomal protein S21	RPS21	RS21_HUMAN	9.1	99.8%	2	2	4	0.00%	22.9%	TYAICGAIR	99.7%	44.6	25	39.7	2	0	0	1024.52	52	60
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	5	6	17	0.02%	29.4%	AHLGTALK	96.5%	29.3	25	8.62	1	0	0	810.48	30	37

40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	5	6	17	0.02%	29.4%	ANPFGGASHAK	99.7%	41.7	25	41.7	9	0	0	1056.52	38	48
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	5	6	17	0.02%	29.4%	GHAVGDIPGVR	99.7%	42.1	25	36	1	0	0	1077.58	109	119
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	5	6	17	0.02%	29.4%	KGHAVGDIPGVR	99.7%	39.4	25	23	2	2	0	1205.68	108	119
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	5	6	17	0.02%	29.4%	VANVSLLALYK	99.7%	88.2	25	88.2	2	0	0	1190.71	125	135
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	8	40	0.04%	30.1%	KQMVIDVLHPGK	99.7%	61	25	61	2	3	0	1380.77	21	32
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	8	40	0.04%	30.1%	QMVIDVLHPGK	99.7%	41.8	25	37.7	3	0	0	1236.68	22	32
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	8	40	0.04%	30.1%	TTGFGMIYDSLDYAK	99.7%	80.2	25	80.2	17	0	0	1681.78	69	83
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	8	40	0.04%	30.1%	TTGFGMIYDSLDYAKK	99.1%	35.2	25	35.2	2	0	0	1809.87	69	84
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	8	40	0.04%	30.1%	TTPDVIFVFGFR	99.7%	63.5	25	61.2	13	0	0	1398.74	50	61
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	6	6	30	0.03%	47.2%	AALQELLSK	99.7%	68.5	25	42.3	11	0	0	972.57	86	94
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	6	6	30	0.03%	47.2%	AQVIYTR	99.2%	35.9	25	26.4	2	0	0	850.48	105	111
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	6	6	30	0.03%	47.2%	ATYDKLCK	99.7%	42.7	25	35.8	2	0	0	998.50	53	60
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	6	6	30	0.03%	47.2%	DKLNNLVLFDK	99.7%	63.3	25	58.1	4	0	0	1318.74	42	52
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	6	6	30	0.03%	47.2%	LITPAVVSER	99.7%	65.8	25	55.9	9	0	0	1084.64	67	76
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	6	6	30	0.03%	47.2%	NTKGGDAPAAGEDA	99.7%	46.4	25	46.4	2	0	0	1273.57	112	125
40S ribosomal protein S26	RPS26	RS26_HUMAN	13.0	100.0%	3	4	27	0.03%	31.3%	DISEASVFDAYVLPK	99.7%	61.8	25	61.1	10	0	0	1653.84	52	66
40S ribosomal protein S26	RPS26	RS26_HUMAN	13.0	100.0%	3	4	27	0.03%	31.3%	LHYCVSCAIHSK	99.7%	58.1	25	54.1	2	2	0	1474.69	71	82
40S ribosomal protein S26	RPS26	RS26_HUMAN	13.0	100.0%	3	4	27	0.03%	31.3%	NIVEAAAVR	99.7%	62.4	25	46.8	13	0	0	942.54	43	51
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	4	6	21	0.02%	39.3%	DLLHPSPEEEK	99.7%	44.1	25	30.2	2	1	0	1293.63	6	16
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	4	6	21	0.02%	39.3%	DLLHPSPEEEKR	99.7%	34.8	25	34.8	0	2	0	1449.73	6	17
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	4	6	21	0.02%	39.3%	LTEGCSFR	99.7%	42.3	25	38.3	6	0	0	969.45	73	80
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	4	6	21	0.02%	39.3%	LVQSPNSYFMDVK	99.7%	71.8	25	71.8	10	0	0	1543.75	24	36
40S ribosomal protein S28	RPS28	RS28_HUMAN	7.8	99.8%	2	3	6	0.01%	30.4%	EGDVLTLLESER	99.7%	72.1	25	70.8	2	0	0	1360.70	52	63
40S ribosomal protein S28	RPS28	RS28_HUMAN	7.8	99.8%	2	3	6	0.01%	30.4%	VEFMDDTSR	99.7%	49.1	25	49.1	4	0	0	1115.47	32	40
40S ribosomal protein S29	RPS29	RS29_HUMAN	6.7	99.8%	2	2	3	0.00%	32.1%	GHQQLYWSHPR	99.6%	30.7	25	27.7	0	1	0	1408.69	2	12
40S ribosomal protein S29	RPS29	RS29_HUMAN	6.7	99.8%	2	2	3	0.00%	32.1%	YGLNMCR	99.7%	44.6	25	40	2	0	0	913.40	34	40
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	22	27	120	0.12%	81.1%	ACYGVLR	99.1%	35.3	25	19.2	2	0	0	838.42	118	124
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	22	27	120	0.12%	81.1%	AELNEFLTR	99.7%	60.5	25	44.3	14	0	0	1092.57	19	27
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	22	27	120	0.12%	81.1%	DEILPTTPISEQK	99.7%	73.9	25	56.8	3	0	0	1470.77	215	227
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	22	27	120	0.12%	81.1%	ELAEDGYSGVEVR	99.7%	86.4	25	73.5	13	0	0	1423.67	28	40
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	22	27	120	0.12%	81.1%	ELTAVVQK	99.7%	53.9	25	35	2	0	0	887.52	68	75
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	22	27	120	0.12%	81.1%	ELTAVVQKR	99.7%	59.8	25	45.7	2	0	0	1043.62	68	76
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	22	27	120	0.12%	81.1%	FGFPEGSVELYAEK	99.7%	107	25	98.4	9	0	0	1572.76	77	90
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	22	27	120	0.12%	81.1%	FIMESGAK	99.7%	45.9	25	21.3	4	0	0	898.43	125	132
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	22	27	120	0.12%	81.1%	FVADGIFK	99.7%	49.8	25	46.6	2	0	0	896.49	11	18
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	22	27	120	0.12%	81.1%	FVDGLMIHSGDPVNYYVDTAVR	99.7%	73	25	72.3	0	4	0	2484.19	152	173
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	22	27	120	0.12%	81.1%	GCEVVVSGK	99.7%	54.2	25	52.5	2	0	0	934.47	133	141
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	22	27	120	0.12%	81.1%	GCEVVVSGKLR	99.7%	41.4	25	33.9	1	0	0	1203.65	133	143
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	22	27	120	0.12%	81.1%	GGKPEPPAMPQPVPTA	99.7%	59.4	25	50.5	9	0	0	1573.80	228	243
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	22	27	120	0.12%	81.1%	GLCAIAQAESLR	99.7%	84.7	25	71.6	11	0	0	1288.67	95	106
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	22	27	120	0.12%	81.1%	IMLPWDPTGK	99.7%	43.7	25	29.7	4	0	0	1157.60	188	197
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	22	27	120	0.12%	81.1%	IRELTAVVQK	99.7%	49.2	25	41.8	2	0	0	1156.70	66	75
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	22	27	120	0.12%	81.1%	KFVADGIFK	99.7%	57.3	25	41.5	4	0	0	1024.58	10	18
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	22	27	120	0.12%	81.1%	KPLPDHVSIVEPK	99.7%	49.6	25	38.9	2	1	0	1458.83	202	214
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	22	27	120	0.12%	81.1%	TEIIILATR	99.7%	75.4	25	74.6	24	0	0	1029.63	46	54
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	22	27	120	0.12%	81.1%	TQNVLGEK	99.6%	39.5	25	25.2	2	0	0	888.48	55	62
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	22	27	120	0.12%	81.1%	VKIMLPWDPTGK	97.4%	30.6	25	26	1	0	0	1400.76	186	197
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	22	27	120	0.12%	81.1%	YKLLGGLAVR	99.4%	37.3	25	37.3	2	0	0	1089.68	107	116
40S ribosomal protein S30	FAU	RS30_HUMAN	6.6	100.0%	2	2	4	0.00%	20.3%	FVNVVPTFGKK	99.4%	37.4	25	37.4	3	0	0	1235.71	42	52
40S ribosomal protein S30	FAU	RS30_HUMAN	6.6	100.0%	2	2	4	0.00%	20.3%	RFVNVVPTFGK	96.2%	29	25	27	1	0	0	1263.72	41	51
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	26	42	92	0.09%	72.3%	ACQSIYPLHDVFVR	99.7%	80.3	25	70.9	2	2	0	1704.85	200	213

40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	26	42	92	0.09%	72.3%	ACQSIYPLHDVFVRK	99.7%	37.2	25	37.2	0	2	0	1832.95	200	214
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	26	42	92	0.09%	72.3%	ADGYEPPVQESV	99.7%	55	25	54.8	2	0	0	1290.58	253	264
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	26	42	92	0.09%	72.3%	APAMFNIR	99.7%	48.4	25	36.4	6	0	0	935.48	35	42
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	26	42	92	0.09%	72.3%	ATGDETGAKVER	99.7%	68.5	25	61.5	2	1	0	1233.61	241	252
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	26	42	92	0.09%	72.3%	DWYDVK	99.4%	37.3	25	22.3	1	0	0	825.38	29	34
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	26	42	92	0.09%	72.3%	EVQTNDLKEVVNK	99.7%	72.1	25	63.4	4	1	0	1515.80	175	187
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	26	42	92	0.09%	72.3%	FELGKLMELHGEGSSSGK	99.7%	35.5	25	33.8	0	2	0	1921.93	223	240
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	26	42	92	0.09%	72.3%	FKLITEDVQGK	99.7%	56.8	25	30.4	2	1	0	1277.71	84	94
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	26	42	92	0.09%	72.3%	IASDGLKGR	99.7%	46	25	34.3	1	0	0	916.52	57	65
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	26	42	92	0.09%	72.3%	KMMEIMTR	99.7%	64.9	25	17.5	3	0	0	1055.50	167	174
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	26	42	92	0.09%	72.3%	KTSYAQHQQVR	99.7%	49.5	25	42.1	2	1	0	1345.70	152	162
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	26	42	92	0.09%	72.3%	LFCVGFTK	99.7%	51.1	25	37.7	6	0	0	971.50	137	144
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	26	42	92	0.09%	72.3%	LFCVGFTKK	99.7%	40.3	25	30.5	2	0	0	1099.60	137	145
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	26	42	92	0.09%	72.3%	LIPDSIGKDIEK	99.7%	52.5	25	43.4	3	0	0	1327.75	188	199
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	26	42	92	0.09%	72.3%	LITEDVQGK	99.7%	56.5	25	42.6	4	0	0	1002.55	86	94
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	26	42	92	0.09%	72.3%	LITEDVQGKNCLTNFHGMDLTR	99.6%	31.6	25	31	0	1	0	2578.24	86	107
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	26	42	92	0.09%	72.3%	LMELHGEGSSSGK	99.7%	83.3	25	75.7	4	4	0	1347.62	228	240
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	26	42	92	0.09%	72.3%	MMEIMTR	99.7%	43.3	25	35.2	4	0	0	911.41	168	174
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	26	42	92	0.09%	72.3%	NCLTNFHGMDLTR	99.7%	82.9	25	74.5	4	4	0	1578.72	95	107
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	26	42	92	0.09%	72.3%	TSYAQHQQVR	99.7%	76.8	25	68.4	2	1	0	1217.60	153	162
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	26	42	92	0.09%	72.3%	TTDGYLLR	99.7%	65.2	25	48.5	8	0	0	938.49	129	136
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	26	42	92	0.09%	72.3%	VERADGYEPPVQESV	99.7%	76.6	25	76.6	2	0	0	1674.80	250	264
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	26	42	92	0.09%	72.3%	VFEVSLADLQNDEVAFR	99.7%	77.6	25	77.6	2	0	0	1951.98	66	82
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	26	42	92	0.09%	72.3%	VFEVSLADLQNDEVAFRK	99.7%	115	25	113	2	2	0	2080.07	66	83
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	26	42	92	0.09%	72.3%	VVDPFSKK	99.6%	39.7	25	21.9	2	0	0	919.52	21	28
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	93	0.09%	60.8%	DANGNSFATR	99.7%	73.5	25	64.6	4	0	0	1052.48	212	221
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	93	0.09%	60.8%	ECLPLIIFLR	99.7%	67	25	60.4	4	0	0	1273.73	40	49
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	93	0.09%	60.8%	ERHPGSFDVVHVK	99.7%	39.2	25	39.2	0	2	0	1506.78	199	211
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	93	0.09%	60.8%	FDTGNLCMVTGGANLGR	99.7%	121	25	118	10	2	0	1782.83	175	191
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	93	0.09%	60.8%	GIPHLVTHDAR	99.7%	51.5	25	44.9	2	3	0	1215.66	135	145
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	93	0.09%	60.8%	GNKPWISLPR	99.5%	38.7	25	33.8	5	0	0	1167.66	231	240
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	93	0.09%	60.8%	HPGSFDVVHVK	99.7%	55.8	25	55.5	2	2	0	1221.64	201	211
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	93	0.09%	60.8%	HWMLDK	96.8%	29.7	25	15.6	1	0	0	829.40	17	22
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	93	0.09%	60.8%	LRECLPLIIFLR	99.7%	48.9	25	48.9	2	2	0	1542.92	38	49
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	93	0.09%	60.8%	LSNIFVIGK	99.7%	72.4	25	64.9	17	0	0	990.60	222	230
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	93	0.09%	60.8%	LTGVFAPRPSTGPHK	99.7%	42.4	25	32.4	2	0	0	1564.86	23	37
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	93	0.09%	60.8%	LTIAEER	99.3%	36.6	25	11.3	6	0	0	831.46	246	252
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	93	0.09%	60.8%	TDITYPAGFMDVISIDK	99.7%	87.3	25	87.3	7	0	0	1901.92	78	94
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	93	0.09%	60.8%	TIRYPDPLIK	99.7%	34.4	25	20.6	0	2	0	1215.71	146	155
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	93	0.09%	60.8%	VNDTIQIDLETGK	99.7%	97.6	25	94.4	7	0	0	1445.75	156	168
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	93	0.09%	60.8%	YALTGDEVK	99.7%	51.3	25	43	6	0	0	995.50	54	62
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	93	0.09%	60.8%	YALTGDEVKK	99.7%	58.1	25	44.2	4	0	0	1123.60	54	63
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	93	0.09%	60.8%	YPDPLIK	95.4%	28.2	25	5.43	1	0	0	845.48	149	155
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	7	8	18	0.02%	31.4%	AQCPIVER	94.8%	27.7	25	20.9	1	0	0	972.49	64	71
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	7	8	18	0.02%	31.4%	KAQCPIVER	99.7%	43.2	25	41.7	2	0	0	1100.59	63	71
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	7	8	18	0.02%	31.4%	LTNSMMMHGR	99.7%	59.8	25	52.2	5	0	0	1177.53	72	81
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	7	8	18	0.02%	31.4%	QAVDVSPLR	99.7%	66.2	25	57.2	3	0	0	984.55	137	145
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	7	8	18	0.02%	31.4%	TIAECLADELINAAK	99.7%	110	25	106	2	0	0	1631.83	168	182
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	7	8	18	0.02%	31.4%	VNQAIWLLCTGAR	99.7%	90.3	25	84.2	4	0	0	1501.79	147	159
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	7	8	18	0.02%	31.4%	YLPHSAGR	95.9%	28.7	25	25.1	1	0	0	900.47	48	55
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	13	19	55	0.06%	46.2%	DIPGLTDTTVPR	99.7%	65	25	55.2	10	0	0	1284.68	120	131

40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	13	19	55	0.06%	46.2%	EDDVRQYVVR	98.0%	31.8	25	22	1	0	0	1278.64	150	159
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	13	19	55	0.06%	46.2%	GCIVDANLSVLNLVIVK	99.7%	130	25	120	6	0	0	1827.04	99	115
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	13	19	55	0.06%	46.2%	GEKDIPGLTDTTVPR	99.7%	36.5	25	35.5	0	2	0	1598.84	117	131
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	13	19	55	0.06%	46.2%	ISGGNDKQGFPMK	99.7%	66.2	25	53.6	3	0	0	1378.68	52	64
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	13	19	55	0.06%	46.2%	KLFNLSK	99.5%	38.2	25	25	2	0	0	849.52	143	149
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	13	19	55	0.06%	46.2%	LFNLSKEDDVR	99.7%	62.5	25	48.8	2	2	0	1335.69	144	154
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	13	19	55	0.06%	46.2%	LIEVDDER	99.7%	57.8	25	49.6	7	0	0	988.49	15	22
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	13	19	55	0.06%	46.2%	LIEVDDERK	99.7%	47.6	25	35.7	2	0	0	1116.59	15	23
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	13	19	55	0.06%	46.2%	MATEVAADALGEEWK	99.7%	121	25	121	6	0	0	1636.75	32	46
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	13	19	55	0.06%	46.2%	MATEVAADALGEEWKGYVVR	99.7%	93.7	25	93.7	4	2	0	2195.08	32	51
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	13	19	55	0.06%	46.2%	MKLNISFPATGCQK	99.7%	78	25	63	2	2	0	1610.80	1	14
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	13	19	55	0.06%	46.2%	NKEEAAEYAK	98.1%	32	25	22.4	2	0	0	1152.55	202	211
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	10	11	22	0.02%	36.6%	AIIIFVPVPQLK	99.7%	84.1	25	84.1	4	0	0	1337.86	59	70
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	10	11	22	0.02%	36.6%	AQQNNVEHKVETFSGVYK	99.7%	73.3	25	73.3	2	2	0	2078.03	161	178
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	10	11	22	0.02%	36.6%	DVNFEFPEFQL	99.7%	68.4	25	67.1	2	0	0	1384.64	184	194
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	10	11	22	0.02%	36.6%	EIEVGGGR	99.6%	39.2	25	35.4	2	0	0	816.42	50	57
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	10	11	22	0.02%	36.6%	ELNITAAK	99.7%	44.1	25	31.2	1	0	0	859.49	42	49
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	10	11	22	0.02%	36.6%	HVVFIAQR	96.0%	28.8	25	28.8	1	0	0	969.56	91	98
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	10	11	22	0.02%	36.6%	KAIIIFVPVPQLK	99.7%	68.3	25	68.3	2	0	0	1465.95	58	70
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	10	11	22	0.02%	36.6%	LTGKDVNFEFPEFQL	99.7%	50.9	25	50.9	2	0	0	1783.89	180	194
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	10	11	22	0.02%	36.6%	VETFSGVYK	99.7%	43.3	25	20.5	2	0	0	1029.53	170	178
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	10	11	22	0.02%	36.6%	VETFSGVYKK	99.7%	42	25	36.2	2	0	0	1157.62	170	179
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	12	15	58	0.06%	58.7%	ADGYVLEGK	99.7%	71.7	25	56.3	2	0	0	951.48	185	193
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	12	15	58	0.06%	58.7%	ELEFYLR	99.7%	44.4	25	34.2	2	0	0	969.50	194	200
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	12	15	58	0.06%	58.7%	ELEFYLRK	96.9%	29.8	25	17.3	1	0	0	1097.60	194	201
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	12	15	58	0.06%	58.7%	IIDVVYNASNNELVR	99.7%	118	25	115	11	2	0	1718.91	78	92
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	12	15	58	0.06%	58.7%	ISSLLEEQFQQGK	99.7%	80.2	25	62.8	13	0	0	1506.78	158	170
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	12	15	58	0.06%	58.7%	KYELGRPAANTK	99.7%	54.3	25	46.7	2	0	0	1347.74	26	37
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	12	15	58	0.06%	58.7%	LDVGNFSWGSECCTR	99.7%	102	25	102	2	0	0	1787.75	60	74
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	12	15	58	0.06%	58.7%	LLACIASRPGQCGR	99.7%	39.7	25	36.7	1	2	0	1558.79	171	184
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	12	15	58	0.06%	58.7%	LTPEEEEILNK	99.7%	69	25	59.1	7	0	0	1314.68	129	139
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	12	15	58	0.06%	58.7%	NCIVLIDSTPYR	99.7%	94.1	25	81.4	7	0	0	1450.74	99	110
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	12	15	58	0.06%	58.7%	QWYESHYALPLGR	99.7%	47.7	25	44.5	2	2	0	1619.80	111	123
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	12	15	58	0.06%	58.7%	YELGRPAANTK	99.7%	50.4	25	44	2	0	0	1219.64	27	37
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	21	68	0.07%	54.6%	ELLTLDEKDPR	99.7%	40.3	25	33.9	1	0	0	1328.71	59	69
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	21	68	0.07%	54.6%	HIDFSLR	99.6%	39.9	25	18.2	2	0	0	887.47	156	162
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	21	68	0.07%	54.6%	IEDFLER	99.7%	58	25	49.8	2	0	0	921.47	102	108
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	21	68	0.07%	54.6%	IEDFLERR	97.9%	31.6	25	17.4	1	0	0	1077.57	102	109
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	21	68	0.07%	54.6%	IGVLDEGK	99.7%	45.5	25	23	8	0	0	830.46	84	91
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	21	68	0.07%	54.6%	IGVLDEGKMK	99.7%	49.2	25	41.3	3	0	0	1089.60	84	93
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	21	68	0.07%	54.6%	KQVVNIPSFIVR	99.7%	54.1	25	54.1	2	2	0	1399.84	139	150
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	21	68	0.07%	54.6%	LDYILGLK	99.7%	54.9	25	45.8	2	0	0	934.56	94	101
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	21	68	0.07%	54.6%	LFEGNALLR	99.7%	66	25	44	17	0	0	1032.58	71	79
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	21	68	0.07%	54.6%	LIGEYGLR	99.7%	59.1	25	37.8	2	0	0	920.52	31	38
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	21	68	0.07%	54.6%	LQTQVFK	99.7%	40.7	25	25.8	2	0	0	863.50	110	116
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	21	68	0.07%	54.6%	MKLDYILGLK	99.7%	55.6	25	38.2	4	0	0	1193.70	92	101
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	21	68	0.07%	54.6%	QVVNIPSFIVR	99.7%	63.7	25	48.8	9	0	0	1271.75	140	150
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	21	68	0.07%	54.6%	RLFEGNALLR	99.7%	54.3	25	32	2	0	0	1188.68	70	79
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	21	68	0.07%	54.6%	RLQTQVFK	97.2%	30.3	25	22.5	1	0	0	1019.60	109	116
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	21	68	0.07%	54.6%	SPYGGGRPGR	99.3%	36.4	25	20.5	4	0	0	1003.51	163	172
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	21	68	0.07%	54.6%	SRLDQELK	99.3%	36.8	25	13.2	2	0	0	988.54	23	30

40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	21	68	0.07%	54.6%	VKFTLAK	97.5%	30.9	25	25.8	2	0	0	806.51	46	52
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	8	8	22	0.02%	25.8%	AIVAIENPADVSVISSR	99.7%	102	25	102	2	0	0	1740.95	64	80
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	8	8	22	0.02%	25.8%	FAAATGATPIAGR	99.7%	101	25	90.6	7	0	0	1203.65	90	102
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	8	8	22	0.02%	25.8%	FTPGTFTNQIQAAFR	99.7%	74	25	64.4	2	0	0	1698.86	103	117
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	8	8	22	0.02%	25.8%	KSDGIYIINLK	99.7%	59	25	31.9	2	0	0	1263.73	42	52
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	8	8	22	0.02%	25.8%	LLVVTDPR	99.7%	55.4	25	46.1	2	0	0	912.55	121	128
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	8	8	22	0.02%	25.8%	SDGIYIINLK	99.7%	63.2	25	45.1	3	0	0	1135.64	43	52
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	8	8	22	0.02%	25.8%	SDGIYIINLKR	98.7%	33.6	25	31.9	2	0	0	1291.74	43	53
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	8	8	22	0.02%	25.8%	YVDIAIPCNNK	99.7%	53.5	25	51	2	0	0	1306.65	156	166
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	19	0.02%	15.1%	EDFDSLLQSAK	99.7%	42.8	25	41.1	1	0	0	1252.61	288	298
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	19	0.02%	15.1%	GENSWFSTQVDTVATK	99.7%	91.8	25	88.7	2	0	0	1769.83	314	329
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	19	0.02%	15.1%	GLVLGPIHK	99.6%	39	25	32.3	1	0	0	933.59	258	266
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	19	0.02%	15.1%	GQSEDPGSLLSLFR	99.7%	76.3	25	72.7	5	0	0	1505.76	511	524
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	19	0.02%	15.1%	GRLDYLSSLK	97.0%	30	25	14.9	1	0	0	1151.64	246	255
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	19	0.02%	15.1%	LLTSFLPAQLLR	99.7%	64.6	25	64.1	2	0	0	1371.84	440	451
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	19	0.02%	15.1%	VAEDEAEAAAAAK	99.7%	78	25	72.2	2	0	0	1245.60	148	160
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	19	0.02%	15.1%	VILDLTPNYR	99.7%	60.9	25	57.7	5	0	0	1203.67	304	313
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	5	5	9	0.01%	6.7%	AALEEVYPDLTPEETRR	97.5%	24.2	25	24.2	0	1	0	1988.99	660	676
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	5	5	9	0.01%	6.7%	ELTMASLPFTFDVER	99.7%	46.3	25	46.3	1	0	0	1755.86	316	330
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	5	5	9	0.01%	6.7%	LFSIVRPR	99.3%	36.5	25	29.6	1	0	0	987.61	88	95
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	5	5	9	0.01%	6.7%	NSLGGDVLFVGK	99.7%	74	25	66	2	0	0	1205.65	677	688
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	5	5	9	0.01%	6.7%	NSPGSQVASNPR	99.7%	72.6	25	71.4	4	0	0	1213.59	447	458
5'-AMP-activated protein kinase catalytic subunit alpha-1	PRKAA1	AAPK1_HUMAN	64.0	100.0%	3	3	5	0.01%	8.2%	MSLQLYQVDSR	99.7%	58.1	25	41	2	0	0	1339.67	458	468
5'-AMP-activated protein kinase catalytic subunit alpha-1	PRKAA1	AAPK1_HUMAN	64.0	100.0%	3	3	5	0.01%	8.2%	TSCGSPNYAAPEVISGR	99.7%	67.9	25	67.9	2	0	0	1765.82	183	199
5'-AMP-activated protein kinase catalytic subunit alpha-1	PRKAA1	AAPK1_HUMAN	64.0	100.0%	3	3	5	0.01%	8.2%	VPFLVAETPR	99.7%	63.4	25	59.2	2	0	0	1128.64	375	384
5'-AMP-activated protein kinase catalytic subunit alpha-1	PRKAA1	AAPK1_HUMAN	64.0	100.0%	3	3	5	0.01%	8.2%	VVNPYYLR	99.7%	43	25	27.9	1	0	0	1023.56	437	444
5'-AMP-activated protein kinase catalytic subunit alpha-2	PRKAA2	AAPK2_HUMAN	62.3	100.0%	3	3	6	0.01%	6.3%	MPPLIADSPK	99.7%	44.2	25	27.3	2	0	0	1084.57	370	379
5'-AMP-activated protein kinase catalytic subunit alpha-2	PRKAA2	AAPK2_HUMAN	62.3	100.0%	3	3	6	0.01%	6.3%	TSCGSPNYAAPEVISGR	99.7%	67.9	25	67.9	2	0	0	1765.82	172	188
5'-AMP-activated protein kinase catalytic subunit alpha-2	PRKAA2	AAPK2_HUMAN	62.3	100.0%	3	3	6	0.01%	6.3%	VVNAYHLR	99.7%	48.4	25	40.7	2	0	0	971.54	432	439
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	4	4	8	0.01%	11.8%	AFFALVTNGVR	99.7%	78.8	25	70.5	2	0	0	1194.66	60	70
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	4	4	8	0.01%	11.8%	FDVINLAAEK	99.7%	63.4	25	52	2	0	0	1119.60	244	253
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	4	4	8	0.01%	11.8%	LVEAEVHR	99.7%	46	25	46	2	0	0	952.52	292	299
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	4	4	8	0.01%	11.8%	VSALPVVDEK	99.3%	36.4	25	30.9	2	0	0	1056.59	225	234
5-methylcytosine rRNA methyltransferase NSUN4	NSUN4	NSUN4_HUMAN	43.1	100.0%	3	3	5	0.01%	8.6%	NLAANDLSPSR	99.7%	49.5	25	41.5	2	0	0	1157.59	199	209
5-methylcytosine rRNA methyltransferase NSUN4	NSUN4	NSUN4_HUMAN	43.1	100.0%	3	3	5	0.01%	8.6%	TLALLQTGCCR	99.7%	58.6	25	50.5	2	0	0	1292.65	188	198
5-methylcytosine rRNA methyltransferase NSUN4	NSUN4	NSUN4_HUMAN	43.1	100.0%	3	3	5	0.01%	8.6%	VLVDVPCTTDR	99.1%	35.4	25	32	1	0	0	1274.64	252	262
5'-nucleotidase domain-containing protein 2	NT5DC2	NT5D2_HUMAN	60.7	100.0%	3	3	5	0.01%	6.5%	MQTYQDAESR	99.7%	45.2	25	45.2	2	0	0	1228.53	411	420
5'-nucleotidase domain-containing protein 2	NT5DC2	NT5D2_HUMAN	60.7	100.0%	3	3	5	0.01%	6.5%	QGNLFDFLR	99.7%	55.8	25	43.2	2	0	0	1109.57	336	344
5'-nucleotidase domain-containing protein 2	NT5DC2	NT5D2_HUMAN	60.7	100.0%	3	3	5	0.01%	6.5%	QLFLITNSPFSFVDK	99.7%	44.8	25	44.8	1	0	0	1755.93	263	277
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	18	24	48	0.05%	33.5%	AAVEEGIVLGGGCALLR	99.7%	129	25	120	2	2	0	1684.91	430	446
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	18	24	48	0.05%	33.5%	CEFQDAYVLLSEK	99.7%	83	25	72.3	2	0	0	1601.75	237	249
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	18	24	48	0.05%	33.5%	CIPALDSLTPANEDQK	99.7%	84.9	25	83.9	2	0	0	1771.85	447	462
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	18	24	48	0.05%	33.5%	GANPVEIR	99.7%	50.2	25	15.5	2	0	0	855.47	134	141
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	18	24	48	0.05%	33.5%	GANPVEIRR	98.6%	33.4	25	22.6	1	0	0	1011.57	134	142
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	18	24	48	0.05%	33.5%	GYISPYFINTSK	99.7%	87.3	25	82.8	2	0	0	1389.70	222	233
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	18	24	48	0.05%	33.5%	IGIEIIKR	99.7%	59.2	25	28.8	2	0	0	941.61	463	470
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	18	24	48	0.05%	33.5%	LSDGVAVLK	99.7%	81.1	25	64.4	1	0	0	901.54	397	405
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	18	24	48	0.05%	33.5%	LVQDVANNTNEEAGDGTTTATVLAR	99.7%	170	25	170	2	2	0	2560.25	97	121
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	18	24	48	0.05%	33.5%	NAGVEGSLIVEK	99.7%	88.2	25	72.1	2	0	0	1215.66	482	493
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	18	24	48	0.05%	33.5%	TLNDELEIIEGMK	99.7%	84.2	25	79.3	2	0	0	1504.76	206	218
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	18	24	48	0.05%	33.5%	TVIIEQSWGSPK	99.7%	73.2	25	67.7	2	0	0	1344.72	61	72

60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	18	24	48	0.05%	33.5%	VGEVIVTK	99.7%	64.2	25	46.4	2	0	0	844.51	345	352
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	18	24	48	0.05%	33.5%	VGEVIVTKDDAMLLK	99.7%	62.7	25	61.2	4	4	0	1630.91	345	359
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	18	24	48	0.05%	33.5%	VGGTSDVEVNEK	99.7%	97.2	25	90	4	0	0	1233.60	406	417
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	18	24	48	0.05%	33.5%	VGGTSDVEVNEKK	99.7%	65.9	25	58.5	2	2	0	1361.69	406	418
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	18	24	48	0.05%	33.5%	VGLQVVAVK	99.7%	80.8	25	75.6	2	0	0	912.59	293	301
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	18	24	48	0.05%	33.5%	VTDALNATR	99.7%	78.6	25	63.7	2	0	0	960.51	421	429
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	7	10	20	0.02%	16.0%	AIADWYNEK	99.7%	45.6	25	43.4	2	0	0	1109.53	151	159
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	7	10	20	0.02%	16.0%	ALDAAFYK	99.1%	35.6	25	32.5	2	0	0	898.47	352	359
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	7	10	20	0.02%	16.0%	ALLQEMPLTALLR	99.7%	88.7	25	85.6	5	0	0	1468.86	271	283
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	7	10	20	0.02%	16.0%	FLCFGSEGGTYYIK	99.7%	72.8	25	68.3	2	0	0	1641.76	36	49
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	7	10	20	0.02%	16.0%	GGMALALAVTK	99.7%	80.8	25	71.2	4	0	0	1031.59	160	170
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	7	10	20	0.02%	16.0%	LGLENAEALIR	99.7%	77.5	25	67.7	3	0	0	1198.68	53	63
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	7	10	20	0.02%	16.0%	MTANSVLEPGNSEVSLVCEK	99.7%	59.1	25	52.9	2	0	0	2180.02	288	307
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	11	14	52	0.05%	49.5%	AFLADPSAFVAAAPVAAATTAAPAAAAAPAK	99.7%	103	25	103	2	4	0	2752.47	267	297
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	11	14	52	0.05%	49.5%	AGAIAPCEVTVPAQNTGLGPEK	99.7%	54.9	25	54.8	3	2	0	2180.10	113	134
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	11	14	52	0.05%	49.5%	CFIVGADNVGSK	99.7%	75	25	65.5	2	0	0	1266.61	27	38
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	11	14	52	0.05%	49.5%	DMLLANKVPAAAR	99.7%	43.2	25	34.2	1	0	0	1369.76	100	112
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	11	14	52	0.05%	49.5%	EDLTEIRDMLLANK	99.7%	45	25	44.3	2	0	0	1660.86	93	106
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	11	14	52	0.05%	49.5%	GHLENNPALEK	99.7%	77.5	25	58.2	2	2	0	1221.62	67	77
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	11	14	52	0.05%	49.5%	GNVGFVFTK	99.7%	52.4	25	42.4	6	0	0	968.52	84	92
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	11	14	52	0.05%	49.5%	GTIEILSDVQLIK	99.7%	77.8	25	64.1	6	0	0	1428.83	150	162
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	11	14	52	0.05%	49.5%	IIQLLDDYPK	99.7%	76.5	25	63.3	2	0	0	1217.68	17	26
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	11	14	52	0.05%	49.5%	TSFFQALGITTK	99.7%	93.2	25	93.2	14	0	0	1313.71	135	146
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	11	14	52	0.05%	49.5%	VLALSVETDYTFPLAEK	99.7%	96.6	25	96.6	4	0	0	1896.00	248	264
60S acidic ribosomal protein P2	RPLP2	RLA2_HUMAN	11.7	100.0%	4	4	8	0.01%	69.6%	ILDSVGIEADDDRLNK	99.7%	63.4	25	54.2	2	0	0	1772.90	26	41
60S acidic ribosomal protein P2	RPLP2	RLA2_HUMAN	11.7	100.0%	4	4	8	0.01%	69.6%	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	99.7%	40.6	25	40.6	0	2	0	2774.43	62	94
60S acidic ribosomal protein P2	RPLP2	RLA2_HUMAN	11.7	100.0%	4	4	8	0.01%	69.6%	NIEDVIAQGIGK	99.7%	98.6	25	82.4	2	0	0	1256.68	50	61
60S acidic ribosomal protein P2	RPLP2	RLA2_HUMAN	11.7	100.0%	4	4	8	0.01%	69.6%	YVASYLLAALGGNSSPSAK	99.7%	67.5	25	59.4	2	0	0	1868.98	3	21
60S ribosomal export protein NMD3	NMD3	NMD3_HUMAN	57.6	99.8%	2	2	3	0.00%	4.0%	DNVVCLSPK	97.6%	31	25	29.8	1	0	0	1031.52	252	260
60S ribosomal export protein NMD3	NMD3	NMD3_HUMAN	57.6	99.8%	2	2	3	0.00%	4.0%	SKVDISQGIPK	99.7%	43.8	25	33.1	2	0	0	1171.67	38	48
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	12	21	45	0.05%	52.3%	AKVDEFPLCGHMVSDEYEQLSSEALEAAR	99.7%	125	25	125	0	2	0	3281.51	41	69
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	12	21	45	0.05%	52.3%	EHVIEALR	99.7%	45.6	25	39.5	3	0	0	966.54	146	153
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	12	21	45	0.05%	52.3%	FNADEFEDMVAEK	99.7%	63.2	25	63.2	6	0	0	1544.66	176	188
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	12	21	45	0.05%	52.3%	FNADEFEDMVAEKR	99.7%	64.4	25	58.8	2	3	0	1700.76	176	189
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	12	21	45	0.05%	52.3%	GAFGKPQGTVAR	99.7%	59.8	25	42.3	4	0	0	1188.65	117	128
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	12	21	45	0.05%	52.3%	ICANKYMVK	95.8%	28.6	25	28.6	1	0	0	1142.57	70	78
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	12	21	45	0.05%	52.3%	IFDLGRK	97.8%	31.3	25	0	1	0	0	848.50	33	39
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	12	21	45	0.05%	52.3%	LQNKEHVIEALR	99.7%	45.4	25	45.4	2	2	0	1449.82	142	153
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	12	21	45	0.05%	52.3%	MLSCAGADR	99.7%	62.1	25	47.5	6	0	0	980.43	102	110
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	12	21	45	0.05%	52.3%	RLIPDGCGVK	99.6%	39.2	25	28	2	0	0	1114.60	189	198
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	12	21	45	0.05%	52.3%	VDEFPLCGHMVSDEYEQLSSEALEAAR	99.7%	75.1	25	72.2	0	4	0	3082.38	43	69
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	12	21	45	0.05%	52.3%	VHIGQVIMSIR	99.7%	55.7	25	55.7	4	3	0	1252.72	129	139
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	16	33	0.03%	39.2%	AVDIPHMDIEALK	99.7%	53.5	25	46	4	0	0	1467.75	79	91
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	16	33	0.03%	39.2%	AVDIPHMDIEALKK	99.5%	38.2	25	33.1	3	1	0	1579.85	79	92
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	16	33	0.03%	39.2%	DTLYEAVR	99.7%	59.4	25	36.4	4	0	0	966.49	8	15
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	16	33	0.03%	39.2%	FPSLLTHNENMVAK	99.7%	43	25	43	3	0	0	1600.82	134	147
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	16	33	0.03%	39.2%	FSVCVLGDQQHCDEAK	99.7%	72.4	25	72.4	3	2	0	1892.83	63	78
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	16	33	0.03%	39.2%	ILGPGLNK	99.7%	41.5	25	30.3	3	0	0	811.50	123	130
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	16	33	0.03%	39.2%	KYDAFLASESLIK	99.7%	76	25	76	3	2	0	1484.80	106	118
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	16	33	0.03%	39.2%	VLCLAVAVGHVK	99.7%	81.5	25	81.5	2	2	0	1265.74	162	173
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	16	33	0.03%	39.2%	YDAFLASESLIK	98.4%	32.7	25	31	1	0	0	1356.70	107	118

60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	11	36	0.04%	39.3%	AEEILEK	97.9%	31.5	25	12.4	2	0	0	831.45	79	85
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	11	36	0.04%	39.3%	AEEILEKGLK	99.0%	34.8	25	25.4	1	0	0	1129.65	79	88
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	11	36	0.04%	39.3%	IAVHCTVR	99.7%	52.3	25	39.7	2	0	0	955.51	68	75
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	11	36	0.04%	39.3%	ISKEEAMR	99.7%	59.4	25	29.4	4	0	0	963.49	157	164
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	11	36	0.04%	39.3%	KLCLNICVGESGDR	99.7%	44.9	25	44.9	1	0	0	1620.78	19	32
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	11	36	0.04%	39.3%	LCLNICVGESGDR	99.7%	77.1	25	74.6	2	0	0	1492.69	20	32
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	11	36	0.04%	39.3%	VLEQLTGQTPVFSK	99.7%	96.9	25	91.4	13	0	0	1546.85	39	52
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	11	36	0.04%	39.3%	VLEQLTGQTPVFSKAR	99.2%	35.7	25	35.7	1	0	0	1773.99	39	54
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	11	36	0.04%	39.3%	WFQQKYDGIILPGK	98.5%	26.1	25	26.1	0	2	0	1692.91	165	178
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	11	36	0.04%	39.3%	YDGIILPGK	99.7%	57.1	25	54.6	8	0	0	975.55	170	178
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	5	7	26	0.03%	43.0%	CTGGEVGATSALAPK	99.7%	105	25	89.7	4	0	0	1418.69	17	31
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	5	7	26	0.03%	43.0%	EILGTAQSVGCNVDGR	99.7%	110	25	110	2	0	0	1675.81	131	146
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	5	7	26	0.03%	43.0%	HSGNITFDEIVNIAR	99.7%	94.4	25	88.8	4	4	0	1685.86	100	114
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	5	7	26	0.03%	43.0%	IGPLGLSPK	99.7%	57.1	25	41.1	6	0	0	881.55	32	40
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	5	7	26	0.03%	43.0%	QAQIEVVPSASALIIK	99.7%	106	25	106	4	2	0	1666.97	68	83
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	91	0.09%	34.1%	GFSLEELR	99.7%	51.6	25	39.3	19	0	0	950.49	75	82
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	91	0.09%	34.1%	LATQLTGPVMPVR	99.7%	77.5	25	76.4	11	0	0	1382.78	146	158
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	91	0.09%	34.1%	NKSTESLQANVQR	99.7%	59.7	25	58.9	2	0	0	1474.76	104	116
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	91	0.09%	34.1%	RVATWFNQPAR	99.7%	48	25	41.3	2	2	0	1345.71	21	31
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	91	0.09%	34.1%	SKLILFPR	99.7%	48.5	25	48.5	3	0	0	973.62	122	129
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	91	0.09%	34.1%	STESLQANVQR	99.7%	88.4	25	75.5	21	0	0	1232.62	106	116
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	91	0.09%	34.1%	TIGISVDPR	99.7%	55.5	25	44.7	13	0	0	957.54	93	101
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	91	0.09%	34.1%	VATWFNQPAR	99.7%	67.2	25	52.8	9	0	0	1189.61	22	31
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	91	0.09%	34.1%	VITEEEKNFK	99.7%	55	25	47.3	9	0	0	1236.65	168	177
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	6	6	17	0.02%	28.6%	CEGINISGNFYR	99.7%	49.5	25	48.9	3	0	0	1429.65	38	49
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	6	6	17	0.02%	28.6%	IDKYTEVLK	99.7%	44.4	25	32.1	1	0	0	1108.63	189	197
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	6	6	17	0.02%	28.6%	KFAYLGR	99.7%	44	25	32.4	2	0	0	854.49	134	140
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	6	6	17	0.02%	28.6%	MVVPAALK	97.4%	30.9	25.3	26.8	1	0	0	844.50	118	125
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	6	6	17	0.02%	28.6%	VFDGIPPPYDK	97.1%	30.1	25	22.3	2	0	0	1247.63	104	114
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	6	6	17	0.02%	28.6%	YQAVTATLEEK	99.7%	62.3	25	55.6	8	0	0	1252.64	149	159
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	10	86	0.09%	27.9%	ALVDGPCTQVR	99.7%	75.5	25	70.1	3	0	0	1215.62	36	46
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	10	86	0.09%	27.9%	CMQLTDFILK	99.7%	56.8	25	48.2	16	0	0	1268.64	54	63
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	10	86	0.09%	27.9%	LVAIVDVIDQNR	99.7%	99.8	25	99.8	41	1	0	1354.77	24	35
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	10	86	0.09%	27.9%	MTDFDRFK	99.7%	40.5	25	40.5	6	0	0	1059.49	104	111
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	10	86	0.09%	27.9%	RFVEVGR	95.2%	28.1	25	17.8	1	0	0	862.49	5	11
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	10	86	0.09%	27.9%	VAYVSFGPHAGK	99.7%	73.6	25	73.6	16	2	0	1232.64	12	23
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	8	10	26	0.03%	38.7%	FFEVILIDPFHK	99.7%	63.2	25	58.9	2	1	0	1504.82	129	140
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	8	10	26	0.03%	38.7%	GATYGKPVHHGVNQLK	99.7%	78.7	25	68.9	2	2	0	1705.91	78	93
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	8	10	26	0.03%	38.7%	NPDTQWITKPVHK	95.0%	21.8	25	21	0	1	0	1563.83	145	157
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	8	10	26	0.03%	38.7%	NTLQLHR	99.7%	41.5	25	26.1	6	0	0	881.50	196	202
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	8	10	26	0.03%	38.7%	QLSALHR	98.2%	32.1	25	4.67	1	0	0	824.47	32	38
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	8	10	26	0.03%	38.7%	RNPDTQWITKPVHK	99.7%	34.1	25	34.1	0	2	0	1719.93	144	157
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	8	10	26	0.03%	38.7%	SLQSVAEER	99.7%	52.7	25	34.8	7	0	0	1018.52	97	105
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	8	10	26	0.03%	38.7%	VLNSYWVGEDSTYK	99.7%	66.1	25	61.7	2	0	0	1660.79	115	128
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	8	11	40	0.04%	38.0%	EQIVPKPEEEVAQK	99.7%	68.6	25	55.2	4	1	0	1623.86	154	167
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	8	11	40	0.04%	38.0%	EQIVPKPEEEVAQKK	99.7%	40.5	25	39.2	1	2	0	1751.95	154	168
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	8	11	40	0.04%	38.0%	GLDVDSLVIEHIQVNK	99.7%	90.6	25	80.9	4	0	0	1778.96	106	121
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	8	11	40	0.04%	38.0%	QWGWTQGR	99.5%	38.7	25	22.1	4	0	0	1018.49	75	82
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	8	11	40	0.04%	38.0%	SAEFLLHMLK	99.7%	53.4	25	42.3	7	0	0	1204.64	87	96
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	8	11	40	0.04%	38.0%	VRYSLDPENPTK	99.0%	34.8	25	31	2	0	0	1418.73	2	13
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	8	11	40	0.04%	38.0%	YLKDVTLQK	99.7%	48	25	39.3	8	0	0	1107.64	47	55

60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	8	11	40	0.04%	38.0%	YSLDPENPTK	99.7%	63	25	56.8	7	0	0	1163.56	4	13
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	11	55	0.06%	42.6%	GCGTVLLSGPR	99.7%	87.2	25	73.2	9	0	0	1116.58	133	143
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	11	55	0.06%	42.6%	ILTFDQLALDSPK	99.7%	122	25	112	20	0	0	1460.80	120	132
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	11	55	0.06%	42.6%	LKVCALR	99.4%	37.3	25	27.5	2	0	0	859.52	98	104
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	11	55	0.06%	42.6%	RTNSTFNQVVLK	99.7%	53	25	18.4	1	0	0	1406.78	38	49
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	11	55	0.06%	42.6%	SQDIYLR	97.4%	30.7	25	15.3	1	0	0	894.47	20	26
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	11	55	0.06%	42.6%	TAVVVGTITDDVR	99.7%	109	25	102	11	0	0	1345.73	79	91
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	11	55	0.06%	42.6%	TAVVVGTITDDVRVQEVPK	99.7%	53	25	53	2	2	0	2026.12	79	97
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	11	55	0.06%	42.6%	TNRPPLSLSR	95.3%	28.1	25	23.2	1	0	0	1140.65	56	65
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	11	55	0.06%	42.6%	TNSTFNQVVLK	99.7%	75.2	25	52.8	3	0	0	1250.67	39	49
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	11	55	0.06%	42.6%	TNSTFNQVVLKR	99.7%	46.9	25	46.9	3	0	0	1406.78	39	50
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	10	12	45	0.05%	43.2%	AHSIQIMK	99.7%	44.7	25	31.2	5	0	0	927.51	121	128
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	10	12	45	0.05%	43.2%	DLTTAGAVTQCYR	99.7%	66.5	25	65.9	6	0	0	1455.69	99	111
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	10	12	45	0.05%	43.2%	EYRDLTTAGAVTQCYR	99.7%	62.4	25	56.5	3	4	0	1903.90	96	111
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	10	12	45	0.05%	43.2%	FWYFVSQLKK	99.7%	45.4	25	40.1	2	0	0	1345.73	44	53
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	10	12	45	0.05%	43.2%	IFAPNHVVAK	99.7%	47.1	25	39.4	6	0	0	1095.63	32	41
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	10	12	45	0.05%	43.2%	KSSGEIVYCGQVFEK	99.7%	37.6	25	36.3	0	1	0	1730.84	56	70
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	10	12	45	0.05%	43.2%	NFGIWLR	99.7%	40.5	25	25.3	4	0	0	905.50	77	83
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	10	12	45	0.05%	43.2%	SSGEIVYCGQVFEK	99.7%	96.4	25	96.4	8	0	0	1602.75	57	70
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	10	12	45	0.05%	43.2%	VEEIAASK	99.7%	45.5	25	35.1	3	0	0	846.46	129	136
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	10	12	45	0.05%	43.2%	VKNFGIWLR	99.5%	38.7	25	28.8	3	0	0	1132.66	75	83
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	7	8	23	0.02%	23.5%	HMYHSLYLK	98.7%	33.7	25	27.9	2	0	0	1191.60	118	126
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	7	8	23	0.02%	23.5%	ILMEHIHK	99.7%	48.3	25	38.9	4	0	0	1020.57	137	144
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	7	8	23	0.02%	23.5%	KLLADQAEAR	99.7%	65.2	25	59.8	2	0	0	1114.62	153	162
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	7	8	23	0.02%	23.5%	KVWLDPNETNEIANANSR	99.7%	46.5	25	46.5	0	2	0	2071.02	21	38
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	7	8	23	0.02%	23.5%	LLADQAEAR	99.7%	71	25	51.5	7	0	0	986.53	154	162
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	7	8	23	0.02%	23.5%	LLADQAEARR	98.1%	32	25	18.3	3	0	0	1142.63	154	163
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	7	8	23	0.02%	23.5%	VWLDPNETNEIANANSR	99.7%	115	25	115	3	0	0	1942.93	22	38
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	8	11	33	0.03%	43.1%	EKGTWVQLK	99.7%	41.7	25	26.4	2	0	0	1088.61	121	129
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	8	11	33	0.03%	43.1%	GDIVDIKGMGTVQK	99.7%	44.2	25	32.6	3	0	0	1476.77	37	50
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	8	11	33	0.03%	43.1%	GTWVQLK	95.3%	28.1	25	20.9	1	0	0	831.47	123	129
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	8	11	33	0.03%	43.1%	GTWVQLKR	99.7%	49.4	25	33.5	4	0	0	987.57	123	130
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	8	11	33	0.03%	43.1%	HGVVPLATYMR	99.7%	61.7	25	61.7	3	1	0	1243.66	22	32
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	8	11	33	0.03%	43.1%	KGDIVDIK	99.7%	49.9	25	17.1	2	0	0	887.52	36	43
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	8	11	33	0.03%	43.1%	TNGKEPELLEPIPYEFMA	99.7%	49.4	25	49.4	5	0	0	2094.01	143	160
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	8	11	33	0.03%	43.1%	VYNVTQHAVGIVVNK	99.7%	106	25	94.9	8	4	0	1640.91	64	78
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	31	0.03%	36.7%	AGNLGGGVVTIER	99.7%	96.7	25	80.9	6	0	0	1242.68	53	65
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	31	0.03%	36.7%	ITVTSEVPFSK	99.7%	70.7	25	60.5	6	0	0	1207.66	70	80
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	31	0.03%	36.7%	ITVTSEVPFSKR	99.7%	69.8	25	64.7	4	2	0	1363.76	70	81
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	31	0.03%	36.7%	NNLRDWLR	98.3%	32.4	25	9.77	3	0	0	1086.58	94	101
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	31	0.03%	36.7%	SKITVTSEVPFSK	99.7%	75.9	25	72.4	4	0	0	1422.78	68	80
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	31	0.03%	36.7%	VVANSKESYELR	99.7%	68.8	25	61	4	2	0	1394.73	102	113
60S ribosomal protein L22-like 1	RPL22L1	RL22L_HUMAN	14.6	99.8%	2	3	6	0.01%	26.2%	NNLRDWLR	98.3%	32.4	25	9.77	3	0	0	1086.58	88	95
60S ribosomal protein L22-like 1	RPL22L1	RL22L_HUMAN	14.6	99.8%	2	3	6	0.01%	26.2%	TGNLGNVVHIER	99.7%	57.4	25	49.3	2	0	0	1308.70	48	59
60S ribosomal protein L22-like 1	RPL22L1	RL22L_HUMAN	14.6	99.8%	2	3	6	0.01%	26.2%	VVASDKETYELR	99.7%	79.2	25	79.2	2	2	0	1409.73	96	107
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	7	13	62	0.06%	46.4%	ECADLWPR	99.7%	53.1	25	39.7	4	0	0	1046.47	124	131
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	7	13	62	0.06%	46.4%	GSAITGPVAK	99.7%	59.4	25	47.6	9	0	0	900.52	114	123
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	7	13	62	0.06%	46.4%	ISLGLPVGAVINCADNTGAK	99.7%	76.9	25	62	6	1	0	1970.04	16	35
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	7	13	62	0.06%	46.4%	LNRLPAAGVGDMVMATVK	99.7%	59.8	25	59.8	2	7	0	1874.98	49	66
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	7	13	62	0.06%	46.4%	LPAAGVGDMVMATVK	99.7%	89	25	29	21	0	0	1475.76	52	66
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	7	13	62	0.06%	46.4%	LPAAGVGDMVMATVKK	99.7%	64.1	25	62.5	5	3	0	1587.86	52	67

60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	7	13	62	0.06%	46.4%	NLYIISVK	99.0%	34.7	25	30.9	4	0	0	949.57	36	43
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	11	14	63	0.06%	51.3%	EAPAPPKAEAK	99.7%	40.1	25	38.1	4	0	0	1108.60	8	18
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	11	14	63	0.06%	51.3%	FPLTTESAMK	99.7%	40.1	25	36.1	10	0	0	1124.57	79	88
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	11	14	63	0.06%	51.3%	FPLTTESAMKK	99.5%	38.5	25	8.86	2	0	0	1268.66	79	89
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	11	14	63	0.06%	51.3%	IEDNNTLVFIVDVK	99.3%	36.9	25	32.6	2	0	0	1618.87	90	103
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	11	14	63	0.06%	51.3%	KLYDIDVAK	99.7%	52.1	25	48.8	2	0	0	1064.60	115	123
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	11	14	63	0.06%	51.3%	LAPDYDALDVANK	99.7%	77.9	25	75.4	14	0	0	1404.70	140	152
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	11	14	63	0.06%	51.3%	LDHYAIIK	99.7%	56.2	25	30.1	3	0	0	972.55	71	78
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	11	14	63	0.06%	51.3%	LYDIDVAK	99.7%	54.9	25	44.8	5	0	0	936.50	116	123
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	11	14	63	0.06%	51.3%	NKLDHYAIIK	99.7%	48.2	25	17.6	2	2	0	1214.69	69	78
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	11	14	63	0.06%	51.3%	VNTLIRPDGEK	99.7%	55.3	25	46.9	12	0	0	1241.69	124	134
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	11	14	63	0.06%	51.3%	VNTLIRPDGEKK	99.3%	28.9	25	28.9	2	3	0	1369.78	124	135
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	13	80	0.08%	35.7%	AITGASLADIMAK	99.7%	106	25	99.7	35	0	0	1261.68	81	93
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	13	80	0.08%	35.7%	AITGASLADIMAKR	99.7%	57.1	25	57.1	2	0	0	1417.78	81	94
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	13	80	0.08%	35.7%	CESAFLSK	99.7%	46.9	25	37.6	8	0	0	941.44	36	43
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	13	80	0.08%	35.7%	CESAFLSKR	99.7%	54.5	25	38.3	2	0	0	1097.54	36	44
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	13	80	0.08%	35.7%	MKVELCSFSGYK	99.7%	66.2	25	61.2	7	2	0	1448.69	1	12
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	13	80	0.08%	35.7%	QINWTVLYR	99.7%	59	25	46.7	8	0	0	1192.65	48	56
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	13	80	0.08%	35.7%	TDGKVFQFLNAK	97.3%	24	25	19.7	0	2	0	1367.73	24	35
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	13	80	0.08%	35.7%	VELCSFSGYK	99.7%	57.6	25	48	2	0	0	1189.56	3	12
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	13	80	0.08%	35.7%	VFQFLNAK	99.7%	64.3	25	46.2	12	0	0	966.54	28	35
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	13	41	0.04%	46.9%	ANGTTVHVGIHPSK	99.7%	71.4	25	65.1	2	1	0	1417.75	90	103
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	13	41	0.04%	46.9%	DDEVQVVR	99.7%	53.4	25	34.2	7	0	0	959.48	52	59
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	13	41	0.04%	46.9%	FNPFVTSDR	99.7%	44.8	25	37.5	6	0	0	1082.53	3	11
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	13	41	0.04%	46.9%	HFNAPSHIR	96.6%	29.5	25	22.1	1	0	0	1078.55	18	26
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	13	41	0.04%	46.9%	IMSSPLSK	99.4%	37	25	27.7	1	0	0	878.47	29	36
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	13	41	0.04%	46.9%	KDDEVQVVR	99.7%	62.8	25	43.5	7	0	0	1087.57	51	59
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	13	41	0.04%	46.9%	KIMSSPLSK	99.7%	41.6	25	28.9	1	0	0	990.57	28	36
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	13	41	0.04%	46.9%	KYVIYIER	99.7%	49.8	25	45	2	0	0	1083.62	77	84
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	13	41	0.04%	46.9%	MKFNPFVTSDR	99.7%	64.3	25	59.5	7	0	0	1357.66	1	11
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	13	41	0.04%	46.9%	YKEETIEK	99.7%	45.2	25	37	2	0	0	1039.53	135	142
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	13	41	0.04%	46.9%	YVIYIER	99.7%	40.7	25	37	4	0	0	955.52	78	84
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	8	12	39	0.04%	52.2%	NIDDGTSDRPYSHALVAGIDR	99.7%	39	25	39	0	2	0	2272.10	28	48
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	8	12	39	0.04%	52.2%	NKWFFQK	96.8%	29.7	25	7.69	2	0	0	997.53	127	133
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	8	12	39	0.04%	52.2%	TVVNKDVFR	99.2%	36.2	25	30.4	1	0	0	1077.61	94	102
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	8	12	39	0.04%	52.2%	VKFEER	96.2%	29	25	18	1	0	0	807.44	116	121
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	8	12	39	0.04%	52.2%	VVLVLAGR	99.7%	48.4	25	41.3	8	0	0	826.55	10	17
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	8	12	39	0.04%	52.2%	VYNYNHLMPTR	99.7%	53.1	25	49.6	7	5	0	1407.68	74	84
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	8	12	39	0.04%	52.2%	YSVDIPLDK	99.4%	37.6	25	37.2	9	0	0	1049.55	85	93
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	8	12	39	0.04%	52.2%	YSVDIPLDKTVVNK	99.7%	63.7	25	63.5	2	2	0	1590.87	85	98
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	6	8	34	0.03%	38.5%	INFDKYHPGYFGK	99.7%	69.1	25	61.5	2	2	0	1585.78	43	55
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	6	8	34	0.03%	38.5%	LWTLVSEQTR	99.7%	47.8	25	37.9	4	0	0	1232.66	78	87
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	6	8	34	0.03%	38.5%	NKTGAAPIIDVVR	99.7%	58	25	50.1	2	2	0	1353.79	93	105
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	6	8	34	0.03%	38.5%	NQSFCPTVNLDK	99.7%	49.1	25	45	3	0	0	1422.67	66	77
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	6	8	34	0.03%	38.5%	SGYYKVLGK	98.9%	34.5	25	25	1	0	0	1014.56	106	114
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	6	8	34	0.03%	38.5%	TGAAPIIDVVR	99.7%	73.1	25	73.1	18	0	0	1111.65	95	105
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	46	0.05%	41.6%	GVVVVIKR	99.7%	46.8	25	37.1	2	0	0	869.59	59	66
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	46	0.05%	41.6%	KPATSYVR	99.7%	50.1	25	33.4	2	0	0	921.52	72	79
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	46	0.05%	41.6%	KTVGVEPAADGK	99.7%	69.6	25	60.1	6	0	0	1171.63	47	58
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	46	0.05%	41.6%	NCSSFLIK	98.8%	34.2	25	15.3	3	0	0	968.49	12	19
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	46	0.05%	41.6%	NCSSFLIKR	99.7%	61	25	50.9	2	0	0	1124.59	12	20

60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	46	0.05%	41.6%	NKQTYSTEPNNLK	99.7%	68.7	25	62.8	7	2	0	1536.77	21	33
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	46	0.05%	41.6%	QTYSTEPNNLK	99.7%	61	25	52.1	7	0	0	1294.63	23	33
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	46	0.05%	41.6%	TVGVEPAADGK	99.7%	63.4	25	61.2	3	0	0	1043.54	48	58
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	46	0.05%	41.6%	TVGVEPAADGKGVVVVIK	99.7%	68.6	25	64.6	4	3	0	1738.01	48	65
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	46	0.05%	41.6%	YNGLIHR	99.7%	42.3	25	28.3	4	0	0	872.47	40	46
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	46	0.05%	41.6%	YNGLIHRK	99.4%	37.1	25	23.7	1	0	0	1000.57	40	47
60S ribosomal protein L29	RPL29	RL29_HUMAN	17.8	100.0%	3	3	18	0.02%	15.1%	AQAAAPASVPAQAPK	99.7%	83.1	25	78.5	14	0	0	1377.75	135	149
60S ribosomal protein L29	RPL29	RL29_HUMAN	17.8	100.0%	3	3	18	0.02%	15.1%	AQAAAPASVPAQAPKR	95.8%	22.4	25	22.4	0	1	0	1533.85	135	150
60S ribosomal protein L29	RPL29	RL29_HUMAN	17.8	100.0%	3	3	18	0.02%	15.1%	LAYIAHPK	97.6%	31	25	26	3	0	0	912.53	96	103
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	18	22	62	0.06%	37.7%	AGMTHIVR	99.7%	59.5	25	51.1	3	0	0	884.48	51	58
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	18	22	62	0.06%	37.7%	AHLMEIQVNGGTVAEK	99.5%	30.5	25	26.5	0	1	0	1696.87	178	193
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	18	22	62	0.06%	37.7%	DDPSKPVHLTAFLGYK	99.7%	69.8	25	69.8	2	1	0	1787.93	35	50
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	18	22	62	0.06%	37.7%	FQTMEEK	95.7%	28.5	25	26.1	1	0	0	912.41	379	385
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	18	22	62	0.06%	37.7%	FQTMEEKK	97.6%	30.9	25	19.8	2	0	0	1040.51	379	386
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	18	22	62	0.06%	37.7%	HGSLGFLPR	99.7%	64.6	25	58	4	0	0	983.54	11	19
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	18	22	62	0.06%	37.7%	IGQGYLIK	99.7%	52.6	25	34.9	4	0	0	891.53	287	294
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	18	22	62	0.06%	37.7%	IGQGYLIKDGK	99.7%	68.4	25	61.5	2	0	0	1191.67	287	297
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	18	22	62	0.06%	37.7%	KSLLVQTK	97.7%	31.1	25	19.1	2	0	0	916.58	349	356
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	18	22	62	0.06%	37.7%	KVACIGAWHPAR	99.7%	59.1	25	55.3	0	2	0	1365.72	250	261
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	18	22	62	0.06%	37.7%	KYCQVIR	99.5%	38.4	25	23.5	1	0	0	966.52	155	161
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	18	22	62	0.06%	37.7%	LEQQVPVNQVFGQDEMIDVIGVTK	99.6%	31.6	25	30.8	0	2	0	2686.38	201	224
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	18	22	62	0.06%	37.7%	NNASTDYDLSDK	99.7%	77.4	25	77.4	8	0	0	1342.58	301	312
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	18	22	62	0.06%	37.7%	TVFAEHISDECK	99.7%	71	25	71	7	2	0	1435.65	104	115
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	18	22	62	0.06%	37.7%	TVFAEHISDECKR	99.7%	63.1	25	58.1	2	4	0	1591.75	104	116
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	18	22	62	0.06%	37.7%	VACIGAWHPAR	99.7%	82.3	25	73	4	2	0	1237.63	251	261
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	18	22	62	0.06%	37.7%	VIAHTQMR	99.7%	50.6	25	42.1	4	0	0	955.51	162	169
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	18	22	62	0.06%	37.7%	YCQVIR	99.1%	35.3	25	23.2	2	0	0	838.42	156	161
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	7	12	27	0.03%	59.1%	KSEIEYYAMLAK	99.7%	43.7	25	42.7	3	3	0	1461.73	57	68
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	7	12	27	0.03%	59.1%	KSLESINSR	99.7%	58.8	25	42.2	2	0	0	1033.56	9	17
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	7	12	27	0.03%	59.1%	LVILANNCPALR	99.7%	85.8	25	65.8	6	0	0	1353.77	45	56
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	7	12	27	0.03%	59.1%	SEIEYYAMLAK	99.7%	80.4	25	64.1	4	0	0	1333.63	58	68
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	7	12	27	0.03%	59.1%	SLESINSR	99.4%	37.2	25	29.5	2	0	0	905.47	10	17
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	7	12	27	0.03%	59.1%	TGVHHYSGNNIELGTACGK	99.7%	53	25	49.3	1	2	0	2014.94	69	87
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	7	12	27	0.03%	59.1%	VCTLAIIDPGDSDIIR	99.7%	95.1	25	86.7	4	0	0	1757.91	91	106
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	9	44	0.04%	49.6%	EMGTPDVR	99.7%	42.3	25	37.4	1	0	0	904.42	56	63
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	9	44	0.04%	49.6%	EYTINIHK	98.5%	33	25	17.4	3	0	0	1017.54	24	31
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	9	44	0.04%	49.6%	EYTINIHKR	99.7%	51.1	25	36.1	4	0	0	1173.64	24	32
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	9	44	0.04%	49.6%	FAMKEMGTPDVR	99.6%	39.3	25	22.7	5	2	0	1397.66	52	63
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	9	44	0.04%	49.6%	IHGVGFKK	96.4%	29.2	25	22.7	1	0	0	885.53	33	40
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	9	44	0.04%	49.6%	LYTLVTYVPVTTFK	99.7%	89.1	25	89.1	8	0	0	1644.92	102	115
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	9	44	0.04%	49.6%	NLQTVNVDEN	99.7%	70.7	25	65.1	5	0	0	1145.54	116	125
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	9	44	0.04%	49.6%	SAINEVVTR	99.7%	76.1	25	62.2	15	0	0	988.54	15	23
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	5	9	39	0.04%	29.6%	ELEVLLMCNK	99.7%	52.8	25	44.3	12	0	0	1264.63	84	93
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	5	9	39	0.04%	29.6%	FKGQILMPNIGYGSNK	99.7%	45.2	25	45.2	2	0	0	1782.92	49	64
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	5	9	39	0.04%	29.6%	GQILMPNIGYGSNK	99.7%	42.1	25	37.2	7	0	0	1491.76	51	64
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	5	9	39	0.04%	29.6%	GQILMPNIGYGSNKK	99.7%	49.9	25	43.4	5	0	0	1619.86	51	65
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	5	9	39	0.04%	29.6%	SYCAEIAHNVSSK	99.7%	85.6	25	85.6	12	1	0	1465.67	94	106
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	10	32	0.03%	41.9%	AFLIEEQK	99.7%	47.9	25	28.8	6	0	0	977.53	94	101
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	10	32	0.03%	41.9%	AFLIEEQKIVVK	99.7%	59.9	25	59.9	2	1	0	1416.85	94	105
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	10	32	0.03%	41.9%	AYGGSMCAK	99.5%	37.8	25	37.8	1	0	0	944.40	77	85
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	10	32	0.03%	41.9%	IVYLYTK	99.7%	40.3	25	30.9	1	0	0	899.52	30	36

60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	10	32	0.03%	41.9%	IVYLYTKK	99.5%	38.3	25	25.4	4	0	0	1027.62	30	37
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	10	32	0.03%	41.9%	LSYNTASNK	99.7%	57.4	25	42.4	8	0	0	997.49	11	19
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	10	32	0.03%	41.9%	RAFLIEEQK	98.1%	32	25	21	1	0	0	1133.63	93	101
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	10	32	0.03%	41.9%	RLSYNTASNK	99.5%	38.5	25	25.5	4	0	0	1153.60	10	19
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	10	32	0.03%	41.9%	SACGVCPGR	99.5%	38.6	25	34.6	4	0	0	963.41	44	52
60S ribosomal protein L35	RPL35	RL35_HUMAN	14.6	100.0%	4	5	20	0.02%	29.3%	QLDDLKVELSQLR	99.7%	77.9	25	57.8	3	2	0	1556.86	20	32
60S ribosomal protein L35	RPL35	RL35_HUMAN	14.6	100.0%	4	5	20	0.02%	29.3%	VLTVINQTQK	99.7%	66.4	25	61.5	12	0	0	1143.67	57	66
60S ribosomal protein L35	RPL35	RL35_HUMAN	14.6	100.0%	4	5	20	0.02%	29.3%	VLTVINQTQKENLR	99.7%	94.5	25	94.5	2	0	0	1655.94	57	70
60S ribosomal protein L35	RPL35	RL35_HUMAN	14.6	100.0%	4	5	20	0.02%	29.3%	YKPLDLRPK	96.4%	29.2	25	29.2	1	0	0	1129.67	78	86
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	22	0.02%	46.4%	AIFAGYKR	99.7%	40.1	25	33.8	2	0	0	925.53	9	16
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	22	0.02%	46.4%	CAYVYK	96.6%	29.4	25	21.7	1	0	0	803.38	47	52
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	22	0.02%	46.4%	DETEFYLGK	99.7%	58.3	25	50.6	4	0	0	1101.51	37	45
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	22	0.02%	46.4%	DETEFYLGKR	99.7%	49.1	25	45.9	3	0	0	1257.61	37	46
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	22	0.02%	46.4%	IEGVYAR	99.5%	38	25	22.9	2	0	0	807.44	30	36
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	22	0.02%	46.4%	NNTVTPGGKPNK	99.7%	42.7	25	36	4	0	0	1226.65	55	66
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	22	0.02%	46.4%	VMLYPSR	95.2%	28.1	25	21.3	2	0	0	881.46	103	109
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	22	0.02%	46.4%	VMLYPSRI	99.5%	37.8	25	29.1	4	0	0	994.54	103	110
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	5	8	21	0.02%	32.4%	ALRYPMAVGLNK	99.7%	46.9	25	37.1	2	2	0	1348.74	2	13
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	5	8	21	0.02%	32.4%	EELSNVLAAMR	99.7%	73.1	25	65.2	6	0	0	1232.63	88	98
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	5	8	21	0.02%	32.4%	EVCGFAPYER	99.7%	50	25	50	5	0	0	1227.55	46	55
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	5	8	21	0.02%	32.4%	REELSNVLAAMR	99.4%	37.5	25	37.5	2	0	0	1388.73	87	98
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	5	8	21	0.02%	32.4%	YPMAVGLNK	99.7%	43.8	25	33.1	4	0	0	992.52	5	13
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	4	4	15	0.02%	21.7%	DSLYAQGR	98.5%	32.9	25	29	1	0	0	909.44	31	38
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	4	4	15	0.02%	21.7%	GKDSLYAQGR	99.7%	60.8	25	56.6	4	0	0	1094.56	29	38
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	4	4	15	0.02%	21.7%	IVLRLECVEPNCR	98.5%	26	25	26	0	2	0	1657.85	66	78
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	4	4	15	0.02%	21.7%	LECVEPNCR	99.7%	47.2	25	47.2	8	0	0	1176.51	70	78
60S ribosomal protein L37a	RPL37A	RL37A_HUMAN	10.3	100.0%	4	5	26	0.03%	51.1%	AVGIWHCGSCMK	99.7%	65.8	25	65.8	5	0	0	1405.62	51	62
60S ribosomal protein L37a	RPL37A	RL37A_HUMAN	10.3	100.0%	4	5	26	0.03%	51.1%	KIEISQHAK	99.7%	42.9	25	36.5	2	0	0	1053.61	28	36
60S ribosomal protein L37a	RPL37A	RL37A_HUMAN	10.3	100.0%	4	5	26	0.03%	51.1%	TVAGGAWTYNTTSAVTVK	99.7%	86.2	25	81.2	18	0	0	1826.93	63	80
60S ribosomal protein L37a	RPL37A	RL37A_HUMAN	10.3	100.0%	4	5	26	0.03%	51.1%	YTCSFCGK	94.6%	27.6	25	27.6	1	0	0	1022.41	37	44
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	5	7	20	0.02%	51.4%	IEEIKDFLLTAR	99.7%	48.7	25	46.1	4	1	0	1447.82	5	16
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	5	7	20	0.02%	51.4%	LKQSLPPGLAVK	99.7%	43.4	25	43.4	3	0	0	1250.78	56	67
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	5	7	20	0.02%	51.4%	QSLPPGLAVK	99.7%	54.9	25	50.9	5	0	0	1009.60	58	67
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	5	7	20	0.02%	51.4%	YLYTLVITDK	99.7%	50.6	25	42.5	2	0	0	1228.68	41	50
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	5	7	20	0.02%	51.4%	YLYTLVITDKEK	99.7%	68.4	25	62.6	4	1	0	1485.82	41	52
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	126	0.13%	47.3%	AAAAAAALQAK	99.7%	92.9	25	86.9	16	0	0	956.55	354	364
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	126	0.13%	47.3%	APIRPDIVNFVHTNLR	99.7%	56.4	25	56.4	2	2	0	1862.04	30	45
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	126	0.13%	47.3%	AWNDIKK	99.0%	35	25	20.1	2	0	0	874.48	176	182
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	126	0.13%	47.3%	EAVLLLKK	99.7%	55.6	25	37.7	2	0	0	913.61	166	173
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	126	0.13%	47.3%	FCIWTESAFR	99.7%	56	25	48	12	0	0	1316.61	249	258
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	126	0.13%	47.3%	GPCIIYNEDNGIIK	99.7%	64.2	25	64.2	4	0	0	1605.79	206	219
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	126	0.13%	47.3%	IEEVPELPLVVEDK	99.7%	56.5	25	56.3	2	0	0	1608.87	144	157
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	126	0.13%	47.3%	IEEVPELPLVVEDKVEGYK	99.7%	54.1	25	54.1	1	0	0	2185.16	144	162
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	126	0.13%	47.3%	KLDELYGTWR	99.7%	67.5	25	67	4	2	0	1280.66	259	268
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	126	0.13%	47.3%	LAPGGHVGR	99.7%	64.2	25	49.3	2	0	0	863.48	240	248
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	126	0.13%	47.3%	LDELYGTWR	99.7%	60.2	25	55	1	0	0	1152.57	260	268
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	126	0.13%	47.3%	MINTDLSR	99.7%	56.9	25	45.5	11	0	0	949.48	284	291
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	126	0.13%	47.3%	NIPGITLLNVSK	99.7%	83.4	25	79.4	15	0	0	1268.76	223	234
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	126	0.13%	47.3%	NIPGITLLNVSKLNILK	99.7%	65.4	25	65.4	2	0	0	1850.15	223	239
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	126	0.13%	47.3%	NVTLPAVFK	99.7%	43.3	25	29.7	3	0	0	988.58	21	29
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	126	0.13%	47.3%	QPYAVSELAGHQTSAESWGTGR	99.7%	119	25	119	1	2	0	2332.10	50	71

60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	126	0.13%	47.3%	RGPCIIYNEDNGIIK	99.7%	74.4	25	56.1	2	2	0	1761.90	205	219
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	126	0.13%	47.3%	SGQGAFGNMCR	99.7%	67.7	25	67.7	7	0	0	1184.49	87	97
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	126	0.13%	47.3%	SNYNLPMHK	99.7%	44.6	25	44.6	10	0	0	1103.53	275	283
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	126	0.13%	47.3%	TKEAVLLLK	99.7%	46.3	25	42.8	4	0	0	1014.66	164	172
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	126	0.13%	47.3%	YAICSALAASALPALVMSK	99.7%	115	25	115	9	6	0	1937.02	122	140
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	30	63	0.06%	42.8%	DIICQIAYAR	99.7%	57.3	25	42.2	2	0	0	1222.63	59	68
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	30	63	0.06%	42.8%	EFNAEVHR	99.7%	42	25	23.6	2	0	0	1001.48	189	196
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	30	63	0.06%	42.8%	EFNAEVHRK	99.2%	35.9	25	28.2	2	0	0	1129.57	189	197
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	30	63	0.06%	42.8%	ENPVYEK	95.3%	28.1	25	5.2	1	0	0	878.43	249	255
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	30	63	0.06%	42.8%	FPGYDSESK	99.1%	35.2	25	30.5	2	0	0	1029.45	180	188
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	30	63	0.06%	42.8%	GAVDGGLSIPHSTK	99.7%	65.2	25	56.2	2	1	0	1338.70	165	178
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	30	63	0.06%	42.8%	GAVDGGLSIPHSTKR	99.7%	53.4	25	42.6	2	2	0	1494.80	165	179
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	30	63	0.06%	42.8%	HIMGQNVADYMR	99.7%	61.7	25	48.9	8	4	0	1434.66	198	209
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	30	63	0.06%	42.8%	IEGDMIVCAAYAHELPK	99.7%	98.2	25	98.2	4	4	0	1916.92	69	85
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	30	63	0.06%	42.8%	NSVTPDMMEEMYK	99.7%	69.2	25	69.2	2	0	0	1574.65	229	241
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	30	63	0.06%	42.8%	NSVTPDMMEEMYKK	99.7%	60.6	25	60.6	5	1	0	1702.75	229	242
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	30	63	0.06%	42.8%	RFPGYDSESK	99.5%	37.8	25	29.3	2	0	0	1185.55	179	188
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	30	63	0.06%	42.8%	VGLTNYAAAYCTGLLLAR	99.7%	104	25	104	3	2	0	1927.01	90	107
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	30	63	0.06%	42.8%	VTNRDIICQIAYAR	99.7%	69.9	25	64.3	2	2	0	1692.89	55	68
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	30	63	0.06%	42.8%	YLMEEDEDAYKK	99.7%	65.4	25	65.4	4	4	0	1549.67	210	221
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	13	17	50	0.05%	42.0%	AIPQLQGYLR	99.7%	62.5	25	50.9	2	0	0	1158.66	263	272
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	13	17	50	0.05%	42.0%	ASITPGTILIILTGR	99.7%	130	25	130	11	1	0	1525.93	142	156
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	13	17	50	0.05%	42.0%	AVDSQILPK	99.7%	50	25	24.6	2	0	0	970.56	252	260
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	13	17	50	0.05%	42.0%	EKYEITEQR	99.7%	42.8	25	36	2	0	0	1195.60	238	246
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	13	17	50	0.05%	42.0%	FVIATSTK	95.7%	28.5	25	28.5	1	0	0	866.50	193	200
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	13	17	50	0.05%	42.0%	HLTDAYFK	97.1%	30.1	25	21.9	1	0	0	994.50	211	218
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	13	17	50	0.05%	42.0%	HLTDAYFKK	98.5%	33.1	25	25.3	2	0	0	1122.59	211	219
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	13	17	50	0.05%	42.0%	KPFSQHVR	98.4%	32.6	25	19.4	1	0	0	998.55	131	138
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	13	17	50	0.05%	42.0%	QLASGLLLVTGPLVLNR	99.7%	94.5	25	94.5	6	4	0	1764.07	167	183
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	13	17	50	0.05%	42.0%	SVFALTNGIYPHK	99.7%	78.7	25	74.1	4	0	0	1446.77	273	285
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	13	17	50	0.05%	42.0%	VLATVTKPVGGDK	99.7%	60.5	25	54	5	2	0	1284.75	88	100
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	13	17	50	0.05%	42.0%	YYPTEDVPR	99.7%	47.3	25	46	3	0	0	1139.54	115	123
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	13	17	50	0.05%	42.0%	YYPTEDVPRK	98.6%	26.2	25	23.6	2	1	0	1267.63	115	124
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	18	42	0.04%	42.3%	AGNFYVPAEPK	99.7%	60.7	25	50	2	0	0	1192.60	78	88
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	18	42	0.04%	42.3%	ASINMLR	99.7%	51	25	33.7	4	0	0	820.43	128	134
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	18	42	0.04%	42.3%	EANNFLWPFK	99.7%	48.4	25	35.5	5	0	0	1265.63	203	212
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	18	42	0.04%	42.3%	EVPAVPETLKK	98.7%	26.6	25	26.6	0	1	0	1210.70	10	20
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	18	42	0.04%	42.3%	FKEANNFLWPFK	99.7%	59.3	25	50	2	0	0	1540.79	201	212
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	18	42	0.04%	42.3%	IALTDNALIAR	99.7%	93.3	25	74.9	4	0	0	1170.68	167	177
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	18	42	0.04%	42.3%	IVEPYIAWGYPNLK	99.7%	65.7	25	36.8	5	0	0	1662.89	135	148
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	18	42	0.04%	42.3%	KAGNFYVPAEPK	99.7%	53.2	25	53.1	2	1	0	1320.69	77	88
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	18	42	0.04%	42.3%	QIFNGTFVK	97.7%	31.2	25	29.2	1	0	0	1053.57	116	124
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	18	42	0.04%	42.3%	RIALTDNALIAR	99.7%	68.5	25	55.6	2	0	0	1326.79	166	177
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	18	42	0.04%	42.3%	SVNELIYK	99.7%	59.8	25	43.6	2	0	0	965.53	149	156
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	18	42	0.04%	42.3%	SVNELIYKR	99.7%	44.4	25	35.1	3	0	0	1121.63	149	157
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	18	42	0.04%	42.3%	TTHFVEGGDAGNR	99.7%	47.7	25	47.7	2	2	0	1360.62	224	236
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	18	42	0.04%	42.3%	TTHFVEGGDAGNREDQINR	99.7%	65.9	25	65.9	2	2	0	2115.98	224	242
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	69	0.07%	45.1%	AGVNTVTTLVENK	99.7%	99.2	25	89.5	7	0	0	1345.73	138	150
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	69	0.07%	45.1%	AGVNTVTTLVENKK	99.7%	90.6	25	83.3	4	4	0	1473.83	138	151
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	69	0.07%	45.1%	HWGGNVLGPK	99.7%	45.3	25	44.3	5	0	0	1064.56	236	245
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	69	0.07%	45.1%	KMGVPYCIIK	99.7%	42	25	33.3	2	4	0	1208.65	176	185

60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	69	0.07%	45.1%	KTCTTVAFTQVNSEDK	99.7%	64	25	64	1	0	0	1828.87	197	212
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	69	0.07%	45.1%	KVAPAPAVVK	99.7%	44.8	25	44.8	3	0	0	979.63	11	20
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	69	0.07%	45.1%	KVVNPLFEK	99.7%	41.1	25	26.2	2	0	0	1073.64	26	34
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	69	0.07%	45.1%	LKVPPAINQFTQALDR	99.7%	43.7	25	43.7	2	2	0	1811.02	74	89
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	69	0.07%	45.1%	MGVPYCIIK	99.7%	41.4	25	34.5	4	0	0	1096.55	177	185
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	69	0.07%	45.1%	NFGIGQDIQPK	99.7%	70.7	25	60.2	4	0	0	1216.63	38	48
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	69	0.07%	45.1%	QTATQLLK	99.7%	56.7	25	36.8	3	0	0	902.53	90	97
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	69	0.07%	45.1%	TCTTVAFTQVNSEDK	99.7%	105	25	99.5	2	0	0	1700.78	198	212
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	69	0.07%	45.1%	TCTTVAFTQVNSEDKGALAK	99.7%	105	25	105	3	4	0	2141.05	198	217
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	69	0.07%	45.1%	TNYNDRYDEIR	99.2%	36.1	25	24.8	2	2	0	1458.66	224	234
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	69	0.07%	45.1%	VPPAINQFTQALDR	99.7%	117	25	108	6	1	0	1569.84	76	89
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	69	0.07%	45.1%	VVNPLFEK	99.5%	38.3	25	38.3	2	0	0	945.54	27	34
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	8	10	28	0.03%	24.1%	ASGNYATVISHNPETK	99.7%	74.7	25	73.2	7	2	0	1688.82	129	144
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	8	10	28	0.03%	24.1%	ASGNYATVISHNPETKK	99.7%	64.9	25	59.2	2	1	0	1816.92	129	145
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	8	10	28	0.03%	24.1%	AVDFAER	99.7%	49.5	25	39.2	2	0	0	807.40	31	37
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	8	10	28	0.03%	24.1%	AVVGVVAGGGR	99.7%	94.9	25	80.7	8	0	0	941.55	164	174
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	8	10	28	0.03%	24.1%	DIIHDPGR	98.9%	34.3	25	24.5	2	0	0	922.47	47	54
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	8	10	28	0.03%	24.1%	GIVKDIIHDPGR	99.7%	37.8	25	35	0	1	0	1319.74	43	54
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	8	10	28	0.03%	24.1%	IDKPILK	98.0%	31.8	25	6.43	2	0	0	826.54	175	181
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	8	10	28	0.03%	24.1%	KVGLIAAR	99.2%	35.9	25	21.1	1	0	0	827.55	234	241
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	16	40	0.04%	45.3%	DFNHINVELSLLGK	99.7%	70.4	25	61.3	4	2	0	1598.85	37	50
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	16	40	0.04%	45.3%	DFNHINVELSLLGKK	99.7%	37	25	35.1	1	2	0	1726.95	37	51
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	16	40	0.04%	45.3%	FLDGIYVSEK	99.7%	77.4	25	66.2	10	0	0	1170.60	175	184
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	16	40	0.04%	45.3%	KFLDGIYVSEK	99.7%	64.3	25	56.7	2	0	0	1298.70	174	184
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	16	40	0.04%	45.3%	MRPGVACSVSQAQK	99.7%	47.8	25	45	4	4	0	1534.75	128	141
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	16	40	0.04%	45.3%	NFLGEKYIR	98.6%	33.4	25	17.9	2	0	0	1139.62	116	124
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	16	40	0.04%	45.3%	TICSHVQNMIK	99.7%	64.6	25	57.6	4	2	0	1330.66	72	82
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	16	40	0.04%	45.3%	TILSNQTVDIPENVDITLK	99.7%	81.7	25	81.7	2	0	0	2113.14	3	21
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	16	40	0.04%	45.3%	VDKWWGNR	96.5%	29.3	25	19.7	1	0	0	1060.53	57	64
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	PFKFB3	F263_HUMAN	59.6	100.0%	5	5	8	0.01%	10.0%	CLLAYFLDK	99.7%	52.7	25	44	2	0	0	1142.59	394	402
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	PFKFB3	F263_HUMAN	59.6	100.0%	5	5	8	0.01%	10.0%	IGGDSGLSSR	99.7%	50.9	25	46.1	2	0	0	948.47	265	274
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	PFKFB3	F263_HUMAN	59.6	100.0%	5	5	8	0.01%	10.0%	LEPVIMELER	99.1%	35.5	25	30.8	2	0	0	1228.66	370	379
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	PFKFB3	F263_HUMAN	59.6	100.0%	5	5	8	0.01%	10.0%	STIQTAEALR	99.7%	53.5	25	41.4	1	0	0	1089.59	303	312
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	PFKFB3	F263_HUMAN	59.6	100.0%	5	5	8	0.01%	10.0%	YPTGESYQDLVQR	99.7%	78.9	25	68.9	1	0	0	1555.74	357	369
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	7	7	12	0.01%	12.9%	AIGVLTSGGDAQGMNAAVR	99.7%	133	25	133	4	1	0	1787.91	26	44
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	7	7	12	0.01%	12.9%	EWSGLLEELAR	99.7%	66.3	25	37.2	2	0	0	1302.67	140	150
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	7	7	12	0.01%	12.9%	GGTPSAFDR	99.3%	36.7	25	26.4	1	0	0	907.43	311	319
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	7	7	12	0.01%	12.9%	NGQIDKEAVQK	99.7%	42.7	25	28.7	2	0	0	1229.65	151	161
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	7	7	12	0.01%	12.9%	NVIFQPVAELKK	99.7%	42.7	25	42.7	2	0	0	1385.82	726	737
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	7	7	12	0.01%	12.9%	SFAGNLNTYK	99.7%	45.1	25	35.5	2	0	0	1114.55	386	395
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	7	7	12	0.01%	12.9%	SFAGNLNTYKR	99.7%	40.8	25	34.6	1	0	0	1270.65	386	396
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	7	7	12	0.01%	12.9%	TFVLEVMGR	99.7%	70.4	25	61.2	2	0	0	1051.56	211	219
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	7	7	12	0.01%	12.9%	VTILGHVQR	99.7%	41.7	25	32	1	0	0	1022.61	302	310
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	7	7	12	0.01%	12.9%	YLEEIATQMR	99.7%	63.5	25	57.1	2	0	0	1253.62	487	496
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	16	19	34	0.03%	26.3%	AIGVLTSGGDAQGMNAAVR	99.7%	133	25	133	4	1	0	1787.91	17	35
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	16	19	34	0.03%	26.3%	AMLWLSEK	99.7%	44.8	25	35.3	2	0	0	977.51	682	689
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	16	19	34	0.03%	26.3%	AVAFSPVTELKK	99.1%	35.1	25	35.1	2	0	0	1289.75	716	727
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	16	19	34	0.03%	26.3%	EQWWLSLR	99.7%	41.6	25	23.8	2	0	0	1117.58	738	745
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	16	19	34	0.03%	26.3%	GGTPSAFDR	99.3%	36.7	25	26.4	1	0	0	907.43	302	310
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	16	19	34	0.03%	26.3%	GQLESIVENIR	99.7%	63.9	25	53.7	2	0	0	1257.68	475	485
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	16	19	34	0.03%	26.3%	IMEVIDAITTTAQSHQR	99.7%	49.9	25	6.69	0	4	0	1929.97	185	201

6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	16	19	34	0.03%	26.3%	LNIIIIAEGAIDR	99.7%	54.7	25	54.7	1	0	0	1410.83	257	269
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	16	19	34	0.03%	26.3%	LPLMECVQMTK	99.7%	58.5	25	53.9	2	0	0	1349.66	346	356
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	16	19	34	0.03%	26.3%	SEWGSLLEELVAEGK	94.7%	27.6	25	15.4	1	0	0	1646.83	130	144
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	16	19	34	0.03%	26.3%	SNFSLAILNVGAPAAGMNAAVR	99.7%	65.4	25	65.4	2	0	0	2144.13	398	419
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	16	19	34	0.03%	26.3%	TFVLEVMGR	99.7%	70.4	25	61.2	2	0	0	1051.56	202	210
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	16	19	34	0.03%	26.3%	TNVLGHLQQGGAPTPFDR	99.7%	52.1	25	49.4	0	2	0	1907.97	655	672
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	16	19	34	0.03%	26.3%	VFANAPDSACVIGLK	99.7%	73.9	25	67.7	2	0	0	1561.80	699	713
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	16	19	34	0.03%	26.3%	VNVEHMTEK	99.7%	54.9	25	50	2	0	0	1086.52	606	614
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	16	19	34	0.03%	26.3%	VTVLGHVQR	99.7%	72.3	25	72.3	2	0	0	1008.59	293	301
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	15	0.02%	19.1%	ALVFQPVAELK	99.7%	54.6	25	49.5	1	0	0	1214.71	717	727
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	15	0.02%	19.1%	DLQANVEHLVQK	99.7%	57.8	25	47.9	2	0	0	1393.74	604	615
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	15	0.02%	19.1%	GGTPSAFDR	99.3%	36.7	25	26.4	1	0	0	907.43	302	310
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	15	0.02%	19.1%	GITNLCVIGGDGSLTGADTFR	99.7%	104	25	104	1	0	0	2124.04	109	129
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	15	0.02%	19.1%	IFANTPDSGCVLGMR	99.7%	55.4	25	48.3	1	0	0	1637.78	700	714
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	15	0.02%	19.1%	IGLIQGNR	99.7%	61	25	53	2	0	0	870.52	425	432
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	15	0.02%	19.1%	LLAHVRPPVSK	96.2%	22.8	25	16.8	0	1	0	1216.75	387	397
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	15	0.02%	19.1%	SEWSDLLSDLQK	99.7%	82.8	25	73	2	0	0	1420.70	130	141
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	15	0.02%	19.1%	SFEQISANITK	99.7%	64.4	25	53.4	1	0	0	1237.64	477	487
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	15	0.02%	19.1%	TFVLEVMGR	99.7%	70.4	25	61.2	2	0	0	1051.56	202	210
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	15	0.02%	19.1%	VGIFTGAR	99.7%	44.3	25	31.5	2	0	0	820.47	40	47
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	15	0.02%	19.1%	VLVVHDGFEGLAK	99.7%	57.1	25	51	2	0	0	1383.76	433	445
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	15	0.02%	19.1%	VTVLGHVQR	99.7%	72.3	25	72.3	2	0	0	1008.59	293	301
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	8	8	14	0.01%	21.3%	AGQAVDDFIEK	99.7%	52.2	25	35.7	2	0	0	1192.58	77	87
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	8	8	14	0.01%	21.3%	CLSSLKDER	98.3%	32.5	25	13.1	1	0	0	1107.55	289	297
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	8	8	14	0.01%	21.3%	GILFVGSGVSGGEEGAR	99.7%	113	25	107	2	0	0	1591.81	120	136
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	8	8	14	0.01%	21.3%	IISYAQGFMLLR	99.7%	78.2	25	72	2	0	0	1411.78	332	343
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	8	8	14	0.01%	21.3%	LVPLLDTGDIIIDGGNSEYR	99.7%	81.5	25	81.5	2	0	0	2160.12	88	107
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	8	8	14	0.01%	21.3%	TIFQGIAAK	99.2%	35.7	25	26.6	2	0	0	948.55	155	163
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	8	8	14	0.01%	21.3%	TVSKVDDFLANEAK	99.7%	60.6	25	60.4	1	0	0	1536.79	35	48
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	8	8	14	0.01%	21.3%	YGPSLMPGGNK	98.9%	34.5	25	31.1	2	0	0	1136.54	137	147
6-phosphogluconolactonase	PGLS	6PGL_HUMAN	27.5	100.0%	2	2	4	0.00%	8.9%	TVIFVATGEGK	99.7%	76.3	25	69.6	2	0	0	1121.62	198	208
6-phosphogluconolactonase	PGLS	6PGL_HUMAN	27.5	100.0%	2	2	4	0.00%	8.9%	VTLTLPVLNAAR	99.7%	58.7	25	58.7	2	0	0	1267.77	186	197
6-pyruvoyl tetrahydrobiopterin synthase	PTS	PTPS_HUMAN	16.4	100.0%	5	5	8	0.01%	33.8%	FLSDEENLK	99.7%	47.8	25	20.6	2	0	0	1094.54	30	38
6-pyruvoyl tetrahydrobiopterin synthase	PTS	PTPS_HUMAN	16.4	100.0%	5	5	8	0.01%	33.8%	FLSDEENLKLFGK	99.5%	37.8	25	31.9	2	0	0	1539.81	30	42
6-pyruvoyl tetrahydrobiopterin synthase	PTS	PTPS_HUMAN	16.4	100.0%	5	5	8	0.01%	33.8%	VLPVGVLYK	99.7%	44.3	25	39	1	0	0	987.62	121	129
6-pyruvoyl tetrahydrobiopterin synthase	PTS	PTPS_HUMAN	16.4	100.0%	5	5	8	0.01%	33.8%	VYETDNNIVVYKGE	99.7%	61.5	25	61.3	2	0	0	1642.80	132	145
6-pyruvoyl tetrahydrobiopterin synthase	PTS	PTPS_HUMAN	16.4	100.0%	5	5	8	0.01%	33.8%	YMEEAIMQPLDHK	95.2%	28	25	11.8	1	0	0	1620.74	79	91
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	19	34	0.03%	37.5%	DAGTIAGLNVMR	99.7%	75.2	25	64.2	1	0	0	1217.63	186	197
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	19	34	0.03%	37.5%	ELEEIVQPIISK	99.7%	53.4	25	40.8	2	0	0	1397.79	622	633
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	19	34	0.03%	37.5%	IINEPTAAAIAYGLDK	99.7%	125	25	123	2	0	0	1659.90	198	213
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	19	34	0.03%	37.5%	IINEPTAAAIAYGLDKR	99.7%	109	25	109	2	2	0	1816.00	198	214
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	19	34	0.03%	37.5%	ITITNDQNR	99.3%	36.4	25	26.1	1	0	0	1074.55	524	532
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	19	34	0.03%	37.5%	ITPSYVAFTPEGER	97.9%	31.5	25	30.6	2	0	0	1566.78	61	74
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	19	34	0.03%	37.5%	LTPEEIER	94.9%	27.8	25	0	1	0	0	986.52	533	540
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	19	34	0.03%	37.5%	LYGSAGPPPTGEEDTAEKDEL	99.7%	44	25	44	1	0	0	2175.99	634	654
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	19	34	0.03%	37.5%	MKETAEAYLGK	99.7%	55.3	25	46.2	2	0	0	1256.62	153	163
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	19	34	0.03%	37.5%	NQLTSNPENTVFDAK	99.7%	109	25	101	2	0	0	1677.81	82	96
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	19	34	0.03%	37.5%	SDIDEIVLVGGSTR	99.7%	53.3	25	53.3	2	0	0	1460.76	354	367
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	19	34	0.03%	37.5%	SQIFSTASDNQPTVTIK	99.7%	81.8	25	73.9	2	0	0	1836.93	448	464
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	19	34	0.03%	37.5%	TFAPEEISAMVLTK	99.7%	88.6	25	84.6	2	0	0	1536.80	139	152
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	19	34	0.03%	37.5%	TKPYIQVDIGGGQTK	99.7%	72	25	64.5	2	0	0	1604.86	124	138

78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	19	34	0.03%	37.5%	TWNDPSVQQDIK	99.7%	93.7	25	86.6	2	0	0	1430.69	102	113
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	19	34	0.03%	37.5%	VEIIANDQGNR	99.7%	59.2	25	0	2	0	0	1228.63	50	60
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	19	34	0.03%	37.5%	VLEDSDLKK	99.7%	40.9	25	26.8	2	0	0	1046.57	345	353
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	19	34	0.03%	37.5%	VMEHFIK	99.7%	42.2	25	30.1	2	0	0	903.48	262	268
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	19	34	0.03%	37.5%	VTHAVVTVPAYFNDAQR	99.7%	37.2	25	35.3	0	2	0	1887.97	165	181
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	19	34	0.03%	37.5%	VYEGERPLTK	99.7%	48.5	25	39.8	2	0	0	1191.64	465	474
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	6	7	24	0.02%	15.2%	FLPGYVGGIQEGAVTPAGVVNK	99.7%	95.8	25	94.1	5	1	0	2173.17	121	142
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	6	7	24	0.02%	15.2%	GYFFPTSAR	97.4%	30.5	25	24.1	1	0	0	1045.51	199	207
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	6	7	24	0.02%	15.2%	LLVSGFWGVAR	99.7%	81.4	25	79.8	6	0	0	1204.68	394	404
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	6	7	24	0.02%	15.2%	SLDGVTNDR	99.3%	36.5	25	25.2	5	0	0	976.47	14	22
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	6	7	24	0.02%	15.2%	VIECSYTSADGQR	99.7%	80.2	25	79.1	4	0	0	1485.66	377	389
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	6	7	24	0.02%	15.2%	YTAAVPYR	99.7%	46.2	25	34.2	2	0	0	940.49	462	469
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	22	43	0.04%	39.6%	AGIPKEEVK	96.9%	29.8	25	16.4	1	0	0	970.56	79	87
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	22	43	0.04%	39.6%	DGLTDVYNK	99.7%	52.8	25	42.1	2	0	0	1024.49	182	190
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	22	43	0.04%	39.6%	EAYMGNVLQGGEGQAPTR	99.7%	113	25	113	4	0	0	1877.88	88	105
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	22	43	0.04%	39.6%	EVVIVSATR	99.7%	69.9	25	63.6	2	0	0	973.57	41	49
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	22	43	0.04%	39.6%	GSTPYGGVKLEDLIVK	99.7%	99.4	25	92.6	2	0	0	1675.93	166	181
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	22	43	0.04%	39.6%	IHMGSCAENTAK	99.7%	55	25	51	2	2	0	1318.59	191	202
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	22	43	0.04%	39.6%	IVGHLTHALK	99.7%	62.3	25	44.7	2	0	0	1088.66	394	403
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	22	43	0.04%	39.6%	LEDLIVK	97.4%	30.6	25	17.4	1	0	0	829.50	175	181
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	22	43	0.04%	39.6%	LEDLIVKDGLTDVYNK	99.7%	53.1	25	52.5	1	0	0	1834.98	175	190
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	22	43	0.04%	39.6%	LNVTPLAR	99.7%	41.3	25	36.9	2	0	0	883.54	304	311
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	22	43	0.04%	39.6%	MLEIDPQK	95.3%	28.1	25	17	4	0	0	989.50	366	373
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	22	43	0.04%	39.6%	NEQDAYAINSYTR	99.7%	110	25	110	3	0	0	1544.70	209	221
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	22	43	0.04%	39.6%	QAVLGAGLPISTPCTTINK	99.7%	101	25	98.7	2	0	0	1941.05	106	124
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	22	43	0.04%	39.6%	RLNVTPLAR	99.6%	39.3	25	33.1	2	0	0	1039.64	303	311
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	22	43	0.04%	39.6%	TPIGSFLGSLSLLPATK	99.7%	114	25	114	5	0	0	1701.98	50	66
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	22	43	0.04%	39.6%	VNINGGAVSLGHPIGMSGAR	99.7%	65.1	25	64.9	2	4	0	1906.99	374	393
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	9	9	11	0.01%	4.4%	AIGIGAYLVR	99.7%	41.8	25	38.2	2	0	0	1032.62	1824	1833
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	9	9	11	0.01%	4.4%	ATLVDHGIR	99.4%	37	25	31.6	1	0	0	981.55	1317	1325
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	9	9	11	0.01%	4.4%	DFTVASPAEFVTR	99.5%	38.6	25	37.2	1	0	0	1439.72	99	111
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	9	9	11	0.01%	4.4%	DIIVIGNDITYR	99.7%	58.1	25	43.2	2	0	0	1391.75	1676	1687
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	9	9	11	0.01%	4.4%	IGSFGPQEDLLFLR	99.7%	52.9	25	47	1	0	0	1591.85	1688	1701
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	9	9	11	0.01%	4.4%	ILNVPQELYEK	99.2%	36	25	34.5	1	0	0	1345.74	278	288
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	9	9	11	0.01%	4.4%	MAALEVYVR	99.7%	59.3	25	39.3	1	0	0	1051.56	1147	1155
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	9	9	11	0.01%	4.4%	VEVGTEVTDYR	99.7%	53.5	25	53.3	1	0	0	1267.62	1410	1420
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	9	9	11	0.01%	4.4%	VQQAELHTGSLPR	99.7%	48.1	25	42.1	1	0	0	1435.77	826	838
Acidic fibroblast growth factor intracellular-binding protein	FIBP	FIBP_HUMAN	41.9	100.0%	3	3	5	0.01%	9.6%	DYAAIVFFANNR	99.0%	34.7	25	34.7	2	0	0	1400.70	172	183
Acidic fibroblast growth factor intracellular-binding protein	FIBP	FIBP_HUMAN	41.9	100.0%	3	3	5	0.01%	9.6%	VLVADKDLLDLHK	99.7%	32.1	25	31.2	0	1	0	1478.86	246	258
Acidic fibroblast growth factor intracellular-binding protein	FIBP	FIBP_HUMAN	41.9	100.0%	3	3	5	0.01%	9.6%	YYAFDEAFVR	99.7%	66.2	25	66.2	2	0	0	1280.59	96	105
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	39	269	0.27%	61.6%	AGFAGDDAPR	99.7%	80.9	25	70.1	22	0	0	976.45	19	28
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	39	269	0.27%	61.6%	AVFPSIVGRPR	99.7%	58.4	25	58.4	7	0	0	1198.71	29	39
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	39	269	0.27%	61.6%	CDVDIRK	99.7%	42.1	25	20.7	3	0	0	905.45	285	291
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	39	269	0.27%	61.6%	DLTDYLMK	99.7%	51.3	25	38	8	0	0	1014.48	184	191
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	39	269	0.27%	61.6%	DLYANTVLSGGTTMYPGIADR	99.7%	134	25	134	24	6	0	2231.07	292	312
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	39	269	0.27%	61.6%	DSYVGDEAQSK	99.7%	79.2	25	73.7	15	0	0	1198.52	51	61
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	39	269	0.27%	61.6%	DSYVGDEAQSKR	99.7%	70.6	25	67.9	13	2	0	1354.62	51	62
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	39	269	0.27%	61.6%	EITALAPSTMK	99.7%	77.6	25	51.8	39	0	0	1161.62	316	326
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	39	269	0.27%	61.6%	GYSFTTTAER	99.7%	79.2	25	72.3	20	0	0	1132.53	197	206
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	39	269	0.27%	61.6%	GYSFTTTAEREIVR	99.6%	31.6	25	31.6	2	2	0	1629.82	197	210
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	39	269	0.27%	61.6%	HQGVMVGMGQK	99.7%	71.2	25	71.2	16	2	0	1171.57	40	50

Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	39	269	0.27%	61.6%	IIAPPERK	99.7%	46.3	25	34.4	2	0	0	923.57	329	336
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	39	269	0.27%	61.6%	IWHHTFYNELR	99.7%	53	25	52.2	2	4	0	1515.75	85	95
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	39	269	0.27%	61.6%	KDLYANTVLSGGTTMYPGIADR	99.7%	72.4	25	72.4	0	2	0	2359.16	291	312
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	39	269	0.27%	61.6%	LCYVALDFEQEMATAASSSSLEK	99.7%	132	25	132	6	10	0	2566.17	216	238
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	39	269	0.27%	61.6%	LDLAGRDLTDYLMK	99.7%	42.9	25	39.4	4	2	0	1639.84	178	191
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	39	269	0.27%	61.6%	QEYDESGPSIVHR	99.7%	64.6	25	55.8	4	8	0	1516.70	360	372
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	39	269	0.27%	61.6%	QEYDESGPSIVHRK	99.7%	52.4	25	49.8	2	2	0	1644.80	360	373
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	39	269	0.27%	61.6%	SYELPDGQVITIGNER	99.7%	120	25	108	19	0	0	1790.89	239	254
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	39	269	0.27%	61.6%	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	99.7%	72.1	25	72.1	0	2	0	3199.61	148	177
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	39	269	0.27%	61.6%	VAPEEHPVLLTEAPLNPK	99.7%	103	25	61.8	11	8	0	1954.06	96	113
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	6	8	13	0.01%	16.5%	GYAFNHSADFETVR	99.7%	63.5	25	50.9	2	2	0	1613.73	201	214
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	6	8	13	0.01%	16.5%	ILLTEPPMNPTK	99.7%	59.7	25	51.9	4	0	0	1353.74	107	118
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	6	8	13	0.01%	16.5%	KVVVCDNGTGFVK	98.8%	34	25	34	1	0	0	1422.74	7	19
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	6	8	13	0.01%	16.5%	LCYVGYNIEQEQK	99.7%	82.2	25	82.2	2	0	0	1643.77	220	232
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	6	8	13	0.01%	16.5%	QLYLER	96.4%	29.2	25	6.48	1	0	0	821.45	323	328
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	6	8	13	0.01%	16.5%	RLDIAGR	95.5%	28.3	25	8.14	1	0	0	800.47	181	187
Actin-related protein 2/3 complex subunit 2	ARPC2	ARPC2_HUMAN	34.3	100.0%	3	3	4	0.00%	9.0%	IIEETLALK	97.0%	30.1	25	17.7	1	0	0	1029.62	10	18
Actin-related protein 2/3 complex subunit 2	ARPC2	ARPC2_HUMAN	34.3	100.0%	3	3	4	0.00%	9.0%	MILLEVNNR	99.7%	42.2	25	36.8	2	0	0	1101.61	1	9
Actin-related protein 2/3 complex subunit 2	ARPC2	ARPC2_HUMAN	34.3	100.0%	3	3	4	0.00%	9.0%	NCFASVFEK	98.2%	32.2	25	27.5	1	0	0	1101.50	119	127
Actin-related protein 2/3 complex subunit 3	ARPC3	ARPC3_HUMAN	20.5	100.0%	4	4	5	0.01%	24.7%	DTDIVDEAIYYFK	99.7%	50.9	25	45.9	1	0	0	1591.75	38	50
Actin-related protein 2/3 complex subunit 3	ARPC3	ARPC3_HUMAN	20.5	100.0%	4	4	5	0.01%	24.7%	LIGNMALLPIR	99.0%	34.8	25	30.8	2	0	0	1210.73	15	25
Actin-related protein 2/3 complex subunit 3	ARPC3	ARPC3_HUMAN	20.5	100.0%	4	4	5	0.01%	24.7%	SQFKGPAPR	97.8%	31.3	25	25.9	1	0	0	987.54	26	34
Actin-related protein 2/3 complex subunit 3	ARPC3	ARPC3_HUMAN	20.5	100.0%	4	4	5	0.01%	24.7%	VFDPQNDKPSK	99.7%	43.4	25	35.4	1	0	0	1274.64	148	158
Actin-related protein 2/3 complex subunit 4	ARPC4	ARPC4_HUMAN	19.7	100.0%	3	3	5	0.01%	13.1%	AENFFILR	96.0%	28.8	25	17.6	1	0	0	1009.55	98	105
Actin-related protein 2/3 complex subunit 4	ARPC4	ARPC4_HUMAN	19.7	100.0%	3	3	5	0.01%	13.1%	ELLLQPVTISR	99.7%	69.4	25	61.9	2	0	0	1268.76	45	55
Actin-related protein 2/3 complex subunit 4	ARPC4	ARPC4_HUMAN	19.7	100.0%	3	3	5	0.01%	13.1%	SSKELLLQPVTISR	99.7%	41.3	25	41.3	2	0	0	1570.92	42	55
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	8	10	15	0.02%	20.3%	DITYFIQQLLR	99.7%	80.9	25	68.7	2	0	0	1409.78	199	209
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	8	10	15	0.02%	20.3%	DYEEIGPSICR	99.3%	36.6	25	36.6	1	0	0	1338.60	399	409
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	8	10	15	0.02%	20.3%	FMEQVIFK	99.7%	42.1	25	25.4	3	0	0	1057.54	92	99
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	8	10	15	0.02%	20.3%	LPACVVDCGTGYTK	99.7%	75.6	25	75.6	1	0	0	1540.71	5	18
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	8	10	15	0.02%	20.3%	LSEELSGGR	99.7%	67.6	25	52.9	2	0	0	947.48	349	357
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	8	10	15	0.02%	20.3%	NIVLSGGSTMFR	99.7%	75.2	25	75	4	0	0	1281.66	318	329
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	8	10	15	0.02%	20.3%	QYTGINAISK	98.4%	32.7	25	31.2	1	0	0	1094.58	255	264
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	8	10	15	0.02%	20.3%	YSYVCPDLVK	99.5%	37.8	25	28.9	1	0	0	1243.60	231	240
Activating signal cointegrator 1 complex subunit 1	ASCC1	ASCC1_HUMAN	45.5	99.8%	2	2	3	0.00%	4.5%	FQASGLIVK	95.2%	28	25	12.5	1	0	0	962.57	289	297
Activating signal cointegrator 1 complex subunit 1	ASCC1	ASCC1_HUMAN	45.5	99.8%	2	2	3	0.00%	4.5%	YNLYTAEGK	99.7%	56.9	25	50.7	2	0	0	1058.52	323	331
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	5	5	8	0.01%	2.3%	DLADWLNIK	99.2%	35.8	25	26.4	1	0	0	1087.58	1498	1506
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	5	5	8	0.01%	2.3%	SVGDVALSQIVR	99.2%	35.9	25	28.8	1	0	0	1243.70	595	606
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	5	5	8	0.01%	2.3%	TGYFSSTDLGR	99.7%	73.8	25	65.5	2	0	0	1203.56	973	983
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	5	5	8	0.01%	2.3%	TVAAELAIFR	99.7%	72.1	25	69.7	2	0	0	1090.63	1356	1365
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	5	5	8	0.01%	2.3%	VFNKYPTSK	98.9%	34.4	25	30.5	2	0	0	1083.58	1366	1374
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	9	10	16	0.02%	28.4%	ADATNVNNWHWTER	99.3%	29.1	25	29.1	0	1	0	1713.77	17	30
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	9	10	16	0.02%	28.4%	DASNWSTDKLK	99.7%	59.2	25	36.6	2	0	0	1264.62	31	41
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	9	10	16	0.02%	28.4%	DEPDTNLVALMK	99.7%	55	25	49.3	1	0	0	1345.67	126	137
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	9	10	16	0.02%	28.4%	EAMGIYISTLK	99.7%	50.6	25	42.6	4	0	0	1225.65	146	156
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	9	10	16	0.02%	28.4%	ETFLTSPEELYR	99.7%	44.1	25	36.4	2	0	0	1484.73	213	224
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	9	10	16	0.02%	28.4%	GIPAPEEERTR	99.7%	50.9	25	49.7	2	0	0	1254.64	306	316
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	9	10	16	0.02%	28.4%	LDGEASINNR	99.7%	64.9	25	36.1	2	0	0	1088.53	64	73
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	9	10	16	0.02%	28.4%	QTFGYGAR	98.4%	32.8	25	21.9	1	0	0	899.44	329	336
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	9	10	16	0.02%	28.4%	WGEGDPR	96.6%	29.5	25	19.7	1	0	0	816.36	4	10
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	18	21	40	0.04%	28.2%	FFTEEVDSR	99.7%	71	25	56.2	2	0	0	1129.52	77	85

Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	18	21	40	0.04%	28.2%	FSMGSVVAGLLK	99.7%	64.1	25	60.5	4	0	0	1224.67	305	316
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	18	21	40	0.04%	28.2%	GIILAGTEEQK	99.7%	60.5	25	45.1	2	0	0	1158.64	152	162
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	18	21	40	0.04%	28.2%	GSNTCEVHFENTK	99.7%	65.8	25	58.5	2	0	0	1522.66	267	279
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	18	21	40	0.04%	28.2%	ILLIFEGTNEILR	99.7%	67.3	25	59.6	2	0	0	1530.89	421	433
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	18	21	40	0.04%	28.2%	IPVENILGEVGDGFK	99.7%	60.6	25	60.6	2	0	0	1586.84	280	294
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	18	21	40	0.04%	28.2%	ITAFIVER	99.7%	56.4	25	44.4	2	0	0	948.55	242	249
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	18	21	40	0.04%	28.2%	LIEMTAEYACTR	99.7%	90.7	25	90.7	4	0	0	1473.67	318	329
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	18	21	40	0.04%	28.2%	LSEFGLIQEK	99.7%	74.9	25	59.9	2	0	0	1163.63	336	345
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	18	21	40	0.04%	28.2%	TEVVDSDGSVK	98.7%	33.7	25	32.9	1	0	0	1135.55	229	239
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	18	21	40	0.04%	28.2%	TEVVDSDGSVKDK	99.7%	63.2	25	56	2	0	0	1378.67	229	241
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	18	21	40	0.04%	28.2%	TIMEEQLVLK	99.7%	53.3	25	37.2	2	0	0	1203.67	522	531
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	18	21	40	0.04%	28.2%	TIMEEQLVLKR	97.3%	30.4	25	18.5	1	0	0	1359.77	522	532
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	18	21	40	0.04%	28.2%	TVETLLLR	99.7%	57.5	25	33.5	2	0	0	944.58	511	518
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	18	21	40	0.04%	28.2%	VAMNILNSGR	99.7%	74.8	25	66	2	0	0	1090.57	295	304
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	18	21	40	0.04%	28.2%	VSQQILEK	99.7%	52.2	25	32.5	2	0	0	944.54	601	608
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	18	21	40	0.04%	28.2%	VSTVMDTVGR	99.7%	88	25	73.5	4	0	0	1064.54	460	469
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	18	21	40	0.04%	28.2%	YAPENLDEQIKK	99.7%	41.1	25	33.3	2	0	0	1447.74	589	600
Acyl-coenzyme A thioesterase 1	ACOT1	ACOT1_HUMAN	46.3	100.0%	3	3	5	0.01%	7.4%	AATLILEPAGR	99.7%	52	25	50.3	1	0	0	1111.65	2	12
Acyl-coenzyme A thioesterase 1	ACOT1	ACOT1_HUMAN	46.3	100.0%	3	3	5	0.01%	7.4%	GALFQAHAR	99.7%	50.7	25	35.7	2	0	0	970.52	43	51
Acyl-coenzyme A thioesterase 1	ACOT1	ACOT1_HUMAN	46.3	100.0%	3	3	5	0.01%	7.4%	GLAPEQPVTLR	99.7%	50.9	25	43.5	2	0	0	1180.67	25	35
Acyl-coenzyme A thioesterase 13	ACOT13	ACO13_HUMAN	15.0	100.0%	3	3	9	0.01%	28.6%	GAPGVSVDMNITYMSPAK	99.7%	58.9	25	58.9	1	0	0	1869.87	78	95
Acyl-coenzyme A thioesterase 13	ACOT13	ACO13_HUMAN	15.0	100.0%	3	3	9	0.01%	28.6%	ITLVSAAPGK	99.7%	53.2	25	40.5	4	0	0	956.58	28	37
Acyl-coenzyme A thioesterase 13	ACOT13	ACO13_HUMAN	15.0	100.0%	3	3	9	0.01%	28.6%	TLAFTSVDLTNK	99.7%	108	25	100	4	0	0	1309.70	112	123
Acyl-coenzyme A thioesterase 8	ACOT8	ACOT8_HUMAN	35.9	100.0%	2	2	4	0.00%	7.8%	LFGGQIVGQALVAAAK	99.7%	101	25	99	2	0	0	1542.90	54	69
Acyl-coenzyme A thioesterase 8	ACOT8	ACOT8_HUMAN	35.9	100.0%	2	2	4	0.00%	7.8%	LPVLYQVER	99.7%	55.3	25	51.3	2	0	0	1116.64	92	100
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	ACOT9_HUMAN	49.9	100.0%	6	6	11	0.01%	13.4%	EIVGASTNWR	99.7%	42.9	25	36.2	1	0	0	1132.57	46	55
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	ACOT9_HUMAN	49.9	100.0%	6	6	11	0.01%	13.4%	FSGHVSWVGK	99.7%	53.6	25	43.1	2	0	0	1103.56	167	176
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	ACOT9_HUMAN	49.9	100.0%	6	6	11	0.01%	13.4%	IAFSSTSLLK	99.7%	41.5	25	41.5	2	0	0	1066.61	241	250
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	ACOT9_HUMAN	49.9	100.0%	6	6	11	0.01%	13.4%	IFGGFLMR	99.7%	55.8	25	48.4	2	0	0	940.51	310	317
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	ACOT9_HUMAN	49.9	100.0%	6	6	11	0.01%	13.4%	SLEICHPQER	99.7%	46.5	25	44.3	2	0	0	1268.61	295	304
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	ACOT9_HUMAN	49.9	100.0%	6	6	11	0.01%	13.4%	VHSEVASLQEK	99.7%	47.8	25	41	2	0	0	1226.64	373	383
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	5	6	12	0.01%	12.3%	ATVFLNPAACK	99.7%	61.2	25	55.5	2	0	0	1191.62	63	73
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	5	6	12	0.01%	12.3%	EQPVFAMTGLR	99.7%	45.6	25	45.6	4	0	0	1248.64	200	210
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	5	6	12	0.01%	12.3%	GDFITIGSR	99.7%	68.4	25	56.9	2	0	0	965.51	343	351
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	5	6	12	0.01%	12.3%	GETVPLDVLQIK	99.7%	52.3	25	42.6	2	0	0	1311.75	185	196
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	5	6	12	0.01%	12.3%	RTDEATFSK	99.7%	43	25	37	2	0	0	1054.52	138	146
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	5	7	22	0.02%	35.6%	AELEIQKDALEPGQR	99.7%	71	25	68.6	4	3	0	1696.89	108	122
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	5	7	22	0.02%	35.6%	DISPVLKDPASFR	99.7%	64.4	25	58.7	4	2	0	1444.78	28	40
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	5	7	22	0.02%	35.6%	IDYIAGLDSR	99.7%	64.3	25	56	4	0	0	1122.58	58	67
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	5	7	22	0.02%	35.6%	LAPVPFFSLLQYE	99.7%	45.9	25	45.9	2	0	0	1523.81	168	180
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	5	7	22	0.02%	35.6%	SFPDFPTPGVVFR	99.4%	37.4	25	32.9	3	0	0	1465.75	15	27
Adenosylhomocysteinase	AHCY	SAHH_HUMAN	47.7	100.0%	5	5	8	0.01%	13.2%	GISEETTTGVHNLYK	99.7%	74.7	25	65	1	0	0	1648.82	152	166
Adenosylhomocysteinase	AHCY	SAHH_HUMAN	47.7	100.0%	5	5	8	0.01%	13.2%	IILLAEGR	99.7%	45.4	25	34.7	2	0	0	884.56	336	343
Adenosylhomocysteinase	AHCY	SAHH_HUMAN	47.7	100.0%	5	5	8	0.01%	13.2%	SKFDNLYGCR	99.7%	42.2	25	39.4	1	0	0	1259.58	187	196
Adenosylhomocysteinase	AHCY	SAHH_HUMAN	47.7	100.0%	5	5	8	0.01%	13.2%	VAVVAGYGDVGK	99.7%	71.3	25	55.3	2	0	0	1134.62	215	226
Adenosylhomocysteinase	AHCY	SAHH_HUMAN	47.7	100.0%	5	5	8	0.01%	13.2%	VPAINVNDSVTK	99.7%	69.5	25	65.4	2	0	0	1256.68	175	186
Adenylate kinase 2, mitochondrial	AK2	KAD2_HUMAN	26.5	100.0%	3	3	4	0.00%	13.8%	AMVASGSELGKK	96.8%	29.8	25	25.9	1	0	0	1177.62	52	63
Adenylate kinase 2, mitochondrial	AK2	KAD2_HUMAN	26.5	100.0%	3	3	4	0.00%	13.8%	AVLLGPPGAGK	99.0%	35	25	29.4	1	0	0	979.59	18	28
Adenylate kinase 2, mitochondrial	AK2	KAD2_HUMAN	26.5	100.0%	3	3	4	0.00%	13.8%	NGFLLDGFPR	99.7%	48.5	25	47.3	2	0	0	1135.59	94	103
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	8	14	0.01%	34.5%	ASTEVGEMAK	99.4%	37.4	25	22.3	1	0	0	1022.48	46	55
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	8	14	0.01%	34.5%	AVILGPPGSGK	99.7%	45.5	25	28.6	2	0	0	995.59	8	18

Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	8	14	0.01%	34.5%	DVAKPVIELYK	99.5%	37.9	25	29.1	2	0	0	1274.74	176	186
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	8	14	0.01%	34.5%	GVLHQFSGTETNK	99.7%	49.7	25	48.3	2	2	0	1417.71	189	201
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	8	14	0.01%	34.5%	IWPYVYTLFSNK	95.8%	28.6	25	19.1	1	0	0	1530.80	202	213
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	8	14	0.01%	34.5%	LMMSELENR	99.7%	49.8	25	46.3	2	0	0	1122.53	72	80
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	8	14	0.01%	34.5%	SLLVPDHVITR	99.4%	37.6	25	35.6	2	0	0	1249.73	61	71
Adenylate kinase isoenzyme 6	AK6	KAD6_HUMAN	20.1	99.8%	2	2	3	0.00%	10.5%	TDTNVLYER	99.7%	71.4	25	59.5	2	0	0	1110.54	97	105
Adenylate kinase isoenzyme 6	AK6	KAD6_HUMAN	20.1	99.8%	2	2	3	0.00%	10.5%	YINVGDLAR	98.8%	34.1	25	22.2	1	0	0	1020.55	31	39
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	7	7	12	0.01%	21.3%	FLEEEVYPLLKPYESVMK	99.7%	39.3	25	31	0	2	0	2214.14	460	477
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	7	7	12	0.01%	21.3%	IQVDAYFSPIHSQLDHLLDPSSFTGR	99.7%	37.7	25	37.7	0	1	0	2943.46	427	452
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	7	7	12	0.01%	21.3%	NALDLLLPK	99.7%	41.1	25	30.2	2	0	0	996.61	126	134
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	7	7	12	0.01%	21.3%	QELPFMATENIIMAMVK	99.7%	55.5	25	50.4	1	0	0	1965.98	375	391
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	7	7	12	0.01%	21.3%	SNLENIDFK	99.7%	45.3	25	38.6	2	0	0	1079.54	67	75
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	7	7	12	0.01%	21.3%	VLSQQAASVVK	99.7%	73.2	25	55.9	2	0	0	1129.66	405	415
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	7	7	12	0.01%	21.3%	YASPEMCFVFSDR	99.7%	46	25	46	2	0	0	1608.68	21	33
Adenylosuccinate synthetase isozyme 2	ADSS	PURA2_HUMAN	50.1	100.0%	3	3	5	0.01%	7.7%	FIEDELQIPVK	99.7%	50.9	25	38.8	2	0	0	1330.73	431	441
Adenylosuccinate synthetase isozyme 2	ADSS	PURA2_HUMAN	50.1	100.0%	3	3	5	0.01%	7.7%	GREFGVTTGR	99.7%	43.7	25	36	1	0	0	1079.56	325	334
Adenylosuccinate synthetase isozyme 2	ADSS	PURA2_HUMAN	50.1	100.0%	3	3	5	0.01%	7.7%	VVDLLAQDADIVCR	99.7%	90.9	25	82.6	2	0	0	1586.82	46	59
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	43.6%	AAYFGVYDTAK	99.7%	88.7	25	88.7	8	0	0	1205.58	189	199
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	43.6%	DFLAGGVAAAVSK	99.7%	113	25	108	5	0	0	1205.65	11	23
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	43.6%	EFHGLGDCIIK	99.7%	40.2	25	33.1	4	0	0	1288.64	153	163
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	43.6%	EQGFLSFWR	99.7%	60.1	25	51.7	6	0	0	1169.57	64	72
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	43.6%	GADIMYTGTVDCWR	99.7%	84.3	25	77.7	7	0	0	1644.71	246	259
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	43.6%	GAWSNVLR	99.7%	58.6	25	40	6	0	0	902.48	273	280
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	43.6%	GMGGAFVLVLYDEIK	99.7%	53.3	25	0	1	0	0	1627.84	281	295
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	43.6%	LLLQVQHASK	99.7%	47.2	25	36.6	26	0	0	1136.68	34	43
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	43.6%	MMMQSGR	99.7%	45.7	25	45.7	3	0	0	840.35	238	244
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	43.6%	QLFLGGVDR	99.7%	47.2	25	30.7	4	0	0	1004.55	97	105
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	43.6%	RMMMQSGR	99.3%	36.5	25	30.4	2	0	0	996.45	237	244
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	43.6%	TAVAPIER	99.7%	44.6	25	29.3	7	0	0	856.49	24	31
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	43.6%	YFPTQALNFAFK	99.7%	87.1	25	71.7	41	0	0	1446.74	81	92
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	43.6%	YFPTQALNFAFKDK	99.7%	74.7	25	72.8	4	0	0	1689.86	81	94
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	163	0.16%	43.6%	AAYFGIYDTAK	99.7%	75.8	25	58.1	6	0	0	1219.60	189	199
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	163	0.16%	43.6%	DFLAGGVAAAISK	99.7%	101	25	91.3	7	0	0	1219.67	11	23
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	163	0.16%	43.6%	EQGVLSFWR	99.7%	69.8	25	64.4	26	0	0	1121.57	64	72
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	163	0.16%	43.6%	GAWSNVLR	99.7%	58.6	25	40	6	0	0	902.48	273	280
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	163	0.16%	43.6%	GLGDCLVK	98.0%	31.7	25	20.8	3	0	0	861.45	156	163
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	163	0.16%	43.6%	GMGGAFVLVLYDEIK	99.7%	53.3	25	0	1	0	0	1627.84	281	295
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	163	0.16%	43.6%	GTDIMYTGTLDCWR	99.7%	82.4	25	82.2	8	0	0	1704.74	246	259
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	163	0.16%	43.6%	GTDIMYTGTLDCWRK	99.4%	37	25	37	2	0	0	1816.84	246	260
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	163	0.16%	43.6%	KGTDIMYTGTLDCWR	99.7%	68	25	66.5	4	2	0	1832.83	245	259
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	163	0.16%	43.6%	LLLQVQHASK	99.7%	47.2	25	36.6	26	0	0	1136.68	34	43
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	163	0.16%	43.6%	MMMQSGR	99.7%	45.7	25	45.7	3	0	0	840.35	238	244
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	163	0.16%	43.6%	QIFLGGVDK	99.7%	48.1	25	28.9	6	0	0	976.55	97	105
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	163	0.16%	43.6%	QIFLGGVDKR	99.7%	41.9	25	29.2	9	0	0	1132.65	97	106
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	163	0.16%	43.6%	RMMMQSGR	99.3%	36.5	25	30.4	2	0	0	996.45	237	244
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	163	0.16%	43.6%	TAVAPIER	99.7%	44.6	25	29.3	7	0	0	856.49	24	31
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	163	0.16%	43.6%	YFPTQALNFAFK	99.7%	87.1	25	71.7	41	0	0	1446.74	81	92
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	163	0.16%	43.6%	YFPTQALNFAFKDK	99.7%	74.7	25	72.8	4	0	0	1689.86	81	94
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	3	4	41	0.04%	42.6%	AAYFGVYDTAK	99.7%	88.7	25	88.7	8	0	0	1205.58	189	199
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	3	4	41	0.04%	42.6%	DFLAGGIAAAISK	99.7%	102	25	96.7	26	0	0	1233.68	11	23
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	3	4	41	0.04%	42.6%	EQGVLSFWR	99.7%	69.8	25	64.4	26	0	0	1121.57	64	72

ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	3	4	41	0.04%	42.6%	GADIMYTGTVDCWR	99.7%	84.3	25	77.7	7	0	0	1644.71	246	259
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	3	4	41	0.04%	42.6%	GAWSNVLR	99.7%	58.6	25	40	6	0	0	902.48	273	280
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	3	4	41	0.04%	42.6%	GLGDCLVK	98.0%	31.7	25	20.8	3	0	0	861.45	156	163
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	3	4	41	0.04%	42.6%	GMGGAFVLVLYDELK	99.7%	53.3	25	0	1	0	0	1627.84	281	295
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	3	4	41	0.04%	42.6%	LLLQVQHASK	99.7%	47.2	25	36.6	26	0	0	1136.68	34	43
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	3	4	41	0.04%	42.6%	MMMQSGR	99.7%	45.7	25	45.7	3	0	0	840.35	238	244
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	3	4	41	0.04%	42.6%	QIFLGGVDK	99.7%	48.1	25	28.9	6	0	0	976.55	97	105
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	3	4	41	0.04%	42.6%	RMMMQSGR	99.3%	36.5	25	30.4	2	0	0	996.45	237	244
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	3	4	41	0.04%	42.6%	TAVAPIER	99.7%	44.6	25	29.3	7	0	0	856.49	24	31
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	3	4	41	0.04%	42.6%	YFPTQALNFAFK	99.7%	87.1	25	71.7	41	0	0	1446.74	81	92
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	3	4	41	0.04%	42.6%	YFPTQALNFAFKDK	99.7%	74.7	25	72.8	4	0	0	1689.86	81	94
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN	20.6	99.8%	2	3	6	0.01%	24.9%	DAVLLVFANK	99.7%	78	25	64.6	4	0	0	1089.63	118	127
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN	20.6	99.8%	2	3	6	0.01%	24.9%	ILMVGLDAAGK	99.7%	73.5	25	58.5	10	0	0	1103.61	20	30
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN	20.6	99.8%	2	3	6	0.01%	24.9%	NISFTVWDVGGQDK	99.7%	89.4	25	81.9	4	0	0	1565.76	60	73
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN	20.6	99.8%	2	3	6	0.01%	24.9%	VNEAREELMR	99.7%	31.9	25	31.1	1	1	0	1262.62	100	109
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	5	7	20	0.02%	32.2%	ILMVGLDAAGK	99.7%	73.5	25	58.5	10	0	0	1103.61	20	30
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	5	7	20	0.02%	32.2%	IQEVADELQK	99.7%	62.9	25	47.3	3	0	0	1172.62	100	109
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	5	7	20	0.02%	32.2%	MLLVDELR	99.7%	42.3	25	32.5	1	0	0	988.55	110	117
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	5	7	20	0.02%	32.2%	NICFTVWDVGGQDR	99.7%	104	25	96	2	0	0	1666.76	60	73
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	5	7	20	0.02%	32.2%	QDLPNAMAISEMTDK	99.7%	67.1	25	66	4	0	0	1695.76	128	142
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	100.0%	4	4	9	0.01%	33.3%	DAVLLVFANK	99.7%	78	25	64.6	4	0	0	1089.63	118	127
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	100.0%	4	4	9	0.01%	33.3%	ILMVGLDAAGK	99.7%	73.5	25	58.5	10	0	0	1103.61	20	30
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	100.0%	4	4	9	0.01%	33.3%	NICFTVWDVGGQDK	99.7%	95.1	25	91	2	0	0	1638.76	60	73
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	100.0%	4	4	9	0.01%	33.3%	QDMPNAMPVSELTDK	99.6%	39.3	25	38.2	1	0	0	1675.77	128	142
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	100.0%	4	4	9	0.01%	33.3%	VQESADELQK	99.7%	55.7	25	48.7	2	0	0	1146.56	100	109
ADP-ribosylation factor 6	ARF6	ARF6_HUMAN	20.1	100.0%	5	7	13	0.01%	34.9%	DAIILIFANK	99.7%	45	25	0	2	0	0	1117.66	114	123
ADP-ribosylation factor 6	ARF6	ARF6_HUMAN	20.1	100.0%	5	7	13	0.01%	34.9%	FNVWDVGGQDK	99.7%	62	25	50.4	2	0	0	1264.60	59	69
ADP-ribosylation factor 6	ARF6	ARF6_HUMAN	20.1	100.0%	5	7	13	0.01%	34.9%	IFGNKEMR	99.7%	43.6	25	28	1	0	0	994.51	8	15
ADP-ribosylation factor 6	ARF6	ARF6_HUMAN	20.1	100.0%	5	7	13	0.01%	34.9%	ILMLGLDAAGK	99.7%	67.9	25	57.7	4	0	0	1101.63	16	26
ADP-ribosylation factor 6	ARF6	ARF6_HUMAN	20.1	100.0%	5	7	13	0.01%	34.9%	LGQSVTTIPTVGFNVETVTYK	99.7%	40.5	25	40.5	2	2	0	2254.20	35	55
ADP-ribosylation factor-like protein 1	ARL1	ARL1_HUMAN	20.4	100.0%	3	4	7	0.01%	16.0%	AILVVFANK	99.7%	64.9	25	64.9	2	0	0	974.60	119	127
ADP-ribosylation factor-like protein 1	ARL1	ARL1_HUMAN	20.4	100.0%	3	4	7	0.01%	16.0%	KWQIFK	99.7%	42.2	25	16.6	2	0	0	849.50	152	157
ADP-ribosylation factor-like protein 1	ARL1	ARL1_HUMAN	20.4	100.0%	3	4	7	0.01%	16.0%	SELVAMLEEEELRK	99.7%	45.8	25	41.8	3	0	0	1691.85	105	118
ADP-ribosylation factor-like protein 10	ARL10	ARL10_HUMAN	27.5	99.8%	2	2	3	0.00%	11.5%	EVLVLGLDGAGK	99.7%	57.8	25	47.7	2	0	0	1170.67	79	90
ADP-ribosylation factor-like protein 10	ARL10	ARL10_HUMAN	27.5	99.8%	2	2	3	0.00%	11.5%	LLDKDPDLPVVVVANK	99.6%	31.3	25	31.3	0	1	0	1735.00	171	186
ADP-ribosylation factor-like protein 2	ARL2	ARL2_HUMAN	20.9	100.0%	4	5	10	0.01%	25.0%	LAGATLLIFANK	99.7%	55.5	25	55.5	2	0	0	1231.74	115	126
ADP-ribosylation factor-like protein 2	ARL2	ARL2_HUMAN	20.9	100.0%	4	5	10	0.01%	25.0%	LLMLGLDNAGK	99.7%	62.4	25	44.4	4	0	0	1144.64	19	29
ADP-ribosylation factor-like protein 2	ARL2	ARL2_HUMAN	20.9	100.0%	4	5	10	0.01%	25.0%	LNIWDVGGQK	99.7%	47.9	25	42.4	2	0	0	1129.60	62	71
ADP-ribosylation factor-like protein 2	ARL2	ARL2_HUMAN	20.9	100.0%	4	5	10	0.01%	25.0%	QDLPGALSSNAIR	99.7%	69.7	25	64.6	2	0	0	1341.71	127	139
ADP-ribosylation factor-like protein 6	ARL6	ARL6_HUMAN	21.1	100.0%	5	6	9	0.01%	29.6%	EGQAIIFVIDSSDR	99.7%	71.7	25	71.7	2	0	0	1549.79	86	99
ADP-ribosylation factor-like protein 6	ARL6	ARL6_HUMAN	21.1	100.0%	5	6	9	0.01%	29.6%	IPILFFANK	99.7%	40.2	25	23.9	2	0	0	1062.63	123	131
ADP-ribosylation factor-like protein 6	ARL6	ARL6_HUMAN	21.1	100.0%	5	6	9	0.01%	29.6%	LSVLLGLK	99.7%	40.2	25	34	2	0	0	842.57	7	14
ADP-ribosylation factor-like protein 6	ARL6	ARL6_HUMAN	21.1	100.0%	5	6	9	0.01%	29.6%	NLWEHYYK	96.1%	28.9	25	18.8	1	0	0	1152.55	78	85
ADP-ribosylation factor-like protein 6	ARL6	ARL6_HUMAN	21.1	100.0%	5	6	9	0.01%	29.6%	SSSLSFTVFDMSGQGR	99.7%	77.2	25	77.2	2	0	0	1705.79	60	75
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	7	7	12	0.01%	8.3%	GLGYAQYLPK	96.7%	29.6	25	20.2	1	0	0	1109.60	602	611
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	7	7	12	0.01%	8.3%	ILINDAYKR	99.7%	48.2	25	39	1	0	0	1105.64	703	711
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	7	7	12	0.01%	8.3%	KTQVLQPEEK	99.6%	38.8	25	13.5	2	0	0	1199.66	559	568
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	7	7	12	0.01%	8.3%	QIFIGPPDIK	97.9%	31.5	25	17.5	2	0	0	1127.65	472	481
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	7	7	12	0.01%	8.3%	VALLLLEK	99.2%	36.1	25	36.1	2	0	0	898.60	726	733
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	7	7	12	0.01%	8.3%	VGQISFDLPR	99.7%	72.2	25	53.9	2	0	0	1131.62	670	679
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	7	7	12	0.01%	8.3%	VSEEIFFGR	99.7%	66	25	46.4	2	0	0	1083.55	633	641

Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	5	5	10	0.01%	11.0%	FAVALLDDSVR	99.7%	81.4	25	59.6	2	0	0	1205.65	166	176
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	5	5	10	0.01%	11.0%	GALLSVGWSTGR	99.7%	68.1	25	59.7	2	0	0	1203.65	467	478
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	5	5	10	0.01%	11.0%	GQWINLPVLQLTK	99.7%	58.3	25	46.9	2	0	0	1509.88	40	52
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	5	5	10	0.01%	11.0%	ILATTPSAVFR	99.7%	61.1	25	52.1	2	0	0	1175.68	302	312
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	5	5	10	0.01%	11.0%	VYNASSTIVPSLK	99.7%	68.9	25	59.3	2	0	0	1378.76	177	189
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	13	13	21	0.02%	15.6%	AAFLNFFR	99.7%	46	25	34.7	2	0	0	985.53	44	51
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	13	13	21	0.02%	15.6%	AGLDPDLETR	99.7%	46.3	25	39.8	2	0	0	1086.54	178	187
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	13	13	21	0.02%	15.6%	AGQEDVLFPVAR	97.7%	31.2	25	26.6	1	0	0	1301.68	581	592
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	13	13	21	0.02%	15.6%	DIWLSLGVPASR	99.4%	37.1	25	31.6	2	0	0	1313.72	188	199
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	13	13	21	0.02%	15.6%	EADGSLQPLPQR	98.0%	31.8	25	26.9	1	0	0	1310.67	251	262
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	13	13	21	0.02%	15.6%	ELGQSLAQEVK	99.7%	55.7	25	44.1	2	0	0	1201.64	791	801
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	13	13	21	0.02%	15.6%	GPLIVDTVSAESLSVLVK	99.7%	56	25	56	1	0	0	1827.05	881	898
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	13	13	21	0.02%	15.6%	HVDTGMGLER	98.3%	32.6	25	32.6	1	0	0	1114.53	263	272
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	13	13	21	0.02%	15.6%	LLAVTGEQAQQAR	99.7%	87.8	25	78.2	2	0	0	1384.75	778	790
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	13	13	21	0.02%	15.6%	LVPSASVRPR	99.7%	43.8	25	41.2	2	0	0	1081.65	58	67
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	13	13	21	0.02%	15.6%	LWISYFDGDPK	99.7%	53.2	25	50.3	2	0	0	1340.65	167	177
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	13	13	21	0.02%	15.6%	TGAVGDLVIIGDR	99.7%	85.2	25	76	2	0	0	1285.71	757	769
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	13	13	21	0.02%	15.6%	TNFYAEQGGQASDR	99.7%	98.9	25	98.9	1	0	0	1543.68	562	575
Alcohol dehydrogenase class-3	ADH5	ADHX_HUMAN	39.7	100.0%	3	3	5	0.01%	9.6%	AFELMHSGK	99.7%	47.4	25	37.5	1	0	0	1019.50	358	366
Alcohol dehydrogenase class-3	ADH5	ADHX_HUMAN	39.7	100.0%	3	3	5	0.01%	9.6%	AGDTVIPLYIPQCGECK	99.7%	55.7	25	51.5	2	0	0	1920.92	85	101
Alcohol dehydrogenase class-3	ADH5	ADHX_HUMAN	39.7	100.0%	3	3	5	0.01%	9.6%	IIGVDINKDK	99.7%	51.4	25	18.4	2	0	0	1114.65	219	228
Aldehyde dehydrogenase family 16 member A1	ALDH16A1	A16A1_HUMAN	85.1	100.0%	3	3	5	0.01%	4.1%	GLDGAVDMGAR	99.7%	50.3	25	34.7	2	0	0	1061.50	335	345
Aldehyde dehydrogenase family 16 member A1	ALDH16A1	A16A1_HUMAN	85.1	100.0%	3	3	5	0.01%	4.1%	GWSAHPGVVR	98.1%	31.9	25	20.9	1	0	0	1065.56	92	101
Aldehyde dehydrogenase family 16 member A1	ALDH16A1	A16A1_HUMAN	85.1	100.0%	3	3	5	0.01%	4.1%	LLWTLESLVTGR	99.7%	68.3	25	61.9	2	0	0	1387.79	118	129
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	8	9	17	0.02%	21.5%	IAKEEIFGPVQPLFK	99.7%	33.4	25	33.4	0	1	0	1715.97	412	426
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	8	9	17	0.02%	21.5%	KIEEVVER	99.7%	63.7	25	46.3	2	0	0	1001.56	429	436
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	8	9	17	0.02%	21.5%	LAPALATGNTVVMK	99.7%	86.2	25	79.5	4	0	0	1401.78	196	209
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	8	9	17	0.02%	21.5%	LLNLLADLVER	99.7%	75.5	25	61.1	2	0	0	1268.76	104	114
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	8	9	17	0.02%	21.5%	TFVEESIYNEFLER	99.7%	88.9	25	75.6	2	0	0	1775.85	325	338
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	8	9	17	0.02%	21.5%	VAEQTPLSALYLASLIK	99.7%	94.9	25	94.9	2	0	0	1817.04	210	226
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	8	9	17	0.02%	21.5%	VGNPFELDTQQGPQVDKEQFER	99.7%	51.2	25	51.2	0	2	0	2561.23	348	369
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	8	9	17	0.02%	21.5%	VLGYIQLGQK	99.7%	61.4	25	53	2	0	0	1118.66	370	379
Aldehyde dehydrogenase, mitochondrial	ALDH2	ALDH2_HUMAN	56.4	99.8%	2	2	3	0.00%	5.8%	VAEQTPLTALYVANLIK	99.7%	59.1	25	59.1	1	0	0	1844.05	210	226
Aldehyde dehydrogenase, mitochondrial	ALDH2	ALDH2_HUMAN	56.4	99.8%	2	2	3	0.00%	5.8%	VIQVAAGSSNLKR	99.7%	47.5	25	47.5	2	0	0	1342.78	269	281
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	5	5	7	0.01%	10.0%	ESISDVGFGMLK	98.8%	33.9	25	33.9	1	0	0	1282.63	629	640
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	5	5	7	0.01%	10.0%	GISDPLTVFEQTEAAAR	99.7%	81.5	25	74.3	2	0	0	1804.91	587	603
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	5	5	7	0.01%	10.0%	GVQFAPFSTCR	99.7%	40.8	25	39.3	1	0	0	1269.60	556	566
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	5	5	7	0.01%	10.0%	IRPVPEYQK	98.0%	31.7	25	22.5	2	0	0	1129.64	381	389
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	5	5	7	0.01%	10.0%	YGSVAFPNFEQGVACLR	99.7%	53.8	25	52.6	1	0	0	1914.92	390	406
All-trans-retinol 13,14-reductase	RETSAT	RETST_HUMAN	66.8	99.8%	2	2	3	0.00%	4.3%	ATVQSVLLDSAGK	99.7%	70.7	25	62.5	2	0	0	1288.71	318	330
All-trans-retinol 13,14-reductase	RETSAT	RETST_HUMAN	66.8	99.8%	2	2	3	0.00%	4.3%	VVSSGAPHAILLK	98.5%	33.1	25	30.9	1	0	0	1291.77	200	212
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	4	4	5	0.01%	9.3%	EGGTVVYGGK	99.6%	38.8	25	18.8	1	0	0	966.49	391	400
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	4	4	5	0.01%	9.3%	IWADIPAPK	98.4%	32.8	25	23.2	1	0	0	1010.57	101	109
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	4	4	5	0.01%	9.3%	VGNPWDPNVLYGPLHTK	95.3%	22.1	25	22.1	0	1	0	1906.98	359	375
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	4	4	5	0.01%	9.3%	VNLLSFTGSTQVGK	99.7%	104	25	104	2	0	0	1450.79	267	280
Alpha-aminoadipic semialdehyde synthase, mitochondrial	AASS	AASS_HUMAN	102.1	100.0%	3	3	4	0.00%	3.9%	EIYGPILER	99.5%	37.8	25	31.4	1	0	0	1089.59	902	910
Alpha-aminoadipic semialdehyde synthase, mitochondrial	AASS	AASS_HUMAN	102.1	100.0%	3	3	4	0.00%	3.9%	NSSQAVQAVR	99.7%	61.7	25	47.6	1	0	0	1059.55	190	199
Alpha-aminoadipic semialdehyde synthase, mitochondrial	AASS	AASS_HUMAN	102.1	100.0%	3	3	4	0.00%	3.9%	SIGPLTFVFTGTGNVSK	99.0%	35	25	35	2	0	0	1724.92	213	229
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	14	29	0.03%	37.0%	ACYLSINPQKDETLETEK	99.7%	77.1	25	77.1	2	2	0	2139.03	221	238
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	14	29	0.03%	37.0%	AGFAGDQIPK	99.7%	61	25	42.4	2	0	0	1003.52	23	32
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	14	29	0.03%	37.0%	AQYYLPDGSTIEIGPSR	99.7%	94.3	25	94.3	2	0	0	1866.92	239	255

Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	14	29	0.03%	37.0%	DQLQTFSEEHPVLLTEAPLNPR	99.7%	66.4	25	59.1	0	2	0	2534.29	97	118
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	14	29	0.03%	37.0%	EGYDFHSSSEFEIVK	99.7%	68.7	25	62.5	2	1	0	1773.80	201	215
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	14	29	0.03%	37.0%	IWQYVYSK	99.7%	42.2	25	31.9	2	0	0	1086.56	89	96
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	14	29	0.03%	37.0%	LLSEVKK	99.5%	38	25	15.4	2	0	0	816.52	314	320
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	14	29	0.03%	37.0%	TLFSNIVLSGGSTLFK	99.7%	131	25	131	4	1	0	1683.93	293	308
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	14	29	0.03%	37.0%	VMAGALEGDIFIGPK	99.7%	89.2	25	0	5	0	0	1533.80	47	61
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	14	29	0.03%	37.0%	YCFPNYVGRPK	99.7%	53.9	25	53.9	2	0	0	1400.68	33	43
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	12	28	0.03%	33.9%	AAVPSGASTGIYEALELR	99.7%	127	25	126	2	0	0	1804.94	33	50
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	12	28	0.03%	33.9%	DATNVGDEGGFAPNILENKEGLELLK	99.7%	56.4	25	56.4	0	2	0	2743.38	203	228
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	12	28	0.03%	33.9%	GNPTVEVDLFTSK	99.7%	80.6	25	30.9	2	0	0	1406.72	16	28
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	12	28	0.03%	33.9%	IEEELGSK	97.2%	30.3	25	13.2	1	0	0	904.46	413	420
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	12	28	0.03%	33.9%	IGAEVYHNLK	99.7%	58.7	25	49.9	4	0	0	1143.62	184	193
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	12	28	0.03%	33.9%	LAMQEFMILPVGAANFR	99.7%	73.8	25	73.8	5	0	0	1939.98	163	179
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	12	28	0.03%	33.9%	SCNCLLLK	99.2%	36	25	27.8	2	0	0	1007.50	336	343
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	12	28	0.03%	33.9%	VNQIGSVTESLQACK	99.7%	140	25	0	4	0	0	1633.82	344	358
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	12	28	0.03%	33.9%	VVIGMDVAASEFFR	99.7%	95.2	25	93.3	2	0	0	1556.78	240	253
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	12	28	0.03%	33.9%	YISPDQLADLYK	99.7%	69.8	25	67.9	2	0	0	1425.73	270	281
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	12	28	0.03%	33.9%	YNQLLR	97.9%	31.5	25	24.5	2	0	0	806.45	407	412
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	15	16	31	0.03%	28.9%	ALEAELAALR	99.7%	67.6	25	56.9	2	0	0	1056.60	121	130
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	15	16	31	0.03%	28.9%	AQLEEASSAR	99.7%	70.5	25	61.6	3	0	0	1061.52	152	161
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	15	16	31	0.03%	28.9%	AQYESLAAK	99.6%	38.9	25	0	2	0	0	980.50	270	278
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	15	16	31	0.03%	28.9%	DGLAEEVQR	99.7%	42.7	25	32.6	1	0	0	1016.50	169	177
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	15	16	31	0.03%	28.9%	DVDGATLAR	99.7%	44.9	25	35.9	2	0	0	917.47	202	210
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	15	16	31	0.03%	28.9%	EYQDLLNVK	99.7%	49.3	25	38.5	6	0	0	1121.58	378	386
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	15	16	31	0.03%	28.9%	FANLNEQAAR	99.7%	80.7	25	34.4	2	0	0	1133.57	291	300
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	15	16	31	0.03%	28.9%	LLEGEETR	99.1%	35.2	25	18.8	2	0	0	946.48	399	406
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	15	16	31	0.03%	28.9%	LSGAGGAGGFR	99.7%	73.4	25	59.6	3	0	0	949.49	29	39
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	15	16	31	0.03%	28.9%	NLQSAEEWYK	99.7%	40.8	25	30.4	1	0	0	1267.60	279	288
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	15	16	31	0.03%	28.9%	QILELEER	98.4%	32.7	25	11.6	2	0	0	1029.56	339	346
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	15	16	31	0.03%	28.9%	SNIEETTISSQK	99.7%	53.4	25	46.3	2	0	0	1336.66	487	498
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	15	16	31	0.03%	28.9%	SNIEETTISSQKI	99.7%	69	25	68.3	2	0	0	1449.74	487	499
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	15	16	31	0.03%	28.9%	TIEIEGLR	99.4%	37.4	25	27.6	2	0	0	930.53	323	330
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	15	16	31	0.03%	28.9%	TNEKEQLQGLNDR	99.7%	68.6	25	58.3	2	1	0	1544.77	92	104
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	15	16	31	0.03%	28.9%	VGELFQR	99.7%	67.5	25	51.1	2	0	0	848.46	139	145
Amidophosphoribosyltransferase	PPAT	PUR1_HUMAN	57.4	99.8%	2	2	3	0.00%	4.5%	HNVQTLDIISR	99.7%	71.5	25	71	1	0	0	1295.71	261	271
Amidophosphoribosyltransferase	PPAT	PUR1_HUMAN	57.4	99.8%	2	2	3	0.00%	4.5%	LYVSNLGIGHTR	99.7%	60	25	57.8	2	0	0	1329.73	82	93
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	9	12	24	0.02%	37.2%	AILQATLREEK	99.7%	43	25	40.6	2	0	0	1271.73	36	46
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	9	12	24	0.02%	37.2%	GAEADQIIEYLK	99.7%	86.4	25	78.7	4	0	0	1349.69	15	26
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	9	12	24	0.02%	37.2%	IGCIITAR	99.7%	70.9	25	57.2	2	0	0	903.51	159	166
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	9	12	24	0.02%	37.2%	ITFDAFPGEPDKELNPK	99.7%	52.2	25	52.2	2	2	0	1917.96	251	267
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	9	12	24	0.02%	37.2%	IWEQIQPDLHTNDECVATYK	99.6%	31.2	25	31.2	0	1	0	2460.15	270	289
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	9	12	24	0.02%	37.2%	KQQSIAGSADSKPIDVSR	99.7%	47.9	25	47.9	0	2	0	1886.99	137	154
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	9	12	24	0.02%	37.2%	MVILLCNLKPAK	99.7%	47.5	25	47.5	1	0	0	1399.82	206	217
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	9	12	24	0.02%	37.2%	QQSIAGSADSKPIDVSR	99.7%	54.4	25	54.4	2	2	0	1758.90	138	154
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	9	12	24	0.02%	37.2%	TVVSGLVNHVPLEQMQNR	99.7%	54.2	25	51.1	0	4	0	2037.05	188	205
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	5	6	15	0.02%	18.1%	FLFSLFGQK	99.5%	38.3	25	30.1	1	0	0	1086.60	216	224
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	5	6	15	0.02%	18.1%	FSIQTMCPIEGEGNIAR	99.7%	85.5	25	83.8	4	0	0	1938.91	199	215
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	5	6	15	0.02%	18.1%	LLCEHFR	99.7%	47.1	25	33	3	0	0	974.49	141	147
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	5	6	15	0.02%	18.1%	SCENLAPFNTALK	99.7%	69.9	25	62.3	2	0	0	1464.72	305	317
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	5	6	15	0.02%	18.1%	VLSTVHTHSSVK	99.7%	56	25	55.5	5	0	0	1294.71	148	159
Aminopeptidase B	RNPEP	AMPB_HUMAN	72.6	100.0%	3	3	3	0.00%	4.6%	GLSGTAVLDLR	99.7%	40.3	25	26.1	1	0	0	1101.63	58	68

Aminopeptidase B	RNPEP	AMPB_HUMAN	72.6	100.0%	3	3	3	0.00%	4.6%	LFGPYVWGR	97.6%	31	25	23.9	1	0	0	1094.58	277	285
Aminopeptidase B	RNPEP	AMPB_HUMAN	72.6	100.0%	3	3	3	0.00%	4.6%	TYQLVYFLDK	99.7%	48.2	25	36.6	1	0	0	1289.68	532	541
Anaphase-promoting complex subunit 1	ANAPC1	APC1_HUMAN	216.5	100.0%	2	2	3	0.00%	1.3%	HSTSVSSLAER	99.0%	35	25	34.7	1	0	0	1173.59	919	929
Anaphase-promoting complex subunit 1	ANAPC1	APC1_HUMAN	216.5	100.0%	2	2	3	0.00%	1.3%	NFDFEGSLSPVIAPK	99.7%	51	25	51	2	0	0	1620.83	680	694
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	14	15	29	0.03%	24.2%	AGQERPSVTSYK	99.7%	55.5	25	48.5	2	0	0	1322.67	182	193
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	14	15	29	0.03%	24.2%	AIQLNSNSVQALLLK	99.7%	86.9	25	78.8	2	0	0	1611.94	365	379
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	14	15	29	0.03%	24.2%	AISTICSLEK	99.7%	47.7	25	38.5	2	0	0	1121.59	254	263
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	14	15	29	0.03%	24.2%	ALTQRPDYIK	97.3%	30.5	25	13.7	1	0	0	1204.67	468	477
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	14	15	29	0.03%	24.2%	AYAFVHTGDNSR	99.7%	58.4	25	58	2	0	0	1337.62	242	253
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	14	15	29	0.03%	24.2%	DMAAAGLHSNVR	99.7%	60.1	25	53.3	4	0	0	1241.61	43	54
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	14	15	29	0.03%	24.2%	EAMVMANNVYK	99.7%	51.8	25	46.4	2	0	0	1269.60	425	435
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	14	15	29	0.03%	24.2%	EQKYEDGIALLR	97.3%	30.4	25	28.4	2	0	0	1434.76	489	500
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	14	15	29	0.03%	24.2%	FEQAQMLDPYLIK	99.7%	88.8	25	81.4	2	0	0	1595.81	294	306
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	14	15	29	0.03%	24.2%	GMDVYGYLLAR	99.7%	62.2	25	49.6	2	0	0	1257.63	307	317
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	14	15	29	0.03%	24.2%	LEDVENLGCR	99.7%	69.2	25	63	2	0	0	1204.56	321	330
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	14	15	29	0.03%	24.2%	MAECYTMLK	99.5%	37.9	25	37.8	2	0	0	1146.50	142	150
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	14	15	29	0.03%	24.2%	YEDGIALLR	99.7%	52.4	25	45.2	2	0	0	1049.56	492	500
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	14	15	29	0.03%	24.2%	YTMALQQK	99.7%	54.8	25	40.5	2	0	0	982.50	100	107
Ancient ubiquitous protein 1	AUP1	AUP1_HUMAN	53.0	100.0%	2	2	4	0.00%	5.0%	GTQSLPTASASK	99.7%	45	25	36.6	2	0	0	1147.60	414	425
Ancient ubiquitous protein 1	AUP1	AUP1_HUMAN	53.0	100.0%	2	2	4	0.00%	5.0%	QLGEANEEFALR	99.7%	62	25	52.3	2	0	0	1376.68	298	309
Angio-associated migratory cell protein	AAMP	AAMP_HUMAN	46.7	99.8%	2	2	4	0.00%	5.5%	AVVGYEDGTIR	99.7%	45	25	42.3	2	0	0	1179.60	230	240
Angio-associated migratory cell protein	AAMP	AAMP_HUMAN	46.7	99.8%	2	2	4	0.00%	5.5%	DASLVVTTSGDHK	99.7%	70	25	62.5	2	0	0	1329.66	411	423
Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	ANFY1_HUMAN	128.4	100.0%	7	7	10	0.01%	7.4%	ESSSESFISR	98.2%	32.1	25	28.1	1	0	0	1128.52	44	53
Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	ANFY1_HUMAN	128.4	100.0%	7	7	10	0.01%	7.4%	FQLQLLR	99.7%	46	25	7.7	1	0	0	917.56	145	151
Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	ANFY1_HUMAN	128.4	100.0%	7	7	10	0.01%	7.4%	GADMSVPDEK	94.8%	27.7	25	20.2	1	0	0	1048.46	678	687
Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	ANFY1_HUMAN	128.4	100.0%	7	7	10	0.01%	7.4%	GDLFAATFLIK	99.7%	51.1	25	34.1	2	0	0	1195.67	300	310
Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	ANFY1_HUMAN	128.4	100.0%	7	7	10	0.01%	7.4%	LGVNNNQGVNIFNYQVATK	99.7%	44.8	25	44.8	2	0	0	2093.08	1070	1088
Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	ANFY1_HUMAN	128.4	100.0%	7	7	10	0.01%	7.4%	TQDGETALQLAIR	99.7%	65.9	25	59.8	2	0	0	1415.75	652	664
Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	ANFY1_HUMAN	128.4	100.0%	7	7	10	0.01%	7.4%	VLLTECTVDAEAFNLR	99.7%	81.9	25	81.9	1	0	0	1850.93	990	1005
Annexin A2	ANXA2	ANXA2_HUMAN	38.6	99.8%	2	2	4	0.00%	6.8%	GVDEVTIVNILTNR	99.7%	72.1	25	59.6	2	0	0	1542.85	50	63
Annexin A2	ANXA2	ANXA2_HUMAN	38.6	99.8%	2	2	4	0.00%	6.8%	QDIAFAYQR	99.7%	61.2	25	49	2	0	0	1111.55	69	77
Annexin A5	ANXA5	ANXA5_HUMAN	35.9	99.8%	2	2	4	0.00%	7.8%	GLGTDEESILTLLTSR	99.7%	61.4	25	61.4	2	0	0	1704.90	30	45
Annexin A5	ANXA5	ANXA5_HUMAN	35.9	99.8%	2	2	4	0.00%	7.8%	VLTEIIASR	99.7%	56.8	25	46	2	0	0	1001.60	109	117
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	17	18	29	0.03%	19.8%	AAMIWIVGEYAER	99.7%	85.4	25	85.4	2	0	0	1508.76	446	458
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	17	18	29	0.03%	19.8%	CVSTLLDLIQTK	99.7%	82.1	25	60.6	2	0	0	1390.76	391	402
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	17	18	29	0.03%	19.8%	DCEDPNPLIR	99.6%	39.3	25	30.5	1	0	0	1228.56	94	103
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	17	18	29	0.03%	19.8%	DCPLNAEAASSK	99.7%	59.8	25	49.1	1	0	0	1262.57	865	876
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	17	18	29	0.03%	19.8%	DLDYYGTLLK	99.7%	60.4	25	41.1	2	0	0	1200.61	273	282
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	17	18	29	0.03%	19.8%	GLEISGTFTR	99.7%	68.1	25	67.4	2	0	0	1080.57	731	740
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	17	18	29	0.03%	19.8%	ITEYLCEPLRK	99.7%	48.4	25	37.2	1	0	0	1421.75	118	128
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	17	18	29	0.03%	19.8%	KGEIFELK	98.9%	34.6	25	10.8	2	0	0	963.55	12	19
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	17	18	29	0.03%	19.8%	LASQANIAQVLAELK	99.7%	85.7	25	80.7	2	0	0	1568.90	345	359
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	17	18	29	0.03%	19.8%	LLSTDPVAAK	99.0%	34.7	25	16.1	2	0	0	1014.58	529	538
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	17	18	29	0.03%	19.8%	LQSSNIFTVAK	99.7%	58.5	25	51.6	2	0	0	1207.67	877	887
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	17	18	29	0.03%	19.8%	LSHANSAVVLSAVK	99.7%	67.1	25	67.1	2	2	0	1395.80	248	261
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	17	18	29	0.03%	19.8%	LTNGIWVLAELR	99.7%	50.1	25	36.4	1	0	0	1384.79	902	913
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	17	18	29	0.03%	19.8%	LVYLYLMNYAK	98.1%	31.9	25	29.2	1	0	0	1406.74	68	78
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	17	18	29	0.03%	19.8%	NINLIVQK	98.8%	34.2	25	30.9	1	0	0	941.58	305	312
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	17	18	29	0.03%	19.8%	VNYVVQEAIVVIK	99.7%	46.8	25	40.6	1	0	0	1473.87	403	415
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	17	18	29	0.03%	19.8%	YNDPIYVK	99.7%	51.7	25	32.8	2	0	0	1011.51	328	335
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	11	12	24	0.02%	13.9%	AALCAVHVIR	99.7%	79.7	25	75.2	2	0	0	1109.62	157	166

AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	11	12	24	0.02%	13.9%	ADCASGIFLAAEK	99.7%	64	25	54.4	2	0	0	1352.65	398	410
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	11	12	24	0.02%	13.9%	AVEYNALFK	99.7%	46	25	37.9	2	0	0	1054.56	563	571
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	11	12	24	0.02%	13.9%	ELLYFLDSCEPEFK	99.7%	75.6	25	73.3	2	0	0	1789.84	384	397
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	11	12	24	0.02%	13.9%	FTCTVNR	99.6%	39.9	25	29.1	2	0	0	897.42	537	543
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	11	12	24	0.02%	13.9%	SSFREEDNTYR	99.7%	36.8	25	22.7	1	2	0	1403.62	36	46
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	11	12	24	0.02%	13.9%	TQAEEREMIQK	97.6%	30.9	25	29	1	0	0	1378.66	19	29
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	11	12	24	0.02%	13.9%	TVQTDHNAVQR	99.7%	45.8	25	34.6	3	0	0	1268.63	335	345
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	11	12	24	0.02%	13.9%	VLAINILGR	99.7%	74.2	25	62.7	3	0	0	968.63	307	315
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	11	12	24	0.02%	13.9%	VLTTAGSYVR	99.7%	71	25	65.1	2	0	0	1066.59	425	434
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	11	12	24	0.02%	13.9%	YVALTSLLK	99.4%	37.5	25	37.5	2	0	0	1007.61	326	334
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	12	18	0.02%	35.0%	FEIPYFTTSGIQVR	99.7%	90.8	25	89	2	0	0	1657.86	380	393
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	12	18	0.02%	35.0%	HNNLYLVATSK	99.7%	57.5	25	47.9	1	0	0	1259.67	62	72
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	12	18	0.02%	35.0%	ILQEYITQEGHK	99.7%	69.9	25	46.1	2	0	0	1458.76	130	141
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	12	18	0.02%	35.0%	LETGAPRPPATVTNAVSWR	99.7%	33.7	25	33.7	0	1	0	2023.07	142	160
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	12	18	0.02%	35.0%	LGLNDKVLFDNTGR	99.7%	49.4	25	44	1	0	0	1561.83	212	225
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	12	18	0.02%	35.0%	SGYQALPWVR	99.1%	35.5	25	22.8	1	0	0	1176.62	401	410
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	12	18	0.02%	35.0%	STANNVEIHIPVPNDADSPK	99.7%	32.8	25	32.8	0	1	0	2118.05	305	324
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	12	18	0.02%	35.0%	SVELEDVKFHQCVR	99.7%	34.8	25	27.3	0	1	0	1745.86	230	243
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	12	18	0.02%	35.0%	VFLSGMPELR	99.7%	53.2	25	39.5	4	0	0	1164.61	202	211
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	12	18	0.02%	35.0%	WVPENSEIVWSIK	98.9%	34.4	25	31.6	2	0	0	1586.82	334	346
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	12	18	0.02%	35.0%	YITQNGDYQLR	99.7%	46.7	25	44.2	2	0	0	1370.67	411	421
AP-1 complex subunit sigma-1A	AP1S1	AP1S1_HUMAN	18.7	100.0%	4	4	9	0.01%	25.3%	AIEQADLLQEEDESPR	99.7%	110	25	110	2	0	0	1842.87	134	149
AP-1 complex subunit sigma-1A	AP1S1	AP1S1_HUMAN	18.7	100.0%	4	4	9	0.01%	25.3%	ELMQVVLAR	99.7%	59.8	25	46.3	4	0	0	1058.60	34	42
AP-1 complex subunit sigma-1A	AP1S1	AP1S1_HUMAN	18.7	100.0%	4	4	9	0.01%	25.3%	FMLLFSR	96.0%	28.8	25	18.9	2	0	0	913.50	4	10
AP-1 complex subunit sigma-1A	AP1S1	AP1S1_HUMAN	18.7	100.0%	4	4	9	0.01%	25.3%	MCSFLEWR	97.8%	31.3	25	31.3	1	0	0	1128.50	46	53
AP-1 complex subunit sigma-2	AP1S2	AP1S2_HUMAN	18.6	99.8%	2	2	12	0.01%	21.0%	AIEQADLLQEEAETPR	99.7%	69.1	25	65.8	4	0	0	1812.90	133	148
AP-1 complex subunit sigma-2	AP1S2	AP1S2_HUMAN	18.6	99.8%	2	2	12	0.01%	21.0%	ELVQTVLAR	99.7%	55.9	25	33.8	8	0	0	1028.61	33	41
AP-1 complex subunit sigma-2	AP1S2	AP1S2_HUMAN	18.6	99.8%	2	2	12	0.01%	21.0%	MCSFLEWR	97.8%	31.3	25	31.3	1	0	0	1128.50	45	52
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	11	11	17	0.02%	12.4%	ACNQLGQFLQHR	99.4%	29.5	25	17.3	0	2	0	1471.72	330	341
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	11	11	17	0.02%	12.4%	ALLLSTYIK	99.7%	55.5	25	55.5	2	0	0	1021.63	539	547
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	11	11	17	0.02%	12.4%	DFLTPPLLSVR	97.9%	31.5	25	31.5	1	0	0	1257.72	833	843
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	11	11	17	0.02%	12.4%	FHLCSVATR	98.0%	31.8	25	17.7	1	0	0	1090.55	530	538
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	11	11	17	0.02%	12.4%	FINLFPETK	99.7%	44	25	38.6	2	0	0	1108.60	548	556
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	11	11	17	0.02%	12.4%	GLAVFISDIR	99.7%	88.8	25	77.3	2	0	0	1090.63	12	21
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	11	11	17	0.02%	12.4%	ILVAGDSMDSVK	98.8%	34.2	25	34	2	0	0	1234.63	154	165
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	11	11	17	0.02%	12.4%	QLSLPQQEAQK	98.5%	32.9	25	27.5	1	0	0	1269.68	881	891
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	11	11	17	0.02%	12.4%	TCVSLAVSR	99.7%	42.4	25	22.8	1	0	0	992.52	224	232
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	11	11	17	0.02%	12.4%	THIDTVINALK	97.4%	30.6	25	30.6	1	0	0	1224.69	368	378
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	11	11	17	0.02%	12.4%	VGGYILGEFGNLIAGDPR	99.7%	92.7	25	91.9	2	0	0	1847.97	499	516
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	7	8	14	0.01%	14.6%	ACNQLGQFLQHR	99.4%	29.5	25	17.3	0	2	0	1471.72	329	340
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	7	8	14	0.01%	14.6%	ALLLSTYIK	99.7%	55.5	25	55.5	2	0	0	1021.63	538	546
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	7	8	14	0.01%	14.6%	EMAEAFAGEIPK	99.7%	63.2	25	53.8	1	0	0	1292.62	142	153
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	7	8	14	0.01%	14.6%	FFQPTEMASQDFFQR	99.7%	63.2	25	17.5	2	0	0	1878.85	826	840
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	7	8	14	0.01%	14.6%	GLAVFISDIR	99.7%	88.8	25	77.3	2	0	0	1090.63	12	21
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	7	8	14	0.01%	14.6%	LTECLETILNK	99.7%	79.6	25	68.5	1	0	0	1333.70	279	289
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	7	8	14	0.01%	14.6%	THIETVINALK	99.7%	53.9	25	51.7	2	0	0	1238.71	367	377
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	7	8	14	0.01%	14.6%	TTQIGCLLR	99.7%	40.5	25	30.9	2	0	0	1061.58	898	906
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	7	8	14	0.01%	14.6%	VGGYILGEFGNLIAGDPR	99.7%	92.7	25	91.9	2	0	0	1847.97	498	515
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	7	8	14	0.01%	14.6%	VLVAGDTMDSVK	99.7%	60	25	43	4	0	0	1250.63	154	165
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	7	8	14	0.01%	14.6%	YGGTFQNVSVQLPITLNK	99.7%	102	25	102	2	0	0	1979.06	808	825
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	8	8	14	0.01%	20.0%	IPTPLNTSGVQVICMK	99.7%	89.7	25	88.1	2	0	0	1757.93	324	339

AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	8	8	14	0.01%	20.0%	LNYSDHDVIK	99.7%	48.7	25	43.3	2	0	0	1203.60	411	420
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	8	8	14	0.01%	20.0%	MCDVMAAYFGK	99.7%	84	25	84	2	0	0	1292.55	85	95
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	8	8	14	0.01%	20.0%	SISFIPPDGEFELMR	99.5%	38	25	30.3	1	0	0	1737.85	262	276
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	8	8	14	0.01%	20.0%	SNFKPSLLAQK	99.7%	45.9	25	39.3	2	0	0	1232.70	309	319
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	8	8	14	0.01%	20.0%	SPVTNIAR	98.0%	31.8	25	18.7	1	0	0	857.48	45	52
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	8	8	14	0.01%	20.0%	TFITQQGIK	99.6%	39.8	25	36.5	2	0	0	1035.58	131	139
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	8	8	14	0.01%	20.0%	VNVIHAR	99.4%	37.1	25	33.9	2	0	0	808.48	34	40
AP-2 complex subunit sigma	AP2S1	AP2S1_HUMAN	17.0	100.0%	3	3	3	0.00%	16.9%	FILIQNR	98.1%	32	25	0.64	1	0	0	903.54	4	10
AP-2 complex subunit sigma	AP2S1	AP2S1_HUMAN	17.0	100.0%	3	3	3	0.00%	16.9%	HTNFVEFR	97.6%	31	25	18.6	1	0	0	1049.52	46	53
AP-2 complex subunit sigma	AP2S1	AP2S1_HUMAN	17.0	100.0%	3	3	3	0.00%	16.9%	QLLMLQSLE	99.5%	38	25	24.2	1	0	0	1090.58	134	142
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	13	13	24	0.02%	13.0%	ASILWLIGENCER	99.7%	72.5	25	69.4	2	0	0	1560.78	497	509
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	13	13	24	0.02%	13.0%	EGSTAQLIINTEK	99.7%	55.3	25	51.5	1	0	0	1403.74	1064	1076
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	13	13	24	0.02%	13.0%	ELKPVLSQG	96.7%	29.6	25	23.7	1	0	0	970.56	1086	1094
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	13	13	24	0.02%	13.0%	LLDSITVPVAR	99.7%	61	25	52.5	1	0	0	1183.70	486	496
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	13	13	24	0.02%	13.0%	LLTQYILNLGK	99.7%	79.9	25	77.6	6	0	0	1275.77	553	563
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	13	13	24	0.02%	13.0%	LQILNLGAK	99.7%	45.5	25	31	2	0	0	969.61	534	542
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	13	13	24	0.02%	13.0%	LVYVYLVR	98.5%	33	25	14.6	1	0	0	1024.62	97	104
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	13	13	24	0.02%	13.0%	NASELFPAVVK	99.7%	60.7	25	41.4	2	0	0	1174.65	75	85
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	13	13	24	0.02%	13.0%	NVEVIELAK	96.4%	29.2	25	25.7	1	0	0	1014.58	650	658
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	13	13	24	0.02%	13.0%	QFAAATIQTIGR	99.7%	87.3	25	80.9	2	0	0	1276.70	419	430
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	13	13	24	0.02%	13.0%	SFTSEDDLVK	98.6%	33.2	25	20.1	2	0	0	1140.54	524	533
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	13	13	24	0.02%	13.0%	YAEEQQDLALLSISTFQR	99.6%	38.9	25	37.4	1	0	0	2112.06	105	122
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	13	13	24	0.02%	13.0%	YDQNYDIR	99.7%	59.1	25	47	2	0	0	1086.49	564	571
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	4	4	5	0.01%	3.5%	AVFHEEEQR	96.4%	29.3	25	23.6	1	0	0	1144.54	643	651
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	4	4	5	0.01%	3.5%	ILIEDSDQNLK	97.5%	30.8	25	22.8	1	0	0	1287.68	310	320
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	4	4	5	0.01%	3.5%	MSFQNLLAK	99.7%	51	25	42.7	2	0	0	1051.56	1079	1087
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	4	4	5	0.01%	3.5%	NYLSLAPLFFK	99.7%	48.1	25	48.1	1	0	0	1312.73	217	227
AP-3 complex subunit mu-1	AP3M1	AP3M1_HUMAN	46.9	100.0%	3	3	3	0.00%	8.9%	LLDDVSFHPCIR	95.8%	22.4	25	19.1	0	1	0	1471.74	227	238
AP-3 complex subunit mu-1	AP3M1	AP3M1_HUMAN	46.9	100.0%	3	3	3	0.00%	8.9%	SVVSQSVCDYFFEAQEK	99.7%	82.4	25	82.4	1	0	0	2022.91	22	38
AP-3 complex subunit mu-1	AP3M1	AP3M1_HUMAN	46.9	100.0%	3	3	3	0.00%	8.9%	VLTWDVGK	98.7%	33.6	25	24	1	0	0	917.51	338	345
AP-3 complex subunit sigma-1	AP3S1	AP3S1_HUMAN	21.7	100.0%	5	6	11	0.01%	27.5%	ETFHLVSK	98.4%	32.7	25	16.8	1	0	0	960.51	34	41
AP-3 complex subunit sigma-1	AP3S1	AP3S1_HUMAN	21.7	100.0%	5	6	11	0.01%	27.5%	FYQPYSEDTQQQIIR	99.7%	78.8	25	72.3	2	0	0	1915.92	19	33
AP-3 complex subunit sigma-1	AP3S1	AP3S1_HUMAN	21.7	100.0%	5	6	11	0.01%	27.5%	NINIGDISIK	99.6%	39.6	25	29.5	2	0	0	1086.62	176	185
AP-3 complex subunit sigma-1	AP3S1	AP3S1_HUMAN	21.7	100.0%	5	6	11	0.01%	27.5%	NMNLPEIPR	99.7%	47.3	25	27.9	4	0	0	1099.56	167	175
AP-3 complex subunit sigma-1	AP3S1	AP3S1_HUMAN	21.7	100.0%	5	6	11	0.01%	27.5%	SEAGLAGAPAR	99.7%	72	25	61	2	0	0	999.52	150	160
AP-3 complex subunit sigma-2	AP3S2	AP3S2_HUMAN	22.0	100.0%	4	4	6	0.01%	21.2%	FPEEIQQQIVR	99.7%	43.3	25	39	2	0	0	1386.74	23	33
AP-3 complex subunit sigma-2	AP3S2	AP3S2_HUMAN	22.0	100.0%	4	4	6	0.01%	21.2%	NINIGDLNIK	95.3%	28.1	25	23	1	0	0	1113.63	176	185
AP-3 complex subunit sigma-2	AP3S2	AP3S2_HUMAN	22.0	100.0%	4	4	6	0.01%	21.2%	NINLPEIPR	99.2%	36.1	25	36.1	1	0	0	1065.61	167	175
AP-3 complex subunit sigma-2	AP3S2	AP3S2_HUMAN	22.0	100.0%	4	4	6	0.01%	21.2%	SEGGLSAAPAR	99.7%	55.2	25	44.4	2	0	0	1015.52	150	160
Apolipoprotein O-like	APOOL	APOOL_HUMAN	29.2	100.0%	3	3	5	0.01%	16.0%	HSVPLPTELSSEAK	99.7%	44.8	25	40.8	1	0	0	1494.78	219	232
Apolipoprotein O-like	APOOL	APOOL_HUMAN	29.2	100.0%	3	3	5	0.01%	16.0%	MGVITVSGLAGLVSAR	99.7%	80.4	25	65.9	2	0	0	1530.87	115	130
Apolipoprotein O-like	APOOL	APOOL_HUMAN	29.2	100.0%	3	3	5	0.01%	16.0%	VYATSQQIFGAVK	99.7%	63.7	25	56.7	2	0	0	1411.76	168	180
Apoptosis regulator BAX	BAX	BAX_HUMAN	21.2	99.8%	2	2	4	0.00%	10.4%	KLSECLK	98.4%	32.8	25	5.68	2	0	0	877.48	58	64
Apoptosis regulator BAX	BAX	BAX_HUMAN	21.2	99.8%	2	2	4	0.00%	10.4%	TGALLLQGFIQDR	99.7%	54.2	25	49.6	2	0	0	1431.80	22	34
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	21	47	0.05%	35.4%	AALSASEGEEVPQDK	99.7%	77.9	25	74	2	0	0	1530.73	113	127
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	21	47	0.05%	35.4%	ALGTEVIQLFPEK	99.7%	99.7	25	95.6	3	0	0	1444.80	325	337
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	21	47	0.05%	35.4%	CLIATGGTPR	99.7%	60.8	25	43.7	2	0	0	1045.55	256	265
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	21	47	0.05%	35.4%	DGEQHEDLNEVAK	99.7%	78.8	25	76.5	2	2	0	1483.67	594	606
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	21	47	0.05%	35.4%	ELWFSDDPNVTK	99.7%	45.2	25	41.4	2	0	0	1450.69	178	189
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	21	47	0.05%	35.4%	ILPEYLSNWTMEK	99.7%	72.3	25	71.2	4	0	0	1639.80	343	355
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	21	47	0.05%	35.4%	ISGLGLTPEQK	99.7%	44.7	25	38.3	4	0	0	1142.64	99	109

Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	21	47	0.05%	35.4%	KVVQLDVR	99.7%	41.9	25	31.5	2	0	0	956.59	232	239
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	21	47	0.05%	35.4%	LFNIHED	97.0%	30	25	30	2	0	0	887.43	607	613
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	21	47	0.05%	35.4%	LNDGSQITYEK	99.7%	72.7	25	67.9	3	0	0	1267.62	245	255
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	21	47	0.05%	35.4%	SATEQSGTGIR	99.7%	70.5	25	44.4	2	0	0	1106.54	519	529
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	21	47	0.05%	35.4%	SITIIGGGFLGSELACALGR	99.7%	54.7	25	54.7	1	0	0	1992.06	302	321
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	21	47	0.05%	35.4%	SNIWVAGDAACFYDIK	99.7%	98.1	25	98.1	3	0	0	1829.85	431	446
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	21	47	0.05%	35.4%	TGGLEIDSDFGGFR	99.7%	74.6	25	74.6	2	0	0	1470.69	409	422
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	21	47	0.05%	35.4%	VLIVSEDPELPYMRPPLSK	99.7%	57.4	25	57.4	0	2	0	2183.18	159	177
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	21	47	0.05%	35.4%	VMPNAIVQSVGVSSGK	99.7%	110	25	94.7	4	0	0	1572.84	363	378
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	21	47	0.05%	35.4%	VNAELQAR	99.7%	63.5	25	50.2	2	0	0	900.49	423	430
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	21	47	0.05%	35.4%	VVQLDVR	99.7%	49.1	25	37.2	3	0	0	828.49	233	239
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	4	4	7	0.01%	3.0%	SGVSITIDDPVR	99.7%	52.9	25	43.6	2	0	0	1258.66	987	998
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	4	4	7	0.01%	3.0%	SQEQEVLER	99.6%	39.2	25	28.5	1	0	0	1117.55	328	336
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	4	4	7	0.01%	3.0%	VTLGDTLTR	99.7%	44.1	25	36	3	0	0	975.55	971	979
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	4	4	7	0.01%	3.0%	WGASTATTQK	95.4%	28.2	25	19.9	1	0	0	1050.52	851	860
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	24	29	66	0.07%	41.8%	AAYPDLENPPLLVTPSQQAK	99.7%	78.2	25	78.2	2	0	0	2152.13	90	109
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	24	29	66	0.07%	41.8%	AYQCVVLLQGK	99.7%	71.8	25	46.8	3	0	0	1278.69	290	300
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	24	29	66	0.07%	41.8%	EIAENITK	98.0%	31.8	25	17.2	1	0	0	917.49	136	143
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	24	29	66	0.07%	41.8%	FPEILQK	99.7%	44	25	13.8	1	0	0	874.50	581	587
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	24	29	66	0.07%	41.8%	GESFYQDR	98.3%	32.4	25	32	1	0	0	1001.43	334	341
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	24	29	66	0.07%	41.8%	GFDILGIKPVQR	99.7%	51.7	25	39.6	2	2	0	1342.78	648	659
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	24	29	66	0.07%	41.8%	GFVQVDDGRK	99.3%	36.2	25	20.5	2	0	0	1120.57	353	362
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	24	29	66	0.07%	41.8%	GNTAAYLLYAFTR	99.7%	44.7	25	44.4	2	0	0	1460.75	528	540
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	24	29	66	0.07%	41.8%	IVFVPGCSIPLTIVK	99.7%	97	25	82	4	0	0	1642.96	363	377
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	24	29	66	0.07%	41.8%	IYDALDVSLIER	99.7%	75.8	25	68.7	4	0	0	1406.75	322	333
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	24	29	66	0.07%	41.8%	LANIDEEMLQK	99.7%	75.1	25	59.6	3	0	0	1303.66	547	557
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	24	29	66	0.07%	41.8%	LFEFAGYDVLR	99.7%	72.3	25	59.4	2	0	0	1329.68	224	234
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	24	29	66	0.07%	41.8%	LLQQEEEIK	99.7%	49.7	25	29	2	0	0	1129.61	12	20
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	24	29	66	0.07%	41.8%	LMDLLGEGLKR	99.7%	58.2	25	44.9	2	1	0	1244.70	462	472
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	24	29	66	0.07%	41.8%	LNDYIFSFDK	99.7%	74.5	25	71.3	4	0	0	1261.61	513	522
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	24	29	66	0.07%	41.8%	MLLCEAVAAVMAK	99.7%	84.5	25	73.7	5	0	0	1422.72	635	647
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	24	29	66	0.07%	41.8%	MNDIVKEFEDR	97.9%	31.6	25	29.5	1	0	0	1395.66	342	352
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	24	29	66	0.07%	41.8%	NCGCLGASPNLEQLQEENLK	99.7%	58.8	25	58.8	1	0	0	2274.05	31	50
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	24	29	66	0.07%	41.8%	NMINIISR	99.7%	44.1	25	20.5	2	0	0	960.53	72	79
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	24	29	66	0.07%	41.8%	SDGGYTYDTSDLAAIK	99.7%	99.3	25	87.4	4	0	0	1676.77	378	393
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	24	29	66	0.07%	41.8%	SLTAEIDR	99.7%	40.5	25	23.5	2	0	0	904.47	21	28
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	24	29	66	0.07%	41.8%	STIIGESISR	99.7%	70.9	25	53.8	4	0	0	1062.58	214	223
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	24	29	66	0.07%	41.8%	VEIAGPGFINVHLR	99.7%	69.4	25	69.4	2	2	0	1521.85	154	167
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	24	29	66	0.07%	41.8%	YADLSHNR	99.7%	55.4	25	55.3	5	0	0	975.46	505	512
Argininosuccinate synthase	ASS1	ASSY_HUMAN	46.5	100.0%	4	4	6	0.01%	8.7%	FELSCYSLAPQIK	99.7%	72	25	57.4	2	0	0	1555.78	128	140
Argininosuccinate synthase	ASS1	ASSY_HUMAN	46.5	100.0%	4	4	6	0.01%	8.7%	GQVYILGR	99.7%	42.7	25	36.1	2	0	0	905.52	356	363
Argininosuccinate synthase	ASS1	ASSY_HUMAN	46.5	100.0%	4	4	6	0.01%	8.7%	MPEFYNR	98.3%	32.5	25	30	1	0	0	956.43	147	153
Argininosuccinate synthase	ASS1	ASSY_HUMAN	46.5	100.0%	4	4	6	0.01%	8.7%	VFIEDVSR	99.7%	48.9	25	36	1	0	0	964.51	59	66
Armadillo repeat-containing protein 6	ARMC6	ARMC6_HUMAN	54.1	100.0%	6	6	8	0.01%	15.6%	AFLDNPGILSELCGTLSR	99.6%	39.9	25	39.9	1	0	0	1963.00	285	302
Armadillo repeat-containing protein 6	ARMC6	ARMC6_HUMAN	54.1	100.0%	6	6	8	0.01%	15.6%	AIAGNDDVKDAIVR	99.7%	94.4	25	93.6	1	0	0	1456.78	353	366
Armadillo repeat-containing protein 6	ARMC6	ARMC6_HUMAN	54.1	100.0%	6	6	8	0.01%	15.6%	DLGCHVELR	99.7%	40.4	25	35.1	1	0	0	1098.54	481	489
Armadillo repeat-containing protein 6	ARMC6	ARMC6_HUMAN	54.1	100.0%	6	6	8	0.01%	15.6%	DQSGVQELVK	97.3%	30.4	25	13.9	1	0	0	1102.57	336	345
Armadillo repeat-containing protein 6	ARMC6	ARMC6_HUMAN	54.1	100.0%	6	6	8	0.01%	15.6%	GAYPIIFTAWK	99.7%	56.6	25	56.6	2	0	0	1266.69	135	145
Armadillo repeat-containing protein 6	ARMC6	ARMC6_HUMAN	54.1	100.0%	6	6	8	0.01%	15.6%	IIVEGGGAVAALQAMK	99.7%	76.7	25	72.9	2	0	0	1527.86	407	422
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	16	19	38	0.04%	32.3%	AMTEDGFLAVCSEAK	99.7%	103	25	103	4	0	0	1644.72	148	162
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	16	19	38	0.04%	32.3%	APSPEKAEEESER	99.7%	70.4	25	67.2	2	0	0	1458.67	380	392

Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	16	19	38	0.04%	32.3%	ASVGMYLISK	99.1%	35.5	25	31.8	2	0	0	1084.57	341	350
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	16	19	38	0.04%	32.3%	DVPLHALYDNVEK	99.7%	76.1	25	76.1	2	0	0	1512.77	209	221
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	16	19	38	0.04%	32.3%	EAFSDGITSVK	99.7%	64.3	25	64.2	4	0	0	1153.57	468	478
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	16	19	38	0.04%	32.3%	ELYLFDVLR	99.0%	35	25	31	3	0	0	1167.64	396	404
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	16	19	38	0.04%	32.3%	ETFEDSNLIPK	99.7%	50.8	25	39.3	2	0	0	1292.64	450	460
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	16	19	38	0.04%	32.3%	FSSYYLSLPPEMR	99.7%	40	25	39.8	2	0	0	1589.77	425	437
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	16	19	38	0.04%	32.3%	HSATPFLK	97.6%	30.9	25	20.8	1	0	0	900.49	169	176
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	16	19	38	0.04%	32.3%	IGCLLSGGLDSSLVAATLLK	99.7%	87.8	25	87.8	2	0	0	1988.11	253	272
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	16	19	38	0.04%	32.3%	ILFNNAVK	98.1%	31.9	25	9.66	2	0	0	918.54	237	244
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	16	19	38	0.04%	32.3%	LAVVDPLFGMQPIR	99.7%	59.3	25	44.7	4	0	0	1555.87	50	63
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	16	19	38	0.04%	32.3%	LFPGFEIETVK	99.5%	37.9	25	22.5	1	0	0	1279.69	222	232
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	16	19	38	0.04%	32.3%	VASVEMVK	99.6%	39.6	25	25.2	3	0	0	878.47	196	203
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	16	19	38	0.04%	32.3%	VPFLDHR	98.0%	31.7	25	26.2	2	0	0	883.48	418	424
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	16	19	38	0.04%	32.3%	WINATDPSAR	99.5%	38.4	25	35	2	0	0	1130.56	541	550
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	7	7	13	0.01%	17.4%	ASAELALGENSEVLK	99.7%	99.6	25	96	2	0	0	1530.80	108	122
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	7	7	13	0.01%	17.4%	FVTVQTISGTGALR	99.7%	96.3	25	91.7	2	0	0	1449.81	126	139
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	7	7	13	0.01%	17.4%	IAAAILNTPDLR	99.7%	66.5	25	50.9	2	0	0	1267.74	326	337
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	7	7	13	0.01%	17.4%	IAAAILNTPDLRK	99.7%	55.3	25	55.3	2	0	0	1395.83	326	338
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	7	7	13	0.01%	17.4%	TCGFDFTGAVEDISK	99.7%	76	25	70.8	2	0	0	1646.74	186	200
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	7	7	13	0.01%	17.4%	TQLVSNLKK	95.9%	28.6	25	26.1	1	0	0	1030.63	356	364
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	7	7	13	0.01%	17.4%	VGAFTMVCK	99.7%	50.5	25	47.4	2	0	0	1012.50	288	296
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	56	0.06%	53.3%	ADEVVWVR	99.7%	62.7	25	56.5	2	0	0	973.51	56	63
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	56	0.06%	53.3%	ALHHGIDLEK	99.3%	36.4	25	24.3	2	0	0	1132.61	442	451
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	56	0.06%	53.3%	EIMDAAEDYAK	99.7%	60.5	25	58.5	3	0	0	1271.55	16	26
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	56	0.06%	53.3%	ESIVDVEGVVR	99.7%	88	25	81.6	2	0	0	1201.64	111	121
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	56	0.06%	53.3%	FGAPPHAGGGIGLER	99.7%	48.6	25	40.1	0	2	0	1435.74	461	475
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	56	0.06%	53.3%	FLEPTLR	99.4%	37.3	25	18.7	2	0	0	875.50	339	345
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	56	0.06%	53.3%	FQTEIQTVNK	98.1%	32	25	19.9	1	0	0	1207.63	321	330
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	56	0.06%	53.3%	GEEILSGAQR	99.7%	70.7	25	36.2	2	0	0	1059.54	422	431
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	56	0.06%	53.3%	GFVEIQTPK	99.7%	51.4	25	32.4	4	0	0	1018.56	214	222
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	56	0.06%	53.3%	IGSCTQQDVELHVQK	99.7%	49.1	25	47.4	1	2	0	1741.85	127	141
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	56	0.06%	53.3%	IHDPQLLTER	99.7%	35.4	25	22	0	2	0	1221.66	432	441
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	56	0.06%	53.3%	IYVISLAEPR	99.7%	58.5	25	54.4	2	0	0	1160.67	142	151
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	56	0.06%	53.3%	LEYCEALAMLR	99.7%	66.1	25	57.8	2	0	0	1368.67	346	356
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	56	0.06%	53.3%	LPLQLDDAVRPEAEGEEEGR	99.7%	63.8	25	63.8	1	2	0	2223.09	152	171
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	56	0.06%	53.3%	LQSGICHLFR	99.7%	65.8	25	55.7	2	2	0	1230.64	198	207
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	56	0.06%	53.3%	NNAYLAQSPQLYK	99.7%	86.2	25	79	2	0	0	1509.77	242	254
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	56	0.06%	53.3%	QCFLVLR	99.7%	46.5	25	15.5	2	0	0	935.51	75	81
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	56	0.06%	53.3%	QQQFNVQALVAVGDHASK	99.7%	46.4	25	46.4	0	2	0	1940.00	82	99
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	56	0.06%	53.3%	QSNSYDMFMR	99.7%	69.7	25	69.7	2	0	0	1278.52	412	421
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	56	0.06%	53.3%	QTSMFPR	94.7%	27.7	25	23.4	1	0	0	882.41	488	494
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	56	0.06%	53.3%	TSTSQAVFR	99.7%	78.8	25	67.2	2	0	0	996.51	189	197
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	56	0.06%	53.3%	VFSIGPVFR	99.7%	62.6	25	56.3	2	0	0	1021.58	265	273
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	56	0.06%	53.3%	VTMLFLGLHNVR	99.7%	71.2	25	62	4	2	0	1399.79	476	487
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	56	0.06%	53.3%	YGISSMIQSQEKPDR	99.7%	50.3	25	49.4	0	1	0	1754.84	29	43
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	9	10	17	0.02%	23.8%	CGLQFLGNIASR	99.7%	70.7	25	63.9	2	0	0	1335.68	134	145
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	9	10	17	0.02%	23.8%	ETTNIFSNCGCVR	99.7%	64.1	25	64.1	1	0	0	1557.68	346	358
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	9	10	17	0.02%	23.8%	ITSDEPLTKDDIPVFLR	99.7%	36.9	25	29.1	0	2	0	1959.04	254	270
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	9	10	17	0.02%	23.8%	LIGNLCYK	99.7%	47.3	25	34.2	2	0	0	980.52	377	384
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	9	10	17	0.02%	23.8%	LSGVMVPAPIQDLEALR	99.7%	45.2	25	45.2	2	0	0	1824.99	11	27
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	9	10	17	0.02%	23.8%	NACIECSVNQNSIR	99.7%	82.1	25	76.7	2	0	0	1664.75	90	103

Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	9	10	17	0.02%	23.8%	SPELVQAMFPK	99.7%	52.6	25	45.8	1	0	0	1262.65	227	237
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	9	10	17	0.02%	23.8%	VEQESLLTAFR	99.7%	68.2	25	58	1	0	0	1292.68	123	133
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	9	10	17	0.02%	23.8%	VTLLDLMIAK	99.7%	76.9	25	71.2	4	0	0	1116.67	244	253
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	8	10	21	0.02%	42.2%	HVVQSISTQQEK	99.7%	74.3	25	67.1	2	0	0	1383.72	222	233
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	8	10	21	0.02%	42.2%	HYLFDVQR	98.9%	34.3	25	28.2	2	0	0	1077.55	164	171
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	8	10	21	0.02%	42.2%	LAQLEEAK	98.9%	34.3	25	21.5	3	0	0	901.50	132	139
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	8	10	21	0.02%	42.2%	NRLDYHISVQNMMR	96.1%	22.6	25	22.5	0	1	0	1776.86	195	208
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	8	10	21	0.02%	42.2%	QASIQHIQNAIDTEK	99.7%	69.7	25	61.3	1	2	0	1695.87	140	154
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	8	10	21	0.02%	42.2%	TGVTGPYVLGTGLILYALSK	99.7%	88.3	25	88.3	2	2	0	2023.15	71	90
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	8	10	21	0.02%	42.2%	YGLIPEEFFQFLYPK	99.7%	51.2	25	51.2	4	0	0	1890.97	56	70
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	8	10	21	0.02%	42.2%	YGPFVADFADKLNEQK	99.7%	66.2	25	66.2	2	0	0	1841.91	116	131
ATP synthase mitochondrial F1 complex assembly factor 2	ATPAF2	ATPF2_HUMAN	32.8	99.9%	2	2	3	0.00%	7.3%	LEEEYQIQK	97.0%	30	25	22.3	2	0	0	1179.59	239	247
ATP synthase mitochondrial F1 complex assembly factor 2	ATPAF2	ATPF2_HUMAN	32.8	99.9%	2	2	3	0.00%	7.3%	VEEPETLVELQR	98.9%	34.6	25	34.6	1	0	0	1441.75	144	155
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	AVDSLVPIGR	99.7%	87.9	25	86.7	11	0	0	1026.59	195	204
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	EAYPGDVFYLHSR	99.7%	82.2	25	75.1	9	3	0	1553.74	335	347
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	EIVTNFLAGFEA	99.7%	96.6	25	96.6	3	0	0	1310.66	542	553
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	ELIIGDR	98.8%	34.1	25	25.7	4	0	0	815.46	208	214
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	EPMQTGIK	99.7%	53.8	25	36	3	0	0	903.46	187	194
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	EVAAFAQFGSDLDAATQQLLSR	99.7%	121	25	121	6	8	0	2338.17	442	463
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	FENAFLSHVVSQHQALLGTIR	99.7%	61.4	25	61.4	0	2	0	2367.26	507	527
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	GIRPAINVGLSVSR	99.7%	68.4	25	64.3	2	5	0	1438.85	403	416
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	GMSLNLEPDNVGVVVFGNDK	99.7%	102	25	99.3	7	0	0	2104.04	104	123
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	GYLDKLEPSK	99.7%	42	25	32.6	8	0	0	1149.62	494	503
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	HALIIYDDLSK	99.7%	78.4	25	77.2	4	0	0	1287.69	306	316
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	ILGADTSVDLEETGR	99.7%	135	25	132	9	0	0	1575.79	59	73
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	ISVREPMQTGIK	99.7%	65.9	25	53.4	2	2	0	1358.75	183	194
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	LELAQYR	99.6%	39.9	25	22.1	2	0	0	892.49	435	441
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	LKEIVTNFLAGFEA	99.7%	98.3	25	98.3	9	0	0	1551.84	540	553
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	LTDADAMK	95.6%	28.4	25	18.5	1	0	0	864.41	263	270
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	LYCIYVAIGQK	99.7%	69.4	25	65.8	4	0	0	1327.71	242	252
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	NVQAEEMVEFSSGLK	99.7%	96.5	25	95.7	5	0	0	1667.79	89	103
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	QGQYSPMAIEEQVAVIYAGVR	99.7%	110	25	103	4	3	0	2309.16	473	493
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	QMSLLLR	99.7%	44.4	25	24.1	5	0	0	860.50	323	329
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	RLTDADAMK	98.9%	34.3	25	21.3	2	0	0	1020.51	262	270
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	RSTVAQLVK	98.7%	33.7	25	15.8	2	0	0	1001.61	253	261
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	STVAQLVK	99.7%	71.2	25	47.7	7	0	0	845.51	254	261
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	TGAIVDVPVGEELLGR	99.7%	92.6	25	90.6	13	0	0	1624.89	134	149
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	TGTAEMSSILEER	99.7%	90.1	25	75.8	8	0	0	1423.67	46	58
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	TSIAIDTIINQK	99.7%	94.5	25	76.9	7	0	0	1316.74	219	230
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	TSIAIDTIINQKR	99.7%	57.5	25	54.2	3	0	0	1472.84	219	231
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	VLSIGDGIAR	99.7%	76.1	25	60.5	16	0	0	1000.58	74	83
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	VVDALGNAIDGK	99.7%	86.1	25	77.2	6	0	0	1171.63	150	161
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	42	203	0.20%	57.5%	VVDALGNAIDGKGPIGSK	99.7%	95.6	25	95.6	10	8	0	1710.94	150	167
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	25	44	217	0.22%	73.0%	AHGGYSVFAGVGER	99.7%	92.3	25	90.5	6	8	0	1406.68	226	239
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	25	44	217	0.22%	73.0%	AIAELGIYPAVDPLDSTSR	99.7%	87.2	25	85	11	0	0	1988.03	388	406
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	25	44	217	0.22%	73.0%	DQEGQDVLLFIDNIFR	99.7%	114	25	114	4	0	0	1921.97	295	310
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	25	44	217	0.22%	73.0%	EGNDLYHEMIESGVINLK	99.7%	76.7	25	66.1	2	2	0	2061.00	242	259
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	25	44	217	0.22%	73.0%	FLSQPFQVAEVFTGHMGK	99.7%	70.1	25	65.2	2	6	0	2023.01	463	480
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	25	44	217	0.22%	73.0%	FTQAGSEVSALLGR	99.7%	109	25	97.1	11	0	0	1435.75	311	324
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	25	44	217	0.22%	73.0%	GFQQILAGEYDHLPEQAFYMVGPIEEAVAK	99.7%	68.8	25	68.8	0	3	0	3366.64	490	519
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	25	44	217	0.22%	73.0%	GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	99.7%	76	25	75.6	0	1	0	3714.89	352	387

ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	25	44	217	0.22%	73.0%	IGLFGGAGVGK	99.7%	63.8	25	56.6	8	0	0	975.56	202	212
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	25	44	217	0.22%	73.0%	IMDPNIVGSEHYDVAR	99.7%	87.8	25	83.2	7	6	0	1815.87	407	422
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	25	44	217	0.22%	73.0%	IMNVIGEPIDER	99.7%	67.6	25	61	9	0	0	1385.71	144	155
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	25	44	217	0.22%	73.0%	IMNVIGEPIDERGPIK	99.7%	69.7	25	63.5	7	2	0	1780.96	144	159
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	25	44	217	0.22%	73.0%	IPSAVGYQPTLATDMGTMQER	99.7%	106	25	106	8	5	0	2266.08	325	345
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	25	44	217	0.22%	73.0%	IPVGPETLGR	99.7%	61	25	56.7	3	0	0	1038.59	134	143
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	25	44	217	0.22%	73.0%	LVLEVAQHLGESTVR	99.7%	109	25	109	8	5	0	1650.92	95	109
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	25	44	217	0.22%	73.0%	LVPLKETIK	97.4%	30.6	25	30.6	1	0	0	1040.67	481	489
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	25	44	217	0.22%	73.0%	QFAPIHAEAPEFMEMSVEQEILVTGIK	95.9%	22.5	25	17.6	0	1	0	3044.51	162	188
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	25	44	217	0.22%	73.0%	SLQDIIAILGMDELSEEDKLTVSR	99.7%	82	25	80.8	0	1	0	2691.38	433	456
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	25	44	217	0.22%	73.0%	TIAMDGTEGLVR	99.7%	76.9	25	61.5	12	0	0	1262.64	110	121
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	25	44	217	0.22%	73.0%	TVLIMELINNVAK	99.7%	93.7	25	92.7	23	0	0	1473.83	213	225
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	25	44	217	0.22%	73.0%	VALTGLTVAEYFR	99.7%	101	25	90.4	10	0	0	1439.79	282	294
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	25	44	217	0.22%	73.0%	VALVYGQMNEPPGAR	99.7%	101	25	91.3	16	0	0	1601.81	265	279
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	25	44	217	0.22%	73.0%	VLDSGAPIK	99.7%	64.5	25	48.3	7	0	0	899.52	125	133
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	25	44	217	0.22%	73.0%	VLDSGAPIKIPVGPETLGR	99.7%	71.1	25	71.1	8	6	0	1919.10	125	143
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	25	44	217	0.22%	73.0%	VVDLLAPYAK	99.7%	58.4	25	58.4	8	0	0	1088.64	189	198
ATP synthase subunit d, mitochondrial	ATP5H	ATP5H_HUMAN	18.5	100.0%	3	3	4	0.00%	17.4%	AGLVDDFEK	98.2%	32.3	25	20.8	1	0	0	993.49	64	72
ATP synthase subunit d, mitochondrial	ATP5H	ATP5H_HUMAN	18.5	100.0%	3	3	4	0.00%	17.4%	SCAEWVSLSK	99.7%	47.2	25	41.2	1	0	0	1166.55	100	109
ATP synthase subunit d, mitochondrial	ATP5H	ATP5H_HUMAN	18.5	100.0%	3	3	4	0.00%	17.4%	SWNETLTSR	98.0%	31.8	25	23.9	2	0	0	1093.53	33	41
ATP synthase subunit e, mitochondrial	ATP5I	ATP5I_HUMAN	7.9	100.0%	3	3	5	0.01%	44.9%	ELAEDDSILK	99.2%	35.7	25	26.4	1	0	0	1132.57	60	69
ATP synthase subunit e, mitochondrial	ATP5I	ATP5I_HUMAN	7.9	100.0%	3	3	5	0.01%	44.9%	YNYLKPR	99.7%	46.7	25	35.2	2	0	0	953.52	30	36
ATP synthase subunit e, mitochondrial	ATP5I	ATP5I_HUMAN	7.9	100.0%	3	3	5	0.01%	44.9%	YSALFLGVAYGATR	99.7%	60.1	25	57.5	2	0	0	1488.78	16	29
ATP synthase subunit f, mitochondrial	ATP5J2	ATPK_HUMAN	10.9	99.8%	2	3	12	0.01%	25.5%	DFSPSGIFGAFQR	99.7%	57.2	25	53.1	5	0	0	1428.69	34	46
ATP synthase subunit f, mitochondrial	ATP5J2	ATPK_HUMAN	10.9	99.8%	2	3	12	0.01%	25.5%	LGELPSWILMR	99.7%	57.9	25	55.5	7	0	0	1330.72	23	33
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	29	0.03%	47.6%	IVNSAQTGSFK	99.7%	81.2	25	63.5	7	0	0	1151.61	56	66
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	29	0.03%	47.6%	KIVNSAQTGSFK	99.7%	61.5	25	61.5	4	0	0	1279.70	55	66
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	29	0.03%	47.6%	LATFWYYAK	99.6%	39.2	25	35.4	4	0	0	1162.59	27	35
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	29	0.03%	47.6%	TPALVNAAVTYSKPR	99.7%	74.6	25	74.6	4	4	0	1587.89	12	26
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	29	0.03%	47.6%	VELVPPTPAEIPR	99.7%	54	25	45.7	6	0	0	1417.81	36	48
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	14	43	0.04%	32.2%	ELIEIISGAAALD	99.7%	69	25	62.9	2	0	0	1314.72	286	298
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	14	43	0.04%	32.2%	EVMLVGIGDK	99.7%	53	25	47.8	5	0	0	1076.57	127	136
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	14	43	0.04%	32.2%	EVMLVGIGDKIR	99.7%	79.3	25	62.3	7	0	0	1329.76	127	138
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	14	43	0.04%	32.2%	GLCGAIHSSIAK	99.7%	70	25	65.8	4	0	0	1213.64	101	112
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	14	43	0.04%	32.2%	HLLIGVSSDR	99.7%	61.7	25	44	4	0	0	1096.61	91	100
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	14	43	0.04%	32.2%	IYGLGSLALYEK	99.7%	92.2	25	86.2	4	0	0	1326.73	68	79
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	14	43	0.04%	32.2%	NASEMIDKLTLTFNR	99.7%	66.2	25	66.2	5	2	0	1752.90	263	277
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	14	43	0.04%	32.2%	SEVATLTAAGK	99.7%	75.2	25	51.3	4	0	0	1047.57	116	126
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	14	43	0.04%	32.2%	THSDQFLVAFK	99.7%	76.6	25	66.9	4	2	0	1292.66	144	154
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	8	11	21	0.02%	50.7%	GEVPCTVTSASPLEEATLSELK	99.7%	70.5	25	70.5	2	0	0	2318.14	137	158
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	8	11	21	0.02%	50.7%	LSNTQGVVSAFSTMMSVHR	99.7%	64.7	25	64.7	2	2	0	2083.99	118	136
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	8	11	21	0.02%	50.7%	LVRPPVQVYGIEGR	99.6%	39.2	25	39.2	1	1	0	1582.91	27	40
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	8	11	21	0.02%	50.7%	SFLSQGQVLK	99.7%	58.8	25	49.5	2	0	0	1106.62	163	172
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	8	11	21	0.02%	50.7%	TDPSILGGMIVR	99.7%	59.1	25	52.5	4	0	0	1274.68	177	188
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	8	11	21	0.02%	50.7%	VAASVLNPYVK	99.7%	77.8	25	70.6	2	0	0	1160.67	74	84
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	8	11	21	0.02%	50.7%	VAQILKEPK	99.7%	44.9	25	33.8	2	0	0	1025.64	65	73
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	8	11	21	0.02%	50.7%	YATALYSAASK	99.7%	90.5	25	79	3	0	0	1145.58	41	51
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	23	25	71	0.07%	39.1%	AEGPGRGDEPSPS	99.7%	57	25	57	4	0	0	1255.56	622	634
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	23	25	71	0.07%	39.1%	AERENADIIR	98.1%	32	25	10.5	2	0	0	1186.62	247	256
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	23	25	71	0.07%	39.1%	ATLNAFLYR	99.7%	80.2	25	69.1	2	0	0	1068.58	479	487
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	23	25	71	0.07%	39.1%	DALNLAQMQEQTLQLEQQSK	99.7%	105	25	102	4	0	0	2316.15	73	92

ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	23	25	71	0.07%	39.1%	DKWSNFDPTGLER	99.4%	29.6	25	29.6	0	2	0	1564.74	45	57
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	23	25	71	0.07%	39.1%	GEGAGPPPPLPPAQPGAEGGGDR	99.7%	73.7	25	73.7	2	0	0	2081.01	13	35
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	23	25	71	0.07%	39.1%	GLGDRPAPK	99.7%	50.6	25	46.3	4	0	0	910.51	36	44
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	23	25	71	0.07%	39.1%	GLLLFVDEADAFLR	99.7%	76.1	25	63.9	2	0	0	1578.85	453	466
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	23	25	71	0.07%	39.1%	ITVLEALR	99.7%	54.7	25	39.9	4	0	0	914.57	339	346
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	23	25	71	0.07%	39.1%	LAQFDYGR	99.7%	53.2	25	28.8	4	0	0	969.48	554	561
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	23	25	71	0.07%	39.1%	LAQFDYGRK	99.2%	36.1	25	36.1	3	0	0	1097.57	554	562
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	23	25	71	0.07%	39.1%	LFDWANTSR	99.7%	57.5	25	41.1	2	0	0	1109.54	443	451
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	23	25	71	0.07%	39.1%	LGKPSLVR	99.7%	45	25	32.1	2	0	0	869.56	327	334
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	23	25	71	0.07%	39.1%	LLSRPQDALEGVVLSPSLEAR	99.7%	53.3	25	53.1	0	2	0	2250.25	355	375
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	23	25	71	0.07%	39.1%	LTEGMSGR	99.7%	52.6	25	46.3	2	0	0	850.41	569	576
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	23	25	71	0.07%	39.1%	MYFDKYVLKPATEGK	98.5%	26	25	26	0	2	0	1789.92	535	549
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	23	25	71	0.07%	39.1%	NATLVAGR	96.1%	28.9	25	10.9	1	0	0	801.46	314	321
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	23	25	71	0.07%	39.1%	NILMYGPPGTGK	99.7%	68.3	25	57.2	8	0	0	1263.64	395	406
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	23	25	71	0.07%	39.1%	QQQLLNEENLR	99.7%	78	25	68.1	4	0	0	1384.72	195	205
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	23	25	71	0.07%	39.1%	QTVLESIR	99.7%	45.8	25	16.5	4	0	0	945.54	268	275
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	23	25	71	0.07%	39.1%	TAGTLFGEGFR	99.7%	77.2	25	71.3	4	0	0	1155.58	276	286
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	23	25	71	0.07%	39.1%	VRDIAIATR	99.7%	42.4	25	38.8	4	0	0	1014.61	376	384
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	23	25	71	0.07%	39.1%	YVLKPATEGK	99.4%	37.4	25	26.1	3	0	0	1105.63	540	549
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	7	8	13	0.01%	34.9%	AERENADIIR	98.1%	32	25	10.5	2	0	0	1186.62	199	208
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	7	8	13	0.01%	34.9%	DKWSNFDPTGLER	99.4%	29.6	25	29.6	0	2	0	1564.74	45	57
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	7	8	13	0.01%	34.9%	EALNLAQMQEQTLQLEQQSK	99.7%	94.9	25	94.9	1	0	0	2330.17	73	92
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	7	8	13	0.01%	34.9%	EYEAAVEQLK	99.7%	40.8	25	29.2	1	0	0	1179.59	95	104
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	7	8	13	0.01%	34.9%	GEGAGPPPPLPPAQPGAEGGGDR	99.7%	73.7	25	73.7	2	0	0	2081.01	13	35
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	7	8	13	0.01%	34.9%	GLGDRPAPK	99.7%	50.6	25	46.3	4	0	0	910.51	36	44
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	7	8	13	0.01%	34.9%	GLLLFMDEADAFLR	99.7%	68.1	25	63	1	0	0	1626.82	405	418
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	7	8	13	0.01%	34.9%	HILLYGPPGTGK	99.5%	37.8	25	19.3	2	0	0	1252.71	347	358
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	7	8	13	0.01%	34.9%	ICSWMGTGLCPGPLSPR	99.7%	63.8	25	61.5	1	0	0	1888.89	615	631
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	7	8	13	0.01%	34.9%	ITVLEALR	99.7%	54.7	25	39.9	4	0	0	914.57	291	298
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	7	8	13	0.01%	34.9%	LAQFDYGR	99.7%	53.2	25	28.8	4	0	0	969.48	506	513
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	7	8	13	0.01%	34.9%	LAQFDYGRK	99.2%	36.1	25	36.1	3	0	0	1097.57	506	514
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	7	8	13	0.01%	34.9%	LFDWANTSR	99.7%	57.5	25	41.1	2	0	0	1109.54	395	403
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	7	8	13	0.01%	34.9%	LGKPSLVR	99.7%	45	25	32.1	2	0	0	869.56	279	286
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	7	8	13	0.01%	34.9%	LHFDNCVLKPATEGK	96.7%	23.3	25	20.9	0	1	0	1728.87	487	501
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	7	8	13	0.01%	34.9%	LKEYEAAVEQLK	99.7%	74.8	25	71.5	4	2	0	1420.77	93	104
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	7	8	13	0.01%	34.9%	LTEGMSGR	99.7%	52.6	25	46.3	2	0	0	850.41	521	528
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	7	8	13	0.01%	34.9%	QQQLLNEENLR	99.7%	78	25	68.1	4	0	0	1384.72	147	157
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	7	8	13	0.01%	34.9%	QTVLESIR	99.7%	45.8	25	16.5	4	0	0	945.54	220	227
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	7	8	13	0.01%	34.9%	TAGTLFGEGFR	99.7%	77.2	25	71.3	4	0	0	1155.58	228	238
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	7	8	13	0.01%	34.9%	VRDIAIATR	99.7%	42.4	25	38.8	4	0	0	1014.61	328	336
ATPase WRNIP1	WRNIP1	WRIP1_HUMAN	72.1	99.8%	2	2	2	0.00%	3.0%	ALAAEEIR	97.9%	31.5	25	20.3	1	0	0	872.48	212	219
ATPase WRNIP1	WRNIP1	WRIP1_HUMAN	72.1	99.8%	2	2	2	0.00%	3.0%	SIEVYSAYNNVK	97.3%	30.5	25	28	1	0	0	1386.69	590	601
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	7	7	13	0.01%	10.0%	LSSDTALLGR	99.7%	53.4	25	47.3	2	0	0	1032.57	275	284
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	7	7	13	0.01%	10.0%	SFQGALEFK	98.6%	33.2	25	15.5	2	0	0	1026.53	487	495
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	7	7	13	0.01%	10.0%	STVLSLLLR	99.7%	57.1	25	24.3	3	0	0	1001.64	534	542
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	7	7	13	0.01%	10.0%	TVLVIAHR	99.7%	45.7	25	41.2	2	0	0	908.57	684	691
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	7	7	13	0.01%	10.0%	VAEVANAVAFIR	99.7%	71.3	25	62.5	2	0	0	1259.71	606	617
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	7	7	13	0.01%	10.0%	VTQDSLAQATQLAEER	99.7%	73.2	25	52.8	1	0	0	1759.88	342	357
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	7	7	13	0.01%	10.0%	VYLMQTSGQR	99.7%	51.1	25	43.1	1	0	0	1198.59	233	242
ATP-binding cassette sub-family B member 7, mitochondrial	ABCB7	ABCB7_HUMAN	82.6	100.0%	3	3	6	0.01%	4.4%	AGAAFFNEVR	99.5%	38	25	26.3	1	0	0	1081.54	201	210
ATP-binding cassette sub-family B member 7, mitochondrial	ABCB7	ABCB7_HUMAN	82.6	100.0%	3	3	6	0.01%	4.4%	AMNIVVPFMFK	97.4%	30.6	25	28.8	1	0	0	1296.68	152	162

ATP-binding cassette sub-family B member 7, mitochondrial	ABCB7	ABCB7_HUMAN	82.6	100.0%	3	3	6	0.01%	4.4%	VAISLGFLGGAK	99.7%	66.4	25	59.9	4	0	0	1132.67	140	151
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	8	9	14	0.01%	14.7%	AVVDKVFFSR	99.2%	36.1	25	32.5	1	0	0	1167.65	57	66
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	8	9	14	0.01%	14.7%	DQVIYPDGREDQK	99.7%	57.3	25	44.9	1	0	0	1562.74	521	533
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	8	9	14	0.01%	14.7%	EYLDNVQLGHILER	99.4%	36.9	25	9.25	1	0	0	1698.88	544	557
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	8	9	14	0.01%	14.7%	FSMGFIDSIIAK	99.7%	59.1	25	52.3	3	0	0	1328.69	311	322
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	8	9	14	0.01%	14.7%	IANPDQLLTQDVEK	99.7%	102	25	98.8	2	0	0	1583.83	182	195
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	8	9	14	0.01%	14.7%	ITELMQVLK	99.6%	40	25	21.7	1	0	0	1090.62	391	399
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	8	9	14	0.01%	14.7%	MTITEQKYEGEYR	99.5%	38.4	25	32.2	1	0	0	1647.77	254	266
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	8	9	14	0.01%	14.7%	VLGELWPLFGGR	99.7%	62.5	25	51.3	4	0	0	1343.75	485	496
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	6	12	0.01%	12.0%	ADIFMFDEPSSYLDVK	99.7%	61.9	25	61.9	2	0	0	1876.87	235	250
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	6	12	0.01%	12.0%	AIIKPQYVDQIPK	99.0%	27.5	25	26.9	0	1	0	1512.88	166	178
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	6	12	0.01%	12.0%	GSELQNYFTK	99.7%	48.4	25	40.2	2	0	0	1186.57	149	158
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	6	12	0.01%	12.0%	GTVGSILDR	96.8%	29.8	25	22	1	0	0	917.51	182	190
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	6	12	0.01%	12.0%	NVEDLSGGELQR	99.7%	58.1	25	46.2	2	0	0	1316.64	213	224
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	6	12	0.01%	12.0%	VAETANEEEVKK	99.7%	77	25	68.9	4	0	0	1346.68	333	344
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	4	4	10	0.01%	5.0%	AVSEEQQPALK	99.7%	56.4	25	46.6	3	0	0	1199.63	164	174
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	4	4	10	0.01%	5.0%	GAVIVVSHDAR	99.7%	53.7	25	32.3	4	0	0	1123.62	790	800
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	4	4	10	0.01%	5.0%	GFNLPYQDAR	99.4%	36.9	25	24.7	1	0	0	1180.57	714	723
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	4	4	10	0.01%	5.0%	STLLLLLTGK	99.7%	54.2	25	54.2	2	0	0	1058.68	665	674
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	17	27	0.03%	18.6%	ETTEVDLLTK	98.7%	33.7	25	28.3	2	0	0	1148.60	49	58
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	17	27	0.03%	18.6%	ILHGLGFTPAMQR	99.7%	56.8	25	51.2	3	1	0	1456.77	211	223
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	17	27	0.03%	18.6%	IPPPVIMVQNVSFK	99.7%	71.6	25	65.8	3	1	0	1568.89	391	404
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	17	27	0.03%	18.6%	LEELDADKAEMR	99.7%	74	25	67.7	2	0	0	1419.68	196	207
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	17	27	0.03%	18.6%	LIQQVAQEIWVCEK	99.7%	65.7	25	56.3	2	0	0	1743.91	575	588
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	17	27	0.03%	18.6%	LLTGELLPTDGMIR	99.7%	73	25	64.8	4	0	0	1528.84	442	455
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	17	27	0.03%	18.6%	LVDEEPQLTK	99.7%	40.7	25	21.2	2	0	0	1171.62	609	618
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	17	27	0.03%	18.6%	MMASGLTER	99.7%	41.7	25	33.4	3	0	0	995.46	366	374
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	17	27	0.03%	18.6%	SMLLSAIGK	96.7%	29.6	25	6.64	2	0	0	935.52	125	133
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	17	27	0.03%	18.6%	YYTGNYDQYVK	99.7%	68.2	25	59.2	2	0	0	1413.63	305	315
ATP-binding cassette sub-family F member 3	ABCF3	ABCF3_HUMAN	79.7	99.8%	2	2	4	0.00%	3.2%	ASVILAGLGFTPK	99.7%	51.2	25	51.2	2	0	0	1273.75	307	319
ATP-binding cassette sub-family F member 3	ABCF3	ABCF3_HUMAN	79.7	99.8%	2	2	4	0.00%	3.2%	LLLGDLAPVR	99.7%	43.3	25	27.2	2	0	0	1066.66	537	546
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	AFDSGIIPMEFVNK	99.7%	101	25	91.3	10	0	0	1567.78	949	962
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	AIVWGMQTR	99.7%	56.5	25	39.1	7	0	0	1061.56	499	507
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	AVQGMLDFDYVCSR	99.7%	100	25	100	6	0	0	1660.75	508	521
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	DEPSVAAMVYPFTGDHK	99.7%	67.5	25	67.5	8	0	0	1863.86	522	538
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	DGVYVLDLAAK	99.7%	75.1	25	68.2	5	0	0	1163.63	210	220
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	DLVSSLTSGLLTIGDR	99.7%	117	25	116	8	0	0	1646.90	919	934
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	DYQGPLKEHEVTIFVR	99.7%	39.7	25	39.7	0	2	0	1931.00	363	378
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	EAGVFVPR	95.7%	28.5	25	10.9	1	0	0	874.48	781	788
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	EAYPEEAYIADLDAK	99.7%	105	25	105	3	0	0	1697.79	245	259
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	EGDYVLFHHEGGVDVGDVDAK	99.7%	45.5	25	45.5	0	2	0	2258.04	128	148
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	EILIPVFK	99.2%	36.1	25	32.2	1	0	0	958.60	547	554
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	FGGALDAAAK	99.7%	77.6	25	54.8	2	0	0	920.48	935	944
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	FICTTSAIQNR	99.7%	70.2	25	65.3	5	0	0	1310.65	18	28
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	GVTIIGPATVGGIKPGCFK	99.7%	90.6	25	90.6	2	2	0	1872.04	617	635
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	IGNTGGMLDNILASK	99.7%	104	25	97.2	9	0	0	1503.78	636	650
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	ILIIGGSIANFTNVAATFK	99.7%	102	25	102	3	0	0	1950.11	337	355
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	LGLVGVNLTLDGVK	99.7%	75	25	72.8	4	0	0	1397.84	69	82
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	LGQEATVGK	99.7%	64.9	25	51.4	4	0	0	902.49	89	97
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	LIMGIGHR	99.7%	43.4	25	31.4	5	0	0	912.51	969	976
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	LLVGVDEK	99.7%	43.3	25	23.9	2	0	0	872.51	152	159

ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	LNPEDIKK	96.7%	29.5	25	19.9	1	0	0	956.54	160	167
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	LYRPGSVAYVSR	99.7%	37.3	25	30.6	3	4	0	1367.74	651	662
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	MIVVLGEIGGTEEYK	99.7%	131	25	131	4	0	0	1637.85	712	726
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	RGGPNYQEGLR	99.7%	42	25	32.2	4	0	0	1246.63	379	389
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	SAYDSTMETMNYAQIR	99.7%	98.7	25	98.7	9	0	0	1880.82	577	592
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	SGGMSNELNNIISR	99.7%	88	25	77	8	0	0	1507.72	663	676
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	SINNPDMR	98.3%	32.5	25	15.3	2	0	0	946.44	979	986
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	SMGFIGHYLDQK	99.7%	53.5	25	43.4	5	0	0	1411.67	1066	1077
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	STTLFSR	96.7%	29.6	25	11.5	2	0	0	811.43	489	495
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	TASFSESR	98.6%	33.2	25	24.9	1	0	0	884.41	453	460
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	TIAIIAEGIPEALTR	99.7%	141	25	131	10	0	0	1567.91	593	607
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	TILSLMTR	99.7%	59.9	25	57.2	6	0	0	950.53	322	329
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	TTDGVYEGVAIGGDR	99.7%	92.3	25	81.8	2	0	0	1509.72	677	691
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	VDATADYICK	99.7%	69.6	25	68.7	4	0	0	1155.54	221	230
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	VTPDTDWAR	99.7%	46.3	25	40	3	0	0	1060.51	34	42
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	WGDIEFPPPFGR	99.7%	54	25	54	1	0	0	1417.69	233	244
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	37	49	162	0.16%	40.9%	YQDTPGVK	96.3%	29.1	25	17.7	2	0	0	907.45	704	711
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	10	10	19	0.02%	19.4%	AAAAADLANR	99.7%	64.2	25	58.2	2	0	0	943.50	453	462
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	10	10	19	0.02%	19.4%	DLIEFGMIPEFVGR	97.4%	30.6	25	30.6	1	0	0	1638.82	486	499
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	10	10	19	0.02%	19.4%	DVGGEGVQQGLLK	99.7%	85.8	25	79.6	2	0	0	1299.69	374	386
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	10	10	19	0.02%	19.4%	LLEGTIVNVPEK	99.7%	64.9	25	64.9	2	0	0	1311.75	387	398
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	10	10	19	0.02%	19.4%	LLQDANYNVEK	99.7%	64.4	25	53.2	2	0	0	1306.66	339	349
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	10	10	19	0.02%	19.4%	SGESNTHQDIEEKDR	99.7%	45.2	25	45.2	0	2	0	1744.77	463	477
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	10	10	19	0.02%	19.4%	SIIKEPESAAEAVK	99.7%	51.1	25	30.8	2	0	0	1471.80	145	158
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	10	10	19	0.02%	19.4%	SNILLLGPTGSGK	99.7%	95.2	25	92.9	2	0	0	1256.72	287	299
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	10	10	19	0.02%	19.4%	TLLAQTLAK	99.7%	49.1	25	43.2	2	0	0	958.59	300	308
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	10	10	19	0.02%	19.4%	YLGFGTPSNLGK	99.7%	59.2	25	49.5	2	0	0	1253.65	438	449
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	AAECNIVVTQPR	99.7%	72.9	25	68	5	0	0	1357.69	435	446
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	AAMEALVVEVTK	99.7%	88.9	25	78.2	4	0	0	1260.69	1105	1116
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	AENNSEVGASGYGVPGPTWDR	99.7%	83.5	25	83.5	2	0	0	2162.97	121	141
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	AIEPPPLDAVIEAEHTLR	99.7%	56.7	25	56.7	2	0	0	1971.05	820	837
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	DFVNYLVR	99.7%	55.9	25	41.9	4	0	0	1025.54	64	71
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	DINTDFLLVVLR	99.7%	81.6	25	70.9	7	0	0	1417.81	517	528
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	DVVQAYPEVR	99.7%	65.1	25	56	4	0	0	1175.61	529	538
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	ELDALDANDELTPLGR	99.7%	114	25	101	5	0	0	1741.86	838	853
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	GANLKDYYSR	99.7%	62.9	25	55.7	1	0	0	1186.59	142	151
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	GISHVIVDEIHER	99.7%	47.8	25	44.4	0	2	0	1503.79	504	516
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	GMTLVTPLQLLLFASK	99.7%	67.8	25	67.8	5	0	0	1748.00	1058	1073
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	ISAVSVAER	99.7%	60.2	25	48.6	6	0	0	931.52	448	456
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	KILTTEGR	96.3%	29.1	25	13.3	1	0	0	917.54	1011	1018
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	KMTPSYEIR	99.7%	47.1	25	36.4	2	0	0	1124.58	16	24
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	KVFDPVPVGVTK	99.7%	58.5	25	50.8	2	0	0	1285.75	697	708
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	LAAQSCALSLVR	99.7%	78	25	63	4	0	0	1288.70	237	248
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	LAQFEPSQR	99.7%	52.8	25	46.9	2	0	0	1075.55	315	323
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	LETHMTPEMFR	97.7%	31.1	25	26.6	1	0	0	1391.64	785	795
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	LGGIGQFLAK	99.7%	78.9	25	69.8	9	0	0	1003.59	810	819
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	LNMATLR	99.7%	45.7	25	28.9	2	0	0	818.46	945	951
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	LNQYFQK	99.7%	45	25	34	4	0	0	940.49	185	191
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	LQISHEAAACITGLR	99.6%	31	25	28.6	0	2	0	1639.86	1090	1104
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	LSMSQLNEK	99.7%	55.4	25	47.4	5	0	0	1065.52	622	630
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	MGGEEAEIR	99.7%	86.5	25	69.7	9	0	0	991.45	930	938

ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	MLNMIR	96.3%	29.1	25	11.7	1	0	0	809.40	1131	1136
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	NFLYAWCGK	99.4%	37.5	25	20.5	2	0	0	1158.54	6	14
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	QPAIISQLDPVNER	99.7%	92.2	25	91.5	2	0	0	1579.84	1117	1130
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	RISAVSVAER	99.7%	40.7	25	23.5	3	0	0	1087.62	447	456
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	SFIAEMTIYIK	99.7%	66.9	25	58.2	3	0	0	1331.69	210	220
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	SSVNCPFSSQDMK	99.7%	51.4	25	51.4	3	0	0	1502.63	1025	1037
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	TPLHEIALSIK	99.7%	36.1	25	36.1	0	4	0	1221.72	796	806
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	TTQVPQFILDDFIQNDR	99.7%	55.9	25	50.6	3	0	0	2050.02	418	434
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	VFDPVPVGVTK	99.7%	58.4	25	57.8	4	0	0	1157.66	698	708
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	VQSDGQIVLVDDWIK	99.7%	81.5	25	75.2	2	0	0	1714.90	1075	1089
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	YGDGPRPPK	98.8%	34	25	31.2	4	0	0	986.51	1155	1163
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	YPSPFFVFGEK	99.7%	52.9	25	49.5	3	0	0	1317.65	1038	1048
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	YQILPLHSQIPR	99.7%	45	25	39.8	2	2	0	1464.83	681	692
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	38	45	130	0.13%	32.6%	YTQVGPDHNR	99.7%	55.8	25	44	2	0	0	1186.56	200	209
ATP-dependent RNA helicase DDX1	DDX1	DDX1_HUMAN	82.4	99.9%	2	2	4	0.00%	2.8%	ELLIIGGVAAR	99.7%	70.4	25	64.7	2	0	0	1111.68	320	330
ATP-dependent RNA helicase DDX1	DDX1	DDX1_HUMAN	82.4	99.9%	2	2	4	0.00%	2.8%	FLICTDVAAR	99.7%	53	25	46	2	0	0	1165.60	568	577
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	8	8	14	0.01%	13.4%	ELAMQTFGVLK	99.7%	83.9	25	78.8	2	0	0	1236.67	262	272
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	8	8	14	0.01%	13.4%	FLLLFTFLK	98.3%	32.3	25	9.31	1	0	0	1141.70	413	421
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	8	8	14	0.01%	13.4%	ISDIQSQLEK	99.7%	62	25	15.9	2	0	0	1160.62	558	567
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	8	8	14	0.01%	13.4%	LGNGINIIVATPGR	99.7%	59.3	25	59.3	2	0	0	1394.81	298	311
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	8	8	14	0.01%	13.4%	QTMLFSATQTR	99.7%	63.5	25	40	2	0	0	1283.64	359	369
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	8	8	14	0.01%	13.4%	SIRPLLEGR	97.2%	30.2	25	22.7	2	0	0	1040.62	209	217
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	8	8	14	0.01%	13.4%	TLAFLIPAVELIVK	99.7%	56.8	25	56.8	2	0	0	1526.96	230	243
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	8	8	14	0.01%	13.4%	VPLSEFDFSWSK	99.7%	71.1	25	71.1	1	0	0	1441.70	546	557
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	13	14	29	0.03%	35.4%	DPNSPLYSVK	99.3%	36.7	25	22.7	2	0	0	1119.57	82	91
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	13	14	29	0.03%	35.4%	GLAVNMVDSK	99.7%	66.1	25	58.3	4	0	0	1033.53	436	445
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	13	14	29	0.03%	35.4%	HSMNILNR	99.7%	42.5	25	32.3	2	0	0	984.50	446	453
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	13	14	29	0.03%	35.4%	IQEHFNK	99.7%	41.7	25	26.6	2	0	0	915.47	454	460
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	13	14	29	0.03%	35.4%	ISEQIVIGTPGTVLDWCSK	99.7%	53.4	25	52.6	1	0	0	2103.08	208	226
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	13	14	29	0.03%	35.4%	LDTDDLDEIEK	99.7%	76.2	25	64.2	2	0	0	1305.61	465	475
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	13	14	29	0.03%	35.4%	REEETLDTIK	95.6%	28.4	25	16.3	1	0	0	1233.63	298	307
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	13	14	29	0.03%	35.4%	SMTNLQIKEEK	99.5%	38.2	25	12.2	1	0	0	1336.68	19	29
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	13	14	29	0.03%	35.4%	SNLVDNTNQVEVLQR	99.7%	103	25	88.9	3	0	0	1728.89	67	81
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	13	14	29	0.03%	35.4%	TAAFVLAMLSR	99.7%	79.4	25	73.6	4	0	0	1179.66	144	154
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	13	14	29	0.03%	35.4%	VEPSDRYPQCLCLSPTYELALQTGK	99.7%	43.6	25	43.6	0	2	0	2925.41	155	179
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	13	14	29	0.03%	35.4%	VFVLDEADVMIATQGHQDQSIR	99.7%	37.3	25	37.3	0	1	0	2472.22	237	258
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	13	14	29	0.03%	35.4%	VLVTTNVCAR	99.7%	49.7	25	44.5	4	0	0	1132.61	385	394
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	23	0.02%	28.3%	CMALAQLLVEQNFPAIAIHR	99.7%	72	25	72	0	4	0	2295.21	299	318
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	23	0.02%	28.3%	DFLLKPELLR	98.6%	33.3	25	26	1	0	0	1243.74	48	57
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	23	0.02%	28.3%	DVQEIFR	99.7%	41	25	19.4	2	0	0	906.47	209	215
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	23	0.02%	28.3%	ELAFQISK	99.7%	40.6	25	32.1	2	0	0	935.52	123	130
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	23	0.02%	28.3%	GLAITFVSDENDAK	99.7%	59.4	25	56.7	1	0	0	1479.73	384	397
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	23	0.02%	28.3%	GSYVSIHSSGFR	99.7%	58	25	48.2	2	0	0	1296.63	36	47
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	23	0.02%	28.3%	ILNDVQDR	99.7%	51.8	25	42.9	2	0	0	972.51	398	405
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	23	0.02%	28.3%	ILVATNLFGR	99.7%	69.1	25	52	2	0	0	1103.66	339	348
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	23	0.02%	28.3%	NCPHVVVGTPGR	99.7%	78.6	25	63.2	2	2	0	1292.65	163	174
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	23	0.02%	28.3%	VSVFFGGLSIK	99.7%	51.4	25	47.8	2	0	0	1153.66	144	154
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	23	0.02%	28.3%	YQQFKDFQR	99.1%	35.5	25	34.5	1	0	0	1259.62	329	337
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	22	23	45	0.05%	36.9%	DKDAYSSFGSR	99.7%	57.8	25	57.7	2	0	0	1232.55	65	75
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	22	23	45	0.05%	36.9%	DLLDLLVEAK	99.7%	80.9	25	70.3	3	0	0	1128.65	555	564
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	22	23	45	0.05%	36.9%	DLMACAQTGSGK	99.7%	60.4	25	52.1	4	0	0	1254.55	219	230

ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	22	23	45	0.05%	36.9%	DREEALHQFR	99.1%	28	25	26.4	0	1	0	1300.64	479	488
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	22	23	45	0.05%	36.9%	EIQMLAR	95.3%	28.1	25	19.3	1	0	0	876.46	388	394
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	22	23	45	0.05%	36.9%	ELAVQIYEEAR	99.7%	70.2	25	58	2	0	0	1320.68	277	287
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	22	23	45	0.05%	36.9%	ELAVQIYEEARK	99.7%	80.8	25	71.9	1	0	0	1448.77	277	288
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	22	23	45	0.05%	36.9%	GLDISNVK	99.7%	43.5	25	31.4	1	0	0	845.47	504	511
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	22	23	45	0.05%	36.9%	IGLDFCK	99.7%	42.7	25	38.2	2	0	0	852.43	336	342
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	22	23	45	0.05%	36.9%	IVEQDTMPPK	99.7%	48	25	48	2	0	0	1173.58	364	373
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	22	23	45	0.05%	36.9%	LEQELFSGGNTGINFEK	99.7%	89.7	25	89.7	1	0	0	1882.92	146	162
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	22	23	45	0.05%	36.9%	MLDMGFEPQIR	99.7%	72.6	25	66.6	7	0	0	1336.64	352	362
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	22	23	45	0.05%	36.9%	QSSGASSSSFSSSR	99.7%	101	25	91.3	2	0	0	1361.59	604	617
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	22	23	45	0.05%	36.9%	QYPISLVLAPTR	99.7%	44.8	25	39	2	0	0	1357.78	265	276
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	22	23	45	0.05%	36.9%	SDYDGIGSR	99.7%	53.4	25	53.4	2	0	0	969.43	102	110
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	22	23	45	0.05%	36.9%	SFLLDLLNATGK	99.7%	102	25	91.2	2	0	0	1291.73	429	440
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	22	23	45	0.05%	36.9%	SPILVATAVAAR	99.7%	119	25	111	5	0	0	1168.70	492	503
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	22	23	45	0.05%	36.9%	VGNLGLATSFFNER	99.7%	82.1	25	77.4	2	0	0	1524.78	535	548
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	22	23	45	0.05%	36.9%	VGSTSENITQK	99.7%	70.6	25	57.3	4	0	0	1163.59	408	418
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	22	23	45	0.05%	36.9%	VRPCVVYGGADIGQQIR	99.7%	46	25	38.2	0	1	0	1887.99	295	311
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	22	23	45	0.05%	36.9%	VVWVEESDKR	99.5%	30.7	25	27.5	0	2	0	1246.64	419	428
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	22	23	45	0.05%	36.9%	YLVLDEADR	99.7%	58	25	40.9	2	0	0	1093.55	343	351
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	22	23	45	0.05%	36.9%	YTRPTPVQK	98.3%	32.4	25	19	1	0	0	1089.61	200	208
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	3	3	8	0.01%	8.0%	EGAFSNFPISEETIK	99.7%	75.1	25	75.1	8	0	0	1668.81	136	150
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	3	3	8	0.01%	8.0%	GVTYLFPIQVK	99.7%	73	25	56.2	2	0	0	1264.73	156	166
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	3	3	8	0.01%	8.0%	NGIDILVGTPGR	99.7%	99.1	25	88.9	3	0	0	1211.67	258	269
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	3	3	8	0.01%	8.0%	TFSFAIPLIER	99.7%	60.8	25	57.1	4	0	0	1293.72	188	198
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	3	3	8	0.01%	8.0%	VLVATNVAAR	99.7%	75.4	25	67.1	2	0	0	1013.61	441	450
ATP-dependent RNA helicase DDX54	DDX54	DDX54_HUMAN	98.6	99.8%	2	2	3	0.00%	2.2%	FEEEELQR	98.2%	32.3	25	16.8	1	0	0	1079.50	552	559
ATP-dependent RNA helicase DDX54	DDX54	DDX54_HUMAN	98.6	99.8%	2	2	3	0.00%	2.2%	TACFLLPMFER	96.9%	29.9	25	24.9	2	0	0	1384.68	147	157
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L_HUMAN	86.5	100.0%	6	6	11	0.01%	9.2%	EIQIVLEGK	99.5%	38.6	25	30.9	2	0	0	1028.60	760	768
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L_HUMAN	86.5	100.0%	6	6	11	0.01%	9.2%	LAETQNIAPSFVK	99.7%	76.9	25	72.4	2	0	0	1417.77	225	237
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L_HUMAN	86.5	100.0%	6	6	11	0.01%	9.2%	LGVMTYSDTGK	99.7%	40.9	25	40.9	2	0	0	1171.57	698	708
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L_HUMAN	86.5	100.0%	6	6	11	0.01%	9.2%	LSPETQSAIEQEIR	99.7%	63.7	25	56.5	2	0	0	1600.82	709	722
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L_HUMAN	86.5	100.0%	6	6	11	0.01%	9.2%	TGFAEGFLK	99.7%	51.5	25	44	2	0	0	969.50	270	278
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L_HUMAN	86.5	100.0%	6	6	11	0.01%	9.2%	TTTGLDSAVDPVQMK	99.7%	86.5	25	75.1	1	0	0	1562.77	320	334
Basic leucine zipper and W2 domain-containing protein 1	BZW1	BZW1_HUMAN	48.0	100.0%	2	2	4	0.00%	4.8%	AEVLSEEPILK	99.7%	69.1	25	58.9	2	0	0	1227.68	369	379
Basic leucine zipper and W2 domain-containing protein 1	BZW1	BZW1_HUMAN	48.0	100.0%	2	2	4	0.00%	4.8%	LMELFPANK	99.7%	60.7	25	46.4	2	0	0	1062.57	215	223
Basic leucine zipper and W2 domain-containing protein 2	BZW2	BZW2_HUMAN	48.2	100.0%	3	3	5	0.01%	6.4%	EGIAASFAVK	99.2%	36	25	27.5	2	0	0	992.54	180	189
Basic leucine zipper and W2 domain-containing protein 2	BZW2	BZW2_HUMAN	48.2	100.0%	3	3	5	0.01%	6.4%	FLDSTGSR	99.3%	36.5	25	13.8	1	0	0	882.43	51	58
Basic leucine zipper and W2 domain-containing protein 2	BZW2	BZW2_HUMAN	48.2	100.0%	3	3	5	0.01%	6.4%	LLELFPVNR	99.1%	35.6	25	26.8	2	0	0	1100.65	216	224
B-cell receptor-associated protein 31	BCAP31	BAP31_HUMAN	28.0	99.9%	2	2	4	0.00%	7.7%	AENQVLAMR	99.7%	40.9	25	33.3	2	0	0	1031.53	205	213
B-cell receptor-associated protein 31	BCAP31	BAP31_HUMAN	28.0	99.9%	2	2	4	0.00%	7.7%	YMEENDQLKK	97.4%	30.7	25	30.5	2	0	0	1297.61	150	159
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	3	3	9	0.01%	3.3%	LLASTLVHSVK	99.7%	62.8	25	59.6	4	0	0	1167.71	570	580
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	3	3	9	0.01%	3.3%	NTEEEGLKYK	99.5%	38.7	25	25.6	1	0	0	1210.60	430	439
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	3	3	9	0.01%	3.3%	TIAPQNAPR	97.4%	30.6	25	20	4	0	0	967.53	304	312
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	10	20	0.02%	16.4%	AGATLDLLVENMGR	99.7%	80	25	69.3	4	0	0	1459.76	469	482
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	10	20	0.02%	16.4%	AYVAVDGIPQGVLER	99.7%	75.6	25	75.6	2	0	0	1586.85	443	457
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	10	20	0.02%	16.4%	MFEIDYSR	99.7%	44.3	25	44.3	2	0	0	1060.48	31	38
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	10	20	0.02%	16.4%	SLYPLTFIQVK	99.7%	64.8	25	64.8	2	0	0	1308.76	400	410
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	10	20	0.02%	16.4%	SSDPDYLAAVDK	99.7%	59	25	37.2	2	0	0	1280.60	149	160
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	10	20	0.02%	16.4%	TEAVASSLYDILAR	99.7%	96.4	25	79.4	2	0	0	1508.80	286	299
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	10	20	0.02%	16.4%	TVGAALDILCPSGPIK	99.7%	96.6	25	88.9	2	0	0	1611.88	384	399
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	10	20	0.02%	16.4%	VNYGAYINDFK	99.7%	81.5	25	76.4	2	0	0	1303.63	483	493

Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	10	20	0.02%	16.4%	YISGSIHYSR	99.7%	70.4	25	65.3	2	0	0	1182.59	50	59
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	6	6	11	0.01%	16.5%	AVAQAGTVGTLLIVK	99.7%	91.6	25	82.3	2	0	0	1440.88	95	109
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	6	6	11	0.01%	16.5%	EGPPPASPAQLLSK	99.7%	51.2	25	51.2	2	0	0	1391.75	421	434
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	6	6	11	0.01%	16.5%	LEQPDPGAVAAAAILR	99.7%	77.4	25	69	2	0	0	1591.88	552	567
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	6	6	11	0.01%	16.5%	SPGADLLQVLTK	99.7%	82.2	25	76.1	2	0	0	1241.71	511	522
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	6	6	11	0.01%	16.5%	VAGALAEAGVGLEEIAK	99.7%	84.1	25	75.3	1	0	0	1597.88	163	179
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	6	6	11	0.01%	16.5%	VAPAEPQEAPDSTAAGGSASK	99.7%	66.4	25	63	2	0	0	1940.92	352	372
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	26	28	83	0.08%	20.3%	AALLNQHYQVNFK	99.7%	54	25	50.3	2	0	0	1545.82	217	229
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	26	28	83	0.08%	20.3%	AYVDDTPAEQMK	99.7%	50.2	25	50.2	1	0	0	1383.61	289	300
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	26	28	83	0.08%	20.3%	DQDLEPGAPSMGAK	99.7%	53.1	25	53.1	4	0	0	1415.65	1464	1477
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	26	28	83	0.08%	20.3%	DQVDIAVQELLQLK	99.7%	105	25	84.3	4	0	0	1611.90	926	939
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	26	28	83	0.08%	20.3%	EYIPGQPPLSQSSDSSPTR	99.7%	55.9	25	48.3	4	0	0	2045.98	871	889
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	26	28	83	0.08%	20.3%	FAGGDYTTTIEAFISASGR	99.7%	67.7	25	67.7	2	0	0	1963.94	1216	1234
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	26	28	83	0.08%	20.3%	FVELPGAEMGK	99.7%	46.7	25	38.2	3	0	0	1177.59	187	197
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	26	28	83	0.08%	20.3%	GDIIQLQR	98.7%	33.5	25	15	1	0	0	942.54	667	674
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	26	28	83	0.08%	20.3%	GNAAWQEQLK	96.4%	29.2	25	16.9	2	0	0	1144.57	130	139
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	26	28	83	0.08%	20.3%	GSQFGQSCCLR	99.7%	48.9	25	48.9	2	0	0	1299.56	329	339
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	26	28	83	0.08%	20.3%	INEAVECLLSLK	99.7%	80.6	25	67.6	6	0	0	1388.75	850	861
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	26	28	83	0.08%	20.3%	KVIDPVAPR	99.7%	42.2	25	36.2	2	0	0	994.60	498	506
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	26	28	83	0.08%	20.3%	LLSVNIR	95.6%	28.4	25	14.9	1	0	0	814.51	1334	1340
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	26	28	83	0.08%	20.3%	LNLNNTVLSK	99.7%	60.7	25	46.8	4	0	0	1115.64	426	435
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	26	28	83	0.08%	20.3%	LQAILEDIQVTLFTR	99.7%	114	25	109	2	0	0	1760.00	1401	1415
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	26	28	83	0.08%	20.3%	LTVAENEAETK	99.7%	77.4	25	76.7	9	0	0	1204.61	1390	1400
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	26	28	83	0.08%	20.3%	MFEIVFEDPK	99.7%	47.4	25	38.7	1	0	0	1254.61	1251	1260
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	26	28	83	0.08%	20.3%	NPEVGLKPVWYSPK	99.7%	45.7	25	45.7	2	0	0	1613.87	536	549
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	26	28	83	0.08%	20.3%	NQGGGLSSSGAGEGQGPK	99.7%	102	25	102	6	0	0	1587.74	992	1009
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	26	28	83	0.08%	20.3%	NSEPAGLETPEAK	99.7%	54.2	25	44.8	3	0	0	1342.65	890	902
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	26	28	83	0.08%	20.3%	SCQFVAVR	99.7%	48.9	25	39.7	4	0	0	966.48	1376	1383
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	26	28	83	0.08%	20.3%	SLYDEVAAQGEVVR	99.7%	99.1	25	94.2	4	0	0	1535.77	825	838
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	26	28	83	0.08%	20.3%	VASQGEVVR	99.7%	42	25	25	4	0	0	944.52	908	916
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	26	28	83	0.08%	20.3%	VAVQGDVVR	99.7%	60	25	43.4	4	0	0	942.54	757	765
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	26	28	83	0.08%	20.3%	VIDPVAPR	99.7%	41.6	25	41.6	4	0	0	866.51	499	506
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	26	28	83	0.08%	20.3%	WFGFLEAQQAFQSVGTK	99.7%	67.1	25	65	2	0	0	1943.97	150	166
Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	MTHFD2	MTDC_HUMAN	37.9	100.0%	3	3	5	0.01%	12.6%	AGYITPVPGGVGPMTVAMLMK	98.5%	32.9	25	32.9	1	0	0	2090.09	302	322
Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	MTHFD2	MTDC_HUMAN	37.9	100.0%	3	3	5	0.01%	12.6%	EGAAVIDVGINR	99.7%	84.5	25	70.2	2	0	0	1213.65	267	278
Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	MTHFD2	MTDC_HUMAN	37.9	100.0%	3	3	5	0.01%	12.6%	LVGDVDFEGVR	99.7%	65.1	25	50.9	2	0	0	1205.62	289	299
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	16	0.02%	11.4%	ANSSVVSVNCK	99.7%	58.8	25	52.6	2	0	0	1164.57	587	597
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	16	0.02%	11.4%	EIPVESIEEVSK	99.7%	66.4	25	55.3	2	0	0	1358.71	258	269
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	16	0.02%	11.4%	ESQATLEER	99.7%	40.2	25	26.1	2	0	0	1062.51	5	13
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	16	0.02%	11.4%	GGLAGEFQR	99.7%	42.8	25	34.4	1	0	0	934.47	683	691
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	16	0.02%	11.4%	LGCFEIAK	99.7%	41.5	25	32.9	2	0	0	937.48	894	901
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	16	0.02%	11.4%	LLPGIEVLWTGPK	99.7%	61.8	25	61.8	2	0	0	1422.84	241	253
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	16	0.02%	11.4%	LLPIDGANDLFFQPPPLTPTSK	96.5%	29.3	25	29.3	1	0	0	2381.28	692	713
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	16	0.02%	11.4%	SFVQWLGCR	99.7%	45.1	25	40.2	2	0	0	1152.56	656	664
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	16	0.02%	11.4%	WELNTYLYAPK	99.7%	72.8	25	69.8	2	0	0	1397.71	88	98
Bifunctional purine biosynthesis protein PURH	ATIC	PUR9_HUMAN	64.6	100.0%	6	6	12	0.01%	12.3%	DVSELTGFPEMLGGR	99.7%	52	25	52	2	0	0	1607.77	50	64
Bifunctional purine biosynthesis protein PURH	ATIC	PUR9_HUMAN	64.6	100.0%	6	6	12	0.01%	12.3%	NLTALGLNLVASGGTAK	99.7%	84.9	25	84.9	2	0	0	1599.91	23	39
Bifunctional purine biosynthesis protein PURH	ATIC	PUR9_HUMAN	64.6	100.0%	6	6	12	0.01%	12.3%	SLFSNVVTK	99.7%	46	25	34.4	2	0	0	994.56	398	406
Bifunctional purine biosynthesis protein PURH	ATIC	PUR9_HUMAN	64.6	100.0%	6	6	12	0.01%	12.3%	TLFGLHLSQK	97.1%	30.2	25	29.2	2	0	0	1143.65	380	389
Bifunctional purine biosynthesis protein PURH	ATIC	PUR9_HUMAN	64.6	100.0%	6	6	12	0.01%	12.3%	TLTPISAAYAR	99.0%	34.9	25	32	2	0	0	1163.64	295	305
Bifunctional purine biosynthesis protein PURH	ATIC	PUR9_HUMAN	64.6	100.0%	6	6	12	0.01%	12.3%	YTQSNSVCYAK	99.7%	59.3	25	59.3	2	0	0	1320.59	427	437

Biliverdin reductase A	BLVRA	BIEA_HUMAN	33.4	100.0%	3	3	5	0.01%	10.8%	DQNIFVQK	99.0%	35.1	25	17.4	1	0	0	991.52	254	261
Biliverdin reductase A	BLVRA	BIEA_HUMAN	33.4	100.0%	3	3	5	0.01%	10.8%	FGVVVVGVGR	99.7%	64.8	25	64	2	0	0	988.59	9	18
Biliverdin reductase A	BLVRA	BIEA_HUMAN	33.4	100.0%	3	3	5	0.01%	10.8%	SGSLENVPNVGVNK	99.7%	51.9	25	51.9	2	0	0	1413.73	235	248
Bloom syndrome protein	BLM	BLM_HUMAN	159.0	99.8%	2	2	2	0.00%	1.4%	SLIVDQVQK	98.2%	32.3	25	16.5	1	0	0	1029.59	718	726
Bloom syndrome protein	BLM	BLM_HUMAN	159.0	99.8%	2	2	2	0.00%	1.4%	SVEGYYQESGR	97.5%	30.7	25	21.3	1	0	0	1274.56	969	979
BolA-like protein 2	BOLA2	BOLA2_HUMAN	10.1	100.0%	3	4	7	0.01%	39.5%	DLEAEHVEVEDTTLNR	99.7%	81.7	25	81.7	2	2	0	1869.88	15	30
BolA-like protein 2	BOLA2	BOLA2_HUMAN	10.1	100.0%	3	4	7	0.01%	39.5%	FEGKPLLQR	99.7%	50	25	45.4	2	0	0	1087.63	44	52
BolA-like protein 2	BOLA2	BOLA2_HUMAN	10.1	100.0%	3	4	7	0.01%	39.5%	TLTPDQWAR	97.1%	30.1	25	23.6	1	0	0	1087.55	74	82
BRCA1-A complex subunit BRE	BRE	BRE_HUMAN	43.6	99.8%	2	2	3	0.00%	7.3%	ISPMLSPFISSVVR	98.4%	32.6	25	32.6	1	0	0	1532.85	10	23
BRCA1-A complex subunit BRE	BRE	BRE_HUMAN	43.6	99.8%	2	2	3	0.00%	7.3%	LPVDFSNIPTYLLK	99.7%	57.2	25	57.2	2	0	0	1619.90	177	190
BRCA1-associated ATM activator 1	BRAT1	BRAT1_HUMAN	88.1	100.0%	3	3	3	0.00%	4.3%	SCDLLLFLR	99.7%	41.5	25	24.1	1	0	0	1136.61	719	727
BRCA1-associated ATM activator 1	BRAT1	BRAT1_HUMAN	88.1	100.0%	3	3	3	0.00%	4.3%	STLAESSDHVEK	99.6%	39.3	25	32.4	1	0	0	1302.62	786	797
BRCA1-associated ATM activator 1	BRAT1	BRAT1_HUMAN	88.1	100.0%	3	3	3	0.00%	4.3%	VQDLSSGVLSFSLR	98.0%	31.8	25	28.6	1	0	0	1507.81	65	78
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	AAEEIGIK	99.7%	61.9	25	37.2	2	0	0	830.46	59	66
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	AAQAPSSFQLLYDLK	99.7%	107	25	104	2	0	0	1651.87	805	819
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	APAEILNGK	99.7%	43.7	25	40.7	2	0	0	912.52	2	10
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	DDSNLYINVK	99.7%	40.2	25	36	1	0	0	1180.58	47	56
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	EIGLLSEEVELYGETK	99.7%	106	25	106	2	0	0	1808.92	337	352
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	EQVPGFTPR	97.3%	30.5	25	26.4	1	0	0	1030.53	29	37
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	ETGVPIAGR	99.6%	39.7	25	36.1	2	0	0	899.49	158	166
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	FSDIQIR	99.7%	46.3	25	16.6	4	0	0	878.47	489	495
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	GALALAQAVQR	99.7%	75.1	25	68.9	5	0	0	1097.64	794	804
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	GDLNDCFIPCTPK	99.7%	42.6	25	42.6	2	0	0	1536.68	138	150
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	GVPTGFILPIR	99.7%	78.2	25	68.7	4	0	0	1169.70	879	889
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	IFHELTQTDK	99.7%	55.2	25	40.9	3	2	0	1231.63	464	473
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	ITIGQAPTEK	99.7%	42.6	25	39.9	2	0	0	1057.59	544	553
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	IYGADDIELLPEAQHK	99.7%	77.3	25	70.4	2	2	0	1811.92	833	848
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	KITIGQAPTEK	99.7%	64.8	25	49.9	2	0	0	1185.68	543	553
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	KVVGDVAYDEAK	99.7%	68.3	25	63.5	2	0	0	1293.67	251	262
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	LAILQVGNR	99.7%	64.9	25	52.9	2	0	0	983.60	38	46
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	LDIDPETITWQR	99.7%	69.5	25	69.5	2	0	0	1486.75	521	532
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	LPVEDKIR	99.7%	47.8	25	38.6	1	0	0	969.57	820	827
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	LVGPEGFVVTEAGFGADIGMEK	99.7%	34.5	25	34.5	0	1	0	2239.10	658	679
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	LVPSVNGVR	96.4%	29.3	25	27.4	2	0	0	940.56	479	487
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	MFGIPVVVAVNAFK	99.7%	81.3	25	73	8	0	0	1491.84	747	760
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	MHGGGPTVTAGLPLPK	98.7%	26.6	25	26.6	0	2	0	1532.83	706	721
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	QGFGNLPICMAK	99.7%	53.3	25	47.1	2	0	0	1335.66	855	866
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	TDPTTLTDEEINR	99.7%	71.1	25	57.3	4	0	0	1504.71	505	517
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	TDTESELDLISR	99.7%	73	25	65.3	2	0	0	1378.67	761	772
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	THLSLSHNPEQK	99.7%	59.6	25	57.4	1	0	0	1390.71	867	878
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	TPVPSDIDISR	99.7%	56	25	56	2	0	0	1199.63	314	324
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	TTTESEVMK	98.5%	33	25	24.8	1	0	0	1025.48	75	83
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	VLLSALER	99.7%	55	25	40.5	5	0	0	900.55	355	362
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	VVGDVAYDEAK	99.7%	70.8	25	68.3	2	0	0	1165.57	252	262
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	VVGDVAYDEAKER	99.7%	74.8	25	65.8	2	0	0	1450.72	252	264
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	WMIQYNNLNLK	99.7%	53.4	25	43.5	3	0	0	1436.74	303	313
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	YSGLCPHVVVLVATVR	99.7%	47.5	25	47.5	0	2	0	1769.97	687	702
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	35	39	88	0.09%	40.5%	YVVVTGITPTPLGEGK	99.7%	124	25	124	2	0	0	1630.91	371	386
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	AAFALGGLGSGFASNR	99.7%	110	25	110	2	0	0	1495.77	556	571
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	ATGYPLAYVAAK	99.7%	53	25	48.5	2	0	0	1224.66	697	708
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	EATAGNPGGQTVR	99.7%	49.6	25	49.6	2	0	0	1257.62	359	371

CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	ELSDLESAR	99.7%	51.5	25	47.4	2	0	0	1019.50	1067	1075
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	FLSSAAAVSK	99.7%	71.7	25	63	2	0	0	980.54	1110	1119
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	IIAHAQLLEQHR	99.7%	40.2	25	39	0	2	0	1428.81	843	854
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	ILALDCGLK	99.7%	46.5	25	28.6	2	0	0	1002.57	178	186
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	LAADFSVPLIIDIK	99.3%	36.7	25	29.2	1	0	0	1514.88	1418	1431
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	LFVEALGQIGPAPPLK	99.7%	65.9	25	65.9	2	0	0	1649.96	1435	1450
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	LGGAVLSFSEATSSVQK	99.7%	102	25	102	2	0	0	1680.88	1987	2003
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	LGYPVLVR	99.4%	37.2	25	30.3	2	0	0	916.56	548	555
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	LLDTIGISQPQWR	99.7%	53.2	25	53.2	2	0	0	1526.83	1054	1066
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	LYLNETFSELR	98.3%	32.5	25	28.5	1	0	0	1384.71	1557	1567
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	MALLATVLGR	99.7%	48.7	25	33.3	2	0	0	1060.62	2215	2224
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	MALLATVLGRF	99.7%	77.2	25	77.2	2	0	0	1207.69	2215	2225
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	NILLTIGSYK	98.7%	33.7	25	31.4	1	0	0	1121.66	1314	1323
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	NKSELLPTVR	99.7%	59.9	25	52.6	1	0	0	1156.67	1324	1333
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	NSVTGGTAAFEPSVDYCVVK	99.7%	91	25	91	2	0	0	2100.99	720	739
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	QELGICPAVK	98.5%	32.9	25	19.7	1	0	0	1114.59	892	901
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	SFEEAFQK	99.3%	36.8	25	22.6	2	0	0	985.46	771	778
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	SILEQLAEK	99.7%	57.3	25	27	2	0	0	1030.58	1379	1387
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	SVGEVMGIGR	99.7%	42.7	25	31.5	2	0	0	1020.51	761	770
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	TLGVDLVALATR	99.7%	83.9	25	72.4	2	0	0	1228.73	1229	1240
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	TSSSFAAAMAR	99.7%	68.4	25	62.8	3	0	0	1115.51	1976	1986
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	VFNTGGAPR	99.7%	49.9	25	41.1	2	0	0	918.48	169	177
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	VHVDCMTSQK	99.5%	38.2	25	32.9	1	0	0	1204.55	1451	1460
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	VIMGEEVEPVGLMTGSGVVGVK	99.4%	37.7	25	33.5	1	0	0	2203.14	1241	1262
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	VLGTSPEAIDSAENR	99.7%	93.7	25	93.5	2	0	0	1558.77	1034	1048
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	VNEISVEVDSDPR	99.7%	87.2	25	77.8	2	0	0	1458.71	2188	2200
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	30	31	54	0.05%	15.6%	VPQFSFSR	99.7%	45.9	25	37.2	2	0	0	967.50	1263	1270
Calcium uniporter protein, mitochondrial	MCU	MCU_HUMAN	39.9	100.0%	2	2	2	0.00%	8.0%	DLLSHENAATLNDVK	99.7%	80.4	25	74.4	1	0	0	1639.83	166	180
Calcium uniporter protein, mitochondrial	MCU	MCU_HUMAN	39.9	100.0%	2	2	2	0.00%	8.0%	LEDLKEQLAPLEK	99.7%	68.7	25	65.1	1	0	0	1525.85	207	219
Calcium/calmodulin-dependent protein kinase type II subunit gamma	CAMK2G	KCC2G_HUMAN	62.6	100.0%	3	3	4	0.00%	6.8%	DLKPENLLLASK	95.4%	28.3	25	16.2	1	0	0	1340.78	136	147
Calcium/calmodulin-dependent protein kinase type II subunit gamma	CAMK2G	KCC2G_HUMAN	62.6	100.0%	3	3	4	0.00%	6.8%	FTDDYQLFEELGK	99.7%	47.9	25	47.9	1	0	0	1604.75	10	22
Calcium/calmodulin-dependent protein kinase type II subunit gamma	CAMK2G	KCC2G_HUMAN	62.6	100.0%	3	3	4	0.00%	6.8%	NLINQMLTINPAK	99.7%	56.9	25	55.6	2	0	0	1469.81	247	259
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	10	0.01%	19.8%	AGQTTYSGVIDCFRK	99.7%	67.5	25	67.5	2	0	0	1702.82	552	566
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	10	0.01%	19.8%	DLGIFGLYK	99.7%	41.2	25	41.2	1	0	0	1025.57	474	482
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	10	0.01%	19.8%	GLIPQLIGVAPEK	99.7%	56.5	25	0	2	0	0	1334.80	391	403
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	10	0.01%	19.8%	IVQLLAGVADQTK	99.7%	70	25	62.8	2	0	0	1355.79	56	68
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	10	0.01%	19.8%	KIYSTLAGTR	99.7%	60.2	25	48.7	2	0	0	1109.63	234	243
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	10	0.01%	19.8%	LATATFAGIENK	99.7%	91.9	25	80.5	2	0	0	1235.66	641	652
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	10	0.01%	19.8%	LQVAGEITTGPR	99.7%	81.4	25	65	2	0	0	1241.69	454	465
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	10	0.01%	19.8%	LTVNDFVR	99.7%	57.6	25	48.8	2	0	0	963.53	407	414
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	10	0.01%	19.8%	NIFLQYASTEVDGER	99.7%	79.8	25	79.8	1	0	0	1741.84	18	32
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	10	0.01%	19.8%	SPSVAVVQPK	99.7%	44.6	25	29.5	2	0	0	1011.58	662	671
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	10	0.01%	19.8%	VSALNVLR	99.7%	47.9	25	24.7	2	0	0	871.54	466	473
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	10	0.01%	19.8%	YEGFFGLYR	99.7%	55.2	25	51.3	2	0	0	1151.55	382	390
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	43	0.04%	40.1%	AGQTTYSGVIDCFRK	99.7%	67.5	25	67.5	2	0	0	1702.82	554	568
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	43	0.04%	40.1%	ASGDSARPVLLQVAESAYR	99.7%	48.3	25	48.3	0	2	0	1990.04	313	331
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	43	0.04%	40.1%	DIPFSAIYFPCYAHVK	99.7%	55.6	25	9.54	2	0	0	1927.94	493	508
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	43	0.04%	40.1%	DLGFFGIYK	99.7%	50.8	25	49.6	2	0	0	1059.55	476	484
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	43	0.04%	40.1%	FGLGSVAGAVGATAVYPIDLVK	99.7%	84.9	25	84.9	2	0	0	2105.16	332	353
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	43	0.04%	40.1%	GLLPQLLGVAPEK	99.7%	56.5	25	0	2	0	0	1334.80	393	405
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	43	0.04%	40.1%	IAPLEEGTLPFNLAEAQR	99.7%	90	25	90	2	1	0	1969.04	293	310

Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	43	0.04%	40.1%	ILREEGPK	99.7%	43.5	25	34.8	2	0	0	941.54	569	576
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	43	0.04%	40.1%	INLPAPNPDHVGGYK	99.7%	59.2	25	51.7	2	0	0	1591.82	627	641
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	43	0.04%	40.1%	KIYSTLAGTR	99.7%	60.2	25	48.7	2	0	0	1109.63	235	244
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	43	0.04%	40.1%	LAVATFAGIENK	99.7%	103	25	94.1	2	0	0	1233.68	642	653
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	43	0.04%	40.1%	LQVAGEITTGPR	99.7%	81.4	25	65	2	0	0	1241.69	456	467
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	43	0.04%	40.1%	LTVNDFVR	99.7%	57.6	25	48.8	2	0	0	963.53	409	416
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	43	0.04%	40.1%	MTLADIER	99.7%	51.2	25	42.6	2	0	0	948.48	285	292
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	43	0.04%	40.1%	NGEFFMSPNDFVTR	99.7%	83.4	25	83.4	3	0	0	1660.74	30	43
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	43	0.04%	40.1%	SSPQFGVTLLTYELLQR	99.7%	113	25	94.6	2	0	0	1952.05	589	605
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	43	0.04%	40.1%	STGSFVGELMYK	99.7%	59.6	25	55.1	2	0	0	1318.63	361	372
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	43	0.04%	40.1%	TVELLSGVVDQTK	99.7%	98.7	25	86.6	2	0	0	1388.76	57	69
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	43	0.04%	40.1%	VSALSVVR	99.7%	56.6	25	51.1	2	0	0	830.51	468	475
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	43	0.04%	40.1%	YEGFFGLYR	99.7%	55.2	25	51.3	2	0	0	1151.55	384	392
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	43	0.04%	40.1%	YLNIFGESQPNPK	99.7%	98.3	25	98.3	1	0	0	1506.76	44	56
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	10	11	22	0.02%	22.0%	EGIPGLYR	99.5%	38	25	28.1	2	0	0	904.49	438	445
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	10	11	22	0.02%	22.0%	FWAYEQYKK	98.9%	34.4	25	27.4	2	0	0	1262.62	269	277
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	10	11	22	0.02%	22.0%	HEGLGAFYK	99.7%	47.6	25	46.1	2	0	0	1021.51	337	345
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	10	11	22	0.02%	22.0%	IMMQVHGSK	99.6%	39.3	25	35.2	2	0	0	1030.52	220	228
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	10	11	22	0.02%	22.0%	MNIFGGFR	99.7%	40.2	25	30.2	2	0	0	941.47	232	239
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	10	11	22	0.02%	22.0%	NLGIPLGQDAEEK	99.7%	49.5	25	48	2	0	0	1383.71	50	62
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	10	11	22	0.02%	22.0%	QLLAGGIAGAVSR	99.7%	102	25	94.8	2	0	0	1212.71	197	209
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	10	11	22	0.02%	22.0%	QTLGVTQK	98.0%	31.8	25	18.2	2	0	0	874.50	470	477
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	10	11	22	0.02%	22.0%	TGQYSGIYDCAK	99.7%	73.6	25	73.6	2	0	0	1362.60	321	332
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	10	11	22	0.02%	22.0%	VLPAVGISYVVYENMK	99.7%	60.8	25	60.8	4	0	0	1797.95	454	469
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	7	7	10	0.01%	7.5%	AAASLAWVLR	99.7%	59.3	25	47.9	1	0	0	1057.62	34	43
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	7	7	10	0.01%	7.5%	ALYTLSGETEELSR	99.7%	59.5	25	57.6	2	0	0	1568.78	1171	1184
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	7	7	10	0.01%	7.5%	APAEEEVGPR	99.7%	50.9	25	47.1	1	0	0	1054.52	964	973
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	7	7	10	0.01%	7.5%	ASPAAPADGAAPAQPSIR	99.7%	52.7	25	52.7	1	0	0	1647.85	192	209
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	7	7	10	0.01%	7.5%	AVASSPAATNSEVK	99.7%	50.8	25	44.5	2	0	0	1331.68	550	563
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	7	7	10	0.01%	7.5%	DLPDGHAASPR	99.7%	52.1	25	43.2	2	0	0	1135.55	326	336
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	7	7	10	0.01%	7.5%	SVSSDSLGPPRPAPAR	95.7%	28.5	25	27	1	0	0	1593.83	429	444
Calpain-2 catalytic subunit	CAPN2	CAN2_HUMAN	80.0	100.0%	2	2	3	0.00%	3.3%	NYPNTFWMNPQYLIK	99.7%	60.6	25	59.6	1	0	0	1928.94	376	390
Calpain-2 catalytic subunit	CAPN2	CAN2_HUMAN	80.0	100.0%	2	2	3	0.00%	3.3%	SDTFINLR	99.7%	76.1	25	41	2	0	0	965.51	462	469
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	6	6	9	0.01%	15.7%	AKEDFLK	99.3%	36.7	25	19	1	0	0	850.47	23	29
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	6	6	9	0.01%	15.7%	ATEQYYAMK	97.6%	30.9	25	30.9	1	0	0	1104.50	65	73
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	6	6	9	0.01%	15.7%	ILQAVNFPFLVR	99.7%	72.7	25	72.7	2	0	0	1416.84	95	106
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	6	6	9	0.01%	15.7%	KVEAPFIPK	99.7%	42.8	25	38	2	0	0	1028.61	310	318
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	6	6	9	0.01%	15.7%	NLLQVDLTK	99.4%	37.2	25	19	1	0	0	1043.61	272	280
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	6	6	9	0.01%	15.7%	TLGTGSFGR	99.7%	46.5	25	36.8	2	0	0	895.46	49	57
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	7	7	10	0.01%	40.0%	GKPLALVEEIR	99.7%	38.8	25	38.8	0	2	0	1224.73	149	159
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	7	7	10	0.01%	40.0%	IGFDVVTLSGTR	99.7%	84.4	25	76.4	2	0	0	1264.69	48	59
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	7	7	10	0.01%	40.0%	QTLSTPGTIILGTIPVPK	99.3%	36.4	25	36.4	1	0	0	1836.08	131	148
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	7	7	10	0.01%	40.0%	RIGFDVVTLSGTR	98.2%	32.1	25	32.1	1	0	0	1420.79	47	59
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	7	7	10	0.01%	40.0%	SSGVPVDGFYTEEVR	99.7%	83.6	25	72.1	2	0	0	1641.78	28	42
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	7	7	10	0.01%	40.0%	VCVIDEIGK	99.2%	35.9	25	28	1	0	0	1032.54	109	117
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	7	7	10	0.01%	40.0%	VGLEPPPGKR	96.1%	28.9	25	22.6	1	0	0	1049.61	65	74
Carbonyl reductase [NADPH] 1	CBR1	CBR1_HUMAN	30.4	100.0%	5	5	14	0.01%	24.2%	EYGGLDVLVNNAGIAFK	99.7%	75.9	25	74.8	4	0	0	1779.93	80	96
Carbonyl reductase [NADPH] 1	CBR1	CBR1_HUMAN	30.4	100.0%	5	5	14	0.01%	24.2%	GQAAVQQLQAEGLSPR	99.7%	100	25	87	4	0	0	1652.87	43	58
Carbonyl reductase [NADPH] 1	CBR1	CBR1_HUMAN	30.4	100.0%	5	5	14	0.01%	24.2%	ILLNACCPGWVR	98.7%	33.8	25	33.8	1	0	0	1458.73	221	232
Carbonyl reductase [NADPH] 1	CBR1	CBR1_HUMAN	30.4	100.0%	5	5	14	0.01%	24.2%	LFSGDVVLTAR	99.7%	87.1	25	71	4	0	0	1177.66	28	38
Carbonyl reductase [NADPH] 1	CBR1	CBR1_HUMAN	30.4	100.0%	5	5	14	0.01%	24.2%	VVNVSSIMSVR	99.7%	102	25	91.4	1	0	0	1190.66	135	145

Carboxymethylenebutenolidase homolog	CMBL	CMBL_HUMAN	28.0	100.0%	4	4	6	0.01%	14.3%	AGVSVYGIVK	99.7%	64	25	56.4	2	0	0	992.58	150	159
Carboxymethylenebutenolidase homolog	CMBL	CMBL_HUMAN	28.0	100.0%	4	4	6	0.01%	14.3%	DSEDIYNLK	99.7%	47.5	25	40.5	2	0	0	1096.52	160	168
Carboxymethylenebutenolidase homolog	CMBL	CMBL_HUMAN	28.0	100.0%	4	4	6	0.01%	14.3%	LEYGGLGR	96.6%	29.5	25	16.9	1	0	0	864.46	16	23
Carboxymethylenebutenolidase homolog	CMBL	CMBL_HUMAN	28.0	100.0%	4	4	6	0.01%	14.3%	NLIEWLNK	98.3%	32.4	25	13.5	1	0	0	1029.57	236	243
Cartilage-associated protein	CRTAP	CRTAP_HUMAN	46.6	100.0%	4	5	9	0.01%	12.7%	AFYECLAACEGSR	99.7%	88.6	25	88.6	1	0	0	1533.65	239	251
Cartilage-associated protein	CRTAP	CRTAP_HUMAN	46.6	100.0%	4	5	9	0.01%	12.7%	FLQFAYFK	98.4%	32.7	25	16.5	2	0	0	1063.56	150	157
Cartilage-associated protein	CRTAP	CRTAP_HUMAN	46.6	100.0%	4	5	9	0.01%	12.7%	SLPGAEDYIKDLETK	99.7%	55.9	25	52.9	2	0	0	1678.85	190	204
Cartilage-associated protein	CRTAP	CRTAP_HUMAN	46.6	100.0%	4	5	9	0.01%	12.7%	TSITDMELALPDFFK	99.7%	49.6	25	49.6	4	0	0	1743.85	224	238
Casein kinase II subunit alpha	CSNK2A1	CSK21_HUMAN	45.2	100.0%	4	4	4	0.00%	13.6%	EAMEHPYFYTVVK	97.8%	31.3	25	26.7	1	0	0	1613.77	317	329
Casein kinase II subunit alpha	CSNK2A1	CSK21_HUMAN	45.2	100.0%	4	4	4	0.00%	13.6%	GGPNIITLADIVK	99.7%	51.2	25	50.7	1	0	0	1310.77	90	102
Casein kinase II subunit alpha	CSNK2A1	CSK21_HUMAN	45.2	100.0%	4	4	4	0.00%	13.6%	QLYQTLTDYDIR	99.7%	46.5	25	41.1	1	0	0	1528.76	123	134
Casein kinase II subunit alpha	CSNK2A1	CSK21_HUMAN	45.2	100.0%	4	4	4	0.00%	13.6%	TPALVFEHVNNTDFK	99.7%	53.5	25	49.7	1	0	0	1731.87	108	122
Casein kinase II subunit alpha'	CSNK2A2	CSK22_HUMAN	41.2	99.8%	2	2	3	0.00%	6.0%	VLGTEELYGYLK	99.7%	57	25	51.2	2	0	0	1384.74	249	260
Casein kinase II subunit alpha'	CSNK2A2	CSK22_HUMAN	41.2	99.8%	2	2	3	0.00%	6.0%	VYAEVNSLR	99.7%	53	25	40.7	1	0	0	1050.56	12	20
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	10	13	24	0.02%	24.6%	ATHDGAPELGAGGTR	99.7%	76.8	25	75.1	2	2	0	1409.68	332	346
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	10	13	24	0.02%	24.6%	IEGVLLLGEPVR	99.7%	61.5	25	53	1	0	0	1294.77	189	200
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	10	13	24	0.02%	24.6%	LFSEYHEK	98.9%	34.5	25	22.1	2	0	0	1052.50	125	132
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	10	13	24	0.02%	24.6%	LFSEYHEKR	99.7%	55.1	25	45.4	2	0	0	1208.61	125	133
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	10	13	24	0.02%	24.6%	LVNSQGQLR	99.7%	59.3	25	47.4	2	0	0	1014.57	74	82
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	10	13	24	0.02%	24.6%	MAFPLLDMVDLER	99.7%	56	25	50.3	4	0	0	1549.78	162	174
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	10	13	24	0.02%	24.6%	MLVSGQGPVMENAQGLGFR	99.7%	88.4	25	79.4	4	0	0	1990.98	134	152
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	10	13	24	0.02%	24.6%	NVVTVDELR	99.7%	54.6	25	33.4	2	0	0	1044.57	153	161
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	10	13	24	0.02%	24.6%	RLVNSQGQLR	98.7%	33.5	25	24.7	1	0	0	1170.67	73	82
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	10	13	24	0.02%	24.6%	VPVVFVTNAGNILQHSK	99.7%	85.5	25	81.1	2	0	0	1823.02	83	99
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	11	11	19	0.02%	12.5%	AAALVLQTIWGYK	99.7%	72.7	25	71.5	2	0	0	1433.82	821	833
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	11	11	19	0.02%	12.5%	ALSAIADLLTNEHER	99.7%	84.7	25	79.4	2	0	0	1652.86	711	725
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	11	11	19	0.02%	12.5%	EIPQAER	99.7%	40.5	25	38	1	0	0	842.44	593	599
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	11	11	19	0.02%	12.5%	FVGDADLER	99.7%	40.8	25	24.7	1	0	0	1021.50	69	77
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	11	11	19	0.02%	12.5%	GIPVLVGLLDHPK	99.7%	64.2	25	64.2	2	0	0	1357.82	409	421
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	11	11	19	0.02%	12.5%	GSLASLDSLRK	99.6%	39.3	25	14.7	1	0	0	1146.65	345	355
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	11	11	19	0.02%	12.5%	GYELLFQPEVVR	99.7%	54.4	25	42	5	0	0	1449.77	655	666
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	11	11	19	0.02%	12.5%	IYISLLK	95.7%	28.5	25	12.3	1	0	0	849.54	667	673
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	11	11	19	0.02%	12.5%	SDFQVNLNNASR	99.7%	78.4	25	66.6	1	0	0	1364.66	847	858
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	11	11	19	0.02%	12.5%	SLDNNYSTPNER	98.9%	34.3	25	34.3	1	0	0	1409.63	899	910
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	11	11	19	0.02%	12.5%	VGGSSVDLHR	99.7%	68.3	25	52.3	2	0	0	1026.53	265	274
CCAAT/enhancer-binding protein zeta	CEBPZ	CEBPZ_HUMAN	121.0	100.0%	2	2	4	0.00%	2.1%	ALLVQVVNK	99.7%	63.5	25	49.1	3	0	0	983.62	382	390
CCAAT/enhancer-binding protein zeta	CEBPZ	CEBPZ_HUMAN	121.0	100.0%	2	2	4	0.00%	2.1%	GKENTDSVVMQPK	99.1%	35.2	25	30.6	1	0	0	1448.71	769	781
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	12	12	22	0.02%	5.9%	AVEGLLDATSGADADLLLR	99.7%	96.9	25	92	2	0	0	1900.00	1665	1683
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	12	12	22	0.02%	5.9%	DAIAALGLLQK	99.7%	65.8	25	59	2	0	0	1112.67	1654	1664
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	12	12	22	0.02%	5.9%	EVTAAQVAR	98.9%	34.5	25	26.3	1	0	0	944.52	284	292
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	12	12	22	0.02%	5.9%	GAFGVGQEQIDAFLK	99.7%	49.4	25	43.1	2	0	0	1579.81	194	208
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	12	12	22	0.02%	5.9%	GQQELLYVVPFVAK	99.7%	45	25	41.9	2	0	0	1590.89	1228	1241
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	12	12	22	0.02%	5.9%	MYYFGIAALDR	99.7%	50.3	25	39.6	2	0	0	1319.65	950	960
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	12	12	22	0.02%	5.9%	NLDEQLSAPK	99.7%	49.2	25	39.7	2	0	0	1114.57	1311	1320
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	12	12	22	0.02%	5.9%	NLILSAFPR	99.7%	49.8	25	34.8	2	0	0	1030.60	2130	2138
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	12	12	22	0.02%	5.9%	SLDLIESLLR	99.7%	79.6	25	66.4	1	0	0	1158.67	450	459
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	12	12	22	0.02%	5.9%	SLLEVVVLSR	99.7%	64.7	25	27.4	2	0	0	1114.68	1641	1650
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	12	12	22	0.02%	5.9%	SPVTFLSDLR	99.7%	54.6	25	45	2	0	0	1134.62	2188	2197
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	12	12	22	0.02%	5.9%	YLFLNAIANQLR	99.7%	52.1	25	52.1	2	0	0	1435.81	2264	2275
CCR4-NOT transcription complex subunit 2	CNOT2	CNOT2_HUMAN	59.7	99.8%	2	2	4	0.00%	5.6%	EGSGNPTPLINPLAGR	99.7%	63.1	25	62.2	2	0	0	1592.84	240	255
CCR4-NOT transcription complex subunit 2	CNOT2	CNOT2_HUMAN	59.7	99.8%	2	2	4	0.00%	5.6%	TNSMSSSGLGSPNR	99.7%	64.8	25	64.8	2	0	0	1410.63	155	168

CCR4-NOT transcription complex subunit 8	CNOT8	CNOT8_HUMAN	33.5	100.0%	3	3	3	0.00%	11.6%	IIQLGLTFTNEK	99.7%	46.7	25	46.7	1	0	0	1376.78	74	85
CCR4-NOT transcription complex subunit 8	CNOT8	CNOT8_HUMAN	33.5	100.0%	3	3	3	0.00%	11.6%	LYGLGTGVAQK	99.7%	41	25	25	1	0	0	1106.62	259	269
CCR4-NOT transcription complex subunit 8	CNOT8	CNOT8_HUMAN	33.5	100.0%	3	3	3	0.00%	11.6%	SSIDYQYQLLR	99.7%	56	25	40.5	1	0	0	1385.71	56	66
CDP-diacylglycerol--inositol 3-phosphatidyltransferase	CDIPT	CDIPT_HUMAN	23.5	100.0%	4	7	14	0.01%	21.1%	FGAMLDMLTDR	99.7%	54	25	28.8	3	0	0	1269.60	63	73
CDP-diacylglycerol--inositol 3-phosphatidyltransferase	CDIPT	CDIPT_HUMAN	23.5	100.0%	4	7	14	0.01%	21.1%	MGLWVTAPIALLK	99.7%	53.8	25	53.8	5	0	0	1428.83	174	186
CDP-diacylglycerol--inositol 3-phosphatidyltransferase	CDIPT	CDIPT_HUMAN	23.5	100.0%	4	7	14	0.01%	21.1%	MIDLSGNPVLR	99.7%	67.8	25	62.5	4	0	0	1214.66	122	132
CDP-diacylglycerol--inositol 3-phosphatidyltransferase	CDIPT	CDIPT_HUMAN	23.5	100.0%	4	7	14	0.01%	21.1%	NMAALDAADR	99.7%	46.8	25	41.5	2	0	0	1047.49	200	209
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	10	10	17	0.02%	12.8%	EAAPDAGAEPITADSDPAYSSK	99.7%	81.1	25	81.1	1	0	0	2162.97	288	309
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	10	10	17	0.02%	12.8%	FSATEVTNK	99.7%	45.7	25	33.8	2	0	0	996.50	847	855
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	10	10	17	0.02%	12.8%	ILLTLGIR	99.7%	43.5	25	42.4	2	0	0	898.61	728	735
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	10	10	17	0.02%	12.8%	LAEAEETAR	99.7%	66.5	25	59.4	3	0	0	989.49	868	876
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	10	10	17	0.02%	12.8%	LTPLQLEIQR	99.7%	42.2	25	33	2	0	0	1210.72	896	905
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	10	10	17	0.02%	12.8%	SPAPPLLHVAALGQK	99.7%	41.8	25	37.4	2	0	0	1498.87	124	138
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	10	10	17	0.02%	12.8%	TLAAEMQELR	99.7%	44.3	25	31.5	1	0	0	1161.59	856	865
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	10	10	17	0.02%	12.8%	VLLLSSPGLEELYR	99.7%	69.3	25	69.3	2	0	0	1588.89	310	323
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	10	10	17	0.02%	12.8%	VQTLSNQPLLK	99.6%	39.5	25	30.8	1	0	0	1240.73	113	123
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	10	10	17	0.02%	12.8%	VVTQNICQYR	99.7%	54.6	25	54.6	1	0	0	1280.64	748	757
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	5	5	10	0.01%	18.7%	IMESGSELSK	98.9%	34.3	25	27.9	2	0	0	1080.52	170	179
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	5	5	10	0.01%	18.7%	IYQWINELSSPETR	99.7%	77.8	25	76.7	2	0	0	1735.87	22	35
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	5	5	10	0.01%	18.7%	LTSLGVIGALVK	99.7%	84.8	25	78.3	2	0	0	1170.75	137	148
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	5	5	10	0.01%	18.7%	NLQEGQVTDPR	99.7%	62.6	25	56.2	2	0	0	1256.62	282	292
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	5	5	10	0.01%	18.7%	TVATFILQK	99.7%	64.1	25	48.6	2	0	0	1020.61	180	188
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	4	5	8	0.01%	8.7%	EFYEVVQSQR	99.7%	64.7	25	55.2	2	0	0	1284.62	9	18
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	4	5	8	0.01%	8.7%	LQEFLADMGLPLK	99.7%	44.3	25	40.6	3	0	0	1474.80	311	323
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	4	5	8	0.01%	8.7%	VLLFVASDVDALCACK	99.7%	41.1	25	41.1	1	0	0	1780.90	19	34
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	4	5	8	0.01%	8.7%	YVTDVGVLQR	99.7%	53	25	38.3	2	0	0	1149.63	238	247
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	6	6	11	0.01%	9.6%	ESDLPSAILQTSGVSEFTK	99.7%	91.5	25	91.5	2	0	0	2009.01	272	290
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	6	6	11	0.01%	9.6%	GVDYNAEIPFEK	99.4%	37.3	25	36.5	1	0	0	1381.66	207	218
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	6	6	11	0.01%	9.6%	ILLGGYQSR	99.3%	36.8	25	25.3	2	0	0	1006.57	719	727
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	6	6	11	0.01%	9.6%	LGLLGLPAPK	99.7%	66	25	66	2	0	0	978.63	478	487
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	6	6	11	0.01%	9.6%	LVLPAPQISDAELQEVVK	99.7%	68.7	25	68	2	0	0	1949.10	295	312
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	6	6	11	0.01%	9.6%	VGQASEIAR	99.7%	58.5	25	41.5	2	0	0	930.50	313	321
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	7	7	13	0.01%	12.7%	ALSIFNELR	99.7%	45.5	25	32.3	2	0	0	1062.59	282	290
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	7	7	13	0.01%	12.7%	AYAVGDVEK	99.0%	34.9	25	26.9	2	0	0	951.48	459	467
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	7	7	13	0.01%	12.7%	IENMDTFSNLLYVR	99.7%	58	25	37.8	2	0	0	1714.85	297	310
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	7	7	13	0.01%	12.7%	MLVALGECYEK	99.7%	47.2	25	47.2	2	0	0	1312.63	435	445
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	7	7	13	0.01%	12.7%	VETCCVIGNYYSLR	99.7%	43	25	43	2	0	0	1733.80	331	344
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	7	7	13	0.01%	12.7%	YLAQYYFK	99.6%	38.9	25	32.2	1	0	0	1095.55	515	522
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	7	7	13	0.01%	12.7%	YQNLIDVGFSK	99.7%	68.8	25	67.3	2	0	0	1283.66	251	261
Cell division cycle protein 27 homolog	CDC27	CDC27_HUMAN	91.9	99.8%	2	2	3	0.00%	3.0%	ESLVYFLIGK	99.7%	40.6	25	40.6	2	0	0	1168.66	736	745
Cell division cycle protein 27 homolog	CDC27	CDC27_HUMAN	91.9	99.8%	2	2	3	0.00%	3.0%	LAEGEQILSGGVFNK	99.7%	64.2	25	57.8	1	0	0	1561.82	85	99
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	5	5	8	0.01%	16.6%	CISEDQKYGGK	99.7%	49.8	25	44.5	2	0	0	1284.59	51	61
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	5	5	8	0.01%	16.6%	ELKLENHQENSR	99.7%	33	25	27	0	1	0	1496.75	205	216
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	5	5	8	0.01%	16.6%	ELLEQISAFDNVPR	99.7%	92.3	25	83.4	2	0	0	1630.84	96	109
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	5	5	8	0.01%	16.6%	VFFTCNACGESVKK	99.7%	54.1	25	54.1	1	0	0	1646.77	2	15
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	5	5	8	0.01%	16.6%	VKDAVEQQGEVK	99.7%	63.8	25	48.2	2	0	0	1329.70	174	185
Cellular nucleic acid-binding protein	CNBP	CNBP_HUMAN	19.5	99.8%	2	2	3	0.00%	11.9%	CGETGHVAINCSK	99.7%	50.7	25	43	1	0	0	1432.63	140	152
Cellular nucleic acid-binding protein	CNBP	CNBP_HUMAN	19.5	99.8%	2	2	3	0.00%	11.9%	TSEVNCYR	97.4%	30.6	25	27.7	2	0	0	1028.45	153	160
Cellular tumor antigen p53	TP53	P53_HUMAN	43.7	100.0%	4	4	9	0.01%	11.5%	ALPNNTSSSPQPK	99.7%	63.8	25	59.8	4	0	0	1340.68	307	319
Cellular tumor antigen p53	TP53	P53_HUMAN	43.7	100.0%	4	4	9	0.01%	11.5%	SVTCTYSPALNK	99.7%	49.5	25	44.8	2	0	0	1340.65	121	132
Cellular tumor antigen p53	TP53	P53_HUMAN	43.7	100.0%	4	4	9	0.01%	11.5%	TYQGSYGFR	99.5%	38.4	25	35.2	2	0	0	1078.50	102	110

Cellular tumor antigen p53	TP53	P53_HUMAN	43.7	100.0%	4	4	9	0.01%	11.5%	VEYLDDRNTFR	95.9%	28.7	25	28.6	1	0	0	1427.69	203	213
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	7	7	12	0.01%	38.9%	CGVQSFYTPR	99.7%	58.5	25	58.5	1	0	0	1214.56	219	228
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	7	7	12	0.01%	38.9%	GAEHITTYTFNTHK	99.7%	38.9	25	38.9	0	2	0	1619.78	197	210
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	7	7	12	0.01%	38.9%	LLLDTFEYQGLVK	99.7%	113	25	90.9	2	0	0	1538.85	135	147
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	7	7	12	0.01%	38.9%	SGASGASAAPAASAAAALAPSATR	99.7%	118	25	111	2	0	0	1985.00	18	41
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	7	7	12	0.01%	38.9%	SMVTEEFNGSDWEK	99.7%	65.6	25	65.6	1	0	0	1658.70	248	261
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	7	7	12	0.01%	38.9%	SNPGGFGIAPHCLDEGTVR	99.7%	48.9	25	48.9	0	2	0	1983.93	229	247
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	7	7	12	0.01%	38.9%	SQAVEKPPSEKPR	99.7%	45.7	25	45.7	2	0	0	1452.78	53	65
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	5	6	9	0.01%	8.1%	AMGTLLNTAISEVIGK	99.7%	62.6	25	61.4	2	0	0	1633.88	652	667
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	5	6	9	0.01%	8.1%	LEKEDLGTR	99.7%	43.9	25	32.4	2	0	0	1060.56	15	23
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	5	6	9	0.01%	8.1%	NLMTSEIHNTVK	99.7%	72.1	25	67.1	2	0	0	1402.70	413	424
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	5	6	9	0.01%	8.1%	QLLDLPLDTDLENEK	99.7%	80.2	25	80.2	2	0	0	1755.90	306	320
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	5	6	9	0.01%	8.1%	YQEEVPVYVPK	99.4%	37.5	25	34.4	1	0	0	1350.69	709	719
Chaperone activity of bc1 complex-like, mitochondrial	ADCK3	ADCK3_HUMAN	72.0	100.0%	3	3	4	0.00%	7.4%	AVLGSSPFLSEANAER	99.7%	70.4	25	67	1	0	0	1647.83	247	262
Chaperone activity of bc1 complex-like, mitochondrial	ADCK3	ADCK3_HUMAN	72.0	100.0%	3	3	4	0.00%	7.4%	ELALECDYQR	99.7%	42.9	25	42.9	1	0	0	1296.59	401	410
Chaperone activity of bc1 complex-like, mitochondrial	ADCK3	ADCK3_HUMAN	72.0	100.0%	3	3	4	0.00%	7.4%	LANFGGLAVGLGFGALAEVAKK	99.7%	59.7	25	58.6	0	2	0	2103.20	214	235
Chitobiosyldiphosphodolichol beta-mannosyltransferase	ALG1	ALG1_HUMAN	52.5	99.8%	2	2	4	0.00%	5.6%	ETPLDLQHR	99.7%	42.1	25	34.8	2	0	0	1108.57	224	232
Chitobiosyldiphosphodolichol beta-mannosyltransferase	ALG1	ALG1_HUMAN	52.5	99.8%	2	2	4	0.00%	5.6%	IQIVGLTELQSLAVGPR	99.7%	51.2	25	51.2	2	0	0	1794.05	83	99
Chloride channel CLIC-like protein 1	CLCC1	CLCC1_HUMAN	62.0	100.0%	6	6	9	0.01%	13.8%	AFDVPDAEAR	98.1%	31.9	25	26	2	0	0	1090.52	444	453
Chloride channel CLIC-like protein 1	CLCC1	CLCC1_HUMAN	62.0	100.0%	6	6	9	0.01%	13.8%	ALAVTFTTFVTEPLK	96.5%	29.4	25	28.8	1	0	0	1637.92	299	313
Chloride channel CLIC-like protein 1	CLCC1	CLCC1_HUMAN	62.0	100.0%	6	6	9	0.01%	13.8%	GQMGPTEQGPYAK	98.8%	33.9	25	17	1	0	0	1379.63	402	414
Chloride channel CLIC-like protein 1	CLCC1	CLCC1_HUMAN	62.0	100.0%	6	6	9	0.01%	13.8%	LAFAQHQAEVAK	99.7%	67.1	25	60.4	3	0	0	1312.70	235	246
Chloride channel CLIC-like protein 1	CLCC1	CLCC1_HUMAN	62.0	100.0%	6	6	9	0.01%	13.8%	SEAAGSPDQGSTYSPAR	99.7%	67.2	25	64.4	1	0	0	1680.75	519	535
Chloride channel CLIC-like protein 1	CLCC1	CLCC1_HUMAN	62.0	100.0%	6	6	9	0.01%	13.8%	SPVLDTKPK	96.8%	29.7	25	15.9	1	0	0	984.57	464	472
Chloride intracellular channel protein 1	CLIC1	CLIC1_HUMAN	26.9	100.0%	3	3	5	0.01%	15.8%	LAALNPESNTAGLDIFAK	99.7%	67.2	25	67.2	2	0	0	1844.98	96	113
Chloride intracellular channel protein 1	CLIC1	CLIC1_HUMAN	26.9	100.0%	3	3	5	0.01%	15.8%	NSNPALNDNLEK	99.7%	47.5	25	39.9	2	0	0	1328.64	120	131
Chloride intracellular channel protein 1	CLIC1	CLIC1_HUMAN	26.9	100.0%	3	3	5	0.01%	15.8%	YLSNAYAR	99.4%	37.2	25	30.5	1	0	0	957.48	209	216
Chromatin target of PRMT1 protein	CHTOP	CHTOP_HUMAN	26.4	100.0%	3	7	18	0.02%	16.9%	ASMQQQQQLASAR	99.7%	84.9	25	71.7	9	0	0	1462.71	39	51
Chromatin target of PRMT1 protein	CHTOP	CHTOP_HUMAN	26.4	100.0%	3	7	18	0.02%	16.9%	EQLDNQLDAYMSK	99.7%	96.3	25	96.3	2	0	0	1570.71	214	226
Chromatin target of PRMT1 protein	CHTOP	CHTOP_HUMAN	26.4	100.0%	3	7	18	0.02%	16.9%	LAQQMENRPSVQAALK	99.7%	49.9	25	24.9	3	4	0	1783.95	55	70
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	5	5	6	0.01%	5.7%	GGQAPGFLLR	98.0%	31.8	25	13.1	1	0	0	1015.57	10	19
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	5	5	6	0.01%	5.7%	GIPTYIYYFPR	99.2%	36.1	25	33.5	1	0	0	1389.72	867	877
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	5	5	6	0.01%	5.7%	LLQPFLLR	99.1%	35.3	25	30.3	2	0	0	999.64	253	260
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	5	5	6	0.01%	5.7%	LQNILSQLR	99.7%	44.1	25	25.5	1	0	0	1084.65	311	319
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	5	5	6	0.01%	5.7%	SYQLEGVNWLAQR	99.7%	48.9	25	42.1	1	0	0	1563.79	48	60
Chromosome transmission fidelity protein 18 homolog	CHTF18	CTF18_HUMAN	107.4	100.0%	3	3	5	0.01%	3.6%	NLIQTLVSGIAPATR	99.7%	57	25	57	2	0	0	1553.90	735	749
Chromosome transmission fidelity protein 18 homolog	CHTF18	CTF18_HUMAN	107.4	100.0%	3	3	5	0.01%	3.6%	TTLAHVIAR	98.6%	33.2	25	29.5	1	0	0	981.58	381	389
Chromosome transmission fidelity protein 18 homolog	CHTF18	CTF18_HUMAN	107.4	100.0%	3	3	5	0.01%	3.6%	VVQGLFDNFLR	99.7%	52.2	25	45.5	2	0	0	1307.71	648	658
Citrate synthase, mitochondrial	CS	CISY_HUMAN	51.7	100.0%	3	3	6	0.01%	6.7%	ALGVLAQLIWSR	99.7%	51.8	25	51.8	2	0	0	1326.79	429	440
Citrate synthase, mitochondrial	CS	CISY_HUMAN	51.7	100.0%	3	3	6	0.01%	6.7%	AYAQGISR	98.8%	34	25	19.6	2	0	0	865.45	184	191
Citrate synthase, mitochondrial	CS	CISY_HUMAN	51.7	100.0%	3	3	6	0.01%	6.7%	IVPNVLLEQGK	99.7%	54.9	25	54.9	2	0	0	1209.72	383	393
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	19	20	47	0.05%	14.0%	ENPYYDSR	99.7%	45.5	25	39.3	1	0	0	1043.44	896	903
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	19	20	47	0.05%	14.0%	ESYVETELIFALAK	99.7%	85.9	25	85.9	2	0	0	1612.85	1166	1179
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	19	20	47	0.05%	14.0%	GQFSTDELVAEVEK	99.7%	68.7	25	68.7	1	0	0	1551.75	838	851
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	19	20	47	0.05%	14.0%	ISGETIFVTAPHEATAGIIGVNR	99.7%	40.7	25	40.7	0	2	0	2353.25	298	320
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	19	20	47	0.05%	14.0%	IVLDNSVFSEHR	99.7%	76.4	25	76.4	2	1	0	1415.73	1011	1022
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	19	20	47	0.05%	14.0%	IYIDSNNNPER	99.7%	59.5	25	48.1	3	0	0	1334.63	882	892
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	19	20	47	0.05%	14.0%	LLLPWLEAR	98.6%	33.3	25	16.7	2	0	0	1110.67	857	865
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	19	20	47	0.05%	14.0%	LLYNNVSNFGR	99.7%	68.8	25	68.8	5	0	0	1296.67	1216	1226
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	19	20	47	0.05%	14.0%	LPVVIGGLLDVDCSEDVIK	99.7%	107	25	107	2	0	0	2041.09	812	830
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	19	20	47	0.05%	14.0%	NLQNLLILTAIK	99.7%	93.6	25	92.8	7	0	0	1353.85	1023	1034

Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	19	20	47	0.05%	14.0%	NNLAGAEELFAR	99.7%	82.5	25	81.2	2	0	0	1304.66	355	366
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	19	20	47	0.05%	14.0%	SVDPTLALSVYLR	99.7%	70.7	25	70.7	3	0	0	1433.80	469	481
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	19	20	47	0.05%	14.0%	TLQIFNIEMK	99.7%	49.2	25	42.1	2	0	0	1252.66	87	96
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	19	20	47	0.05%	14.0%	VANVELYYR	99.7%	75.7	25	73.7	2	0	0	1126.59	1398	1406
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	19	20	47	0.05%	14.0%	VDKLDASESLR	99.0%	35	25	33.6	1	0	0	1232.65	1610	1620
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	19	20	47	0.05%	14.0%	VIQCFAETGQVQK	99.7%	79.1	25	72.3	2	0	0	1507.76	488	500
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	19	20	47	0.05%	14.0%	VVGAMQLYSVDR	99.7%	82	25	80.4	2	0	0	1337.69	177	188
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	19	20	47	0.05%	14.0%	WLLLTGISAQQNR	99.7%	73.9	25	67.8	3	0	0	1499.83	164	176
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	19	20	47	0.05%	14.0%	YIEIYVQK	98.9%	34.4	25	30.1	2	0	0	1055.58	799	806
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	7	7	13	0.01%	5.8%	EVLLVALGSR	99.7%	84.9	25	69.2	2	0	0	1056.64	848	857
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	7	7	13	0.01%	5.8%	NVLDGELLNR	99.7%	57.6	25	46.5	2	0	0	1142.62	1397	1406
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	7	7	13	0.01%	5.8%	SSFLPSYIIDVR	99.7%	57.5	25	46.8	2	0	0	1396.75	183	194
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	7	7	13	0.01%	5.8%	VLVDSSFGQPTTQGEAR	99.5%	38.2	25	37.8	2	0	0	1791.89	817	833
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	7	7	13	0.01%	5.8%	VYAVATSTNTPCAR	99.7%	43.9	25	39	2	0	0	1510.73	1033	1046
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	7	7	13	0.01%	5.8%	YIVQVSPLGIR	99.7%	41.6	25	29.6	2	0	0	1244.74	617	627
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	7	7	13	0.01%	5.8%	YLYLSTMER	96.0%	28.8	25	17.4	1	0	0	1175.58	1407	1415
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	4	4	6	0.01%	20.7%	LFLVQLQEK	99.7%	66.8	25	45.9	2	0	0	1117.66	174	182
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	4	4	6	0.01%	20.7%	LMTEILGR	99.7%	55.3	25	44.5	1	0	0	932.52	124	131
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	4	4	6	0.01%	20.7%	LPGGELNPGEDEVEGLKR	99.7%	76.8	25	76.1	0	2	0	1908.97	106	123
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	4	4	6	0.01%	20.7%	YIQQTKPLTLER	99.7%	45.1	25	26.8	1	0	0	1489.84	24	35
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	6	8	13	0.01%	12.5%	AISSSAISR	99.6%	39.5	25	24.6	2	0	0	891.49	423	431
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	6	8	13	0.01%	12.5%	GAAPNVVYTYTGK	99.7%	87.1	25	86.8	2	0	0	1340.68	67	79
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	6	8	13	0.01%	12.5%	GDYGPPGR	96.4%	29.2	25	15.6	1	0	0	818.38	393	400
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	6	8	13	0.01%	12.5%	GFALVGVGSEASSK	99.7%	105	25	98.7	2	0	0	1308.68	125	138
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	6	8	13	0.01%	12.5%	QFLSQFEMQSR	99.7%	47	25	45.6	2	0	0	1400.66	162	172
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	6	8	13	0.01%	12.5%	TPLSEAEFEEIMNR	99.7%	99.9	25	99.9	4	0	0	1665.78	407	420
CLIP-associating protein 2	CLASP2	CLAP2_HUMAN	141.1	100.0%	3	3	4	0.00%	4.1%	SAEEAASVLATSISPEQCIK	95.2%	28	25	28	1	0	0	2091.03	1162	1181
CLIP-associating protein 2	CLASP2	CLAP2_HUMAN	141.1	100.0%	3	3	4	0.00%	4.1%	VLNTGSDVEEAVADALK	99.7%	45	25	45	1	0	0	1730.88	591	607
CLIP-associating protein 2	CLASP2	CLAP2_HUMAN	141.1	100.0%	3	3	4	0.00%	4.1%	VLTTTALSTVSSGVQR	99.7%	90.2	25	81.3	2	0	0	1619.90	467	482
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	24	26	57	0.06%	22.1%	ASNLENSTYDLYTIPK	99.7%	85	25	80.1	2	0	0	1828.90	383	398
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	24	26	57	0.06%	22.1%	CPLSGACYSPEFK	99.7%	44	25	44	1	0	0	1515.66	1185	1197
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	24	26	57	0.06%	22.1%	DADSITLFDVQQK	99.7%	77.7	25	69.2	2	0	0	1479.73	468	480
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	24	26	57	0.06%	22.1%	DVAVMQLR	99.7%	49.1	25	35.9	3	0	0	931.50	351	358
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	24	26	57	0.06%	22.1%	GFFEGTIASK	99.7%	59.8	25	56.9	5	0	0	1056.54	816	825
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	24	26	57	0.06%	22.1%	GITGVDLFGTTDAVVK	99.7%	72.8	25	71.3	4	0	0	1592.85	183	198
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	24	26	57	0.06%	22.1%	LLELGPKPEVAQQTR	99.7%	35	25	34.2	0	2	0	1678.95	1128	1142
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	24	26	57	0.06%	22.1%	LNDLIQR	99.7%	67.1	25	50.7	2	0	0	871.50	1003	1009
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	24	26	57	0.06%	22.1%	LSFLYLITGNLEK	99.7%	57.9	25	51	2	0	0	1510.85	703	715
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	24	26	57	0.06%	22.1%	LVGQSIIAYLQK	99.7%	76.7	25	75	1	0	0	1332.79	620	631
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	24	26	57	0.06%	22.1%	NLSPGAVESDVR	99.7%	46.4	25	34.2	3	0	0	1243.63	171	182
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	24	26	57	0.06%	22.1%	QELILSNSEDK	99.4%	37.6	25	35.1	1	0	0	1275.64	261	271
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	24	26	57	0.06%	22.1%	QLDFNSSK	97.9%	31.5	25	15.8	1	0	0	938.46	343	350
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	24	26	57	0.06%	22.1%	QLFLQTYAR	99.7%	62	25	50.6	2	0	0	1139.62	957	965
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	24	26	57	0.06%	22.1%	QQPLFVSGGDDYK	99.6%	39.3	25	38.5	1	0	0	1453.70	62	74
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	24	26	57	0.06%	22.1%	SILLSVPLLVVDNK	99.7%	81.6	25	81.6	6	0	0	1509.93	1031	1044
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	24	26	57	0.06%	22.1%	SSGLTAVWVAR	99.7%	69	25	37.5	2	0	0	1146.63	413	423
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	24	26	57	0.06%	22.1%	TALNLFFK	99.7%	55.2	25	49.2	2	0	0	953.55	1107	1114
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	24	26	57	0.06%	22.1%	TGVQTFR	98.3%	32.5	25	24.3	1	0	0	808.43	282	288
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	24	26	57	0.06%	22.1%	TLDLPIYVTR	99.7%	49.1	25	49.1	2	0	0	1190.68	563	572
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	24	26	57	0.06%	22.1%	VLTIDPTEFK	99.7%	45.7	25	37.9	4	0	0	1162.64	589	598
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	24	26	57	0.06%	22.1%	VTTVTEIGKDVIGLR	99.7%	85.1	25	85.1	2	0	0	1600.93	1203	1217

Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	24	26	57	0.06%	22.1%	VWDISGLR	98.9%	34.3	25	18.7	2	0	0	945.52	161	168
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	24	26	57	0.06%	22.1%	YAVTTGDHGIIR	99.7%	67.9	25	61.7	3	1	0	1302.68	551	562
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	25	31	64	0.06%	31.7%	AAAQCYIDLIIK	99.7%	85.1	25	68.7	2	0	0	1378.74	280	291
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	25	31	64	0.06%	31.7%	ALSGYCGFMAANLYAR	99.7%	70.2	25	70.2	1	0	0	1764.82	883	898
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	25	31	64	0.06%	31.7%	CIYNLLQSSSPAVK	99.7%	82.7	25	82.6	2	0	0	1579.81	248	261
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	25	31	64	0.06%	31.7%	DLQHPNEFIR	96.8%	29.7	25	20.4	1	0	0	1268.64	108	117
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	25	31	64	0.06%	31.7%	EAELLEPLMPAIR	99.7%	63.7	25	50.6	2	0	0	1481.80	129	141
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	25	31	64	0.06%	31.7%	EAGELKPEEEITVGPVQK	99.7%	65.4	25	65.4	2	0	0	1953.02	496	513
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	25	31	64	0.06%	31.7%	GALWILGEYCSTK	99.7%	61	25	60.9	2	0	0	1497.74	457	469
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	25	31	64	0.06%	31.7%	KPITDDDVDR	99.7%	48.5	25	29.5	2	0	0	1173.57	603	612
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	25	31	64	0.06%	31.7%	LLLVFWEIVPK	99.7%	67.1	25	49.8	2	0	0	1356.83	77	87
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	25	31	64	0.06%	31.7%	LPGLLMTIIR	99.7%	61.6	25	49.6	3	0	0	1126.70	55	64
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	25	31	64	0.06%	31.7%	LVTEMGTYATQSALSSSRPTK	99.7%	44.9	25	42.4	0	4	0	2244.12	514	534
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	25	31	64	0.06%	31.7%	MLEVFHAIK	99.7%	43.7	25	34.1	3	0	0	1087.60	442	450
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	25	31	64	0.06%	31.7%	NAVLAIYTIYR	99.7%	81.2	25	81.2	4	0	0	1296.73	154	164
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	25	31	64	0.06%	31.7%	NVEELVIVLK	99.5%	38	25	35	2	0	0	1155.70	352	361
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	25	31	64	0.06%	31.7%	NVEELVIVLKK	99.6%	39	25	39	2	0	0	1283.79	352	362
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	25	31	64	0.06%	31.7%	NVTVQPDDPISFMQLTAK	99.7%	105	25	104	5	0	0	2004.01	662	679
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	25	31	64	0.06%	31.7%	SLGEIPIVESEIKK	99.7%	66.8	25	64.3	2	0	0	1541.88	482	495
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	25	31	64	0.06%	31.7%	SQGMALSLGDK	99.7%	40.5	25	23.8	2	0	0	1106.55	933	943
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	25	31	64	0.06%	31.7%	TLQLALDLVSSR	99.7%	92.1	25	92.1	3	0	0	1315.76	340	351
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	25	31	64	0.06%	31.7%	TNNVSEHEDTDKYR	99.7%	48.7	25	48.7	0	3	0	1707.76	367	380
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	25	31	64	0.06%	31.7%	VIIMILNGEK	99.7%	53.2	25	47.2	3	0	0	1145.66	45	54
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	25	31	64	0.06%	31.7%	VLQDLVMDILR	99.7%	70.5	25	59.3	6	0	0	1314.75	317	327
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	25	31	64	0.06%	31.7%	VLSECSPLMNDIFNK	99.7%	70.1	25	69.4	2	0	0	1766.85	619	633
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	25	31	64	0.06%	31.7%	VLSTPDLEVR	99.7%	41.1	25	27.4	2	0	0	1128.63	328	337
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	25	31	64	0.06%	31.7%	YVALVQEK	99.7%	41.6	25	30.2	2	0	0	949.54	568	575
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	4	4	7	0.01%	5.2%	AAESLADPTEYENLFPGLK	99.7%	48.7	25	48.7	2	0	0	2065.01	784	802
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	4	4	7	0.01%	5.2%	HSEVQQANLK	99.7%	46.5	25	37	2	0	0	1153.60	319	328
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	4	4	7	0.01%	5.2%	LPEAAFLAR	99.7%	63.7	25	48.9	2	0	0	987.56	751	759
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	4	4	7	0.01%	5.2%	VFNYNTLER	99.7%	44.4	25	37.2	1	0	0	1155.58	83	91
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	16	29	0.03%	32.3%	ENVNLAQIR	99.7%	69.1	25	56.8	2	0	0	1056.58	123	131
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	16	29	0.03%	32.3%	GKEVDNFVDK	99.6%	39.7	25	35.9	1	0	0	1150.57	232	241
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	16	29	0.03%	32.3%	GVQLQTHPNVDKK	95.2%	22	25	16	0	1	0	1463.80	324	336
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	16	29	0.03%	32.3%	IEGLLAAFPK	99.7%	50	25	32.7	2	0	0	1058.62	29	38
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	16	29	0.03%	32.3%	KNYCNIQVTK	99.7%	54.5	25	50.7	2	0	0	1267.65	476	485
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	16	29	0.03%	32.3%	LFTAESLIGLK	99.7%	69.5	25	57.1	2	0	0	1191.70	337	347
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	16	29	0.03%	32.3%	LYMVLITTK	99.7%	60.1	25	60.1	2	0	0	1081.63	64	72
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	16	29	0.03%	32.3%	NSNILEDLETLR	99.7%	71.6	25	65.8	2	0	0	1416.73	73	84
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	16	29	0.03%	32.3%	NTLEWCLPVIDAK	99.7%	56.6	25	52.1	2	0	0	1558.79	436	448
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	16	29	0.03%	32.3%	NYCNIQVTK	99.6%	39.8	25	31.4	2	0	0	1139.55	477	485
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	16	29	0.03%	32.3%	QHTFVETESVR	98.7%	33.8	25	30.9	1	0	0	1332.65	45	55
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	16	29	0.03%	32.3%	SEGETIMSSSMGK	99.7%	61.3	25	48.1	2	0	0	1343.58	244	256
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	16	29	0.03%	32.3%	SFPVNSDVGVLK	99.7%	67	25	55.9	2	0	0	1261.68	352	363
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	16	29	0.03%	32.3%	TFTEMDSHEEK	99.7%	49.6	25	45.7	2	0	0	1353.56	132	142
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	16	29	0.03%	32.3%	VLLAAAVCTK	99.7%	82.9	25	73.9	2	0	0	1045.61	2	11
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	16	29	0.03%	32.3%	VTQVDGNSPVR	97.8%	31.2	25	26.9	2	0	0	1171.61	486	496
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	9	9	17	0.02%	40.3%	APPAPGPASGGSGEVDELFDVK	99.7%	89.5	25	89.5	2	0	0	2097.01	2	23
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	9	9	17	0.02%	40.3%	DSIVAELDREMSR	99.7%	45.3	25	45.2	1	0	0	1536.73	98	110
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	9	9	17	0.02%	40.3%	DVERDVFLYR	99.3%	36.6	25	26.4	2	0	0	1311.67	49	58
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	9	9	17	0.02%	40.3%	ENDFDRLVLQYAPSA	99.0%	34.8	25	21.5	2	0	0	1737.84	294	308

Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	9	9	17	0.02%	40.3%	FGVVLDEIKPSSAPELQAVR	99.7%	68.9	25	62.5	0	2	0	2155.18	66	85
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	9	9	17	0.02%	40.3%	LDRLDLAR	94.9%	27.8	25	18.9	1	0	0	971.56	159	166
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	9	9	17	0.02%	40.3%	LQDAYYIFQEMADK	99.7%	64.1	25	42.3	3	0	0	1734.80	198	211
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	9	9	17	0.02%	40.3%	MFADYLAHESRR	99.6%	31.4	25	27.8	0	2	0	1495.71	86	97
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	9	9	17	0.02%	40.3%	YLSQLKDAHR	99.7%	37.8	25	34.4	0	2	0	1230.66	273	282
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	15	18	39	0.04%	23.2%	ALQQYTLEPSEKPFDLK	98.5%	26	25	21.5	0	1	0	2007.04	561	577
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	15	18	39	0.04%	23.2%	ATFYLNVLEQK	99.7%	65.8	25	55.1	2	0	0	1325.71	528	538
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	15	18	39	0.04%	23.2%	DSPLFDFIESCLR	96.0%	28.8	25	27.9	1	0	0	1598.75	248	260
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	15	18	39	0.04%	23.2%	ELAPAVSVLQLFCSSPK	99.7%	108	25	108	5	1	0	1845.98	284	300
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	15	18	39	0.04%	23.2%	FGAQNEEMLPSILVLLK	99.7%	45.6	25	40.7	2	0	0	1918.04	498	514
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	15	18	39	0.04%	23.2%	ILHLLGQEGPK	99.7%	54.8	25	54.8	2	2	0	1204.71	455	465
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	15	18	39	0.04%	23.2%	LLLLDTVTMQVTAR	99.7%	82.7	25	82.7	1	0	0	1589.89	846	859
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	15	18	39	0.04%	23.2%	QEIFQEQLAAVPEFR	99.7%	66.9	25	56.6	2	0	0	1804.92	610	624
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	15	18	39	0.04%	23.2%	SAVLQEAR	98.1%	31.9	25	11.8	2	0	0	873.48	25	32
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	15	18	39	0.04%	23.2%	SIATLAITTLLK	99.7%	97.7	25	97.7	6	0	0	1244.78	339	350
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	15	18	39	0.04%	23.2%	SLPYNQPGTCYTLVALPK	99.7%	70.1	25	66.7	2	0	0	2022.04	697	714
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	15	18	39	0.04%	23.2%	SSPEPVALTESETEYVIR	99.7%	98.1	25	92.4	2	0	0	2006.99	632	649
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	15	18	39	0.04%	23.2%	VFNETPINPR	99.5%	38.2	25	33.8	2	0	0	1186.62	33	42
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	15	18	39	0.04%	23.2%	VVLEHEEVR	99.7%	63.8	25	58.5	4	0	0	1109.59	480	488
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	15	18	39	0.04%	23.2%	VVVVQAISALCQK	99.7%	69.1	25	62.9	2	0	0	1414.81	377	389
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	10	11	22	0.02%	16.8%	AEITLVATKPEK	99.7%	47.2	25	39.6	2	0	0	1299.75	591	602
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	10	11	22	0.02%	16.8%	AIVDCIISIVEENPESK	99.7%	75.3	25	75.3	2	0	0	1915.97	416	432
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	10	11	22	0.02%	16.8%	ATFYLNVLQQR	99.7%	69.8	25	63.1	4	0	0	1352.73	528	538
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	10	11	22	0.02%	16.8%	DDGGFEYKR	94.7%	27.6	25	21.4	1	0	0	1086.49	407	415
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	10	11	22	0.02%	16.8%	DMTGKEDVYR	95.2%	28	25	28	1	0	0	1213.55	112	121
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	10	11	22	0.02%	16.8%	IFNETPINPR	99.7%	54.8	25	41.5	3	0	0	1200.64	33	42
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	10	11	22	0.02%	16.8%	ITDGTMLQAIER	99.7%	45.3	25	31.5	1	0	0	1347.69	131	142
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	10	11	22	0.02%	16.8%	SAVLQEAR	98.1%	31.9	25	11.8	2	0	0	873.48	25	32
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	10	11	22	0.02%	16.8%	SIATLAITTLLK	99.7%	97.7	25	97.7	6	0	0	1244.78	339	350
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	10	11	22	0.02%	16.8%	SIPLAMAPVFEQK	99.7%	67.7	25	64.1	3	0	0	1430.77	578	590
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	10	11	22	0.02%	16.8%	SQFAYCMLIR	99.7%	42.4	25	28.9	1	0	0	1288.62	225	234
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	10	11	22	0.02%	16.8%	VVLENEAVR	99.7%	65.3	25	59.4	4	0	0	1028.57	480	488
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	10	11	22	0.02%	16.8%	VVVVQAISALCQK	99.7%	69.1	25	62.9	2	0	0	1414.81	377	389
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	4	4	8	0.01%	28.3%	AVLFCLSEDKK	99.7%	53.8	25	50.8	2	0	0	1309.68	35	45
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	4	4	8	0.01%	28.3%	LGGSAVISLEGKPL	99.7%	80.9	25	78.6	2	0	0	1340.78	153	166
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	4	4	8	0.01%	28.3%	MIYASSKDAIK	98.6%	33.3	25	23.4	1	0	0	1242.64	115	125
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	4	4	8	0.01%	28.3%	YALYDATYETK	99.7%	68.4	25	63.7	3	0	0	1337.63	82	92
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	6	6	10	0.01%	5.7%	FALTFGLDQLK	99.7%	57.1	25	0	2	0	0	1252.69	955	965
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	6	6	10	0.01%	5.7%	HMQNSEIIR	97.4%	30.5	25	22	1	0	0	1127.56	138	146
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	6	6	10	0.01%	5.7%	ITELFAVALPQLLAK	99.7%	70.1	25	70.1	2	0	0	1626.98	563	577
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	6	6	10	0.01%	5.7%	MYSDAFLNDSYLK	99.7%	48.4	25	48.4	1	0	0	1566.71	318	330
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	6	6	10	0.01%	5.7%	SSFCEFIGVLVR	99.7%	76.2	25	71.1	2	0	0	1413.72	173	184
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	6	6	10	0.01%	5.7%	YYNDYGDIIK	99.7%	63.8	25	57.8	2	0	0	1263.59	892	901
Coiled-coil domain-containing protein 137	CCDC137	CC137_HUMAN	33.2	99.8%	2	2	2	0.00%	6.6%	KGESDGAYIHR	98.9%	27.3	25	25.1	0	1	0	1232.60	118	128
Coiled-coil domain-containing protein 137	CCDC137	CC137_HUMAN	33.2	99.8%	2	2	2	0.00%	6.6%	QRIVEEER	96.0%	28.9	25.2	4.92	1	0	0	1058.56	248	255
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	13	19	0.02%	24.0%	ARVEENFLK	99.7%	59	25	39.9	2	0	0	1105.60	411	419
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	13	19	0.02%	24.0%	ELLESNFTLVGDDGTNK	99.7%	92.3	25	92.3	2	0	0	1851.90	173	189
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	13	19	0.02%	24.0%	EMQDLSEFCSDKPK	99.7%	54.9	25	48.9	2	0	0	1713.75	275	288
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	13	19	0.02%	24.0%	IMNEEDPEKQR	99.7%	45.7	25	44.6	3	1	0	1388.65	444	454
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	13	19	0.02%	24.0%	IMQEEGQPLK	98.5%	33.1	25	21.5	1	0	0	1172.60	342	351
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	13	19	0.02%	24.0%	IMQEEGQPLKLPDTK	95.3%	22	25	21.6	0	1	0	1726.90	342	356

Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	13	19	0.02%	24.0%	MMRPVSDQVQIK	98.3%	25.7	25	18.7	0	1	0	1463.73	237	248
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	13	19	0.02%	24.0%	RQDLLNVLAR	99.7%	44.8	25	37	2	0	0	1197.71	227	236
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	13	19	0.02%	24.0%	TLLFTFNVPGSGNTYPK	99.7%	49.8	25	49.5	2	0	0	1855.96	358	374
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	13	19	0.02%	24.0%	VCCEGMLIQLR	99.7%	61.7	25	55.6	2	0	0	1378.66	213	223
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	7	8	12	0.01%	28.6%	AAANEQLTR	99.7%	41.4	25	24	1	0	0	973.51	96	104
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	7	8	12	0.01%	28.6%	LSENVIDR	99.7%	57.4	25	51	2	0	0	945.50	28	35
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	7	8	12	0.01%	28.6%	VAEELALEQAK	99.7%	56.3	25	51.9	2	0	0	1200.65	66	76
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	7	8	12	0.01%	28.6%	VTTEQYQK	99.7%	43.6	25	30.7	1	0	0	996.50	158	165
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	7	8	12	0.01%	28.6%	YESHPVCADLQAK	97.6%	31	25	31	1	0	0	1517.71	177	189
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	7	8	12	0.01%	28.6%	YSGAYGASVSDEELK	99.7%	109	25	109	2	0	0	1575.72	49	63
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	7	8	12	0.01%	28.6%	YSGAYGASVSDEELKR	99.7%	84.9	25	76.2	2	1	0	1731.82	49	64
Coiled-coil-helix-coiled-coil-helix domain-containing protein 6, mitochondrial	CHCHD6	CHCH6_HUMAN	26.5	99.8%	2	2	3	0.00%	11.9%	ASLPTGEGSISHEEQK	99.7%	65	25	65	2	0	0	1669.80	118	133
Coiled-coil-helix-coiled-coil-helix domain-containing protein 6, mitochondrial	CHCHD6	CHCH6_HUMAN	26.5	99.8%	2	2	3	0.00%	11.9%	LSSEQFHEAASK	98.1%	31.9	25	31.8	1	0	0	1333.64	172	183
Coilin	COIL	COIL_HUMAN	62.6	99.8%	2	2	4	0.00%	4.2%	NSSTIIQNPVETPK	99.7%	40.9	25	40.5	1	0	0	1527.80	445	458
Coilin	COIL	COIL_HUMAN	62.6	99.8%	2	2	4	0.00%	4.2%	VVTDLISLIR	99.7%	57.8	25	50.4	3	0	0	1128.70	37	46
Cold-inducible RNA-binding protein	CIRBP	CIRBP_HUMAN	18.6	99.8%	2	2	3	0.00%	14.0%	DSYDSYATHNE	99.7%	75.9	25	75.9	2	0	0	1301.49	162	172
Cold-inducible RNA-binding protein	CIRBP	CIRBP_HUMAN	18.6	99.8%	2	2	3	0.00%	14.0%	YGQISEVVVVKDR	99.7%	52.3	25	52.3	1	0	0	1491.82	29	41
COMM domain-containing protein 3	COMMD3	COMD3_HUMAN	22.2	100.0%	3	3	4	0.00%	17.9%	NSLEILLGSIGR	99.7%	45.1	25	31.6	1	0	0	1271.73	109	120
COMM domain-containing protein 3	COMMD3	COMD3_HUMAN	22.2	100.0%	3	3	4	0.00%	17.9%	SFDSNAFTLLLR	99.7%	72.2	25	66.8	2	0	0	1383.73	19	30
COMM domain-containing protein 3	COMMD3	COMD3_HUMAN	22.2	100.0%	3	3	4	0.00%	17.9%	SLPHITDVSWR	97.8%	31.4	25	29.3	1	0	0	1310.69	121	131
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	C1QBP_HUMAN	31.4	100.0%	5	8	13	0.01%	22.0%	AFVDFLSDEIK	99.7%	55.1	25	51.3	1	0	0	1283.65	81	91
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	C1QBP_HUMAN	31.4	100.0%	5	8	13	0.01%	22.0%	AFVDFLSDEIKEER	99.7%	81.6	25	76.4	2	2	0	1697.84	81	94
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	C1QBP_HUMAN	31.4	100.0%	5	8	13	0.01%	22.0%	EVSFQSTGESEWK	99.7%	78	25	69.5	2	0	0	1513.68	208	220
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	C1QBP_HUMAN	31.4	100.0%	5	8	13	0.01%	22.0%	MSGGWELELNGTEAK	99.7%	109	25	109	3	0	0	1637.75	105	119
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	C1QBP_HUMAN	31.4	100.0%	5	8	13	0.01%	22.0%	VEEQEPELTSTPNFVVEVIK	99.7%	67.8	25	67.8	2	1	0	2287.17	155	174
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	10	10	17	0.02%	8.1%	DLAYCVSQLPLTER	99.7%	57.2	25	57.2	1	0	0	1664.83	1225	1238
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	10	10	17	0.02%	8.1%	EAVLNAYR	99.7%	54.1	25	42.3	4	0	0	935.49	691	698
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	10	10	17	0.02%	8.1%	FQAVVALAVGR	99.7%	53.7	25	46	2	0	0	1130.67	402	412
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	10	10	17	0.02%	8.1%	GNAIYNLLPDIISR	99.7%	46.1	25	35	2	0	0	1558.86	1160	1173
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	10	10	17	0.02%	8.1%	LRDPAQQVR	99.3%	36.3	25	21.8	1	0	0	1082.61	1101	1109
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	10	10	17	0.02%	8.1%	LSDADLAGPLQK	99.7%	42.4	25	30.8	1	0	0	1227.66	441	452
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	10	10	17	0.02%	8.1%	QTLAAFVPLLLK	99.4%	37.5	25	37.5	2	0	0	1313.82	1009	1020
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	10	10	17	0.02%	8.1%	VACCPLER	98.7%	33.8	25	28.2	1	0	0	1004.47	764	771
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	10	10	17	0.02%	8.1%	VLQLFTR	99.6%	39.8	25	25.3	2	0	0	876.53	384	390
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	10	10	17	0.02%	8.1%	YQPLASTASDNDFVTPEPR	99.7%	60.1	25	60.1	1	0	0	2107.99	1325	1343
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	6	6	10	0.01%	8.6%	APLQQCAEDR	99.7%	57	25	54.1	2	0	0	1187.55	304	313
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	6	6	10	0.01%	8.6%	LLASPSSR	98.7%	33.8	25	24.6	1	0	0	830.47	84	91
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	6	6	10	0.01%	8.6%	QSMWSLLTALSGK	98.9%	34.6	25	34.6	1	0	0	1421.75	649	661
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	6	6	10	0.01%	8.6%	VAAGTLDASTK	99.6%	38.7	25	33.4	2	0	0	1033.55	153	163
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	6	6	10	0.01%	8.6%	VDAVHADVYR	99.7%	42.2	25	20.6	2	0	0	1144.57	169	178
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	6	6	10	0.01%	8.6%	VFDLQFSTDSPR	99.7%	105	25	99.6	2	0	0	1411.69	72	83
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	10	10	23	0.02%	11.4%	APIVTVGVNNDPADVR	99.7%	58.3	25	58.3	2	0	0	1636.87	471	486
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	10	10	23	0.02%	11.4%	ASELKEEIK	99.4%	37.3	25	18.7	2	0	0	1046.57	518	526
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	10	10	23	0.02%	11.4%	EFIGQQLILIIK	99.7%	59.7	25	50.6	3	0	0	1414.87	399	410
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	10	10	23	0.02%	11.4%	GDFSYIGNLMTK	99.7%	48	25	46.9	1	0	0	1345.65	387	398
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	10	10	23	0.02%	11.4%	IQAVLALSR	99.7%	41.7	25	34.9	2	0	0	970.60	160	168
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	10	10	23	0.02%	11.4%	LLSDFLDSEVSELR	99.7%	92.3	25	87.7	4	0	0	1622.83	695	708
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	10	10	23	0.02%	11.4%	LMFSGLLVSSR	99.7%	74.5	25	69.1	3	0	0	1209.67	718	728
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	10	10	23	0.02%	11.4%	SLDTSEEGGR	97.9%	31.5	25	24.6	1	0	0	1050.47	411	420
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	10	10	23	0.02%	11.4%	TQIVTEIISEIR	99.7%	86.3	25	79.3	4	0	0	1401.79	459	470
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	10	10	23	0.02%	11.4%	VMLLQQGLNDR	99.7%	58.9	25	50.9	1	0	0	1286.69	247	257

Condensin-2 complex subunit D3	NCAPD3	CNDD3_HUMAN	168.9	99.8%	2	2	4	0.00%	1.6%	SALQVLVSILK	99.7%	46.9	25	43.1	2	0	0	1170.75	560	570
Condensin-2 complex subunit D3	NCAPD3	CNDD3_HUMAN	168.9	99.8%	2	2	4	0.00%	1.6%	TFAAQSLVQLLSK	99.7%	65.7	25	62.9	2	0	0	1405.81	372	384
Condensin-2 complex subunit G2	NCAPG2	CNDG2_HUMAN	131.0	99.8%	2	2	3	0.00%	1.6%	GFSEAAAPR	99.7%	46.2	25	37.3	2	0	0	905.45	812	820
Condensin-2 complex subunit G2	NCAPG2	CNDG2_HUMAN	131.0	99.8%	2	2	3	0.00%	1.6%	YSLHDNSEK	99.3%	36.7	25	25.1	1	0	0	1092.50	466	474
Conserved oligomeric Golgi complex subunit 1	COG1	COG1_HUMAN	109.0	100.0%	2	2	4	0.00%	1.9%	ALQLLYDLR	99.7%	48.2	25	43.1	2	0	0	1104.64	806	814
Conserved oligomeric Golgi complex subunit 1	COG1	COG1_HUMAN	109.0	100.0%	2	2	4	0.00%	1.9%	QALTDFLLAR	99.7%	79.6	25	76.1	2	0	0	1147.65	225	234
Conserved oligomeric Golgi complex subunit 4	COG4	COG4_HUMAN	89.1	100.0%	3	3	4	0.00%	4.7%	ELDPILTEVTLMNAR	99.7%	60.5	25	59.3	1	0	0	1714.90	351	365
Conserved oligomeric Golgi complex subunit 4	COG4	COG4_HUMAN	89.1	100.0%	3	3	4	0.00%	4.7%	LFSQGIGGEQAQAK	99.7%	70.3	25	65.6	1	0	0	1433.74	572	585
Conserved oligomeric Golgi complex subunit 4	COG4	COG4_HUMAN	89.1	100.0%	3	3	4	0.00%	4.7%	LLQEAEQR	99.6%	39.7	25	25.2	2	0	0	986.53	187	194
Conserved oligomeric Golgi complex subunit 5	COG5	COG5_HUMAN	92.7	99.9%	2	2	2	0.00%	2.5%	AVELFIR	97.4%	30.6	25	10.9	1	0	0	847.50	679	685
Conserved oligomeric Golgi complex subunit 5	COG5	COG5_HUMAN	92.7	99.9%	2	2	2	0.00%	2.5%	LFDPINLVFPPGGR	99.7%	51.2	25	45.1	1	0	0	1541.85	493	506
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	10	10	15	0.02%	11.6%	AEGSSTASSGSQLAEGK	99.7%	84.6	25	84.6	2	0	0	1566.72	503	519
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	10	10	15	0.02%	11.6%	APSHSESALNNDSK	96.5%	23	25	20.6	0	1	0	1456.67	1073	1086
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	10	10	15	0.02%	11.6%	EAALEAAVLNKEE	99.7%	40.7	25	35.1	1	0	0	1386.71	1106	1118
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	10	10	15	0.02%	11.6%	GVISTPVIR	99.7%	43.8	25	28.2	2	0	0	941.58	987	995
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	10	10	15	0.02%	11.6%	LPPEFSPVIIK	95.0%	27.9	25	22.4	1	0	0	1239.73	633	643
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	10	10	15	0.02%	11.6%	LYEPDQLQELK	96.9%	29.9	25	20.9	1	0	0	1375.71	748	758
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	10	10	15	0.02%	11.6%	NIQDTSDLDAIAK	99.7%	67.6	25	62.1	2	0	0	1403.70	292	304
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	10	10	15	0.02%	11.6%	QYVYGVLFSLAESR	99.7%	76.9	25	76.9	2	0	0	1631.84	607	620
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	10	10	15	0.02%	11.6%	SPQTPELVEALAFR	99.7%	52.5	25	52.1	2	0	0	1557.83	652	665
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	10	10	15	0.02%	11.6%	SQGGVQPIPSQGGK	99.7%	47.9	25	43.6	1	0	0	1339.70	933	946
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	5	5	10	0.01%	10.4%	AESTPEIAEQR	99.7%	46.4	25	43.4	2	0	0	1230.60	225	235
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	5	5	10	0.01%	10.4%	DSQTQAILTK	99.7%	42.5	25	31.2	2	0	0	1104.59	239	248
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	5	5	10	0.01%	10.4%	EGSQGELTPANSQSR	99.7%	73.5	25	73.5	4	0	0	1560.72	472	486
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	5	5	10	0.01%	10.4%	MALSFVQR	99.3%	36.6	25	30.2	1	0	0	967.50	77	84
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	5	5	10	0.01%	10.4%	TLYTQIR	98.2%	32.1	25	28.1	1	0	0	894.50	364	370
COP9 signalosome complex subunit 4	COPS4	CSN4_HUMAN	46.3	99.8%	2	3	3	0.00%	5.4%	ATTADGSSILDR	99.7%	75.3	25	65.2	1	0	0	1206.60	291	302
COP9 signalosome complex subunit 4	COPS4	CSN4_HUMAN	46.3	99.8%	2	3	3	0.00%	5.4%	IASQMITEGR	99.7%	72.2	25	64.9	2	0	0	1105.57	338	347
COP9 signalosome complex subunit 7a	COPS7A	CSN7A_HUMAN	30.3	100.0%	3	3	6	0.01%	12.7%	ELAESDFASTFR	99.4%	37.4	25	35.3	2	0	0	1372.64	54	65
COP9 signalosome complex subunit 7a	COPS7A	CSN7A_HUMAN	30.3	100.0%	3	3	6	0.01%	12.7%	LEVDYSIGR	99.7%	54.5	25	36.8	2	0	0	1051.54	152	160
COP9 signalosome complex subunit 7a	COPS7A	CSN7A_HUMAN	30.3	100.0%	3	3	6	0.01%	12.7%	VTGQNQEQFLLLAK	99.7%	48.4	25	39.7	2	0	0	1588.87	7	20
COP9 signalosome complex subunit 8	COPS8	CSN8_HUMAN	23.2	99.8%	2	2	3	0.00%	13.9%	GILEQGWQADSTTR	99.7%	71.9	25	63.7	2	0	0	1561.76	147	160
COP9 signalosome complex subunit 8	COPS8	CSN8_HUMAN	23.2	99.8%	2	2	3	0.00%	13.9%	SANSELGGIWSVGQR	99.4%	36.9	25	36.9	1	0	0	1560.78	66	80
Coronin-1C	CORO1C	COR1C_HUMAN	53.3	99.8%	2	2	3	0.00%	6.1%	AIFLADGNVFTTGFSR	95.9%	28.7	25	28.7	1	0	0	1715.88	224	239
Coronin-1C	CORO1C	COR1C_HUMAN	53.3	99.8%	2	2	3	0.00%	6.1%	KTTDTASVQNEAK	99.7%	66	25	50.7	2	0	0	1392.70	428	440
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	4	4	8	0.01%	12.3%	FCTGLTQIETLFK	99.7%	76	25	67.6	2	0	0	1557.80	253	265
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	4	4	8	0.01%	12.3%	FSEVLKR	99.6%	38.9	25	20.6	2	0	0	878.51	308	314
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	4	4	8	0.01%	12.3%	LAVEALSSLDGDLAGR	99.7%	107	25	107	2	0	0	1586.84	157	172
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	4	4	8	0.01%	12.3%	VLTPELYAELR	99.7%	61.3	25	52.5	2	0	0	1303.73	33	43
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	3	3	10	0.01%	8.4%	IGSGFDNIDIK	99.7%	55.3	25	40.8	4	0	0	1178.61	98	108
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	3	3	10	0.01%	8.4%	QGAFLVNTAR	99.7%	42.7	25	34.6	2	0	0	1076.58	257	266
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	3	3	10	0.01%	8.4%	VGQAVALR	99.7%	70.3	25	56.3	4	0	0	813.49	185	192
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	3	3	10	0.01%	8.4%	VQSVEQIR	99.7%	46.3	25	22.7	2	0	0	958.53	156	163
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	7	7	10	0.01%	16.0%	EAAATEIRR	99.5%	38.3	25	22.4	1	0	0	1016.55	335	343
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	7	7	10	0.01%	16.0%	GAALDVHESEPFSFAQGPLK	99.7%	54.1	25	52.7	0	2	0	2100.04	292	311
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	7	7	10	0.01%	16.0%	GETLGLIGFGR	99.7%	66.1	25	59.7	1	0	0	1119.62	180	190
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	7	7	10	0.01%	16.0%	IGSGYDNVDIK	99.7%	50.6	25	41.3	2	0	0	1180.58	104	114
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	7	7	10	0.01%	16.0%	IRGETLGLIGFGR	99.6%	38.8	25	38.8	1	0	0	1388.80	178	190
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	7	7	10	0.01%	16.0%	QGAFLVNAAR	99.7%	44.2	25	38.8	1	0	0	1046.57	263	272
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	7	7	10	0.01%	16.0%	VQSVEQIR	99.7%	46.3	25	22.7	2	0	0	958.53	162	169
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	23	44	0.04%	39.8%	ALEHSALAINHK	99.7%	53.9	25	50.5	2	2	0	1303.71	320	331

CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	23	44	0.04%	39.8%	CSNPLDTSVK	99.7%	48.3	25	47.7	2	0	0	1120.53	218	227
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	23	44	0.04%	39.8%	ENFCNIHVSLVPQPSSTGEQK	99.6%	31.5	25	31.5	0	2	0	2371.13	173	193
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	23	44	0.04%	39.8%	FEVNPVWK	94.6%	27.6	25	11.8	1	0	0	1018.54	482	489
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	23	44	0.04%	39.8%	FSDSYASVIK	99.7%	70.3	25	54	2	0	0	1116.56	310	319
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	23	44	0.04%	39.8%	FVGQDVEGER	99.7%	69.3	25	57.1	2	0	0	1135.54	499	508
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	23	44	0.04%	39.8%	GIIASSVGTILK	99.7%	76.1	25	72.4	2	0	0	1158.71	17	28
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	23	44	0.04%	39.8%	GLGLSPDLVVCR	99.7%	51.2	25	41.3	2	0	0	1285.69	206	217
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	23	44	0.04%	39.8%	IQAIAWAR	99.7%	67	25	49.2	2	0	0	928.54	382	389
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	23	44	0.04%	39.8%	IYQYVINK	99.7%	46.6	25	35.6	2	0	0	1040.58	93	100
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	23	44	0.04%	39.8%	KLYGDADYLEER	99.7%	76.5	25	73.2	2	2	0	1471.71	466	477
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	23	44	0.04%	39.8%	LCSAHGVLVPGGFGVR	99.7%	47.4	25	40.9	1	2	0	1625.86	361	376
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	23	44	0.04%	39.8%	LLETCSIALVGK	99.7%	95.5	25	88.6	3	0	0	1303.73	295	306
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	23	44	0.04%	39.8%	LYGDADYLEER	99.7%	71.6	25	54	2	0	0	1343.61	467	477
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	23	44	0.04%	39.8%	RLDLPIER	99.7%	42.5	25	28.3	2	0	0	1011.59	269	276
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	23	44	0.04%	39.8%	SCGLHVTSIK	99.7%	46.2	25	37.7	2	0	0	1101.57	29	38
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	23	44	0.04%	39.8%	TVQVVPHITDAIQEWVMR	99.7%	41.5	25	41.5	0	2	0	2122.11	110	127
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	23	44	0.04%	39.8%	VPLLLEEQGVVDYFLR	99.7%	78.1	25	77.5	1	0	0	1890.04	253	268
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	23	44	0.04%	39.8%	YIDSADLEPITSQEEPVR	99.7%	89.5	25	78.8	2	0	0	2062.00	336	353
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	23	44	0.04%	39.8%	YILVTGGVISGIGK	99.7%	116	25	116	2	0	0	1376.82	3	16
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	5	5	11	0.01%	13.3%	ALEHSALAINHK	99.7%	53.9	25	50.5	2	2	0	1303.71	320	331
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	5	5	11	0.01%	13.3%	GIIASSIGTILK	99.7%	65.1	25	39.1	2	0	0	1172.73	17	28
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	5	5	11	0.01%	13.3%	GLGLSPDLIVCR	99.7%	53.4	25	47.4	4	0	0	1299.71	206	217
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	5	5	11	0.01%	13.3%	IYQHVINK	99.0%	34.8	25	17.9	1	0	0	1014.57	93	100
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	5	5	11	0.01%	13.3%	LQAISWAR	99.7%	54.7	25	41.5	2	0	0	944.53	382	389
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	5	5	11	0.01%	13.3%	VPVLLEEQSIVK	99.7%	72.7	25	72.7	2	0	0	1353.80	253	264
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	5	5	11	0.01%	13.3%	YILVTGGVISGIGK	99.7%	116	25	116	2	0	0	1376.82	3	16
Cullin-1	CUL1	CUL1_HUMAN	89.7	99.8%	2	2	2	0.00%	2.7%	LLIQAAIVR	99.7%	48.3	25	35.5	1	0	0	996.66	709	717
Cullin-1	CUL1	CUL1_HUMAN	89.7	99.8%	2	2	2	0.00%	2.7%	QIGLDQIWDDLR	99.7%	51.7	25	51.7	1	0	0	1471.75	14	25
Cullin-4B	CUL4B	CUL4B_HUMAN	104.0	100.0%	3	3	5	0.01%	3.6%	ETVEEQASTTER	99.7%	96	25	91.9	2	0	0	1379.63	830	841
Cullin-4B	CUL4B	CUL4B_HUMAN	104.0	100.0%	3	3	5	0.01%	3.6%	QYQIDAAIVR	99.7%	64.2	25	56.4	1	0	0	1176.64	847	856
Cullin-4B	CUL4B	CUL4B_HUMAN	104.0	100.0%	3	3	5	0.01%	3.6%	TIDGILLLIER	99.7%	66.1	25	58.9	2	0	0	1255.76	346	356
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	AADIDQEVK	99.7%	53.5	25	39.2	2	0	0	988.49	578	586
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	AADIDQEVKER	99.7%	60.4	25	49.4	5	2	0	1273.64	578	588
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	ADVFHAYLSLLK	99.7%	48.6	25	45.9	2	0	0	1376.76	392	403
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	ALTLIAGSPLK	99.7%	84.2	25	84.2	6	0	0	1083.68	631	641
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	AVAALLTIPEAEK	99.7%	83.7	25	68.2	2	0	0	1325.77	1179	1191
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	CLGPLVSK	98.9%	34.5	25	20.9	1	0	0	873.49	71	78
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	DLLDTVLPHLYNETK	99.7%	60.1	25	60.1	2	0	0	1770.93	1043	1057
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	DSIKLDDDSER	99.3%	36.4	25	28.1	1	0	0	1292.60	37	47
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	DSSSTNLESMDTS	96.3%	29.1	25	29.1	1	0	0	1389.53	1218	1230
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	EGPAVVGQFIQDVK	99.7%	65.3	25	59.9	4	0	0	1486.79	813	826
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	EYCIQAFESFVR	99.7%	62.6	25	62.6	2	0	0	1548.72	273	284
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	FMATNDLMTELQK	99.7%	97.5	25	91.5	8	0	0	1541.73	24	36
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	FTISDHPQPIDPLLK	98.5%	26.2	25	24.4	0	1	0	1720.93	991	1005
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	GYLISGSSYAR	99.7%	52.3	25	38.1	3	0	0	1173.59	972	982
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	HTVDDGLDIR	99.7%	61.6	25	54.5	2	0	0	1140.56	1073	1082
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	HTVDDGLDIRK	99.5%	38.5	25	32.2	1	0	0	1268.66	1073	1083
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	IGEYLEK	99.7%	46.1	25	37.8	2	0	0	851.45	249	255
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	ISGSILNELIGLVR	99.7%	60.5	25	50.7	2	0	0	1483.88	730	743
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	ITSEALLVTQQLVK	99.7%	89.1	25	80.5	4	2	0	1542.91	535	548
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	LGTLSALDILIK	99.7%	85.8	25	74.3	4	0	0	1256.78	668	679

Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	LLEDKNGEVQNLAVK	99.7%	39.9	25	30.3	0	1	0	1669.91	56	70
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	LSTLCPSAVLQR	99.7%	56	25	46.7	2	0	0	1344.73	1130	1141
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	LTLIDPETLLPR	99.7%	67.1	25	67.1	8	0	0	1380.81	958	969
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	MLTFLMLVR	99.7%	65.5	25	50.3	9	0	0	1123.64	1121	1129
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	MLTGPVYSQSTALTHK	99.7%	97.5	25	80.9	4	4	0	1733.89	778	793
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	MTSSDKDFR	98.0%	31.8	25	28.7	1	0	0	1086.49	15	23
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	NCIGDFLK	97.6%	30.9	25	23.3	1	0	0	966.47	1006	1013
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	NVVAECLGK	96.2%	29	25	28.4	1	0	0	989.51	949	957
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	SVILEAFSSPSEEVK	99.7%	106	25	100	5	0	0	1621.83	859	873
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	TLEDPDLNVR	99.7%	61.5	25	56.5	3	0	0	1171.60	1014	1023
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	TVIGELPPASSGSALAANVCK	99.7%	89	25	89	2	2	0	2042.06	112	132
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	TVSPALISR	98.5%	32.9	25	17.4	2	0	0	943.56	374	382
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	TYIQCIAAISR	99.7%	98	25	89	3	0	0	1295.68	233	243
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	34	42	109	0.11%	31.8%	VIRPLDQPSSFDATPYIK	99.7%	59.9	25	59.9	2	0	0	2047.09	549	566
Cullin-associated NEDD8-dissociated protein 2	CAND2	CAND2_HUMAN	135.3	100.0%	4	4	5	0.01%	6.0%	AVLLEALGSPSEDVR	99.7%	51.4	25	46.4	2	0	0	1555.83	864	878
Cullin-associated NEDD8-dissociated protein 2	CAND2	CAND2_HUMAN	135.3	100.0%	4	4	5	0.01%	6.0%	FLISDQPHPIDPLLK	96.0%	22.6	25	18.5	0	1	0	1732.96	996	1010
Cullin-associated NEDD8-dissociated protein 2	CAND2	CAND2_HUMAN	135.3	100.0%	4	4	5	0.01%	6.0%	LLEDKNGEVQNLAVK	99.7%	39.9	25	30.3	0	1	0	1669.91	56	70
Cullin-associated NEDD8-dissociated protein 2	CAND2	CAND2_HUMAN	135.3	100.0%	4	4	5	0.01%	6.0%	MTSSDKDFR	98.0%	31.8	25	28.7	1	0	0	1086.49	15	23
Cullin-associated NEDD8-dissociated protein 2	CAND2	CAND2_HUMAN	135.3	100.0%	4	4	5	0.01%	6.0%	TLIQCLGSVGR	99.7%	57.9	25	38.8	1	0	0	1203.65	236	246
Cullin-associated NEDD8-dissociated protein 2	CAND2	CAND2_HUMAN	135.3	100.0%	4	4	5	0.01%	6.0%	VPTSPTAIR	99.7%	51	25	39.5	1	0	0	941.54	227	235
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	58	0.06%	56.2%	ALGTPNNEVWPEVESLQDYK	99.7%	44.9	25	44.9	2	0	0	2289.10	219	238
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	58	0.06%	56.2%	DLKPQNLLIDDKGTIK	99.7%	62.4	25	62.4	2	2	0	1811.03	128	143
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	58	0.06%	56.2%	IGEGTYGVVYK	99.7%	95.9	25	47.8	5	0	0	1185.62	10	20
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	58	0.06%	56.2%	IRLESEEEGVPSTAIR	99.7%	102	25	100	3	1	0	1785.93	35	50
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	58	0.06%	56.2%	LADFGLAR	99.7%	52.4	25	0	7	0	0	862.48	144	151
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	58	0.06%	56.2%	LESEEEGVPSTAIR	99.7%	57.8	25	51.7	2	0	0	1516.75	37	50
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	58	0.06%	56.2%	MALNHPYFNDLDNQIK	99.7%	81.5	25	78.2	4	4	0	1932.93	280	295
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	58	0.06%	56.2%	MLIYDPAK	99.7%	40.5	25	34.1	2	0	0	950.50	267	274
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	58	0.06%	56.2%	MLIYDPAKR	99.7%	48	25	43.5	4	0	0	1122.60	267	275
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	58	0.06%	56.2%	NLDENGLDLLSK	99.7%	79.2	25	56.7	3	0	0	1330.69	255	266
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	58	0.06%	56.2%	SPEVLLGSAR	99.7%	93	25	83.7	6	0	0	1028.57	171	180
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	58	0.06%	56.2%	TTGQVVAMK	99.7%	49.5	25	37.3	2	0	0	934.50	25	33
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	58	0.06%	56.2%	VYTHEVVTLWYR	99.7%	67.8	25	66.7	2	0	0	1565.81	159	170
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	58	0.06%	56.2%	WKPGSLASHVK	99.6%	31.5	25	30.8	0	2	0	1209.67	244	254
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	58	0.06%	56.2%	YLDSIPPGQYMDSSLVK	99.7%	51.5	25	51.5	5	0	0	1912.94	90	106
Cyclin-dependent kinase 11B	CDK11B	CD11B_HUMAN	92.7	100.0%	7	7	9	0.01%	8.8%	APELLLGAK	99.3%	36.5	25	32.9	1	0	0	911.56	605	613
Cyclin-dependent kinase 11B	CDK11B	CD11B_HUMAN	92.7	100.0%	7	7	9	0.01%	8.8%	AQHPNIVTVR	99.7%	41.2	25	24.5	1	0	0	1134.64	492	501
Cyclin-dependent kinase 11B	CDK11B	CD11B_HUMAN	92.7	100.0%	7	7	9	0.01%	8.8%	EGFPITSLR	97.6%	31	25	17.1	1	0	0	1019.55	476	484
Cyclin-dependent kinase 11B	CDK11B	CD11B_HUMAN	92.7	100.0%	7	7	9	0.01%	8.8%	FGALLSDQGFDLMNK	99.3%	36.6	25	36.6	1	0	0	1671.81	688	702
Cyclin-dependent kinase 11B	CDK11B	CD11B_HUMAN	92.7	100.0%	7	7	9	0.01%	8.8%	FLTYFPGR	99.2%	35.7	25	28.3	1	0	0	1000.53	703	710
Cyclin-dependent kinase 11B	CDK11B	CD11B_HUMAN	92.7	100.0%	7	7	9	0.01%	8.8%	IEEGTYGVVYR	99.7%	67.5	25	65	2	0	0	1285.64	444	454
Cyclin-dependent kinase 11B	CDK11B	CD11B_HUMAN	92.7	100.0%	7	7	9	0.01%	8.8%	TLMIQLLR	99.0%	35	25	27	2	0	0	987.60	541	548
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	10	19	0.02%	33.6%	ALFPGDSEIDQLFR	99.7%	71.6	25	64.8	2	0	0	1607.81	201	214
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	10	19	0.02%	33.6%	APEILLGCK	99.7%	59.3	25	58.3	2	0	0	1000.55	170	178
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	10	19	0.02%	33.6%	DLKPQNLLINTEGAIK	99.7%	74.3	25	74.3	2	2	0	1767.00	127	142
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	10	19	0.02%	33.6%	FMDASALTGIPLPLIK	99.7%	72	25	72	4	0	0	1702.95	90	105
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	10	19	0.02%	33.6%	IGEGTYGVVYK	99.7%	95.9	25	47.8	5	0	0	1185.62	10	20
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	10	19	0.02%	33.6%	IRLDTETEGVPSTAIR	99.7%	75.4	25	72.2	2	2	0	1757.94	35	50
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	10	19	0.02%	33.6%	LADFGLAR	99.7%	52.4	25	0	7	0	0	862.48	143	150
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	10	19	0.02%	33.6%	LDTETEGVPSTAIR	97.9%	31.5	25	30.6	1	0	0	1488.75	37	50
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	10	19	0.02%	33.6%	LTGEVVALKK	99.7%	47.7	25	38.3	2	0	0	1057.66	25	34

Cyclin-dependent kinase 5	CDK5	CDK5_HUMAN	33.3	100.0%	3	3	4	0.00%	14.4%	DLLQNLLK	99.7%	40.5	25	30.3	1	0	0	956.58	261	268
Cyclin-dependent kinase 5	CDK5	CDK5_HUMAN	33.3	100.0%	3	3	4	0.00%	14.4%	IGEGTYGTVFK	99.7%	73.3	25	66	2	0	0	1171.60	10	20
Cyclin-dependent kinase 5	CDK5	CDK5_HUMAN	33.3	100.0%	3	3	4	0.00%	14.4%	LADFGLAR	99.7%	52.4	25	0	7	0	0	862.48	142	149
Cyclin-dependent kinase 5	CDK5	CDK5_HUMAN	33.3	100.0%	3	3	4	0.00%	14.4%	LLGTPTEEQWPSMTK	99.5%	37.8	25	37	1	0	0	1717.85	218	232
Cyclin-dependent kinase 9	CDK9	CDK9_HUMAN	42.8	100.0%	3	3	6	0.01%	11.3%	GSQITQQSTNQSR	99.7%	73.8	25	63.9	2	0	0	1434.69	346	358
Cyclin-dependent kinase 9	CDK9	CDK9_HUMAN	42.8	100.0%	3	3	6	0.01%	11.3%	LADFGLAR	99.7%	52.4	25	0	7	0	0	862.48	165	172
Cyclin-dependent kinase 9	CDK9	CDK9_HUMAN	42.8	100.0%	3	3	6	0.01%	11.3%	LLVLDPAQR	99.7%	46.4	25	46	2	0	0	1024.62	295	303
Cyclin-dependent kinase 9	CDK9	CDK9_HUMAN	42.8	100.0%	3	3	6	0.01%	11.3%	NPATTNQTEFER	99.7%	71.1	25	70.8	2	0	0	1407.65	359	370
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	6	6	11	0.01%	12.2%	AAQELQEGQR	99.7%	75.5	25	59.3	2	0	0	1129.56	360	369
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	6	6	11	0.01%	12.2%	CVVILPDSVR	99.4%	37.6	25	31.3	2	0	0	1157.63	370	379
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	6	6	11	0.01%	12.2%	GFLKEEDLTEK	99.7%	69.8	25	59.2	2	0	0	1308.67	395	405
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	6	6	11	0.01%	12.2%	IGDTPMVR	98.6%	33.2	25	22.5	2	0	0	904.46	84	91
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	6	6	11	0.01%	12.2%	PSETPQAEVGPTGCPHR	99.7%	41.5	25	37.3	0	1	0	1819.84	2	18
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	6	6	11	0.01%	12.2%	SNDEEAFTFAR	99.7%	83.1	25	83.1	2	0	0	1286.56	326	336
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	7	7	9	0.01%	15.3%	AIGTDEDLAHSSIR	99.7%	57.8	25	52.6	1	0	0	1484.73	394	407
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	7	7	9	0.01%	15.3%	GVGAIYIR	99.7%	44.2	25	27.6	2	0	0	848.50	264	271
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	7	7	9	0.01%	15.3%	KVYFHTDAAQAVGK	97.8%	24.8	25	23.4	0	1	0	1534.80	226	239
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	7	7	9	0.01%	15.3%	QPIAEIGR	99.7%	46.6	25	35.1	2	0	0	883.50	213	220
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	7	7	9	0.01%	15.3%	QQVASLIGADPR	99.7%	79.4	25	68.2	1	0	0	1254.68	108	119
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	7	7	9	0.01%	15.3%	VEALQSGGGQER	96.7%	29.5	25	21.9	1	0	0	1230.61	278	289
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	7	7	9	0.01%	15.3%	VRVEALQSGGGQER	99.4%	29.8	25	29.3	0	1	0	1485.78	276	289
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	9	11	17	0.02%	22.7%	ADLTEYLSTHYK	99.7%	65.3	25	65.3	2	0	0	1440.70	214	225
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	9	11	17	0.02%	22.7%	EHTAYYIK	96.0%	28.8	25	16.6	1	0	0	1024.51	127	134
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	9	11	17	0.02%	22.7%	EMQENDASMR	99.7%	42	25	40.8	1	0	0	1210.48	171	180
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	9	11	17	0.02%	22.7%	IAEVDASVVR	99.7%	78	25	48.1	2	0	0	1058.58	433	442
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	9	11	17	0.02%	22.7%	LCTSATESEVAR	99.7%	93.3	25	86.3	2	0	0	1323.62	379	390
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	9	11	17	0.02%	22.7%	MVLAAAGGVEHQQLLDLAQK	99.7%	55.4	25	55.4	0	4	0	2092.12	229	248
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	9	11	17	0.02%	22.7%	NALVSHLDGTTPVCEDIGR	99.7%	39.9	25	39.9	0	1	0	2054.00	397	415
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	9	11	17	0.02%	22.7%	RIPLAEWESR	96.6%	29.4	25	29.4	1	0	0	1256.67	423	432
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	9	11	17	0.02%	22.7%	SGMFWLRF	99.4%	36.9	25	36.9	3	0	0	1059.51	473	480
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	23	44	0.04%	45.3%	ATAAPAGAPPQPQDLEFTK	99.7%	72.1	25	70.1	2	0	0	1909.97	24	42
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	23	44	0.04%	45.3%	AVAFQNPQTHVIENLHAAAYR	99.7%	48.6	25	48.6	0	2	0	2350.21	163	183
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	23	44	0.04%	45.3%	ENMAYTVECLR	99.7%	70.6	25	65.4	4	0	0	1401.61	117	127
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	23	44	0.04%	45.3%	GSNTTSHLHQAVAK	99.7%	67	25	58.4	3	0	0	1450.74	302	315
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	23	44	0.04%	45.3%	LPNGLVIASLENYSPVSR	99.7%	131	25	131	2	1	0	1929.04	43	60
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	23	44	0.04%	45.3%	LTSSLTTK	99.2%	36.2	25	36.2	1	0	0	850.49	85	92
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	23	44	0.04%	45.3%	MALIGLGVSHPVLK	99.7%	76.2	25	74.1	2	3	0	1450.85	218	231
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	23	44	0.04%	45.3%	NALANPLYCPDYR	99.7%	63.1	25	54.4	2	0	0	1566.74	184	196
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	23	44	0.04%	45.3%	QVAEQFLNMR	99.7%	74.8	25	64.1	4	0	0	1251.62	232	241
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	23	44	0.04%	45.3%	RWEVADLQPQLK	99.7%	50.4	25	42.6	2	2	0	1482.81	148	159
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	23	44	0.04%	45.3%	SMAASGNLGHTPFVDEL	99.7%	82.7	25	79.4	4	0	0	1761.81	437	453
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	23	44	0.04%	45.3%	TIAQGNLSNTDVQAAK	99.7%	102	25	95.6	4	0	0	1630.84	360	375
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	23	44	0.04%	45.3%	VTSEELHYFVQNHFTSAR	99.7%	34.8	25	34.8	0	2	0	2165.04	200	217
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	23	44	0.04%	45.3%	WEVADLQPQLK	99.7%	60.2	25	51.7	1	0	0	1326.71	149	159
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	23	44	0.04%	45.3%	YEDFSNLGTTHLLR	99.7%	82.9	25	80.9	2	1	0	1665.82	71	84
Cytochrome b-c1 complex subunit 8	UQCRQ	QCR8_HUMAN	9.9	100.0%	4	4	10	0.01%	47.6%	GREFGNLTR	99.1%	35.4	25	4.49	3	0	0	1049.55	2	10
Cytochrome b-c1 complex subunit 8	UQCRQ	QCR8_HUMAN	9.9	100.0%	4	4	10	0.01%	47.6%	HVISYSLSPFEQR	99.7%	49.3	25	44.7	4	0	0	1562.80	13	25
Cytochrome b-c1 complex subunit 8	UQCRQ	QCR8_HUMAN	9.9	100.0%	4	4	10	0.01%	47.6%	IRESFFR	96.1%	28.9	25	13.2	2	0	0	954.52	42	48
Cytochrome b-c1 complex subunit 8	UQCRQ	QCR8_HUMAN	9.9	100.0%	4	4	10	0.01%	47.6%	KNPAAYENDK	99.3%	36.4	25	27.6	1	0	0	1149.55	73	82
Cytochrome b-c1 complex subunit 9	UQCR10	QCR9_HUMAN	7.3	99.8%	2	3	5	0.01%	38.1%	AFDQGADAIYDHINEGK	99.7%	76.2	25	76.2	2	2	0	1863.85	35	51
Cytochrome b-c1 complex subunit 9	UQCR10	QCR9_HUMAN	7.3	99.8%	2	3	5	0.01%	38.1%	LYSLLFR	96.2%	29	25	22.2	1	0	0	911.53	10	16

Cytochrome b-c1 complex subunit Rieske, mitochondrial	UQCRFS1	UCRI_HUMAN	29.7	100.0%	5	5	9	0.01%	19.0%	EIEQEAAVELSQLR	99.7%	61.5	25	43.9	2	0	0	1614.83	183	196
Cytochrome b-c1 complex subunit Rieske, mitochondrial	UQCRFS1	UCRI_HUMAN	29.7	100.0%	5	5	9	0.01%	19.0%	LEVLDSTK	97.4%	30.7	25	6.45	2	0	0	904.50	94	101
Cytochrome b-c1 complex subunit Rieske, mitochondrial	UQCRFS1	UCRI_HUMAN	29.7	100.0%	5	5	9	0.01%	19.0%	NAVTQFVSSMSASADVLALAK	99.7%	87.6	25	87.6	2	0	0	2126.08	131	151
Cytochrome b-c1 complex subunit Rieske, mitochondrial	UQCRFS1	UCRI_HUMAN	29.7	100.0%	5	5	9	0.01%	19.0%	RLEVLDSTK	99.7%	46	25	46	2	0	0	1060.60	93	101
Cytochrome b-c1 complex subunit Rieske, mitochondrial	UQCRFS1	UCRI_HUMAN	29.7	100.0%	5	5	9	0.01%	19.0%	VPDFSEYR	98.9%	34.5	25	34.5	1	0	0	1012.47	85	92
Cytochrome c	CYCS	CYC_HUMAN	11.7	100.0%	3	3	6	0.01%	24.8%	KTGQAPGYSYTAANK	99.7%	46.6	25	43.9	2	0	0	1556.77	40	54
Cytochrome c	CYCS	CYC_HUMAN	11.7	100.0%	3	3	6	0.01%	24.8%	TGPNLHGLFGR	99.7%	46.7	25	38.9	2	0	0	1168.62	29	39
Cytochrome c	CYCS	CYC_HUMAN	11.7	100.0%	3	3	6	0.01%	24.8%	TGQAPGYSYTAANK	99.7%	57.3	25	57.1	2	0	0	1428.68	41	54
Cytochrome c oxidase assembly factor 3 homolog, mitochondrial	COA3	COA3_HUMAN	11.7	99.8%	2	2	2	0.00%	17.9%	FLDELEDEAK	99.1%	35.4	25	31.1	1	0	0	1208.57	84	93
Cytochrome c oxidase assembly factor 3 homolog, mitochondrial	COA3	COA3_HUMAN	11.7	99.8%	2	2	2	0.00%	17.9%	RGEAPFAQR	95.2%	28	25	19.5	1	0	0	1031.54	14	22
Cytochrome c oxidase assembly protein COX15 homolog	COX15	COX15_HUMAN	46.0	99.8%	2	2	2	0.00%	5.4%	SGLEEKSDSHDIPR	96.6%	23.1	25	23.1	0	1	0	1569.75	204	217
Cytochrome c oxidase assembly protein COX15 homolog	COX15	COX15_HUMAN	46.0	99.8%	2	2	2	0.00%	5.4%	YQQFPEFK	96.8%	29.7	25	27.3	1	0	0	1086.53	124	131
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	5	7	19	0.02%	18.9%	IFEMGPVFTL	97.9%	31.4	25	24.8	2	0	0	1153.60	218	227
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	5	7	19	0.02%	18.9%	ILYMTDEVNDPSLTIK	99.7%	91.9	25	89.2	8	0	0	1867.94	83	98
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	5	7	19	0.02%	18.9%	LLDVDNR	99.7%	44.7	25	28.4	3	0	0	844.45	135	141
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	5	7	19	0.02%	18.9%	LLDVDNRVVLPIEAPIR	99.7%	36.1	25	31.8	0	2	0	1932.13	135	151
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	5	7	19	0.02%	18.9%	VVLPIEAPIR	99.7%	55.3	25	55.3	4	0	0	1106.69	142	151
Cytochrome c oxidase subunit 7A2, mitochondrial	COX7A2	CX7A2_HUMAN	9.4	99.8%	2	2	4	0.00%	27.7%	GGVADALLYR	99.7%	73.7	25	52.1	2	0	0	1034.56	47	56
Cytochrome c oxidase subunit 7A2, mitochondrial	COX7A2	CX7A2_HUMAN	9.4	99.8%	2	2	4	0.00%	27.7%	LFQEDDEIPLYLK	99.7%	67.5	25	54.9	2	0	0	1622.83	34	46
Cytochrome P450 20A1	CYP20A1	CP20A_HUMAN	52.4	99.8%	2	2	3	0.00%	5.4%	YGPVVSFWFGR	99.7%	62.4	25	62.4	2	0	0	1314.66	65	75
Cytochrome P450 20A1	CYP20A1	CP20A_HUMAN	52.4	99.8%	2	2	3	0.00%	5.4%	YQSGGGSVSENHMR	95.7%	28.5	25	28.5	1	0	0	1524.65	110	123
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	5	5	9	0.01%	6.4%	FVEFFGPGVAQLSIADR	99.7%	88	25	88	2	0	0	1852.96	277	293
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	5	5	9	0.01%	6.4%	GPFLLGIK	99.7%	44.5	25	40.2	2	0	0	844.53	786	793
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	5	5	9	0.01%	6.4%	NIEVPFKPAR	94.7%	27.6	25	15.9	1	0	0	1170.66	73	82
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	5	5	9	0.01%	6.4%	VLLEAAIR	99.7%	51.2	25	35.3	2	0	0	884.56	41	48
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	5	5	9	0.01%	6.4%	YQQAGLPLIVLAGK	99.7%	77.1	25	77.1	2	0	0	1470.87	759	772
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	AATSPALFNR	99.7%	62.8	25	46.2	2	0	0	1047.56	3079	3088
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	ALGEYLER	99.7%	51.9	25	45.7	2	0	0	950.49	1614	1621
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	ALGHQLGR	97.0%	30	25	16.5	1	0	0	851.48	1918	1925
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	ANEVEQMIR	99.7%	52.6	25	38.2	2	0	0	1089.54	3430	3438
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	ASVVTLPVYLNFTR	99.7%	51	25	49.2	3	0	0	1579.88	4602	4615
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	CYLTMTQALEAR	99.7%	71.2	25	70.2	2	0	0	1456.69	1888	1899
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	DLFQVAFNR	99.7%	68.7	25	63.3	5	0	0	1109.57	3862	3870
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	DSAIQQQVANLQMK	99.7%	82.2	25	75.4	2	0	0	1573.80	1229	1242
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	DYIPVDQEELRDYVK	98.5%	33.1	25	31	1	0	0	1881.92	2880	2894
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	EALELTDTGLLSGSEER	99.7%	98.1	25	88.2	2	0	0	1819.89	1302	1318
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	EGLMLDSHEELYK	99.7%	59.4	25	51.8	1	0	0	1563.74	3040	3052
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	ESPEVLLTLDILK	99.7%	79.3	25	68.3	2	0	0	1469.85	293	305
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	EWTDGLFTHVLR	99.7%	54.1	25	45.3	2	0	0	1473.75	2274	2285
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	EYQTQLIQR	99.7%	58.2	25	37.7	2	0	0	1178.62	603	611
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	FLSDPQVHTVLVER	99.7%	66.2	25	66.1	1	0	0	1639.88	68	81
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	FNYGFEYLGVQDK	99.7%	105	25	105	2	0	0	1579.74	1866	1878
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	FTQDTQPHYIYSPR	99.7%	65.5	25	65.5	1	0	0	1752.83	2784	2797
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	FYFVGDEDLLEIIGNSK	95.8%	28.6	25	28.6	1	0	0	1958.97	1629	1645
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	HLLPVETQR	99.5%	37.8	25	36	2	0	0	1092.62	1559	1567
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	IAFIMDESNVLDSGFLER	99.7%	68.9	25	68.9	2	0	0	2072.00	2990	3007
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	IFTIESTR	99.7%	65.6	25	48.3	2	0	0	966.53	717	724
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	IFVFEPPPGVK	99.7%	44.7	25	38.5	3	0	0	1229.69	4144	4154
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	IMFEVQDLK	99.7%	50.5	25	39.1	2	0	0	1138.58	2341	2349
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	INEWLTLVEK	99.7%	54.6	25	48.8	2	0	0	1244.69	1698	1707
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	INMLVIELK	99.7%	61.6	25	51.8	2	0	0	1088.64	1396	1404

Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	IQFVGACNPPTDPGR	99.7%	82.2	25	75.6	2	0	0	1628.79	2706	2720
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	IQGLTVEQAEAVVR	99.7%	84.7	25	78.1	3	0	0	1512.84	3924	3937
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	KIIDSVR	94.9%	27.8	25	3.64	1	0	0	830.51	2286	2292
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	KYEFGESDLR	99.7%	44.1	25	27.8	2	0	0	1243.60	4204	4213
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	LAETVFNFQEK	99.7%	51.4	25	51.4	1	0	0	1325.67	836	846
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	LEGVEGVAHIIDPK	99.7%	70.5	25	62	2	0	0	1476.81	2244	2257
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	LFLTMEINPK	99.7%	49.5	25	39.2	4	0	0	1205.66	4124	4133
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	LGGSPFGPAGTGK	99.7%	65.3	25	58.8	2	0	0	1145.60	1900	1912
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	LKQDGDSFR	99.7%	49.3	25	49.3	2	0	0	1065.53	682	690
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	LLAESVTEVEIFGK	99.7%	99.8	25	99.8	2	0	0	1534.84	1716	1729
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	LLNTFLER	99.7%	55.7	25	43.3	3	0	0	1005.57	4264	4271
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	LNTQEIFDDWAR	99.7%	51	25	48.8	1	0	0	1507.72	693	704
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	LQGEFQLR	99.7%	53	25	36.9	3	0	0	990.54	3734	3741
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	LRDQLGTAK	99.6%	39.9	25	26.1	2	0	0	1001.57	568	576
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	LSLSNAISTALPLTQLR	99.7%	44.6	25	44.4	1	0	0	1798.04	4575	4591
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	LVPLLLEDGGEAPAALEAALEEK	99.7%	32.7	25	32.7	0	1	0	2348.26	37	59
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	MLSAVSQQVQCIQEALR	99.7%	43.4	25	43.4	2	0	0	1960.99	1967	1983
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	MVVLSLPR	99.7%	48.1	25	46.3	2	0	0	914.55	991	998
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	NTISLLVAGLK	99.7%	66	25	46.3	2	0	0	1128.70	799	809
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	NVVHELR	97.0%	30	25	20.5	1	0	0	866.48	957	963
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	NYMSNPSYNYEIVNR	99.7%	92.1	25	84.9	2	0	0	1863.83	3370	3384
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	QLTAYMK	98.0%	31.8	25	23.6	1	0	0	854.44	657	663
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	QNLDALLNQLK	99.7%	61.1	25	48.3	2	0	0	1269.72	1361	1371
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	QYASYEFVQR	99.7%	49	25	45	2	0	0	1290.61	1379	1388
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	SLETCMYDHK	99.7%	43.8	25	43.8	2	0	0	1283.54	863	872
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	SLLQALNEVK	99.7%	70.5	25	62.8	4	0	0	1114.65	3748	3757
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	SMANPPAAVK	99.4%	36.9	25	36.9	1	0	0	985.51	3309	3318
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	SNSLAFIK	98.9%	34.5	25	21.4	2	0	0	879.49	113	120
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	SPLVMDVLNIQGVQR	99.7%	61	25	59.4	3	0	0	1684.91	1585	1599
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	SSLQSQCLNEVLK	99.7%	72.8	25	63.3	2	0	0	1505.76	3706	3718
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	SVLVSAGNVK	99.1%	35.5	25	26.1	2	0	0	973.57	2095	2104
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	SVLVSAGNVKR	99.7%	47.9	25	40.3	2	0	0	1129.67	2095	2105
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	TEYLSNADER	99.7%	57.8	25	57.8	3	0	0	1197.54	3550	3559
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	TFSEILNR	99.6%	39.7	25	31.2	1	0	0	979.52	873	880
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	TFSSIPVSR	99.7%	43.9	25	37	3	0	0	993.54	4160	4168
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	TLINELVK	99.7%	43.7	25	22.8	2	0	0	929.57	4450	4457
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	TLMAQSIYGGR	99.7%	55.6	25	46.6	1	0	0	1196.61	4245	4255
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	TMTLFSALR	99.7%	53.2	25	48.8	2	0	0	1055.56	2602	2610
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	TPNGVVLAPVQLGK	99.7%	55.8	25	55.8	2	0	0	1392.82	2644	2657
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	TPVIDADKPVSSQLR	99.7%	68.1	25	66.3	2	2	0	1625.89	122	136
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	TPVSITEHPK	99.7%	59.3	25	54.7	2	0	0	1108.60	1688	1697
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	TSAPITCELLNK	99.7%	65.6	25	55.7	2	0	0	1346.70	1993	2004
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	TSFLDDAFRK	99.7%	65.9	25	61	2	0	0	1199.61	3612	3621
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	TVENIKDPLFR	99.7%	42.4	25	33.5	1	0	0	1331.73	4401	4411
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	VAAPDVVVPTLDTVR	99.7%	42.7	25	42.7	2	0	0	1551.87	2562	2576
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	VDNEFDQR	99.7%	52.7	25	43.3	2	0	0	1022.45	4256	4263
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	VLLTTQGVDMISK	99.7%	95.3	25	89.3	5	0	0	1404.78	4330	4342
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	VMSQEIQEQLHK	99.6%	39	25	34.6	1	0	0	1469.74	3255	3266
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	VPQIEVETHK	99.7%	44.4	25	31.3	2	0	0	1179.64	2552	2561
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	VPVNLLR	98.5%	33.1	25	21.9	2	0	0	810.52	4134	4140
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	VTFVNFTVTR	99.7%	91.9	25	86.4	2	0	0	1183.65	3696	3705

Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	WTDENIDTVALK	99.7%	63.3	25	56.7	2	0	0	1404.70	2845	2856
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	78	83	158	0.16%	18.8%	YATLATVSR	99.7%	55.5	25	45.8	2	0	0	981.54	2350	2358
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	6	6	8	0.01%	16.4%	AGATSEGVLANFFNSLLSK	99.7%	89.1	25	85.3	1	0	0	1926.00	436	454
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	6	6	8	0.01%	16.4%	IGILHENFQTLK	96.6%	23.1	25	20.1	0	1	0	1412.79	333	344
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	6	6	8	0.01%	16.4%	IPAVVVEK	99.7%	44.2	25	35.1	2	0	0	854.53	311	318
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	6	6	8	0.01%	16.4%	QPPTAAGRPVDASPR	98.1%	25.3	25	23.9	0	2	0	1519.80	386	400
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	6	6	8	0.01%	16.4%	SGQKPVLDVHAELDR	99.3%	28.8	25	26.8	0	1	0	1663.88	487	501
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	6	6	8	0.01%	16.4%	SVSSNVASVSPIPAGSK	99.7%	67.9	25	56.2	1	0	0	1586.84	412	428
Cytoplasmic dynein 2 heavy chain 1	DYNC2H1	DYHC2_HUMAN	492.6	100.0%	5	5	5	0.01%	1.4%	FYEFSLSDLR	95.0%	27.9	25	26.2	1	0	0	1276.62	3888	3897
Cytoplasmic dynein 2 heavy chain 1	DYNC2H1	DYHC2_HUMAN	492.6	100.0%	5	5	5	0.01%	1.4%	NSLLTILDQLQR	99.3%	36.4	25	14.8	1	0	0	1413.81	1399	1410
Cytoplasmic dynein 2 heavy chain 1	DYNC2H1	DYHC2_HUMAN	492.6	100.0%	5	5	5	0.01%	1.4%	TVAGGGLETISNLK	99.7%	45.1	25	35	1	0	0	1359.75	999	1012
Cytoplasmic dynein 2 heavy chain 1	DYNC2H1	DYHC2_HUMAN	492.6	100.0%	5	5	5	0.01%	1.4%	VLSFPGGSLLLAGR	99.7%	49.8	25	49.8	1	0	0	1386.81	2643	2656
Cytoplasmic dynein 2 heavy chain 1	DYNC2H1	DYHC2_HUMAN	492.6	100.0%	5	5	5	0.01%	1.4%	VTTLTTHAGIR	99.7%	46.7	25	37.6	1	0	0	1169.66	1388	1398
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	22	25	38	0.04%	20.7%	AVGPSSTQLYMVR	99.7%	63.2	25	50.1	3	0	0	1424.72	551	563
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	22	25	38	0.04%	20.7%	DFVSEAYLITLGK	99.7%	62.4	25	0	3	0	0	1455.77	151	163
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	22	25	38	0.04%	20.7%	EANHNVSAPYGR	99.7%	58.2	25	56.7	2	1	0	1314.62	827	838
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	22	25	38	0.04%	20.7%	EFFLELTMGR	99.7%	60.2	25	54.6	1	0	0	1258.61	625	634
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	22	25	38	0.04%	20.7%	FALVEVIAMIK	99.7%	58	25	50.8	1	0	0	1233.73	449	459
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	22	25	38	0.04%	20.7%	FINMFAVLDELK	99.7%	45	25	40.9	1	0	0	1439.76	164	175
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	22	25	38	0.04%	20.7%	FQILNDEIITILDK	99.7%	58	25	42.9	2	0	0	1674.93	1211	1224
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	22	25	38	0.04%	20.7%	LCCGLSMFEVILTR	98.9%	34.5	25	34.5	1	0	0	1698.84	1086	1099
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	22	25	38	0.04%	20.7%	LGTPQQIAIAR	99.7%	79.1	25	68.7	2	0	0	1167.68	1066	1076
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	22	25	38	0.04%	20.7%	MESVFNHAIR	98.6%	33.4	25	26.3	1	0	0	1203.59	468	477
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	22	25	38	0.04%	20.7%	NAFVTGIAR	99.7%	47.9	25	37.6	2	0	0	948.53	50	58
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	22	25	38	0.04%	20.7%	NVIQSVLQAIR	99.7%	78.2	25	48.9	2	0	0	1240.74	505	515
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	22	25	38	0.04%	20.7%	QLQVVPLFGDMQIELAR	97.4%	30.6	25	30.6	1	0	0	1957.06	301	317
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	22	25	38	0.04%	20.7%	SFLDDPIWR	98.1%	31.9	25	24.7	2	0	0	1148.57	1102	1110
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	22	25	38	0.04%	20.7%	SGDGEGTPVEHVR	99.7%	43.5	25	37.9	2	0	0	1339.62	1228	1240
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	22	25	38	0.04%	20.7%	SLLQGTILQYVK	99.7%	60.6	25	60.6	2	0	0	1362.80	939	950
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	22	25	38	0.04%	20.7%	TMLESLIADK	99.5%	37.9	25	36.4	1	0	0	1136.59	564	573
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	22	25	38	0.04%	20.7%	TVEVLEPEVTK	99.7%	42.9	25	35.5	1	0	0	1243.68	111	121
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	22	25	38	0.04%	20.7%	TVLPFSQEFQR	97.1%	30.1	25	24	1	0	0	1351.70	867	877
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	22	25	38	0.04%	20.7%	YAPLHLVPLIER	98.9%	34.3	25	34.3	1	0	0	1420.83	1054	1065
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	22	25	38	0.04%	20.7%	YLTLDGFDAMFR	99.7%	45.3	25	45.3	3	0	0	1448.69	815	826
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	22	25	38	0.04%	20.7%	YSNSEVVTGSGR	99.7%	89	25	86.2	2	0	0	1255.59	366	377
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	99.8%	2	2	3	0.00%	13.5%	DFVSEAYLLTLGK	99.7%	62.4	25	0	3	0	0	1455.77	151	163
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	99.8%	2	2	3	0.00%	13.5%	EANHNVSAPYGR	99.7%	58.2	25	56.7	2	1	0	1314.62	851	862
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	99.8%	2	2	3	0.00%	13.5%	EFFLELTMGR	99.7%	60.2	25	54.6	1	0	0	1258.61	649	658
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	99.8%	2	2	3	0.00%	13.5%	FINMFAVLDELK	99.7%	45	25	40.9	1	0	0	1439.76	164	175
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	99.8%	2	2	3	0.00%	13.5%	LCCGLSMFEVILTR	98.9%	34.5	25	34.5	1	0	0	1698.84	1110	1123
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	99.8%	2	2	3	0.00%	13.5%	LGTPQQIAIAR	99.7%	79.1	25	68.7	2	0	0	1167.68	1090	1100
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	99.8%	2	2	3	0.00%	13.5%	NAFVTGIAR	99.7%	47.9	25	37.6	2	0	0	948.53	50	58
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	99.8%	2	2	3	0.00%	13.5%	QLQVVPLFGDMQIELAR	97.4%	30.6	25	30.6	1	0	0	1957.06	301	317
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	99.8%	2	2	3	0.00%	13.5%	SLLQGTILQYVK	99.7%	60.6	25	60.6	2	0	0	1362.80	963	974
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	99.8%	2	2	3	0.00%	13.5%	SVETDSSTVEHVR	99.7%	65.8	25	60.6	2	0	0	1445.69	1252	1264
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	99.8%	2	2	3	0.00%	13.5%	TMLESLIADK	99.5%	37.9	25	36.4	1	0	0	1136.59	588	597
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	99.8%	2	2	3	0.00%	13.5%	TVEVLEPEVTK	99.7%	42.9	25	35.5	1	0	0	1243.68	111	121
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	99.8%	2	2	3	0.00%	13.5%	YAPLHLVPLIER	98.9%	34.3	25	34.3	1	0	0	1420.83	1078	1089
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	99.8%	2	2	3	0.00%	13.5%	YSNSEVVTGSGLDSQK	99.7%	81	25	81	1	0	0	1670.79	366	381
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	7	7	10	0.01%	4.1%	EGLDEVAGIINDAK	99.7%	66.8	25	53.6	2	0	0	1443.73	879	892
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	7	7	10	0.01%	4.1%	FVTDSNAVVQLK	99.6%	39.6	25	25.8	1	0	0	1320.72	56	67

Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	7	7	10	0.01%	4.1%	HINDSAPEVR	95.2%	28	25	28	1	0	0	1137.56	447	456
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	7	7	10	0.01%	4.1%	LEAGDYADLVK	99.7%	52.5	25	42.7	1	0	0	1193.61	312	322
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	7	7	10	0.01%	4.1%	NLGIPIITVLGDSK	96.4%	29.2	25	29.2	2	0	0	1439.85	941	954
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	7	7	10	0.01%	4.1%	TALAATNPAVR	99.7%	66.4	25	57.8	2	0	0	1084.61	762	772
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	7	7	10	0.01%	4.1%	TTGEVVSGVVSK	99.6%	39.8	25	31.5	1	0	0	1162.63	85	96
Cytosolic carboxypeptidase 1	AGTPBP1	CBPC1_HUMAN	138.5	99.8%	2	2	4	0.00%	1.7%	IVGLLAQLEK	99.7%	47	25	42.5	2	0	0	1083.68	18	27
Cytosolic carboxypeptidase 1	AGTPBP1	CBPC1_HUMAN	138.5	99.8%	2	2	4	0.00%	1.7%	VALDTLAALLK	99.7%	41	25	40.2	2	0	0	1127.70	222	232
Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	NUBP2_HUMAN	28.8	100.0%	3	3	7	0.01%	13.3%	GWAPVFLDR	96.3%	29.1	25	15.1	1	0	0	1060.56	75	83
Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	NUBP2_HUMAN	28.8	100.0%	3	3	7	0.01%	13.3%	STISTELALALR	99.7%	67.6	25	58.8	2	0	0	1274.73	29	40
Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	NUBP2_HUMAN	28.8	100.0%	3	3	7	0.01%	13.3%	VGILDVDLCGPSIPR	99.7%	72.8	25	69.9	4	0	0	1610.86	46	60
Cytosolic non-specific dipeptidase	CNDP2	CNDP2_HUMAN	52.9	100.0%	4	4	5	0.01%	9.1%	LYDDIDFDIEEFAK	99.7%	49.8	25	49.8	1	0	0	1732.80	276	289
Cytosolic non-specific dipeptidase	CNDP2	CNDP2_HUMAN	52.9	100.0%	4	4	5	0.01%	9.1%	TGQEIPVNVR	98.2%	32.1	25	23.7	2	0	0	1112.61	150	159
Cytosolic non-specific dipeptidase	CNDP2	CNDP2_HUMAN	52.9	100.0%	4	4	5	0.01%	9.1%	TVFGVEPDLTR	99.7%	40.5	25	33.6	1	0	0	1233.65	403	413
Cytosolic non-specific dipeptidase	CNDP2	CNDP2_HUMAN	52.9	100.0%	4	4	5	0.01%	9.1%	YNYIEGTK	99.5%	37.9	25	34.1	1	0	0	987.48	454	461
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	21	28	107	0.11%	47.7%	AGTGVDNVDLEAATR	99.7%	111	25	101	7	0	0	1488.73	76	90
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	21	28	107	0.11%	47.7%	AGTGVDNVDLEAATRK	99.7%	107	25	107	2	1	0	1616.82	76	91
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	21	28	107	0.11%	47.7%	ALQSGQCAGAALDVFTEEPPRDR	99.7%	78.3	25	78.3	0	2	0	2488.19	248	270
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	21	28	107	0.11%	47.7%	ALVDHENVISCPHLGASTK	99.7%	59.3	25	59.3	0	2	0	2048.02	271	289
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	21	28	107	0.11%	47.7%	CGEEIAVQFVDMVK	99.7%	97.1	25	92.6	7	0	0	1624.77	295	308
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	21	28	107	0.11%	47.7%	DLPLLLFR	99.7%	55.8	25	48.4	13	0	0	986.60	462	469
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	21	28	107	0.11%	47.7%	EELIAELQDCEGLIVR	99.7%	84.3	25	84.3	2	0	0	1886.95	39	54
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	21	28	107	0.11%	47.7%	FMGTELNGK	99.7%	48.1	25	39.7	4	0	0	996.48	138	146
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	21	28	107	0.11%	47.7%	GGIVDEGALLR	99.7%	101	25	69.5	7	0	0	1099.61	237	247
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	21	28	107	0.11%	47.7%	GTIQVITQGTSLK	99.7%	92.2	25	88.1	8	0	0	1345.77	352	364
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	21	28	107	0.11%	47.7%	ILQDGGLQVVEK	99.7%	76.3	25	68.9	2	0	0	1298.73	22	33
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	21	28	107	0.11%	47.7%	MQSFGMK	98.5%	33	25	23.9	1	0	0	828.37	164	170
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	21	28	107	0.11%	47.7%	NAGNCLSPAVIVGLLK	99.7%	72.8	25	71.4	6	0	0	1625.90	365	380
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	21	28	107	0.11%	47.7%	QADVNLVNAK	99.7%	60.8	25	56.4	2	0	0	1071.58	385	394
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	21	28	107	0.11%	47.7%	QHVTEAFQFHF	99.6%	39.6	25	30	1	0	0	1390.65	523	533
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	21	28	107	0.11%	47.7%	QIPQATASMK	99.7%	48.6	25	43	4	0	0	1090.56	120	129
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	21	28	107	0.11%	47.7%	QNLSKEELIAELQDCEGLIVR	99.0%	27.6	25	26.8	0	1	0	2457.27	34	54
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	21	28	107	0.11%	47.7%	TLGILGLGR	99.7%	66.3	25	53.3	10	0	0	899.57	147	155
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	21	28	107	0.11%	47.7%	TQTSDPAMLPTMIGLLAEAGVR	99.7%	112	25	45.3	9	4	0	2288.16	470	491
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	21	28	107	0.11%	47.7%	VLISDSLDPCCR	99.7%	71	25	71	2	0	0	1434.67	9	20
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	21	28	107	0.11%	47.7%	VTADVINAAEK	99.7%	92	25	73.5	10	0	0	1130.61	59	69
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	2	2	3	0.00%	4.3%	ESVLTATSILNNPIVK	99.7%	88.2	25	85.7	2	0	0	1698.96	444	459
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	2	2	3	0.00%	4.3%	NSLDSFGGR	99.7%	45.8	25	37.1	1	0	0	952.45	117	125
DDB1- and CUL4-associated factor 7	DCAF7	DCAF7_HUMAN	38.9	100.0%	5	5	8	0.01%	19.3%	DMFASVGADGSVR	99.7%	71.3	25	69	1	0	0	1311.60	190	202
DDB1- and CUL4-associated factor 7	DCAF7	DCAF7_HUMAN	38.9	100.0%	5	5	8	0.01%	19.3%	GVYPDLLATSGDYLR	99.7%	103	25	103	2	0	0	1639.83	82	96
DDB1- and CUL4-associated factor 7	DCAF7	DCAF7_HUMAN	38.9	100.0%	5	5	8	0.01%	19.3%	LALGSFVEEYNNK	99.7%	80.8	25	80.8	2	0	0	1483.74	34	46
DDB1- and CUL4-associated factor 7	DCAF7	DCAF7_HUMAN	38.9	100.0%	5	5	8	0.01%	19.3%	VNLVSGHVK	98.7%	33.8	25	21.9	2	0	0	952.56	159	167
DDB1- and CUL4-associated factor 7	DCAF7	DCAF7_HUMAN	38.9	100.0%	5	5	8	0.01%	19.3%	VQLVGLDEESSEFICR	99.7%	84.1	25	83.1	1	0	0	1880.91	47	62
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	6	6	10	0.01%	3.8%	ESFCITSFLCSTK	99.6%	39.9	25	39.9	2	0	0	1579.71	565	577
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	6	6	10	0.01%	3.8%	ESGVSLIATVTR	99.7%	65.4	25	49.3	2	0	0	1232.68	1146	1157
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	6	6	10	0.01%	3.8%	ILSNVFCLIK	95.9%	28.7	25	24.5	1	0	0	1206.69	854	863
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	6	6	10	0.01%	3.8%	NSAPASVSPDGTR	95.6%	28.4	25	28.3	1	0	0	1258.60	1613	1625
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	6	6	10	0.01%	3.8%	TSLYLVQSLPGISR	99.4%	37.3	25	37.3	2	0	0	1533.86	1441	1454
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	6	6	10	0.01%	3.8%	TVESQLYTNPDSR	99.7%	60.4	25	48.4	2	0	0	1509.72	815	827
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	8	11	25	0.03%	31.7%	GTIMDTTVDVDKR	97.2%	30.3	25	30.3	1	0	0	1450.72	149	161
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	8	11	25	0.03%	31.7%	LLQWVR	98.7%	33.8	25	18.8	1	0	0	814.49	40	45
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	8	11	25	0.03%	31.7%	NAVVVITGATSGLGK	99.7%	101	25	90.5	4	0	0	1386.80	52	66

Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	8	11	25	0.03%	31.7%	QGHIVAISSIQGK	99.7%	69.3	25	67.2	1	0	0	1337.75	186	198
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	8	11	25	0.03%	31.7%	SPVEVAQDVLAAVGKK	99.7%	54.7	25	54.7	2	0	0	1610.91	268	283
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	8	11	25	0.03%	31.7%	TLAPGLFFSLMASR	99.7%	80	25	74.4	4	0	0	1510.81	302	315
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	8	11	25	0.03%	31.7%	VMETNYFGPVALTK	99.7%	102	25	75	6	0	0	1569.80	162	175
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	8	11	25	0.03%	31.7%	YGVMDTTTAQGR	99.7%	83.8	25	83	6	0	0	1299.60	256	267
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	4	4	7	0.01%	9.8%	NAAGNFYINDK	98.2%	32.3	25	32.3	1	0	0	1226.58	499	509
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	4	4	7	0.01%	9.8%	SADVESVVSGTLR	99.7%	90.9	25	81.2	2	0	0	1319.68	326	338
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	4	4	7	0.01%	9.8%	STGSIVGQQPFGGAR	99.7%	61.2	25	54.8	2	0	0	1461.74	510	524
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	4	4	7	0.01%	9.8%	VANEPVLAFTQGSPER	99.7%	78.9	25	78.9	2	0	0	1714.88	32	47
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	CEYPAACNALETLLIHR	99.7%	46.3	25	46.3	0	2	0	2030.98	606	622
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	DLEEAEGR	99.7%	44.4	25	32.8	2	0	0	918.42	410	417
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	EAVQLVNTR	99.7%	52.5	25	43.2	2	0	0	1029.57	531	539
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	EAVQLVNTREEVEDLCR	99.7%	43.7	25	41.3	0	2	0	2060.01	531	547
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	EEVEDLCR	95.5%	28.3	25	28	1	0	0	1049.46	540	547
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	EMAIPVLEAR	99.7%	52.7	25	44.9	2	0	0	1144.60	150	159
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	EMMLVTSGAVAFGK	99.7%	66.6	25	10.1	4	0	0	1456.72	111	124
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	FASYLTFSPSEVK	99.7%	93.3	25	92.2	5	0	0	1475.74	650	662
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	FGLGAEVGISTSR	99.7%	85.4	25	78.7	1	0	0	1293.68	733	745
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	GPVGLEGLLTTK	99.7%	75.8	25	75.8	2	0	0	1184.69	750	761
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	LAAPLLKR	99.7%	42.5	25	39.3	2	0	0	881.59	418	425
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	LASIVEQVSVLQNQGR	99.7%	107	25	94.8	2	0	0	1740.96	95	110
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	LGSAVVTR	99.7%	79.8	25	58	4	0	0	802.48	77	84
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	LIDIFYPGDQQSVTFGTK	99.7%	86.6	25	82.1	5	0	0	2029.03	283	300
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	LNSLAIGLR	99.7%	77.8	25	62.5	4	0	0	956.59	433	441
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	LRHEILLSQSVR	99.7%	35.7	25	35.7	0	2	0	1450.85	127	138
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	MIDLIIPR	99.7%	57.9	25	46.3	6	0	0	970.58	551	558
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	MLATLEPEQR	99.7%	69.5	25	53.7	4	0	0	1203.60	376	385
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	NLNGTLHELLR	99.7%	56.1	25	48.8	2	0	0	1279.71	202	212
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	QALHSGQNQLK	99.7%	34.7	25	31.2	0	1	0	1223.65	139	149
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	QIAASSQDSVGR	99.7%	77.7	25	70.3	2	0	0	1218.61	442	453
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	SWSNIPFITVPLSR	99.7%	55.2	25	48.9	2	0	0	1616.88	42	55
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	TPLFDQIIDMLR	99.7%	74.4	25	70.8	4	0	0	1477.77	627	638
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	VGMGGMEAK	99.7%	50.5	25	43	2	0	0	879.41	303	311
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	VGTFFSEVKPAGPTVEQQGEMAR	99.7%	88	25	88	0	4	0	2465.21	349	371
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	VSGHVITDIVEGK	99.7%	74.2	25	66	2	2	0	1353.74	335	347
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	VSGHVITDIVEGKK	99.7%	52.4	25	52.4	0	2	0	1481.83	335	348
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	28	33	77	0.08%	39.0%	YLHENLPIPQR	99.5%	38.4	25	37.8	2	0	0	1379.74	782	792
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	14	15	24	0.02%	25.1%	EWNDSTSVQNPTR	99.7%	56.9	25	42.3	2	0	0	1533.69	597	609
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	14	15	24	0.02%	25.1%	FAEQLIR	99.7%	47.7	25	21.6	1	0	0	876.49	545	551
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	14	15	24	0.02%	25.1%	FENLGVSSLGER	99.7%	58.1	25	46	1	0	0	1307.66	86	97
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	14	15	24	0.02%	25.1%	FIPLARPEVK	98.7%	33.8	25	23	2	0	0	1169.70	221	230
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	14	15	24	0.02%	25.1%	GGFEEPVLLK	99.7%	45.8	25	28.6	2	0	0	1088.60	57	66
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	14	15	24	0.02%	25.1%	IIDTPQFQR	99.7%	63.6	25	53	2	0	0	1117.60	135	143
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	14	15	24	0.02%	25.1%	ISTAIDDMEAYTK	99.7%	90.2	25	82.8	2	0	0	1457.68	409	421
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	14	15	24	0.02%	25.1%	LLSYIQR	97.7%	31.2	25	16.6	1	0	0	892.53	100	106
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	14	15	24	0.02%	25.1%	NQVSQLLPEK	98.5%	32.9	25	10.2	1	0	0	1155.64	535	544
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	14	15	24	0.02%	25.1%	QLGGGYYVFPGASHNR	99.7%	34.8	25	34.8	0	1	0	1722.83	149	164
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	14	15	24	0.02%	25.1%	SFLYEIVSNKR	99.7%	61.6	25	61.6	2	0	0	1355.73	295	305
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	14	15	24	0.02%	25.1%	TWGPEQVCSFLR	99.7%	47.5	25	39.4	2	0	0	1479.71	44	55
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	14	15	24	0.02%	25.1%	VGNIIDTMITDAFLK	99.7%	96	25	96	3	0	0	1650.88	378	392
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	14	15	24	0.02%	25.1%	YVGETQPTGQIK	99.7%	58.7	25	50	2	0	0	1320.68	456	467

Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial	DUT	DUT_HUMAN	26.6	99.8%	2	2	4	0.00%	7.1%	IAQLICER	99.7%	46.8	25	35.6	2	0	0	1002.54	217	224
Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial	DUT	DUT_HUMAN	26.6	99.8%	2	2	4	0.00%	7.1%	LSEHATAPTR	99.7%	41.5	25	30.8	2	0	0	1082.56	119	128
Dephospho-CoA kinase domain-containing protein	DCAKD	DCAKD_HUMAN	26.6	100.0%	5	5	8	0.01%	19.9%	HTVVVYCDR	97.0%	30.1	25	23.5	1	0	0	1148.55	129	137
Dephospho-CoA kinase domain-containing protein	DCAKD	DCAKD_HUMAN	26.6	100.0%	5	5	8	0.01%	19.9%	INAQLPLTDK	99.7%	54.7	25	38.7	2	0	0	1112.63	159	168
Dephospho-CoA kinase domain-containing protein	DCAKD	DCAKD_HUMAN	26.6	100.0%	5	5	8	0.01%	19.9%	MFLVGLTGGIASGK	99.7%	111	25	111	2	0	0	1350.75	1	14
Dephospho-CoA kinase domain-containing protein	DCAKD	DCAKD_HUMAN	26.6	100.0%	5	5	8	0.01%	19.9%	VLGDLIFNQPDR	99.7%	48.8	25	36.6	1	0	0	1386.74	68	79
Dephospho-CoA kinase domain-containing protein	DCAKD	DCAKD_HUMAN	26.6	100.0%	5	5	8	0.01%	19.9%	VLGDLIFNQPDRR	99.3%	28.8	25	20.8	0	2	0	1542.84	68	80
Dermcidin	DCD	DCD_HUMAN	11.3	100.0%	3	4	53	0.05%	22.7%	DAVEDLESVGK	99.7%	75.4	25	68.6	9	0	0	1161.56	86	96
Dermcidin	DCD	DCD_HUMAN	11.3	100.0%	3	4	53	0.05%	22.7%	ENAGEDPGLAR	99.7%	89	25	83.9	35	0	0	1128.53	43	53
Dermcidin	DCD	DCD_HUMAN	11.3	100.0%	3	4	53	0.05%	22.7%	LGKDAVEDLESVGK	99.7%	84.2	25	79	7	2	0	1459.76	83	96
Desmoglein-1	DSG1	DSG1_HUMAN	113.7	100.0%	6	6	10	0.01%	7.1%	EMQDLGGGER	99.3%	36.6	25	30.9	2	0	0	1091.48	641	650
Desmoglein-1	DSG1	DSG1_HUMAN	113.7	100.0%	6	6	10	0.01%	7.1%	ESSNVVVTER	99.7%	55.1	25	50.6	2	0	0	1119.56	916	925
Desmoglein-1	DSG1	DSG1_HUMAN	113.7	100.0%	6	6	10	0.01%	7.1%	MTGFELTEGVK	98.7%	33.7	25	30.2	1	0	0	1211.60	651	661
Desmoglein-1	DSG1	DSG1_HUMAN	113.7	100.0%	6	6	10	0.01%	7.1%	QEPSDSPMFIINR	96.6%	29.5	25	28.4	1	0	0	1549.73	201	213
Desmoglein-1	DSG1	DSG1_HUMAN	113.7	100.0%	6	6	10	0.01%	7.1%	YQGTILSIDDNLQR	97.2%	30.2	25	30.2	2	0	0	1635.83	460	473
Desmoglein-1	DSG1	DSG1_HUMAN	113.7	100.0%	6	6	10	0.01%	7.1%	YVMGNNPADLLAVDSR	99.7%	63	25	63	2	0	0	1750.84	423	438
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	19	19	48	0.05%	7.2%	AELIVQPELK	99.7%	53.2	25	34.4	7	0	0	1139.67	85	94
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	19	19	48	0.05%	7.2%	ALLQAILQTEDMLK	99.7%	87.9	25	87.9	2	0	0	1586.88	772	785
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	19	19	48	0.05%	7.2%	FGDSNTVMR	99.0%	35	25	29.1	1	0	0	1026.47	917	925
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	19	19	48	0.05%	7.2%	GFFDPNTEENLTYLQLK	99.7%	71.7	25	69.8	2	0	0	2028.99	2414	2430
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	19	19	48	0.05%	7.2%	GIHNSIGDYR	98.5%	33.1	25	33.1	1	0	0	1131.55	223	232
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	19	19	48	0.05%	7.2%	GLVGIEFKEK	99.2%	35.6	25	35.6	2	0	0	1119.64	2319	2328
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	19	19	48	0.05%	7.2%	IEVLEEELR	99.7%	49.4	25	38.2	5	0	0	1129.61	1034	1042
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	19	19	48	0.05%	7.2%	IQSQFTDAQK	99.7%	57.7	25	47.5	3	0	0	1165.58	608	617
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	19	19	48	0.05%	7.2%	ITNLTQQLEQASIVK	99.7%	41	25	41	1	0	0	1685.94	1612	1626
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	19	19	48	0.05%	7.2%	LASLEELKR	99.7%	43.3	25	33.4	2	0	0	1058.62	1076	1084
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	19	19	48	0.05%	7.2%	LLEAQIATGGIIDPK	99.7%	82.1	25	76.7	5	0	0	1538.88	2367	2381
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	19	19	48	0.05%	7.2%	LNDSILQATEQR	99.7%	57.3	25	51.1	1	0	0	1387.72	1256	1267
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	19	19	48	0.05%	7.2%	NQCTQVVQER	99.6%	39	25	32.6	4	0	0	1261.60	1803	1812
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	19	19	48	0.05%	7.2%	QLLQEQESVK	99.0%	34.8	25	26.2	1	0	0	1201.64	1667	1676
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	19	19	48	0.05%	7.2%	QLQNIIQATSR	99.7%	79.1	25	79.1	4	0	0	1271.71	271	281
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	19	19	48	0.05%	7.2%	QVQNLVNK	95.7%	28.5	25	19.6	1	0	0	942.54	434	441
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	19	19	48	0.05%	7.2%	RVEEDIQQQK	99.2%	35.7	25	27.5	1	0	0	1272.65	1425	1434
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	19	19	48	0.05%	7.2%	TVSVSEAIKK	99.0%	35.1	25	31.5	1	0	0	1061.62	2104	2113
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	19	19	48	0.05%	7.2%	YGDGIQLTR	99.7%	69.3	25	60.5	4	0	0	1022.53	95	103
Developmentally-regulated GTP-binding protein 2	DRG2	DRG2_HUMAN	40.7	99.8%	2	2	3	0.00%	6.6%	TADVIIMMLDATK	99.7%	46.5	25	45.3	1	0	0	1421.74	139	151
Developmentally-regulated GTP-binding protein 2	DRG2	DRG2_HUMAN	40.7	99.8%	2	2	3	0.00%	6.6%	VALIGFPSVGK	99.7%	41.4	25	36.6	2	0	0	1087.65	65	75
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	6	7	12	0.01%	40.1%	EAMNHPGHLK	95.4%	28.2	25	13.5	1	0	0	1133.55	124	133
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	6	7	12	0.01%	40.1%	INLVLSR	99.7%	47.8	25	30	2	0	0	814.51	72	78
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	6	7	12	0.01%	40.1%	LLPEYPGVLSDVQEEK	99.7%	81.1	25	78.9	2	0	0	1815.94	159	174
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	6	7	12	0.01%	40.1%	LTEQPELANK	99.5%	38	25	33	2	0	0	1142.61	100	109
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	6	7	12	0.01%	40.1%	VDMVWIVGGSSVYK	99.7%	49.1	25	44.2	2	0	0	1539.79	110	123
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	6	7	12	0.01%	40.1%	VGSLNCIVAVSQNMGIGK	99.7%	69.9	25	57.8	2	1	0	1862.95	2	19
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	20	25	47	0.05%	55.8%	ADGGTQVIDTK	99.7%	69.1	25	54.9	2	0	0	1104.55	167	177
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	20	25	47	0.05%	55.8%	AEVITCDVLLVCIGR	99.7%	55	25	54.8	2	0	0	1717.90	301	315
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	20	25	47	0.05%	55.8%	ALLNNSHYYHMAHGK	99.7%	41.1	25	41.1	0	2	0	1755.84	90	104
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	20	25	47	0.05%	55.8%	ALTGGIAHLFK	99.7%	65	25	53.2	2	0	0	1127.66	133	143
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	20	25	47	0.05%	55.8%	EANLAASFGK	99.7%	61.7	25	55.7	2	0	0	1007.52	496	505
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	20	25	47	0.05%	55.8%	FPFAANSR	99.6%	39.6	25	26	2	0	0	909.46	421	428
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	20	25	47	0.05%	55.8%	GIEMSEVR	99.7%	45.6	25	32	3	0	0	920.45	110	117
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	20	25	47	0.05%	55.8%	GRIPVNTR	96.8%	29.8	25	18.7	2	0	0	912.54	335	342

Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	20	25	47	0.05%	55.8%	IPNIYAIGDVVAGPMLAHK	99.7%	97.6	25	97.6	2	4	0	1979.08	347	365
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	20	25	47	0.05%	55.8%	LGADVTAVEFLGHVGGVGIDMEISK	99.7%	90.8	25	90.8	0	2	0	2530.29	235	259
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	20	25	47	0.05%	55.8%	LNLDKMMEQK	99.7%	43.6	25	41.4	2	0	0	1281.62	118	127
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	20	25	47	0.05%	55.8%	MVVIGAGVIGVELGSVWQR	99.7%	76.6	25	76.6	1	0	0	1970.09	216	234
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	20	25	47	0.05%	55.8%	NETLGGTCLNVGCIPSK	99.7%	119	25	118	2	0	0	1819.87	73	89
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	20	25	47	0.05%	55.8%	NLGLEELGIELDPR	99.7%	83.7	25	82	3	0	0	1567.83	321	334
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	20	25	47	0.05%	55.8%	SDGKIDVSIEAASGGK	99.7%	32.4	25	29.4	0	1	0	1533.78	285	300
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	20	25	47	0.05%	55.8%	SEEQLKEEGIEYK	99.7%	69.7	25	69.7	2	2	0	1581.76	405	417
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	20	25	47	0.05%	55.8%	TNADTDGMVK	99.7%	62.8	25	47.1	2	0	0	1051.47	431	440
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	20	25	47	0.05%	55.8%	VCHAHPTLSEAFR	99.7%	52	25	46.9	1	2	0	1524.74	483	495
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	20	25	47	0.05%	55.8%	VLGAHILGPGAGEMVNEAALALEYGASCEDIAR	99.7%	74.5	25	70.1	0	2	0	3354.65	450	482
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	20	25	47	0.05%	55.8%	VVHVNGYGK	99.7%	47.8	25	46.6	2	0	0	972.53	147	155
Dihydrolipoyl lysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	8	9	14	0.01%	15.8%	DIDSFVPSK	98.1%	32	25	28	1	0	0	1007.50	388	396
Dihydrolipoyl lysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	8	9	14	0.01%	15.8%	DVPLGTPLCIIVEK	99.7%	70.1	25	63.7	2	0	0	1553.86	283	296
Dihydrolipoyl lysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	8	9	14	0.01%	15.8%	GVETIANDVVSLATK	99.7%	73.1	25	69.5	2	0	0	1516.82	533	547
Dihydrolipoyl lysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	8	9	14	0.01%	15.8%	ILVAEGTR	95.2%	28.1	25	15.5	1	0	0	858.50	148	155
Dihydrolipoyl lysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	8	9	14	0.01%	15.8%	VPEANSSWMDTVIR	99.7%	63.3	25	63.3	1	0	0	1604.77	491	504
Dihydrolipoyl lysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	8	9	14	0.01%	15.8%	VPLPSLSPTMQAGTIAR	99.7%	92.6	25	92.6	4	0	0	1738.95	94	110
Dihydrolipoyl lysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	8	9	14	0.01%	15.8%	VVDGAVGAQWLAEFR	99.7%	51.7	25	51.7	1	0	0	1617.84	622	636
Dihydrolipoyl lysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	8	9	14	0.01%	15.8%	YLEKPITMLL	99.2%	35.8	25	32	2	0	0	1236.69	638	647
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	8	9	14	0.01%	16.3%	GMYDGPVYEVPATPK	99.7%	60	25	60	3	0	0	1639.77	497	511
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	8	9	14	0.01%	16.3%	INCPVYITK	99.6%	40	25	28.4	1	0	0	1107.59	246	254
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	8	9	14	0.01%	16.3%	IVFEDGNINVNK	99.7%	59.5	25	58.7	2	0	0	1361.71	452	463
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	8	9	14	0.01%	16.3%	MDENQFVAVTSTNAAK	99.7%	84.8	25	74.1	2	0	0	1725.81	375	390
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	8	9	14	0.01%	16.3%	QIGENLIVPGGVK	99.7%	45.5	25	44.2	1	0	0	1323.76	44	56
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	8	9	14	0.01%	16.3%	SAADIIALAR	99.7%	89.9	25	70.5	2	0	0	1000.58	259	268
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	8	9	14	0.01%	16.3%	SIPHITSDR	95.1%	28	25	23.6	1	0	0	1025.54	8	16
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	8	9	14	0.01%	16.3%	VFGLQGVSR	99.7%	58.3	25	46.6	2	0	0	962.54	488	496
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	6	6	10	0.01%	11.4%	GAPAVVISQGR	99.7%	77.3	25	73.8	2	0	0	1054.60	441	451
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	6	6	10	0.01%	11.4%	IFNFYPR	97.1%	30.2	25	9.22	1	0	0	956.50	391	397
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	6	6	10	0.01%	11.4%	LAEIHGVPR	99.7%	60.1	25	49.6	2	0	0	991.57	488	496
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	6	6	10	0.01%	11.4%	MDENEFVAVTSTNAAK	99.7%	76.8	25	76.8	1	0	0	1726.80	375	390
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	6	6	10	0.01%	11.4%	MFVTPGAGR	97.0%	30	25	30	2	0	0	935.48	459	467
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	6	6	10	0.01%	11.4%	QIGENLIVPGGIK	99.7%	43	25	43	2	0	0	1337.78	44	56
Dihydropyrimidinase-related protein 5	DPYSL5	DPYL5_HUMAN	61.4	100.0%	3	3	5	0.01%	7.3%	EMGTPLADTPTRPVTR	95.7%	22.3	25	18	0	1	0	1757.89	506	521
Dihydropyrimidinase-related protein 5	DPYSL5	DPYL5_HUMAN	61.4	100.0%	3	3	5	0.01%	7.3%	FVAVTSSNAAK	99.7%	52.7	25	52.7	2	0	0	1094.58	373	383
Dihydropyrimidinase-related protein 5	DPYSL5	DPYL5_HUMAN	61.4	100.0%	3	3	5	0.01%	7.3%	VHAENGELVAEGAK	99.7%	66.8	25	66.8	2	0	0	1423.72	190	203
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	8	10	15	0.02%	24.9%	DGPFVYGR	99.3%	36.4	25	32.2	1	0	0	910.44	162	169
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	8	10	15	0.02%	24.9%	FIPGLQMLSDAAPGK	99.7%	65.9	25	64.3	4	0	0	1544.81	90	104
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	8	10	15	0.02%	24.9%	LLELADIDPTLRPR	99.7%	40.3	25	33.5	1	1	0	1621.93	280	293
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	8	10	15	0.02%	24.9%	LPPLPTIR	98.0%	31.8	25	31.8	1	0	0	906.58	12	19
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	8	10	15	0.02%	24.9%	LSVMAQYLCNVR	99.7%	70.7	25	65.2	2	0	0	1453.73	196	207
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	8	10	15	0.02%	24.9%	QLSQNFLLDLR	99.7%	58.2	25	31.9	2	0	0	1346.74	32	42
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	8	10	15	0.02%	24.9%	TQMTLTFQK	99.7%	53.6	25	47.8	1	0	0	1097.57	170	178
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	8	10	15	0.02%	24.9%	VVQNVFQFR	99.7%	63.2	25	55.9	2	0	0	1136.62	248	256
Dimethyladenosine transferase 2, mitochondrial	TFB2M	TFB2M_HUMAN	45.4	100.0%	3	3	5	0.01%	8.6%	LYLIQMIPR	99.7%	46.7	25	35.9	2	0	0	1146.67	296	304
Dimethyladenosine transferase 2, mitochondrial	TFB2M	TFB2M_HUMAN	45.4	100.0%	3	3	5	0.01%	8.6%	NLGIEAVPWTADIPLK	99.7%	55.4	25	54	2	0	0	1736.96	175	190
Dimethyladenosine transferase 2, mitochondrial	TFB2M	TFB2M_HUMAN	45.4	100.0%	3	3	5	0.01%	8.6%	SATVIDHLR	99.7%	41.5	25	29.3	1	0	0	1011.56	332	340
Diphosphoinositol polyphosphate phosphohydrolase 3-beta	NUDT11	NUD11_HUMAN	18.6	99.8%	2	2	4	0.00%	12.2%	EVYEEAGVK	99.7%	43.3	25	26.5	2	0	0	1023.50	65	73
Diphosphoinositol polyphosphate phosphohydrolase 3-beta	NUDT11	NUD11_HUMAN	18.6	99.8%	2	2	4	0.00%	12.2%	LLGVFEQNQDR	96.9%	29.8	25	29.8	2	0	0	1318.68	79	89
DNA ligase 3	LIG3	DNLI3_HUMAN	112.9	100.0%	4	4	6	0.01%	4.2%	GASFVTSTNPR	98.3%	32.4	25	25.5	1	0	0	1136.57	214	224

DNA ligase 3	LIG3	DNLI3_HUMAN	112.9	100.0%	4	4	6	0.01%	4.2%	TQIIQDFLR	97.3%	30.5	25	23.3	1	0	0	1133.63	283	291
DNA ligase 3	LIG3	DNLI3_HUMAN	112.9	100.0%	4	4	6	0.01%	4.2%	VIQEGLEGLVLK	99.7%	103	25	95.7	2	0	0	1297.77	649	660
DNA ligase 3	LIG3	DNLI3_HUMAN	112.9	100.0%	4	4	6	0.01%	4.2%	VLLDIFTGVR	99.7%	76.2	25	76.2	2	0	0	1132.67	933	942
DNA methyltransferase 1-associated protein 1	DMAP1	DMAP1_HUMAN	53.0	100.0%	4	4	5	0.01%	10.9%	AAEEGKDYPFAR	99.1%	35.5	25	35.5	1	0	0	1353.64	117	128
DNA methyltransferase 1-associated protein 1	DMAP1	DMAP1_HUMAN	53.0	100.0%	4	4	5	0.01%	10.9%	AETDHLFDLSR	99.7%	49.5	25	46.1	1	0	0	1303.63	155	165
DNA methyltransferase 1-associated protein 1	DMAP1	DMAP1_HUMAN	53.0	100.0%	4	4	5	0.01%	10.9%	DTIIDVVGAPLTPNSR	99.7%	45.8	25	43.2	1	0	0	1667.90	434	449
DNA methyltransferase 1-associated protein 1	DMAP1	DMAP1_HUMAN	53.0	100.0%	4	4	5	0.01%	10.9%	LITAADTTAEQR	99.7%	71	25	55.8	2	0	0	1289.67	271	282
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	13.8%	DSLIIIDELGR	99.7%	76	25	66.1	2	0	0	1243.69	742	752
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	13.8%	LDSSAQFGYYFR	99.7%	85.3	25	79.2	2	0	0	1453.67	513	524
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	13.8%	LLLAVFVTPLTDLR	99.7%	70.7	25	70.7	2	0	0	1570.96	431	444
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	13.8%	LNLVEAFVEDAELR	99.7%	106	25	102	1	0	0	1617.85	360	373
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	13.8%	LTSLNEEYTK	99.7%	58.5	25	58.5	2	0	0	1197.60	556	565
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	13.8%	LYQGINQLPNVIQALEK	99.7%	62.8	25	62.8	2	0	0	1941.08	407	423
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	13.8%	NLQSVVLSK	99.7%	53.8	25	31.9	2	0	0	987.58	74	82
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	13.8%	NNSFVNEIISR	99.7%	59.1	25	43.3	2	0	0	1292.66	919	929
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	13.8%	QAANLQDCYR	99.2%	36.1	25	27.2	2	0	0	1238.56	397	406
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	13.8%	QTLQEDLLR	99.7%	43.6	25	31.9	2	0	0	1115.61	374	382
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	13.8%	QVGVGYVDSIQR	99.7%	43.5	25	33.6	1	0	0	1320.69	160	171
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	14	15	26	0.03%	11.9%	AYGVCFVDTSLGK	99.7%	63.3	25	63.1	2	0	0	1416.68	555	567
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	14	15	26	0.03%	11.9%	EVCLASER	96.8%	29.7	25	26.7	1	0	0	963.46	1335	1342
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	14	15	26	0.03%	11.9%	GTATFDGTAIANAVVK	99.7%	85.2	25	71.6	2	0	0	1535.81	1218	1233
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	14	15	26	0.03%	11.9%	GTQTYSVLEGDPSENYSK	99.7%	48.7	25	48.7	2	0	0	1974.89	520	537
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	14	15	26	0.03%	11.9%	IHNVGSPLK	94.6%	27.6	25	22.4	1	0	0	964.56	825	833
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	14	15	26	0.03%	11.9%	IIDFLSALEGFK	99.7%	68.9	25	61.1	3	0	0	1352.75	855	866
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	14	15	26	0.03%	11.9%	IIGIMEEVADGFK	99.7%	65.3	25	59.3	3	0	0	1421.73	871	883
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	14	15	26	0.03%	11.9%	LANLPEEVIQK	99.7%	48.5	25	40.2	2	0	0	1253.71	1305	1315
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	14	15	26	0.03%	11.9%	LSDGIGVMLPQVLK	99.7%	63.3	25	43.6	3	0	0	1469.84	647	660
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	14	15	26	0.03%	11.9%	QVISLQTK	97.8%	31.3	25	22.9	1	0	0	916.55	889	896
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	14	15	26	0.03%	11.9%	STVDAEAVHK	99.5%	38.7	25	28.2	1	0	0	1056.53	1343	1352
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	14	15	26	0.03%	11.9%	TIVYWGIGR	97.0%	30	25	24.7	1	0	0	1064.59	966	974
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	14	15	26	0.03%	11.9%	TLLEEEYFR	99.7%	44.1	25	30.7	2	0	0	1199.59	636	644
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	14	15	26	0.03%	11.9%	YQLEIPENFTTR	99.7%	45.2	25	35.2	2	0	0	1510.75	977	988
DNA polymerase alpha catalytic subunit	POLA1	DPOLA_HUMAN	165.9	100.0%	2	2	3	0.00%	1.9%	AAYAGGLVLDPK	99.7%	43.8	25	33.2	1	0	0	1174.65	837	848
DNA polymerase alpha catalytic subunit	POLA1	DPOLA_HUMAN	165.9	100.0%	2	2	3	0.00%	1.9%	DTGNFVIGQILSDQSR	99.7%	44.8	25	39.2	2	0	0	1749.88	1090	1105
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	20	23	42	0.04%	22.2%	DLEDQEQLLR	99.7%	65.1	25	49	1	0	0	1258.63	1088	1097
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	20	23	42	0.04%	22.2%	DNCPLVANLVTASLR	99.7%	56.4	25	56.4	2	0	0	1642.86	835	849
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	20	23	42	0.04%	22.2%	ELNLAISR	99.7%	44.5	25	28.9	2	0	0	915.53	167	174
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	20	23	42	0.04%	22.2%	ELTGPAVLAVELCSR	99.7%	86.1	25	84.8	2	0	0	1614.85	181	195
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	20	23	42	0.04%	22.2%	EVSHLNALEER	99.7%	53.5	25	42.6	1	0	0	1296.65	1040	1050
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	20	23	42	0.04%	22.2%	FGVSSVAEAMALGR	99.7%	103	25	103	4	0	0	1394.71	763	776
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	20	23	42	0.04%	22.2%	IDISQLVITK	99.7%	85.5	25	54.3	2	0	0	1129.68	876	885
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	20	23	42	0.04%	22.2%	IFEPILGEGR	99.7%	53.1	25	47.4	2	0	0	1130.62	969	978
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	20	23	42	0.04%	22.2%	LGLTEDQFIR	99.7%	72	25	60.4	2	0	0	1191.64	630	639
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	20	23	42	0.04%	22.2%	LLEQGIR	99.4%	37.5	25	0	1	0	0	828.49	226	232
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	20	23	42	0.04%	22.2%	LMVLVNAVEMAR	99.7%	69	25	69	5	0	0	1345.73	526	537
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	20	23	42	0.04%	22.2%	LPCLEISQSVTGFGR	99.7%	85.1	25	85.1	2	0	0	1663.85	711	725
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	20	23	42	0.04%	22.2%	SEGGEDYTGATVIEPLK	99.7%	94.7	25	94.7	2	0	0	1765.85	575	591
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	20	23	42	0.04%	22.2%	TPTGDEFVK	99.5%	38.5	25	28.8	2	0	0	993.49	640	648
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	20	23	42	0.04%	22.2%	VLSFDIECAGR	99.7%	64.6	25	63.7	2	0	0	1266.61	312	322
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	20	23	42	0.04%	22.2%	VQMDMLQVLLR	99.7%	61.8	25	49.3	3	0	0	1345.73	455	465
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	20	23	42	0.04%	22.2%	VQTFPFLGR	97.7%	31.2	25	21.1	2	0	0	1064.59	415	423

DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	20	23	42	0.04%	22.2%	VSANSVYGFTGAQVGK	99.7%	72.7	25	65.4	2	0	0	1584.80	695	710
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	20	23	42	0.04%	22.2%	VTGVPLSYLLSR	99.7%	43	25	34.6	2	0	0	1304.76	538	549
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	20	23	42	0.04%	22.2%	VVYGDTDSVMCR	99.7%	65.9	25	65.9	1	0	0	1417.61	751	762
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	20	23	42	0.04%	22.2%	YTVENGYSTSAK	99.7%	67.3	25	67.3	1	0	0	1319.61	739	750
DNA polymerase delta subunit 2	POLD2	DPOD2_HUMAN	51.3	99.8%	2	2	4	0.00%	6.0%	FLGTSGQNVSDIFR	99.7%	94.1	25	87.8	2	0	0	1540.78	341	354
DNA polymerase delta subunit 2	POLD2	DPOD2_HUMAN	51.3	99.8%	2	2	4	0.00%	6.0%	LVTGTVLAVFGSVR	99.7%	92.4	25	90.6	2	0	0	1418.84	153	166
DNA polymerase delta subunit 3	POLD3	DPOD3_HUMAN	51.4	100.0%	5	5	7	0.01%	14.4%	DSGPLFNTDYDILK	99.7%	64	25	54.8	2	0	0	1597.77	110	123
DNA polymerase delta subunit 3	POLD3	DPOD3_HUMAN	51.4	100.0%	5	5	7	0.01%	14.4%	EVTNASAAGNKAPGK	99.2%	35.8	25	32	1	0	0	1414.73	217	231
DNA polymerase delta subunit 3	POLD3	DPOD3_HUMAN	51.4	100.0%	5	5	7	0.01%	14.4%	FSAIQCAAAVPR	99.6%	39	25	27.9	1	0	0	1290.66	132	143
DNA polymerase delta subunit 3	POLD3	DPOD3_HUMAN	51.4	100.0%	5	5	7	0.01%	14.4%	IVEQPTVSVTEPK	99.7%	70.7	25	70.6	2	0	0	1426.78	262	274
DNA polymerase delta subunit 3	POLD3	DPOD3_HUMAN	51.4	100.0%	5	5	7	0.01%	14.4%	VNLDSEQAVKEEK	99.7%	44.2	25	32.7	1	0	0	1488.75	249	261
DNA primase large subunit	PRIM2	PRI2_HUMAN	58.8	100.0%	4	4	7	0.01%	9.0%	IPFADALDLFR	99.7%	69.8	25	62.9	2	0	0	1277.69	186	196
DNA primase large subunit	PRIM2	PRI2_HUMAN	58.8	100.0%	4	4	7	0.01%	9.0%	ISPGGISQILDLVK	99.7%	67.6	25	61.1	2	0	0	1439.85	403	416
DNA primase large subunit	PRIM2	PRI2_HUMAN	58.8	100.0%	4	4	7	0.01%	9.0%	SLPAVQSDER	99.6%	39.2	25	35.7	2	0	0	1101.55	236	245
DNA primase large subunit	PRIM2	PRI2_HUMAN	58.8	100.0%	4	4	7	0.01%	9.0%	WFIQQEMDLLR	99.7%	46.7	25	25.6	1	0	0	1478.75	119	129
DNA primase small subunit	PRIM1	PRI1_HUMAN	49.9	100.0%	4	4	5	0.01%	9.5%	ISVPIDLQK	94.9%	27.8	25	24.8	1	0	0	1012.60	330	338
DNA primase small subunit	PRIM1	PRI1_HUMAN	49.9	100.0%	4	4	5	0.01%	9.5%	LGAFQAQEK	99.7%	57.2	25	32.7	1	0	0	991.52	96	104
DNA primase small subunit	PRIM1	PRI1_HUMAN	49.9	100.0%	4	4	5	0.01%	9.5%	SGIVEYLSLVK	99.6%	39.4	25	36.4	2	0	0	1207.69	183	193
DNA primase small subunit	PRIM1	PRI1_HUMAN	49.9	100.0%	4	4	5	0.01%	9.5%	VFEHFLENLDK	99.7%	54.5	25	50.8	1	0	0	1390.70	394	404
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	20	22	38	0.04%	15.4%	DVNGELIAVQR	99.7%	73.6	25	63.4	2	0	0	1213.65	88	98
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	20	22	38	0.04%	15.4%	EQVSPLETTLEK	99.7%	46.2	25	41.7	2	0	0	1373.72	910	921
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	20	22	38	0.04%	15.4%	GQDIEYIEIR	99.7%	81.5	25	66.4	2	0	0	1235.63	1157	1166
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	20	22	38	0.04%	15.4%	ILELDQELIK	99.7%	56.7	25	22.2	2	0	0	1213.70	474	483
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	20	22	38	0.04%	15.4%	LEENIDNIKR	99.6%	39.5	25	33.4	2	1	0	1243.66	1060	1069
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	20	22	38	0.04%	15.4%	LIQDQQEQIQHLK	99.7%	55.2	25	47	2	0	0	1620.87	852	864
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	20	22	38	0.04%	15.4%	LKEIEHNLSK	98.5%	33	25	18.2	1	0	0	1210.68	255	264
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	20	22	38	0.04%	15.4%	LQGIDLDR	99.7%	55.6	25	45.5	2	0	0	929.51	816	823
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	20	22	38	0.04%	15.4%	MEVISLQNEK	99.5%	38.1	25	19.3	1	0	0	1190.61	502	511
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	20	22	38	0.04%	15.4%	NIDQCSEIVK	99.7%	54.2	25	40.6	2	0	0	1205.58	1292	1301
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	20	22	38	0.04%	15.4%	SDADENVSASDK	99.7%	68.8	25	68.8	2	0	0	1237.52	1167	1178
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	20	22	38	0.04%	15.4%	SELLVEQGR	99.7%	62.5	25	46.8	2	0	0	1030.55	344	352
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	20	22	38	0.04%	15.4%	SYENELDPLK	99.7%	46.3	25	40.5	2	0	0	1207.58	243	252
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	20	22	38	0.04%	15.4%	TLDQAIMK	99.7%	43.3	25	34.1	2	0	0	935.49	1127	1134
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	20	22	38	0.04%	15.4%	VCLTDVTIMER	99.7%	58.4	25	46	2	0	0	1336.66	787	797
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	20	22	38	0.04%	15.4%	VIAQLSECEK	99.7%	52.9	25	52.9	2	0	0	1176.59	983	992
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	20	22	38	0.04%	15.4%	VKEYQMELK	99.1%	35.2	25	20.8	1	0	0	1167.61	203	211
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	20	22	38	0.04%	15.4%	VLASLIIR	99.7%	59.8	25	45.8	2	0	0	884.59	1207	1214
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	20	22	38	0.04%	15.4%	WLQDNLTLR	99.7%	44.5	25	30.8	2	0	0	1158.63	1017	1025
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	20	22	38	0.04%	15.4%	YELQQLEGSSDR	99.7%	84.5	25	80.7	2	0	0	1424.67	462	473
DNA repair protein RAD51 homolog 3	RAD51C	RA51C_HUMAN	42.2	99.8%	2	2	3	0.00%	6.1%	AEALETLQIIR	99.7%	53.5	25	40.2	1	0	0	1256.72	55	65
DNA repair protein RAD51 homolog 3	RAD51C	RA51C_HUMAN	42.2	99.8%	2	2	3	0.00%	6.1%	DLVSFPLSPAVR	99.7%	43.4	25	37.8	2	0	0	1300.73	13	24
DNA replication licensing factor MCM2	MCM2	MCM2_HUMAN	101.9	99.9%	2	2	4	0.00%	2.4%	AGIVTSLQAR	99.2%	35.8	25	31.7	2	0	0	1015.59	614	623
DNA replication licensing factor MCM2	MCM2	MCM2_HUMAN	101.9	99.9%	2	2	4	0.00%	2.4%	GLALALFGGEPK	99.7%	77.7	25	66.4	2	0	0	1172.67	494	505
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	26	29	56	0.06%	36.6%	AILCLLLGGVER	99.7%	86.1	25	71.9	7	0	0	1313.76	316	327
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	26	29	56	0.06%	36.6%	ALKDFVASIDATYAK	99.7%	59.6	25	59.5	2	0	0	1612.86	79	93
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	26	29	56	0.06%	36.6%	APAGQLPR	99.7%	52.2	25	33.7	3	0	0	809.46	208	215
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	26	29	56	0.06%	36.6%	CSVLAAANPVYGR	99.7%	74.1	25	62.2	2	0	0	1377.69	446	458
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	26	29	56	0.06%	36.6%	DAQPSFSAEDIAK	99.7%	70.2	25	66.1	2	0	0	1378.65	271	283
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	26	29	56	0.06%	36.6%	DLENGSHIR	99.4%	37.6	25	25.7	2	0	0	1040.51	328	336
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	26	29	56	0.06%	36.6%	DSEEPFSSVEIQAALSK	99.7%	98.3	25	91.8	1	0	0	1836.89	775	791
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	26	29	56	0.06%	36.6%	DYLDFLDDEEDQGIYQSK	99.7%	50.4	25	50.4	1	0	0	2192.95	18	35

DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	26	29	56	0.06%	36.6%	EAHAQSIGMNR	99.7%	58.8	25	50.5	2	0	0	1213.57	757	767
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	26	29	56	0.06%	36.6%	ELISDNQYR	99.7%	64.6	25	57.8	2	0	0	1137.55	38	46
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	26	29	56	0.06%	36.6%	GDINILLIGDPSVAK	99.7%	81.7	25	81.7	3	0	0	1524.86	337	351
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	26	29	56	0.06%	36.6%	GGYTSGTFR	99.7%	49.3	25	43.7	2	0	0	945.44	249	257
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	26	29	56	0.06%	36.6%	GSSGVGLTAAVTTDQETGER	99.7%	128	25	128	1	0	0	1935.93	372	391
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	26	29	56	0.06%	36.6%	LIVNVNDLR	99.7%	66	25	53	2	0	0	1055.62	47	55
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	26	29	56	0.06%	36.6%	LIVNVNDLRR	99.4%	37.4	25	33.2	1	0	0	1211.72	47	56
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	26	29	56	0.06%	36.6%	LLNNAFEELVAFQR	99.7%	94.6	25	92.8	2	0	0	1663.88	65	78
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	26	29	56	0.06%	36.6%	SKDIFDQLAK	99.7%	51.9	25	42.7	2	0	0	1164.63	292	301
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	26	29	56	0.06%	36.6%	SLAPSIHGHDYVK	99.7%	49.6	25	48.4	1	0	0	1423.73	302	314
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	26	29	56	0.06%	36.6%	SVDVILDDDLVDK	99.7%	56.3	25	49.8	2	0	0	1445.74	216	228
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	26	29	56	0.06%	36.6%	SVHYCPATK	97.8%	31.3	25	20	2	0	0	1062.50	144	152
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	26	29	56	0.06%	36.6%	TAIHEVMEQGR	99.7%	49.2	25	49.2	2	1	0	1270.62	420	430
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	26	29	56	0.06%	36.6%	TLETLIR	99.0%	34.8	25	8.95	2	0	0	845.51	617	623
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	26	29	56	0.06%	36.6%	TPMENIGLQDSLLSR	99.7%	85.8	25	85.8	4	0	0	1689.85	464	478
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	26	29	56	0.06%	36.6%	TVLIACNVK	97.9%	31.6	25	17.1	1	0	0	1017.58	258	266
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	26	29	56	0.06%	36.6%	VALLDVFR	99.7%	57.7	25	51.1	2	0	0	932.56	749	756
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	26	29	56	0.06%	36.6%	YVLCTAPR	99.7%	48.1	25	37.5	2	0	0	979.50	357	364
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	11	11	21	0.02%	16.1%	ALADDDFLTVTGK	99.7%	97.4	25	97.4	2	0	0	1365.69	846	858
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	11	11	21	0.02%	16.1%	GILLQLFGGTR	99.7%	77.3	25	77.3	4	0	0	1174.69	479	489
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	11	11	21	0.02%	16.1%	GMVSAYPR	95.9%	28.7	25	24.1	1	0	0	896.43	725	732
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	11	11	21	0.02%	16.1%	IAEPSVCGR	99.7%	47.6	25	24.1	2	0	0	988.49	322	330
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	11	11	21	0.02%	16.1%	LASALAPSIYEHEDIKK	95.8%	22.5	25	22	0	1	0	1885.01	462	478
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	11	11	21	0.02%	16.1%	LVIWGTDVNVAACK	99.7%	81.3	25	81.3	2	0	0	1545.81	150	163
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	11	11	21	0.02%	16.1%	QRPDLGSAQK	99.7%	40.4	25	28.4	2	0	0	1099.59	114	123
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	11	11	21	0.02%	16.1%	SQLLQYVYNLVPR	99.7%	55.4	25	49.9	1	0	0	1592.88	517	529
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	11	11	21	0.02%	16.1%	TGIVDISILTTGMSATSR	99.7%	68.8	25	68.8	2	0	0	1822.96	778	795
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	11	11	21	0.02%	16.1%	TSVLAAANPIESQWNPK	99.7%	82.3	25	76.2	2	0	0	1825.94	611	627
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	11	11	21	0.02%	16.1%	YQQLFEDIR	99.7%	65.7	25	42.4	2	0	0	1211.61	820	828
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	27	0.03%	22.1%	AGITTTLNSR	99.7%	55.4	25	37.7	1	0	0	1033.56	472	481
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	27	0.03%	22.1%	AIACLLFGGSR	99.7%	81.4	25	76.7	5	0	0	1164.62	352	362
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	27	0.03%	22.1%	CSVLAAANSVFGR	99.7%	92.5	25	89.4	2	0	0	1351.68	482	494
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	27	0.03%	22.1%	FAIGSQVSEHSIIK	99.7%	61.1	25	53.2	1	0	0	1515.82	683	696
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	27	0.03%	22.1%	HMQLYCDR	98.5%	33.1	25	27.1	1	0	0	1138.48	244	251
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	27	0.03%	22.1%	IPGIIIAASAVR	99.7%	87	25	87	2	0	0	1180.74	151	162
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	27	0.03%	22.1%	LAALPNVYEVISK	99.7%	62.1	25	62.1	2	0	0	1416.81	325	337
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	27	0.03%	22.1%	LQELPDAVPHGEMPR	95.0%	21.8	25	21.5	0	1	0	1704.84	229	243
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	27	0.03%	22.1%	LQPFATEADVEEALR	99.7%	93.3	25	91.8	2	0	0	1688.85	628	642
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	27	0.03%	22.1%	QLEAIVR	95.8%	28.6	25	10.1	1	0	0	828.49	612	618
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	27	0.03%	22.1%	SIAPSIFGGTDMKK	99.7%	46.9	25	44.6	3	0	0	1451.76	338	351
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	27	0.03%	22.1%	VLGIQVDTDGSGR	99.7%	68.9	25	68.9	2	0	0	1316.68	296	308
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	27	0.03%	22.1%	VLQLMLR	99.7%	47	25	27.3	2	0	0	872.54	711	717
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	27	0.03%	22.1%	VTIMGIYSIK	99.7%	48	25	34.2	2	0	0	1124.64	263	272
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	20	33	0.03%	24.5%	AEAVESAQAGDK	99.3%	36.7	25	35.9	1	0	0	1175.55	230	241
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	20	33	0.03%	24.5%	DFYVAFQDLPTR	99.7%	82.1	25	68.7	2	0	0	1471.72	109	120
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	20	33	0.03%	24.5%	ELRDEEQTAESIK	99.7%	60.3	25	52.8	1	0	0	1547.75	314	326
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	20	33	0.03%	24.5%	GDINVCIVGDPSTAK	99.7%	67.2	25	66.7	1	0	0	1545.76	388	402
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	20	33	0.03%	24.5%	GVLLMLFGGVPK	99.7%	64.8	25	44	2	0	0	1230.73	367	378
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	20	33	0.03%	24.5%	HVEEFSPR	99.5%	38.1	25	38.1	2	0	0	1000.48	408	415
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	20	33	0.03%	24.5%	IQETQAELPR	99.7%	70.4	25	46.6	2	0	0	1184.63	208	217
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	20	33	0.03%	24.5%	ISNLIVLHLR	99.7%	42.4	25	37.8	2	0	0	1177.74	723	732

DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	20	33	0.03%	24.5%	LGFSEYCR	99.2%	35.9	25	35.9	2	0	0	1031.46	715	722
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	20	33	0.03%	24.5%	LVFLACCVAPTNPR	99.7%	90.1	25	89.6	2	0	0	1617.82	296	309
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	20	33	0.03%	24.5%	QNINLSAPIMSR	99.7%	45.8	25	37.6	1	0	0	1343.71	518	529
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	20	33	0.03%	24.5%	SELVNWYLK	99.6%	39.9	25	33.7	2	0	0	1151.61	746	754
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	20	33	0.03%	24.5%	SLEVILR	98.9%	34.5	25	27.3	2	0	0	829.51	223	229
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	20	33	0.03%	24.5%	TSILAAANPISGHYDR	99.7%	69.7	25	69.7	2	2	0	1685.86	497	512
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	20	33	0.03%	24.5%	VSGVDGYETEGIR	99.7%	72.1	25	50.7	1	0	0	1381.66	270	282
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	20	33	0.03%	24.5%	VYSLDDIRR	99.3%	36.6	25	27.2	1	0	0	1136.61	566	574
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	20	33	0.03%	24.5%	YLQLAEELIRPER	99.7%	50.4	25	39.4	2	1	0	1629.90	46	58
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	20	33	0.03%	24.5%	YTQPNICR	99.0%	34.9	25	28	2	0	0	1051.50	174	181
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	22	44	0.04%	31.6%	AGILTTLNAR	99.7%	71.1	25	59.3	2	0	0	1029.61	472	481
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	22	44	0.04%	31.6%	ALLLLLVGGVDQSPR	99.7%	73.8	25	73.8	6	0	0	1550.93	353	367
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	22	44	0.04%	31.6%	CSILAAANPAYGR	99.7%	63.6	25	55	2	0	0	1363.68	482	494
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	22	44	0.04%	31.6%	DSLLGDKGQTAR	99.7%	48.2	25	43.4	2	0	0	1260.65	642	653
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	22	44	0.04%	31.6%	GNINICLMGDPGVAK	99.7%	43.4	25	43.4	2	0	0	1558.77	373	387
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	22	44	0.04%	31.6%	GSSGVGLTAAVLR	99.7%	98	25	78	2	0	0	1187.67	408	420
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	22	44	0.04%	31.6%	IAQPGDHVSVTGIFLPILR	99.7%	41.2	25	32.8	0	1	0	2033.15	264	282
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	22	44	0.04%	31.6%	LFADAVQELLPQYK	99.7%	70	25	49.3	4	0	0	1634.88	76	89
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	22	44	0.04%	31.6%	MQEHSDQVPVGNIPR	99.7%	37.3	25	23.6	0	1	0	1722.82	237	251
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	22	44	0.04%	31.6%	QIAEEDFYEK	99.7%	44.9	25	42.8	2	0	0	1271.58	326	335
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	22	44	0.04%	31.6%	QVVQGLLSETYLEAHR	99.7%	74	25	73.8	1	2	0	1842.97	287	302
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	22	44	0.04%	31.6%	SITVLVEGENTR	99.7%	88.4	25	77.9	2	0	0	1317.70	252	263
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	22	44	0.04%	31.6%	SLEQNIQLPAALLSR	99.7%	121	25	121	2	0	0	1652.93	500	514
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	22	44	0.04%	31.6%	SPQNQYPAELMR	99.7%	47.6	25	45.1	4	0	0	1449.68	121	132
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	22	44	0.04%	31.6%	SQLLSYIDR	99.7%	56.3	25	33.2	2	0	0	1094.58	388	396
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	22	44	0.04%	31.6%	TLLAILR	99.7%	40.5	25	13.3	1	0	0	799.54	605	611
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	22	44	0.04%	31.6%	TQRPADVIFATVR	99.7%	41.7	25	35.8	2	2	0	1473.82	654	666
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	22	44	0.04%	31.6%	YGNQLVR	99.7%	52.5	25	34.9	2	0	0	849.46	33	39
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	12	31	0.03%	15.7%	AEEVATFFAK	99.7%	59	25	43.6	4	0	0	1112.56	253	262
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	12	31	0.03%	15.7%	AVAILCNHQR	99.7%	58.1	25	41.2	2	0	0	1181.62	625	634
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	12	31	0.03%	15.7%	AVALYFIDK	99.7%	47	25	28.1	2	0	0	1039.58	476	484
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	12	31	0.03%	15.7%	ELTAPDENIPAK	97.6%	31	25	28.6	1	0	0	1297.66	604	615
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	12	31	0.03%	15.7%	GPVFAPPYEPLPENVK	99.7%	54.8	25	54.8	4	0	0	1753.92	224	239
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	12	31	0.03%	15.7%	HLQDLMEGLTAK	99.7%	54.5	25	30.9	2	0	0	1355.70	576	587
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	12	31	0.03%	15.7%	LEVQATDREENK	99.7%	63.4	25	54.3	4	0	0	1431.71	701	712
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	12	31	0.03%	15.7%	LNTGILNK	97.6%	30.9	25	13.9	1	0	0	872.52	568	575
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	12	31	0.03%	15.7%	MLDHEYTTK	99.7%	45.7	25	37.4	6	0	0	1137.52	263	271
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	12	31	0.03%	15.7%	TYNASITLQQQLK	99.7%	88.4	25	75.3	4	0	0	1507.81	591	603
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	12	31	0.03%	15.7%	YIMLNPSSR	98.7%	33.6	25	32.3	1	0	0	1080.55	426	434
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	12	12	23	0.02%	9.3%	DKYGVFPLR	98.8%	33.9	25	28.9	1	0	0	1094.60	479	487
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	12	12	23	0.02%	9.3%	ELILFSNSDNER	99.7%	67.9	25	61.4	2	0	0	1436.70	702	713
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	12	12	23	0.02%	9.3%	FLEEFITPIVK	99.7%	47.7	25	44.4	2	0	0	1335.76	569	579
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	12	12	23	0.02%	9.3%	FTVETASR	99.7%	45.6	25	42.5	2	0	0	910.46	177	184
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	12	12	23	0.02%	9.3%	GFQQISFVNSIATSK	99.7%	73.2	25	70.1	2	0	0	1626.85	307	321
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	12	12	23	0.02%	9.3%	HVDYVADQIVTK	99.7%	64.1	25	64.1	2	0	0	1387.72	325	336
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	12	12	23	0.02%	9.3%	IFDEILVNAADNK	99.7%	102	25	102	4	0	0	1461.76	84	96
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	12	12	23	0.02%	9.3%	LCNIFSTK	98.2%	32.2	25	23.2	1	0	0	982.50	169	176
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	12	12	23	0.02%	9.3%	NSTECTLILTEGDSAK	99.7%	63.7	25	52.3	1	0	0	1738.82	451	466
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	12	12	23	0.02%	9.3%	TLAVSGLGVVGR	99.7%	63.6	25	59.9	2	0	0	1128.67	467	478
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	12	12	23	0.02%	9.3%	YIFTMLSSLAR	99.7%	52.6	25	52.6	3	0	0	1301.69	805	815
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	12	12	23	0.02%	9.3%	YSGPEDDAAISLAFSK	99.7%	60.2	25	53	1	0	0	1670.79	640	655

DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	6	6	12	0.01%	6.0%	DLIQMLVQR	99.5%	37.9	25	22.9	1	0	0	1115.62	1093	1101
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	6	6	12	0.01%	6.0%	ELILFSNSDNER	99.7%	67.9	25	61.4	2	0	0	1436.70	723	734
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	6	6	12	0.01%	6.0%	GFQQISFVNSIATTK	99.7%	42.2	25	34.4	1	0	0	1640.86	328	342
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	6	6	12	0.01%	6.0%	IFDEILVNAADNK	99.7%	102	25	102	4	0	0	1461.76	105	117
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	6	6	12	0.01%	6.0%	LAQAEAAGLHK	99.7%	61.4	25	51.3	2	0	0	1108.61	998	1008
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	6	6	12	0.01%	6.0%	LCNIFSTK	98.2%	32.2	25	23.2	1	0	0	982.50	190	197
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	6	6	12	0.01%	6.0%	LLFPAVDDNLLK	99.7%	50	25	41.2	4	0	0	1357.77	837	848
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	6	6	12	0.01%	6.0%	LPNYDAR	95.2%	28.1	25	21.3	1	0	0	848.43	885	891
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	6	6	12	0.01%	6.0%	YIFTMLSTLAR	99.7%	43.5	25	28.2	3	0	0	1315.71	826	836
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	AALSALESFLK	99.7%	79.2	25	56.8	8	0	0	1149.65	311	321
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	AAYLSDPR	95.6%	28.4	25	18.2	1	0	0	892.45	3826	3833
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	AQEPESGLSEETQVK	99.7%	76.6	25	60.8	2	0	0	1631.78	4091	4105
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	ATQMPEGGQGAPPMYQLYK	99.7%	49.2	25	47.7	3	0	0	2082.96	945	963
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	ATQQQHDFTLTQTADGR	99.7%	48.6	25	48.6	1	2	0	1917.91	2637	2653
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	AYVPALQMAFK	99.7%	45.8	25	27.4	2	0	0	1254.66	747	757
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	CFFLSK	97.6%	30.9	25	17.6	1	0	0	801.40	3187	3192
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	CFGTGAAGNR	99.7%	40.3	25	33.1	1	0	0	1010.45	1312	1321
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	CGAALAGHQLIR	99.7%	63.6	25	59	2	0	0	1266.67	25	36
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	CLMDQATDPNILGR	99.7%	79.1	25	79.1	1	0	0	1603.76	4106	4119
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	DCLSIPYR	99.0%	34.7	25	26.4	1	0	0	1023.49	2247	2254
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	DFGLLVFVR	99.7%	70.1	25	56.6	4	0	0	1065.61	62	70
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	DFSAFINLVEFCR	99.7%	51.6	25	51.6	2	0	0	1617.77	619	631
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	DILETHLR	99.7%	41.2	25	31.9	2	0	0	996.55	1413	1420
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	DILPCLDGYLK	98.5%	33.2	25	12.9	1	0	0	1306.67	791	801
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	DLCNTHLMR	99.6%	38.9	25	35.7	2	0	0	1175.53	1362	1370
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	DQNILLGTTYR	99.7%	87.8	25	80.7	4	0	0	1293.68	3325	3335
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	DVDFMYVELIQR	99.7%	68.7	25	59.6	4	0	0	1543.75	380	391
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	EIFNFVLK	98.3%	32.5	25	16.4	1	0	0	1009.57	247	254
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	ELLNPVVEFVSHPSTTCR	99.7%	62.9	25	62.5	2	1	0	2085.04	2453	2470
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	EQQHVMEELFQSSFR	99.3%	28.7	25	28.7	0	1	0	1910.87	1769	1783
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	ETGLMYSIMVHALR	95.6%	28.4	25	28.4	1	0	0	1620.82	3976	3989
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	FMNAVFFLLPK	99.7%	72	25	60.9	4	0	0	1326.73	2378	2388
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	FNNYVDCMK	98.8%	34.1	25	27	1	0	0	1190.50	1736	1744
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	FNNYVDCMKK	95.4%	28.3	25	15.4	1	0	0	1318.59	1736	1745
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	FVPLLPGNR	96.3%	29.1	25	22.6	2	0	0	1012.59	1194	1202
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	FYQGFLFSEKPEK	99.7%	56.8	25	50.1	2	0	0	1619.81	1961	1973
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	GIFTSEIGTK	99.7%	62.5	25	55.7	4	0	0	1052.56	2941	2950
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	GLSSLLCNFTK	99.7%	52.4	25	41.6	2	0	0	1239.64	226	236
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	HGDLPDIQIK	99.7%	54.7	25	46.8	3	0	0	1135.61	2777	2786
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	HNLEIIK	99.7%	48.7	25	18.9	2	0	0	866.51	2233	2239
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	HSSLITPLQAVAQR	99.7%	44.3	25	42.8	2	2	0	1520.85	2787	2800
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	IAGFDER	98.2%	32.2	25	25.7	1	0	0	807.40	3719	3725
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	IAPYSVEIK	99.7%	41.2	25	27.9	2	0	0	1019.58	100	108
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	ICSKPVVLPK	97.3%	30.5	25	19.8	1	0	0	1140.68	490	499
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	ILDVMYSR	99.7%	55.3	25	45.9	4	0	0	996.52	1876	1883
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	ILELSGSSSEDSEK	99.7%	96.3	25	92.5	3	0	0	1480.70	3359	3372
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	IMEFTTTLLNTSPEGWK	99.7%	43.8	25	40.1	2	0	0	1967.98	1341	1357
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	INQVFHGSCITEGNELTK	99.7%	64.7	25	64.7	2	0	0	2046.99	1896	1913
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	IPALDLLIK	95.9%	28.7	25	22.6	1	0	0	995.65	125	133
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	KNILEESLCELVAK	99.7%	43.2	25	40.4	2	0	0	1645.88	2334	2347
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	KQNNFSLAMK	99.7%	50.6	25	40.5	1	0	0	1180.61	3248	3257

DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LAAVVSACK	99.7%	62.8	25	51.3	2	0	0	918.51	1448	1456
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LACDVDQVTR	99.7%	64.2	25	45.9	2	0	0	1176.57	972	981
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LATTILQHWK	99.7%	60.1	25	60.1	2	0	0	1210.69	1618	1627
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LGASLAFNNIYR	99.7%	72.5	25	45	2	0	0	1338.72	1076	1087
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LGLPGDEVDNK	99.7%	48.1	25	48.1	1	0	0	1156.58	2705	2715
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LGLPGDEVDNKVK	99.7%	55.2	25	52	2	0	0	1383.75	2705	2717
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LGNPIVPLNIR	99.7%	62.8	25	62.8	2	0	0	1205.74	2133	2143
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LLEEALLR	99.7%	57	25	51.3	4	0	0	956.58	2892	2899
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LLLQGEADQSLLTFIDK	99.7%	91.7	25	91.7	4	0	0	1904.04	3051	3067
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LLNFLMK	98.4%	32.7	25	22.2	3	0	0	878.52	2215	2221
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LLNTWTNR	99.1%	35.4	25	30.4	3	0	0	1017.55	3160	3167
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LLPAELPAKR	98.0%	31.8	25	31.8	2	0	0	1107.69	2900	2909
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LLQDFNR	99.7%	43	25	21.6	2	0	0	905.48	2836	2842
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LLQIIER	99.7%	44	25	32.2	4	0	0	884.56	3468	3474
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LLSITVR	99.7%	40.5	25	21.7	2	0	0	801.52	669	675
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LNESTFDTQITK	99.7%	82.7	25	77.4	2	0	0	1396.70	1858	1869
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LNESTFDTQITKK	99.7%	56	25	54.7	2	0	0	1524.79	1858	1870
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LPKDDVHAK	99.7%	45.6	25	32.6	2	0	0	1022.56	1884	1892
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LPPDVLR	96.3%	29.1	25	29.1	1	0	0	809.49	2916	2922
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LPSNTLDR	99.7%	44.3	25	33.3	2	0	0	915.49	2531	2538
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LPVLAGCLK	99.7%	51	25	51	2	0	0	970.58	217	225
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LQETLSAADR	99.7%	84.7	25	63.4	4	0	0	1103.57	15	24
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LQYFMEQFYGIIR	99.7%	57.1	25	57.1	2	0	0	1723.85	338	350
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LSDFNDITNMLLLK	99.7%	90.9	25	81.7	5	0	0	1636.86	3656	3669
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LSFAVPFR	99.7%	48	25	39.8	3	0	0	936.53	892	899
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LSLMYAR	99.7%	53.3	25	30.1	4	0	0	869.46	2739	2745
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LVINTEEVFRPYAK	99.7%	56.4	25	56.4	2	2	0	1678.92	2149	2162
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	LYSLALHPNAFK	99.4%	29.4	25	24.3	1	2	0	1373.76	1063	1074
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	MAVLALLAK	99.7%	51.6	25	40.4	3	0	0	945.58	1643	1651
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	MKQDAQVVLYR	99.7%	73	25	65.3	2	1	0	1350.72	2763	2773
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	MSTSPEAFLALR	99.7%	76.2	25	70.2	6	0	0	1322.68	3890	3901
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	MYAALGDPK	99.7%	50.2	25	46	4	0	0	965.48	3613	3621
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	NCISTVVHQGLIR	99.7%	71.8	25	66.2	2	2	0	1496.80	477	489
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	NLDLAVLELMQSSVDNTK	99.7%	75.2	25	75.2	2	0	0	1990.02	1574	1591
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	NLLIFENLIDLK	99.7%	85.2	25	69.9	2	0	0	1444.84	1974	1985
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	NLLIFENLIDLKR	99.7%	63.8	25	63.8	2	0	0	1600.94	1974	1986
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	NLLTVTSSDEMMK	99.7%	87.3	25	83.8	7	0	0	1500.69	869	881
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	NLSSNEAISLEEIR	99.7%	110	25	87.7	2	0	0	1574.80	839	852
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	NNWEVSALSR	99.7%	54.7	25	46.1	2	0	0	1175.58	811	820
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	NVDSNNKELSIAIR	99.7%	71.8	25	59.6	2	1	0	1572.83	351	364
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	QCLPSLDLSCK	99.7%	53.1	25	40.4	2	0	0	1320.63	1498	1508
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	QDAQVVLYR	98.0%	31.6	25	16.2	1	0	0	1091.58	2765	2773
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	QFINLMLPMK	97.8%	31.3	25	13.4	3	0	0	1266.66	3966	3975
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	QGNLSSQVPLKR	94.6%	27.6	25	23.9	1	0	0	1326.75	3148	3159
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	QITQSALLAEAR	99.7%	90.9	25	71.9	4	0	0	1300.72	2951	2962
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	QLFSSLFSGILK	99.7%	81.8	25	69.8	3	0	0	1339.76	2807	2818
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	QMFLTQTDTGDDR	99.7%	52	25	47.5	1	0	0	1527.67	394	406
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	RLSFAVPFR	98.8%	33.9	25	28.4	1	0	0	1092.63	891	899
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	SDPGLLTNTMDVFVK	99.7%	69.4	25	67.8	5	0	0	1636.83	3993	4007
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	SIELFYK	95.7%	28.5	25	7.11	1	0	0	899.49	1187	1193
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	SIGEYDVLR	99.7%	51.7	25	46.1	3	0	0	1051.54	2932	2940

DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	SKDFVQVMR	99.7%	56.1	25	42.7	2	0	0	1109.58	2417	2425
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	SLEYCSTASIDSENPPDLNK	99.7%	69.6	25	69.6	2	0	0	2240.00	3010	3029
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	SLGPPQGEEDSVPR	99.7%	69.6	25	68.4	2	0	0	1467.71	2107	2120
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	SLNSIEFR	99.7%	45.2	25	32.7	2	0	0	965.51	72	79
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	SMEEDPQTSR	97.3%	30.5	25	26	1	0	0	1179.49	237	246
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	SQGCSEQVLTVLK	99.7%	80.1	25	75.2	5	0	0	1448.74	3290	3302
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	STVLTPMFVETQASQGTLQTR	99.7%	100	25	100	2	1	0	2295.17	2599	2619
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	TETVTSFR	99.7%	45.7	25	37.7	4	0	0	940.47	3865	3872
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	TLCLEVVLCR	99.7%	65.1	25	60	2	0	0	1262.66	2395	2404
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	TVGALQVLGTEAQSSLLK	99.7%	121	25	120	4	0	0	1815.02	1275	1292
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	TVSLLDENNVSSYLSK	99.7%	114	25	113	4	0	0	1768.90	3303	3318
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	TYSVVPMTSR	97.4%	30.5	25	29	2	0	0	1140.57	3790	3799
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	VCLDIIYK	99.1%	35.4	25	15.7	2	0	0	1023.55	2434	2441
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	VEGMTELYFQLK	99.7%	82.7	25	76.3	2	0	0	1457.73	2405	2416
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	VFLALAAK	99.0%	35	25	23.2	2	0	0	832.53	464	471
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	VLEQLIVAHFPMQSR	98.7%	33.5	25	32.7	2	0	0	1783.95	1713	1727
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	VPADLLKR	99.7%	52	25	35.9	2	0	0	911.57	3878	3885
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	VTELALTASDR	99.7%	109	25	94.1	4	0	0	1175.63	914	924
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	VTVMASLR	99.7%	55.8	25	39	2	0	0	876.50	3726	3733
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	VVQMLGSLGGQINK	99.7%	82.1	25	74.9	5	0	0	1443.80	855	868
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	YAVPSAGLR	99.4%	37.3	25	28.1	1	0	0	933.52	265	273
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	YNFPVEVEVPMER	99.7%	60	25	56.8	3	0	0	1608.77	1988	2000
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	YPEETLSLMTK	99.7%	48.2	25	43.9	2	0	0	1311.65	3475	3485
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	117	144	294	0.30%	30.3%	YSCFALFVK	98.7%	33.8	25	29.5	2	0	0	1134.57	701	709
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	7	7	11	0.01%	6.1%	EGEEQLQTQHQK	99.0%	34.7	25	23.6	1	0	0	1454.69	135	146
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	7	7	11	0.01%	6.1%	GPIQILNR	99.7%	56.8	25	47	2	0	0	910.55	1065	1072
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	7	7	11	0.01%	6.1%	IVATLPYIK	96.9%	29.8	25	29.8	1	0	0	1017.63	256	264
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	7	7	11	0.01%	6.1%	NLTYSAPLYVDITK	99.7%	55.1	25	50.4	2	0	0	1597.85	117	130
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	7	7	11	0.01%	6.1%	QEVPIIIVFR	99.7%	42.1	25	29.8	2	0	0	1213.73	265	274
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	7	7	11	0.01%	6.1%	VSGDDVIIGK	99.6%	39.1	25	35.7	2	0	0	1002.55	860	869
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	7	7	11	0.01%	6.1%	YAYTGECR	96.6%	29.5	25	19.4	1	0	0	1019.43	215	222
DNA-directed RNA polymerase II subunit RPB7	POLR2G	RPB7_HUMAN	19.3	99.8%	2	2	5	0.01%	13.4%	LFTEVEGTCTGK	98.5%	33.1	25	33.1	2	0	0	1341.64	30	41
DNA-directed RNA polymerase II subunit RPB7	POLR2G	RPB7_HUMAN	19.3	99.8%	2	2	5	0.01%	13.4%	YFGPNLLNTVK	99.7%	40.8	25	31.9	3	0	0	1265.69	17	27
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	8	8	16	0.02%	5.8%	AEALVLMGTK	99.7%	42.3	25	35.6	2	0	0	1048.57	517	526
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	8	8	16	0.02%	5.8%	IDEVAVPVHVAK	99.7%	60.6	25	50.4	2	0	0	1276.73	377	388
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	8	8	16	0.02%	5.8%	LAPVYLSNR	99.7%	42.1	25	33.9	2	0	0	1032.58	686	694
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	8	8	16	0.02%	5.8%	LLVEGDNLR	99.7%	46.4	25	35.3	2	0	0	1028.57	1225	1233
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	8	8	16	0.02%	5.8%	LTEIIFLNDVIK	99.7%	53.8	25	46.3	2	0	0	1417.83	283	294
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	8	8	16	0.02%	5.8%	NELILTTESIMK	99.7%	41.8	25	26.4	2	0	0	1391.75	943	954
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	8	8	16	0.02%	5.8%	NNIFYILLR	99.2%	36.2	25	22.8	2	0	0	1165.67	661	669
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	8	8	16	0.02%	5.8%	YGDIVER	99.6%	38.8	25	32.3	2	0	0	851.43	446	452
DNA-directed RNA polymerase III subunit RPC10	POLR3K	RPC10_HUMAN	12.3	99.8%	2	2	3	0.00%	18.5%	AYFMQLQTR	99.3%	36.4	25	22.1	2	0	0	1173.57	77	85
DNA-directed RNA polymerase III subunit RPC10	POLR3K	RPC10_HUMAN	12.3	99.8%	2	2	3	0.00%	18.5%	SADEPMTTFYK	97.9%	31.5	25	31.5	1	0	0	1305.57	86	96
DNA-directed RNA polymerase III subunit RPC3	POLR3C	RPC3_HUMAN	60.6	99.8%	2	2	3	0.00%	3.2%	LADTHFVQR	99.1%	35.3	25	25	1	0	0	1086.57	151	159
DNA-directed RNA polymerase III subunit RPC3	POLR3C	RPC3_HUMAN	60.6	99.8%	2	2	3	0.00%	3.2%	SIANLIER	96.5%	29.3	25	19.4	2	0	0	915.53	442	449
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	11	11	17	0.02%	10.8%	ELVYVLFMVK	99.7%	49.6	25	43.7	2	0	0	1256.70	279	288
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	11	11	17	0.02%	10.8%	ILEASQLK	97.8%	31.4	25	6.54	1	0	0	901.54	1198	1205
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	11	11	17	0.02%	10.8%	LQALFTAVLLSEEDR	99.7%	58.1	25	58.1	1	0	0	1704.92	330	344
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	11	11	17	0.02%	10.8%	LQMPFQSGEFK	99.4%	37.6	25	32.4	1	0	0	1327.64	144	154
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	11	11	17	0.02%	10.8%	LSLAQHLR	99.7%	63.7	25	53.5	2	0	0	937.56	783	790
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	11	11	17	0.02%	10.8%	QLQAESVSEVVVNR	99.7%	84.1	25	78.8	2	0	0	1557.82	72	85

DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	11	11	17	0.02%	10.8%	QYWEELGAPEALR	99.7%	57.2	25	46.7	1	0	0	1561.76	551	563
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	11	11	17	0.02%	10.8%	VAQVLEGFITR	99.7%	91.5	25	86.2	2	0	0	1232.70	977	987
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	11	11	17	0.02%	10.8%	VLDLVLQLFQAK	99.7%	82.1	25	64.6	2	0	0	1386.84	713	724
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	11	11	17	0.02%	10.8%	VSGQVQALQNHYR	99.7%	55	25	47.2	2	0	0	1499.77	519	531
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	11	11	17	0.02%	10.8%	YLCLLASDAEVPEPCLPR	99.1%	35.5	25	31.5	1	0	0	2103.03	533	550
DNA-directed RNA polymerases I and III subunit RPAC1	POLR1C	RPAC1_HUMAN	39.2	99.9%	2	3	4	0.00%	7.5%	DSSDPNELYVNHK	98.7%	33.8	25	33.8	1	0	0	1517.69	155	167
DNA-directed RNA polymerases I and III subunit RPAC1	POLR1C	RPAC1_HUMAN	39.2	99.9%	2	3	4	0.00%	7.5%	ILLAEVPTMAVEK	99.7%	99.9	25	99.9	3	0	0	1413.80	79	91
DNA-directed RNA polymerases I, II, and III subunit RPABC1	POLR2E	RPAB1_HUMAN	24.6	100.0%	2	2	3	0.00%	11.4%	ALIVVQQGMTPSAK	99.7%	51.6	25	47.2	1	0	0	1442.80	102	115
DNA-directed RNA polymerases I, II, and III subunit RPABC1	POLR2E	RPAB1_HUMAN	24.6	100.0%	2	2	3	0.00%	11.4%	IIRPSETAGR	99.7%	41.3	25	28.8	2	0	0	1099.62	193	202
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	5	7	11	0.01%	37.3%	ADQFEYVMYGK	99.7%	67.8	25	67.8	2	0	0	1350.60	85	95
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	5	7	11	0.01%	37.3%	IEGDETSTEAATR	99.7%	96	25	96	2	0	0	1379.63	99	111
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	5	7	11	0.01%	37.3%	LQGDANNLHGFEVDSR	99.7%	48.6	25	48.6	1	1	0	1771.84	125	140
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	5	7	11	0.01%	37.3%	LSAYVSYGGLLMR	99.7%	82.7	25	78.3	4	0	0	1429.75	112	124
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	5	7	11	0.01%	37.3%	VYRIEGDETSTEAATR	97.5%	30.9	25	30.9	1	0	0	1797.86	96	111
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	5	6	12	0.01%	14.1%	ELYDKGGEQAIK	99.7%	52.8	25	37.2	2	2	0	1350.69	62	73
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	5	6	12	0.01%	14.1%	ILEVHIDK	99.7%	46.1	25	12.8	2	0	0	966.56	207	214
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	5	6	12	0.01%	14.1%	NVICDKCEGR	99.2%	36.2	25	30.1	2	0	0	1250.56	131	140
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	5	6	12	0.01%	14.1%	QISQAYEVLSDAK	99.7%	103	25	101	2	0	0	1451.74	47	59
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	5	6	12	0.01%	14.1%	TIVITSHPGQIVK	99.7%	73.2	25	73.2	2	0	0	1392.82	284	296
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	11	13	20	0.02%	27.7%	DGNDLHMTYK	99.7%	45.7	25	43.7	3	0	0	1193.53	263	272
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	11	13	20	0.02%	27.7%	EISFAYEVLSNPEK	99.7%	76.4	25	76.4	1	0	0	1625.81	49	62
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	11	13	20	0.02%	27.7%	EISFAYEVLSNPEKR	99.7%	67.8	25	58.6	2	0	0	1781.91	49	63
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	11	13	20	0.02%	27.7%	IGLVEALCGFQFTFK	99.7%	71.9	25	68.7	1	0	0	1729.90	273	287
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	11	13	20	0.02%	27.7%	ILEVHVDK	99.7%	46.1	25	26.2	2	0	0	952.55	216	223
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	11	13	20	0.02%	27.7%	LYDILGVPPGASENELKK	98.5%	33.1	25	28.7	1	1	0	1943.05	9	26
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	11	13	20	0.02%	27.7%	NVLCSACSGQGGK	99.7%	88.2	25	88.2	2	0	0	1337.59	140	152
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	11	13	20	0.02%	27.7%	RGEDMMHPLK	99.5%	30.5	25	13.6	0	1	0	1213.58	112	121
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	11	13	20	0.02%	27.7%	VIEPGCVR	99.5%	38.6	25	29.7	2	0	0	929.49	303	310
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	11	13	20	0.02%	27.7%	VSLEDLYNGK	99.7%	63.8	25	48.8	2	0	0	1137.58	122	131
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	11	13	20	0.02%	27.7%	YGEQGLR	99.7%	53.2	25	33.2	2	0	0	822.41	69	75
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	7	9	14	0.01%	21.9%	EFTVNIMDTCER	99.7%	40.8	25	40.8	1	0	0	1514.66	227	238
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	7	9	14	0.01%	21.9%	FSQLAEAYEVLSDEVK	99.7%	57.7	25	57.6	2	0	0	1827.90	135	150
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	7	9	14	0.01%	21.9%	GGPTVDPEELFR	99.7%	42.1	25	42.1	2	0	0	1316.65	176	187
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	7	9	14	0.01%	21.9%	GSIIISPCVVCR	99.7%	56.6	25	44.3	2	0	0	1360.71	282	293
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	7	9	14	0.01%	21.9%	INSYGYGDHYIHIK	98.6%	33.3	25	30.2	1	0	0	1679.82	396	409
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	7	9	14	0.01%	21.9%	QYDAYGSAGFDPGASGSQHSYWK	99.7%	58.3	25	58.3	0	1	0	2479.06	153	175
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	7	9	14	0.01%	21.9%	VMIPVPAGVEDGQTVR	99.7%	87.7	25	82.2	4	1	0	1683.87	304	319
DnaJ homolog subfamily B member 11	DNAJB11	DJB11_HUMAN	40.5	100.0%	3	3	6	0.01%	9.8%	EQLTEEAR	99.2%	36.2	25	28	2	0	0	975.47	329	336
DnaJ homolog subfamily B member 11	DNAJB11	DJB11_HUMAN	40.5	100.0%	3	3	6	0.01%	9.8%	FQDLGAAYEVLSDSEK	99.7%	120	25	115	2	0	0	1771.84	67	82
DnaJ homolog subfamily B member 11	DNAJB11	DJB11_HUMAN	40.5	100.0%	3	3	6	0.01%	9.8%	TLEVEIEPGVR	99.7%	64.2	25	51.5	2	0	0	1241.67	207	217
DnaJ homolog subfamily B member 12	DNAJB12	DJB12_HUMAN	41.8	100.0%	4	4	6	0.01%	12.3%	AIGTAYAVLSNPEK	99.7%	68.2	25	62	2	0	0	1433.76	153	166
DnaJ homolog subfamily B member 12	DNAJB12	DJB12_HUMAN	41.8	100.0%	4	4	6	0.01%	12.3%	DYYEILGVSR	99.5%	37.9	25	31.5	1	0	0	1214.61	110	119
DnaJ homolog subfamily B member 12	DNAJB12	DJB12_HUMAN	41.8	100.0%	4	4	6	0.01%	12.3%	GYTAEQVAAVK	99.2%	36	25	32.8	1	0	0	1136.59	93	103
DnaJ homolog subfamily B member 12	DNAJB12	DJB12_HUMAN	41.8	100.0%	4	4	6	0.01%	12.3%	NVEDDYIANLR	99.7%	74.7	25	73.9	2	0	0	1321.64	316	326
DnaJ homolog subfamily B member 6	DNAJB6	DNJB6_HUMAN	36.1	100.0%	3	3	7	0.01%	11.0%	APGPWDPLASAAGLK	99.7%	51	25	51	2	0	0	1450.77	288	302
DnaJ homolog subfamily B member 6	DNAJB6	DNJB6_HUMAN	36.1	100.0%	3	3	7	0.01%	11.0%	VDYYEVLGVQR	99.7%	55.8	25	29.6	3	0	0	1340.68	2	12
DnaJ homolog subfamily B member 6	DNAJB6	DNJB6_HUMAN	36.1	100.0%	3	3	7	0.01%	11.0%	VEVEEDGQLK	99.6%	38.9	25	30	2	0	0	1145.57	216	225
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	11	11	28	0.03%	14.8%	AIAALISEK	99.7%	41.2	25	35.9	2	0	0	915.55	770	778
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	11	11	28	0.03%	14.8%	ALLPELR	95.3%	28.1	25	27.1	1	0	0	811.50	485	491
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	11	11	28	0.03%	14.8%	ASNLLYGQLK	99.7%	60.2	25	51.5	4	0	0	1106.62	493	502
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	11	11	28	0.03%	14.8%	GGDCLTSQTR	99.2%	35.9	25	23.8	1	0	0	1094.49	267	276

DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	11	11	28	0.03%	14.8%	GLEDNQGGQYESWNYYR	99.7%	63.3	25	63.3	1	0	0	2078.88	103	119
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	11	11	28	0.03%	14.8%	GVNSYPSLFIFR	99.7%	59.4	25	59.3	2	0	0	1399.74	197	208
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	11	11	28	0.03%	14.8%	ILYDILAFAK	99.7%	64.2	25	61.8	7	0	0	1166.68	439	448
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	11	11	28	0.03%	14.8%	NDHIQVGR	98.5%	32.9	25	25.6	1	0	0	938.48	393	400
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	11	11	28	0.03%	14.8%	NFQEEQINTR	99.7%	72.9	25	46.9	3	0	0	1278.61	757	766
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	11	11	28	0.03%	14.8%	NSILFLNSLDAK	99.7%	90.9	25	88.5	4	0	0	1334.73	326	337
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	11	11	28	0.03%	14.8%	VDCQAYAQTCQK	99.7%	54.8	25	54.8	2	0	0	1471.63	726	737
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	7	7	16	0.02%	15.0%	AGFFGTVVEYGAER	99.7%	93.7	25	82.8	4	0	0	1502.73	328	341
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	7	7	16	0.02%	15.0%	AGLPGFYDPCVGEEK	99.7%	46.4	25	46.4	2	0	0	1638.75	509	523
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	7	7	16	0.02%	15.0%	ESAATDVLQK	99.7%	55.2	25	46.5	2	0	0	1061.55	425	434
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	7	7	16	0.02%	15.0%	GIRPGLTTVLAR	98.6%	33.3	25	17.1	2	0	0	1253.77	249	260
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	7	7	16	0.02%	15.0%	GLEMEGWEVVER	99.7%	82.8	25	76.2	1	0	0	1433.67	85	96
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	7	7	16	0.02%	15.0%	IIEAEESR	99.7%	47.4	25	33.2	3	0	0	946.48	452	459
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	7	7	16	0.02%	15.0%	VIDVTVPLQCLVK	99.7%	55.9	25	55.2	2	0	0	1483.86	485	497
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	4	4	7	0.01%	2.1%	DSLLASLLDGVR	99.7%	49.8	25	42.1	1	0	0	1258.70	312	323
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	4	4	7	0.01%	2.1%	ELIVGEIFVR	99.7%	64.5	25	64.2	2	0	0	1174.68	1685	1694
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	4	4	7	0.01%	2.1%	IFIAQPAWVLR	99.7%	61.6	25	54	2	0	0	1313.77	1987	1997
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	4	4	7	0.01%	2.1%	IVDGPDPENIILILK	99.7%	48.6	25	47.1	2	0	0	1648.95	1360	1374
DnaJ homolog subfamily C member 7	DNAJC7	DNJC7_HUMAN	56.4	100.0%	3	3	6	0.01%	6.9%	AVQFFVQALR	99.7%	41.2	25	34.2	2	0	0	1178.67	229	238
DnaJ homolog subfamily C member 7	DNAJC7	DNJC7_HUMAN	56.4	100.0%	3	3	6	0.01%	6.9%	EALGDAQQSVR	99.7%	74.3	25	67.7	3	0	0	1173.59	80	90
DnaJ homolog subfamily C member 7	DNAJC7	DNJC7_HUMAN	56.4	100.0%	3	3	6	0.01%	6.9%	YPEAQSVASDILR	99.7%	50.7	25	50.1	1	0	0	1448.74	192	204
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	9	23	0.02%	31.5%	DVAEQLEK	95.6%	28.4	25	11.1	1	0	0	931.47	73	80
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	9	23	0.02%	31.5%	EGNFDIVSGTR	99.7%	81.3	25	74.6	2	0	0	1194.58	137	147
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	9	23	0.02%	31.5%	GYVFQMEMIVR	99.7%	46.9	25	46.9	3	0	0	1404.67	206	216
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	9	23	0.02%	31.5%	LGGNEIVSFLK	99.7%	70.2	25	70.2	4	0	0	1176.66	241	251
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	9	23	0.02%	31.5%	LGLGTAYIHGMK	99.7%	49.7	25	41.8	3	0	0	1276.67	96	107
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	9	23	0.02%	31.5%	QKEGNFDIVSGTR	99.7%	36	25	29.8	0	4	0	1450.73	135	147
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	9	23	0.02%	31.5%	QLNYTIGEVPISFVDR	99.7%	75.2	25	72.3	4	0	0	1850.96	219	234
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	9	23	0.02%	31.5%	YSVLLPTYNER	99.7%	42.1	25	39.4	2	0	0	1354.70	27	37
Dolichyldiphosphatase 1	DOLPP1	DOPP1_HUMAN	27.0	99.8%	2	2	2	0.00%	8.4%	FLDLLWR	98.2%	32.3	25	16.6	1	0	0	962.55	130	136
Dolichyldiphosphatase 1	DOLPP1	DOPP1_HUMAN	27.0	99.8%	2	2	2	0.00%	8.4%	IAAWPVSEFFLIR	99.7%	44.7	25	37	1	0	0	1548.86	194	206
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	7	7	15	0.02%	17.1%	LPDVYGVFQFK	99.7%	57.6	25	48.9	2	0	0	1312.69	381	391
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	7	7	15	0.02%	17.1%	NTLLIAGLQAR	99.7%	95.9	25	72.4	3	0	0	1169.70	240	250
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	7	7	15	0.02%	17.1%	SSLNPILFR	99.7%	63.3	25	43.3	2	0	0	1046.60	190	198
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	7	7	15	0.02%	17.1%	TADDPSLSLIK	99.2%	35.9	25	29.1	2	0	0	1159.62	78	88
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	7	7	15	0.02%	17.1%	TLVLLDNLNVR	99.7%	75.7	25	61.1	2	0	0	1269.75	47	57
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	7	7	15	0.02%	17.1%	WVFKEEGVLR	99.7%	46.5	25	36.4	2	0	0	1262.69	298	307
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	7	7	15	0.02%	17.1%	YSQTGNYELAVALSR	99.7%	116	25	111	2	0	0	1671.83	283	297
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	20	39	0.04%	31.6%	ALTSEIALLQSR	99.7%	73.3	25	68.1	2	0	0	1301.74	525	536
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	20	39	0.04%	31.6%	ATSFLLALEPELEAR	99.7%	70.2	25	69.1	4	0	0	1659.90	66	80
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	20	39	0.04%	31.6%	DISTLNSGKK	97.1%	30.1	25	16.4	2	0	0	1062.58	508	517
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	20	39	0.04%	31.6%	DTYIENEKLISGK	99.6%	39.9	25	39.9	2	0	0	1509.78	580	592
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	20	39	0.04%	31.6%	DVPAYSQDTFK	99.7%	42.8	25	32.5	2	0	0	1270.60	205	215
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	20	39	0.04%	31.6%	FPLFGGWK	97.8%	31.4	25	15.1	1	0	0	951.51	320	327
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	20	39	0.04%	31.6%	FVDHVFDEQVIDSLTVK	99.7%	49.3	25	48.5	1	0	0	1991.01	355	371
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	20	39	0.04%	31.6%	GEDEEENNLEVR	99.7%	59.2	25	47.3	2	0	0	1432.62	90	101
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	20	39	0.04%	31.6%	HFDETVNR	99.0%	34.9	25	21.4	2	0	0	1017.47	495	502
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	20	39	0.04%	31.6%	LKTEGSDLCDR	99.7%	57.6	25	42.5	2	2	0	1293.61	537	547
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	20	39	0.04%	31.6%	LPVALDPGAK	99.6%	38.8	25	38.8	2	0	0	980.58	117	126
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	20	39	0.04%	31.6%	NIEIDSPYEISR	99.7%	77.9	25	68.4	2	0	0	1435.71	380	391
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	20	39	0.04%	31.6%	QPDSGISSIR	99.7%	51.1	25	37.2	2	0	0	1059.54	269	278

Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	20	39	0.04%	31.6%	SEDLLDYGPFR	99.7%	67.3	25	66.6	2	0	0	1311.62	194	204
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	20	39	0.04%	31.6%	VACITEQVLTLVNK	99.7%	66.7	25	57.9	1	0	0	1587.88	475	488
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	20	39	0.04%	31.6%	VACITEQVLTLVNKR	99.7%	88.9	25	75.4	2	2	0	1743.98	475	489
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	20	39	0.04%	31.6%	VTAEVVLAHLGGGSTSR	99.7%	112	25	112	2	2	0	1653.89	49	65
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	7	7	14	0.01%	12.8%	FELDTSER	98.7%	33.8	25	19.2	3	0	0	996.46	461	468
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	7	7	14	0.01%	12.8%	LQVTNVLSQPLTQATVK	99.7%	130	25	114	4	0	0	1840.05	290	306
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	7	7	14	0.01%	12.8%	MLAQQAVK	97.0%	30	25	14.2	2	0	0	904.49	620	627
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	7	7	14	0.01%	12.8%	SIVEEIEDLVAR	99.7%	59	25	40	1	0	0	1372.73	179	190
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	7	7	14	0.01%	12.8%	TGQEVVFVAEPDNK	99.7%	78.5	25	64.5	2	0	0	1532.76	443	456
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	7	7	14	0.01%	12.8%	TGQEVVFVAEPDNKNVYK	99.7%	48.2	25	45.1	1	0	0	2037.03	443	460
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	7	7	14	0.01%	12.8%	TSFTPVGDVFELNFMNVK	99.7%	67.5	25	66	1	0	0	2045.00	323	340
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	DAD1	DAD1_HUMAN	12.5	100.0%	3	3	7	0.01%	24.8%	ADFQGISPER	99.7%	49.4	25	41.9	3	0	0	1119.54	83	92
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	DAD1	DAD1_HUMAN	12.5	100.0%	3	3	7	0.01%	24.8%	IQINPQNK	97.2%	30.3	25	18.6	2	0	0	954.54	75	82
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	DAD1	DAD1_HUMAN	12.5	100.0%	3	3	7	0.01%	24.8%	SASVVSVISR	99.7%	47.8	25	40.8	2	0	0	1004.57	2	11
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	5	5	8	0.01%	7.5%	EGSPVLLNCLMYK	99.7%	46.6	25	46.6	1	0	0	1523.76	629	641
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	5	5	8	0.01%	7.5%	FGQVYTEAK	99.7%	51.1	25	45.6	2	0	0	1042.52	647	655
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	5	5	8	0.01%	7.5%	FLAEEGFYK	99.7%	47.7	25	34	2	0	0	1103.54	59	67
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	5	5	8	0.01%	7.5%	FYSLLDPSYAK	99.7%	43.8	25	40.3	2	0	0	1303.66	330	340
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	5	5	8	0.01%	7.5%	VGQAMASTEEK	99.3%	36.7	25	23.2	1	0	0	1150.54	555	565
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	STT3B	STT3B_HUMAN	93.7	99.8%	2	2	3	0.00%	2.2%	FYSLWDTGYAK	99.6%	38.9	25	38.9	1	0	0	1350.64	384	394
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	STT3B	STT3B_HUMAN	93.7	99.8%	2	2	3	0.00%	2.2%	VTNIFPK	96.9%	29.8	25	21.9	2	0	0	818.48	787	793
Dolichyl-phosphate beta-glucosyltransferase	ALG5	ALG5_HUMAN	36.9	100.0%	3	3	6	0.01%	13.6%	ETLPSIWDSPTK	99.7%	53.5	25	46.7	2	0	0	1373.69	54	65
Dolichyl-phosphate beta-glucosyltransferase	ALG5	ALG5_HUMAN	36.9	100.0%	3	3	6	0.01%	13.6%	GLNDLQPWPNQMAIACGSR	99.2%	36.1	25	36.1	2	0	0	2128.01	179	197
Dolichyl-phosphate beta-glucosyltransferase	ALG5	ALG5_HUMAN	36.9	100.0%	3	3	6	0.01%	13.6%	QLSVVVPSYNEEK	99.7%	59.5	25	52.5	2	0	0	1491.77	66	78
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	3	3	4	0.00%	5.7%	LAQIQQAK	97.5%	30.7	25	20.9	1	0	0	899.53	291	298
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	3	3	4	0.00%	5.7%	VPQAQPTKPALK	99.4%	37.4	25	34	2	0	0	1277.76	356	367
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	3	3	4	0.00%	5.7%	VSVGEFVGEGEGK	99.7%	53	25	47	1	0	0	1293.63	220	232
Double-stranded RNA-specific adenosine deaminase	ADAR	DSRAD_HUMAN	136.1	100.0%	3	4	9	0.01%	3.0%	AMTILLEEAK	99.7%	46.2	25	25.6	4	0	0	1118.61	565	574
Double-stranded RNA-specific adenosine deaminase	ADAR	DSRAD_HUMAN	136.1	100.0%	3	4	9	0.01%	3.0%	LVDQSGPPHEPK	99.7%	47.5	25	44.2	2	0	0	1303.66	746	757
Double-stranded RNA-specific adenosine deaminase	ADAR	DSRAD_HUMAN	136.1	100.0%	3	4	9	0.01%	3.0%	YLNTNPVGGLLEYAR	99.7%	89.8	25	86.2	3	0	0	1679.88	722	736
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	10	11	17	0.02%	26.5%	DVKPSNILVNSR	99.7%	62.6	25	60.8	2	0	0	1341.75	194	205
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	10	11	17	0.02%	26.5%	ISELGAGNGGVVTK	99.7%	92.6	25	89.6	2	0	0	1301.71	75	88
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	10	11	17	0.02%	26.5%	LNQPGTPTR	99.7%	53.4	25	47.4	2	0	0	983.53	389	397
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	10	11	17	0.02%	26.5%	RIPEEILGK	99.7%	42	25	39.4	2	0	0	1054.63	164	172
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	10	11	17	0.02%	26.5%	RLEAFLTQK	99.7%	40.3	25	29.3	1	0	0	1105.64	53	61
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	10	11	17	0.02%	26.5%	SEVEEVDFAGWLCK	99.7%	63.5	25	63.5	1	0	0	1668.76	372	385
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	10	11	17	0.02%	26.5%	SYMAPER	97.2%	30.3	25	13	1	0	0	869.38	232	238
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	10	11	17	0.02%	26.5%	VGELKDDDFER	99.7%	68.6	25	60.2	2	2	0	1322.62	64	74
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	10	11	17	0.02%	26.5%	VQHRPSGLIMAR	98.8%	26.9	25	26.9	0	1	0	1364.76	89	100
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	10	11	17	0.02%	26.5%	YPIPPPDAK	99.0%	34.9	25	17	1	0	0	997.54	265	273
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	9	11	19	0.02%	32.6%	DVKPSNVLINK	97.3%	30.5	25	23.9	1	0	0	1226.71	190	200
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	9	11	19	0.02%	32.6%	FPYESWGTPFQQLK	99.7%	62	25	57.5	2	0	0	1727.84	266	279
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	9	11	19	0.02%	32.6%	FSPEFVDFTAQCLR	99.7%	74.1	25	74.1	2	0	0	1716.81	294	307
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	9	11	19	0.02%	32.6%	GAYGVVEK	96.4%	29.2	25	21.1	1	0	0	822.44	73	80
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	9	11	19	0.02%	32.6%	HAQSGTIMAVK	99.5%	38.4	25	24.9	2	0	0	1142.60	83	93
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	9	11	19	0.02%	32.6%	ISCMSKPPAPNPTPPR	99.7%	42.4	25	42.4	0	3	0	1749.88	27	42
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	9	11	19	0.02%	32.6%	KTDIAAFVK	98.5%	33.2	25	16.3	2	0	0	992.58	332	340
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	9	11	19	0.02%	32.6%	MCDFGISGYLVDSVAK	99.7%	74.5	25	74.5	4	0	0	1777.81	206	221
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	9	11	19	0.02%	32.6%	QVVEEPSPQLPADR	99.7%	49.5	25	46.3	2	0	0	1564.80	280	293
Dual specificity protein phosphatase 3	DUSP3	DUS3_HUMAN	20.5	100.0%	2	2	4	0.00%	14.1%	AADFIDQALAQK	99.7%	54.7	25	48.6	2	0	0	1290.67	105	116
Dual specificity protein phosphatase 3	DUSP3	DUS3_HUMAN	20.5	100.0%	2	2	4	0.00%	14.1%	IYVGNASVAQDIPK	99.7%	70.3	25	68.2	2	0	0	1474.79	37	50

Dual specificity protein phosphatase 9	DUSP9	DUS9_HUMAN	41.9	100.0%	2	2	2	0.00%	8.3%	ASFPVQILPNLYLGSAR	97.8%	31.2	25	31.2	1	0	0	1846.02	201	217
Dual specificity protein phosphatase 9	DUSP9	DUS9_HUMAN	41.9	100.0%	2	2	2	0.00%	8.3%	IGGALSVALPALLLR	99.5%	37.8	25	37.8	1	0	0	1463.93	38	52
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	AEITDAEGLGLK	99.7%	80.4	25	69.4	1	0	0	1216.64	933	944
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	AESLQQEVEALK	99.7%	70.7	25	60	2	0	0	1344.70	318	329
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	AFLQGGQEATDIALLLR	99.7%	84.2	25	68.5	2	0	0	1816.00	769	785
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	AIEMELR	97.5%	30.7	25	19	1	0	0	877.44	568	574
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	ASEQIYGTPSSSPYECLR	99.7%	59.8	25	50.2	1	0	0	2044.93	873	890
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	ASLASLPPLHVAK	99.7%	46.4	25	39.1	2	0	0	1303.77	1121	1133
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	DLEEKLETLR	99.7%	54.9	25	38.7	2	0	0	1245.67	226	235
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	DLETSCSDIR	99.7%	68.2	25	57.3	2	0	0	1195.53	786	795
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	DQLDETVNVEPLTK	99.4%	37.5	25	31.4	1	0	0	1600.81	709	722
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	DSPLLLQQISAMR	99.7%	73.2	25	68.1	4	0	0	1471.79	1089	1101
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	ELTNQQEASVER	99.7%	79.6	25	79.6	2	0	0	1403.68	533	544
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	EQLDMAGAR	99.7%	53	25	49.8	2	0	0	990.47	487	495
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	FTQSALDCMSVEVGR	99.7%	75.2	25	75.2	4	0	0	1699.78	752	766
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	GSDGAASSYQLK	99.7%	66.5	25	57.9	2	0	0	1183.56	350	361
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	GTVAYVGATLFATGK	99.7%	82.4	25	82.4	2	0	0	1455.78	42	56
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	IKGEELSEANVR	99.7%	50.6	25	44	2	1	0	1344.71	961	972
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	IQLEQVQEWK	99.7%	54.8	25	48.3	2	0	0	1300.69	253	262
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	LKDALVR	98.4%	32.6	25	12.4	1	0	0	814.51	370	376
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	LSHEGPGSELPAGALYR	99.7%	32.6	25	31.2	0	2	0	1753.89	1134	1150
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	MQEQQADLQR	99.7%	73	25	65.7	4	0	0	1246.58	265	274
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	NQELEVVR	99.7%	59.7	25	41.7	2	0	0	986.53	399	406
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	QLTAHLQDVNR	99.7%	48.9	25	42	2	2	0	1294.69	522	532
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	QSCNILISTMNK	99.3%	36.8	25	26.6	1	0	0	1408.69	891	902
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	SPSAQLMEQVAQLK	99.7%	93.9	25	85.5	4	0	0	1529.80	1180	1193
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	VDELTTDLEILK	99.7%	102	25	79.1	2	0	0	1388.75	332	343
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	VEAAQETVADYQQTIK	99.7%	74.5	25	71.3	1	0	0	1793.89	503	518
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	VTFSCAAGFGQR	99.7%	88.5	25	79.5	2	0	0	1300.61	1248	1259
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	28	34	60	0.06%	26.6%	WVGVILDEAK	99.7%	45.6	25	36.7	2	0	0	1129.63	57	66
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	10	10	14	0.01%	17.4%	AEELLAEEK	98.8%	33.8	25	26.4	1	0	0	1031.53	598	606
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	10	10	14	0.01%	17.4%	FATEYCNTIEGTAK	99.7%	67.9	25	60.8	2	0	0	1604.73	340	353
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	10	10	14	0.01%	17.4%	GVSPEPIHLK	98.4%	32.8	25	23.8	2	0	0	1076.61	124	133
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	10	10	14	0.01%	17.4%	IFSPNVVNLTLVDLPGMTK	99.7%	59.7	25	59.7	2	0	0	2074.13	134	152
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	10	10	14	0.01%	17.4%	LGIIGVVNR	99.7%	78.4	25	68.1	2	0	0	940.59	239	247
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	10	10	14	0.01%	17.4%	RLEEPSLR	99.7%	48.4	25	37.2	1	0	0	999.56	423	430
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	10	10	14	0.01%	17.4%	SQLDINNKK	98.3%	32.5	25	16.3	1	0	0	1059.58	248	256
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	10	10	14	0.01%	17.4%	SSLLDDLLTESEDMAQR	98.3%	32.5	25	32.5	1	0	0	1922.90	693	709
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	10	10	14	0.01%	17.4%	TLESVDPLGGLNTIDILTAIR	99.7%	80.2	25	80.2	1	0	0	2211.22	377	397
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	10	10	14	0.01%	17.4%	YIETSELCGGAR	99.7%	50.8	25	43.4	1	0	0	1355.63	354	365
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	14	25	0.03%	16.4%	ALLQMVQQFGVDFEK	99.7%	69	25	69	1	0	0	1752.90	328	342
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	14	25	0.03%	16.4%	DMILQFISR	99.7%	56.6	25	27.5	2	0	0	1122.60	158	166
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	14	25	0.03%	16.4%	ESSLILAVTPANMDLANSDALK	99.7%	77.7	25	75.5	2	0	0	2273.17	167	188
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	14	25	0.03%	16.4%	EVDPQGLR	98.4%	32.8	25	19.5	2	0	0	913.47	192	199
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	14	25	0.03%	16.4%	FPFELVK	99.7%	42.5	25	0	2	0	0	879.50	370	376
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	14	25	0.03%	16.4%	GMEELIPLVNK	99.7%	69.9	25	59.7	2	0	0	1242.68	5	15
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	14	25	0.03%	16.4%	GYIGVVNR	99.4%	37.1	25	31.3	3	0	0	877.49	230	237
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	14	25	0.03%	16.4%	IVTTYIR	99.7%	44.3	25	26.2	1	0	0	865.51	459	465
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	14	25	0.03%	16.4%	LQSQLLSLEK	99.7%	58.8	25	0	2	0	0	1158.67	300	309
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	14	25	0.03%	16.4%	NLVDSYVAIINK	99.7%	81.9	25	64.1	3	0	0	1348.75	658	669
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	14	25	0.03%	16.4%	SSVLENFVGR	99.7%	57.5	25	41.2	2	0	0	1107.58	45	54

Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	14	25	0.03%	16.4%	TGLFTPDLAFEAIVK	99.7%	83.9	25	75	2	0	0	1621.88	400	414
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	14	25	0.03%	16.4%	YMLPLDNLK	97.8%	31.3	25	12.4	1	0	0	1106.59	563	571
Dynamin-like 120 kDa protein, mitochondrial	OPA1	OPA1_HUMAN	111.6	100.0%	3	3	4	0.00%	3.1%	ESVEQQADSFK	99.7%	41.7	25	41.7	1	0	0	1267.58	558	568
Dynamin-like 120 kDa protein, mitochondrial	OPA1	OPA1_HUMAN	111.6	100.0%	3	3	4	0.00%	3.1%	QQLTNTEVR	99.5%	38.7	25	27.9	2	0	0	1088.57	896	904
Dynamin-like 120 kDa protein, mitochondrial	OPA1	OPA1_HUMAN	111.6	100.0%	3	3	4	0.00%	3.1%	VIQHNALEDR	99.7%	51.8	25	34	1	0	0	1194.62	724	733
Dynein light chain 1, cytoplasmic	DYNLL1	DYL1_HUMAN	10.4	100.0%	3	3	10	0.01%	49.4%	NADMSEEMQQDSVECATQALEK	98.7%	26.7	25	26.7	0	2	0	2546.03	10	31
Dynein light chain 1, cytoplasmic	DYNLL1	DYL1_HUMAN	10.4	100.0%	3	3	10	0.01%	49.4%	NFGSYVTHETK	99.3%	36.2	25	27.9	4	0	0	1282.61	61	71
Dynein light chain 1, cytoplasmic	DYNLL1	DYL1_HUMAN	10.4	100.0%	3	3	10	0.01%	49.4%	YNPTWHCIVGR	99.7%	52.6	25	52.1	4	0	0	1402.67	50	60
Dynein light chain Tctex-type 1	DYNLT1	DYLT1_HUMAN	12.5	99.8%	2	3	5	0.01%	23.0%	EAIESAIGGNAYQHSK	99.7%	71.3	25	71.3	2	0	0	1674.81	23	38
Dynein light chain Tctex-type 1	DYNLT1	DYLT1_HUMAN	12.5	99.8%	2	3	5	0.01%	23.0%	YIVTCVIMQK	99.7%	55.3	25	47.3	3	0	0	1254.66	63	72
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	13	13	21	0.02%	5.2%	ELLQSFDSALQSVK	99.7%	75.6	25	72.5	4	0	0	1564.82	257	270
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	13	13	21	0.02%	5.2%	ELVGPPLAETVFTPK	99.7%	80.1	25	76.5	2	0	0	1597.88	1384	1398
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	13	13	21	0.02%	5.2%	FGESTTGFNFSFK	99.6%	39.5	25	39.3	1	0	0	1468.67	2260	2272
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	13	13	21	0.02%	5.2%	FGISEPGNQEK	97.9%	31.6	25	20.6	1	0	0	1205.58	1900	1910
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	13	13	21	0.02%	5.2%	GVIFGQTSSTFTFADLAK	99.7%	58.7	25	58.7	2	0	0	1889.96	1935	1952
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	13	13	21	0.02%	5.2%	IAVAVLEETTR	99.7%	79.5	25	76.2	2	0	0	1201.68	2467	2477
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	13	13	21	0.02%	5.2%	IIDDSDSNLSVVK	99.7%	82.1	25	0	2	0	0	1404.72	721	733
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	13	13	21	0.02%	5.2%	LLVQHEINTLR	99.5%	38.1	25	38.1	1	0	0	1335.77	553	563
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	13	13	21	0.02%	5.2%	SGFEGMFTK	96.7%	29.6	25	28.3	1	0	0	1003.46	1597	1605
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	13	13	21	0.02%	5.2%	SGQSALYDALFSSQSPK	99.7%	65.4	25	60.8	1	0	0	1785.87	380	396
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	13	13	21	0.02%	5.2%	SGSSFVHQASFK	99.0%	34.9	25	26.5	1	0	0	1281.62	1447	1458
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	13	13	21	0.02%	5.2%	STSGEGFQFGK	98.7%	33.6	25	27.3	1	0	0	1144.53	1953	1963
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	13	13	21	0.02%	5.2%	YIASVQGSTPSPR	99.7%	73.2	25	69	2	0	0	1362.70	11	23
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	21	21	28	0.03%	5.8%	AALPLTTSDTK	99.7%	42.4	25	40.5	2	0	0	1117.61	1498	1508
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	21	21	28	0.03%	5.8%	AIQDPAFSDGIR	99.7%	45.1	25	45.1	1	0	0	1289.65	518	529
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	21	21	28	0.03%	5.8%	ALAELFGLLVK	99.7%	79.9	25	67.5	2	0	0	1173.72	1062	1072
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	21	21	28	0.03%	5.8%	DGGSGNSTIIVSR	99.7%	43.8	25	36	1	0	0	1262.63	2359	2371
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	21	21	28	0.03%	5.8%	DSAVAISGADSR	99.7%	68.2	25	61.7	1	0	0	1148.55	2930	2941
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	21	21	28	0.03%	5.8%	EMFNPMYALFR	99.7%	41.7	25	36.7	1	0	0	1418.66	4072	4082
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	21	21	28	0.03%	5.8%	EVLGSLPNVFSALCLNAR	99.5%	38.3	25	38.3	1	0	0	1960.03	599	616
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	21	21	28	0.03%	5.8%	IVNQPSSLFGSK	96.4%	29.2	25	9.11	1	0	0	1276.69	2256	2267
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	21	21	28	0.03%	5.8%	LGSSGLGSASSIQAAVR	99.7%	70.8	25	70.8	1	0	0	1560.83	3750	3766
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	21	21	28	0.03%	5.8%	LLSLISIALPENK	99.4%	37.6	25	37.6	3	0	0	1410.86	3456	3468
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	21	21	28	0.03%	5.8%	LPGGVQNFPQFSALR	99.5%	38.6	25	38	1	0	0	1630.87	1226	1240
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	21	21	28	0.03%	5.8%	LYIVFEGEEGQDAGGLLR	99.4%	37.5	25	32.2	1	0	0	1965.99	4046	4063
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	21	21	28	0.03%	5.8%	NLCYHAQTR	96.1%	28.9	25	23.9	1	0	0	1162.54	3211	3219
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	21	21	28	0.03%	5.8%	NPDIFTEVANCCIR	99.7%	58	25	58	1	0	0	1708.78	1881	1894
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	21	21	28	0.03%	5.8%	QIGTLLAELR	95.1%	28	25	12.6	1	0	0	1113.66	3637	3646
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	21	21	28	0.03%	5.8%	SILTLSHEPK	99.6%	38.9	25	30.8	2	0	0	1124.63	830	839
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	21	21	28	0.03%	5.8%	SLLSILQR	99.1%	35.5	25	18.4	1	0	0	929.58	3225	3232
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	21	21	28	0.03%	5.8%	SSESELCIETPK	99.0%	34.8	25	34.8	1	0	0	1379.64	3233	3244
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	21	21	28	0.03%	5.8%	TLTSIVHLER	99.7%	46	25	35.5	2	0	0	1168.67	330	339
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	21	21	28	0.03%	5.8%	TNIFQIQR	99.6%	39.2	25	18.7	1	0	0	1019.56	3298	3305
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	21	21	28	0.03%	5.8%	TPTEAPADCR	98.8%	34	25	34	2	0	0	1117.49	11	20
E3 ubiquitin-protein ligase RING2	RNF2	RING2_HUMAN	37.7	100.0%	4	4	5	0.01%	14.3%	FCADCIITALR	99.7%	54	25	47.8	1	0	0	1339.65	71	81
E3 ubiquitin-protein ligase RING2	RNF2	RING2_HUMAN	37.7	100.0%	4	4	5	0.01%	14.3%	IYPSRDEYEAHQER	95.4%	22.1	25	16.6	0	1	0	1792.82	113	126
E3 ubiquitin-protein ligase RING2	RNF2	RING2_HUMAN	37.7	100.0%	4	4	5	0.01%	14.3%	TSGNATVDHLSK	99.7%	62	25	52.8	2	0	0	1229.61	250	261
E3 ubiquitin-protein ligase RING2	RNF2	RING2_HUMAN	37.7	100.0%	4	4	5	0.01%	14.3%	TWELSLYELQR	99.7%	53	25	44.8	1	0	0	1437.74	16	26
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	14	16	29	0.03%	27.2%	ALCWVCAQSR	99.7%	56.4	25	48.1	2	0	0	1250.58	109	118
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	14	16	29	0.03%	27.2%	DLDITSPELR	99.7%	53.9	25	43.4	2	0	0	1158.60	261	270
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	14	16	29	0.03%	27.2%	EAWDLGVCR	99.7%	56	25	56	2	0	0	1105.51	352	360

E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	14	16	29	0.03%	27.2%	GGGSVCPVCR	99.0%	34.9	25	30.4	1	0	0	1048.47	46	55
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	14	16	29	0.03%	27.2%	HYWEVDVTGK	99.6%	39.7	25	34.3	2	0	0	1233.59	342	351
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	14	16	29	0.03%	27.2%	IHAEFVQQK	99.7%	42.6	25	28.4	2	0	0	1099.59	178	186
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	14	16	29	0.03%	27.2%	LGDTQQSIPGNEER	99.7%	56.2	25	54	2	0	0	1543.73	311	324
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	14	16	29	0.03%	27.2%	LQVALGELR	99.7%	55.7	25	27.7	2	0	0	998.60	139	147
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	14	16	29	0.03%	27.2%	LQVALGELRR	99.7%	43.6	25	39.1	1	0	0	1154.70	139	148
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	14	16	29	0.03%	27.2%	NFLVEEEQR	99.7%	56	25	30.3	2	0	0	1163.57	187	195
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	14	16	29	0.03%	27.2%	QLANMVNNLK	99.7%	56.3	25	50.7	3	0	0	1144.61	68	77
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	14	16	29	0.03%	27.2%	SESWNLKDLDITSPELR	99.7%	73.6	25	69.4	2	2	0	2003.01	254	270
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	14	16	29	0.03%	27.2%	SGFWTIWLWNK	99.7%	59	25	53.2	2	0	0	1437.73	375	385
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	14	16	29	0.03%	27.2%	SVCHVPGLKK	96.6%	29.5	25	18.6	2	0	0	1124.62	271	280
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	15	15	23	0.02%	19.8%	AQFAEATQR	99.7%	46.4	25	33.3	2	0	0	1021.51	18	26
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	15	15	23	0.02%	19.8%	AVFVPDIYSR	98.4%	32.8	25	30.9	1	0	0	1166.62	242	251
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	15	15	23	0.02%	19.8%	CVPQIIAFLNSK	99.4%	37.1	25	36.4	1	0	0	1389.76	708	719
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	15	15	23	0.02%	19.8%	ELQELSSSIK	99.0%	34.7	25	30.2	1	0	0	1133.60	771	780
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	15	15	23	0.02%	19.8%	FFADDTQAALTK	99.7%	90.2	25	86.5	2	0	0	1327.65	560	571
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	15	15	23	0.02%	19.8%	FINDCTELFR	99.7%	42.9	25	36.2	1	0	0	1314.61	368	377
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	15	15	23	0.02%	19.8%	GVIFTEAFVAR	99.7%	87.4	25	73.7	2	0	0	1209.66	175	185
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	15	15	23	0.02%	19.8%	IISGHIDLDNR	99.6%	39.6	25	33.8	2	0	0	1252.66	164	174
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	15	15	23	0.02%	19.8%	LAADFQR	99.7%	40.1	25	23.8	2	0	0	820.43	11	17
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	15	15	23	0.02%	19.8%	LGIPDAVSYIK	97.9%	31.5	25	24.2	1	0	0	1175.67	275	285
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	15	15	23	0.02%	19.8%	QISTLESVSTSK	99.7%	50.4	25	46.8	1	0	0	1279.67	403	414
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	15	15	23	0.02%	19.8%	TQSTWVDSFFR	99.7%	40.8	25	39.5	2	0	0	1373.65	252	262
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	15	15	23	0.02%	19.8%	TTQLLFLK	95.1%	28	25	19.5	2	0	0	963.59	290	297
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	15	15	23	0.02%	19.8%	TYDLPGNFLTQALTQR	99.7%	102	25	87.1	2	0	0	1837.94	145	160
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	15	15	23	0.02%	19.8%	TYLEVVR	97.7%	31.1	25	29.9	1	0	0	879.49	512	518
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	11	14	20	0.02%	23.6%	ADQIETQQLMR	99.7%	60.1	25	52.3	3	0	0	1332.66	221	231
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	11	14	20	0.02%	23.6%	EHQISPGDFPSLR	99.7%	41.4	25	30.7	1	2	0	1482.73	345	357
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	11	14	20	0.02%	23.6%	ELVNNLGEIYQK	99.7%	73.2	25	73.2	2	0	0	1419.75	330	341
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	11	14	20	0.02%	23.6%	EPELFQTVAEGLR	99.7%	44.3	25	39.6	2	0	0	1488.77	14	26
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	11	14	20	0.02%	23.6%	KLNDLIK	97.6%	31	25	7.61	1	0	0	843.53	293	299
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	11	14	20	0.02%	23.6%	LLDTVDDMLANDIAR	99.7%	61.2	25	61.2	1	0	0	1674.84	378	392
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	11	14	20	0.02%	23.6%	LLPLEEHYR	95.9%	28.7	25	16.5	2	0	0	1169.63	33	41
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	11	14	20	0.02%	23.6%	LNAFGNAFLNR	99.7%	69.2	25	59.7	2	0	0	1236.65	125	135
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	11	14	20	0.02%	23.6%	MQELLQTQDFSK	99.7%	62.4	25	52.1	1	0	0	1467.72	359	370
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	11	14	20	0.02%	23.6%	QEESLMPSQVVK	99.7%	42.8	25	34.1	2	0	0	1374.69	399	410
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	11	14	20	0.02%	23.6%	VYGALMWSLGK	99.5%	38.2	25	38.2	1	0	0	1240.64	232	242
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	5	5	7	0.01%	13.7%	AGGADAVQTVTGGLR	99.7%	71.7	25	64	2	0	0	1372.72	15	29
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	5	5	7	0.01%	13.7%	EGADEEEWVVAK	98.6%	33.4	25	33.4	1	0	0	1361.62	435	446
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	5	5	7	0.01%	13.7%	EYQISAGDFPEVK	99.7%	67.8	25	61.6	2	0	0	1482.71	348	360
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	5	5	7	0.01%	13.7%	FGNAFLNR	99.7%	52.2	25	42.6	1	0	0	938.48	131	138
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	5	5	7	0.01%	13.7%	KLNDLIK	97.6%	31	25	7.61	1	0	0	843.53	296	302
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	5	5	7	0.01%	13.7%	LPNSVLGK	97.6%	30.9	25	23.1	1	0	0	827.50	479	486
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	5	5	7	0.01%	13.7%	VYGALMWSLGK	99.5%	38.2	25	38.2	1	0	0	1240.64	235	245
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	9	11	23	0.02%	32.5%	AINTLNGLR	99.7%	50.9	25	38.8	2	0	0	971.56	77	85
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	9	11	23	0.02%	32.5%	FAANPNQNK	97.0%	30	25	25.3	1	0	0	1003.50	183	191
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	9	11	23	0.02%	32.5%	LGDKILQVSFK	99.7%	45.4	25	45.4	1	2	0	1247.74	310	320
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	9	11	23	0.02%	32.5%	NVALLSQLYHSPAR	99.7%	62.2	25	59.7	2	0	0	1568.85	192	205
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	9	11	23	0.02%	32.5%	SLFSSIGEVESAK	99.7%	85	25	74.8	4	0	0	1353.69	38	50
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	9	11	23	0.02%	32.5%	TNLIVNYLPQNMTQDELR	99.7%	72.1	25	69.6	4	0	0	2162.09	20	37
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	9	11	23	0.02%	32.5%	VIRDFNTNK	98.9%	34.4	25	23.1	2	0	0	1106.60	275	283

ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	9	11	23	0.02%	32.5%	VLVDQTTGLSR	99.7%	88	25	67.8	3	0	0	1188.66	137	147
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	9	11	23	0.02%	32.5%	VSYARPSSEVIK	99.7%	48	25	23.1	2	0	0	1335.73	93	104
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	13	17	45	0.05%	53.2%	AAVDAGFVPNDMQVGQTGK	99.7%	88.2	25	87.2	4	0	0	1920.91	250	268
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	13	17	45	0.05%	53.2%	ASSTSPVEISEWLDQK	99.7%	83.6	25	76.8	3	0	0	1776.87	188	203
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	13	17	45	0.05%	53.2%	CDKVAQDLCK	99.7%	42.3	25	31.4	2	0	0	1236.57	60	69
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	13	17	45	0.05%	53.2%	GLLPEELTPLILATQK	99.7%	88.6	25	88.2	4	2	0	1736.02	86	101
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	13	17	45	0.05%	53.2%	GTSFDAAATSGGSASSEK	99.7%	136	25	134	3	0	0	1630.72	170	187
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	13	17	45	0.05%	53.2%	LEVAPISDIIAIK	99.7%	99.8	25	85.2	7	0	0	1381.83	127	139
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	13	17	45	0.05%	53.2%	LGGEVSCLVAGTK	99.7%	91.1	25	88.6	4	0	0	1290.67	47	59
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	13	17	45	0.05%	53.2%	LLYDLADQLHAAVGASR	99.7%	67.9	25	59.5	2	2	0	1812.96	233	249
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	13	17	45	0.05%	53.2%	QFNYTHICAGASAFGK	99.7%	44.7	25	40.8	1	0	0	1771.82	102	117
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	13	17	45	0.05%	53.2%	SPDTFVR	99.7%	42	25	24.6	2	0	0	821.42	140	146
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	13	17	45	0.05%	53.2%	TIYAGNALCTVK	99.7%	82.6	25	74	2	0	0	1310.68	147	158
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	13	17	45	0.05%	53.2%	VLVAQHDVYK	99.7%	62	25	52.8	4	0	0	1171.65	76	85
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	13	17	45	0.05%	53.2%	VVPEMTEILK	99.5%	38	25	32.9	3	0	0	1158.64	322	331
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	18	0.02%	48.6%	EIDGGLETLR	99.7%	82.9	25	75.7	2	0	0	1102.57	165	174
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	18	0.02%	48.6%	EKVDLVLLGK	98.7%	33.7	25	30	1	0	0	1113.69	115	124
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	18	0.02%	48.6%	EVIAVSCGPAQCQETIR	99.7%	106	25	102	2	0	0	1917.92	60	76
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	18	0.02%	48.6%	GIHVEVPPAEAER	96.4%	22.9	25	22.2	0	1	0	1403.73	86	98
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	18	0.02%	48.6%	IEVIKPGDLGVDLTSK	99.7%	52.8	25	52.8	1	0	0	1683.95	206	221
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	18	0.02%	48.6%	LGPLQVAR	99.7%	71.4	25	62.7	2	0	0	853.53	99	106
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	18	0.02%	48.6%	LPAVVTADLR	99.7%	45.1	25	33.3	1	0	0	1054.63	177	186
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	18	0.02%	48.6%	LSVISVEDPPQR	99.7%	50.6	25	45.9	2	0	0	1339.72	222	233
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	18	0.02%	48.6%	TALAMGADR	99.7%	48.6	25	35.1	2	0	0	905.45	77	85
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	18	0.02%	48.6%	TGVVTDGVK	99.7%	41.2	25	26.2	2	0	0	875.48	27	35
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	18	0.02%	48.6%	VETTEDLVAK	99.7%	61.3	25	46	2	0	0	1104.58	239	248
ELMO domain-containing protein 2	ELMOD2	ELMD2_HUMAN	35.0	100.0%	5	6	10	0.01%	16.7%	IENSLTYSK	99.4%	37.7	25	33.7	2	0	0	1054.54	47	55
ELMO domain-containing protein 2	ELMOD2	ELMD2_HUMAN	35.0	100.0%	5	6	10	0.01%	16.7%	IFDTYVGAQR	99.7%	67.9	25	59.2	2	0	0	1169.60	34	43
ELMO domain-containing protein 2	ELMOD2	ELMD2_HUMAN	35.0	100.0%	5	6	10	0.01%	16.7%	LWNLLMPTK	99.6%	39.7	25	31.2	2	0	0	1115.63	134	142
ELMO domain-containing protein 2	ELMOD2	ELMD2_HUMAN	35.0	100.0%	5	6	10	0.01%	16.7%	MCLLQITGYK	99.7%	48.3	25	48.3	3	0	0	1242.62	97	106
ELMO domain-containing protein 2	ELMOD2	ELMD2_HUMAN	35.0	100.0%	5	6	10	0.01%	16.7%	NINPEKDASFK	97.0%	30	25	12.1	1	0	0	1262.64	82	92
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	28	231	0.23%	45.5%	EHALLAYTLGVK	99.7%	73.9	25	63	28	6	0	1314.74	135	146
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	28	231	0.23%	45.5%	EVSTYIK	97.4%	30.6	25	0.47	2	0	0	839.45	173	179
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	28	231	0.23%	45.5%	EVSTYIKK	99.7%	46.4	25	36.2	9	0	0	967.55	173	180
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	28	231	0.23%	45.5%	FEKEAAEMGK	99.7%	52.6	25	40.2	4	0	0	1139.54	42	51
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	28	231	0.23%	45.5%	IGGIGTVPVGR	99.7%	86.7	25	81.3	33	0	0	1025.61	256	266
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	28	231	0.23%	45.5%	LPLQDVYK	99.7%	60	25	47.3	16	0	0	975.55	248	255
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	28	231	0.23%	45.5%	MDSTEPPYSQK	99.7%	50.9	25	49.4	1	0	0	1298.56	155	165
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	28	231	0.23%	45.5%	NMITGTSQADCAVLIVAAGVGEFEAGISK	99.6%	31.2	25	31.2	0	1	0	2925.43	101	129
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	28	231	0.23%	45.5%	QLIVGVNK	99.7%	44.5	25	28.5	8	0	0	870.54	147	154
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	28	231	0.23%	45.5%	QTVAVGVIK	99.7%	63.9	25	43.9	11	0	0	914.57	431	439
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	28	231	0.23%	45.5%	RYEEIVK	98.5%	33	25	6.8	2	0	0	936.51	166	172
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	28	231	0.23%	45.5%	SGDAAIVDMVPGKPMCVESFSDYPPLGR	99.7%	59	25	59	0	4	0	3027.39	396	423
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	28	231	0.23%	45.5%	STTTGHLIYK	99.7%	49	25	38.3	34	0	0	1120.60	21	30
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	28	231	0.23%	45.5%	THINIVVIGHVDSGK	99.7%	116	25	116	4	12	0	1588.88	6	20
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	28	231	0.23%	45.5%	TIEKFEK	99.2%	35.8	25	27.3	5	0	0	894.49	38	44
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	28	231	0.23%	45.5%	VETGVLKPGMVVTFAPVNVTTEVK	99.7%	49.8	25	49.8	4	11	0	2531.38	267	290
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	28	231	0.23%	45.5%	YEEIVKEVSTYIK	99.7%	65.2	25	58.8	4	0	0	1600.85	167	179
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	28	231	0.23%	45.5%	YYVTIIDAPGHR	99.7%	73.7	25	70.9	21	5	0	1404.73	85	96
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	28	231	0.23%	45.5%	YYVTIIDAPGHRDFIK	99.7%	58.5	25	58.5	2	4	0	1908.00	85	100
Elongation factor 1-beta	EEF1B2	EF1B_HUMAN	24.8	100.0%	3	3	5	0.01%	15.1%	LEECVR	99.7%	40.2	25	20.7	1	0	0	805.39	158	163

Elongation factor 1-beta	EEF1B2	EF1B_HUMAN	24.8	100.0%	3	3	5	0.01%	15.1%	SIQADGLVWGSSK	99.7%	77.9	25	72.8	2	0	0	1347.69	164	176
Elongation factor 1-beta	EEF1B2	EF1B_HUMAN	24.8	100.0%	3	3	5	0.01%	15.1%	SPAGLQVLNDYLADK	99.7%	102	25	102	2	0	0	1603.83	8	22
Elongation factor 1-delta	EEF1D	EF1D_HUMAN	31.1	100.0%	5	6	8	0.01%	25.3%	ATAPQTQHVSPMR	99.6%	39.1	25	35.8	2	0	0	1423.71	124	136
Elongation factor 1-delta	EEF1D	EF1D_HUMAN	31.1	100.0%	5	6	8	0.01%	25.3%	IASLEVENQSLR	99.7%	82.5	25	60.7	2	0	0	1358.73	84	95
Elongation factor 1-delta	EEF1D	EF1D_HUMAN	31.1	100.0%	5	6	8	0.01%	25.3%	LVPVGYGIR	99.6%	38.9	25	28.6	1	0	0	973.58	233	241
Elongation factor 1-delta	EEF1D	EF1D_HUMAN	31.1	100.0%	5	6	8	0.01%	25.3%	SIQLDGLVWGASK	99.7%	57.2	25	57.2	1	0	0	1373.74	220	232
Elongation factor 1-delta	EEF1D	EF1D_HUMAN	31.1	100.0%	5	6	8	0.01%	25.3%	SLAGSSGPGASSGTSGDHGELVVR	99.7%	42.3	25	42.3	0	2	0	2185.05	60	83
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	15	31	0.03%	29.1%	AKDPFAHLPK	98.9%	34.5	25	22.6	2	0	0	1123.63	276	285
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	15	31	0.03%	29.1%	ALIAAQYSGAQVR	99.7%	98	25	98	4	0	0	1347.74	18	30
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	15	31	0.03%	29.1%	EYFSWEGAFQHVGK	99.7%	71	25	63.5	2	2	0	1684.78	415	428
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	15	31	0.03%	29.1%	FAETQPK	98.7%	33.8	25	15.8	2	0	0	820.42	221	227
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	15	31	0.03%	29.1%	ILGLLDAYLK	99.7%	60.5	25	52.1	4	0	0	1118.68	138	147
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	15	31	0.03%	29.1%	KLDPGSEETQTLVR	99.7%	79.7	25	72.6	2	2	0	1572.82	401	414
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	15	31	0.03%	29.1%	MAQFDAK	97.3%	30.5	25	25.1	1	0	0	810.38	213	219
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	15	31	0.03%	29.1%	QAFPNTNR	98.1%	32	25	23.2	1	0	0	947.47	182	189
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	15	31	0.03%	29.1%	STFVLDEFKR	99.7%	51.6	25	51.4	2	1	0	1241.65	286	295
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	15	31	0.03%	29.1%	TFLVGER	99.6%	39.8	25	29	2	0	0	821.45	150	156
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	15	31	0.03%	29.1%	VLSAPPHFHFGQTNR	99.7%	39.2	25	38	0	2	0	1707.87	31	45
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	15	31	0.03%	29.1%	WFLTCINQPQFR	99.7%	65.2	25	53.2	2	0	0	1609.79	190	201
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	20	22	53	0.05%	26.7%	AYLPVNESFGFTADLR	99.7%	113	25	113	2	0	0	1799.90	786	801
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	20	22	53	0.05%	26.7%	CLYASVLTAQPR	99.7%	70.7	25	66.9	2	0	0	1378.71	728	739
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	20	22	53	0.05%	26.7%	EGALCEENMR	99.7%	56.6	25	45.6	3	0	0	1208.50	689	698
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	20	22	53	0.05%	26.7%	EGIPALDNFLDKL	99.7%	65.6	25	59.6	3	0	0	1444.77	846	858
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	20	22	53	0.05%	26.7%	ETVSEESNVLCLSK	99.7%	96.1	25	86.7	2	0	0	1594.76	581	594
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	20	22	53	0.05%	26.7%	GEGQLGPAER	99.7%	45.2	25	32.6	4	0	0	1013.50	240	249
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	20	22	53	0.05%	26.7%	GGGQIIPTAR	98.6%	33.3	25	25.6	6	0	0	969.55	717	726
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	20	22	53	0.05%	26.7%	GPLMMYISK	99.7%	46.3	25	42.8	4	0	0	1039.53	392	400
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	20	22	53	0.05%	26.7%	IMGPNYTPGK	99.7%	46.1	25	45.9	2	0	0	1077.54	429	438
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	20	22	53	0.05%	26.7%	IMGPNYTPGKK	98.7%	33.6	25	26.8	1	0	0	1205.63	429	439
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	20	22	53	0.05%	26.7%	IWCFGPDGTGPNILTDITK	99.7%	43.5	25	25.1	1	0	0	2105.04	649	667
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	20	22	53	0.05%	26.7%	KEDLYLKPIQR	99.7%	41	25	40.7	0	3	0	1402.81	439	449
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	20	22	53	0.05%	26.7%	NMSVIAHVDHGK	99.7%	40.8	25	32.4	2	0	0	1323.65	21	32
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	20	22	53	0.05%	26.7%	QFAEMYVAK	99.7%	52.8	25	45.4	2	0	0	1086.53	227	235
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	20	22	53	0.05%	26.7%	STLTDSLVCK	99.7%	63.2	25	56	2	0	0	1123.57	33	42
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	20	22	53	0.05%	26.7%	TFCQLILDPIFK	99.7%	55.1	25	55.1	4	0	0	1494.80	288	299
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	20	22	53	0.05%	26.7%	TGTITTFEHAHNMR	98.6%	26.2	25	26.2	0	1	0	1615.76	482	495
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	20	22	53	0.05%	26.7%	VFDAIMNFK	99.7%	48.8	25	45	2	0	0	1084.55	300	308
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	20	22	53	0.05%	26.7%	VFSGLVSTGLK	99.7%	90.4	25	77.8	5	0	0	1107.64	416	426
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	20	22	53	0.05%	26.7%	VNFTVDQIR	99.7%	88.5	25	70	6	0	0	1091.58	2	10
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	20	22	53	0.05%	26.7%	YEWDVAEAR	99.7%	64.2	25	58.8	2	0	0	1138.52	639	647
Elongation factor Ts, mitochondrial	TSFM	EFTS_HUMAN	35.4	99.8%	2	2	3	0.00%	9.2%	GFLNSSELSGLPAGPDR	99.7%	81.5	25	80.4	2	0	0	1716.86	162	178
Elongation factor Ts, mitochondrial	TSFM	EFTS_HUMAN	35.4	99.8%	2	2	3	0.00%	9.2%	YGALVICETSEQK	99.7%	62.2	25	54.4	1	0	0	1497.73	234	246
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	35	110	0.11%	54.2%	ADAVQDSEMVELVELEIR	99.7%	79.4	25	77.6	3	1	0	2062.00	183	200
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	35	110	0.11%	54.2%	AEAGDNLGALVR	99.7%	103	25	88.1	6	0	0	1185.62	316	327
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	35	110	0.11%	54.2%	DLEKPFLLPVEAVYSVPGR	99.7%	77	25	75.8	4	3	0	2129.16	253	271
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	35	110	0.11%	54.2%	EHLLLAR	99.6%	39.2	25	35.2	5	0	0	851.51	163	169
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	35	110	0.11%	54.2%	ELAMPGEDLK	99.6%	39.9	25	35.4	4	0	0	1102.55	396	405
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	35	110	0.11%	54.2%	ELLTEFGYK	99.7%	43.1	25	42.5	2	0	0	1099.57	201	209
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	35	110	0.11%	54.2%	GDECELLGHSK	99.7%	54.7	25	53.7	2	0	0	1244.56	287	297
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	35	110	0.11%	54.2%	GITINAAHVEYSTAAR	99.7%	100	25	91.3	3	2	0	1673.86	105	120
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	35	110	0.11%	54.2%	GLVMVKPGSIKPHQK	95.2%	21.9	25	21.9	0	1	0	1618.95	337	351

Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	35	110	0.11%	54.2%	GTVVTGTLER	99.7%	66.9	25	44.6	8	0	0	1032.57	272	281
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	35	110	0.11%	54.2%	HYAHTDCPGHADYVK	99.7%	37.8	25	37.8	0	2	0	1770.77	121	135
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	35	110	0.11%	54.2%	IILPPEKELAMPGEDLK	99.7%	35.2	25	35.2	0	4	0	1893.04	389	405
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	35	110	0.11%	54.2%	KGDECELLGHSK	99.7%	70.2	25	58.3	2	4	0	1372.65	286	297
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	35	110	0.11%	54.2%	KYEEIDNAPEER	99.7%	42.4	25	29.8	0	1	0	1492.69	91	102
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	35	110	0.11%	54.2%	LLDAVDTYIPVPAR	99.7%	95.4	25	92.2	10	0	0	1542.85	239	252
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	35	110	0.11%	54.2%	QIGVEHVVVYVNK	99.7%	76.3	25	73.2	2	2	0	1483.83	170	182
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	35	110	0.11%	54.2%	TIGTGLVTNTLAMTEEEK	99.7%	112	25	104	7	0	0	1923.96	430	447
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	35	110	0.11%	54.2%	TIGTGLVTNTLAMTEEEKNIK	96.7%	23.2	25	23	0	1	0	2279.18	430	450
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	35	110	0.11%	54.2%	TTLTAAITK	99.7%	68.6	25	55.7	2	0	0	919.55	71	79
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	35	110	0.11%	54.2%	TVVTGIEMFHK	99.7%	68.8	25	41.7	13	2	0	1261.66	301	311
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	35	110	0.11%	54.2%	VEAQVYILSK	99.7%	72.7	25	66.1	8	0	0	1149.65	352	361
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	35	110	0.11%	54.2%	VEAQVYILSKEEGGR	99.7%	66.5	25	60	2	2	0	1677.88	352	366
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	35	110	0.11%	54.2%	YEEIDNAPEER	99.7%	66.4	25	59.6	2	0	0	1364.60	92	102
Elongator complex protein 1	IKBKAP	ELP1_HUMAN	150.3	100.0%	8	8	13	0.01%	6.8%	ALVLAQIR	99.7%	41.5	25	35.4	2	0	0	883.57	723	730
Elongator complex protein 1	IKBKAP	ELP1_HUMAN	150.3	100.0%	8	8	13	0.01%	6.8%	DIQGPGNPQCFSLR	99.7%	53.5	25	53.5	1	0	0	1588.75	14	27
Elongator complex protein 1	IKBKAP	ELP1_HUMAN	150.3	100.0%	8	8	13	0.01%	6.8%	EYLPFLNTLK	98.9%	34.3	25	25	2	0	0	1237.68	916	925
Elongator complex protein 1	IKBKAP	ELP1_HUMAN	150.3	100.0%	8	8	13	0.01%	6.8%	IVSLMWDPVTPYR	97.3%	30.4	25	25.5	1	0	0	1576.82	346	358
Elongator complex protein 1	IKBKAP	ELP1_HUMAN	150.3	100.0%	8	8	13	0.01%	6.8%	IVTVVPQDTK	99.4%	37.3	25	26	2	0	0	1099.64	697	706
Elongator complex protein 1	IKBKAP	ELP1_HUMAN	150.3	100.0%	8	8	13	0.01%	6.8%	SVVLQLADGQIFK	99.7%	66.2	25	55.3	2	0	0	1417.81	568	580
Elongator complex protein 1	IKBKAP	ELP1_HUMAN	150.3	100.0%	8	8	13	0.01%	6.8%	TTPELEIVLQK	99.7%	43.8	25	36.9	1	0	0	1270.73	847	857
Elongator complex protein 1	IKBKAP	ELP1_HUMAN	150.3	100.0%	8	8	13	0.01%	6.8%	VFLGNVETFIK	99.7%	45	25	40.7	2	0	0	1266.71	762	772
Elongator complex protein 3	ELP3	ELP3_HUMAN	62.3	100.0%	3	3	6	0.01%	6.8%	AVCESFHLAK	99.7%	50.1	25	40	2	0	0	1161.57	266	275
Elongator complex protein 3	ELP3	ELP3_HUMAN	62.3	100.0%	3	3	6	0.01%	6.8%	LEIGVQSVYEDVAR	99.7%	55.3	25	55.3	2	0	0	1577.82	243	256
Elongator complex protein 3	ELP3	ELP3_HUMAN	62.3	100.0%	3	3	6	0.01%	6.8%	SYSPSDLVELVAR	99.7%	65	25	58.1	2	0	0	1435.74	339	351
Emerin	EMD	EMD_HUMAN	29.0	100.0%	7	8	15	0.02%	33.9%	APGAGLGQDR	99.7%	69.1	25	59.6	2	0	0	941.48	212	221
Emerin	EMD	EMD_HUMAN	29.0	100.0%	7	8	15	0.02%	33.9%	DSAYQSITHYRPVSASR	99.7%	33.3	25	33.3	0	2	0	1937.95	158	174
Emerin	EMD	EMD_HUMAN	29.0	100.0%	7	8	15	0.02%	33.9%	GYNDDYYEESYFTTR	99.7%	67.2	25	67.2	2	0	0	1922.77	89	103
Emerin	EMD	EMD_HUMAN	29.0	100.0%	7	8	15	0.02%	33.9%	KEDALLYQSK	99.7%	70.2	25	55.3	2	0	0	1194.64	79	88
Emerin	EMD	EMD_HUMAN	29.0	100.0%	7	8	15	0.02%	33.9%	KIFEYETQR	99.7%	50.1	25	43.6	1	0	0	1213.62	37	45
Emerin	EMD	EMD_HUMAN	29.0	100.0%	7	8	15	0.02%	33.9%	TYGEPESAGPSR	99.7%	87	25	72.6	2	0	0	1250.56	104	115
Emerin	EMD	EMD_HUMAN	29.0	100.0%	7	8	15	0.02%	33.9%	YNIPHGPVVGSTR	99.7%	42	25	41.7	2	2	0	1396.73	19	31
Endonuclease III-like protein 1	NTHL1	NTH_HUMAN	34.4	100.0%	2	2	4	0.00%	8.3%	GLTVDSILQTDDATLGK	99.7%	71.9	25	71.9	2	0	0	1746.91	158	174
Endonuclease III-like protein 1	NTHL1	NTH_HUMAN	34.4	100.0%	2	2	4	0.00%	8.3%	LIYPVGFWR	94.7%	27.6	25	24.2	2	0	0	1150.64	175	183
Endoplasmic reticulum-Golgi intermediate compartment protein 1	ERGIC1	ERGI1_HUMAN	32.6	99.8%	2	2	2	0.00%	8.3%	LTSNPLASHDYILK	98.1%	25.2	25	25.2	0	1	0	1571.84	177	190
Endoplasmic reticulum-Golgi intermediate compartment protein 1	ERGIC1	ERGI1_HUMAN	32.6	99.8%	2	2	2	0.00%	8.3%	YSYQYTVANK	99.7%	68.3	25	66.4	1	0	0	1236.59	205	214
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	2	2	3	0.00%	4.9%	ELISNASDALDK	99.7%	78.7	25	63.9	7	0	0	1275.64	103	114
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	2	2	3	0.00%	4.9%	ELISNASDALDKIR	99.7%	98.3	25	80	8	2	0	1544.83	103	116
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	2	2	3	0.00%	4.9%	GVVDSDDLPLNVSR	99.7%	58.1	25	55.9	1	0	0	1485.75	435	448
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	2	2	3	0.00%	4.9%	SILFVPTSAPR	99.0%	34.7	25	28.1	2	0	0	1187.68	385	395
Enhancer of mRNA-decapping protein 3	EDC3	EDC3_HUMAN	56.1	100.0%	4	4	6	0.01%	10.0%	AGDITELK	99.7%	47.2	25	14.6	2	0	0	846.46	56	63
Enhancer of mRNA-decapping protein 3	EDC3	EDC3_HUMAN	56.1	100.0%	4	4	6	0.01%	10.0%	KPASSSSAPQNIPK	99.7%	60	25	51.4	2	0	0	1411.75	106	119
Enhancer of mRNA-decapping protein 3	EDC3	EDC3_HUMAN	56.1	100.0%	4	4	6	0.01%	10.0%	MLESITNELSLFSK	99.7%	46.2	25	44.5	1	0	0	1627.82	374	387
Enhancer of mRNA-decapping protein 3	EDC3	EDC3_HUMAN	56.1	100.0%	4	4	6	0.01%	10.0%	SQDVAVSPQQQQCSK	99.7%	51.8	25	51.8	1	0	0	1689.79	125	139
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	4	5	9	0.01%	37.5%	ADTQTYQPYNK	99.7%	40.3	25	37.5	2	0	0	1328.61	74	84
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	4	5	9	0.01%	37.5%	ADTQTYQPYNKDWIK	96.0%	22.5	25	21	0	2	0	1870.90	74	88
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	4	5	9	0.01%	37.5%	IYVLLRR	98.5%	32.9	25	12.5	1	0	0	932.60	91	97
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	4	5	9	0.01%	37.5%	TYADYESVNECMEGVCK	99.7%	96	25	96	4	0	0	2070.81	18	34
Enoyl-CoA delta isomerase 1, mitochondrial	ECI1	ECI1_HUMAN	32.8	100.0%	3	3	5	0.01%	11.9%	AVQELWLR	98.6%	33.5	25	21	1	0	0	1014.57	127	134
Enoyl-CoA delta isomerase 1, mitochondrial	ECI1	ECI1_HUMAN	32.8	100.0%	3	3	5	0.01%	11.9%	DADVQNFVSFISK	99.7%	87.7	25	85.6	2	0	0	1469.73	271	283
Enoyl-CoA delta isomerase 1, mitochondrial	ECI1	ECI1_HUMAN	32.8	100.0%	3	3	5	0.01%	11.9%	VLVEPDAGAGVAVMK	99.7%	57.8	25	57.8	2	0	0	1455.79	47	61

Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	7	10	22	0.02%	31.0%	AFAAGADIK	99.7%	45.3	25	26	2	0	0	863.46	93	101
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	7	10	22	0.02%	31.0%	AQFAQPEILIGTIPGAGGTQR	99.7%	87.7	25	82.9	2	2	0	2125.14	158	178
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	7	10	22	0.02%	31.0%	EGMTAFVEK	99.7%	58.3	25	50.3	2	0	0	1011.48	274	282
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	7	10	22	0.02%	31.0%	EMQNLSFQDCYSSK	99.7%	72.5	25	72.5	3	0	0	1752.72	102	115
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	7	10	22	0.02%	31.0%	LFYSTFATDDRK	99.5%	38.2	25	32.4	1	0	0	1463.72	262	273
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	7	10	22	0.02%	31.0%	NNTVGLIQLNRPK	99.7%	75.9	25	75.9	2	0	0	1466.84	44	56
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	7	10	22	0.02%	31.0%	SLAMEMVLTGDR	99.7%	82.3	25	69.5	8	0	0	1322.64	186	197
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	5	5	7	0.01%	5.9%	FNVEDGEIVQQVR	99.7%	66.7	25	57.8	1	0	0	1532.77	202	214
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	5	5	7	0.01%	5.9%	LFGIESSSGTILWK	99.7%	76.8	25	72.6	2	0	0	1537.83	545	558
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	5	5	7	0.01%	5.9%	NVIAALNSR	99.1%	35.3	25	32.4	1	0	0	957.55	61	69
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	5	5	7	0.01%	5.9%	TFIGIFLIDGVTGR	99.6%	39.3	25	37.9	2	0	0	1508.85	755	768
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	5	5	7	0.01%	5.9%	TVAAVMACR	99.6%	38.9	25	33.4	1	0	0	978.49	331	339
ER membrane protein complex subunit 3	EMC3	EMC3_HUMAN	30.0	100.0%	5	5	8	0.01%	19.9%	AGPELLLDSNIR	99.7%	75.1	25	58	2	0	0	1297.71	2	13
ER membrane protein complex subunit 3	EMC3	EMC3_HUMAN	30.0	100.0%	5	5	8	0.01%	19.9%	KLTQEQVSDSQVLIR	99.7%	32.6	25	27.7	0	1	0	1743.96	43	57
ER membrane protein complex subunit 3	EMC3	EMC3_HUMAN	30.0	100.0%	5	5	8	0.01%	19.9%	LTQEQVSDSQVLIR	99.7%	100	25	76.8	2	0	0	1615.87	44	57
ER membrane protein complex subunit 3	EMC3	EMC3_HUMAN	30.0	100.0%	5	5	8	0.01%	19.9%	SIYSLILGQDNAADQSR	99.7%	96.9	25	95	2	0	0	1850.92	181	197
ER membrane protein complex subunit 3	EMC3	EMC3_HUMAN	30.0	100.0%	5	5	8	0.01%	19.9%	VPFPLTLR	98.4%	32.7	25	19.1	1	0	0	942.58	140	147
ER membrane protein complex subunit 4	EMC4	EMC4_HUMAN	20.1	100.0%	2	2	7	0.01%	15.8%	GSGQGDSLYPVGYLDK	99.7%	79.9	25	76.6	4	0	0	1655.79	35	50
ER membrane protein complex subunit 4	EMC4	EMC4_HUMAN	20.1	100.0%	2	2	7	0.01%	15.8%	WAIELSGPGGGSR	99.7%	62.7	25	55.3	3	0	0	1286.65	17	29
ER membrane protein complex subunit 6	EMC6	EMC6_HUMAN	12.0	99.8%	2	2	5	0.01%	20.0%	EGPPFISEAAVR	99.7%	50	25	42.6	3	0	0	1272.66	9	20
ER membrane protein complex subunit 6	EMC6	EMC6_HUMAN	12.0	99.8%	2	2	5	0.01%	20.0%	GNAAVLDYCR	99.7%	63.2	25	55.3	2	0	0	1138.53	21	30
ER membrane protein complex subunit 7	EMC7	EMC7_HUMAN	26.5	100.0%	3	3	6	0.01%	13.6%	SSGPPSYFIK	99.7%	41.8	25	30.1	2	0	0	1082.55	142	151
ER membrane protein complex subunit 7	EMC7	EMC7_HUMAN	26.5	100.0%	3	3	6	0.01%	13.6%	VLVDGEEHVGFLK	99.7%	55.5	25	55.5	2	0	0	1441.77	67	79
ER membrane protein complex subunit 7	EMC7	EMC7_HUMAN	26.5	100.0%	3	3	6	0.01%	13.6%	VVNTSDPDMR	99.5%	38.7	25	38.7	2	0	0	1133.53	182	191
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	8	10	17	0.02%	36.1%	ADAEYYAAHK	99.7%	62.1	25	61.8	2	0	0	1138.52	258	267
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	8	10	17	0.02%	36.1%	DLNLMAPGLTIQAVR	99.7%	101	25	93.4	5	0	0	1611.89	155	169
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	8	10	17	0.02%	36.1%	EALEPSGENVIQNK	99.7%	82	25	80.1	2	0	0	1527.77	329	342
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	8	10	17	0.02%	36.1%	ESSLPSKEALEPSGENVIQNK	99.2%	28.3	25	20.5	0	1	0	2256.14	322	342
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	8	10	17	0.02%	36.1%	IPEAIRR	95.5%	28.3	25	20.3	1	0	0	854.52	175	181
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	8	10	17	0.02%	36.1%	ISEIEDAAFLAR	99.7%	94.5	25	83.1	4	0	0	1334.70	242	253
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	8	10	17	0.02%	36.1%	IYFGSNIPNMFVDSSCALK	99.7%	45.3	25	45.3	3	0	0	2163.03	295	313
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	8	10	17	0.02%	36.1%	LTPEYLELKK	97.7%	31.2	25	24.9	1	0	0	1233.71	276	285
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	8	10	17	0.02%	36.1%	NFELMEAEK	99.7%	43	25	14.1	2	0	0	1110.51	182	190
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	8	10	17	0.02%	36.1%	SVQTTLQTDEVK	99.7%	84.6	25	70	4	0	0	1348.70	61	72
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	8	10	17	0.02%	36.1%	VVEKEAETER	99.7%	62.3	25	61.4	4	0	0	1189.61	202	211
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	14	35	0.04%	31.6%	ADAECYTAMK	99.7%	65.1	25	65.1	4	0	0	1159.48	258	267
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	14	35	0.04%	31.6%	AKADAECYTAMK	99.7%	60.8	25	60.8	1	0	0	1358.61	256	267
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	14	35	0.04%	31.6%	DIPNMFMDSAGSVSK	99.7%	98.5	25	92.3	4	0	0	1598.72	300	314
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	14	35	0.04%	31.6%	IEEGHIGVYYR	99.7%	42	25	29.2	2	0	0	1335.67	26	36
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	14	35	0.04%	31.6%	ISEIEDAAFLAR	99.7%	94.5	25	83.1	4	0	0	1334.70	242	253
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	14	35	0.04%	31.6%	KISEIEDAAFLAR	99.7%	79.2	25	75.2	2	0	0	1462.79	241	253
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	14	35	0.04%	31.6%	LTPEYLQLMK	99.6%	39.7	25	36.7	5	0	0	1251.67	276	285
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	14	35	0.04%	31.6%	SVQTTLQTDEVK	99.7%	84.6	25	70	4	0	0	1348.70	61	72
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	14	35	0.04%	31.6%	VAQVAEITYGQK	99.7%	84.3	25	82.3	2	0	0	1306.70	221	232
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	14	35	0.04%	31.6%	VTKPNIPEAIR	99.7%	50	25	50	2	0	0	1237.73	170	180
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	14	35	0.04%	31.6%	VTKPNIPEAIRR	98.0%	25.1	25	19.2	0	1	0	1393.83	170	181
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	14	35	0.04%	31.6%	VVEKEAETER	99.7%	62.3	25	61.4	4	0	0	1189.61	202	211
ERO1-like protein alpha	ERO1L	ERO1A_HUMAN	54.4	99.8%	2	2	4	0.00%	5.6%	LGAVDESLSEETQK	99.7%	78.8	25	78.8	2	0	0	1505.73	137	150
ERO1-like protein alpha	ERO1L	ERO1A_HUMAN	54.4	99.8%	2	2	4	0.00%	5.6%	QEIVSLFNAFGR	99.7%	70.1	25	65.3	2	0	0	1380.73	438	449
Erythrocyte band 7 integral membrane protein	STOM	STOM_HUMAN	31.7	100.0%	2	2	4	0.00%	6.9%	LLAQTTLR	99.7%	47.5	25	39.2	2	0	0	915.56	145	152
Erythrocyte band 7 integral membrane protein	STOM	STOM_HUMAN	31.7	100.0%	2	2	4	0.00%	6.9%	VIAAEGEMNASR	99.7%	47.9	25	37.2	2	0	0	1263.60	221	232

Estradiol 17-beta-dehydrogenase 11	HSD17B11	DHB11_HUMAN	32.9	100.0%	3	3	4	0.00%	8.7%	FAAVGFHK	99.7%	46.3	25	10.2	2	0	0	876.47	190	197
Estradiol 17-beta-dehydrogenase 11	HSD17B11	DHB11_HUMAN	32.9	100.0%	3	3	4	0.00%	8.7%	FDAVIGYK	99.6%	39.1	25	39.1	1	0	0	912.48	289	296
Estradiol 17-beta-dehydrogenase 11	HSD17B11	DHB11_HUMAN	32.9	100.0%	3	3	4	0.00%	8.7%	LMHGILTEQK	98.6%	33.2	25	24.5	1	0	0	1169.63	246	255
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	12	36	0.04%	35.9%	GVFVQSVLPYFVATK	99.7%	52.7	25	52.7	3	0	0	1654.92	224	238
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	12	36	0.04%	35.9%	ISYSLFTALR	99.7%	100	25	82.7	6	0	0	1170.65	26	35
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	12	36	0.04%	35.9%	KPTLDKPSPETFVK	99.7%	32.7	25	31.3	0	1	0	1586.88	244	257
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	12	36	0.04%	35.9%	LDQVSSEIKEK	99.7%	49.7	25	30	2	0	0	1275.68	87	97
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	12	36	0.04%	35.9%	MININILSVCK	99.7%	84.5	25	80.8	6	0	0	1304.71	157	167
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	12	36	0.04%	35.9%	MTQLVLPGMVER	99.7%	70.1	25	57.5	7	0	0	1389.72	168	179
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	12	36	0.04%	35.9%	SYAEELAK	98.7%	33.8	25	24.5	1	0	0	910.45	65	72
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	12	36	0.04%	35.9%	TFVDFFSQCLHEEYR	99.7%	74.8	25	74.8	4	2	0	1977.88	207	221
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	12	36	0.04%	35.9%	TIAVDFASEDIYDKIK	99.7%	90.2	25	89.8	4	0	0	1827.94	104	119
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	9	9	23	0.02%	37.5%	DLLGTVWGGPANLEAIAK	99.7%	66.4	25	66.4	2	0	0	1824.99	284	301
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	9	9	23	0.02%	37.5%	ELYLEEALQNER	99.7%	70.9	25	70.9	2	0	0	1506.74	272	283
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	9	9	23	0.02%	37.5%	EMGIIPSWGGTTR	98.8%	34	25	33	1	0	0	1404.69	186	198
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	9	9	23	0.02%	37.5%	LVEIIGSR	99.7%	54.5	25	50.8	2	0	0	886.54	199	206
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	9	9	23	0.02%	37.5%	NALNIGMVEEVLQSSDETK	99.7%	80	25	78.5	1	0	0	2093.01	222	240
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	9	9	23	0.02%	37.5%	NTFSSGSDLNAVK	99.7%	61.4	25	60.3	4	0	0	1339.65	109	121
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	9	9	23	0.02%	37.5%	QFIQGPPEVIR	99.7%	55.6	25	34.1	4	0	0	1283.71	251	261
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	9	9	23	0.02%	37.5%	SLEEAQEWLK	99.7%	60	25	45.9	4	0	0	1232.62	241	250
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	9	9	23	0.02%	37.5%	VIELENWTEGK	99.7%	82.1	25	82.1	3	0	0	1317.67	90	100
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	48	0.05%	47.3%	ATQALVLAPTR	99.7%	57.1	25	56.2	2	0	0	1140.67	100	110
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	48	0.05%	47.3%	DFTVSAMHGDMDQKER	99.7%	40.1	25	40.1	0	5	0	1898.80	296	311
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	48	0.05%	47.3%	EELTLEGIR	99.7%	51.3	25	34.7	2	0	0	1059.57	239	247
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	48	0.05%	47.3%	ELAQQIQK	99.7%	49	25	27.8	2	0	0	957.54	111	118
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	48	0.05%	47.3%	GFKDQIYDIFQK	99.7%	71.2	25	65	2	1	0	1501.77	191	202
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	48	0.05%	47.3%	GIYAYGFEKPSAIQQR	99.7%	95.7	25	91.9	2	0	0	1827.94	46	61
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	48	0.05%	47.3%	GVAINMVTEEDKR	99.7%	66.3	25	66.3	2	0	0	1461.74	370	382
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	48	0.05%	47.3%	GYDVIAQAQSGTGK	99.7%	128	25	117	2	0	0	1394.69	69	82
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	48	0.05%	47.3%	KEELTLEGIR	99.7%	56	25	43.3	2	0	0	1187.66	238	247
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	48	0.05%	47.3%	KVDWLTEK	99.7%	40.2	25	24.3	2	0	0	1018.56	284	291
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	48	0.05%	47.3%	LNSNTQVVLLSATMPSDVLEVTK	99.7%	83.1	25	83.1	4	0	0	2475.30	203	225
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	48	0.05%	47.3%	LQMEAPHIIVGTPGR	99.7%	81.9	25	79.5	4	4	0	1618.87	147	161
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	48	0.05%	47.3%	MFVLDEADEMLSR	99.7%	119	25	112	6	0	0	1555.71	178	190
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	48	0.05%	47.3%	VLITTDLLAR	99.7%	76.8	25	73	5	0	0	1114.68	325	334
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	48	0.05%	47.3%	VVMALGDYMGASCHACIGGTNVR	99.7%	34.1	25	34.1	0	1	0	2471.09	119	141
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	12	21	0.02%	32.4%	ELAVQIQK	99.7%	45	25	35.1	2	0	0	928.55	117	124
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	12	21	0.02%	32.4%	ETQALILAPTR	99.7%	49.2	25	32.4	2	0	0	1212.69	106	116
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	12	21	0.02%	32.4%	GFKEQIYDVYR	99.7%	50.3	25	50.3	1	0	0	1417.71	196	206
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	12	21	0.02%	32.4%	GIYAYGFEKPSAIQQR	99.7%	95.7	25	91.9	2	0	0	1827.94	52	67
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	12	21	0.02%	32.4%	GRDVIAQSQSGTGK	99.7%	90.5	25	84.2	2	2	0	1403.72	75	88
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	12	21	0.02%	32.4%	KGVAINFVK	99.7%	45.1	25	34.9	2	0	0	975.60	374	382
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	12	21	0.02%	32.4%	KLDYGQHVVAGTPGR	99.7%	41.2	25	34.2	0	2	0	1597.84	152	166
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	12	21	0.02%	32.4%	KVDWLTEK	99.7%	40.2	25	24.3	2	0	0	1018.56	289	296
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	12	21	0.02%	32.4%	LDYGQHVVAGTPGR	96.7%	23.3	25	20	0	1	0	1469.75	153	166
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	12	21	0.02%	32.4%	MLVLDEADEMLNK	99.7%	57.5	25	52.2	1	0	0	1520.73	183	195
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	12	21	0.02%	32.4%	QFFVAVER	99.7%	42.7	25	25.8	2	0	0	995.53	253	260
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	12	21	0.02%	32.4%	RDELTLEGIK	99.4%	37.4	25	24.2	2	0	0	1173.65	243	252
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	12	21	0.02%	32.4%	VLISTDVWAR	99.7%	55.4	25	48.4	2	0	0	1159.65	330	339
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	6	7	11	0.01%	31.6%	AIVQQWLEYR	99.7%	58.9	25	51	2	0	0	1305.70	69	78
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	6	7	11	0.01%	31.6%	EYLLGSTAEEK	99.7%	57	25	48.9	1	0	0	1239.61	58	68

Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	6	7	11	0.01%	31.6%	FIVDLTVQEKEK	99.7%	62.5	25	57.2	2	0	0	1448.80	127	138
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	6	7	11	0.01%	31.6%	NDIHTLLK	94.6%	27.5	25	19.5	1	0	0	953.54	89	96
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	6	7	11	0.01%	31.6%	QANKEYLLGSTAEEK	99.7%	58.5	25	55.1	2	2	0	1680.84	54	68
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	6	7	11	0.01%	31.6%	QHLSSVVFIK	97.2%	30.3	25	26	1	0	0	1157.67	157	166
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	9	11	19	0.02%	29.8%	AGLNCSTENMPIK	99.7%	67.4	25	67.4	3	0	0	1434.67	214	226
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	9	11	19	0.02%	29.8%	GVFNVQMEPK	99.7%	48.4	25	37.2	2	0	0	1148.58	267	276
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	9	11	19	0.02%	29.8%	INLIAPPR	96.8%	29.7	25	25.2	1	0	0	893.56	227	234
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	9	11	19	0.02%	29.8%	NECVVVIR	99.7%	51.9	25	37.2	1	0	0	988.52	68	75
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	9	11	19	0.02%	29.8%	RLTPQAVK	99.4%	37.2	25	20.7	2	0	0	912.56	183	190
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	9	11	19	0.02%	29.8%	TAWVFDDKYK	99.6%	39.1	25	39.1	1	0	0	1272.63	134	143
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	9	11	19	0.02%	29.8%	TEGLSVLSQAMAVIK	99.7%	74.2	25	69.7	4	0	0	1546.85	245	259
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	9	11	19	0.02%	29.8%	VVTDTDETELAR	99.7%	102	25	91.6	3	0	0	1348.66	277	288
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	9	11	19	0.02%	29.8%	YVMTTTTLER	99.7%	45.3	25	45.3	2	0	0	1230.60	235	244
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	IF2G_HUMAN	51.1	100.0%	4	4	7	0.01%	8.1%	AISGVHTVR	99.7%	45	25	45	2	0	0	939.54	60	68
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	IF2G_HUMAN	51.1	100.0%	4	4	7	0.01%	8.1%	LIGWGQIR	97.5%	30.7	25	17.2	1	0	0	942.55	453	460
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	IF2G_HUMAN	51.1	100.0%	4	4	7	0.01%	8.1%	LTPLSHEVISR	99.7%	44.4	25	40.2	2	0	0	1251.71	28	38
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	IF2G_HUMAN	51.1	100.0%	4	4	7	0.01%	8.1%	QDLTTLDVTK	99.7%	52.7	25	42.7	2	0	0	1133.61	18	27
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	ANEFLEVGK	99.7%	52.7	25	42.7	4	0	0	1006.52	15	23
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	ANEFLEVGKK	99.4%	37.5	25	20.3	3	0	0	1134.62	15	24
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	AVEDIHGLFSLSK	99.7%	88.3	25	86.4	2	0	0	1415.75	252	264
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	EDAPIGPHLQSMPSEQIR	99.7%	44.8	25	44.8	0	4	0	2020.98	503	520
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	EEELREYQER	99.7%	44	25	38	2	0	0	1380.64	838	847
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	ELEIEERER	98.8%	34	25	1.1	1	0	0	1202.60	862	870
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	FCLQYTR	99.7%	41.7	25	36.6	4	0	0	987.47	184	190
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	FLWESYR	97.5%	30.8	25	27.3	1	0	0	1000.49	152	158
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	FNVLQYVVPEVK	99.7%	76	25	64.7	8	0	0	1434.80	377	388
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	IGLINDMVR	99.7%	61.7	25	46.7	11	0	0	1046.57	368	376
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	ILQEHEQIK	99.7%	51.5	25	45.6	8	0	0	1137.63	624	632
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	ITTMQLER	99.7%	62.4	25	44.3	5	0	0	991.52	733	740
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	KGPEADSEWR	99.7%	47.3	25	37.3	2	0	0	1174.55	901	910
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	KIDYFER	99.1%	35.5	25	24.1	4	0	0	970.50	694	700
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	KLCDNLR	98.0%	31.7	25	17.6	1	0	0	918.48	196	202
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	LATLLGLQAPPTR	99.7%	43.6	25	43.6	4	0	0	1350.81	355	367
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	LEEIPLIK	98.0%	31.7	25	18.2	1	0	0	954.59	704	711
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	LESLNIQR	99.7%	57.1	25	15.8	3	0	0	972.55	582	589
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	LKQFEER	99.4%	37	25	9.59	2	0	0	949.51	776	782
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	LLDMDGIIVEK	99.7%	78.1	25	70.7	10	0	0	1245.68	341	351
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	LLLTPWVK	99.7%	47.2	25	25.4	4	0	0	969.61	144	151
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	LLQQVSQIYQSIEFSR	99.7%	96.1	25	96.1	5	0	0	1939.03	439	454
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	LTSLVPFVDAFQLER	99.7%	72.7	25	72.7	6	0	0	1734.94	455	469
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	LYHDIAQQAFK	99.7%	65.1	25	49.8	3	0	0	1333.69	173	183
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	MHLSQIQR	98.8%	34	25	26.9	3	0	0	1028.53	203	210
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	MLEDRDLFVMR	98.1%	25.2	25	21	0	1	0	1440.70	753	763
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	NICQQVNIK	99.7%	45.1	25	26.4	4	0	0	1116.58	76	84
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	NLTQDEMQR	99.7%	48.2	25	45.2	5	0	0	1134.52	309	317
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	NMDDDRLSR	95.8%	28.6	25	16.6	1	0	0	1121.50	1142	1150
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	NQLTAMSSVLAK	99.7%	97.4	25	82.9	11	0	0	1262.68	521	532
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	PAYFQRPENALK	99.2%	36.1	25	26.2	2	0	0	1433.75	2	13
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	QCLDLLR	99.7%	42.4	25	3.36	4	0	0	917.49	159	165
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	RGPAEESSSWR	96.0%	28.8	25	28.8	1	0	0	1261.59	1250	1260
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	RLEEIPLIK	99.7%	49.3	25	42	2	0	0	1110.69	703	711

Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	RLGDSSLSR	99.7%	40.7	25	20.5	2	0	0	990.53	877	885
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	RVPPPALSR	98.2%	32.1	25	23.1	2	0	0	992.60	1329	1337
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	SGNALFHASTLHR	99.7%	59.4	25	55.9	0	6	0	1410.72	286	298
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	SLEDVVR	99.7%	40.6	25	17.8	2	0	0	817.44	85	91
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	TLSFGSDLNYATR	99.7%	94.4	25	86.9	6	0	0	1444.71	490	502
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	VLLATLSIPITPER	99.7%	58.5	25	58.5	8	0	0	1522.92	322	335
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	41	47	159	0.16%	28.7%	YLELCVDLR	95.2%	28.1	25	19.3	1	0	0	1180.60	54	62
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	30	79	0.08%	35.4%	AQAVSEDAGGNEGR	99.7%	117	25	117	8	0	0	1360.61	121	134
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	30	79	0.08%	35.4%	DQYSVIFESGDR	99.7%	74.6	25	72.3	1	0	0	1415.64	304	315
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	30	79	0.08%	35.4%	ETIIAFAWEPNGSK	99.7%	66.6	25	63.9	2	0	0	1562.79	563	576
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	30	79	0.08%	35.4%	FAVLHGEAPR	99.7%	59.6	25	54.2	3	0	0	1096.59	577	586
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	30	79	0.08%	35.4%	FSHQGVQLIDFSPCER	99.7%	40.4	25	40.4	0	2	0	1919.91	371	386
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	30	79	0.08%	35.4%	GIALWGGEK	99.7%	46	25	34.1	2	0	0	930.50	356	364
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	30	79	0.08%	35.4%	GTQGVVTNFEIFR	99.7%	77.6	25	77.6	11	0	0	1467.76	536	548
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	30	79	0.08%	35.4%	GTYLATFHQR	99.7%	70.4	25	57.6	4	0	0	1193.61	346	355
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	30	79	0.08%	35.4%	GYIFLEYASPAHAVDAVK	99.7%	78.2	25	78.2	2	2	0	1951.00	231	248
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	30	79	0.08%	35.4%	ISVSFYHVK	99.1%	35.5	25	25.3	1	0	0	1079.59	587	595
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	30	79	0.08%	35.4%	ITNDFYPEEDGK	99.7%	60.3	25	60.3	2	0	0	1427.63	217	228
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	30	79	0.08%	35.4%	ITNDFYPEEDGKTK	99.7%	60.6	25	60.6	2	2	0	1656.78	217	230
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	30	79	0.08%	35.4%	MAQELYMEQK	99.7%	72.4	25	56.5	8	0	0	1270.58	763	772
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	30	79	0.08%	35.4%	MTLDTLSIYETPSMGLLDK	99.6%	38.9	25	36.2	1	0	0	2128.06	441	459
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	30	79	0.08%	35.4%	NADGYKLDK	99.6%	39.3	25	20	1	0	0	1023.51	249	257
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	30	79	0.08%	35.4%	NGDYLCVK	99.7%	54	25	40.2	2	0	0	968.45	522	529
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	30	79	0.08%	35.4%	NLFNVVDCK	99.7%	53.3	25	46.9	4	0	0	1108.55	508	516
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	30	79	0.08%	35.4%	QVPVDVVEMK	99.5%	38	25	34.1	2	0	0	1143.61	553	562
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	30	79	0.08%	35.4%	TMMEDFRK	98.2%	32.3	25	19.1	1	0	0	1057.48	752	759
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	30	79	0.08%	35.4%	TSIFWNDVKDPVSIEER	99.7%	47.2	25	46.4	0	2	0	2035.01	316	332
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	30	79	0.08%	35.4%	VDNAYWLWTFQGR	99.7%	83.2	25	83.2	3	0	0	1655.80	677	689
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	30	79	0.08%	35.4%	VNLFTDFDK	99.7%	43.4	25	35.9	1	0	0	1098.55	263	271
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	30	79	0.08%	35.4%	VTLMQLPTR	99.7%	55.5	25	48.1	6	0	0	1058.60	493	501
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	30	79	0.08%	35.4%	WTETYVR	96.7%	29.6	25	16.5	1	0	0	954.47	335	341
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	30	79	0.08%	35.4%	YVVTSVSWWSHK	99.7%	41.2	25	40.5	2	0	0	1478.74	665	676
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	30	79	0.08%	35.4%	YWLEEAECR	99.1%	35.5	25	35.5	1	0	0	1255.54	295	303
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	13	13	22	0.02%	14.5%	DAHNALLDIQSSGR	98.8%	34.1	25	34.1	1	0	0	1496.75	628	641
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	13	13	22	0.02%	14.5%	DFESHITSYK	98.6%	33.2	25	26.6	2	0	0	1226.57	151	160
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	13	13	22	0.02%	14.5%	ELLGQGLLLR	99.7%	59.4	25	45.3	2	0	0	1111.68	644	653
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	13	13	22	0.02%	14.5%	FEELTNLIR	99.7%	63.2	25	44.3	2	0	0	1134.62	57	65
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	13	13	22	0.02%	14.5%	GCILTLVER	99.7%	67.8	25	51	2	0	0	1060.58	442	450
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	13	13	22	0.02%	14.5%	GTEITHAVVIK	99.7%	60	25	41.8	2	0	0	1167.67	321	331
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	13	13	22	0.02%	14.5%	ILHTYYK	95.7%	28.5	25	21	1	0	0	937.51	507	513
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	13	13	22	0.02%	14.5%	KIQEESLR	98.2%	32.3	25	20	2	0	0	1002.56	782	789
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	13	13	22	0.02%	14.5%	KLNEILQAR	99.7%	41	25	19.7	1	0	0	1084.65	332	340
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	13	13	22	0.02%	14.5%	LGSLVENNER	99.7%	65.4	25	46.8	2	0	0	1130.58	863	872
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	13	13	22	0.02%	14.5%	QGTYGGYFR	99.0%	34.8	25	27.2	1	0	0	1048.48	878	886
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	13	13	22	0.02%	14.5%	SIVDKEGVPR	99.7%	43	25	32.7	2	0	0	1099.61	95	104
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	13	13	22	0.02%	14.5%	TEPTAQQNLALQLAEK	99.7%	108	25	107	2	0	0	1754.93	847	862
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	12	13	33	0.03%	19.3%	GAVIATELK	99.7%	42.8	25	25.3	2	0	0	901.54	418	426
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	12	13	33	0.03%	19.3%	GAVIATELKNNSYK	99.7%	69.4	25	53.1	1	0	0	1507.81	418	431
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	12	13	33	0.03%	19.3%	IFHTVTTTDDPVIR	99.7%	74	25	65.5	4	1	0	1614.85	223	236
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	12	13	33	0.03%	19.3%	IFHTVTTTDDPVIRK	98.5%	26	25	24.4	0	1	0	1742.94	223	237
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	12	13	33	0.03%	19.3%	LGDDIDLIVR	99.7%	100	25	91.7	4	0	0	1128.63	365	374

Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	12	13	33	0.03%	19.3%	NMLQFNLQILPK	99.7%	64	25	64	4	0	0	1458.81	113	124
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	12	13	33	0.03%	19.3%	SVYSWDIVVQR	99.7%	69.3	25	64	4	0	0	1351.70	261	271
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	12	13	33	0.03%	19.3%	TLNEWDSR	96.5%	29.4	25	25.4	1	0	0	1020.47	395	402
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	12	13	33	0.03%	19.3%	VADWTGATYQDK	99.7%	60.2	25	55.2	2	0	0	1354.63	42	53
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	12	13	33	0.03%	19.3%	VADWTGATYQDKR	99.7%	73.2	25	73.2	5	0	0	1510.73	42	54
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	12	13	33	0.03%	19.3%	WTCCALLAGSEYLK	99.7%	57.5	25	51.4	3	0	0	1671.79	435	448
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	12	13	33	0.03%	19.3%	YLILKDPNK	99.2%	35.9	25	28.2	1	0	0	1103.65	506	514
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	50.6%	EIYNEKELLQGK	99.7%	68.8	25	40.6	2	0	0	1463.77	30	41
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	50.6%	ETIDNNSVSSPLQSLQQR	99.7%	96.4	25	88.5	1	0	0	2016.00	194	211
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	50.6%	IAHFLDR	99.7%	42.9	25	28.8	2	0	0	871.48	10	16
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	50.6%	LASEILMQNWDAAMEDLTR	99.7%	87.6	25	87.6	1	0	0	2207.05	173	191
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	50.6%	LFIFETFCR	99.7%	63.7	25	53.7	6	0	0	1232.61	338	346
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	50.6%	LGHVVMGNNAVSPYQQVIEK	99.7%	86.6	25	86.6	1	3	0	2183.13	388	407
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	50.6%	LKETIDNNSVSSPLQSLQQR	99.7%	46.7	25	46.7	0	2	0	2257.18	192	211
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	50.6%	LNMTPEEAER	97.0%	30	25	30	1	0	0	1189.55	360	369
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	50.6%	MFEDPETTR	99.7%	47.7	25	35.1	4	0	0	1141.48	94	102
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	50.6%	MLFDYLADK	99.7%	57.9	25	46.3	5	0	0	1115.54	112	120
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	50.6%	NALSSLWGK	99.7%	49.3	25	46.9	2	0	0	975.53	164	172
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	50.6%	NLYSDDIPHALR	99.7%	64.8	25	58.1	3	2	0	1413.71	60	71
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	50.6%	QEYLDTLYR	99.7%	40.8	25	32.3	2	0	0	1200.59	125	133
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	50.6%	QLQAETEPIVK	99.7%	59.8	25	38.7	3	0	0	1255.69	83	93
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	50.6%	QVLKDLVK	96.2%	29	25	19	1	0	0	942.60	272	279
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	50.6%	RTTVVAQLK	97.2%	30.2	25	16.4	2	0	0	1015.63	74	82
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	50.6%	SEAPNWATQDSGFY	99.7%	71.8	25	71.8	2	0	0	1572.66	432	445
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	50.6%	SQMLAMNIEK	99.7%	62.6	25	44	4	0	0	1164.58	415	424
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	50.6%	TTVVAQLK	99.6%	39	25	23.8	1	0	0	859.52	75	82
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	50.6%	VLVPATDR	99.7%	43.1	25	36.6	2	0	0	870.50	156	163
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	50.6%	WIVNLIR	99.6%	39.5	25	12.8	2	0	0	913.56	370	376
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	50.6%	YLTTAVITNK	99.7%	68.3	25	61.4	5	0	0	1123.64	256	265
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	50.6%	YLTTAVITNKDVR	99.7%	65.8	25	58.7	2	1	0	1493.83	256	268
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	8	16	0.02%	22.4%	AYVSTLMGVPGR	99.7%	61.6	25	55.9	4	0	0	1250.66	215	226
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	8	16	0.02%	22.4%	FLMSLVNQVPK	99.7%	75	25	62.5	2	0	0	1275.71	307	317
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	8	16	0.02%	22.4%	TMGVMFTPLTVK	99.7%	52.3	25	48.6	2	0	0	1324.70	227	238
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	8	16	0.02%	22.4%	VIGLSSDLQQVGGASAR	99.7%	150	25	149	3	0	0	1657.89	262	278
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	8	16	0.02%	22.4%	VIGTLLGTVDK	99.7%	52.9	25	45.6	2	0	0	1115.67	116	126
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	8	16	0.02%	22.4%	VSADNTVGR	99.6%	39.1	25	31.4	1	0	0	918.46	298	306
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	8	16	0.02%	22.4%	YAYYDTER	99.7%	41.2	25	41.2	2	0	0	1080.46	239	246
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	8	9	15	0.02%	23.4%	CPYKDTLGPMQK	99.7%	47.5	25	46.5	1	1	0	1437.69	169	180
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	8	9	15	0.02%	23.4%	EKLPGELEPVQATQNK	99.7%	43.4	25	38.8	0	2	0	1780.94	194	209
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	8	9	15	0.02%	23.4%	ELAEQLGLSTGEK	99.7%	72.3	25	65.2	2	0	0	1374.71	181	193
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	8	9	15	0.02%	23.4%	ELAEQLGLSTGEKEK	99.7%	69.4	25	58.8	1	0	0	1631.85	181	195
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	8	9	15	0.02%	23.4%	ETDLQELFRPFGSISR	99.7%	34.9	25	34.9	0	2	0	1894.97	252	267
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	8	9	15	0.02%	23.4%	GFAFISFHR	99.7%	45.1	25	35.9	2	0	0	1081.56	281	289
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	8	9	15	0.02%	23.4%	LPGELEPVQATQNK	99.7%	69.4	25	66.2	2	0	0	1523.81	196	209
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	8	9	15	0.02%	23.4%	VTNLSEDTR	99.7%	50.3	25	30.9	2	0	0	1034.51	243	251
Eukaryotic translation initiation factor 3 subunit H	EIF3H	EIF3H_HUMAN	39.9	100.0%	2	2	3	0.00%	8.8%	EGTGSTATSSSSTAGAAGK	99.7%	81.5	25	73.9	2	0	0	1627.74	6	24
Eukaryotic translation initiation factor 3 subunit H	EIF3H	EIF3H_HUMAN	39.9	100.0%	2	2	3	0.00%	8.8%	LFMAQALQEYNN	99.7%	59.9	25	59.9	1	0	0	1441.68	341	352
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	17	50	0.05%	44.6%	DMTMFVTASK	99.7%	71.6	25	65.8	8	0	0	1130.52	199	208
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	17	50	0.05%	44.6%	EGDLLFTVAK	99.7%	60.4	25	57.7	3	0	0	1092.59	21	30
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	17	50	0.05%	44.6%	GHFGPINSVAFHPDGK	99.7%	37.8	25	37.7	0	4	0	1679.83	283	298
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	17	50	0.05%	44.6%	HVLTGSADNSCR	99.7%	69.3	25	69.3	4	0	0	1316.60	66	77

Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	17	50	0.05%	44.6%	IGKFEAR	98.8%	34.2	25	24.7	2	0	0	820.47	262	268
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	17	50	0.05%	44.6%	LFDSTTLEHQK	99.7%	68	25	51.9	3	2	0	1318.66	214	224
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	17	50	0.05%	44.6%	LWDCETGK	96.0%	28.8	25	28.8	1	0	0	1008.45	78	85
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	17	50	0.05%	44.6%	MKPILLQGHER	99.7%	38.1	25	31.3	0	6	0	1321.74	1	11
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	17	50	0.05%	44.6%	QINDIQLSR	99.7%	84.3	25	21.5	4	0	0	1086.59	190	198
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	17	50	0.05%	44.6%	SGEVLVNVK	99.7%	85.8	25	77.9	4	0	0	944.54	177	185
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	17	50	0.05%	44.6%	SGEVLVNVKEHSR	99.7%	49.2	25	45.5	0	2	0	1453.78	177	189
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	17	50	0.05%	44.6%	SITQIKYNR	99.7%	42.6	25	42.6	1	0	0	1122.63	12	20
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	17	50	0.05%	44.6%	SYSSGGEDGYVR	99.7%	76.1	25	73.4	4	0	0	1276.54	299	310
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	17	50	0.05%	44.6%	TCGFDFGGNIIMFSTDK	99.7%	61.6	25	61.6	2	0	0	1909.85	98	114
Eukaryotic translation initiation factor 3 subunit K	EIF3K	EIF3K_HUMAN	25.1	100.0%	5	6	11	0.01%	26.1%	ALTNLPHTDFTLCK	99.7%	53.7	25	47.9	2	0	0	1630.83	73	86
Eukaryotic translation initiation factor 3 subunit K	EIF3K	EIF3K_HUMAN	25.1	100.0%	5	6	11	0.01%	26.1%	CMIDQAHQEERPIR	97.0%	23.6	25	23.6	0	1	0	1798.83	87	100
Eukaryotic translation initiation factor 3 subunit K	EIF3K	EIF3K_HUMAN	25.1	100.0%	5	6	11	0.01%	26.1%	ENAYDLEANLAVLK	99.7%	98.4	25	89.8	2	0	0	1562.81	39	52
Eukaryotic translation initiation factor 3 subunit K	EIF3K	EIF3K_HUMAN	25.1	100.0%	5	6	11	0.01%	26.1%	GIDRYNPENLATLER	99.7%	48.7	25	47.1	1	2	0	1760.89	17	31
Eukaryotic translation initiation factor 3 subunit K	EIF3K	EIF3K_HUMAN	25.1	100.0%	5	6	11	0.01%	26.1%	YNPENLATLER	99.7%	55.2	25	44.1	3	0	0	1319.66	21	31
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	21	23	56	0.06%	37.9%	EPFLQQLK	99.3%	36.9	25	20.5	2	0	0	1002.56	438	445
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	21	23	56	0.06%	37.9%	IDESIHLQLR	99.7%	51.2	25	40.6	2	1	0	1223.67	382	391
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	21	23	56	0.06%	37.9%	KSEEEIDFLR	99.7%	62.2	25	54.2	2	0	0	1265.64	207	216
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	21	23	56	0.06%	37.9%	LAGFLDLTEQEFR	99.7%	105	25	99.4	7	0	0	1538.79	475	487
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	21	23	56	0.06%	37.9%	LHSLLGDYYQAIK	99.7%	65.5	25	65.5	2	2	0	1520.81	280	292
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	21	23	56	0.06%	37.9%	LYTTMPVAK	99.7%	56.2	25	34.6	2	0	0	1039.55	466	474
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	21	23	56	0.06%	37.9%	MLGYFSLVGLLR	99.7%	71.8	25	61.1	2	0	0	1384.77	268	279
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	21	23	56	0.06%	37.9%	NFIQYFHK	96.7%	29.6	25	12.3	1	0	0	1096.56	54	61
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	21	23	56	0.06%	37.9%	QDLAYER	98.2%	32.1	25	22.6	2	0	0	894.43	32	38
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	21	23	56	0.06%	37.9%	QLEVYTSGGDPESVAGEYGR	99.7%	114	25	109	3	0	0	2113.97	243	262
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	21	23	56	0.06%	37.9%	SEEEIDFLR	99.7%	58.7	25	47.3	2	0	0	1137.54	208	216
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	21	23	56	0.06%	37.9%	TTYKYEMINK	99.7%	42.6	25	39.1	1	0	0	1290.64	353	362
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	21	23	56	0.06%	37.9%	TVSDLIDQK	94.8%	27.7	25	16.5	1	0	0	1018.54	62	70
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	21	23	56	0.06%	37.9%	VFANILLYIQR	99.6%	39.1	25	38.7	2	0	0	1349.79	335	345
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	21	23	56	0.06%	37.9%	VFSDEVQQQAQLSTIR	99.7%	106	25	106	4	0	0	1848.95	446	461
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	21	23	56	0.06%	37.9%	VLENIELNKK	99.7%	53.5	25	40.4	2	0	0	1199.70	293	302
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	21	23	56	0.06%	37.9%	VSGGPSLEQR	99.7%	77.8	25	63.6	4	0	0	1029.53	144	153
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	21	23	56	0.06%	37.9%	VSSDVIDQK	99.7%	69.8	25	52.9	4	0	0	990.51	79	87
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	21	23	56	0.06%	37.9%	VYEIQDIYENSWTK	99.7%	99.1	25	95.3	2	0	0	1787.85	88	101
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	21	23	56	0.06%	37.9%	VYELQASR	99.7%	57.6	25	48.1	4	0	0	965.51	71	78
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	21	23	56	0.06%	37.9%	YGDFFIR	99.7%	51.8	25	33.7	2	0	0	917.45	539	545
Eukaryotic translation initiation factor 3 subunit M	EIF3M	EIF3M_HUMAN	42.5	99.7%	2	2	3	0.00%	5.6%	LLTFMGMAVENK	99.7%	78.4	25	59.4	2	0	0	1353.69	279	290
Eukaryotic translation initiation factor 3 subunit M	EIF3M	EIF3M_HUMAN	42.5	99.7%	2	2	3	0.00%	5.6%	YTVYCSLIK	94.9%	27.8	25	16.6	1	0	0	1146.59	121	129
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	7	7	11	0.01%	7.7%	GLSFLFPLLK	99.7%	46	25	42.1	2	0	0	1134.69	723	732
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	7	7	11	0.01%	7.7%	GVILLIVDK	99.7%	66.9	25	51.8	2	0	0	969.63	113	121
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	7	7	11	0.01%	7.7%	LEVDIPLVK	99.2%	35.7	25	35.7	1	0	0	1025.62	632	640
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	7	7	11	0.01%	7.7%	SDFFLEGPFMPPR	98.2%	32.1	25	28.3	1	0	0	1539.73	348	360
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	7	7	11	0.01%	7.7%	SYLAQFAAR	99.7%	49.3	25	41.8	2	0	0	1026.54	641	649
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	7	7	11	0.01%	7.7%	TNPPLIQEKPAK	99.7%	47.2	25	42	1	0	0	1335.76	521	532
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	7	7	11	0.01%	7.7%	VIILSLDR	99.2%	35.8	25	26.8	2	0	0	928.58	585	592
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	11	14	62	0.06%	19.1%	AASIFGGAKPVDTAAR	99.7%	52.2	25	48.7	8	5	0	1531.82	357	372
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	11	14	62	0.06%	19.1%	DSDKTDTDWR	99.1%	35.2	25	20.3	2	0	0	1238.53	191	200
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	11	14	62	0.06%	19.1%	GLNISAVR	99.7%	69.6	25	39.2	6	0	0	829.49	118	125
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	11	14	62	0.06%	19.1%	QLDEPKLER	99.2%	36.1	25	18.7	1	0	0	1127.61	390	398
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	11	14	62	0.06%	19.1%	SILPTAPR	99.0%	34.8	25	23.2	3	0	0	854.51	71	78
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	11	14	62	0.06%	19.1%	SQSSDTEQQSPTSGGGK	99.7%	105	25	105	6	0	0	1680.73	495	511

Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	11	14	62	0.06%	19.1%	SRTGSESSQTGTSTTSSR	98.8%	26.9	25	26.9	0	2	0	1816.83	418	435
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	11	14	62	0.06%	19.1%	STPKEDDSSASTSQSTR	99.7%	82.7	25	82.7	5	3	0	1783.79	340	356
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	11	14	62	0.06%	19.1%	TGSESSQTGTSTTSSR	99.7%	86.1	25	85.8	3	0	0	1573.69	420	435
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	11	14	62	0.06%	19.1%	VAPAQPSEEGPGR	99.7%	59.2	25	59.2	14	0	0	1294.64	512	524
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	11	14	62	0.06%	19.1%	VAPAQPSEEGPGRK	99.7%	49.2	25	47.4	3	1	0	1422.73	512	525
Eukaryotic translation initiation factor 4E type 2	EIF4E2	IF4E2_HUMAN	28.4	99.8%	2	2	4	0.00%	9.8%	FQEDIISIWNK	99.7%	72.3	25	54.1	2	0	0	1392.72	175	185
Eukaryotic translation initiation factor 4E type 2	EIF4E2	IF4E2_HUMAN	28.4	99.8%	2	2	4	0.00%	9.8%	QIGTFASVEQFWR	99.7%	59.5	25	57.3	2	0	0	1568.79	84	96
Eukaryotic translation initiation factor 6	EIF6	IF6_HUMAN	26.6	99.8%	2	2	4	0.00%	9.8%	LNEAQPSTIATSMR	99.7%	60.3	25	60.3	2	0	0	1534.75	224	237
Eukaryotic translation initiation factor 6	EIF6	IF6_HUMAN	26.6	99.8%	2	2	4	0.00%	9.8%	NSLPDTVQIR	99.7%	46.3	25	38.6	2	0	0	1142.62	86	95
Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	ECSIT	ECSIT_HUMAN	49.1	100.0%	4	4	5	0.01%	16.9%	ALVPFEDLFGQAPGGER	99.7%	52.8	25	52.5	2	0	0	1802.91	68	84
Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	ECSIT	ECSIT_HUMAN	49.1	100.0%	4	4	5	0.01%	16.9%	DLAVYNQLLNIFPK	99.4%	37.3	25	37.3	1	0	0	1647.91	125	138
Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	ECSIT	ECSIT_HUMAN	49.1	100.0%	4	4	5	0.01%	16.9%	DLPQDPVELAMFGLR	99.7%	60.9	25	58.1	1	0	0	1700.87	218	232
Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	ECSIT	ECSIT_HUMAN	49.1	100.0%	4	4	5	0.01%	16.9%	DSTGAADPPQPHIVGIQSPDQQAALAR	99.7%	42.9	25	42.9	0	1	0	2740.37	252	278
Exocyst complex component 2	EXOC2	EXOC2_HUMAN	104.1	100.0%	4	4	5	0.01%	5.0%	ASNTADTLFQEVLGR	99.7%	92.3	25	79.8	1	0	0	1621.82	249	263
Exocyst complex component 2	EXOC2	EXOC2_HUMAN	104.1	100.0%	4	4	5	0.01%	5.0%	GALLPLSIR	99.5%	38.7	25	38.7	1	0	0	939.60	519	527
Exocyst complex component 2	EXOC2	EXOC2_HUMAN	104.1	100.0%	4	4	5	0.01%	5.0%	LVLSQLPNFWK	99.7%	53	25	53	2	0	0	1344.77	458	468
Exocyst complex component 2	EXOC2	EXOC2_HUMAN	104.1	100.0%	4	4	5	0.01%	5.0%	VIEAVSEELSR	95.5%	28.3	25	6.31	1	0	0	1231.65	828	838
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	4	4	7	0.01%	5.2%	DASVPLIDVTNLPTPR	99.7%	87.7	25	81.4	2	0	0	1707.93	224	239
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	4	4	7	0.01%	5.2%	ESEVLIGNLGDK	99.7%	82.4	25	75.1	2	0	0	1273.66	682	693
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	4	4	7	0.01%	5.2%	NITVIFHPLLR	99.7%	45.2	25	45.2	2	0	0	1322.79	495	505
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	4	4	7	0.01%	5.2%	STTQVADSGYQR	99.7%	48.8	25	44.5	1	0	0	1312.61	314	325
Exocyst complex component 5	EXOC5	EXOC5_HUMAN	81.9	99.8%	2	2	3	0.00%	3.0%	LIQNVFEIK	95.6%	28.4	25	19.3	1	0	0	1103.65	275	283
Exocyst complex component 5	EXOC5	EXOC5_HUMAN	81.9	99.8%	2	2	3	0.00%	3.0%	NVDTVLMELGVR	99.7%	65.7	25	58.8	2	0	0	1345.71	598	609
Exocyst complex component 8	EXOC8	EXOC8_HUMAN	81.8	100.0%	2	2	2	0.00%	3.5%	IQALAEETAQNLKR	98.3%	25.5	25	21.8	0	1	0	1584.87	48	61
Exocyst complex component 8	EXOC8	EXOC8_HUMAN	81.8	100.0%	2	2	2	0.00%	3.5%	RFEEGVGKPAK	99.7%	33.2	25	27.6	0	1	0	1217.66	692	702
Exosome complex component CSL4	EXOSC1	EXOS1_HUMAN	21.5	99.8%	2	2	4	0.00%	12.8%	SFRPGDIVLAK	99.7%	40.8	25	22.5	2	0	0	1202.69	121	131
Exosome complex component CSL4	EXOSC1	EXOS1_HUMAN	21.5	99.8%	2	2	4	0.00%	12.8%	SSENGALPVVSVVR	99.7%	62.6	25	45.3	2	0	0	1413.77	44	57
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	7	7	15	0.02%	28.3%	ELALALQEALEPAVR	99.7%	64.3	25	63.8	2	0	0	1622.91	121	135
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	7	7	15	0.02%	28.3%	GGGPAGAGGEAPAALR	99.7%	80.8	25	77.1	4	0	0	1308.67	78	93
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	7	7	15	0.02%	28.3%	GSAYLEAGGTK	99.7%	56.1	25	48.6	2	0	0	1053.52	51	61
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	7	7	15	0.02%	28.3%	LGLEGCQR	98.2%	32.2	25	22.2	2	0	0	932.46	243	250
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	7	7	15	0.02%	28.3%	LRPVYAR	97.8%	31.3	25	15.6	1	0	0	874.53	36	42
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	7	7	15	0.02%	28.3%	LYPVLQQSLVR	99.7%	49.3	25	37.9	2	0	0	1315.77	251	261
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	7	7	15	0.02%	28.3%	VLCAVSGPR	99.7%	67.8	25	58.8	2	0	0	958.51	62	70
Exosome complex component RRP4	EXOSC2	EXOS2_HUMAN	32.8	100.0%	3	3	7	0.01%	12.3%	LGQGVLVQVSPSLVK	99.7%	71.1	25	57.6	2	0	0	1523.92	166	180
Exosome complex component RRP4	EXOSC2	EXOS2_HUMAN	32.8	100.0%	3	3	7	0.01%	12.3%	LIASVAGSVER	99.7%	55.6	25	45.4	3	0	0	1101.63	52	62
Exosome complex component RRP4	EXOSC2	EXOS2_HUMAN	32.8	100.0%	3	3	7	0.01%	12.3%	NCIISLVTQR	99.7%	61.6	25	53.8	2	0	0	1203.65	239	248
Exosome complex component RRP41	EXOSC4	EXOS4_HUMAN	26.4	100.0%	3	3	6	0.01%	12.7%	ALAVVYGPHEIR	99.6%	39.5	25	37.9	2	0	0	1324.74	48	59
Exosome complex component RRP41	EXOSC4	EXOS4_HUMAN	26.4	100.0%	3	3	6	0.01%	12.7%	SCEMGLQLR	99.7%	56.9	25	42.8	2	0	0	1093.51	96	104
Exosome complex component RRP41	EXOSC4	EXOS4_HUMAN	26.4	100.0%	3	3	6	0.01%	12.7%	VLEAAAQAAR	99.7%	91.5	25	79.4	2	0	0	999.56	213	222
Exosome complex component RRP43	EXOSC8	EXOS8_HUMAN	30.0	99.8%	2	2	4	0.00%	10.9%	LGNTTVICGVK	99.7%	57.7	25	47.1	2	0	0	1161.63	53	63
Exosome complex component RRP43	EXOSC8	EXOS8_HUMAN	30.0	99.8%	2	2	4	0.00%	10.9%	TTTVNIGSISTADGSALVK	99.7%	107	25	98.5	2	0	0	1834.98	34	52
Exosome complex component RRP45	EXOSC9	EXOS9_HUMAN	49.0	100.0%	3	3	6	0.01%	7.7%	FGFAESIANQR	99.7%	51.5	25	46.1	1	0	0	1239.61	282	292
Exosome complex component RRP45	EXOSC9	EXOS9_HUMAN	49.0	100.0%	3	3	6	0.01%	7.7%	VAEITELILK	99.7%	71.3	25	59.5	4	0	0	1128.69	258	267
Exosome complex component RRP45	EXOSC9	EXOS9_HUMAN	49.0	100.0%	3	3	6	0.01%	7.7%	VLGQVSCELVSPK	99.7%	66.2	25	65.9	1	0	0	1415.76	55	67
Exosome complex component RRP46	EXOSC5	EXOS5_HUMAN	25.2	100.0%	3	3	6	0.01%	14.9%	AVLTFALDSVER	99.7%	101	25	70.9	2	0	0	1320.72	179	190
Exosome complex component RRP46	EXOSC5	EXOS5_HUMAN	25.2	100.0%	3	3	6	0.01%	14.9%	IGLPGVAEK	96.8%	29.7	25	12.9	2	0	0	883.52	84	92
Exosome complex component RRP46	EXOSC5	EXOS5_HUMAN	25.2	100.0%	3	3	6	0.01%	14.9%	NTCEAVVLGTLHPR	99.7%	80.8	25	77.5	2	0	0	1566.81	100	113
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	10	10	17	0.02%	12.5%	GALTLSSPEVR	99.6%	39.9	25	23	1	0	0	1129.62	628	638
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	10	10	17	0.02%	12.5%	IEDTVFHVFDK	99.5%	38	25	38	2	0	0	1349.67	896	906
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	10	10	17	0.02%	12.5%	IIFSEHLPLSK	99.7%	52.2	25	44	2	0	0	1283.74	226	236

Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	10	10	17	0.02%	12.5%	IIVAIDGWPR	99.7%	74	25	67.4	2	0	0	1139.66	398	407
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	10	10	17	0.02%	12.5%	LACLSEEGNEIESGK	99.7%	71.9	25	71.9	1	0	0	1635.75	211	225
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	10	10	17	0.02%	12.5%	LLAVAIGADCTYPELTDK	99.7%	74.8	25	74	1	0	0	1949.99	790	807
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	10	10	17	0.02%	12.5%	NVIVLQTVLQEVR	99.7%	94.7	25	94.7	4	0	0	1510.90	87	99
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	10	10	17	0.02%	12.5%	SLTANPELIDR	97.6%	31	25	20.1	1	0	0	1228.65	200	210
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	10	10	17	0.02%	12.5%	YADVIVHR	99.7%	44.1	25	37.7	2	0	0	972.53	782	789
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	10	10	17	0.02%	12.5%	YGLEGTVFFEEK	99.7%	42.5	25	42.5	1	0	0	1418.68	867	878
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	6	6	11	0.01%	7.1%	AAAEQAISVR	99.7%	62.7	25	40.4	1	0	0	1015.55	759	768
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	6	6	11	0.01%	7.1%	FALGSVVAVTK	99.7%	81.3	25	73.1	2	0	0	1091.65	38	48
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	6	6	11	0.01%	7.1%	LAQVQVQK	99.5%	38.5	25	22.7	2	0	0	913.55	726	733
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	6	6	11	0.01%	7.1%	LYCNVDSNK	99.3%	36.6	25	31.5	2	0	0	1112.50	409	417
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	6	6	11	0.01%	7.1%	TEDFIIDTLELR	99.7%	71.8	25	58.8	2	0	0	1464.76	335	346
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	6	6	11	0.01%	7.1%	VGILLDEASGVNK	99.7%	72.2	25	71.8	2	0	0	1314.73	124	136
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	AIIASNIMYIVGQYPR	99.7%	89.9	25	87.9	4	2	0	1808.97	538	553
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	AVGHPFVIQLGR	99.7%	44.8	25	33.3	2	2	0	1293.74	701	712
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	EFAGEDTSDLFLEER	99.7%	122	25	104	2	0	0	1757.79	1024	1038
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	EFMKDTDSINLYK	99.7%	63.8	25	58.8	1	0	0	1619.76	443	455
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	EPEVLSTMAIIVNK	99.7%	99.3	25	99.3	4	0	0	1543.84	797	810
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	ETLVYLTHLDYVDTER	99.7%	97.2	25	97.2	2	2	0	1966.98	459	474
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	FLNWIPLGYIFETK	96.2%	29	25	28.6	1	0	0	1740.94	232	245
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	FLVTVIK	99.7%	45.9	25	16.8	2	0	0	819.53	516	522
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	IYLDMLNVYK	99.7%	65.9	25	60.7	6	0	0	1271.67	713	722
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	LFVTGLFSLNQDIPAFK	99.7%	74.3	25	74.3	1	0	0	1910.04	996	1012
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	LISGWVSR	99.7%	58.6	25	38.9	2	0	0	917.52	758	765
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	LISTLIYK	99.7%	53.5	25	47.9	2	0	0	950.59	246	253
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	LLSEEVFDFSSGQITQVK	99.7%	104	25	104	3	2	0	2027.03	173	190
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	LNMILVQILK	99.7%	81.6	25	62.2	4	0	0	1184.74	130	139
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	LVLDSIIWAFK	99.7%	83.1	25	83.1	5	0	0	1304.76	873	883
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	MAKPEEVLVVENDQGEVVR	99.7%	45.1	25	43.9	0	2	0	2157.09	424	442
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	MAQEVLTHLK	99.7%	63.7	25	56.1	4	0	0	1185.63	45	54
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	NVDILKDPETVK	99.7%	58	25	53.5	2	2	0	1370.75	675	686
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	PAIMTMLADHAAR	99.7%	52.3	25	52.3	0	1	0	1397.70	2	14
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	QLLDFSQK	96.9%	29.8	25	21.1	1	0	0	978.53	15	22
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	QLYLPMLFK	97.3%	30.4	25	17	1	0	0	1168.64	407	415
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	QMLPLNTNIR	99.7%	59.8	25	47	4	0	0	1199.66	296	305
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	SAFPHLQDAQVK	99.7%	63.4	25	53.1	2	0	0	1340.70	984	995
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	TSESLCQNNMVILK	99.7%	84.2	25	68.9	4	0	0	1636.80	159	172
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	TSSDPTCVEK	99.7%	56.9	25	39.6	2	0	0	1123.49	113	122
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	TSSDPTCVEKEK	99.7%	63.5	25	46.4	2	0	0	1380.63	113	124
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	VDTILEFSQNMNTK	99.7%	92.9	25	85.1	4	0	0	1639.80	63	76
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	YVVGLIIK	99.7%	52.1	25	40.9	2	0	0	904.59	105	112
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	29	42	88	0.09%	31.9%	YYGLQILENVIK	99.7%	87.1	25	83	6	0	0	1452.81	77	88
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	AACDLVR	99.5%	38.7	25	24.9	2	0	0	804.40	385	391
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	AADEEAFEDNSEEYIR	99.7%	110	25	110	2	0	0	1887.79	356	371
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	AADEEAFEDNSEEYIRR	99.7%	38.9	25	38.9	1	2	0	2043.89	356	372
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	ALTLPGSSENEYIMK	99.7%	99.3	25	90.3	4	0	0	1668.82	560	574
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	ANIVHLMLSSPEQIQK	99.7%	82.9	25	81.8	3	2	0	1807.97	94	109
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	ATIELCSTHANDASALR	99.7%	105	25	103	2	2	0	1829.88	190	206
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	DAAIYLVTSLASK	99.7%	96.6	25	96.3	2	0	0	1351.75	428	440
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	DLEGSDIDTR	99.7%	51.3	25	44.2	2	0	0	1120.51	373	382
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	DLEGSDIDTRR	99.7%	41.4	25	19.1	2	0	0	1276.61	373	383

Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	EHDPVGQMVNNPK	99.7%	73.6	25	73.6	2	2	0	1480.69	913	925
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	FQSGDFHVINGVLR	96.7%	23.2	25	22.8	0	1	0	1588.82	138	151
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	FVTAIWNLLVTTGQEVK	99.7%	42.7	25	42.7	1	0	0	1919.06	293	309
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	GSNTIASAAADK	99.7%	46.8	25	39.8	2	0	0	1105.55	715	726
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	GSNTIASAAADKIPGLLGVFQK	99.7%	41.6	25	39.4	0	2	0	2158.19	715	736
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	IHLAQSLHK	99.7%	44.9	25	42.9	2	0	0	1046.61	926	934
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	ILFSSLILISK	99.7%	83.2	25	83.2	3	0	0	1233.78	207	217
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	IVEDEPNKICEADR	99.7%	89.6	25	89.6	2	1	0	1687.80	76	89
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	KICAVGITK	99.6%	39.2	25	32.7	3	0	0	989.58	840	848
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	LLQAFLER	99.7%	62.2	25	43.3	8	0	0	989.58	707	714
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	LLQTDDEEEAGLLELLK	99.7%	119	25	114	2	0	0	1929.01	252	268
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	LLTECPPMMDTEYTK	99.7%	65.6	25	65.6	4	0	0	1828.82	849	863
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	LSTACPGR	97.1%	30.2	25	23.9	2	0	0	861.42	935	942
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	LVLDAFALPLTNLFK	99.7%	58.6	25	58.6	2	0	0	1674.98	175	189
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	MFGMVLEK	98.6%	33.2	25	21.6	2	0	0	954.48	817	824
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	NLFEDQNTLTSICEK	99.7%	103	25	103	2	0	0	1811.85	332	346
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	NPSVNWK	97.7%	31.1	25	22.1	1	0	0	844.43	419	425
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	QIFILLFQR	99.7%	59.7	25	53.3	5	0	0	1177.71	769	777
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	QLSDAISIIGR	99.7%	76.5	25	53.8	2	0	0	1172.66	110	120
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	SANVNEFPVLK	99.7%	51.7	25	37	2	0	0	1217.65	471	481
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	SNELWTEIK	99.7%	57.9	25	42.7	2	0	0	1119.57	166	174
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	SQICDNAALYAQK	99.7%	88.2	25	73	2	0	0	1481.71	269	281
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	TGNIPALVR	99.7%	55.1	25	45.5	4	0	0	940.56	698	706
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	VIVPNMEFR	99.6%	39.2	25	33.5	2	0	0	1104.59	347	355
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	YDEEFQR	99.7%	44.3	25	44.3	2	0	0	986.42	282	288
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	YGALALQEIFDGIQPK	99.7%	122	25	121	3	0	0	1762.94	801	816
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.10%	41.0%	YIMIFR	97.6%	31	25	18.8	1	0	0	842.46	487	492
Exportin-4	XPO4	XPO4_HUMAN	130.1	99.9%	2	2	3	0.00%	2.0%	AQETDSPLFLATR	99.7%	63	25	51.1	1	0	0	1448.74	1039	1051
Exportin-4	XPO4	XPO4_HUMAN	130.1	99.9%	2	2	3	0.00%	2.0%	LVFDMLVLQK	99.7%	66	25	53.4	2	0	0	1205.70	1056	1065
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	23	23	45	0.05%	23.4%	AGGFVVGYTSSGNPIFR	99.7%	106	25	106	2	0	0	1728.87	746	762
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	23	23	45	0.05%	23.4%	ALDMLDAEK	99.7%	42.2	25	40	2	0	0	1021.49	802	810
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	23	23	45	0.05%	23.4%	AVMEQIPEIQK	99.7%	56.1	25	50.8	2	0	0	1285.68	1113	1123
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	23	23	45	0.05%	23.4%	AVTVMMDPNSTQR	99.7%	64.9	25	64.9	1	0	0	1481.67	16	28
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	23	23	45	0.05%	23.4%	CPICVPCGLR	96.7%	29.6	25	22.7	1	0	0	1231.57	44	53
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	23	23	45	0.05%	23.4%	DIQQTLTQNMER	99.7%	43.6	25	43.6	2	0	0	1492.71	177	188
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	23	23	45	0.05%	23.4%	DPLLLAIIPK	99.7%	45.8	25	37.8	7	0	0	1092.70	387	396
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	23	23	45	0.05%	23.4%	EVMDLITVCCVSK	96.4%	29.2	25	29.2	1	0	0	1569.73	968	980
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	23	23	45	0.05%	23.4%	IFSFLLNTLQENVNK	99.7%	77.8	25	64.4	2	0	0	1779.96	189	203
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	23	23	45	0.05%	23.4%	IVVEMIKR	97.8%	31.2	25	17.5	2	0	0	987.60	119	126
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	23	23	45	0.05%	23.4%	LIAGCIGKPLGEQFR	98.1%	25.1	25	17.6	0	1	0	1658.91	1153	1167
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	23	23	45	0.05%	23.4%	LLDNLLALIR	99.7%	73.6	25	52.5	4	0	0	1153.73	772	781
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	23	23	45	0.05%	23.4%	LLNPSLQK	97.5%	30.9	25	13.3	1	0	0	912.55	1133	1140
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	23	23	45	0.05%	23.4%	NPCTEQILK	99.4%	37.1	25	30	2	0	0	1102.56	763	771
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	23	23	45	0.05%	23.4%	QGETQTELVMFILLR	99.7%	52.8	25	52.8	1	0	0	1793.95	145	159
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	23	23	45	0.05%	23.4%	QLLSNELLLTQMEK	99.7%	79.7	25	70	2	0	0	1659.90	632	645
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	23	23	45	0.05%	23.4%	SAILGLPQPLLELNDSPVFK	99.7%	68.3	25	68.3	2	0	0	2151.21	811	830
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	23	23	45	0.05%	23.4%	TCWPTDLEEAK	99.7%	54.6	25	44.5	1	0	0	1349.60	735	745
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	23	23	45	0.05%	23.4%	TDSPSCEYSR	99.7%	48.8	25	48.8	2	0	0	1201.48	414	423
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	23	23	45	0.05%	23.4%	THNTLYAPEMLAK	99.7%	61.9	25	58.6	1	0	0	1504.75	782	794
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	23	23	45	0.05%	23.4%	TSFQMAGEWLK	99.7%	55.1	25	54	2	0	0	1297.62	457	467
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	23	23	45	0.05%	23.4%	TTSQLCWPLLK	99.1%	35.6	25	27.7	2	0	0	1346.71	1047	1057

Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	23	23	45	0.05%	23.4%	VLSDVDAFIAYVGTDQK	99.7%	101	25	97.2	2	0	0	1840.93	688	704
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	5	5	6	0.01%	4.5%	AELFELLFR	99.7%	48.9	25	38.3	2	0	0	1137.63	936	944
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	5	5	6	0.01%	4.5%	FCLYFLSSTR	99.7%	41.3	25	36.1	1	0	0	1293.63	47	56
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	5	5	6	0.01%	4.5%	FNDALTVVER	99.7%	75.8	25	66.5	1	0	0	1163.61	580	589
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	5	5	6	0.01%	4.5%	LAEYFIGDVFAAR	99.6%	39.1	25	39.1	1	0	0	1471.76	567	579
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	5	5	6	0.01%	4.5%	STVLASVQR	99.7%	50.4	25	34.8	1	0	0	960.55	956	964
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	30	0.03%	18.5%	AALSGSYVNFGVFR	99.7%	96.2	25	92.2	2	0	0	1487.76	841	854
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	30	0.03%	18.5%	ALVEFTNSPDCLSK	99.7%	46.5	25	41.2	1	0	0	1580.76	33	46
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	30	0.03%	18.5%	DSSLFDIFTLSCNLLK	99.4%	37.3	25	37.3	1	0	0	1872.94	183	198
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	30	0.03%	18.5%	GIAFAFNAK	99.7%	50.8	25	39.7	2	0	0	938.51	728	736
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	30	0.03%	18.5%	GSSSYSQLLAATCLTK	99.7%	63.1	25	59.2	2	0	0	1686.84	54	69
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	30	0.03%	18.5%	IYIGDQVQK	99.7%	46.7	25	38.4	2	0	0	1063.58	560	568
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	30	0.03%	18.5%	LESVHIILR	99.7%	65.7	25	65.7	2	0	0	1079.66	418	426
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	30	0.03%	18.5%	LMAELVHNR	99.7%	53.3	25	43.1	2	0	0	1082.58	774	782
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	30	0.03%	18.5%	LQFDVSSPNGILLFR	99.7%	79.4	25	79.4	2	0	0	1705.93	786	800
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	30	0.03%	18.5%	LYGDDALDNALQTFIK	99.7%	91.1	25	90.3	2	0	0	1796.91	855	870
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	30	0.03%	18.5%	NSIVNSQPPEK	99.7%	53.5	25	49	2	0	0	1212.62	1021	1031
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	30	0.03%	18.5%	NYVLNYLATRPK	99.7%	77	25	77	2	0	0	1451.80	88	99
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	30	0.03%	18.5%	QLYETTDTTTR	99.7%	64.7	25	57	2	0	0	1328.63	17	27
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	30	0.03%	18.5%	SNYQLGELVK	99.7%	41.4	25	35.7	2	0	0	1150.61	339	348
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	30	0.03%	18.5%	TNNPLPLEQR	99.7%	54.9	25	39.8	2	0	0	1181.63	74	83
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	30	0.03%	18.5%	TTFYTALGR	95.5%	28.3	25	20.4	1	0	0	1029.54	666	674
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	30	0.03%	18.5%	VLQLMNLTDSR	99.7%	68.3	25	63.8	1	0	0	1289.69	527	537
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	22	39	0.04%	20.6%	ALAYFEQLK	99.7%	58.6	25	50.8	2	0	0	1082.59	21	29
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	22	39	0.04%	20.6%	ANVEAIMLAVMK	99.7%	98.9	25	90.3	2	0	0	1289.70	370	381
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	22	39	0.04%	20.6%	ASALQDMMR	99.7%	56.7	25	51.8	3	0	0	1022.48	475	483
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	22	39	0.04%	20.6%	DGPVGFADFVYK	99.7%	66.9	25	66.9	2	0	0	1314.64	860	871
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	22	39	0.04%	20.6%	DLQEFIPLINQITAK	99.7%	73.7	25	73.7	1	0	0	1742.97	738	752
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	22	39	0.04%	20.6%	DVVHTSEEAR	98.2%	32.3	25	32.1	1	0	0	1142.54	157	166
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	22	39	0.04%	20.6%	FFCFQVLEHQVK	99.7%	62	25	62	2	2	0	1581.79	54	65
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	22	39	0.04%	20.6%	FMEVEVAIR	99.7%	54.6	25	44.3	2	0	0	1109.57	443	451
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	22	39	0.04%	20.6%	LAQVSPELLLASVR	99.7%	107	25	107	4	0	0	1495.88	415	428
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	22	39	0.04%	20.6%	LMLAQDEER	99.7%	42	25	34	2	0	0	1104.54	635	643
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	22	39	0.04%	20.6%	NAQEALQAIETK	99.7%	68.6	25	40.1	2	0	0	1315.69	317	328
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	22	39	0.04%	20.6%	QLTVLSDQQK	99.1%	35.5	25	23	2	0	0	1159.63	360	369
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	22	39	0.04%	20.6%	QMNPFIEDILNR	99.7%	74.4	25	66.3	4	0	0	1489.75	558	569
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	22	39	0.04%	20.6%	TCFIILSK	99.7%	45.4	25	39.7	1	0	0	981.54	844	851
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	22	39	0.04%	20.6%	VFSSTLQNWQTTR	99.7%	85.8	25	84	2	0	0	1567.79	430	442
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	22	39	0.04%	20.6%	VLVTVIQGAVEYPDPIAQK	99.7%	103	25	103	2	1	0	2040.14	825	843
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	22	39	0.04%	20.6%	YSELTTVQQQLIR	99.7%	75.2	25	71	2	0	0	1578.85	68	80
Extended synaptotagmin-1	ESYT1	ESYT1_HUMAN	122.9	100.0%	3	3	4	0.00%	3.6%	ALTLGALTLPLAR	99.7%	46.2	25	43.7	2	0	0	1309.82	551	563
Extended synaptotagmin-1	ESYT1	ESYT1_HUMAN	122.9	100.0%	3	3	4	0.00%	3.6%	LLAETVAPAVR	99.7%	40.5	25	39.3	1	0	0	1139.68	160	170
Extended synaptotagmin-1	ESYT1	ESYT1_HUMAN	122.9	100.0%	3	3	4	0.00%	3.6%	LLVPLVPDLQDVAQLR	95.0%	27.9	25	27.9	1	0	0	1789.06	308	323
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	4	4	7	0.01%	5.1%	ALALLEDEER	99.7%	45.4	25	42.2	1	0	0	1158.60	163	172
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	4	4	7	0.01%	5.1%	ITVPLVSEVQIAQLR	99.7%	92.6	25	92.6	2	0	0	1665.99	365	379
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	4	4	7	0.01%	5.1%	LLDEWFTLDEVPK	99.7%	63.5	25	56.8	2	0	0	1604.82	484	496
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	4	4	7	0.01%	5.1%	VDVGQQPLR	99.7%	49.7	25	34.1	2	0	0	1011.56	240	248
FACT complex subunit SPT16	SUPT16H	SP16H_HUMAN	119.9	100.0%	4	4	4	0.00%	4.8%	AASITSEVFNK	99.7%	48.1	25	46.4	1	0	0	1166.61	186	196
FACT complex subunit SPT16	SUPT16H	SP16H_HUMAN	119.9	100.0%	4	4	4	0.00%	4.8%	APGEQTVPALNLQNAFR	97.1%	30.1	25	30.1	1	0	0	1825.96	607	623
FACT complex subunit SPT16	SUPT16H	SP16H_HUMAN	119.9	100.0%	4	4	4	0.00%	4.8%	LTEQKGEQQIQK	99.7%	41.8	25	36	1	0	0	1429.76	493	504
FACT complex subunit SPT16	SUPT16H	SP16H_HUMAN	119.9	100.0%	4	4	4	0.00%	4.8%	QDSLVINLNR	98.6%	33.5	25	26.1	1	0	0	1171.64	648	657

F-actin-capping protein subunit alpha-1	CAPZA1	CAZA1_HUMAN	32.9	99.9%	2	2	4	0.00%	8.7%	FTITPPTAQVVGVLK	99.7%	51.9	25	51.9	2	0	0	1570.92	179	193
F-actin-capping protein subunit alpha-1	CAPZA1	CAZA1_HUMAN	32.9	99.9%	2	2	4	0.00%	8.7%	LLLNNDNLLR	99.7%	72.1	25	53.6	2	0	0	1197.70	38	47
Fanconi anemia group D2 protein	FANCD2	FACD2_HUMAN	166.5	100.0%	4	4	5	0.01%	3.0%	LLLGIDILQPAIIK	99.6%	38.8	25	38.8	1	0	0	1519.98	138	151
Fanconi anemia group D2 protein	FANCD2	FACD2_HUMAN	166.5	100.0%	4	4	5	0.01%	3.0%	LVSPLCLAPYFR	98.1%	32	25	32	2	0	0	1435.78	724	735
Fanconi anemia group D2 protein	FANCD2	FACD2_HUMAN	166.5	100.0%	4	4	5	0.01%	3.0%	SESPSLTQER	99.3%	36.9	25	10.2	1	0	0	1133.54	590	599
Fanconi anemia group D2 protein	FANCD2	FACD2_HUMAN	166.5	100.0%	4	4	5	0.01%	3.0%	TLELLVCR	99.3%	36.4	25	18	1	0	0	1003.56	1363	1370
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	28	0.03%	15.0%	DLQLLQGSK	99.7%	41.3	25	31.1	2	0	0	1001.56	340	348
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	28	0.03%	15.0%	DVPLTAEEVEFVVEK	99.7%	73.1	25	68.8	2	0	0	1703.87	183	197
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	28	0.03%	15.0%	EALLLVTVLTSLSK	99.7%	66.8	25	66.8	2	0	0	1486.91	981	994
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	28	0.03%	15.0%	EGDLTNLLQNQAVK	99.7%	75.3	25	66.2	2	0	0	1542.81	26	39
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	28	0.03%	15.0%	ETGHVSGPDGQNPEK	99.5%	38.3	25	35.4	1	0	0	1551.70	855	869
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	28	0.03%	15.0%	FVSSLLTALFR	99.7%	62.8	25	59.7	2	0	0	1253.73	809	819
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	28	0.03%	15.0%	GSPCSEEAGTLR	99.7%	66.9	25	66.9	1	0	0	1263.56	53	64
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	28	0.03%	15.0%	IFQNLCDITR	99.7%	53.8	25	32.1	1	0	0	1279.65	870	879
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	28	0.03%	15.0%	IFSAVQQFYQPK	99.7%	74.6	25	56.5	2	0	0	1455.76	915	926
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	28	0.03%	15.0%	LMLYEGFYDVLR	99.7%	42.7	25	36.8	2	0	0	1534.76	603	614
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	28	0.03%	15.0%	SADFSQSTSIGIK	99.7%	53.2	25	46	2	0	0	1340.67	726	738
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	28	0.03%	15.0%	SLLNLLSSQEEDFNSK	99.7%	76.9	25	76.9	2	0	0	1823.90	965	980
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	28	0.03%	15.0%	TAAPTVCLLVLSQAEK	99.7%	67.5	25	59.6	2	0	0	1700.93	1079	1094
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	28	0.03%	15.0%	TIETSPSLSR	98.9%	34.3	25	31.7	1	0	0	1090.57	403	412
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	28	0.03%	15.0%	VLEEVDWLITK	99.7%	42	25	29.1	2	0	0	1344.74	1095	1105
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	28	0.03%	15.0%	YAVNVALQK	99.4%	37.7	25	37.7	2	0	0	1005.57	841	849
Far upstream element-binding protein 2	KHSRP	FUBP2_HUMAN	73.1	100.0%	5	5	8	0.01%	8.4%	AINQQTGAFVEISR	99.7%	75.7	25	71	1	0	0	1533.80	449	462
Far upstream element-binding protein 2	KHSRP	FUBP2_HUMAN	73.1	100.0%	5	5	8	0.01%	8.4%	DAFADAVQR	99.7%	52.1	25	41.3	2	0	0	992.48	72	80
Far upstream element-binding protein 2	KHSRP	FUBP2_HUMAN	73.1	100.0%	5	5	8	0.01%	8.4%	IGGGIDVPVPR	99.7%	73.1	25	67.8	2	0	0	1079.62	321	331
Far upstream element-binding protein 2	KHSRP	FUBP2_HUMAN	73.1	100.0%	5	5	8	0.01%	8.4%	SVSLTGAPESVQK	99.7%	45.9	25	38	2	0	0	1302.69	191	203
Far upstream element-binding protein 2	KHSRP	FUBP2_HUMAN	73.1	100.0%	5	5	8	0.01%	8.4%	VQISPDSGGLPER	99.7%	41	25	36.6	1	0	0	1354.70	178	190
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	5	5	7	0.01%	9.6%	AAQVMGPPDR	97.3%	30.5	25	30.5	1	0	0	1057.51	300	309
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	5	5	7	0.01%	9.6%	AEGFVDALHR	99.6%	39.6	25	30.9	2	0	0	1114.56	16	25
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	5	5	7	0.01%	9.6%	IQFKPDDGISPER	99.6%	30.7	25	27	0	1	0	1501.76	287	299
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	5	5	7	0.01%	9.6%	LLGQIVDR	99.7%	41.9	25	31.9	2	0	0	913.55	140	147
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	5	5	7	0.01%	9.6%	SINQQSGAHVELQR	99.7%	55.1	25	46.5	1	0	0	1566.80	379	392
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	7	12	23	0.02%	19.6%	ATPEQYQILK	99.7%	44.5	25	40.2	2	0	0	1190.64	344	353
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	7	12	23	0.02%	19.6%	CSWLVVQCLQR	99.7%	77.5	25	67.5	2	0	0	1448.71	333	343
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	7	12	23	0.02%	19.6%	GLTVVVAFR	99.7%	72	25	63.3	2	0	0	961.58	127	135
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	7	12	23	0.02%	19.6%	IGTDIQDNK	99.7%	46	25	31	2	0	0	1003.51	324	332
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	7	12	23	0.02%	19.6%	LKEVLEYNAIGGK	99.7%	62.3	25	57.3	2	2	0	1433.80	111	123
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	7	12	23	0.02%	19.6%	QDFVQHFSQIVR	99.7%	38.1	25	31.5	2	2	0	1503.77	81	92
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	7	12	23	0.02%	19.6%	VLTEDEMGHPEIGDAIAR	99.7%	70.4	25	70.4	3	4	0	1952.94	93	110
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	8	10	17	0.02%	24.7%	AHPVFYQGTYSQALNDAK	99.7%	45.6	25	45.6	0	1	0	2009.97	150	167
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	8	10	17	0.02%	24.7%	DLTQEQTEK	99.7%	45.7	25	32.7	2	0	0	1091.52	8	16
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	8	10	17	0.02%	24.7%	ENTYPFLAMIMLK	99.7%	58.5	25	57.8	2	0	0	1570.80	227	239
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	8	10	17	0.02%	24.7%	FTYYTILDIFR	99.7%	82	25	75	3	0	0	1451.76	105	115
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	8	10	17	0.02%	24.7%	HTLEQHNWNIEAAVQDR	99.0%	27.6	25	27.6	0	1	0	2060.99	34	50
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	8	10	17	0.02%	24.7%	IYSYVVSRPQPR	99.7%	49.3	25	46.9	1	1	0	1464.80	78	89
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	8	10	17	0.02%	24.7%	QQQDEAYLASLR	99.7%	75.7	25	64.5	2	0	0	1421.70	291	302
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	8	10	17	0.02%	24.7%	VTDPVGDIVSFMHSFEEK	99.7%	94.2	25	94.2	3	1	0	2036.96	129	146
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	12	14	23	0.02%	20.0%	DAPIALKR	99.7%	54.8	25	17.5	2	0	0	883.54	320	327
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	12	14	23	0.02%	20.0%	DIISELLTSDDMK	99.7%	80.2	25	72.6	4	0	0	1479.73	523	535
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	12	14	23	0.02%	20.0%	IEDVFTLQVVMK	99.5%	38.1	25	23.2	1	0	0	1437.77	304	315
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	12	14	23	0.02%	20.0%	IVEDPESLNMK	99.7%	61.2	25	48.6	2	0	0	1274.63	444	454

FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	12	14	23	0.02%	20.0%	LDDTVYLR	99.7%	56.5	25	45.1	2	0	0	994.52	549	556
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	12	14	23	0.02%	20.0%	LGIPQNTILVQTLLR	99.7%	40.9	25	38	2	0	0	1679.02	242	256
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	12	14	23	0.02%	20.0%	NQVLPLSDVDTTSATDIQR	99.7%	139	25	139	2	0	0	2073.05	615	633
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	12	14	23	0.02%	20.0%	SAYCLGSSHPR	99.7%	53.6	25	53.6	2	0	0	1234.56	642	652
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	12	14	23	0.02%	20.0%	SLILLDECSK	99.7%	44.3	25	35.9	2	0	0	1177.61	359	368
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	12	14	23	0.02%	20.0%	VAVLCVSR	99.7%	48.1	25	31	2	0	0	903.51	634	641
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	12	14	23	0.02%	20.0%	VNLNHEVSNEDVLTK	99.7%	39	25	36.9	0	1	0	1710.87	133	147
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	12	14	23	0.02%	20.0%	VVLDNIHGCPLR	99.7%	53.2	25	40.1	1	0	0	1392.74	369	380
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	44	0.04%	9.4%	AALQEELQLCK	99.7%	49.7	25	31.9	2	0	0	1302.67	1132	1142
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	44	0.04%	9.4%	AINCATSGVVGLVNCLR	99.6%	39.9	25	39.9	1	0	0	1803.92	1445	1461
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	44	0.04%	9.4%	AQVADVVVSR	99.7%	57.2	25	43.1	1	0	0	1043.58	1073	1082
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	44	0.04%	9.4%	DNLEFFLAGIGR	99.7%	64.6	25	48	2	0	0	1351.70	791	802
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	44	0.04%	9.4%	EDGLAQQQTQLNLR	99.7%	73.1	25	67.4	3	0	0	1613.82	2207	2220
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	44	0.04%	9.4%	FDASFFGVHPK	99.7%	52.1	25	43.2	2	0	0	1251.62	60	70
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	44	0.04%	9.4%	FPQLDSTSFANSR	99.7%	84.3	25	71	3	0	0	1469.70	1712	1724
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	44	0.04%	9.4%	GLVQALQTK	99.7%	46.6	25	28	4	0	0	957.57	1143	1151
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	44	0.04%	9.4%	GVDLVLNSLAEEK	99.7%	72.1	25	60.8	2	0	0	1386.75	1740	1752
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	44	0.04%	9.4%	LLEQGLR	99.4%	37.5	25	0	1	0	0	828.49	437	443
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	44	0.04%	9.4%	LPEDPLLSGLLDSPALK	99.7%	95.4	25	95.4	4	0	0	1778.00	1209	1225
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	44	0.04%	9.4%	LQVVDQPLPVR	99.7%	60	25	60	2	0	0	1263.74	374	384
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	44	0.04%	9.4%	SEGVVAVLLTK	99.7%	61.9	25	53.7	2	0	0	1115.67	225	235
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	44	0.04%	9.4%	SFYGSTLFLCR	99.7%	65.2	25	49.2	2	0	0	1350.65	1394	1404
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	44	0.04%	9.4%	SLLVNPEGPTLMR	97.8%	31.4	25	31.4	1	0	0	1442.77	2221	2233
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	44	0.04%	9.4%	TGTVSLEVR	99.7%	47.2	25	37	2	0	0	961.53	928	936
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	44	0.04%	9.4%	VAAAVDLIIK	99.2%	36	25	36	2	0	0	1012.64	2397	2406
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	44	0.04%	9.4%	VLEALLPLK	99.7%	45.5	25	42.6	2	0	0	995.65	2383	2391
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	44	0.04%	9.4%	VLQGDLVMNVYR	99.7%	60.4	25	60.4	2	0	0	1406.75	1496	1507
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	44	0.04%	9.4%	VVVQVLAEEPEAVLK	99.7%	89	25	70.4	4	0	0	1622.94	1852	1866
Fermitin family homolog 2	FERMT2	FERM2_HUMAN	77.9	100.0%	4	4	5	0.01%	7.1%	GCEVTPDVNISGQK	99.4%	37.3	25	34.3	1	0	0	1503.71	425	438
Fermitin family homolog 2	FERMT2	FERM2_HUMAN	77.9	100.0%	4	4	5	0.01%	7.1%	INQLYEQAK	99.3%	36.8	25	16.1	1	0	0	1106.58	291	299
Fermitin family homolog 2	FERMT2	FERM2_HUMAN	77.9	100.0%	4	4	5	0.01%	7.1%	LLIPVAEGMNEIWLR	99.4%	37.5	25	36.6	1	0	0	1769.96	443	457
Fermitin family homolog 2	FERMT2	FERM2_HUMAN	77.9	100.0%	4	4	5	0.01%	7.1%	YYSFFDLNPK	99.7%	67.3	25	52.7	2	0	0	1293.62	276	285
Filaggrin-2	FLG2	FILA2_HUMAN	248.1	100.0%	3	3	24	0.02%	2.0%	FSNSSSSNEFSK	99.7%	52.9	25	52.7	7	0	0	1320.57	404	415
Filaggrin-2	FLG2	FILA2_HUMAN	248.1	100.0%	3	3	24	0.02%	2.0%	SGQSSYGQHSSGSSQSSGYGQHGSR	99.7%	34.9	25	34.9	0	1	0	2500.05	613	637
Filaggrin-2	FLG2	FILA2_HUMAN	248.1	100.0%	3	3	24	0.02%	2.0%	SVVTVIDVFYK	99.7%	65.8	25	65.8	16	0	0	1269.71	7	17
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	21	21	28	0.03%	10.3%	AFGPGLQGGSAGSPAR	99.7%	62.6	25	58	1	0	0	1429.72	1072	1087
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	21	21	28	0.03%	10.3%	AGQSAAGAAPGGGVDTR	99.3%	36.7	25	36.7	1	0	0	1442.70	8	24
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	21	21	28	0.03%	10.3%	AGVAPLQVK	99.6%	40	25	35.1	1	0	0	882.54	1478	1486
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	21	21	28	0.03%	10.3%	ALTQTGGPHVK	99.5%	38.7	25	35.8	2	0	0	1108.61	1284	1294
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	21	21	28	0.03%	10.3%	ANLPQSFQVDTSK	99.7%	59.2	25	54	2	0	0	1434.72	1465	1477
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	21	21	28	0.03%	10.3%	EATTEFSVDAR	99.1%	35.5	25	35.5	1	0	0	1225.57	1273	1283
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	21	21	28	0.03%	10.3%	ENGVYLIDVK	99.7%	47.3	25	43.2	1	0	0	1149.62	2396	2405
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	21	21	28	0.03%	10.3%	GAGTGGLGLAVEGPSEAK	99.7%	45.3	25	33.3	1	0	0	1570.81	1382	1399
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	21	21	28	0.03%	10.3%	IVGPSGAAVPCK	96.3%	29.2	25	21.7	1	0	0	1155.62	1008	1019
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	21	21	28	0.03%	10.3%	LYSVSYLLK	95.3%	28.1	25	11.6	1	0	0	1085.62	2613	2621
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	21	21	28	0.03%	10.3%	SPFEVYVDK	94.7%	27.6	25	22.5	1	0	0	1083.54	368	376
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	21	21	28	0.03%	10.3%	SPFSVAVSPSLDLSK	99.7%	54.3	25	46.9	2	0	0	1533.82	959	973
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	21	21	28	0.03%	10.3%	SPYTVTVGQACNPSACR	99.7%	76.2	25	76.2	1	0	0	1867.84	468	484
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	21	21	28	0.03%	10.3%	TGVAVNKPAEFTVDAK	94.8%	27.7	25	19.9	1	0	0	1646.87	685	700
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	21	21	28	0.03%	10.3%	TPCEEILVK	96.5%	29.4	25	15.3	1	0	0	1088.57	2599	2607
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	21	21	28	0.03%	10.3%	VANPSGNLTETYVQDR	99.7%	97.5	25	97.5	2	0	0	1763.86	1297	1312

Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	21	21	28	0.03%	10.3%	VPVHDVTDASK	99.7%	43.8	25	35.3	2	0	0	1167.60	1440	1450
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	21	21	28	0.03%	10.3%	VTAQGPGLEPSGNIANK	99.7%	61.1	25	60.8	2	0	0	1652.86	384	400
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	21	21	28	0.03%	10.3%	VTVLFAGQHIAK	99.7%	53.1	25	53.1	2	0	0	1283.75	356	367
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	21	21	28	0.03%	10.3%	YGGDEIPFSPYR	99.7%	57.7	25	23.8	1	0	0	1400.65	1622	1633
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	21	21	28	0.03%	10.3%	YGGQPVPNFPSK	95.5%	28.3	25	19.2	1	0	0	1290.65	1235	1246
Flap endonuclease 1	FEN1	FEN1_HUMAN	42.6	100.0%	3	4	7	0.01%	10.0%	KLPIQEFHLSR	99.7%	32.1	25	30.5	0	2	0	1367.78	201	211
Flap endonuclease 1	FEN1	FEN1_HUMAN	42.6	100.0%	3	4	7	0.01%	10.0%	LIADVAPSAIR	99.7%	58.5	25	43.6	2	0	0	1125.66	9	19
Flap endonuclease 1	FEN1	FEN1_HUMAN	42.6	100.0%	3	4	7	0.01%	10.0%	QLQQAQAAGAEQEVEK	99.7%	123	25	117	2	1	0	1727.86	110	125
Formin-like protein 2	FMNL2	FMNL2_HUMAN	123.3	99.8%	2	2	3	0.00%	2.3%	AAAVSLENVLLDVK	99.7%	56.3	25	43.6	2	0	0	1441.83	891	904
Formin-like protein 2	FMNL2	FMNL2_HUMAN	123.3	99.8%	2	2	3	0.00%	2.3%	LQSLDLLLDTK	96.2%	29	25	26	1	0	0	1258.73	845	855
Fragile X mental retardation protein 1	FMR1	FMR1_HUMAN	71.2	100.0%	3	3	4	0.00%	6.2%	LIQEIVDK	97.5%	30.7	25	13.5	1	0	0	957.56	303	310
Fragile X mental retardation protein 1	FMR1	FMR1_HUMAN	71.2	100.0%	3	3	4	0.00%	6.2%	LQIDEQLR	99.7%	50.6	25	41.3	3	0	0	1014.56	435	442
Fragile X mental retardation protein 1	FMR1	FMR1_HUMAN	71.2	100.0%	3	3	4	0.00%	6.2%	SFLEFAEDVIQVPR	99.7%	64.3	25	57	1	0	0	1649.85	277	290
Fragile X mental retardation protein 1	FMR1	FMR1_HUMAN	71.2	100.0%	3	3	4	0.00%	6.2%	VRIEAENEK	99.7%	40.6	25	28.6	2	0	0	1087.57	316	324
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	99.9%	2	2	4	0.00%	2.7%	IYGETPEACR	99.2%	35.8	25	26.2	1	0	0	1195.54	274	283
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	99.9%	2	2	4	0.00%	2.7%	LQIDEQLR	99.7%	50.6	25	41.3	3	0	0	1014.56	379	386
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	8	8	13	0.01%	27.5%	AAQEEYVKR	99.0%	34.8	25	22	2	0	0	1093.56	323	331
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	8	8	13	0.01%	27.5%	ADDGRPFPQVIK	98.9%	34.5	25	27	1	0	0	1342.71	88	99
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	8	8	13	0.01%	27.5%	ALANSLACQGK	99.7%	62.1	25	50.8	2	0	0	1132.58	332	342
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	8	8	13	0.01%	27.5%	ELSDIAHR	99.7%	44.4	25	27	2	0	0	940.48	15	22
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	8	8	13	0.01%	27.5%	GGVVGIKVDK	99.7%	48.7	25	42	2	0	0	971.59	102	111
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	8	8	13	0.01%	27.5%	GILAADESTGSIAK	99.7%	87.8	25	85.6	2	0	0	1332.70	29	42
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	8	8	13	0.01%	27.5%	LQSIGTENTEENRR	95.3%	22.1	25	18.4	0	1	0	1646.81	44	57
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	8	8	13	0.01%	27.5%	YTPSGQAGAAASESLFVSNHAY	99.7%	89.9	25	89.9	1	0	0	2228.03	343	364
Fumarylacetoacetate hydrolase domain-containing protein 2A	FAHD2A	FAH2A_HUMAN	34.6	100.0%	4	4	8	0.01%	15.9%	ALAAQLPVLPR	99.7%	52.5	25	40.6	1	0	0	1148.72	83	93
Fumarylacetoacetate hydrolase domain-containing protein 2A	FAHD2A	FAH2A_HUMAN	34.6	100.0%	4	4	8	0.01%	15.9%	DSVADPHNLK	99.7%	56.2	25	51.6	2	0	0	1095.54	225	234
Fumarylacetoacetate hydrolase domain-containing protein 2A	FAHD2A	FAH2A_HUMAN	34.6	100.0%	4	4	8	0.01%	15.9%	SEVTFLAPVTRPDK	99.7%	51.7	25	51.7	2	0	0	1559.84	94	107
Fumarylacetoacetate hydrolase domain-containing protein 2A	FAHD2A	FAH2A_HUMAN	34.6	100.0%	4	4	8	0.01%	15.9%	TFDTFCPLGPALVTK	99.7%	76	25	73.8	3	0	0	1666.85	210	224
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	10	10	17	0.02%	28.6%	EVQLEELEAAR	99.7%	88	25	79.3	2	0	0	1286.66	257	267
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	10	10	17	0.02%	28.6%	GHALLIDCR	99.7%	51	25	40.8	2	0	0	1054.55	196	204
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	10	10	17	0.02%	28.6%	HSLASSEYPVR	99.7%	49.8	25	44.5	2	0	0	1245.62	229	239
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	10	10	17	0.02%	28.6%	KDGLVSLLTTSEGADEPQR	97.4%	24.1	25	13.2	0	1	0	2016.02	69	87
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	10	10	17	0.02%	28.6%	LAVLITNSNVR	99.7%	57.6	25	34.3	2	0	0	1199.71	218	228
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	10	10	17	0.02%	28.6%	LMVESHR	95.4%	28.2	25	12	1	0	0	871.45	306	312
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	10	10	17	0.02%	28.6%	LQFPLPTAQR	99.0%	34.7	25	21.9	1	0	0	1170.66	88	97
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	10	10	17	0.02%	28.6%	QPQVAELLAEAR	99.7%	73.6	25	70.9	2	0	0	1324.72	6	17
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	10	10	17	0.02%	28.6%	SLETSLVPLSDPK	99.7%	70.3	25	68.6	2	0	0	1385.75	205	217
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	10	10	17	0.02%	28.6%	TAQAAAALR	99.7%	52.6	25	39.5	2	0	0	872.49	288	296
Gamma-glutamyl hydrolase	GGH	GGH_HUMAN	36.0	99.8%	2	2	2	0.00%	8.5%	NLDGISHAPNAVK	99.5%	37.9	25	27.9	1	0	0	1335.70	254	266
Gamma-glutamyl hydrolase	GGH	GGH_HUMAN	36.0	99.8%	2	2	2	0.00%	8.5%	TAFYLAEFFVNEAR	99.2%	35.8	25	35.8	1	0	0	1677.83	267	280
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	3	3	4	0.00%	3.8%	LWFYIQPAMR	99.7%	42.5	25	35.4	1	0	0	1324.69	324	333
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	3	3	4	0.00%	3.8%	NLDPLVYLLSK	99.7%	56	25	50.1	1	0	0	1274.74	77	87
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	3	3	4	0.00%	3.8%	TFLVDPNLDLSIR	99.7%	68.1	25	51.6	2	0	0	1502.82	245	257
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	8	9	15	0.02%	23.4%	FYQASTSELYGK	99.7%	69.1	25	63.8	2	0	0	1393.66	150	161
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	8	9	15	0.02%	23.4%	GYEVHGIVR	99.7%	41.2	25	39.2	2	0	0	1029.55	47	55
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	8	9	15	0.02%	23.4%	IYLGQLECFSLGNLDAK	99.7%	40.2	25	40.2	1	0	0	1940.98	230	246
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	8	9	15	0.02%	23.4%	LHYGDLTDSTCLVK	99.7%	75.4	25	71.2	2	0	0	1621.79	82	95
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	8	9	15	0.02%	23.4%	NPQAHIEGNMK	99.7%	54.7	25	50.1	4	0	0	1238.59	71	81
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	8	9	15	0.02%	23.4%	SFLHIGK	94.9%	27.8	25	18.7	1	0	0	801.46	288	294
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	8	9	15	0.02%	23.4%	TCGLINSVK	99.7%	43.8	25	18.1	1	0	0	991.52	141	149
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	8	9	15	0.02%	23.4%	VHVTVDLK	99.5%	38.3	25	26.4	2	0	0	910.54	315	322

Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	4	4	4	0.00%	5.0%	EWGEELQAVLR	99.7%	42.9	25	33.4	1	0	0	1329.68	326	336
Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	4	4	4	0.00%	5.0%	MLSLLVVDVGNPEEVR	99.7%	63.8	25	63.8	1	0	0	1785.94	832	847
Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	4	4	4	0.00%	5.0%	SIAEGIGPEER	99.7%	48	25	44.5	1	0	0	1157.58	1037	1047
Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	4	4	4	0.00%	5.0%	VLQPHPVTPSDTETR	99.5%	30.1	25	23.7	0	1	0	1676.86	77	91
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	7	7	16	0.02%	5.4%	GVLQTAAER	99.7%	51	25	24.5	4	0	0	944.52	934	942
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	7	7	16	0.02%	5.4%	LSGEAFDINK	99.7%	44.5	25	40.1	1	0	0	1093.55	515	524
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	7	7	16	0.02%	5.4%	SLEAFFLYGR	99.7%	84.5	25	75.6	3	0	0	1202.62	1275	1284
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	7	7	16	0.02%	5.4%	TVIESSPESPVTITEPYR	99.7%	65.2	25	65.2	2	0	0	2005.01	616	633
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	7	7	16	0.02%	5.4%	VGPGAGESPGTPPFR	99.7%	41.3	25	40.7	2	0	0	1425.71	41	55
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	7	7	16	0.02%	5.4%	VIGELVGHTER	99.7%	51.4	25	50.2	2	0	0	1209.66	56	66
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	7	7	16	0.02%	5.4%	VYEAVELLK	99.7%	42.9	25	42.9	2	0	0	1063.60	991	999
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	4	4	6	0.01%	1.9%	DMLTQTYDLIER	95.6%	28.4	25	28.4	1	0	0	1497.73	367	378
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	4	4	6	0.01%	1.9%	GISQAEIR	96.4%	29.3	25	17	1	0	0	873.48	383	390
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	4	4	6	0.01%	1.9%	IASNVLNTK	99.7%	48.4	25	33.5	2	0	0	959.55	1278	1286
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	4	4	6	0.01%	1.9%	NLIIEAVTNLR	99.7%	70	25	63.5	2	0	0	1255.74	619	629
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	3	3	6	0.01%	3.7%	AIFAVLTSVLTK	99.7%	92.2	25	91	2	0	0	1262.77	611	622
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	3	3	6	0.01%	3.7%	ILNLLSPSDGER	99.7%	46.8	25	38	2	0	0	1313.71	277	288
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	3	3	6	0.01%	3.7%	YNLAVVWLR	99.7%	76.7	25	61	2	0	0	1133.65	453	461
General transcription factor 3C polypeptide 4	GTF3C4	TF3C4_HUMAN	92.0	100.0%	3	3	4	0.00%	3.8%	LSDVFGSVR	96.3%	29.1	25	16.3	1	0	0	979.52	468	476
General transcription factor 3C polypeptide 4	GTF3C4	TF3C4_HUMAN	92.0	100.0%	3	3	4	0.00%	3.8%	NYQVQFVTLK	99.7%	54.4	25	52.3	2	0	0	1239.67	507	516
General transcription factor 3C polypeptide 4	GTF3C4	TF3C4_HUMAN	92.0	100.0%	3	3	4	0.00%	3.8%	QLIPIFTDVALK	98.2%	32.2	25	12.2	1	0	0	1357.81	449	460
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	9	11	18	0.02%	20.4%	EGYNNPPISGENLIGLSR	99.7%	75.2	25	75.2	2	0	0	1929.97	192	209
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	9	11	18	0.02%	20.4%	FSTSSLLLR	99.7%	55.3	25	38.3	2	0	0	1023.58	79	87
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	9	11	18	0.02%	20.4%	HGYAPSDLPVK	99.7%	46.1	25	46.1	1	0	0	1183.61	329	339
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	9	11	18	0.02%	20.4%	IYQVLDFR	99.7%	65.4	25	47.8	2	0	0	1053.57	315	322
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	9	11	18	0.02%	20.4%	MLPTLGGEEGVSR	99.7%	65.6	25	56.4	4	0	0	1361.67	39	51
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	9	11	18	0.02%	20.4%	MVCVEYPGVVR	99.7%	50.4	25	39.2	2	0	0	1308.64	24	34
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	9	11	18	0.02%	20.4%	QGLGPSGTSGAR	99.7%	54.1	25	40.7	1	0	0	1087.55	368	379
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	9	11	18	0.02%	20.4%	STYNYSLPITVK	99.7%	64.8	25	64.8	2	0	0	1385.73	343	354
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	9	11	18	0.02%	20.4%	TSSQLVTMHDLK	99.7%	40.4	25	28.4	2	0	0	1359.69	356	367
General transcription factor II-I	GTF2I	GTF2I_HUMAN	112.4	100.0%	7	7	8	0.01%	7.8%	ANELPQPPVPEPANAGK	99.7%	45.6	25	37	1	0	0	1728.89	327	343
General transcription factor II-I	GTF2I	GTF2I_HUMAN	112.4	100.0%	7	7	8	0.01%	7.8%	APSYLEISSMR	99.7%	52.9	25	52.9	1	0	0	1253.62	917	927
General transcription factor II-I	GTF2I	GTF2I_HUMAN	112.4	100.0%	7	7	8	0.01%	7.8%	EQVNDLFSR	99.7%	49.9	25	43.1	1	0	0	1107.54	870	878
General transcription factor II-I	GTF2I	GTF2I_HUMAN	112.4	100.0%	7	7	8	0.01%	7.8%	FAEALGSTEAK	99.7%	66.3	25	57	1	0	0	1123.56	478	488
General transcription factor II-I	GTF2I	GTF2I_HUMAN	112.4	100.0%	7	7	8	0.01%	7.8%	FAQALGLTEAVK	99.7%	78.7	25	61.1	2	0	0	1247.70	583	594
General transcription factor II-I	GTF2I	GTF2I_HUMAN	112.4	100.0%	7	7	8	0.01%	7.8%	SPSWYGIPR	99.5%	38	25	19.5	1	0	0	1062.54	515	523
General transcription factor II-I	GTF2I	GTF2I_HUMAN	112.4	100.0%	7	7	8	0.01%	7.8%	SPTWFGIPR	99.7%	42.2	25	27.6	1	0	0	1060.56	620	628
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	13	15	24	0.02%	17.5%	EQDDLLVLLADQDQK	99.7%	79.6	25	55.5	1	0	0	1742.88	905	919
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	13	15	24	0.02%	17.5%	EQDLQLEELR	95.9%	28.7	25	2	1	0	0	1272.64	661	670
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	13	15	24	0.02%	17.5%	IVAFENAFER	99.7%	73	25	71.4	2	0	0	1195.61	203	212
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	13	15	24	0.02%	17.5%	LMDLLADSR	99.7%	68.8	25	51.9	4	0	0	1033.53	171	179
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	13	15	24	0.02%	17.5%	LSALLQETK	99.7%	50.1	25	39.7	2	0	0	1002.58	850	858
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	13	15	24	0.02%	17.5%	NDGVLLLQALTR	99.7%	87.6	25	81.6	2	0	0	1312.76	184	195
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	13	15	24	0.02%	17.5%	QLGPQVQQIILVSPMGVSR	99.7%	47.1	25	47.1	1	0	0	2050.15	152	170
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	13	15	24	0.02%	17.5%	QSEDLGSQFTEIFIK	99.7%	95.1	25	88	2	0	0	1741.86	105	119
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	13	15	24	0.02%	17.5%	SQLNSQSVEITK	99.7%	87.2	25	81.6	2	0	0	1333.70	799	810
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	13	15	24	0.02%	17.5%	SSQTSGTNEQSSAIVSAR	99.7%	136	25	124	2	0	0	1809.86	765	782
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	13	15	24	0.02%	17.5%	SVEVQGETETIIATK	99.7%	100	25	88.6	2	0	0	1604.84	828	842
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	13	15	24	0.02%	17.5%	TLEQHDNIVTHYK	97.8%	24.6	25	22.2	0	1	0	1597.80	644	656
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	13	15	24	0.02%	17.5%	VASSTLLDDRR	99.5%	38	25	13.4	1	1	0	1232.66	30	40
Geranylgeranyl transferase type-2 subunit alpha	RABGGTA	PGTA_HUMAN	65.1	100.0%	3	3	4	0.00%	5.8%	AELGFLESCLR	99.7%	65.8	25	58.2	1	0	0	1294.65	91	101

Geranylgeranyl transferase type-2 subunit alpha	RABGGTA	PGTA_HUMAN	65.1	100.0%	3	3	4	0.00%	5.8%	LQELLLCNNR	99.7%	52.6	25	46.9	1	0	0	1272.67	510	519
Geranylgeranyl transferase type-2 subunit alpha	RABGGTA	PGTA_HUMAN	65.1	100.0%	3	3	4	0.00%	5.8%	LYQSATQAVFQK	99.7%	61.1	25	56	2	0	0	1383.73	27	38
Girdin	CCDC88A	GRDN_HUMAN	216.0	99.8%	2	2	2	0.00%	1.0%	MLKVEQEK	97.8%	31.4	25	0.6	1	0	0	1020.54	1218	1225
Girdin	CCDC88A	GRDN_HUMAN	216.0	99.8%	2	2	2	0.00%	1.0%	TSELSEAPQK	99.5%	37.9	25	37.9	1	0	0	1089.54	439	448
Glomulin	GLMN	GLMN_HUMAN	68.2	100.0%	4	5	9	0.01%	7.6%	GLELLENSLLR	99.7%	63.7	25	50.3	2	0	0	1256.72	335	345
Glomulin	GLMN	GLMN_HUMAN	68.2	100.0%	4	5	9	0.01%	7.6%	IEDNSLLYQYLEIK	96.6%	29.5	25	29.5	1	0	0	1740.91	346	359
Glomulin	GLMN	GLMN_HUMAN	68.2	100.0%	4	5	9	0.01%	7.6%	IMASLNLLR	99.7%	57.5	25	42.8	4	0	0	1030.61	471	479
Glomulin	GLMN	GLMN_HUMAN	68.2	100.0%	4	5	9	0.01%	7.6%	SLAMLQLYINK	99.3%	36.6	25	21.2	2	0	0	1293.72	384	394
Glucose-6-phosphate 1-dehydrogenase	G6PD	G6PD_HUMAN	59.3	100.0%	2	2	2	0.00%	3.5%	GGYFDEFGIIR	99.7%	67.7	25	56.4	1	0	0	1273.62	247	257
Glucose-6-phosphate 1-dehydrogenase	G6PD	G6PD_HUMAN	59.3	100.0%	2	2	2	0.00%	3.5%	IDHYLGK	99.0%	34.8	25	22.3	1	0	0	845.45	199	205
Glucose-6-phosphate isomerase	GPI	G6PI_HUMAN	63.1	100.0%	3	5	7	0.01%	8.4%	ILLANFLAQTEALMR	99.7%	93.1	25	86.1	3	1	0	1703.95	424	438
Glucose-6-phosphate isomerase	GPI	G6PI_HUMAN	63.1	100.0%	3	5	7	0.01%	8.4%	TLAQLNPESSLFIIASK	99.7%	55.9	25	55.9	2	0	0	1832.02	195	211
Glucose-6-phosphate isomerase	GPI	G6PI_HUMAN	63.1	100.0%	3	5	7	0.01%	8.4%	VFEGNRPTNSIVFTK	98.5%	33	25	17.6	1	0	0	1708.90	467	481
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	6	6	12	0.01%	17.7%	AQTGAPCLSFDIVR	99.7%	41.4	25	41.1	2	0	0	1534.77	60	73
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	6	6	12	0.01%	17.7%	GQVEVFALR	99.7%	56.5	25	40.2	2	0	0	1018.57	173	181
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	6	6	12	0.01%	17.7%	LLQVVEEPQALAAFLR	99.7%	101	25	98.6	2	0	0	1797.03	183	198
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	6	6	12	0.01%	17.7%	REPFLLSGGDDGALK	99.7%	33.8	25	33.8	0	2	0	1574.82	319	333
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	6	6	12	0.01%	17.7%	SGSPVATFK	98.7%	33.5	25	29.9	2	0	0	893.47	342	350
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	6	6	12	0.01%	17.7%	VSWLGEEPVAGVWSEK	99.7%	61.8	25	61.8	2	0	0	1772.89	157	172
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	9	9	15	0.02%	14.7%	EIFEQPESVVNTMR	99.7%	67.8	25	60.1	1	0	0	1678.81	346	359
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	9	9	15	0.02%	14.7%	EILETLIK	99.5%	38	25	24.2	2	0	0	958.58	18	25
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	9	9	15	0.02%	14.7%	ESQDTSFTTLVER	99.7%	69.4	25	69.4	1	0	0	1512.72	164	176
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	9	9	15	0.02%	14.7%	EVLSMDDEIQK	99.7%	57.1	25	52.4	1	0	0	1322.61	537	547
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	9	9	15	0.02%	14.7%	GSPLLIGVR	99.7%	52.9	25	42.1	2	0	0	911.57	204	212
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	9	9	15	0.02%	14.7%	GYDFESETDTETIAK	99.7%	86.1	25	86.1	2	0	0	1705.74	140	154
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	9	9	15	0.02%	14.7%	GYDVDFPR	99.7%	40.4	25	40.4	2	0	0	968.45	683	690
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	9	9	15	0.02%	14.7%	LATELYHQK	99.7%	41.2	25	21.2	2	0	0	1102.59	548	556
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	9	9	15	0.02%	14.7%	VIFLEDDDVAAVVDGR	99.7%	72.1	25	65.3	2	0	0	1732.88	291	306
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	10	10	19	0.02%	13.4%	AINFNFGYAK	99.7%	52.9	25	40.9	2	0	0	1144.58	283	292
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	10	10	19	0.02%	13.4%	DVLNDTAPR	98.4%	32.7	25	28.4	2	0	0	1000.51	559	567
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	10	10	19	0.02%	13.4%	FDDTNPEKEEAK	99.7%	72.8	25	68.8	2	0	0	1422.64	302	313
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	10	10	19	0.02%	13.4%	FSEGEATLR	99.7%	49.4	25	40.3	2	0	0	1009.49	395	403
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	10	10	19	0.02%	13.4%	GLAYVCHQR	99.7%	61.8	25	37	2	0	0	1103.54	353	361
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	10	10	19	0.02%	13.4%	ILQLVATGAVR	99.7%	89.1	25	85.4	2	0	0	1140.71	499	509
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	10	10	19	0.02%	13.4%	LAWGQPVGLR	99.7%	66.9	25	54.2	2	0	0	1096.63	630	639
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	10	10	19	0.02%	13.4%	LGYFSVDPDSHQGK	99.7%	41	25	41	1	0	0	1549.73	746	759
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	10	10	19	0.02%	13.4%	LSFLVSYIASK	99.7%	63.6	25	63.6	2	0	0	1227.70	69	79
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	10	10	19	0.02%	13.4%	NSALSAQLR	99.7%	71.3	25	61	2	0	0	959.53	26	34
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	8	11	24	0.02%	20.7%	ELRVPLIGSLPEAR	99.7%	49.8	25	49.6	2	2	0	1549.91	67	80
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	8	11	24	0.02%	20.7%	FLEATLR	99.7%	48.8	25	36.6	2	0	0	849.48	118	124
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	8	11	24	0.02%	20.7%	GLMEPLLPPK	99.7%	50.8	25	31.7	5	0	0	1110.62	17	26
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	8	11	24	0.02%	20.7%	HLAQLMESIPHSPGPTR	98.7%	26.5	25	26.5	0	2	0	1870.96	242	258
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	8	11	24	0.02%	20.7%	HLTLACHYDSK	99.7%	52.8	25	51.6	2	1	0	1344.64	162	172
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	8	11	24	0.02%	20.7%	TPGSPGNLQVR	99.7%	70.6	25	61	3	0	0	1125.60	106	116
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	8	11	24	0.02%	20.7%	VPLIGSLPEAR	99.7%	57	25	50.8	2	0	0	1151.68	70	80
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	8	11	24	0.02%	20.7%	VVGQLDPQR	99.7%	48.8	25	48.8	3	0	0	1011.56	84	92
Glutaryl-CoA dehydrogenase, mitochondrial	GCDH	GCDH_HUMAN	48.1	100.0%	3	3	3	0.00%	10.5%	AITGIQAFTASK	99.7%	72.7	25	70.1	1	0	0	1207.67	427	438
Glutaryl-CoA dehydrogenase, mitochondrial	GCDH	GCDH_HUMAN	48.1	100.0%	3	3	3	0.00%	10.5%	EIISEMGELGVLGPTIK	99.4%	36.9	25	36.9	1	0	0	1785.97	95	111
Glutaryl-CoA dehydrogenase, mitochondrial	GCDH	GCDH_HUMAN	48.1	100.0%	3	3	3	0.00%	10.5%	GYGCAGVSSVAYGLLAR	99.7%	66	25	64.8	1	0	0	1700.84	112	128
Glutathione S-transferase kappa 1	GSTK1	GSTK1_HUMAN	25.5	100.0%	3	3	5	0.01%	17.3%	AGMSAEQAQGLLEK	99.7%	91.7	25	79.9	2	0	0	1432.71	145	158
Glutathione S-transferase kappa 1	GSTK1	GSTK1_HUMAN	25.5	100.0%	3	3	5	0.01%	17.3%	DFLSVMLEK	99.7%	41	25	29.3	2	0	0	1097.55	86	94

Glutathione S-transferase kappa 1	GSTK1	GSTK1_HUMAN	25.5	100.0%	3	3	5	0.01%	17.3%	NEDITEPQSILAAAEK	99.7%	42.6	25	42.6	1	0	0	1728.87	129	144
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	9	12	36	0.04%	35.2%	GALQNIIPASTGAAK	99.7%	90.7	25	88	9	0	0	1411.79	201	215
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	9	12	36	0.04%	35.2%	IISNASCTTNCLAPLAK	99.7%	108	25	102	4	0	0	1833.92	146	162
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	9	12	36	0.04%	35.2%	LISWYDNEFGYSNR	99.7%	85.3	25	85.3	2	0	0	1763.80	310	323
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	9	12	36	0.04%	35.2%	LTGMAFR	98.9%	34.4	25	29.2	2	0	0	811.41	228	234
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	9	12	36	0.04%	35.2%	LVINGNPITIFQER	99.7%	85.3	25	76.3	2	0	0	1613.90	67	80
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	9	12	36	0.04%	35.2%	LVINGNPITIFQERDPSK	99.7%	59	25	59	1	1	0	2041.11	67	84
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	9	12	36	0.04%	35.2%	VPTANVSVVDLTCR	99.7%	87.8	25	85.9	6	1	0	1530.79	235	248
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	9	12	36	0.04%	35.2%	VVDLMAHMASKE	99.7%	64.1	25	55.2	7	0	0	1330.65	324	335
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	9	12	36	0.04%	35.2%	WGDAGAEYVVESTGVFTTMEK	99.7%	53.5	25	53.5	1	0	0	2277.04	87	107
Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	GPD1L_HUMAN	38.4	100.0%	2	2	4	0.00%	5.7%	ICDEITGR	99.7%	40.1	25	26.6	2	0	0	963.46	103	110
Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	GPD1L_HUMAN	38.4	100.0%	2	2	4	0.00%	5.7%	LQGPQTSAEVYR	99.7%	59.2	25	59.2	2	0	0	1348.69	299	310
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	9	9	15	0.02%	15.0%	ELSEALTR	96.2%	29	25	15.7	1	0	0	918.49	633	640
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	9	9	15	0.02%	15.0%	IYLYLTK	96.3%	29.2	25	6.58	2	0	0	913.54	413	419
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	9	9	15	0.02%	15.0%	LPFAAAQIGNSFR	99.7%	74.8	25	66.8	2	0	0	1391.74	319	331
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	9	9	15	0.02%	15.0%	SCYDLSCHAR	99.6%	39.1	25	39.1	1	0	0	1268.51	465	474
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	9	9	15	0.02%	15.0%	SPITGNDLSPPVSFNLMFK	99.2%	36.2	25	36.2	1	0	0	2064.05	265	283
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	9	9	15	0.02%	15.0%	TFFSFPAVVAPFK	99.7%	40.7	25	39.2	2	0	0	1457.78	603	615
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	9	9	15	0.02%	15.0%	TLYVEEVVPNVIEPSFGLGR	99.7%	69.3	25	69.3	2	0	0	2218.18	564	583
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	9	9	15	0.02%	15.0%	TVNVVQFEPSK	99.7%	49.5	25	41.9	2	0	0	1247.66	491	501
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	9	9	15	0.02%	15.0%	VDDSSGSIGR	99.7%	40.2	25	24.7	2	0	0	992.46	647	656
Glycogen [starch] synthase, muscle	GYS1	GYS1_HUMAN	83.8	99.8%	2	2	4	0.00%	3.0%	GADVFLEALAR	99.7%	67.2	25	54	2	0	0	1161.63	338	348
Glycogen [starch] synthase, muscle	GYS1	GYS1_HUMAN	83.8	99.8%	2	2	4	0.00%	3.0%	VGGIYTVLQTK	99.7%	67.4	25	0	2	0	0	1178.68	40	50
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	7	7	12	0.01%	12.8%	DYFFALAHTVR	99.7%	57	25	46.4	2	0	0	1339.68	51	61
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	7	7	12	0.01%	12.8%	GLAGLGDVAEVR	99.7%	76.7	25	69.8	2	0	0	1156.63	18	29
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	7	7	12	0.01%	12.8%	LLPLVSDEVFIR	99.7%	43.7	25	43.4	2	0	0	1400.81	522	533
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	7	7	12	0.01%	12.8%	LVTSIGDVVNHDPVVGDR	99.7%	33.5	25	33.5	0	1	0	1891.99	623	640
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	7	7	12	0.01%	12.8%	NLAENISR	99.7%	46.5	25	23.1	2	0	0	916.48	271	278
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	7	7	12	0.01%	12.8%	VEDVEALDR	99.7%	47.3	25	41.3	2	0	0	1045.52	716	724
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	7	7	12	0.01%	12.8%	VEHTPDGVK	97.1%	30.2	25	21.4	1	0	0	981.50	207	215
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	7	7	12	0.01%	12.8%	VIFLENYR	99.7%	53.9	25	43.3	4	0	0	1053.57	643	650
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	7	7	12	0.01%	12.8%	VLYPNDNFFEGK	99.7%	60.4	25	60.4	2	0	0	1442.70	279	290
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	7	7	12	0.01%	12.8%	YEFGIFNQK	99.7%	44	25	31.5	2	0	0	1145.56	162	170
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	APNDFNLR	99.7%	50.8	25	39.9	2	0	0	946.47	249	256
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	AWNTMVLK	99.3%	36.7	25	21.5	1	0	0	962.51	797	804
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	DFNVGDYIQAVLDR	99.7%	89.4	25	82	1	0	0	1624.80	257	270
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	DFSELEPDKFQNK	99.7%	54.9	25	43.7	2	0	0	1596.75	471	483
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	DYYFALAHTVR	99.7%	62.7	25	51.8	2	0	0	1355.67	51	61
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	EYAQNIWNVEPSDLK	99.7%	50	25	45.8	2	0	0	1805.87	820	834
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	EYYEALPELK	99.4%	37.6	25	32.3	2	0	0	1254.63	731	740
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	FSQFLETEYK	99.7%	69.8	25	65.9	3	0	0	1291.62	546	555
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	GIVGVENVAELKK	99.7%	68.5	25	66.2	2	0	0	1355.79	18	30
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	HLEIIYEINQK	99.7%	61.1	25	49	1	0	0	1399.76	400	410
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	IDDVAALDK	99.7%	40.9	25	35.3	1	0	0	959.50	716	724
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	IFVDIEKLPWSK	99.0%	27.7	25	26.5	0	1	0	1474.83	353	364
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	IGEDYVK	96.7%	29.6	25	21	1	0	0	823.42	508	514
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	IGEDYVKDLSQLTK	98.4%	32.7	25	29.7	1	0	0	1608.85	508	521
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	INPSSMFDVQVK	99.7%	75.3	25	61.8	3	0	0	1364.69	558	569
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	LHSFLGDDVFLR	99.7%	65.9	25	53.6	2	2	0	1418.74	522	533
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	LITSVADVVNNDPMVGSK	99.7%	121	25	116	3	0	0	1874.95	623	640
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	LVIDQIDNGFFSPK	99.7%	83.2	25	83.2	3	0	0	1592.83	741	754

Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	MSLIEEEGSKR	99.7%	61.4	25	44.4	3	0	0	1278.64	429	439
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	NLAENISR	99.7%	46.5	25	23.1	2	0	0	916.48	271	278
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	TFAYTNHTVLPEALER	99.7%	45.4	25	39.4	0	2	0	1861.94	372	387
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	VFADYEAYVK	99.7%	52.7	25	49.2	2	0	0	1204.59	774	783
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	VIFLENYR	99.7%	53.9	25	43.3	4	0	0	1053.57	643	650
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	VIPATDLSEQISTAGTEASGTGNMK	99.7%	42.8	25	42.5	0	2	0	2478.20	657	681
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	VLYPNDNFFEGK	99.7%	60.4	25	60.4	2	0	0	1442.70	279	290
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	VSQLYMNPK	99.7%	62.4	25	51.6	4	0	0	1079.56	788	796
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	WPVDLVEK	95.0%	27.9	25	21.5	2	0	0	985.54	388	395
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	33	60	0.06%	37.8%	YEYGIFNQK	99.7%	42.7	25	42.7	2	0	0	1161.56	162	170
Glycosylphosphatidylinositol anchor attachment 1 protein	GPAA1	GPAA1_HUMAN	67.6	99.8%	2	2	2	0.00%	3.2%	SGALPVAWLER	95.6%	28.4	25	17.1	1	0	0	1198.66	84	94
Glycosylphosphatidylinositol anchor attachment 1 protein	GPAA1	GPAA1_HUMAN	67.6	99.8%	2	2	2	0.00%	3.2%	VVSTQAPDR	99.4%	37	25	33.8	1	0	0	972.51	485	493
Glyoxylate reductase/hydroxypyruvate reductase	GRHPR	GRHPR_HUMAN	35.7	100.0%	5	5	7	0.01%	21.3%	IAAAGLDVTSPEPLPTNHPLLTLK	99.7%	62.1	25	62.1	0	1	0	2468.38	263	286
Glyoxylate reductase/hydroxypyruvate reductase	GRHPR	GRHPR_HUMAN	35.7	100.0%	5	5	7	0.01%	21.3%	ILDAAGANLK	99.7%	73.8	25	60.7	2	0	0	985.57	67	76
Glyoxylate reductase/hydroxypyruvate reductase	GRHPR	GRHPR_HUMAN	35.7	100.0%	5	5	7	0.01%	21.3%	MKETAVFINISR	99.6%	31.2	25	26.5	0	1	0	1408.76	234	245
Glyoxylate reductase/hydroxypyruvate reductase	GRHPR	GRHPR_HUMAN	35.7	100.0%	5	5	7	0.01%	21.3%	NCVILPHIGSATHR	97.4%	24.1	25	24.1	0	1	0	1574.82	287	300
Glyoxylate reductase/hydroxypyruvate reductase	GRHPR	GRHPR_HUMAN	35.7	100.0%	5	5	7	0.01%	21.3%	RLPEAIEEVK	99.7%	46.5	25	35.5	2	0	0	1183.67	125	134
GMP synthase [glutamine-hydrolyzing]	GMPS	GUAA_HUMAN	76.7	100.0%	4	4	6	0.01%	7.5%	ELGLPEELVSR	99.6%	39.8	25	32	2	0	0	1241.67	425	435
GMP synthase [glutamine-hydrolyzing]	GMPS	GUAA_HUMAN	76.7	100.0%	4	4	6	0.01%	7.5%	EPPTDVTPTFLTTGVLSTLR	99.7%	41.5	25	41.5	2	0	0	2145.14	570	589
GMP synthase [glutamine-hydrolyzing]	GMPS	GUAA_HUMAN	76.7	100.0%	4	4	6	0.01%	7.5%	ESQSVEEALKK	98.8%	33.9	25	31	1	0	0	1247.65	279	289
GMP synthase [glutamine-hydrolyzing]	GMPS	GUAA_HUMAN	76.7	100.0%	4	4	6	0.01%	7.5%	VVYIFGPPVK	96.0%	28.8	25	22.2	1	0	0	1118.66	560	569
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	5	5	6	0.01%	3.2%	GATPEGIFLR	98.2%	32.3	25	18.2	2	0	0	1060.58	907	916
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	5	5	6	0.01%	3.2%	LLEAFTER	99.6%	39.3	25	29.8	1	0	0	978.53	801	808
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	5	5	6	0.01%	3.2%	LLITGTEQFNQKPK	99.0%	34.8	25	28.3	1	0	0	1616.90	702	715
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	5	5	6	0.01%	3.2%	MQALTYLQR	98.3%	32.4	25	26.8	1	0	0	1123.59	1562	1570
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	5	5	6	0.01%	3.2%	SEDTTGPITGLALTSVNK	99.7%	53.4	25	52	1	0	0	1803.93	74	91
GPI transamidase component PIG-T	PIGT	PIGT_HUMAN	65.7	100.0%	4	4	7	0.01%	6.1%	LYVHTLTITSK	99.7%	61.2	25	54.6	2	0	0	1275.73	395	405
GPI transamidase component PIG-T	PIGT	PIGT_HUMAN	65.7	100.0%	4	4	7	0.01%	6.1%	TFHIEEPR	95.0%	27.9	25	16.1	1	0	0	1028.52	550	557
GPI transamidase component PIG-T	PIGT	PIGT_HUMAN	65.7	100.0%	4	4	7	0.01%	6.1%	VSIQFER	99.7%	47.2	25	16	2	0	0	878.47	442	448
GPI transamidase component PIG-T	PIGT	PIGT_HUMAN	65.7	100.0%	4	4	7	0.01%	6.1%	YVSGYGLQK	96.0%	28.8	25	25.3	2	0	0	1014.53	357	365
GPI-anchor transamidase	PIGK	GPI8_HUMAN	45.3	100.0%	4	4	7	0.01%	10.4%	HVANTLSVYR	99.7%	41.5	25	41.5	1	0	0	1159.62	61	70
GPI-anchor transamidase	PIGK	GPI8_HUMAN	45.3	100.0%	4	4	7	0.01%	10.4%	KVEITTETIK	99.6%	39.3	25	28.4	2	0	0	1161.67	309	318
GPI-anchor transamidase	PIGK	GPI8_HUMAN	45.3	100.0%	4	4	7	0.01%	10.4%	NPKPATVFSHK	96.9%	23.5	25	22.5	0	2	0	1225.67	96	106
GPI-anchor transamidase	PIGK	GPI8_HUMAN	45.3	100.0%	4	4	7	0.01%	10.4%	SLCVSTPGHR	99.7%	41	25	41	2	0	0	1113.55	278	287
Growth arrest and DNA damage-inducible proteins-interacting protein 1	GADD45GIP1	G45IP_HUMAN	25.4	100.0%	3	3	4	0.00%	17.1%	EREQHIAECMAK	95.5%	22.2	25	22.2	0	1	0	1501.69	116	127
Growth arrest and DNA damage-inducible proteins-interacting protein 1	GADD45GIP1	G45IP_HUMAN	25.4	100.0%	3	3	4	0.00%	17.1%	FQELLQDLEK	99.7%	56	25	32.7	2	0	0	1262.66	175	184
Growth arrest and DNA damage-inducible proteins-interacting protein 1	GADD45GIP1	G45IP_HUMAN	25.4	100.0%	3	3	4	0.00%	17.1%	LQAEAQELLGYQVDPR	99.7%	46.4	25	46.4	1	0	0	1829.94	156	171
GrpE protein homolog 1, mitochondrial	GRPEL1	GRPE1_HUMAN	24.3	100.0%	4	4	7	0.01%	18.4%	ALADTENLR	99.7%	45.9	25	35.4	2	0	0	1002.52	81	89
GrpE protein homolog 1, mitochondrial	GRPEL1	GRPE1_HUMAN	24.3	100.0%	4	4	7	0.01%	18.4%	DLLEVADVLEK	99.7%	68.2	25	55.1	2	0	0	1243.68	110	120
GrpE protein homolog 1, mitochondrial	GRPEL1	GRPE1_HUMAN	24.3	100.0%	4	4	7	0.01%	18.4%	LYGIQAFCK	96.8%	29.7	25	22.1	1	0	0	1099.56	101	109
GrpE protein homolog 1, mitochondrial	GRPEL1	GRPE1_HUMAN	24.3	100.0%	4	4	7	0.01%	18.4%	TLRPALVGVVK	99.7%	42.6	25	41.6	2	0	0	1152.75	205	215
GTP:AMP phosphotransferase AK3, mitochondrial	AK3	KAD3_HUMAN	25.6	100.0%	2	2	2	0.00%	9.7%	LALHELK	96.6%	29.4	25	12.9	1	0	0	823.50	74	80
GTP:AMP phosphotransferase AK3, mitochondrial	AK3	KAD3_HUMAN	25.6	100.0%	2	2	2	0.00%	9.7%	TVGIDDLTGEPLIQR	99.7%	50.1	25	47.7	1	0	0	1626.87	147	161
GTPase Era, mitochondrial	ERAL1	ERAL1_HUMAN	48.3	100.0%	6	6	10	0.01%	18.8%	DPNTQSVGNPQR	99.7%	44.8	25	39.6	2	0	0	1312.62	285	296
GTPase Era, mitochondrial	ERAL1	ERAL1_HUMAN	48.3	100.0%	6	6	10	0.01%	18.8%	EIFMLSALSQEDVK	99.7%	62.3	25	58.2	2	0	0	1609.81	304	317
GTPase Era, mitochondrial	ERAL1	ERAL1_HUMAN	48.3	100.0%	6	6	10	0.01%	18.8%	ETQVILLDTPGIISPGK	99.7%	66.3	25	66.3	2	0	0	1781.01	160	176
GTPase Era, mitochondrial	ERAL1	ERAL1_HUMAN	48.3	100.0%	6	6	10	0.01%	18.8%	STLSNQLLGR	99.7%	58.4	25	21.4	2	0	0	1088.61	127	136
GTPase Era, mitochondrial	ERAL1	ERAL1_HUMAN	48.3	100.0%	6	6	10	0.01%	18.8%	TAVWEEGPGGELVIQQK	99.7%	66.1	25	62.3	1	0	0	1840.94	372	388
GTPase Era, mitochondrial	ERAL1	ERAL1_HUMAN	48.3	100.0%	6	6	10	0.01%	18.8%	YSQIPSVLVMNK	98.4%	32.6	25	32.6	1	0	0	1378.74	226	237
GTPase NRas	NRAS	RASN_HUMAN	21.2	99.8%	2	2	3	0.00%	12.2%	LVVVGAGGVGK	97.9%	31.4	25	30.8	1	0	0	955.59	6	16
GTPase NRas	NRAS	RASN_HUMAN	21.2	99.8%	2	2	3	0.00%	12.2%	QGVEDAFYTLVR	96.0%	28.8	25	28.8	2	0	0	1397.71	150	161

GTPase-activating protein and VPS9 domain-containing protein 1	GAPVD1	GAPD1_HUMAN	165.0	100.0%	2	2	2	0.00%	1.6%	ILEDTQFVDGYK	99.7%	72.7	25	72.7	1	0	0	1427.71	76	87
GTPase-activating protein and VPS9 domain-containing protein 1	GAPVD1	GAPD1_HUMAN	165.0	100.0%	2	2	2	0.00%	1.6%	VQEMVESNEAK	96.9%	29.8	25	22.6	1	0	0	1263.59	247	257
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	35	0.04%	52.3%	DGYYIQAQCAIIMFDVTSR	99.7%	83.9	25	83.9	2	0	0	2251.05	77	95
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	35	0.04%	52.3%	GPIKFNVWDTAGQEK	99.7%	84.7	25	79.3	1	2	0	1689.86	57	71
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	35	0.04%	52.3%	HLTGEFEK	98.6%	33.5	25	20.2	2	0	0	960.48	30	37
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	35	0.04%	52.3%	KYVATLGVEVHPLVFHTNR	99.7%	52.4	25	52.4	0	1	0	2180.20	38	56
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	35	0.04%	52.3%	LVLVGDGGTGK	99.7%	64	25	4.81	6	0	0	1015.58	13	23
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	35	0.04%	52.3%	NLQYYDISAK	99.7%	48.9	25	45.4	10	0	0	1214.61	143	152
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	35	0.04%	52.3%	SNYNFEKPFLWLAR	99.7%	50.1	25	50.1	2	4	0	1784.91	153	166
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	35	0.04%	52.3%	VCENIPIVLCGNK	99.7%	63	25	55.5	2	0	0	1515.77	111	123
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	35	0.04%	52.3%	VCENIPIVLCGNKVDIK	98.2%	25.3	25	23.8	0	1	0	1971.04	111	127
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	35	0.04%	52.3%	YVATLGVEVHPLVFHTNR	99.7%	41.1	25	41.1	0	2	0	2052.10	39	56
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	5	7	13	0.01%	33.7%	ALAESWNAAFLESSAK	99.7%	89.3	25	89.3	2	0	0	1694.84	136	151
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	5	7	13	0.01%	33.7%	ENQTAVDVFR	99.7%	90.2	25	86.4	2	0	0	1178.58	152	161
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	5	7	13	0.01%	33.7%	IILEAEKMDGAASQGK	99.7%	86	25	86	4	2	0	1660.86	163	178
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	5	7	13	0.01%	33.7%	KIAILGYR	99.7%	42.1	25	25.5	2	0	0	933.59	8	15
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	5	7	13	0.01%	33.7%	VQIPIMLVGNKK	99.7%	34.6	25	31.2	0	1	0	1355.81	110	121
GTP-binding protein SAR1a	SAR1A	SAR1A_HUMAN	22.4	99.8%	2	2	4	0.00%	9.6%	LVFLGLDNAGK	99.7%	55.2	25	49	2	0	0	1146.65	28	38
GTP-binding protein SAR1a	SAR1A	SAR1A_HUMAN	22.4	99.8%	2	2	4	0.00%	9.6%	QGYGEGFR	99.7%	43.4	25	33.3	2	0	0	913.42	184	191
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	GBB2_HUMAN	37.3	100.0%	4	4	5	0.01%	15.3%	ACGDSTLTQITAGLDPVGR	99.7%	110	25	110	2	0	0	1931.95	24	42
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	GBB2_HUMAN	37.3	100.0%	4	4	5	0.01%	15.3%	LIIWDSYTTNK	99.7%	48.7	25	48.5	1	0	0	1353.71	79	89
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	GBB2_HUMAN	37.3	100.0%	4	4	5	0.01%	15.3%	LLVSASQDGK	99.7%	41.6	25	35	1	0	0	1017.56	69	78
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	GBB2_HUMAN	37.3	100.0%	4	4	5	0.01%	15.3%	TFVSGACDASIK	99.7%	62	25	54	1	0	0	1255.60	198	209
Guanine nucleotide-binding protein G(k) subunit alpha	GNAI3	GNAI3_HUMAN	40.5	99.9%	2	2	3	0.00%	10.7%	ISQSNYIPTQQDVLR	99.7%	59.6	25	47	2	0	0	1761.91	162	176
Guanine nucleotide-binding protein G(k) subunit alpha	GNAI3	GNAI3_HUMAN	40.5	99.9%	2	2	3	0.00%	10.7%	LLLLGAGESGK	99.7%	69.7	25	0	6	0	0	1057.63	36	46
Guanine nucleotide-binding protein G(k) subunit alpha	GNAI3	GNAI3_HUMAN	40.5	99.9%	2	2	3	0.00%	10.7%	TTGIVETHFTFK	98.9%	34.5	25	18.7	1	0	0	1380.72	181	192
Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	GNAS	GNAS1_HUMAN	45.7	100.0%	4	4	6	0.01%	5.2%	LLLLGAGESGK	99.7%	69.7	25	0	6	0	0	1057.63	43	53
Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	GNAS	GNAS1_HUMAN	45.7	100.0%	4	4	6	0.01%	5.2%	SKIEDYFPEFAR	99.7%	64.5	25	64.5	1	0	0	1501.73	306	317
Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	GNAS	GNAS1_HUMAN	45.7	100.0%	4	4	6	0.01%	5.2%	TISVILFLNK	99.7%	58.4	25	55.8	2	0	0	1147.71	284	293
Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	GNAS	GNAS1_HUMAN	45.7	100.0%	4	4	6	0.01%	5.2%	VFNDCRDIIQR	99.2%	36	25	29	1	0	0	1435.71	375	385
Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	GNAS	GNAS1_HUMAN	45.7	100.0%	4	4	6	0.01%	5.2%	VLTSGIFETK	99.7%	61	25	55	2	0	0	1094.61	202	211
Guanine nucleotide-binding protein subunit alpha-11	GNA11	GNA11_HUMAN	42.1	99.8%	2	2	4	0.00%	9.5%	IATLGYLPTQQDVLR	99.7%	43.3	25	42	2	0	0	1687.94	167	181
Guanine nucleotide-binding protein subunit alpha-11	GNA11	GNA11_HUMAN	42.1	99.8%	2	2	4	0.00%	9.5%	LLLLGTGESGK	99.7%	58.4	25	24.8	2	0	0	1087.64	42	52
Guanine nucleotide-binding protein subunit alpha-11	GNA11	GNA11_HUMAN	42.1	99.8%	2	2	4	0.00%	9.5%	MVDVGGQR	98.7%	33.8	25	32.6	2	0	0	861.42	203	210
Guanine nucleotide-binding protein subunit alpha-13	GNA13	GNA13_HUMAN	44.1	100.0%	4	5	12	0.01%	10.9%	APMAAQGMVETR	99.7%	51.4	25	51.4	2	0	0	1293.59	129	140
Guanine nucleotide-binding protein subunit alpha-13	GNA13	GNA13_HUMAN	44.1	100.0%	4	5	12	0.01%	10.9%	IIHGQDFDQR	98.8%	26.9	25	18.5	1	1	0	1228.61	70	79
Guanine nucleotide-binding protein subunit alpha-13	GNA13	GNA13_HUMAN	44.1	100.0%	4	5	12	0.01%	10.9%	ILLLGAGESGK	99.7%	69.7	25	0	6	0	0	1057.63	51	61
Guanine nucleotide-binding protein subunit alpha-13	GNA13	GNA13_HUMAN	44.1	100.0%	4	5	12	0.01%	10.9%	MVDVGGQR	98.7%	33.8	25	32.6	2	0	0	861.42	220	227
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	19	82	0.08%	45.4%	DETNYGIPQR	99.7%	69	25	62.2	4	0	0	1192.56	48	57
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	19	82	0.08%	45.4%	DGQAMLWDLNEGK	99.7%	105	25	98.7	10	0	0	1492.67	213	225
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	19	82	0.08%	45.4%	DKTIIMWK	99.7%	43.5	25	30.9	4	0	0	1034.57	37	44
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	19	82	0.08%	45.4%	DVLSVAFSSDNR	99.7%	88.6	25	88.1	10	0	0	1309.64	107	118
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	19	82	0.08%	45.4%	FSPNSSNPIIVSCGWDK	99.7%	85.3	25	73.8	4	0	0	1907.90	156	172
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	19	82	0.08%	45.4%	IIVDELK	94.8%	27.7	25	14.4	1	0	0	829.50	265	271
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	19	82	0.08%	45.4%	IIVDELKQEVISTSSK	99.7%	112	25	109	5	4	0	1789.00	265	280
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	19	82	0.08%	45.4%	LTRDETNYGIPQR	99.7%	53.3	25	50.8	4	2	0	1562.79	45	57
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	19	82	0.08%	45.4%	LWDLTTGTTTR	99.7%	69.6	25	65.5	3	0	0	1264.65	89	99
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	19	82	0.08%	45.4%	LWNTLGVCK	99.7%	63	25	56.1	6	0	0	1090.57	131	139
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	19	82	0.08%	45.4%	QEVISTSSK	99.7%	41.2	25	34.3	1	0	0	978.51	272	280
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	19	82	0.08%	45.4%	VWNLANCK	99.7%	42.8	25	38.4	4	0	0	1004.50	176	183
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	19	82	0.08%	45.4%	VWQVTIGTR	99.7%	76.1	25	70	6	0	0	1059.59	309	317

Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	19	82	0.08%	45.4%	YTVQDESHSEWVSCVR	99.7%	96.3	25	96.3	4	6	0	1981.87	140	155
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	19	82	0.08%	45.4%	YWLCAATGPSIK	99.7%	76.4	25	69.9	4	0	0	1366.68	246	257
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	6	6	9	0.01%	12.9%	CPQVEEAIVQSGQK	99.7%	48	25	42.9	1	0	0	1572.77	158	171
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	6	6	9	0.01%	12.9%	ELPTVVFR	97.8%	31.3	25	31.3	1	0	0	960.55	198	205
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	6	6	9	0.01%	12.9%	KDPGVPNSAPFK	99.2%	35.6	25	28.4	1	0	0	1256.66	46	57
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	6	6	9	0.01%	12.9%	LLGGFQETCSK	99.7%	58	25	55.2	2	0	0	1239.60	243	253
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	6	6	9	0.01%	12.9%	VGVIGFPNVGK	99.6%	39.8	25	28.9	3	0	0	1086.63	257	267
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	6	6	9	0.01%	12.9%	VIEASDVVLEVLDAR	99.7%	60.9	25	45.2	1	0	0	1627.89	137	151
H/ACA ribonucleoprotein complex subunit 1	GAR1	GAR1_HUMAN	22.3	100.0%	3	3	5	0.01%	10.6%	DFYFSVK	98.6%	33.4	25	24.9	1	0	0	905.44	122	128
H/ACA ribonucleoprotein complex subunit 1	GAR1	GAR1_HUMAN	22.3	100.0%	3	3	5	0.01%	10.6%	FYIDPYK	99.7%	48.4	25	42.2	2	0	0	945.47	144	150
H/ACA ribonucleoprotein complex subunit 1	GAR1	GAR1_HUMAN	22.3	100.0%	3	3	5	0.01%	10.6%	VDEIFGQLR	99.7%	72.1	25	59	2	0	0	1076.57	113	121
H/ACA ribonucleoprotein complex subunit 2	NHP2	NHP2_HUMAN	17.2	99.8%	2	3	5	0.01%	19.0%	NLPYVYIPSK	97.4%	30.7	25	15.1	1	0	0	1193.66	102	111
H/ACA ribonucleoprotein complex subunit 2	NHP2	NHP2_HUMAN	17.2	99.8%	2	3	5	0.01%	19.0%	TYQELLVNQNPIAQPLASR	99.7%	92.4	25	90.6	2	2	0	2155.15	23	41
H/ACA ribonucleoprotein complex subunit 3	NOP10	NOP10_HUMAN	7.7	99.8%	2	2	5	0.01%	31.2%	FSPDDKYSR	98.1%	31.9	25	11.3	3	0	0	1114.52	35	43
H/ACA ribonucleoprotein complex subunit 3	NOP10	NOP10_HUMAN	7.7	99.8%	2	2	5	0.01%	31.2%	VLMTQQPRPVL	99.7%	53.4	25	53.4	2	0	0	1281.73	54	64
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	7	7	11	0.01%	13.4%	APQVVAEAAK	99.7%	41.4	25	41.4	2	0	0	983.55	434	443
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	7	7	11	0.01%	13.4%	DSAVNAICYGAK	99.7%	52.6	25	49	2	0	0	1268.59	303	314
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	7	7	11	0.01%	13.4%	EIGDYIR	94.7%	27.7	25	22.2	1	0	0	865.44	82	88
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	7	7	11	0.01%	13.4%	EVVAEVVK	99.6%	39.7	25	27.3	2	0	0	872.51	426	433
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	7	7	11	0.01%	13.4%	IMLPGVLR	97.6%	31	25	12.6	1	0	0	914.55	315	322
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	7	7	11	0.01%	13.4%	LDTSQWPLLLK	99.7%	64.9	25	54	1	0	0	1313.75	47	57
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	7	7	11	0.01%	13.4%	LHNAIEGGTQLSR	99.7%	83	25	83	2	0	0	1395.73	159	171
HCLS1-associated protein X-1	HAX1	HAX1_HUMAN	31.6	100.0%	3	4	6	0.01%	12.5%	GFFGFPGPR	99.5%	37.9	25	29.2	2	0	0	981.49	9	17
HCLS1-associated protein X-1	HAX1	HAX1_HUMAN	31.6	100.0%	3	4	6	0.01%	12.5%	IFGGVLESDAR	99.7%	81.3	25	57.5	2	0	0	1163.61	140	150
HCLS1-associated protein X-1	HAX1	HAX1_HUMAN	31.6	100.0%	3	4	6	0.01%	12.5%	TVVDSEGRTETTVTR	98.4%	32.8	25	28.9	1	1	0	1650.83	228	242
HEAT repeat-containing protein 1	HEATR1	HEAT1_HUMAN	242.4	100.0%	3	3	4	0.00%	1.7%	LDDTYSFQVINK	99.7%	51.3	25	43	1	0	0	1442.72	1337	1348
HEAT repeat-containing protein 1	HEATR1	HEAT1_HUMAN	242.4	100.0%	3	3	4	0.00%	1.7%	LVPDLLAIVQR	99.2%	35.9	25	35.9	2	0	0	1236.77	1644	1654
HEAT repeat-containing protein 1	HEATR1	HEAT1_HUMAN	242.4	100.0%	3	3	4	0.00%	1.7%	VSLLNEQFLPLIR	99.5%	38.5	25	31	1	0	0	1541.91	418	430
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	9	9	18	0.02%	13.6%	AIQDAILEVLK	99.7%	71	25	60.5	2	0	0	1212.72	804	814
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	9	9	18	0.02%	13.6%	CSLLDPFAAVR	99.7%	47.8	25	40.1	2	0	0	1248.64	173	183
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	9	9	18	0.02%	13.6%	EGSGLFPDLLVR	99.7%	50.2	25	43.5	2	0	0	1302.71	815	826
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	9	9	18	0.02%	13.6%	LFDDVPQVR	99.7%	57.4	25	50	2	0	0	1088.57	254	262
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	9	9	18	0.02%	13.6%	LIPLLLSSLNDEVPEVR	99.7%	94.1	25	89.1	1	0	0	1907.09	286	302
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	9	9	18	0.02%	13.6%	LLPGLEADSKPGR	99.7%	61	25	57.4	2	0	0	1352.75	34	46
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	9	9	18	0.02%	13.6%	SAELVGTFVSPEVFLK	99.7%	77.2	25	76.3	4	0	0	1722.93	423	438
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	9	9	18	0.02%	13.6%	SVDDVLSHFAQR	99.0%	34.8	25	32.5	1	0	0	1373.68	242	253
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	9	9	18	0.02%	13.6%	TPSASGLLVLASAMR	99.7%	105	25	105	2	0	0	1473.81	447	461
HEAT repeat-containing protein 3	HEATR3	HEAT3_HUMAN	74.6	99.9%	2	2	2	0.00%	4.0%	DIMTPLVALLK	99.4%	37.7	25	29.8	1	0	0	1213.72	122	132
HEAT repeat-containing protein 3	HEATR3	HEAT3_HUMAN	74.6	99.9%	2	2	2	0.00%	4.0%	VNVVSILGITGSVLAK	98.8%	34.2	25	34.2	1	0	0	1569.96	557	572
HEAT repeat-containing protein 6	HEATR6	HEAT6_HUMAN	128.8	100.0%	3	3	5	0.01%	3.1%	IWNALVTALQK	99.7%	43.7	25	43.7	2	0	0	1256.74	1042	1052
HEAT repeat-containing protein 6	HEATR6	HEAT6_HUMAN	128.8	100.0%	3	3	5	0.01%	3.1%	LEALQVLTLLAR	99.7%	63.7	25	55.7	2	0	0	1339.83	689	700
HEAT repeat-containing protein 6	HEATR6	HEAT6_HUMAN	128.8	100.0%	3	3	5	0.01%	3.1%	YLPELLGNTGLLMK	96.4%	29.2	25	29.2	1	0	0	1577.86	157	170
Heat shock 70 kDa protein 12A	HSPA12A	HS12A_HUMAN	75.0	100.0%	2	2	4	0.00%	3.9%	ETAPTSAYSSPAR	99.7%	49.1	25	49.1	2	0	0	1337.63	14	26
Heat shock 70 kDa protein 12A	HSPA12A	HS12A_HUMAN	75.0	100.0%	2	2	4	0.00%	3.9%	GAVLFGLDPAVIK	99.7%	69.6	25	62.9	2	0	0	1299.77	517	529
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	28	66	0.07%	40.7%	AFYPEEISSMVLTK	99.7%	91	25	85.4	5	0	0	1630.80	113	126
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	28	66	0.07%	40.7%	AQIHDLVLVGGSTR	99.7%	79	25	70.7	2	2	0	1465.81	329	342
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	28	66	0.07%	40.7%	ARFEELCSDLFR	99.7%	50.2	25	49.5	2	2	0	1542.74	300	311
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	28	66	0.07%	40.7%	ATAGDTHLGGEDFDNR	99.7%	67.6	25	67.6	3	2	0	1675.73	221	236
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	28	66	0.07%	40.7%	DAGVIAGLNVLR	99.7%	98.7	25	87.9	4	0	0	1197.70	160	171
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	28	66	0.07%	40.7%	DNNLLGR	99.3%	36.7	25	27.1	2	0	0	801.42	452	458
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	28	66	0.07%	40.7%	FEELCSDLFR	99.7%	46.4	25	46.4	2	0	0	1315.60	302	311

Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	28	66	0.07%	40.7%	FGDPVVQSDMK	99.7%	61.3	25	61.3	2	0	0	1222.58	78	88
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	28	66	0.07%	40.7%	GGSGSGPTIEEVD	98.4%	32.6	25	25.4	2	0	0	1204.53	629	641
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	28	66	0.07%	40.7%	HWPFQVINDGDKPK	99.7%	49.4	25	49.4	0	2	0	1680.85	89	102
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	28	66	0.07%	40.7%	IINEPTAAAIAYGLDR	99.7%	118	25	117	4	2	0	1687.90	172	187
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	28	66	0.07%	40.7%	ITITNDKGR	99.7%	45.7	25	33.5	2	0	0	1017.57	501	509
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	28	66	0.07%	40.7%	KFGDPVVQSDMK	99.7%	42	25	42	2	0	0	1350.67	77	88
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	28	66	0.07%	40.7%	LLQDFFNGR	99.7%	54.3	25	41.2	4	0	0	1109.57	349	357
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	28	66	0.07%	40.7%	LSKEEIER	99.7%	53.6	25	28.2	2	0	0	1003.54	510	517
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	28	66	0.07%	40.7%	LVNHFVEEFKR	99.7%	38.8	25	38.3	0	2	0	1417.76	237	247
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	28	66	0.07%	40.7%	MVQEAEKYK	98.4%	32.8	25	26.3	1	0	0	1125.56	518	526
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	28	66	0.07%	40.7%	NALESYAFNMK	99.7%	74.8	25	74.8	5	0	0	1287.60	540	550
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	28	66	0.07%	40.7%	NQVALNPQNTVFDAK	99.7%	110	25	99.7	2	0	0	1658.85	57	71
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	28	66	0.07%	40.7%	NQVALNPQNTVFDAKR	95.9%	22.5	25	22.2	0	2	0	1814.95	57	72
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	28	66	0.07%	40.7%	SAVEDEGLK	99.7%	50.2	25	44.8	2	0	0	947.47	551	559
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	28	66	0.07%	40.7%	STLEPVEK	95.1%	27.9	25	14.9	1	0	0	902.48	312	319
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	28	66	0.07%	40.7%	TTPSYVAFTDTER	99.7%	86.5	25	84.7	5	0	0	1487.70	37	49
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	28	66	0.07%	40.7%	VEIIANDQGNR	99.7%	59.2	25	0	2	0	0	1228.63	26	36
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	28	66	0.07%	40.7%	VQVSYKGETK	99.7%	51.4	25	44.4	2	0	0	1138.61	103	112
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	28	66	0.07%	40.7%	YKAEDEVQR	99.7%	46	25	32.3	4	0	0	1137.55	525	533
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	12	0.01%	13.3%	AFSDPFVEAEK	99.2%	36.2	25	34.4	2	0	0	1239.59	74	84
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	12	0.01%	13.3%	AGGIETIANEYSDR	99.7%	64.1	25	64.1	1	0	0	1495.70	20	33
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	12	0.01%	13.3%	EFSITDVVPYPISLR	99.7%	40.4	25	40.4	1	0	0	1735.93	391	405
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	12	0.01%	13.3%	FQESEERPK	99.7%	42	25	24.1	3	0	0	1149.55	689	697
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	12	0.01%	13.3%	GCALQCAILSPAFK	99.7%	99	25	87.2	2	0	0	1535.77	375	388
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	12	0.01%	13.3%	MIMQDKLEK	98.3%	32.5	25	21.2	1	0	0	1135.59	604	612
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	12	0.01%	13.3%	SNLAYDIVQLPTGLTGIK	99.7%	80.5	25	80.5	2	0	0	1903.05	85	102
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	12	0.01%	13.3%	VEPPKEEQK	99.7%	42.4	25	37.1	1	0	0	1083.57	790	798
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	12	0.01%	13.3%	VLATAFDTTLGGR	99.7%	105	25	96.6	2	0	0	1321.71	222	234
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	ARFEELNADLFR	99.7%	61.2	25	48.6	2	2	0	1480.75	300	311
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	DAGTIAGLNVLR	99.7%	90.9	25	78.7	4	0	0	1199.67	160	171
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	EIAEAYLGK	99.7%	51.9	25	41.7	2	0	0	993.53	129	137
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	FDDAVVQSDMK	99.7%	58.6	25	49.9	2	0	0	1254.57	78	88
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	FEELNADLFR	99.7%	73.9	25	66.3	2	0	0	1253.62	302	311
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	GTLDPVEK	94.9%	27.8	25	13.9	1	0	0	858.46	312	319
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	IINEPTAAAIAYGLDK	99.7%	125	25	123	2	0	0	1659.90	172	187
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	IINEPTAAAIAYGLDKK	99.7%	112	25	112	2	1	0	1787.99	172	188
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	ITITNDKGR	99.7%	45.7	25	33.5	2	0	0	1017.57	501	509
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	LDKSQIHDIVLVGGSTR	99.7%	38.9	25	38.9	0	1	0	1838.01	326	342
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	LLQDFFNGK	99.4%	37.7	25	24.9	2	0	0	1081.57	349	357
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	LSKEDIER	99.7%	61.9	25	13.2	2	0	0	989.53	510	517
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	MKEIAEAYLGK	99.7%	66.9	25	55.4	4	0	0	1268.66	127	137
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	MVNHFIAEFK	99.7%	50.5	25	29.9	4	2	0	1235.62	237	246
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	MVQEAEKYK	98.4%	32.8	25	26.3	1	0	0	1125.56	518	526
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	NQVAMNPTNTVFDAK	99.7%	114	25	108	4	0	0	1649.80	57	71
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	NQVAMNPTNTVFDAKR	96.6%	23.2	25	23.2	0	1	0	1805.90	57	72
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	NSLESYAFNMK	99.7%	49.2	25	49.2	2	0	0	1319.59	540	550
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	RFDDAVVQSDMK	99.7%	61.5	25	56.9	2	0	0	1410.67	77	88
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	SFYPEEVSSMVLTK	99.7%	83.1	25	83.1	4	0	0	1616.79	113	126
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	SQIHDIVLVGGSTR	99.7%	81.2	25	75.2	2	2	0	1481.81	329	342
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	STAGDTHLGGEDFDNR	99.7%	63.7	25	63.7	2	1	0	1691.73	221	236
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	TTPSYVAFTDTER	99.7%	86.5	25	84.7	5	0	0	1487.70	37	49

Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	TVTNAVVTVPAYFNDSQR	99.7%	80.7	25	78.9	2	1	0	1982.00	138	155
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	VCNPIITK	99.7%	43.3	25	23.6	2	0	0	944.52	602	609
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	VEIIANDQGNR	99.7%	59.2	25	0	2	0	0	1228.63	26	36
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	73	0.07%	38.9%	VQVEYKGETK	99.7%	50	25	46	3	0	0	1180.62	103	112
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	18	18	31	0.03%	22.4%	CTPSVISFGSK	97.0%	30	25	25	2	0	0	1182.58	34	44
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	18	18	31	0.03%	22.4%	DISTTLNADEAVAR	99.7%	102	25	93.7	2	0	0	1475.73	361	374
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	18	18	31	0.03%	22.4%	DKLCGPYEK	95.5%	28.3	25	20.1	1	0	0	1109.53	647	655
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	18	18	31	0.03%	22.4%	DLLNMYIETEGK	99.7%	69.3	25	69.3	2	0	0	1425.69	609	620
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	18	18	31	0.03%	22.4%	EKENLSYDLVPLK	99.7%	52	25	43.7	1	0	0	1547.83	83	95
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	18	18	31	0.03%	22.4%	FQEAEERPK	99.7%	46.3	25	33.1	2	0	0	1133.56	706	714
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	18	18	31	0.03%	22.4%	FVVQNVSAQK	99.7%	42.7	25	39.5	1	0	0	1119.62	462	471
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	18	18	31	0.03%	22.4%	GCALQCAILSPAFK	99.7%	99	25	87.2	2	0	0	1535.77	375	388
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	18	18	31	0.03%	22.4%	KSLDQDPVVR	99.6%	39.5	25	30.5	1	0	0	1156.63	772	781
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	18	18	31	0.03%	22.4%	LKETAENSLK	99.7%	51	25	23.5	2	0	0	1132.62	125	134
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	18	18	31	0.03%	22.4%	MFEELGQR	98.6%	33.4	25	33.4	1	0	0	1009.48	715	722
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	18	18	31	0.03%	22.4%	MIMQDKLEK	98.3%	32.5	25	21.2	1	0	0	1135.59	621	629
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	18	18	31	0.03%	22.4%	NAVEEYVYEFR	99.7%	60.4	25	60.4	2	0	0	1418.66	636	646
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	18	18	31	0.03%	22.4%	QDLPSLDEKPR	99.7%	32.1	25	30.5	0	1	0	1297.67	186	196
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	18	18	31	0.03%	22.4%	SLDQDPVVR	99.7%	43.2	25	36.9	2	0	0	1028.54	773	781
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	18	18	31	0.03%	22.4%	SQFEELCAELLQK	99.7%	91.7	25	84	2	0	0	1594.78	304	316
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	18	18	31	0.03%	22.4%	SVLDAAQIVGLNCLR	99.7%	109	25	100	2	0	0	1628.88	155	169
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	18	18	31	0.03%	22.4%	VLGTAFDPFLGGK	99.7%	80.6	25	64.4	4	0	0	1321.72	222	234
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	28	0.03%	24.7%	AFLDALQNQAEASSK	99.7%	120	25	116	2	0	0	1592.79	182	196
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	28	0.03%	24.7%	AQLLQPTLEINPR	99.7%	82.1	25	79.7	2	0	0	1492.85	635	647
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	28	0.03%	24.7%	ELGSSVALYSR	99.7%	66.2	25	61.8	2	0	0	1181.62	358	368
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	28	0.03%	24.7%	ELISNASDALEK	99.7%	87	25	77.2	2	0	0	1289.66	115	126
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	28	0.03%	24.7%	ELLQESALIR	99.7%	66	25	52.3	2	0	0	1171.67	403	412
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	28	0.03%	24.7%	FFEDYGLFMR	99.7%	54.4	25	54.4	4	0	0	1324.60	440	449
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	28	0.03%	24.7%	GVVDSEDIPLNLSR	99.7%	114	25	0	13	0	0	1513.79	389	402
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	28	0.03%	24.7%	LNELLVK	98.7%	33.8	25	12.8	1	0	0	828.52	693	699
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	28	0.03%	24.7%	MNTLQAIWMMDPK	99.7%	46.8	25	46.8	2	0	0	1578.75	292	304
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	28	0.03%	24.7%	NIYYLCAPNR	99.7%	43.2	25	40.8	2	0	0	1283.62	496	505
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	28	0.03%	24.7%	SDCKEFSSEAR	99.7%	46.6	25	37.7	1	0	0	1315.56	259	269
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	28	0.03%	24.7%	TDAPLNIR	99.7%	45	25	37.6	2	0	0	899.49	333	340
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	28	0.03%	24.7%	YESSALPSGQLTSLSEYASR	99.7%	115	25	112	2	0	0	2146.03	470	489
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	28	0.03%	24.7%	YSNFVSFPLYLNGR	99.7%	47.9	25	47.9	2	0	0	1676.84	277	290
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	28	0.03%	24.7%	YTLHYK	96.4%	29.3	25	21.3	2	0	0	824.43	327	332
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	ADLINNLGTIAK	99.7%	84.3	25	70.8	19	0	0	1242.71	101	112
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	ALLFVPR	99.7%	45	25	0	5	0	0	815.51	339	345
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	APFDLFENR	99.7%	65.7	25	62.5	2	0	0	1108.54	347	355
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	DNSTMGYMAAK	99.7%	68.3	25	62.5	4	0	0	1188.50	621	631
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	DQVANSAFVER	99.7%	73.5	25	66.2	7	0	0	1235.60	500	510
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	EDQTEYLEER	99.7%	61.1	25	56.1	3	0	0	1311.57	192	201
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	EGLELPEDEEEK	98.7%	33.7	25	32.9	1	0	0	1416.64	547	558
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	EGLELPEDEEEKK	99.7%	49	25	47.6	2	0	0	1544.73	547	559
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	EKYIDQEELNK	99.7%	53.9	25	41.5	2	0	0	1408.70	282	292
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	ELHINLIPNK	98.1%	32.1	25	25.5	2	0	0	1190.69	75	84
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	ELHINLIPNKQDR	99.7%	51.7	25	51.7	2	2	0	1589.88	75	87
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	ELISNSSDALDK	99.7%	88.9	25	77.8	2	0	0	1291.64	47	58
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	ELISNSSDALDKIR	99.7%	92.1	25	83.5	2	0	0	1560.82	47	60
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	FENLCK	99.3%	36.4	25	24	1	0	0	810.38	568	573

Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	FYEQFSK	99.7%	47.9	25	31.9	3	0	0	948.45	437	443
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	GVVDSEDLPLNISR	99.7%	114	25	0	13	0	0	1513.79	387	400
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	HFSVEGQLEFR	99.7%	73	25	69.9	8	2	0	1348.66	328	338
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	HIYYITGETK	99.7%	48.8	25	46.4	2	0	0	1224.63	490	499
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	HLEINPDHSIIETLR	99.7%	39.9	25	39.9	0	2	0	1786.94	633	647
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	HSQFIGYPITLFVEK	99.7%	42	25	42	2	0	0	1778.95	210	224
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	IMKDILEK	99.7%	49.9	25	12.4	2	0	0	989.57	574	581
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	IRYESLTDPSK	99.7%	47.5	25	42.4	2	2	0	1308.68	59	69
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	KLSELLR	94.7%	27.6	25	11.4	1	0	0	858.54	458	464
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	LGIHEDSQNR	99.7%	46	25	42	4	0	0	1168.57	447	456
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	LVTSPCCIVTSTYGWTANMER	99.7%	66.3	25	66.3	4	0	0	2446.12	592	612
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	NPDDITNEEYGEFYK	99.7%	106	25	103	4	0	0	1833.78	300	314
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	RAPFDLFENR	99.7%	49.5	25	43.8	2	0	0	1264.64	346	355
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	SLTNDWEDHLAVK	99.7%	83.4	25	76.5	6	3	0	1527.74	315	327
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	TDTGEPMGR	99.7%	50.9	25	39.8	2	0	0	963.42	174	182
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	TKFENLCK	97.1%	30.1	25	28.4	1	0	0	1039.52	566	573
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	TLTIVDTGIGMTK	99.7%	109	25	0	27	0	0	1365.73	88	100
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	VILHLKEDQTEYLEER	99.7%	41.3	25	40.9	1	3	0	2015.04	186	201
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	YESLTDPSK	99.7%	62.4	25	56.6	4	0	0	1039.49	61	69
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	YESLTDPSKLDSGK	99.7%	74.6	25	62.7	6	1	0	1539.75	61	74
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	YIDQEELNK	99.7%	60.4	25	36.7	13	0	0	1151.56	284	292
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	YYTSASGDEMVSLK	99.7%	79.3	25	79.3	4	0	0	1550.70	465	478
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	22	25	62	0.06%	44.7%	YYTSASGDEMVSLKDYCTR	99.7%	33.4	25	33.4	0	1	0	2245.97	465	483
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	ADHGEPIGR	98.5%	33.1	25	26.2	2	0	0	951.46	169	177
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	ADLINNLGTIAK	99.7%	84.3	25	70.8	19	0	0	1242.71	96	107
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	AKFENLCK	99.7%	45.2	25	35.9	1	0	0	1009.51	558	565
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	ALLFIPR	99.7%	43	25	15.5	8	0	0	829.53	331	337
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	APFDLFENK	99.7%	43.9	25	40.2	4	0	0	1080.54	339	347
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	APFDLFENKK	99.7%	53.2	25	43.5	2	0	0	1208.63	339	348
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	DNSTMGYMMAK	99.7%	72.4	25	19.7	12	0	0	1280.50	613	623
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	EDQTEYLEER	99.7%	61.1	25	56.1	3	0	0	1311.57	187	196
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	EGLELPEDEEEK	98.7%	33.7	25	32.9	1	0	0	1416.64	539	550
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	EGLELPEDEEEKK	99.7%	49	25	47.6	2	0	0	1544.73	539	551
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	EKYIDQEELNK	99.7%	53.9	25	41.5	2	0	0	1408.70	274	284
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	ELISNASDALDK	99.7%	78.7	25	63.9	7	0	0	1275.64	42	53
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	ELISNASDALDKIR	99.7%	98.3	25	80	8	2	0	1544.83	42	55
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	ELKIDIIPNPQER	99.7%	50.8	25	48.5	2	0	0	1564.87	70	82
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	EQVANSAFVER	99.7%	75.4	25	65.2	16	0	0	1249.62	492	502
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	FENLCK	99.3%	36.4	25	24	1	0	0	810.38	560	565
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	FYEAFSK	99.0%	35.1	25	30.7	4	0	0	891.42	429	435
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	GFEVVYMTEPIDEYCVQQLK	99.7%	90.9	25	44.9	4	0	0	2464.14	507	526
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	GVVDSEDLPLNISR	99.7%	114	25	0	13	0	0	1513.79	379	392
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	HFSVEGQLEFR	99.7%	73	25	69.9	8	2	0	1348.66	320	330
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	HLEINPDHPIVETLR	99.7%	72.7	25	65.7	2	2	0	1782.95	625	639
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	HSQFIGYPITLYLEK	99.7%	38.3	25	0	2	2	0	1808.96	205	219
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	IDIIPNPQER	99.7%	47.8	25	42.5	5	0	0	1194.65	73	82
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	IRYESLTDPSK	99.7%	47.5	25	42.4	2	2	0	1308.68	54	64
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	KFYEAFSK	99.5%	38.6	25	29.5	2	0	0	1019.52	428	435
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	LGIHEDSTNR	99.7%	54	25	52.1	5	0	0	1141.56	439	448
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	LGIHEDSTNRR	99.7%	43.8	25	41.7	0	3	0	1297.66	439	449
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	LVSSPCCIVTSTYGWTANMER	99.7%	112	25	112	4	3	0	2448.10	584	604

Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	NPDDITQEEYGEFYK	99.7%	103	25	103	8	0	0	1847.80	292	306
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	RAPFDLFENK	99.7%	44.5	25	31.6	6	0	0	1236.64	338	347
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	RLSELLR	99.7%	43.8	25	8.09	4	0	0	886.55	450	456
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	SIYYITGESK	99.7%	68.8	25	61.6	9	0	0	1160.58	482	491
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	SLTNDWEDHLAVK	99.7%	83.4	25	76.5	6	3	0	1527.74	307	319
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	TLTLVDTGIGMTK	99.7%	109	25	0	27	0	0	1365.73	83	95
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	VILHLKEDQTEYLEER	99.7%	41.3	25	40.9	1	3	0	2015.04	181	196
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	YESLTDPSK	99.7%	62.4	25	56.6	4	0	0	1039.49	56	64
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	YESLTDPSKLDSGK	99.7%	74.6	25	62.7	6	1	0	1539.75	56	69
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	YHTSQSGDEMTSLSEYVSR	99.7%	121	25	121	4	9	0	2176.95	457	475
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	261	0.26%	47.2%	YIDQEELNK	99.7%	60.4	25	36.7	13	0	0	1151.56	276	284
Helicase SKI2W	SKIV2L	SKIV2_HUMAN	137.8	100.0%	3	3	6	0.01%	3.4%	GPATAEVPYPDDLVGFK	98.9%	34.2	25	34.2	1	0	0	1775.89	889	905
Helicase SKI2W	SKIV2L	SKIV2_HUMAN	137.8	100.0%	3	3	6	0.01%	3.4%	TQGELFLLLDSR	99.7%	49	25	49	3	0	0	1391.75	499	510
Helicase SKI2W	SKIV2L	SKIV2_HUMAN	137.8	100.0%	3	3	6	0.01%	3.4%	TVVAEYAIALAQK	99.7%	76	25	71.4	2	0	0	1376.78	339	351
Helicase-like transcription factor	HLTF	HLTF_HUMAN	113.9	100.0%	3	3	4	0.00%	2.8%	ASGFVFTR	99.7%	40	25	37.3	1	0	0	884.46	873	880
Helicase-like transcription factor	HLTF	HLTF_HUMAN	113.9	100.0%	3	3	4	0.00%	2.8%	ELAAGAFGTK	98.0%	31.8	25	31.8	1	0	0	964.51	979	988
Helicase-like transcription factor	HLTF	HLTF_HUMAN	113.9	100.0%	3	3	4	0.00%	2.8%	VILDEGHAIR	99.7%	60.9	25	49.9	2	0	0	1122.63	554	563
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	4	4	10	0.01%	8.3%	LEDVLPLAFTR	99.7%	54.6	25	43.2	5	0	0	1273.72	259	269
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	4	4	10	0.01%	8.3%	SGASVVAIR	99.7%	63.1	25	47.1	1	0	0	859.50	176	184
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	4	4	10	0.01%	8.3%	SSAVDPEPQVK	99.7%	43.7	25	32.5	2	0	0	1156.58	248	258
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	4	4	10	0.01%	8.3%	TIPSWATLSASQLAR	99.7%	86.2	25	82.6	2	0	0	1601.86	132	146
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	4	5	10	0.01%	15.7%	DLKDYFTK	99.7%	42.7	25	32.5	2	0	0	1029.53	84	91
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	4	5	10	0.01%	15.7%	EVYQQQQYGSGGR	99.7%	88.4	25	82.3	2	0	0	1499.69	233	245
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	4	5	10	0.01%	15.7%	FGEVVDCTIK	99.7%	57.8	25	0	5	0	0	1167.57	92	101
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	4	5	10	0.01%	15.7%	GFGFILFK	99.7%	41.8	25	33.2	2	0	0	928.53	111	118
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	4	5	10	0.01%	15.7%	MFVGGLSWDTSKK	99.7%	67.9	25	65.3	4	0	0	1455.73	71	83
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	6	6	11	0.01%	25.9%	AEIIADKQSGK	99.7%	54.1	25	42.4	2	0	0	1159.63	127	137
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	6	6	11	0.01%	25.9%	AVPKEDIYSGGGGGGSR	99.7%	97.3	25	88.9	2	0	0	1606.78	173	189
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	6	6	11	0.01%	25.9%	EDIYSGGGGGGSR	99.7%	78.9	25	78.9	2	0	0	1211.53	177	189
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	6	6	11	0.01%	25.9%	GDVAEGDLIEHFSQFGTVEK	99.7%	52.3	25	52.3	0	2	0	2178.04	107	126
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	6	6	11	0.01%	25.9%	GFGFVYFQNHDAADK	97.1%	30.1	25	30.1	1	0	0	1715.78	140	154
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	6	6	11	0.01%	25.9%	LFIGGLNVQTSESGLR	99.7%	98	25	90.1	2	0	0	1690.91	9	24
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	8	10	25	0.03%	26.9%	EDSQRPGAHLTVK	99.7%	56.5	25	32.3	2	0	0	1437.74	93	105
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	8	10	25	0.03%	26.9%	EDSQRPGAHLTVKK	97.6%	24.4	25	16	0	1	0	1565.84	93	106
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	8	10	25	0.03%	26.9%	GFAFVTFDDHDSVDK	99.7%	63.6	25	58	1	0	0	1699.76	147	161
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	8	10	25	0.03%	26.9%	IEVIEIMTDR	99.7%	75.5	25	66.5	3	0	0	1234.64	131	140
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	8	10	25	0.03%	26.9%	LFIGGLSFETTDESLR	99.7%	106	25	87.8	5	0	0	1784.91	16	31
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	8	10	25	0.03%	26.9%	NQGGYGGSSSSSSYGSGR	99.7%	124	25	124	3	0	0	1694.70	353	370
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	8	10	25	0.03%	26.9%	SESPKEPEQLR	99.7%	48.6	25	42.2	2	2	0	1299.65	4	14
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	8	10	25	0.03%	26.9%	SSGPYGGGGQYFAKPR	99.7%	100	25	93.5	4	2	0	1628.78	337	352
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	7	11	18	0.02%	27.2%	EDSVKPGAHLTVK	99.7%	68.3	25	60.1	2	1	0	1380.75	114	126
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	7	11	18	0.02%	27.2%	GFAFVTFDDHDTVDK	99.7%	49.9	25	45.8	2	0	0	1713.78	168	182
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	7	11	18	0.02%	27.2%	IETIEVMEDR	99.7%	72.6	25	65.3	4	0	0	1234.60	152	161
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	7	11	18	0.02%	27.2%	IFVGGIKEDTEEYNLR	99.7%	74.8	25	67.7	2	2	0	1882.95	128	143
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	7	11	18	0.02%	27.2%	LFIGGLSFETTDDSLR	99.7%	62.6	25	62.6	1	0	0	1770.89	37	52
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	7	11	18	0.02%	27.2%	SSGSPYGGGYGSGGGSGGYGSR	99.7%	134	25	134	2	0	0	1910.79	355	376
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	7	11	18	0.02%	27.2%	WGTLTDCVVMR	97.2%	30.3	25	28.5	2	0	0	1353.63	58	68
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	7	7	21	0.02%	19.7%	FGEVVDCTLK	99.7%	57.8	25	0	5	0	0	1167.57	120	129
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	7	7	21	0.02%	19.7%	FGEVVDCTLKLDPITGR	99.7%	32.2	25	31.2	0	2	0	1919.99	120	136
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	7	7	21	0.02%	19.7%	GFGFVLFK	99.5%	38.1	25	30.2	5	0	0	914.51	139	146
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	7	7	21	0.02%	19.7%	IDASKNEEDEGHSNSSPR	99.7%	53	25	53	0	2	0	1971.86	68	85

Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	7	7	21	0.02%	19.7%	IFVGGLSPDTPEEK	99.7%	78	25	69.6	5	0	0	1488.76	184	197
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	7	7	21	0.02%	19.7%	MFIGGLSWDTTK	95.2%	28.1	25	28.1	1	0	0	1355.67	99	110
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	7	7	21	0.02%	19.7%	MFIGGLSWDTTKK	99.7%	64.8	25	61.3	1	0	0	1483.76	99	111
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	5	6	11	0.01%	23.6%	ATENDIYNFFSPLNPVR	99.7%	75.9	25	75.9	3	2	0	1996.98	300	316
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	5	6	11	0.01%	23.6%	DLSYCLSGMYDHR	99.7%	52.1	25	52.1	2	0	0	1632.68	263	275
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	5	6	11	0.01%	23.6%	HSGPNSADSANDGFVR	99.7%	97.6	25	97.6	2	2	0	1630.72	99	114
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	5	6	11	0.01%	23.6%	QSGEAFVELGSEDDVK	99.7%	122	25	119	2	0	0	1709.79	53	68
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	5	6	11	0.01%	23.6%	RYIGIVK	96.7%	29.6	25	16.9	1	0	0	848.54	218	224
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	5	6	11	0.01%	23.6%	VHIEIGPDGR	99.7%	58.9	25	56.9	8	0	0	1092.58	317	326
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	5	6	11	0.01%	23.6%	YGDSEFTVQSTTGHCVHMR	99.7%	76	25	76	0	2	0	2211.95	276	294
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	16	76	0.08%	41.2%	ATENDIYNFFSPLNPVR	99.7%	75.9	25	75.9	3	2	0	1996.98	300	316
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	16	76	0.08%	41.2%	DLNYCFSGMSDHR	99.7%	69.4	25	69.4	8	0	0	1601.65	263	275
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	16	76	0.08%	41.2%	EGRPSGEAFVELESEDEVK	99.7%	62	25	60.9	0	5	0	2106.98	50	68
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	16	76	0.08%	41.2%	GLPWSCSADEVQR	99.7%	78.2	25	75.6	7	0	0	1504.69	17	29
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	16	76	0.08%	41.2%	HTGPNSPDTANDGFVR	99.7%	81.8	25	76.1	6	9	0	1684.77	99	114
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	16	76	0.08%	41.2%	IQNGAQGIR	99.7%	57.1	25	42.8	4	0	0	956.53	36	44
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	16	76	0.08%	41.2%	SNNVEMDWVLK	99.7%	63	25	58.8	4	0	0	1334.64	88	98
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	16	76	0.08%	41.2%	STGEAFVQFASQEIAEK	99.7%	94.4	25	94.4	9	0	0	1841.89	151	167
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	16	76	0.08%	41.2%	VHIEIGPDGR	99.7%	58.9	25	56.9	8	0	0	1092.58	317	326
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	16	76	0.08%	41.2%	VTGEADVEFATHEDAVAAMSK	99.7%	36.5	25	36.5	0	2	0	2194.00	327	347
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	16	76	0.08%	41.2%	YGDGGSTFQSTTGHCVHMR	99.7%	66.4	25	66.4	0	8	0	2097.89	276	294
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	16	76	0.08%	41.2%	YVELFLNSTAGASGGAYEHR	99.2%	28.6	25	22	0	1	0	2142.03	356	375
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	7	12	0.01%	30.5%	ATENDIYNFFSPLNPMR	99.7%	71.9	25	71.9	4	0	0	2044.94	300	316
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	7	12	0.01%	30.5%	DLNYCFSGMSDHR	99.7%	69.4	25	69.4	8	0	0	1601.65	263	275
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	7	12	0.01%	30.5%	GLPWSCSADEVMR	99.7%	61.9	25	54.9	2	0	0	1523.66	17	29
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	7	12	0.01%	30.5%	HTGPNSPDTANDGFVR	99.7%	81.8	25	76.1	6	9	0	1684.77	99	114
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	7	12	0.01%	30.5%	SNSVEMDWVLK	99.7%	46.2	25	39.5	1	0	0	1307.63	88	98
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	7	12	0.01%	30.5%	STGEAFVQFASQEIAEK	99.7%	94.4	25	94.4	9	0	0	1841.89	151	167
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	7	12	0.01%	30.5%	VHIEIGPDGR	99.7%	58.9	25	56.9	8	0	0	1092.58	317	326
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	7	12	0.01%	30.5%	VTGEADVEFATHEDAVAAMAK	96.1%	22.7	25	7.94	0	1	0	2178.00	327	347
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	7	12	0.01%	30.5%	YGDGGSSFQSTTGHCVHMR	99.7%	60.8	25	60.8	0	4	0	2083.87	276	294
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	5	5	9	0.01%	17.6%	ATENDIANFFSPLNPIR	99.7%	53.6	25	51.5	2	0	0	1918.97	206	222
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	5	5	9	0.01%	17.6%	EIAENALGK	99.4%	37.3	25	37.3	2	0	0	944.50	68	76
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	5	5	9	0.01%	17.6%	HNGPNDASDGTVR	98.5%	32.9	25	32.9	1	0	0	1339.60	7	19
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	5	5	9	0.01%	17.6%	STGEAFVQFASK	99.7%	81.9	25	75.7	2	0	0	1271.63	56	67
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	5	5	9	0.01%	17.6%	VHIDIGADGR	99.7%	48.5	25	38.4	2	0	0	1052.55	223	232
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	17	22	50	0.05%	38.4%	DLAGSIIGK	99.7%	48	25	29.7	2	0	0	873.50	397	405
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	17	22	50	0.05%	38.4%	DYDDMSPR	99.7%	42	25	42	2	0	0	998.39	279	286
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	17	22	50	0.05%	38.4%	GGDLMAYDR	99.7%	65	25	61.8	4	0	0	1013.44	317	325
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	17	22	50	0.05%	38.4%	GGDLMAYDRR	98.4%	32.8	25	20.2	2	0	0	1153.54	317	326
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	17	22	50	0.05%	38.4%	GSDFDCELR	99.7%	53.9	25	50	2	0	0	1098.45	140	148
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	17	22	50	0.05%	38.4%	GSYGDLGGPIITTQVTIPK	99.7%	115	25	111	3	0	0	1917.03	378	396
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	17	22	50	0.05%	38.4%	IDEPLEGSEDR	99.7%	75.6	25	68.8	2	0	0	1259.58	423	433
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	17	22	50	0.05%	38.4%	IILDLISESPIK	99.7%	96.1	25	89.1	8	0	0	1340.80	208	219
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	17	22	50	0.05%	38.4%	IITITGTQDQIQNAQYLLQNSVK	99.7%	55.2	25	52.6	0	3	0	2589.39	434	456
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	17	22	50	0.05%	38.4%	LFQECCPHSTDR	99.7%	85.5	25	85.5	2	2	0	1549.65	180	191
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	17	22	50	0.05%	38.4%	LLIHQSLAGGIIGVK	99.7%	54.5	25	54.5	1	2	0	1518.94	149	163
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	17	22	50	0.05%	38.4%	NLPLPPPPPPR	97.1%	30.1	25	18.3	1	0	0	1194.70	306	316
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	17	22	50	0.05%	38.4%	NTDEMVELR	99.7%	76.1	25	60.2	4	0	0	1106.51	38	46
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	17	22	50	0.05%	38.4%	RDYDDMSPR	99.0%	35	25	30.2	1	0	0	1154.49	278	286
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	17	22	50	0.05%	38.4%	SRNTDEMVELR	99.6%	31.1	25	5.76	1	1	0	1349.65	36	46

Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	17	22	50	0.05%	38.4%	TDYNASVSVPDSSGPER	99.7%	80	25	80	2	0	0	1780.80	70	86
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	17	22	50	0.05%	38.4%	VVLIGGKPDR	99.7%	52.3	25	26.9	5	0	0	1053.64	192	201
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	8	9	22	0.02%	15.6%	AITHLNNNFMFGQK	99.7%	83.9	25	73.7	2	1	0	1634.81	435	448
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	8	9	22	0.02%	15.6%	ASLNGADIYSGCCTLK	99.7%	69.4	25	67.4	2	0	0	1729.79	249	264
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	8	9	22	0.02%	15.6%	IEYAKPTR	99.6%	39.5	25	33.8	4	0	0	977.54	265	272
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	8	9	22	0.02%	15.6%	ISRPGDSDDSR	98.1%	25.2	25	25.2	0	1	0	1204.56	179	189
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	8	9	22	0.02%	15.6%	LCFSTAQHAS	99.7%	43.2	25	43.2	4	0	0	1121.50	580	589
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	8	9	22	0.02%	15.6%	MGPPVGGHR	98.9%	34.5	25	19.6	2	0	0	907.46	345	353
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	8	9	22	0.02%	15.6%	NPNGPYPYTLK	99.7%	42.2	25	29.7	2	0	0	1263.64	569	579
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	8	9	22	0.02%	15.6%	VFNVFCLYGNVEK	99.7%	91.5	25	84	4	0	0	1588.78	399	411
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	ACQIFVR	99.7%	45.1	25	32.9	2	0	0	893.47	652	658
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	ADILEDKDGK	99.7%	49.3	25	39.4	5	0	0	1103.56	233	242
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	AFITNIPFDVK	99.7%	88.9	25	72.2	7	0	0	1264.69	73	83
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	EVFSMAGVVVR	99.7%	68	25	59.8	2	0	0	1193.63	222	232
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	FESPEVAER	99.7%	41.4	25	31.4	3	0	0	1063.51	699	707
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	FGSGMNMGR	99.7%	59.9	25	58.8	10	0	0	956.41	363	371
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	GCAVVEFK	99.7%	45.5	25	32.1	2	0	0	909.45	113	120
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	GGNRFEPYANPTK	99.7%	46.2	25	36.4	2	0	0	1450.71	57	69
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	GIGMGNIGPAGMGMEGIGFGINK	99.7%	116	25	68.5	9	1	0	2194.05	323	345
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	GNFGGSFAGSFGGAGGHAPGVAR	99.7%	99.5	25	99.5	2	2	0	2034.95	628	650
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	HSLSGRPLK	95.3%	28.1	25	14.1	1	0	0	994.58	135	143
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	INEILSNALK	99.7%	69.4	25	53.9	10	0	0	1114.65	372	381
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	INEILSNALKR	99.7%	50.9	25	43.7	2	0	0	1270.75	372	382
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	KACQIFVR	99.7%	58.1	25	43.8	2	0	0	1021.56	651	658
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	LGSTVFVANLDYK	99.7%	72	25	66.3	4	0	0	1426.76	202	214
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	LKEVFSMAGVVVR	99.7%	96.5	25	82.3	3	2	0	1434.81	220	232
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	MGAGLGHGMDR	99.7%	93.3	25	84.8	9	0	0	1117.49	419	429
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	MGAGMGFGLER	99.7%	84.5	25	60	11	0	0	1141.51	486	496
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	MGANNLER	99.7%	71	25	61.2	4	0	0	904.43	558	565
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	MGANSLER	99.7%	70.8	25	61.2	4	0	0	877.42	571	578
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	MGGMEGPFGGGMENMGR	99.7%	51.7	25	51.7	4	0	0	1778.66	346	362
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	MGLAMGGGGGASFDR	99.7%	94.6	25	50	10	0	0	1399.61	607	621
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	MGLSMER	99.7%	59.9	25	50.3	7	0	0	823.38	525	531
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	MGLVMDR	99.7%	53	25	44.2	6	0	0	821.40	437	443
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	MGPAMGPALGAGIER	99.7%	86.1	25	78.3	8	0	0	1459.70	592	606
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	MGPLGLDHMASSIER	99.7%	76.7	25	76.7	8	4	0	1613.78	457	471
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	MGPVMDR	99.7%	45.8	25	24.5	1	0	0	821.36	544	550
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	MVPAGMGAGLER	99.7%	56.6	25	45.5	7	0	0	1188.59	532	543
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	NLPFDFTWK	98.5%	33	25	27.6	1	0	0	1167.58	659	667
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	QGGGGGGGSVPGIER	99.7%	106	25	103	6	0	0	1284.63	389	403
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	VGEVTYVELLMDAEGK	99.7%	111	25	105	4	0	0	1768.87	95	110
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	32	49	167	0.17%	46.6%	VGQTIER	99.7%	59.2	25.4	36.6	2	0	0	802.44	504	510
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	11	12	29	0.03%	18.6%	AGPIWDLR	99.7%	65.8	25	52.1	2	0	0	927.50	185	192
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	11	12	29	0.03%	18.6%	DLFEDELVPLFEK	99.7%	97.4	25	92.6	4	0	0	1593.80	172	184
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	11	12	29	0.03%	18.6%	DSDLSHVQNK	99.6%	39	25	30.2	2	0	0	1142.54	82	91
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	11	12	29	0.03%	18.6%	GFCFLEYEDHK	99.7%	45.2	25	45.2	2	0	0	1444.62	287	297
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	11	12	29	0.03%	18.6%	GYAFVTFCTK	99.7%	57.2	25	57.2	1	0	0	1193.57	204	213
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	11	12	29	0.03%	18.6%	LMMDPLTGLNR	99.7%	76.9	25	68.2	4	0	0	1260.64	193	203
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	11	12	29	0.03%	18.6%	LYNNHEIR	99.6%	39.1	25	28.6	3	0	0	1058.54	222	229
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	11	12	29	0.03%	18.6%	NLANTVTEEILEK	99.7%	110	25	102	3	0	0	1473.78	344	356
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	11	12	29	0.03%	18.6%	SAFLCGVMK	99.7%	41.9	25	35.3	2	0	0	1012.50	92	100

Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	11	12	29	0.03%	18.6%	TGYTLDVTTGQR	99.7%	76.9	25	73.6	4	0	0	1311.65	131	142
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	11	12	29	0.03%	18.6%	TKEQILEEFSK	99.7%	63.4	25	59.6	2	0	0	1351.71	255	265
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	10	10	32	0.03%	25.6%	AGPIWDLR	99.7%	65.8	25	52.1	2	0	0	927.50	188	195
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	10	10	32	0.03%	25.6%	DLYEDELVPLFEK	99.7%	102	25	97.1	4	0	0	1609.80	175	187
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	10	10	32	0.03%	25.6%	EFNEEGALSVLQQFK	99.7%	52.8	25	33.6	2	0	0	1738.86	70	84
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	10	10	32	0.03%	25.6%	GFCFLEYEDHK	99.7%	45.2	25	45.2	2	0	0	1444.62	290	300
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	10	10	32	0.03%	25.6%	GYAFITFCGK	99.7%	61.5	25	57.6	3	0	0	1163.56	207	216
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	10	10	32	0.03%	25.6%	LCDSYEIRPGK	99.7%	52.9	25	29.5	2	0	0	1337.65	225	235
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	10	10	32	0.03%	25.6%	LKDYAFVHFEDR	99.7%	44.4	25	44.4	0	2	0	1539.76	373	384
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	10	10	32	0.03%	25.6%	LMMDPLSGQNR	99.7%	51.7	25	26.3	2	0	0	1261.60	196	206
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	10	10	32	0.03%	25.6%	NLATTVTEEILEK	99.7%	111	25	100	9	0	0	1460.78	347	359
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	10	10	32	0.03%	25.6%	SAFLCGVMK	99.7%	41.9	25	35.3	2	0	0	1012.50	95	103
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	10	10	32	0.03%	25.6%	STAYEDYYYHPPPR	99.6%	30.8	25	30.8	0	2	0	1758.78	428	441
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	10	10	32	0.03%	25.6%	TGYTLDVTTGQR	99.7%	76.9	25	73.6	4	0	0	1311.65	134	145
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	10	10	32	0.03%	25.6%	TKENILEEFSK	99.7%	58	25	47.8	2	0	0	1337.69	258	268
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	10	10	32	0.03%	25.6%	VQESTKGPDEAK	99.7%	62.3	25	52.9	4	0	0	1288.64	115	126
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	AEGGGGGGRPGAPAAGDGK	99.7%	48.8	25	48.8	2	2	0	1538.73	216	234
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	AEGGGGGGRPGAPAAGDGKTEQK	99.7%	34.8	25	34.8	0	2	0	2024.97	216	238
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	AVVVCPKDEDYK	99.1%	35.3	25	35.3	2	0	0	1422.69	603	614
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	DCEVVMMIGLPGAGK	99.7%	78.5	25	78.5	6	0	0	1608.74	496	510
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	DIDIHEVR	99.7%	45.5	25	37	10	0	0	996.51	353	360
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	DLPEHAVLK	98.9%	34.5	25	25.7	8	0	0	1021.57	627	635
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	EKPYFPIPEEYTFIQNVPLEDR	99.1%	28	25	28	0	2	0	2724.36	463	484
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	FIEIAAR	99.7%	46.5	25	31.3	11	0	0	819.47	566	572
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	GKVCFEMK	98.9%	34.4	25	24.5	2	0	0	998.48	332	339
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	GYFEYIEENK	99.7%	66.4	25	59.3	2	0	0	1291.58	256	265
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	GYFEYIEENKYSR	99.7%	73	25	73	8	2	0	1697.78	256	268
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	KAEGGGGGGRPGAPAAGDGK	99.4%	29.6	25	29.6	0	3	0	1666.83	215	234
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	KDCEVVMMIGLPGAGK	99.7%	57	25	3.73	6	2	0	1720.84	495	510
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	KMCLFAGFQR	99.7%	46.6	25	45	2	0	0	1273.62	592	601
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	LLEQYKEESK	99.7%	57.7	25	51.5	9	0	0	1266.66	665	674
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	LNTLLQR	99.5%	37.9	25	16.3	2	0	0	857.52	552	558
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	LQAALDDEEAGGRPAMEPGNGSLDLGGDSAGR	99.7%	84.6	25	84.6	0	4	0	3142.43	38	69
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	LSASSLTMESFAFLWAGGR	99.7%	92.1	25	92.1	2	0	0	2047.00	306	324
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	MCLFAGFQR	99.7%	62.5	25	51.8	11	0	0	1129.53	593	601
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	MMVAGFK	97.4%	30.5	25	16.5	3	0	0	815.38	537	543
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	NFILDQTNVSAAAQR	99.7%	135	25	122	18	2	0	1647.84	576	590
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	NGQDLGVAFK	99.7%	64.4	25	60.1	8	0	0	1048.54	424	433
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	SSGPTSLFAVTVAPPGAR	99.7%	76.9	25	71.3	11	2	0	1714.91	187	204
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	TCNCETEDYGEK	99.7%	52.2	25	52.2	2	0	0	1505.55	388	399
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	VCFEMK	97.8%	31.3	25	14	1	0	0	813.36	334	339
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	VSELKEELK	99.7%	43.3	25	21.6	2	0	0	1074.60	13	21
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	VTEKIPVR	99.7%	52	25	44.2	6	0	0	941.58	340	347
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	28	39	171	0.17%	34.9%	YNILGTNTIMDK	99.7%	88.9	25	75.1	16	0	0	1398.69	525	536
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	4	4	6	0.01%	6.9%	HLPSTEPDPHVVR	99.7%	40.9	25	40.9	0	3	0	1483.77	271	283
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	4	4	6	0.01%	6.9%	NCAVEFNFGQR	99.7%	64.2	25	64.2	1	0	0	1341.60	376	386
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	4	4	6	0.01%	6.9%	NYILDQTNVYGSAQR	99.7%	126	25	121	1	0	0	1741.85	501	515
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	4	4	6	0.01%	6.9%	VCFEMK	97.8%	31.3	25	14	1	0	0	813.36	257	262
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	4	4	6	0.01%	6.9%	WDVLIQQATQCLNR	99.7%	76.2	25	73.6	1	0	0	1744.88	477	490
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	6	8	15	0.02%	10.2%	DLLVQQASQCLSK	99.7%	102	25	99.4	2	0	0	1489.77	509	521
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	6	8	15	0.02%	10.2%	EGCTEVSLLR	99.7%	52.3	25	33.1	2	0	0	1163.57	306	315

Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	6	8	15	0.02%	10.2%	GLEEPEMDPK	99.7%	42.5	25	40.9	3	0	0	1144.52	497	506
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	6	8	15	0.02%	10.2%	NFILDQCNVYNSGQR	99.7%	93.6	25	93.6	2	0	0	1827.84	532	546
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	6	8	15	0.02%	10.2%	SGDETPGSEVPGDK	99.7%	45.5	25	45.5	2	0	0	1374.60	161	174
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	6	8	15	0.02%	10.2%	YNVLGAETVLNQMR	99.7%	87.3	25	80.3	4	0	0	1607.82	481	494
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	11	11	25	0.03%	39.9%	EESGKPGAHVTVK	99.7%	42.5	25	40.4	3	0	0	1338.70	100	112
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	11	11	25	0.03%	39.9%	GFGFVTFDDHDPVDK	99.7%	61.5	25	61.5	1	0	0	1695.77	154	168
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	11	11	25	0.03%	39.9%	GGGGNFGPGPGSNFR	99.7%	46.1	25	44.8	4	0	0	1377.63	214	228
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	11	11	25	0.03%	39.9%	GGNFGFGDSR	99.7%	44.7	25	35.1	3	0	0	1013.44	204	213
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	11	11	25	0.03%	39.9%	IDTIEIITDR	99.7%	92.2	25	84.6	1	0	0	1188.65	138	147
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	11	11	25	0.03%	39.9%	LFIGGLSFETTEESLR	99.7%	118	25	118	4	0	0	1798.92	23	38
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	11	11	25	0.03%	39.9%	LTDCVVMR	98.3%	32.5	25	28.2	1	0	0	993.49	47	54
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	11	11	25	0.03%	39.9%	NMGGPYGGGNYGPGGSGGSGGYGGR	99.7%	112	25	112	1	0	0	2205.90	326	350
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	11	11	25	0.03%	39.9%	NYYEQWGK	98.7%	33.6	25	33.6	3	0	0	1087.48	39	46
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	11	11	25	0.03%	39.9%	TLETVPLER	99.7%	44.1	25	44.1	3	0	0	1057.59	4	12
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	11	11	25	0.03%	39.9%	YHTINGHNAEVR	94.7%	21.6	25	21.6	0	1	0	1410.69	174	185
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	10	13	30	0.03%	28.4%	GFAFVQYVNER	99.7%	97.8	25	97.1	4	0	0	1329.66	51	61
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	10	13	30	0.03%	28.4%	KSDVEAIFSK	99.7%	65.7	25	53.3	3	0	0	1123.60	30	39
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	10	13	30	0.03%	28.4%	LKGDDLQAIK	99.2%	35.9	25	21.8	1	0	0	1100.63	188	197
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	10	13	30	0.03%	28.4%	MIAGQVLDINLAAEPK	99.7%	126	25	77.7	5	0	0	1698.91	74	89
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	10	13	30	0.03%	28.4%	MYSYPAR	98.9%	34.6	25	29	4	0	0	903.40	136	142
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	10	13	30	0.03%	28.4%	QKVDSLLENLEK	99.7%	47.2	25	37.2	2	2	0	1415.77	205	216
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	10	13	30	0.03%	28.4%	SDVEAIFSK	99.7%	54.4	25	47.9	2	0	0	995.50	31	39
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	10	13	30	0.03%	28.4%	VDSLLENLEK	99.7%	44.5	25	35.2	2	0	0	1159.62	207	216
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	10	13	30	0.03%	28.4%	VFIGNLNTLVVK	99.7%	90.1	25	90.1	4	0	0	1316.79	18	29
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	10	13	30	0.03%	28.4%	VPPPPPIAR	97.4%	30.6	25	29	1	0	0	943.57	143	151
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	12	13	19	0.02%	14.2%	ASGVEGADVVK	99.7%	55.4	25	36.7	2	0	0	1031.54	177	187
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	12	13	19	0.02%	14.2%	FLLSESGSGK	99.7%	41.4	25	31.7	2	0	0	1024.53	442	451
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	12	13	19	0.02%	14.2%	FLSQIESDR	99.7%	55.2	25	44.3	2	0	0	1094.55	786	794
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	12	13	19	0.02%	14.2%	GAAMVTAVAYR	99.7%	77.9	25	67.1	1	0	0	1125.57	452	462
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	12	13	19	0.02%	14.2%	GDFIALDLGGSSFR	99.7%	67.2	25	67.2	2	0	0	1454.73	78	91
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	12	13	19	0.02%	14.2%	IDEAILITWTK	99.7%	55.4	25	55.3	1	0	0	1302.73	163	173
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	12	13	19	0.02%	14.2%	LALLQVR	99.2%	36	25	17.4	2	0	0	812.54	795	801
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	12	13	19	0.02%	14.2%	LPVGFTFSFPCQQSK	97.8%	31.4	25	24.9	1	0	0	1742.86	148	162
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	12	13	19	0.02%	14.2%	LSDETLIDIMTR	99.7%	58.2	25	50.7	2	0	0	1406.72	31	42
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	12	13	19	0.02%	14.2%	MLPTFVR	95.3%	28.2	25	11.7	1	0	0	879.48	63	69
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	12	13	19	0.02%	14.2%	NILIDFTK	97.5%	30.8	25	29.2	1	0	0	963.55	756	763
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	12	13	19	0.02%	14.2%	SANLVAATLGAILNR	99.7%	80.1	25	71.3	1	1	0	1483.86	382	396
Hexokinase-2	HK2	HXK2_HUMAN	102.4	99.9%	2	2	3	0.00%	5.1%	GAALITAVACR	98.4%	32.7	25	21.3	1	0	0	1102.60	900	910
Hexokinase-2	HK2	HXK2_HUMAN	102.4	99.9%	2	2	3	0.00%	5.1%	GAAMVTAVAYR	99.7%	77.9	25	67.1	1	0	0	1125.57	452	462
Hexokinase-2	HK2	HXK2_HUMAN	102.4	99.9%	2	2	3	0.00%	5.1%	LSPELLNTGR	99.2%	35.9	25	28.9	2	0	0	1099.61	324	333
Hexokinase-2	HK2	HXK2_HUMAN	102.4	99.9%	2	2	3	0.00%	5.1%	MLPTFVR	95.3%	28.2	25	11.7	1	0	0	879.48	63	69
Hexokinase-2	HK2	HXK2_HUMAN	102.4	99.9%	2	2	3	0.00%	5.1%	NILIDFTK	97.5%	30.8	25	29.2	1	0	0	963.55	756	763
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	13	0.01%	16.2%	ISICSSDKR	99.7%	40.9	25	34.2	2	0	0	1065.54	405	413
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	13	0.01%	16.2%	LGCFNLTIK	99.7%	53	25	37	2	0	0	1065.58	271	279
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	13	0.01%	16.2%	LHISPSNMTNQNTNEYLEK	99.7%	34.8	25	34.8	0	1	0	2249.05	343	361
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	13	0.01%	16.2%	SIRPDNMSEYSK	99.7%	45.1	25	32.4	3	0	0	1426.66	78	89
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	13	0.01%	16.2%	VMTVSFHK	99.6%	39.1	25	30.1	2	0	0	948.50	193	200
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	13	0.01%	16.2%	YGEYFPGTGDLR	99.7%	66.3	25	65.2	2	0	0	1374.63	201	212
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	13	0.01%	16.2%	YYAVNYPLR	99.7%	46.1	25	39.7	1	0	0	1158.59	221	229
Histone deacetylase 2	HDAC2	HDAC2_HUMAN	55.4	99.9%	2	3	4	0.00%	10.2%	LGCFNLTVK	99.7%	55.4	25	46.7	2	0	0	1051.56	272	280
Histone deacetylase 2	HDAC2	HDAC2_HUMAN	55.4	99.9%	2	3	4	0.00%	10.2%	SIRPDNMSEYSK	99.7%	45.1	25	32.4	3	0	0	1426.66	79	90

Histone deacetylase 2	HDAC2	HDAC2_HUMAN	55.4	99.9%	2	3	4	0.00%	10.2%	VMTVSFHK	99.6%	39.1	25	30.1	2	0	0	948.50	194	201
Histone deacetylase 2	HDAC2	HDAC2_HUMAN	55.4	99.9%	2	3	4	0.00%	10.2%	YGEYFPGTGDLR	99.7%	66.3	25	65.2	2	0	0	1374.63	202	213
Histone deacetylase 2	HDAC2	HDAC2_HUMAN	55.4	99.9%	2	3	4	0.00%	10.2%	YYAVNFPMR	99.7%	48.1	25	48.1	2	0	0	1160.56	222	230
Histone deacetylase 8	HDAC8	HDAC8_HUMAN	41.8	99.8%	2	2	3	0.00%	7.4%	FSPGFFPGTGDVSDVGLGK	99.7%	52.4	25	51.6	2	0	0	1883.92	203	221
Histone deacetylase 8	HDAC8	HDAC8_HUMAN	41.8	99.8%	2	2	3	0.00%	7.4%	IQQILNYIK	97.5%	30.8	25	23.4	1	0	0	1132.67	362	370
Histone deacetylase complex subunit SAP18	SAP18	SAP18_HUMAN	17.6	100.0%	3	3	9	0.01%	15.7%	GTDDSMTLQSQK	99.6%	39	25	38.5	1	0	0	1326.58	115	126
Histone deacetylase complex subunit SAP18	SAP18	SAP18_HUMAN	17.6	100.0%	3	3	9	0.01%	15.7%	KGTDDSMTLQSQK	99.7%	76.8	25	62.6	4	0	0	1438.68	114	126
Histone deacetylase complex subunit SAP18	SAP18	SAP18_HUMAN	17.6	100.0%	3	3	9	0.01%	15.7%	VKEIGSTMSGR	99.4%	37	25	29.2	4	0	0	1164.60	103	113
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	7	9	133	0.13%	17.4%	ALAAAGYDVEK	99.7%	76.9	25	64.4	35	0	0	1107.57	65	75
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	7	9	133	0.13%	17.4%	ALAAAGYDVEKNNSR	99.7%	96.2	25	96.2	10	2	0	1578.79	65	79
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	7	9	133	0.13%	17.4%	ASGPPVSELITK	99.7%	72.6	25	63.1	26	0	0	1198.67	35	46
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	7	9	133	0.13%	17.4%	KALAAAGYDVEK	99.7%	76.8	25	68.7	4	0	0	1235.66	64	75
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	7	9	133	0.13%	17.4%	KASGPPVSELITK	99.7%	92.1	25	88.4	17	4	0	1326.76	34	46
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	7	9	133	0.13%	17.4%	SGVSLAALK	99.7%	68.2	25	41.5	2	0	0	845.51	55	63
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	7	9	133	0.13%	17.4%	SGVSLAALKK	99.7%	76.9	25	74.2	33	0	0	973.60	55	64
Histone H1.5	HIST1H1B	H15_HUMAN	22.6	99.8%	2	2	3	0.00%	10.2%	ALAAGGYDVEK	98.8%	34.1	25	29.2	2	0	0	1093.55	68	78
Histone H1.5	HIST1H1B	H15_HUMAN	22.6	99.8%	2	2	3	0.00%	10.2%	ATGPPVSELITK	97.0%	30	25	16.4	1	0	0	1212.68	38	49
Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	4	4	21	0.02%	17.8%	ALVQNDTLLQVK	99.7%	77.8	25	68.6	7	0	0	1341.77	95	106
Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	4	4	21	0.02%	17.8%	GAPAAATAPAPTAHK	99.7%	72.5	25	72.5	6	0	0	1331.71	129	143
Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	4	4	21	0.02%	17.8%	RGAPAAATAPAPTAHK	98.4%	25.9	25	25.9	0	1	0	1487.81	128	143
Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	4	4	21	0.02%	17.8%	YSQLVVETIR	99.7%	84.4	25	65.7	7	0	0	1207.67	48	57
Histone H2A type 1-B/E	HIST1H2AB	H2A1B_HUMAN	14.1	100.0%	3	3	16	0.02%	26.9%	AGLQFPVGR	99.7%	86.3	25	70	11	0	0	944.53	22	30
Histone H2A type 1-B/E	HIST1H2AB	H2A1B_HUMAN	14.1	100.0%	3	3	16	0.02%	26.9%	HLQLAIR	98.0%	31.8	25	21.8	2	0	0	850.53	83	89
Histone H2A type 1-B/E	HIST1H2AB	H2A1B_HUMAN	14.1	100.0%	3	3	16	0.02%	26.9%	VTIAQGGVLPNIQAVLLPK	99.7%	52	25	52	3	0	0	1931.17	101	119
Histone H2B type 1-C/E/F/G/I	HIST1H2BC	H2B1C_HUMAN	13.9	100.0%	4	4	16	0.02%	27.0%	AMGIMNSFVNDIFER	99.7%	77	25	77	6	0	0	1775.81	59	73
Histone H2B type 1-C/E/F/G/I	HIST1H2BC	H2B1C_HUMAN	13.9	100.0%	4	4	16	0.02%	27.0%	ESYSVYVYK	99.7%	42	25	42	1	0	0	1137.55	36	44
Histone H2B type 1-C/E/F/G/I	HIST1H2BC	H2B1C_HUMAN	13.9	100.0%	4	4	16	0.02%	27.0%	KESYSVYVYK	99.7%	59.9	25	50.7	1	0	0	1265.64	35	44
Histone H2B type 1-C/E/F/G/I	HIST1H2BC	H2B1C_HUMAN	13.9	100.0%	4	4	16	0.02%	27.0%	LLLPGELAK	99.7%	42.3	25	17.8	8	0	0	953.60	101	109
Histone H3.1t	HIST3H3	H31T_HUMAN	15.5	100.0%	2	2	4	0.00%	13.2%	EIAQDFKTDLR	99.7%	40.5	25	30.2	2	0	0	1335.69	74	84
Histone H3.1t	HIST3H3	H31T_HUMAN	15.5	100.0%	2	2	4	0.00%	13.2%	STELLIR	99.6%	39.3	25	28.6	2	0	0	831.49	58	64
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	5	7	25	0.03%	50.5%	DAVTYTEHAK	99.7%	53.8	25	53.6	5	0	0	1134.54	69	78
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	5	7	25	0.03%	50.5%	DNIQGITKPAIR	99.7%	59.8	25	41.5	6	2	0	1325.75	25	36
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	5	7	25	0.03%	50.5%	ISGLIYEETR	99.7%	63.8	25	54.7	4	0	0	1180.62	47	56
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	5	7	25	0.03%	50.5%	TVTAMDVVYALK	99.7%	40.1	25	33.6	4	0	0	1326.70	81	92
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	5	7	25	0.03%	50.5%	VFLENVIR	99.7%	45.8	25	32.8	4	0	0	989.58	61	68
Histone-binding protein RBBP4	RBBP4	RBBP4_HUMAN	47.7	100.0%	2	2	3	0.00%	3.5%	LMIWDTR	99.4%	37	25	28.3	2	0	0	934.48	252	258
Histone-binding protein RBBP4	RBBP4	RBBP4_HUMAN	47.7	100.0%	2	2	3	0.00%	3.5%	TVALWDLR	99.7%	59.7	25	38.8	1	0	0	973.55	297	304
Hornerin	HRNR	HORN_HUMAN	282.4	100.0%	4	4	11	0.01%	2.7%	GEQHGSSSGSSSSYGQHGSGSR	97.1%	23.7	25	23.7	0	1	0	2122.88	1910	1931
Hornerin	HRNR	HORN_HUMAN	282.4	100.0%	4	4	11	0.01%	2.7%	GPYESGSGHSSGLGHQESR	99.6%	31.2	25	31.2	0	1	0	1928.85	572	590
Hornerin	HRNR	HORN_HUMAN	282.4	100.0%	4	4	11	0.01%	2.7%	GPYESGSGHSSGLGHR	99.7%	33.1	25	33.1	0	7	0	1584.72	1038	1053
Hornerin	HRNR	HORN_HUMAN	282.4	100.0%	4	4	11	0.01%	2.7%	QSLGHGQHGSGSGQSPSPSR	99.7%	32.9	25	30.9	0	2	0	1947.90	992	1011
Hydroxyacylglutathione hydrolase, mitochondrial	HAGH	GLO2_HUMAN	33.8	99.8%	2	2	2	0.00%	5.8%	ALLEVLGR	96.7%	29.6	25	21.6	1	0	0	870.54	203	210
Hydroxyacylglutathione hydrolase, mitochondrial	HAGH	GLO2_HUMAN	33.8	99.8%	2	2	2	0.00%	5.8%	HVEPGNAAIR	98.7%	33.7	25	33.7	1	0	0	1063.56	233	242
Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	HMGCL_HUMAN	34.4	100.0%	4	4	8	0.01%	16.0%	AAQSANISVR	99.7%	49.2	25	41.8	2	0	0	1016.55	156	165
Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	HMGCL_HUMAN	34.4	100.0%	4	4	8	0.01%	16.0%	EVVIFGAASELFTK	99.7%	95.1	25	95.1	2	0	0	1510.82	123	136
Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	HMGCL_HUMAN	34.4	100.0%	4	4	8	0.01%	16.0%	FPGINYPVLTPNLK	99.7%	54.7	25	54.7	2	0	0	1572.88	98	111
Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	HMGCL_HUMAN	34.4	100.0%	4	4	8	0.01%	16.0%	LLEAGNFICQALNR	99.7%	89.9	25	81.3	2	0	0	1618.84	299	312
Hydroxysteroid dehydrogenase-like protein 2	HSDL2	HSDL2_HUMAN	45.4	100.0%	3	3	7	0.01%	9.6%	LAGCTVFITGASR	99.7%	107	25	87.5	2	0	0	1352.70	8	20
Hydroxysteroid dehydrogenase-like protein 2	HSDL2	HSDL2_HUMAN	45.4	100.0%	3	3	7	0.01%	9.6%	LLGTIYTAAEEIEAVGGK	99.7%	105	25	105	3	0	0	1834.98	50	67
Hydroxysteroid dehydrogenase-like protein 2	HSDL2	HSDL2_HUMAN	45.4	100.0%	3	3	7	0.01%	9.6%	SGAVEETFR	99.7%	51.8	25	45.7	2	0	0	995.48	307	315
Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	HPRT_HUMAN	24.6	100.0%	4	5	9	0.01%	21.1%	SYCNDQSTGDIK	99.7%	65.3	25	65.3	1	0	0	1387.58	104	115

Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	HPRT_HUMAN	24.6	100.0%	4	5	9	0.01%	21.1%	TMQTLLSLVR	99.7%	71.1	25	47.3	4	0	0	1161.67	142	151
Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	HPRT_HUMAN	24.6	100.0%	4	5	9	0.01%	21.1%	VFIPHGLIMDR	99.7%	43.1	25	40.1	0	2	0	1297.71	35	45
Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	HPRT_HUMAN	24.6	100.0%	4	5	9	0.01%	21.1%	VIGGDDLSTLTGK	99.7%	93.8	25	88.1	2	0	0	1275.68	116	128
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	19	34	0.03%	21.9%	AANSLEAFIFETQDK	99.7%	70.8	25	58	2	0	0	1683.82	739	753
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	19	34	0.03%	21.9%	AEAGPEGVAPAPEGEK	99.7%	72.4	25	67.6	2	0	0	1508.72	670	685
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	19	34	0.03%	21.9%	AEAGPEGVAPAPEGEKK	99.7%	56.4	25	50.1	2	1	0	1636.82	670	686
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	19	34	0.03%	21.9%	DAVITVPVFFNQAER	99.7%	42	25	40	2	0	0	1705.89	171	185
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	19	34	0.03%	21.9%	DAVVYPILVEFTR	99.7%	72.7	25	72.7	2	0	0	1521.83	439	451
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	19	34	0.03%	21.9%	EAGMQPQLQIR	99.7%	42.2	25	36	2	0	0	1270.66	252	262
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	19	34	0.03%	21.9%	FFGDSAASMAIK	99.7%	77.1	25	72.4	2	0	0	1244.60	80	91
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	19	34	0.03%	21.9%	LAGLFNEQR	99.7%	63.7	25	53.2	2	0	0	1047.56	283	291
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	19	34	0.03%	21.9%	LGNTISSLFGGGTTPDAK	99.7%	99.5	25	99.3	2	0	0	1735.89	577	594
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	19	34	0.03%	21.9%	LPATEKPVLLSK	96.7%	23.2	25	21.2	0	1	0	1295.79	878	889
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	19	34	0.03%	21.9%	NINADEAAAMGAVYQAAALSK	99.7%	77.9	25	77.9	2	0	0	2079.02	408	428
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	19	34	0.03%	21.9%	QADNPHVALYQAR	99.0%	35.1	25	35.1	1	0	0	1482.74	107	119
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	19	34	0.03%	21.9%	TLGGLEMELR	99.7%	70.9	25	66.8	4	0	0	1118.59	269	278
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	19	34	0.03%	21.9%	VEFEELCADLFER	99.7%	83.4	25	81	2	0	0	1656.76	346	358
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	19	34	0.03%	21.9%	VESVFETLVEDSAEEESTLTK	99.7%	69.6	25	69.6	2	0	0	2342.11	556	576
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	19	34	0.03%	21.9%	VLQLINDNTATALSYGVFR	99.7%	138	25	138	2	1	0	2095.12	199	217
Ig kappa chain V-I region Lay	IGKV1-13	KV113_HUMAN	11.8	99.8%	2	3	9	0.01%	25.0%	DIQMTQSPSSLSVSVGDR	99.7%	62.4	25	62.4	5	0	0	1922.91	1	18
Ig kappa chain V-I region Lay	IGKV1-13	KV113_HUMAN	11.8	99.8%	2	3	9	0.01%	25.0%	LLIYGASTR	99.7%	67	25	17.2	4	0	0	993.57	46	54
Ig kappa chain V-II region RPMI 6410	IGKV2-30	KV206_HUMAN	14.7	99.8%	2	3	434	0.44%	12.0%	FSGSGSGTDFTLK	99.7%	103	25	0	410	0	0	1303.62	87	99
Ig kappa chain V-II region RPMI 6410	IGKV2-30	KV206_HUMAN	14.7	99.8%	2	3	434	0.44%	12.0%	FSGSGSGTDFTLKISR	99.7%	93.2	25	0	11	13	0	1659.83	87	102
Ig kappa chain V-IV region (Fragment)	IGKV4-1	KV401_HUMAN	13.4	99.8%	2	2	22	0.02%	19.8%	LLIYWASTR	99.7%	64.3	25	54.3	21	0	0	1122.63	72	80
Ig kappa chain V-IV region (Fragment)	IGKV4-1	KV401_HUMAN	13.4	99.8%	2	2	22	0.02%	19.8%	NYLAWYQQKPGQPPK	99.7%	57.5	25	51	1	0	0	1817.93	57	71
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	4	4	6	0.01%	12.1%	FVSFLGR	98.7%	33.5	25	23.9	1	0	0	825.46	124	130
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	4	4	6	0.01%	12.1%	LLGASELPIVTPALR	99.7%	63.3	25	63.3	2	0	0	1549.93	301	315
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	4	4	6	0.01%	12.1%	NKNPAPPIDAVEQILPTLVR	99.7%	53	25	53	1	0	0	2185.23	239	258
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	4	4	6	0.01%	12.1%	QDQIQQVVNHGLVPFLVSVLSK	99.7%	71.1	25	70	0	2	0	2448.36	367	388
Importin subunit alpha-4	KPNA3	IMA4_HUMAN	57.8	99.8%	2	2	3	0.00%	4.2%	DSQVVQVVLDGLK	99.7%	64.7	25	53.5	2	0	0	1399.78	424	436
Importin subunit alpha-4	KPNA3	IMA4_HUMAN	57.8	99.8%	2	2	3	0.00%	4.2%	SGILPILVK	96.5%	29.4	25	29.4	1	0	0	939.62	113	121
Importin subunit alpha-5	KPNA1	IMA5_HUMAN	60.2	100.0%	4	4	7	0.01%	10.8%	EAAWAITNATSGGSAEQIK	99.7%	99.7	25	91	1	0	0	1904.93	399	417
Importin subunit alpha-5	KPNA1	IMA5_HUMAN	60.2	100.0%	4	4	7	0.01%	10.8%	EACWTISNITAGNR	99.7%	64.3	25	64.3	2	0	0	1592.75	357	370
Importin subunit alpha-5	KPNA1	IMA5_HUMAN	60.2	100.0%	4	4	7	0.01%	10.8%	IVQVALNGLENILR	99.7%	62	25	58.1	2	0	0	1551.92	439	452
Importin subunit alpha-5	KPNA1	IMA5_HUMAN	60.2	100.0%	4	4	7	0.01%	10.8%	NAVWALSNLCR	99.7%	49.8	25	44.5	2	0	0	1303.66	231	241
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	18	21	42	0.04%	26.7%	AAVENLPTFLVELSR	99.7%	117	25	114	4	0	0	1658.91	28	42
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	18	21	42	0.04%	26.7%	ANFDKESER	99.7%	41.8	25	35.1	2	0	0	1095.51	207	215
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	18	21	42	0.04%	26.7%	DTAAWTVGR	99.7%	56	25	44.3	1	0	0	976.48	426	434
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	18	21	42	0.04%	26.7%	ESCLEAYTGIVQGLK	99.7%	95.9	25	88.1	2	0	0	1667.83	763	777
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	18	21	42	0.04%	26.7%	GALQYLVPILTQTLTK	99.7%	53.3	25	53.3	2	0	0	1759.04	317	332
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	18	21	42	0.04%	26.7%	LAATNALLNSLEFTK	99.7%	105	25	100	3	0	0	1605.88	192	206
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	18	21	42	0.04%	26.7%	LLETTDRPDGHQNNLR	99.7%	45.4	25	42	0	2	0	1878.94	510	525
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	18	21	42	0.04%	26.7%	LQQVLQMESHIQSTSDR	99.7%	37.2	25	30.8	0	1	0	2015.98	558	574
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	18	21	42	0.04%	26.7%	SDYDMVDYLNELR	99.7%	82.4	25	82.4	2	0	0	1632.72	750	762
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	18	21	42	0.04%	26.7%	SNEILTAIIQGMR	99.7%	86.2	25	80.7	4	0	0	1445.78	170	182
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	18	21	42	0.04%	26.7%	SSAYESLMEIVK	99.7%	90	25	81.5	4	0	0	1356.67	526	537
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	18	21	42	0.04%	26.7%	TTLVIMER	99.7%	52.7	25	46.9	3	0	0	962.53	550	557
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	18	21	42	0.04%	26.7%	TVSPDRLELEAAQK	99.7%	57.2	25	48.5	2	0	0	1556.83	10	23
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	18	21	42	0.04%	26.7%	VAAGLQIK	99.7%	46.2	25	33.6	2	0	0	799.50	55	62
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	18	21	42	0.04%	26.7%	VAALQNLVK	99.7%	44.8	25	35.7	2	0	0	955.59	235	243
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	18	21	42	0.04%	26.7%	VLANPGNSQVAR	99.7%	83.4	25	73.4	2	0	0	1225.66	43	54

Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	18	21	42	0.04%	26.7%	YLEVVLNTLQQASQAQVDK	99.7%	113	25	112	2	0	0	2147.13	731	749
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	18	21	42	0.04%	26.7%	YMEAFKPFLGIGLK	99.7%	46.7	25	39.1	2	0	0	1613.88	646	659
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	5	5	8	0.01%	5.7%	ALLTFYHVTK	99.7%	47	25	35.9	2	0	0	1192.67	147	156
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	5	5	8	0.01%	5.7%	LTVDDFEFR	99.7%	50.7	25	49.6	2	0	0	1141.55	541	549
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	5	5	8	0.01%	5.7%	NFEDSSPETLEAHK	99.7%	40.4	25	31.9	1	0	0	1603.72	338	351
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	5	5	8	0.01%	5.7%	SIGTDNVCR	99.7%	50.2	25	40.8	2	0	0	1021.47	255	263
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	5	5	8	0.01%	5.7%	VTEDEEPPTEQDKR	94.7%	27.6	25	27.6	1	0	0	1672.77	905	918
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	24	50	0.05%	22.6%	ACYALENFVENLGPK	99.7%	93.1	25	93.1	2	0	0	1724.83	458	472
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	24	50	0.05%	22.6%	AQELQAVLGLS	99.7%	43.9	25	36.5	1	0	0	1128.63	1071	1081
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	24	50	0.05%	22.6%	ATEQLQIVLR	99.7%	55.8	25	35	2	0	0	1170.68	24	33
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	24	50	0.05%	22.6%	DNICGALAR	99.7%	54.3	25	40.7	2	0	0	989.48	959	967
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	24	50	0.05%	22.6%	EDLQPVQIQSLETLGVLAR	99.7%	46.9	25	46.9	1	0	0	2109.16	535	553
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	24	50	0.05%	22.6%	EVMPLLLAYLK	99.7%	69.2	25	55.8	5	0	0	1289.75	435	445
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	24	50	0.05%	22.6%	GLEDPSQVVR	99.7%	51.1	25	29	2	0	0	1099.57	402	411
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	24	50	0.05%	22.6%	ICSLILADNK	99.7%	50.8	25	38.1	1	0	0	1146.62	1026	1035
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	24	50	0.05%	22.6%	ILCCLTFLVK	99.7%	45.2	25	39.2	2	0	0	1266.70	267	276
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	24	50	0.05%	22.6%	LAELCGVLK	99.7%	56.8	25	45.1	4	0	0	1002.57	793	801
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	24	50	0.05%	22.6%	LIMAMQTLIPIDEAK	99.7%	70.5	25	67.6	7	0	0	1686.92	206	220
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	24	50	0.05%	22.6%	LLECPHLNVR	99.1%	35.3	25	30.7	2	0	0	1250.67	705	714
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	24	50	0.05%	22.6%	LLMASPTR	99.7%	44.5	25	32.3	2	0	0	904.49	968	975
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	24	50	0.05%	22.6%	LLNETLGEVGSPGLLFYSLR	99.7%	74.9	25	74.9	1	0	0	2178.18	163	182
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	24	50	0.05%	22.6%	LLPVLLSTAQEADPEVR	99.7%	81.6	25	80.8	2	0	0	1851.02	900	916
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	24	50	0.05%	22.6%	QFAAVLTR	99.7%	47.8	25	30.4	2	0	0	905.52	55	62
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	24	50	0.05%	22.6%	SCGTLTLKPPGR	98.0%	31.7	25	28	1	0	0	1286.69	781	792
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	24	50	0.05%	22.6%	SLILTALQR	99.7%	59.9	25	45.3	3	0	0	1014.63	82	90
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	24	50	0.05%	22.6%	TLTTMAPYLSTEDVPLAR	99.7%	71.5	25	71	2	0	0	1979.02	183	200
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	24	50	0.05%	22.6%	VRDNICGALAR	99.7%	43.9	25	31.6	2	0	0	1244.65	957	967
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	24	50	0.05%	22.6%	VVPSYMQAVNR	99.7%	61.2	25	56.9	4	0	0	1279.65	751	761
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	23	29	80	0.08%	27.5%	AKLEEHFK	99.7%	48.6	25	24.3	1	0	0	1001.54	799	806
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	23	29	80	0.08%	27.5%	ATAAFILANEHNVALFK	99.7%	84.3	25	81.4	2	0	0	1829.99	196	212
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	23	29	80	0.08%	27.5%	EFQQYLPVVMGPLMK	99.7%	54.8	25	47.9	4	0	0	1811.91	618	632
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	23	29	80	0.08%	27.5%	EGFVEYTEQVVK	99.7%	67.8	25	61.5	2	0	0	1427.71	694	705
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	23	29	80	0.08%	27.5%	FLFDSVSSQNVGLR	99.7%	97.1	25	93.6	5	0	0	1568.81	135	148
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	23	29	80	0.08%	27.5%	FMQDASDVMQLLLK	99.7%	143	25	134	7	0	0	1638.82	573	586
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	23	29	80	0.08%	27.5%	FVPYYDLFMPSLK	99.7%	69.9	25	0	7	0	0	1635.81	527	539
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	23	29	80	0.08%	27.5%	HIVENAVQK	99.7%	42.6	25	39	2	0	0	1037.57	540	548
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	23	29	80	0.08%	27.5%	LCGDTSLNNMQR	99.7%	59.9	25	54.8	1	0	0	1424.63	265	276
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	23	29	80	0.08%	27.5%	LQELIQK	99.7%	46.1	25	14.8	4	0	0	871.52	497	503
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	23	29	80	0.08%	27.5%	LVLEQVVTSIASVADTAEEK	99.7%	91.6	25	89.3	2	3	0	2102.12	507	526
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	23	29	80	0.08%	27.5%	QAEETYENIPGQSK	99.7%	77.7	25	71.9	2	0	0	1593.74	28	41
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	23	29	80	0.08%	27.5%	QMAAVLLR	98.3%	32.4	25	13.4	2	0	0	901.53	60	67
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	23	29	80	0.08%	27.5%	SELLMIIQMETQSSMR	99.7%	80.8	25	63.8	1	0	0	1928.91	91	106
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	23	29	80	0.08%	27.5%	SLLIPYLDNLVK	99.7%	48.1	25	31.1	3	0	0	1387.82	476	487
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	23	29	80	0.08%	27.5%	SLVEIADTVPK	99.7%	96	25	81.8	8	0	0	1171.66	239	249
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	23	29	80	0.08%	27.5%	STACQMLVCYAK	99.7%	67.3	25	60.6	2	0	0	1431.64	679	690
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	23	29	80	0.08%	27.5%	TIECISLIGLAVGK	99.7%	102	25	101	7	0	0	1473.83	557	570
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	23	29	80	0.08%	27.5%	VAAAESMPLLLECAR	99.7%	85.8	25	76.5	2	0	0	1630.83	721	735
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	23	29	80	0.08%	27.5%	VCDIAAELAR	99.7%	69.5	25	50.9	5	0	0	1117.57	109	118
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	23	29	80	0.08%	27.5%	VIAALLQTMEDQGNQR	99.7%	131	25	127	4	0	0	1786.91	442	457
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	23	29	80	0.08%	27.5%	VSDILHSIFSSYK	99.7%	64.4	25	60.8	2	1	0	1495.78	842	854
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	23	29	80	0.08%	27.5%	YAACNAVGQMATDFAPGFQK	99.7%	56.7	25	44.9	1	0	0	2146.97	417	436

Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	61	0.06%	21.8%	AFAVGVQQVLLK	99.7%	85.9	25	72.5	7	0	0	1272.77	295	306
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	61	0.06%	21.8%	AIFQTIQNR	99.7%	54.2	25	45.9	6	0	0	1090.60	964	972
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	61	0.06%	21.8%	DGALHMIGSLAEILLK	99.5%	38.4	25	38.4	1	0	0	1696.93	430	445
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	61	0.06%	21.8%	ENIVEAIIHSPELIR	99.7%	75.3	25	65.5	3	2	0	1732.96	93	107
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	61	0.06%	21.8%	ETENDDLTNVIQK	99.7%	88.2	25	80.9	2	0	0	1518.73	552	564
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	61	0.06%	21.8%	EYNEFAEVFLK	99.7%	66.8	25	66.8	7	0	0	1388.67	284	294
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	61	0.06%	21.8%	FIQLLSDQSDQSVLIQK	99.7%	125	25	120	2	0	0	1962.05	185	201
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	61	0.06%	21.8%	GIDQCIPLFVEAALER	99.7%	83	25	79.2	2	0	0	1830.94	753	768
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	61	0.06%	21.8%	GTMDPALR	99.7%	51.6	25	35.5	3	0	0	876.42	12	19
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	61	0.06%	21.8%	KVLTGVAGEDAECHAAK	96.4%	22.9	25	22.9	0	1	0	1755.87	724	740
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	61	0.06%	21.8%	LLEVIILQCK	99.7%	72	25	72	6	0	0	1228.73	741	750
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	61	0.06%	21.8%	QAGVIYLK	98.7%	33.6	25	14.2	1	0	0	891.53	54	61
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	61	0.06%	21.8%	QLQDIATLADQR	99.7%	61.2	25	54.5	2	0	0	1371.72	991	1002
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	61	0.06%	21.8%	SDQNLQTALELTR	99.7%	74.4	25	62.4	3	0	0	1488.77	490	502
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	61	0.06%	21.8%	SPLVAAMQHFLPVLK	99.7%	76.6	25	76.6	2	0	0	1650.94	168	182
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	61	0.06%	21.8%	TMGFCYQILTEPNADPR	99.7%	68.4	25	68.4	2	0	0	2012.92	411	427
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	61	0.06%	21.8%	VLTGVAGEDAECHAAK	99.7%	92.5	25	92.5	3	2	0	1627.77	725	740
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	61	0.06%	21.8%	WALHILAR	99.7%	43.7	25	38.8	2	0	0	979.58	263	270
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	61	0.06%	21.8%	YGSPGNVSK	98.9%	34.2	25	26.2	2	0	0	908.45	275	283
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	3	3	4	0.00%	4.2%	EYFEFSEFFLK	99.7%	47.8	25	47.8	1	0	0	1485.69	285	295
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	3	3	4	0.00%	4.2%	IINFAPSLLR	99.7%	55.3	25	48.1	2	0	0	1143.69	32	41
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	3	3	4	0.00%	4.2%	LLEVIILQCK	99.7%	72	25	72	6	0	0	1228.73	741	750
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	3	3	4	0.00%	4.2%	TYAVGIQQVLLK	99.7%	81.2	25	79.5	1	0	0	1332.79	296	307
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	16	31	0.03%	15.3%	AIWGYCDQLK	99.7%	50.7	25	48.2	2	0	0	1253.60	540	549
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	16	31	0.03%	15.3%	EALVDTLTGILSPVQEVR	99.7%	62.1	25	58	2	0	0	1940.07	23	40
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	16	31	0.03%	15.3%	EVTDTQMPLVAPVILPEMYK	99.7%	57.6	25	57.6	4	0	0	2274.18	176	195
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	16	31	0.03%	15.3%	FRPPETTER	96.6%	29.5	25	14	1	0	0	1132.57	96	104
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	16	31	0.03%	15.3%	ICPFTIAIFLK	97.3%	30.5	25	29.9	1	0	0	1322.75	605	615
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	16	31	0.03%	15.3%	IFTMAEVYGIR	99.7%	69	25	63.5	4	0	0	1299.68	196	206
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	16	31	0.03%	15.3%	LIINELSNVMEANAAR	99.7%	116	25	116	5	0	0	1773.92	920	935
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	16	31	0.03%	15.3%	LLQHGINADDKR	99.7%	51.9	25	45.7	2	0	0	1379.74	866	877
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	16	31	0.03%	15.3%	QLASVILK	99.7%	50.1	25	23.5	2	0	0	871.56	75	82
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	16	31	0.03%	15.3%	TSEFTAAFVGR	99.7%	99.3	25	81.8	2	0	0	1185.59	755	765
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	16	31	0.03%	15.3%	VSSVALCK	97.7%	31.1	25	11.5	2	0	0	863.47	858	865
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	16	31	0.03%	15.3%	WTNIPLLVK	98.0%	31.8	25	17	1	0	0	1083.66	908	916
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	16	31	0.03%	15.3%	YSNDPVVASLAQDIFK	99.7%	78.8	25	70.9	3	0	0	1766.90	616	631
Inactive hydroxysteroid dehydrogenase-like protein 1	HSDL1	HSDL1_HUMAN	37.0	100.0%	4	4	7	0.01%	13.6%	AYAEELASR	99.7%	54.2	25	43.4	2	0	0	1009.49	82	90
Inactive hydroxysteroid dehydrogenase-like protein 1	HSDL1	HSDL1_HUMAN	37.0	100.0%	4	4	7	0.01%	13.6%	GLNIILISR	99.7%	49.1	25	44.5	2	0	0	998.64	91	99
Inactive hydroxysteroid dehydrogenase-like protein 1	HSDL1	HSDL1_HUMAN	37.0	100.0%	4	4	7	0.01%	13.6%	VYAHHAVSTLGISK	96.6%	23.1	25	23.1	0	1	0	1482.81	274	287
Inactive hydroxysteroid dehydrogenase-like protein 1	HSDL1	HSDL1_HUMAN	37.0	100.0%	4	4	7	0.01%	13.6%	WAVVSGATDGIGK	99.7%	46.2	25	40.4	2	0	0	1260.66	69	81
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	5	5	8	0.01%	31.4%	ALLELQEYFGSLAA	99.5%	37.9	25	37.7	1	0	0	1524.79	181	194
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	5	5	8	0.01%	31.4%	IDLPEYQGEPDEISIQK	99.7%	69.7	25	66.9	2	0	0	1973.97	40	56
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	5	5	8	0.01%	31.4%	IVFVTGNAK	99.7%	48	25	34.9	2	0	0	948.55	10	18
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	5	5	8	0.01%	31.4%	KIVFVTGNAK	98.5%	33	25	33	1	0	0	1076.65	9	18
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	5	5	8	0.01%	31.4%	SAYALCTFALSTGDPSQPVR	99.7%	68.7	25	68.7	2	0	0	2141.03	111	130
Inosine-5'-monophosphate dehydrogenase 2	IMPDH2	IMDH2_HUMAN	55.8	100.0%	5	5	8	0.01%	12.1%	EANEILQR	99.5%	38.4	25	24.1	1	0	0	972.51	196	203
Inosine-5'-monophosphate dehydrogenase 2	IMPDH2	IMDH2_HUMAN	55.8	100.0%	5	5	8	0.01%	12.1%	LPIVNEDDELVAIIAR	99.7%	101	25	101	2	0	0	1779.99	209	224
Inosine-5'-monophosphate dehydrogenase 2	IMPDH2	IMDH2_HUMAN	55.8	100.0%	5	5	8	0.01%	12.1%	TSSAQVEGGVHSLHSYEK	99.7%	34.3	25	34.3	0	2	0	1915.91	494	511
Inosine-5'-monophosphate dehydrogenase 2	IMPDH2	IMDH2_HUMAN	55.8	100.0%	5	5	8	0.01%	12.1%	VAQGVSGAVQDK	99.7%	73.3	25	55.9	2	0	0	1158.61	439	450
Inosine-5'-monophosphate dehydrogenase 2	IMPDH2	IMDH2_HUMAN	55.8	100.0%	5	5	8	0.01%	12.1%	VRDVFEAK	94.7%	27.7	25	16	1	0	0	963.53	127	134
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	21	28	74	0.07%	43.5%	AIETFSGK	99.6%	39.5	25	34.8	2	0	0	852.45	53	60

Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	21	28	74	0.07%	43.5%	AISVHSTPEGCSSACK	99.7%	65.3	25	65.3	3	2	0	1690.75	243	258
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	21	28	74	0.07%	43.5%	DQTPDENDQVIVK	99.7%	85.4	25	78	4	0	0	1500.72	526	538
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	21	28	74	0.07%	43.5%	EEVKLETHIR	99.7%	49.2	25	40	2	0	0	1253.68	484	493
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	21	28	74	0.07%	43.5%	IIGHFYASQMAQR	99.7%	49.5	25	49.5	4	4	0	1521.76	539	551
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	21	28	74	0.07%	43.5%	ILAHNNFVGR	99.7%	53.2	25	46.8	4	0	0	1140.63	281	290
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	21	28	74	0.07%	43.5%	IRDILAQVK	99.7%	45.4	25	24.8	2	0	0	1055.66	553	561
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	21	28	74	0.07%	43.5%	ISYSGQFLVK	99.7%	53.3	25	44.4	1	0	0	1141.63	27	36
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	21	28	74	0.07%	43.5%	ITISSLQDLTLYNPER	99.7%	86.5	25	85.4	3	0	0	1862.99	310	325
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	21	28	74	0.07%	43.5%	LKEENFFGPK	99.7%	50.3	25	50.3	2	0	0	1208.63	474	483
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	21	28	74	0.07%	43.5%	LLVPTQYVGAIIGK	99.7%	94.5	25	93.5	6	0	0	1471.89	200	213
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	21	28	74	0.07%	43.5%	LNGHQLENHALK	99.6%	31.7	25	30.3	0	2	0	1373.73	139	150
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	21	28	74	0.07%	43.5%	LYIGNLNESVTPADLEK	99.7%	102	25	89.2	2	0	0	1875.97	4	20
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	21	28	74	0.07%	43.5%	MILEIMHK	99.7%	41.8	25	29.7	2	0	0	1014.55	259	266
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	21	28	74	0.07%	43.5%	MVIITGPPEAQFK	99.7%	83.8	25	72.4	8	0	0	1430.77	453	465
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	21	28	74	0.07%	43.5%	QGSPVAAGAPAK	99.7%	60.2	25	57.2	4	0	0	1053.57	179	190
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	21	28	74	0.07%	43.5%	QQQVDIPLR	99.7%	43.6	25	29.6	4	0	0	1096.61	191	199
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	21	28	74	0.07%	43.5%	RLEIEHSVPK	98.1%	31.9	25	30	1	2	0	1207.68	67	76
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	21	28	74	0.07%	43.5%	SGYAFVDCPDEHWAMK	99.7%	76.9	25	76.9	2	0	0	1912.80	37	52
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	21	28	74	0.07%	43.5%	TADEVPLK	99.7%	47.6	25	37.5	2	0	0	872.47	273	280
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	21	28	74	0.07%	43.5%	TVNELQNLTAAEVVVPR	99.7%	92.2	25	79.3	4	2	0	1853.01	509	525
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	10	10	19	0.02%	26.8%	ALQSGPPQSR	99.1%	35.5	25	22.1	2	0	0	1040.55	568	577
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	10	10	19	0.02%	26.8%	DQTPDENDQVVVK	99.7%	55.7	25	50.4	1	0	0	1486.70	526	538
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	10	10	19	0.02%	26.8%	IAPAEAPDAK	99.7%	46	25	46	2	0	0	982.52	441	450
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	10	10	19	0.02%	26.8%	IKEENFVSPK	97.5%	30.8	25	20.9	2	0	0	1190.64	474	483
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	10	10	19	0.02%	26.8%	ILAHNNFVGR	99.7%	53.2	25	46.8	4	0	0	1140.63	281	290
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	10	10	19	0.02%	26.8%	IPVSGPFLVK	99.7%	41.8	25	41.8	2	0	0	1056.65	27	36
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	10	10	19	0.02%	26.8%	ITISPLQELTLYNPER	99.7%	76.3	25	76.3	2	0	0	1887.02	310	325
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	10	10	19	0.02%	26.8%	LLVPTQFVGAIIGK	99.7%	78.9	25	0	3	0	0	1455.89	200	213
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	10	10	19	0.02%	26.8%	MVIITGPPEAQFK	99.7%	83.8	25	72.4	8	0	0	1430.77	453	465
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	10	10	19	0.02%	26.8%	SITILSTPEGTSAACK	99.7%	58.5	25	54.3	1	0	0	1635.83	243	258
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	10	10	19	0.02%	26.8%	TGYAFVDCPDESWALK	99.7%	70.1	25	70.1	2	0	0	1858.83	37	52
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	10	10	19	0.02%	26.8%	TVNELQNLSSAEVVVPR	99.7%	65.8	25	64.7	2	0	0	1854.99	509	525
Integrator complex subunit 11	CPSF3L	INT11_HUMAN	67.7	100.0%	3	3	5	0.01%	5.7%	SCILVSIAGK	97.2%	30.3	25	22.1	1	0	0	1047.59	18	27
Integrator complex subunit 11	CPSF3L	INT11_HUMAN	67.7	100.0%	3	3	5	0.01%	5.7%	VPIYFSTGLTEK	99.7%	41.9	25	41.9	2	0	0	1354.73	263	274
Integrator complex subunit 11	CPSF3L	INT11_HUMAN	67.7	100.0%	3	3	5	0.01%	5.7%	VTPLGAGQDVGR	99.7%	57.5	25	51	2	0	0	1169.63	6	17
Integrator complex subunit 7	INTS7	INT7_HUMAN	106.8	99.9%	2	2	3	0.00%	2.4%	QIQLLLQYLK	99.7%	42.8	25	42.8	2	0	0	1259.77	252	261
Integrator complex subunit 7	INTS7	INT7_HUMAN	106.8	99.9%	2	2	3	0.00%	2.4%	YPFPILINSAFLK	99.7%	59.8	25	59.8	1	0	0	1522.87	55	67
Interferon-induced protein with tetratricopeptide repeats 5	IFIT5	IFIT5_HUMAN	55.8	99.8%	2	2	2	0.00%	5.6%	IDPENAEFLTALCELR	95.3%	28.1	25	28.1	1	0	0	1890.93	464	479
Interferon-induced protein with tetratricopeptide repeats 5	IFIT5	IFIT5_HUMAN	55.8	99.8%	2	2	2	0.00%	5.6%	LALYNLLAYVK	99.7%	62.5	25	62.5	1	0	0	1280.76	51	61
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	99.8%	2	2	4	0.00%	4.5%	IGDFGLVTSLK	99.7%	59.8	25	56.7	2	0	0	1149.65	430	440
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	99.8%	2	2	4	0.00%	4.5%	LAYLQILSEETSVK	99.7%	64.2	25	64.2	2	0	0	1593.87	160	173
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	11	14	31	0.03%	33.1%	GTMTTGHNVADLVVILK	99.7%	56.3	25	52.3	1	2	0	1768.96	111	127
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	11	14	31	0.03%	33.1%	ILITTVPPNLR	99.6%	39.8	25	39.3	3	0	0	1236.77	175	185
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	11	14	31	0.03%	33.1%	ILPTLEAVAALGNK	99.7%	85.7	25	80.9	8	0	0	1409.84	128	141
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	11	14	31	0.03%	33.1%	ILSHGGFR	99.7%	41.7	25	30.6	2	0	0	886.49	320	327
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	11	14	31	0.03%	33.1%	KLDPELHLDIK	99.7%	52.2	25	30.2	1	1	0	1320.75	186	196
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	11	14	31	0.03%	33.1%	LDPELHLDIK	99.7%	42.6	25	39	2	0	0	1192.66	187	196
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	11	14	31	0.03%	33.1%	NQDLAPNSAEQASILSLVTK	99.7%	118	25	118	2	2	0	2099.10	61	80
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	11	14	31	0.03%	33.1%	QPLALNVAYR	99.7%	67.3	25	55.9	2	0	0	1144.65	260	269
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	11	14	31	0.03%	33.1%	VKPAPDETSFSEALLK	99.7%	64.1	25	61.2	2	0	0	1731.92	44	59
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	11	14	31	0.03%	33.1%	VLQSALAAIR	99.7%	93.5	25	86.6	2	0	0	1041.64	197	206

Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	11	14	31	0.03%	33.1%	WFEENASQSTVK	99.7%	69.6	25	66	1	0	0	1425.66	210	221
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	19	25	56	0.06%	23.9%	AYAALAALEK	99.7%	88	25	62.1	4	0	0	1020.57	578	587
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	19	25	56	0.06%	23.9%	CLAALASLR	99.7%	46.4	25	37.3	2	0	0	974.55	203	211
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	19	25	56	0.06%	23.9%	EATDAIGHLDR	99.7%	92.3	25	69.9	3	0	0	1197.59	298	308
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	19	25	56	0.06%	23.9%	EDITQSAQHALR	99.7%	64.6	25	55	2	2	0	1368.69	312	323
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	19	25	56	0.06%	23.9%	FNYSGSGGR	98.4%	32.6	25	24.7	2	0	0	944.42	807	815
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	19	25	56	0.06%	23.9%	FVMEVEVDGQK	99.7%	54.8	25	41.6	4	0	0	1280.62	555	565
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	19	25	56	0.06%	23.9%	GDLDLELVLLCK	99.7%	60	25	56.5	2	0	0	1387.75	106	117
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	19	25	56	0.06%	23.9%	GWPLELLCEK	99.7%	50	25	0	2	0	0	1244.63	248	257
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	19	25	56	0.06%	23.9%	LAAFGQLHK	99.7%	54.5	25	50.8	4	0	0	984.56	324	332
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	19	25	56	0.06%	23.9%	LFPDTPLALDANK	99.7%	70.5	25	68.3	3	0	0	1414.76	588	600
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	19	25	56	0.06%	23.9%	LFPDTPLALDANKK	99.7%	57.2	25	48.4	2	0	0	1542.85	588	601
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	19	25	56	0.06%	23.9%	LNQLKPGLQYK	99.7%	43.2	25	29.5	5	1	0	1301.76	409	419
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	19	25	56	0.06%	23.9%	NPVMELNEK	99.7%	42	25	34.1	2	0	0	1089.52	527	535
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	19	25	56	0.06%	23.9%	RPMEEDGEEKSPSK	99.7%	31.8	25	31.8	0	2	0	1634.73	372	385
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	19	25	56	0.06%	23.9%	SIGTANRPMGAGEALRR	99.3%	29.1	25	29.1	0	1	0	1756.92	258	274
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	19	25	56	0.06%	23.9%	VLAGETLSVNDPPDVLDR	99.7%	114	25	113	2	0	0	1909.99	183	200
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	19	25	56	0.06%	23.9%	VLGMDPLPSK	99.7%	44.6	25	36.3	3	0	0	1056.58	333	342
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	19	25	56	0.06%	23.9%	VLQDMGLPTGAEGR	99.7%	81.7	25	71.3	4	0	0	1443.73	461	474
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	19	25	56	0.06%	23.9%	YELISETGGSHDKR	99.7%	62	25	53.2	2	2	0	1591.77	541	554
Interleukin-1 receptor-associated kinase 1	IRAK1	IRAK1_HUMAN	76.5	99.9%	2	2	4	0.00%	2.7%	LGDFGLAR	99.7%	55.7	25	0	2	0	0	848.46	356	363
Interleukin-1 receptor-associated kinase 1	IRAK1	IRAK1_HUMAN	76.5	99.9%	2	2	4	0.00%	2.7%	TASVLWPWINR	99.7%	47.7	25	39.9	2	0	0	1342.73	66	76
Iron-sulfur protein NUBPL	NUBPL	NUBPL_HUMAN	34.1	100.0%	3	3	7	0.01%	16.9%	AIGLLDVDVYGPSVPK	99.7%	86.9	25	86.9	4	0	0	1642.91	100	115
Iron-sulfur protein NUBPL	NUBPL	NUBPL_HUMAN	34.1	100.0%	3	3	7	0.01%	16.9%	EASDTGQPIVFSQPESDEAK	99.7%	43.4	25	43.4	1	0	0	2134.98	282	301
Iron-sulfur protein NUBPL	NUBPL	NUBPL_HUMAN	34.1	100.0%	3	3	7	0.01%	16.9%	STTAVNLALALAANDSSK	99.7%	82.8	25	82.7	2	0	0	1746.92	82	99
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	12	15	27	0.03%	33.3%	APIQWEER	99.7%	66.5	25	57.8	2	0	0	1028.52	59	66
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	12	15	27	0.03%	33.3%	CSDFTEEICR	99.7%	67.9	25	63.7	2	0	0	1316.52	351	360
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	12	15	27	0.03%	33.3%	EVAESCKDIK	98.7%	33.8	25	9.26	2	0	0	1178.57	217	226
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	12	15	27	0.03%	33.3%	HMGLFDHAAR	99.3%	36.9	25	36.6	1	0	0	1170.55	317	326
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	12	15	27	0.03%	33.3%	IAEFAFEYAR	99.7%	75.3	25	68.3	2	0	0	1216.60	179	188
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	12	15	27	0.03%	33.3%	IEAACFATIK	99.7%	62.8	25	53.9	2	0	0	1123.58	327	336
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	12	15	27	0.03%	33.3%	LITEGASKR	99.7%	41.1	25	19.9	1	0	0	974.56	170	178
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	12	15	27	0.03%	33.3%	MGLKGPLK	95.4%	28.2	25	16.8	1	0	0	843.51	93	100
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	12	15	27	0.03%	33.3%	MSDGLFLQK	99.7%	52.4	25	19.9	4	0	0	1054.52	206	214
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	12	15	27	0.03%	33.3%	NVTAIQGPGGK	99.7%	58.6	25	58.2	2	0	0	1041.57	67	77
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	12	15	27	0.03%	33.3%	TPIAAGHPSMNLLLR	99.7%	78.4	25	78.2	4	2	0	1590.88	101	115
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	12	15	27	0.03%	33.3%	TPYTDVNIVTIR	99.7%	74.2	25	65.1	2	0	0	1391.75	135	146
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	12	15	31	0.03%	31.9%	DMGGYSTTTDFIK	99.7%	79.3	25	72.2	4	0	0	1435.64	362	374
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	12	15	31	0.03%	31.9%	EQTEGEYSSLEHESAR	99.7%	85.2	25	81.1	2	2	0	1851.80	165	180
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	12	15	31	0.03%	31.9%	FAFDYATK	99.2%	35.7	25	35.7	2	0	0	962.46	200	207
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	12	15	31	0.03%	31.9%	FAFDYATKK	99.7%	48.7	25	42	2	0	0	1090.56	200	208
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	12	15	31	0.03%	31.9%	GVIECLK	99.7%	40.1	25	17	1	0	0	818.44	181	187
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	12	15	31	0.03%	31.9%	HNNLDLVIIR	99.7%	72.4	25	56	2	0	0	1206.70	155	164
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	12	15	31	0.03%	31.9%	HPFAQAVGR	99.6%	39.7	25	30.1	1	0	0	982.52	309	317
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	12	15	31	0.03%	31.9%	LEQVLSSMKENK	98.3%	32.6	25	27.7	1	0	0	1421.73	97	108
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	12	15	31	0.03%	31.9%	LGDGLFLQCCEEVAELYPK	99.7%	59.4	25	59.4	2	0	0	2241.06	224	242
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	12	15	31	0.03%	31.9%	NIANPTAMLLSASNMLR	99.7%	112	25	111	8	0	0	1816.94	318	334
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	12	15	31	0.03%	31.9%	SVIGHLQTK	99.7%	42.2	25	41.3	2	0	0	982.57	375	383
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	12	15	31	0.03%	31.9%	TRDMGGYSTTTDFIK	99.7%	44.8	25	42.1	2	0	0	1708.79	360	374
Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G	IDH3G_HUMAN	42.8	100.0%	6	6	9	0.01%	13.2%	HKDIDILIVR	99.3%	29.1	25	29.1	0	1	0	1221.73	158	167
Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G	IDH3G_HUMAN	42.8	100.0%	6	6	9	0.01%	13.2%	LGDGLFLQCCR	99.7%	71.9	25	71.9	2	0	0	1338.63	227	237

Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G	IDH3G_HUMAN	42.8	100.0%	6	6	9	0.01%	13.2%	LHSYATSIR	99.4%	37.7	25	29.2	2	0	0	1047.56	341	349
Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G	IDH3G_HUMAN	42.8	100.0%	6	6	9	0.01%	13.2%	LHSYATSIRK	94.8%	27.8	25	24.1	1	0	0	1175.65	341	350
Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G	IDH3G_HUMAN	42.8	100.0%	6	6	9	0.01%	13.2%	SLPGVVTR	99.7%	40.3	25	26.4	1	0	0	828.49	150	157
Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G	IDH3G_HUMAN	42.8	100.0%	6	6	9	0.01%	13.2%	TSLDLYANVIHCK	99.7%	68.2	25	64.2	2	0	0	1533.77	137	149
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	25	47	0.05%	41.8%	ATDFVADR	99.4%	37.2	25	31.5	2	0	0	894.43	181	188
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	25	47	0.05%	41.8%	CATITPDEAR	99.7%	50.7	25	38.8	2	0	0	1133.53	113	122
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	25	47	0.05%	41.8%	CATITPDEARVEEFK	99.0%	27.5	25	24.7	0	2	0	1765.84	113	127
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	25	47	0.05%	41.8%	DQTDDQVTIDSALATQK	99.7%	122	25	122	2	0	0	1848.88	90	106
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	25	47	0.05%	41.8%	FAQMLEK	98.7%	33.6	25	19.3	1	0	0	882.44	394	400
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	25	47	0.05%	41.8%	FKDIFQEIFDK	99.7%	67.6	25	60	2	0	0	1429.74	262	272
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	25	47	0.05%	41.8%	GKLDGNQDLIR	99.7%	60.8	25	46.4	2	2	0	1228.66	383	393
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	25	47	0.05%	41.8%	IIWQFIK	99.6%	39.7	25	34.1	2	0	0	947.57	61	67
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	25	47	0.05%	41.8%	LIDDMVAQVLK	99.7%	93.4	25	76.8	3	0	0	1244.69	289	299
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	25	47	0.05%	41.8%	LILPHVDIQLK	99.7%	52	25	35.7	2	0	0	1288.80	70	80
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	25	47	0.05%	41.8%	LNEHFLNTTDFLDTIK	99.7%	51.7	25	51.7	1	2	0	1920.97	427	442
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	25	47	0.05%	41.8%	NILGGTVFR	99.7%	42	25	31.9	2	0	0	976.56	141	149
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	25	47	0.05%	41.8%	NILGGTVFREPIICK	99.7%	68.1	25	68.1	2	0	0	1716.95	141	155
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	25	47	0.05%	41.8%	SSGGFVWACK	99.7%	77.7	25	67.9	2	0	0	1098.50	300	309
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	25	47	0.05%	41.8%	TIEAEAAHGTVTR	99.7%	106	25	100	4	1	0	1355.69	341	353
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	25	47	0.05%	41.8%	VAKPVVEMDGDEMTR	99.7%	62	25	62	2	3	0	1708.79	46	60
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	25	47	0.05%	41.8%	VCVETVESGAMTK	99.7%	117	25	109	4	0	0	1426.66	401	413
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	25	47	0.05%	41.8%	YFDLGLPNR	99.7%	45.7	25	41.1	2	0	0	1094.56	81	89
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	APLKPYPVSPSDK	99.7%	39	25	38.7	2	2	0	1398.76	1039	1051
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	AVPSWFVR	97.3%	30.5	25	20.9	2	0	0	961.53	411	418
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	DVLLPWYNAYR	99.0%	34.9	25	32.5	1	0	0	1409.72	651	661
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	EFEDAFPADFIAEGIDQTR	99.7%	74.2	25	74.2	1	0	0	2170.99	547	565
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	EIVVIHQDPEALK	99.7%	78.4	25	63.8	2	0	0	1490.82	849	861
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	ESVDHLTIPSR	99.7%	55.2	25	41.9	2	0	0	1253.65	501	511
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	FLIQNVLR	99.7%	41.5	25	25.9	6	0	0	1002.61	662	669
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	FVDILTNWYVR	99.7%	72.2	25	65.8	5	0	0	1425.75	726	736
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	GSELEITLTR	99.7%	77	25	50.2	2	0	0	1118.61	1062	1071
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	LESDYEILER	99.7%	82.9	25	67.5	2	0	0	1266.62	269	278
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	LFLNETQTQEITEDIPVK	99.7%	92.8	25	80.2	2	0	0	2118.10	1227	1244
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	LLILMEAR	99.7%	66.5	25	48.2	4	0	0	974.57	255	262
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	LRAEPDHMVLGK	94.6%	21.5	25	21.5	0	1	0	1365.73	892	903
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	LYLINSPVVR	99.7%	68.9	25	60.3	6	0	0	1173.70	625	634
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	LYTVVPR	96.7%	29.6	25	20	1	0	0	847.50	716	722
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	MGITEYNNQCR	99.7%	56.1	25	56.1	4	0	0	1401.59	111	121
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	NNDLCYWVPELVR	99.7%	47.2	25	44.9	3	0	0	1677.81	429	441
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	NTELAVFHDETEIQNQTDLLSLSGK	99.7%	42.6	25	42.6	0	1	0	2802.38	1126	1150
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	QLSSEELEQFQK	99.7%	71	25	69.5	2	0	0	1465.72	918	929
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	SDTPLIYK	98.1%	32	25	22.8	2	0	0	936.50	403	410
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	TESAVSQMQSVIELGR	99.7%	94.8	25	85.3	4	0	0	1734.87	818	833
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	TVYVSVLPTTADF	97.1%	30.2	25	22.7	1	0	0	1412.73	1250	1262
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	VCMDFNIIR	99.7%	49.4	25	45.6	2	0	0	1183.56	335	343
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	VENMVDQLLR	99.7%	71.3	25	60	2	0	0	1232.63	419	428
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	VLIDPVSVQDK	99.5%	38.2	25	34.8	1	0	0	1212.68	786	796
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	VREELIDK	98.9%	34.3	25	13.6	2	0	0	1001.56	809	816
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	27	31	67	0.07%	24.9%	YIIEELNVR	99.7%	60.6	25	14.4	2	0	0	1148.63	869	877
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	21	25	48	0.05%	24.8%	ASPLLPANHVTMAK	99.7%	43.6	25	43.3	2	0	0	1465.78	373	386
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	21	25	48	0.05%	24.8%	AVLEEGTDVVIK	99.7%	89.9	25	76.8	4	0	0	1272.70	434	445

Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	21	25	48	0.05%	24.8%	DQLGGWFQSSLLTSVAAR	99.7%	87.4	25	87.4	2	0	0	1935.99	626	643
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	21	25	48	0.05%	24.8%	DSFLGSIPGK	99.7%	55	25	42.6	2	0	0	1020.54	887	896
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	21	25	48	0.05%	24.8%	EAQNLSAMEIR	99.7%	68.8	25	59.2	4	0	0	1261.62	171	181
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	21	25	48	0.05%	24.8%	ELSNFYFSIIK	99.7%	70.9	25	59.6	2	0	0	1360.71	793	803
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	21	25	48	0.05%	24.8%	EMTADVIELK	99.7%	52.3	25	29.4	4	0	0	1148.59	948	957
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	21	25	48	0.05%	24.8%	EPPYGADVLR	99.7%	44.2	25	30.7	2	0	0	1116.57	688	697
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	21	25	48	0.05%	24.8%	FLINLEGGDIR	99.7%	80.6	25	49.8	2	0	0	1246.68	960	970
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	21	25	48	0.05%	24.8%	FLINLEGGDIREESSYK	99.7%	32.8	25	30.1	0	2	0	1969.99	960	976
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	21	25	48	0.05%	24.8%	FPLLKPSPK	99.6%	39.9	25	31	2	0	0	1026.63	273	281
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	21	25	48	0.05%	24.8%	LVHSYPYDWR	99.3%	36.7	25	30.8	1	0	0	1335.65	459	468
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	21	25	48	0.05%	24.8%	QQPDTELEIQQK	99.7%	58.1	25	47.2	2	0	0	1456.73	79	90
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	21	25	48	0.05%	24.8%	SCQTALVEILDVIVR	99.7%	103	25	97.8	2	0	0	1715.94	818	832
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	21	25	48	0.05%	24.8%	SGDLYVLAADK	99.7%	84.2	25	76.3	2	0	0	1151.59	326	336
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	21	25	48	0.05%	24.8%	SYKPVFWSPSSR	97.8%	31.4	25	29.5	1	0	0	1440.73	239	250
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	21	25	48	0.05%	24.8%	TALAEAELEYNPEHVSR	99.7%	74.5	25	74.5	2	2	0	1928.93	251	267
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	21	25	48	0.05%	24.8%	TGWISTSSIWK	99.7%	50.7	25	41.3	2	0	0	1265.65	861	871
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	21	25	48	0.05%	24.8%	TKDEYLINSQTTEHIVK	99.7%	38	25	37.7	0	2	0	2019.04	539	555
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	21	25	48	0.05%	24.8%	TVIVHGFTLGEK	99.7%	59.3	25	53.5	1	1	0	1300.73	650	661
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	21	25	48	0.05%	24.8%	YTAESSDTLCPR	99.7%	96	25	84.3	2	0	0	1399.62	993	1004
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	6	6	11	0.01%	9.1%	ALMGSPQLVAAVVR	99.7%	91.1	25	82.3	2	0	0	1411.81	178	191
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	6	6	11	0.01%	9.1%	LAEPSQLLK	99.7%	43.4	25	31.2	2	0	0	998.59	116	124
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	6	6	11	0.01%	9.1%	LLNDEDPVVVTK	99.7%	84.7	25	78.9	3	0	0	1341.73	150	161
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	6	6	11	0.01%	9.1%	LNYGIPAIVK	96.4%	29.3	25	17.6	1	0	0	1087.65	478	487
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	6	6	11	0.01%	9.1%	TMQNTSDLDTAR	99.7%	60.5	25	50.6	1	0	0	1352.61	192	203
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	6	6	11	0.01%	9.1%	VSVELTNSLFK	99.7%	54.3	25	44.5	2	0	0	1236.68	664	674
Katanin p60 ATPase-containing subunit A1	KATNA1	KTNA1_HUMAN	56.0	100.0%	5	5	12	0.01%	13.2%	DIISQNPNVR	99.7%	58	25	50	3	0	0	1155.61	198	207
Katanin p60 ATPase-containing subunit A1	KATNA1	KTNA1_HUMAN	56.0	100.0%	5	5	12	0.01%	13.2%	EAVVLPMWMPEFFK	99.7%	41.1	25	41.1	1	0	0	1723.86	223	236
Katanin p60 ATPase-containing subunit A1	KATNA1	KTNA1_HUMAN	56.0	100.0%	5	5	12	0.01%	13.2%	FYSPATIFIDEIDSICSR	99.7%	96.9	25	96.9	4	0	0	2134.02	299	316
Katanin p60 ATPase-containing subunit A1	KATNA1	KTNA1_HUMAN	56.0	100.0%	5	5	12	0.01%	13.2%	SVSAADIER	99.7%	55.3	25	28.8	2	0	0	947.48	472	480
Katanin p60 ATPase-containing subunit A1	KATNA1	KTNA1_HUMAN	56.0	100.0%	5	5	12	0.01%	13.2%	TTFFNVSSSTLTSK	99.7%	70.5	25	64.9	2	0	0	1519.76	268	281
Katanin p80 WD40 repeat-containing subunit B1	KATNB1	KTNB1_HUMAN	72.3	100.0%	3	3	4	0.00%	5.7%	ASDFLPAVK	98.6%	33.2	25	28.2	1	0	0	947.52	467	475
Katanin p80 WD40 repeat-containing subunit B1	KATNB1	KTNB1_HUMAN	72.3	100.0%	3	3	4	0.00%	5.7%	LLATGGDDCR	99.3%	36.8	25	32.6	1	0	0	1077.50	35	44
Katanin p80 WD40 repeat-containing subunit B1	KATNB1	KTNB1_HUMAN	72.3	100.0%	3	3	4	0.00%	5.7%	LNTPEELIVAGSQSGSIR	99.7%	112	25	109	2	0	0	1870.99	71	88
Keratinocyte proline-rich protein	KPRP	KPRP_HUMAN	64.1	99.7%	2	2	3	0.00%	3.6%	RLDQCPESPLQR	99.3%	36.4	25	26.3	2	0	0	1498.74	387	398
Keratinocyte proline-rich protein	KPRP	KPRP_HUMAN	64.1	99.7%	2	2	3	0.00%	3.6%	RSEPIYNSR	94.6%	27.5	25	16.8	1	0	0	1121.57	300	308
Kidney mitochondrial carrier protein 1	SLC25A30	KMCP1_HUMAN	32.5	99.8%	2	2	4	0.00%	7.2%	ALYSGIAPAMLR	99.7%	61	25	56.2	2	0	0	1278.69	67	78
Kidney mitochondrial carrier protein 1	SLC25A30	KMCP1_HUMAN	32.5	99.8%	2	2	4	0.00%	7.2%	NEGFFALYK	99.3%	36.8	25	31.6	2	0	0	1088.54	255	263
Kinesin-like protein KIF11	KIF11	KIF11_HUMAN	119.2	100.0%	5	5	9	0.01%	5.8%	EAGNINQSLLTLGR	99.6%	38.8	25	38.8	1	0	0	1485.80	284	297
Kinesin-like protein KIF11	KIF11	KIF11_HUMAN	119.2	100.0%	5	5	9	0.01%	5.8%	ETTIDGEELVK	95.5%	28.3	25	25.2	1	0	0	1233.62	247	257
Kinesin-like protein KIF11	KIF11	KIF11_HUMAN	119.2	100.0%	5	5	9	0.01%	5.8%	LNLVDLAGSENIGR	99.7%	83.1	25	83.1	2	0	0	1470.79	261	274
Kinesin-like protein KIF11	KIF11	KIF11_HUMAN	119.2	100.0%	5	5	9	0.01%	5.8%	NILNKPEVNQK	99.5%	38.2	25	31	1	0	0	1296.73	358	368
Kinesin-like protein KIF11	KIF11	KIF11_HUMAN	119.2	100.0%	5	5	9	0.01%	5.8%	TVLQELINVLK	99.7%	54.1	25	47.5	4	0	0	1269.78	619	629
Kinesin-like protein KIF23	KIF23	KIF23_HUMAN	110.1	100.0%	3	3	5	0.01%	3.7%	ALLQEFDNAVLSK	99.7%	60.6	25	50.4	2	0	0	1447.78	524	536
Kinesin-like protein KIF23	KIF23	KIF23_HUMAN	110.1	100.0%	3	3	5	0.01%	3.7%	NLQQELETQNQK	99.7%	53.5	25	42	1	0	0	1472.73	588	599
Kinesin-like protein KIF23	KIF23	KIF23_HUMAN	110.1	100.0%	3	3	5	0.01%	3.7%	TTTIYEEDKR	99.6%	38.8	25	32.1	2	0	0	1255.62	578	587
Kinetochore-associated protein 1	KNTC1	KNTC1_HUMAN	250.8	100.0%	3	3	3	0.00%	1.6%	FSLDTLYVSTAK	97.4%	30.6	25	30.6	1	0	0	1344.70	1629	1640
Kinetochore-associated protein 1	KNTC1	KNTC1_HUMAN	250.8	100.0%	3	3	3	0.00%	1.6%	LGISFQPVFR	99.7%	50.3	25	49.8	1	0	0	1163.66	1414	1423
Kinetochore-associated protein 1	KNTC1	KNTC1_HUMAN	250.8	100.0%	3	3	3	0.00%	1.6%	VLAPELIPSILEK	98.8%	34	25	34	1	0	0	1421.86	727	739
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	5	5	8	0.01%	14.7%	GLLEESSFATLFPK	99.7%	85.4	25	80.1	2	0	0	1538.81	53	66
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	5	5	8	0.01%	14.7%	ILQDDVACDIIK	99.7%	79.1	25	63.3	2	0	0	1402.73	135	146
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	5	5	8	0.01%	14.7%	LGALTAEEIALK	99.7%	67.7	25	41.7	1	0	0	1228.71	358	369

KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	5	5	8	0.01%	14.7%	SVSFEQAVR	98.8%	34.1	25	25.1	1	0	0	1022.53	126	134
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	5	5	8	0.01%	14.7%	TFDPYIIIR	99.7%	44.6	25	34.9	2	0	0	1137.63	107	115
Kynurenine--oxoglutarate transaminase 3	CCBL2	KAT3_HUMAN	51.4	100.0%	5	6	7	0.01%	12.8%	AIILNTPHNPLGK	99.7%	40.2	25	40.2	1	0	0	1387.81	210	222
Kynurenine--oxoglutarate transaminase 3	CCBL2	KAT3_HUMAN	51.4	100.0%	5	6	7	0.01%	12.8%	DSTLDAAEEIIK	99.7%	44.5	25	36.3	1	0	0	1304.66	436	447
Kynurenine--oxoglutarate transaminase 3	CCBL2	KAT3_HUMAN	51.4	100.0%	5	6	7	0.01%	12.8%	GFGHPSLVK	95.5%	28.3	25	20.4	1	0	0	941.52	100	108
Kynurenine--oxoglutarate transaminase 3	CCBL2	KAT3_HUMAN	51.4	100.0%	5	6	7	0.01%	12.8%	IAAIDSLNQYTR	99.7%	82.3	25	78.4	1	0	0	1364.72	88	99
Kynurenine--oxoglutarate transaminase 3	CCBL2	KAT3_HUMAN	51.4	100.0%	5	6	7	0.01%	12.8%	MAGATPVFIPLR	99.7%	60.3	25	41.4	3	0	0	1272.71	168	179
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	9	10	17	0.02%	19.7%	ACFLGATVK	99.7%	42.4	25	29.7	2	0	0	966.51	375	383
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	9	10	17	0.02%	19.7%	FIPEITISDILR	99.7%	69.7	25	66.8	2	0	0	1416.81	388	399
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	9	10	17	0.02%	19.7%	FPFLGVHFTPR	97.7%	24.5	25	22.9	0	1	0	1317.71	308	318
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	9	10	17	0.02%	19.7%	GNIYPVPDSR	99.6%	39.1	25	28.5	1	0	0	1117.56	298	307
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	9	10	17	0.02%	19.7%	ISELSGCTPDPR	99.7%	52.2	25	46.5	2	0	0	1331.63	266	277
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	9	10	17	0.02%	19.7%	LIQQEDIK	99.6%	39.8	25	19.9	2	0	0	986.55	166	173
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	9	10	17	0.02%	19.7%	LIQQEDIKK	99.6%	39.3	25	13.5	2	0	0	1114.65	166	174
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	9	10	17	0.02%	19.7%	LIVAVEQEEIPR	99.7%	80.8	25	57.2	2	0	0	1395.78	137	148
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	9	10	17	0.02%	19.7%	MDGSIWLGPNAVLAFK	99.7%	59.9	25	59.9	3	0	0	1734.89	319	334
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	5	7	11	0.01%	22.8%	DFLLQQTMLR	99.7%	50.1	25	22.6	2	0	0	1264.67	29	38
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	5	7	11	0.01%	22.8%	IAWALSR	99.7%	44.3	25	28.4	2	0	0	816.47	89	95
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	5	7	11	0.01%	22.8%	KSLDFYTR	99.6%	39.4	25	14.5	2	0	0	1029.54	44	51
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	5	7	11	0.01%	22.8%	RFEELGVK	99.7%	43.6	25	12	2	0	0	977.54	141	148
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	5	7	11	0.01%	22.8%	VLGMTLIQK	99.7%	55.1	25	52.8	3	0	0	1002.60	52	60
Lamina-associated polypeptide 2, isoform alpha	TMPO	LAP2A_HUMAN	75.5	99.8%	2	2	5	0.01%	4.2%	SSTPLPTISSSAENTR	99.7%	42.9	25	21.4	2	0	0	1647.82	158	173
Lamina-associated polypeptide 2, isoform alpha	TMPO	LAP2A_HUMAN	75.5	99.8%	2	2	5	0.01%	4.2%	YGVNPGPIVGTTR	99.7%	52.7	25	50.2	3	0	0	1330.71	127	139
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	7	23	0.02%	13.7%	KFADGEVVR	99.7%	55.4	25	46.8	3	0	0	1020.55	5	13
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	7	23	0.02%	13.7%	LTPLILKPFGNSISR	99.7%	45.5	25	45.5	2	0	0	1655.98	117	131
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	7	23	0.02%	13.7%	NDLSPASSGNAVYDFFIGR	99.7%	66.2	25	66.2	7	0	0	2029.96	354	372
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	7	23	0.02%	13.7%	NLLVSGWWGFVR	99.7%	67.5	25	60.8	2	0	0	1433.77	533	544
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	7	23	0.02%	13.7%	TFEVTPIR	99.7%	40.4	25	38.6	2	0	0	962.53	196	203
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	7	23	0.02%	13.7%	VVEGTPLIDGR	99.7%	75.2	25	62.5	6	0	0	1155.64	280	290
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	7	23	0.02%	13.7%	YNGEPEHIER	99.1%	35.4	25	22	1	0	0	1243.57	132	141
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	AEHDQLLLNYAK	98.6%	26.4	25	23.5	0	1	0	1414.73	112	123
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	AGGPTTPLSPTR	99.7%	50.9	25	50.9	4	0	0	1154.62	15	26
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	AKLQIELGK	99.7%	46.9	25	20	2	0	0	999.62	101	109
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	ALYETELADAR	99.7%	72.5	25	56	4	0	0	1251.62	80	90
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	ALYETELADARR	99.1%	35.3	25	31.9	2	0	0	1407.72	80	91
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	CQSLTEDLEFRK	99.7%	64.8	25	58.7	2	2	0	1525.73	198	209
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	DAALATALGDKK	99.7%	73.3	25	50.3	6	0	0	1173.65	146	157
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	DQMQQQLNDYEQLLDVK	99.7%	74.5	25	74.5	1	0	0	2108.00	351	367
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	EYEAALNSK	99.6%	40	25	34.9	2	0	0	1024.49	137	145
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	IESLSSQLSNLQK	99.7%	90.4	25	81.5	2	0	0	1446.78	300	312
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	IGDTSVSYK	99.7%	65.6	25	61.4	2	0	0	969.49	475	483
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	IQELEDLLAK	99.7%	70.9	25	37.7	4	0	0	1171.66	321	330
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	KESDLNGAQIK	99.7%	44.1	25	25.9	2	0	0	1202.64	124	134
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	KIGDTSVSYK	99.7%	43	25	36.5	1	0	0	1097.58	474	483
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	KLLEGEEER	99.7%	71.5	25	48.4	2	0	0	1102.57	379	387
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	KQLADETLLK	99.1%	35.2	25	28.9	1	0	0	1158.67	182	191
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	LALDMEISAYR	99.7%	65.6	25	62.2	2	0	0	1297.65	368	378
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	LALDMEISAYRK	99.7%	45.8	25	44.1	2	0	0	1425.74	368	379
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	LAQALHEMR	99.7%	68.6	25	50.3	4	0	0	1068.56	242	250
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	LAVYIDK	99.2%	35.7	25	33.9	2	0	0	821.48	43	49
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	LAVYIDKVR	99.7%	43.3	25	43.3	2	0	0	1076.65	43	51

Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	LLEGEEER	99.7%	40.4	25	33	2	0	0	974.48	380	387
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	LLEGEEERLK	99.7%	48.9	25	41.8	2	0	0	1215.66	380	389
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	LQEKEELR	99.7%	43	25	16.9	4	0	0	1044.57	30	37
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	LQIELGK	99.0%	34.8	25	0	1	0	0	800.49	103	109
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	LREYEAALNSK	99.7%	62	25	44.7	5	0	0	1293.68	135	145
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	LSSEMNTSTVNSAR	99.7%	116	25	105	6	0	0	1496.70	277	290
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	LVEVDSGR	99.7%	44.9	25	33.5	4	0	0	874.46	227	234
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	LYKEELEQTYHAK	99.7%	83.6	25	73.9	2	4	0	1651.83	259	271
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	MRIESLSSQLSNLQK	99.7%	49.7	25	42.3	2	3	0	1749.92	298	312
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	NQNSWGTGEDVK	99.7%	62.5	25	62.5	2	0	0	1334.60	517	528
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	NTSEQDQPMGGWEMIR	99.7%	45.1	25	0.88	1	0	0	1894.81	458	473
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	QIEYEYK	99.4%	36.9	25	29.6	2	0	0	972.47	235	241
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	QLADETLLK	96.2%	29	25	20.1	1	0	0	1030.58	183	191
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	SLETENSALQLQVTEREEVR	99.7%	51.1	25	51.1	0	1	0	2331.18	52	71
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	SMYEEEINETR	99.7%	71.5	25	66.8	2	0	0	1416.59	210	220
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	37	43	97	0.10%	51.7%	SMYEEEINETRR	96.9%	29.8	25	26.2	1	0	0	1556.70	210	221
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	AELDEVNK	99.7%	41	25	33.3	1	0	0	917.46	106	113
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	AGGPATPLSPTR	99.7%	67	25	55.4	4	0	0	1124.61	9	20
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	ALELENDRLLLK	99.7%	52.5	25	45	2	0	0	1426.83	46	57
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	ALYESELADAR	99.7%	65.9	25	56.1	2	0	0	1237.61	74	84
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	ATSSSSGSLSATGR	99.7%	101	25	101	4	0	0	1268.61	397	410
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	EGELTVAQGR	99.7%	68.7	25	39.9	3	0	0	1059.54	119	128
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	ELEEAMAGER	99.7%	41.2	25	33.2	1	0	0	1134.51	317	326
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	GLESDVAELR	99.7%	88.6	25	66.9	2	0	0	1088.56	152	161
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	ISEKEEVTTR	99.7%	66.4	25	44.5	2	0	0	1191.62	58	67
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	KLLEGEEER	99.7%	71.5	25	48.4	2	0	0	1102.57	373	381
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	LESLSYQLSGLQK	99.7%	64.4	25	52.7	2	0	0	1465.79	294	306
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	LLEGEEER	99.7%	40.4	25	33	2	0	0	974.48	374	381
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	LLEGEEERLK	99.7%	48.9	25	41.8	2	0	0	1215.66	374	383
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	LQEKEELR	99.7%	43	25	16.9	4	0	0	1044.57	24	31
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	LQIEIGK	99.0%	34.8	25	0	1	0	0	800.49	97	103
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	LRAELDEVNK	99.7%	42.6	25	24.7	2	0	0	1186.64	104	113
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	LSSDQNDKAASAAR	99.7%	91.2	25	85.9	4	0	0	1433.70	271	284
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	LVEVDSSR	99.0%	34.8	25	23	2	0	0	904.47	221	228
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	LYKLELEQTYQAK	99.7%	63.9	25	63.4	1	0	0	1626.87	253	265
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	MAQALEELR	99.5%	38.6	25	27.7	1	0	0	1060.55	236	244
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	QVLEGEEIAYK	99.7%	76.1	25	67.3	2	0	0	1278.66	486	496
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	RLVEVDSSR	99.7%	45.3	25	33.8	4	0	0	1060.57	220	228
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	RVLDETAR	96.3%	29.2	25	19.6	1	0	0	959.53	85	92
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	SEVELAAALSDKR	99.7%	76.6	25	70.1	2	0	0	1388.74	139	151
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	SVFEEEVR	97.8%	31.3	25	22.6	1	0	0	994.48	204	211
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	TVLVNADGEEVAMR	99.7%	113	25	112	4	0	0	1503.75	542	555
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	22	24	53	0.05%	41.2%	VKDLESLFHR	99.7%	52.7	25	45.6	2	4	0	1243.68	129	138
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	8	9	19	0.02%	8.1%	ETESAPGSPR	98.5%	33	25	33	2	0	0	1030.48	514	523
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	8	9	19	0.02%	8.1%	FQQVPTDALANK	99.7%	47.6	25	39.5	2	0	0	1331.70	742	753
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	8	9	19	0.02%	8.1%	FWSFFLR	96.3%	29.1	25	23.3	1	0	0	1002.52	918	924
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	8	9	19	0.02%	8.1%	LFGAPEPSTIAR	99.5%	38.6	25	22.7	2	0	0	1258.68	754	765
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	8	9	19	0.02%	8.1%	LGIGQSQEMNTLFR	99.7%	66.1	25	66.1	5	0	0	1609.80	904	917
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	8	9	19	0.02%	8.1%	QIEYYFSVDNLER	99.7%	42.7	25	42.7	1	0	0	1675.80	410	422
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	8	9	19	0.02%	8.1%	SLPTTVPESPNYR	99.3%	36.5	25	22	2	0	0	1460.74	766	778
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	8	9	19	0.02%	8.1%	YGLECLFR	99.7%	62	25	57.4	4	0	0	1057.51	949	956

La-related protein 7	LARP7	LARP7_HUMAN	66.9	100.0%	3	3	5	0.01%	7.0%	AIEFLNNPPEEAPR	99.7%	70.8	25	70.8	2	0	0	1596.80	182	195
La-related protein 7	LARP7	LARP7_HUMAN	66.9	100.0%	3	3	5	0.01%	7.0%	DRVEASSLPEVR	98.2%	32.3	25	25.1	1	0	0	1357.71	280	291
La-related protein 7	LARP7	LARP7_HUMAN	66.9	100.0%	3	3	5	0.01%	7.0%	VNATGPQFVSGVIVK	99.7%	54.9	25	47.2	2	0	0	1515.85	444	458
Large neutral amino acids transporter small subunit 1	SLC7A5	LAT1_HUMAN	55.0	100.0%	3	4	7	0.01%	9.5%	ALAAPAAEEKEEAR	99.7%	98	25	98	3	1	0	1455.74	10	23
Large neutral amino acids transporter small subunit 1	SLC7A5	LAT1_HUMAN	55.0	100.0%	3	4	7	0.01%	9.5%	GDVSNLDPNFSFEGTK	99.1%	35.2	25	30.9	1	0	0	1726.79	222	237
Large neutral amino acids transporter small subunit 1	SLC7A5	LAT1_HUMAN	55.0	100.0%	3	4	7	0.01%	9.5%	SADGSAPAGEGEGVTLQR	99.7%	97.6	25	97.6	2	0	0	1701.80	31	48
Lethal(2) giant larvae protein homolog 1	LLGL1	L2GL1_HUMAN	115.4	99.9%	2	2	5	0.01%	2.4%	APVVAIAVLDGR	99.7%	101	25	89.2	4	0	0	1180.70	788	799
Lethal(2) giant larvae protein homolog 1	LLGL1	L2GL1_HUMAN	115.4	99.9%	2	2	5	0.01%	2.4%	TGPLPWPAGFQPR	98.7%	33.5	25	33.5	1	0	0	1423.75	578	590
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	AENQPIRDVLK	98.2%	32.1	25	20.5	1	0	0	1282.71	673	683
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	AFAETHIK	99.7%	50.7	25	46.2	2	0	0	916.49	1091	1098
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	AGDMENAENILTVMR	99.7%	61.7	25	61.7	4	0	0	1695.77	245	259
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	AGYPQYVSEILEK	99.7%	68.6	25	65.4	2	0	0	1496.76	315	327
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	CVANNQVETLEK	99.7%	70.5	25	62.5	2	0	0	1404.68	930	941
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	DAHLLVESK	99.7%	52.8	25	43.2	2	0	0	1011.55	641	649
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	EKDIQEESTFSSR	99.7%	75.4	25	65.4	1	0	0	1555.72	65	77
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	EQNIVFNAETYSNLIK	99.7%	83.9	25	83.9	2	0	0	1882.95	1060	1075
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	FSPTDFLAK	97.1%	30.2	25	20.4	2	0	0	1025.53	179	187
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	GAYDIFLNAK	99.7%	50.7	25	47.5	1	0	0	1111.58	1050	1059
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	GDLSTALEVAIDCYEK	99.7%	65.5	25	58.2	2	0	0	1783.84	836	851
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	GDVENIEVVQK	99.7%	78.2	25	64.8	2	0	0	1229.64	1153	1163
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	GFTLNDAANSR	99.7%	78.9	25	68.2	2	0	0	1165.56	1099	1109
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	IPENIYR	95.4%	28.2	25	10.1	1	0	0	904.49	618	624
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	IQEENVIPR	99.7%	70.8	25	62	2	0	0	1097.60	981	989
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	KIIETPGIR	99.7%	56.9	25	48.4	2	0	0	1026.63	909	917
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	LDDLFLK	98.3%	32.5	25	13.5	1	0	0	863.49	1351	1357
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	LDDLFLKR	99.7%	54.7	25	40.4	2	0	0	1019.59	1351	1358
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	LDSSAVLDTGK	99.7%	85.2	25	76.2	2	0	0	1105.57	740	750
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	LGAVYDVSHYNALLK	99.7%	65.3	25	61.9	2	0	0	1662.89	156	170
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	LIASYCNVGDIEGASK	99.7%	119	25	113	2	0	0	1696.82	203	218
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	LIITQVR	96.4%	29.3	25	10.2	2	0	0	842.55	1110	1116
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	LLMSEDYFTQAMEVK	99.7%	94.5	25	93.7	8	0	0	1820.84	1076	1090
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	LQDAINILK	99.7%	54.2	25	42.5	2	0	0	1027.61	764	772
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	LVEKGETDLIQK	99.7%	65.5	25	55.2	2	0	0	1372.77	865	876
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	MEEANIQPNR	99.7%	63.2	25	56	2	0	0	1201.56	188	197
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	MLNGLEDSIGLSK	99.7%	88.9	25	77.9	4	0	0	1392.70	1164	1176
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	MVFINNIALAQIK	99.7%	93.5	25	93.5	4	0	0	1474.85	1177	1189
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	NLLESYHVPELIK	99.7%	65	25	55.5	2	0	0	1554.85	628	640
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	NVQGIIEILK	99.7%	68.2	25	59.8	2	0	0	1126.68	454	463
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	QLILVLCSEENMQK	99.7%	73	25	68.8	2	0	0	1704.87	684	697
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	SCGSLLPELK	99.7%	50.6	25	43.9	2	0	0	1103.58	129	138
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	SEAANGNLDFVLSFLK	99.7%	61.4	25	61.4	2	0	0	1724.89	514	529
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	SGGLGGSHALLLLR	99.7%	68.1	25	60.9	2	2	0	1350.79	115	128
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	SVLELIPELNEK	99.7%	45.1	25	39.8	2	0	0	1383.77	1306	1317
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	SYVSEKDVTSAK	99.7%	83.7	25	76.2	2	0	0	1313.66	1327	1338
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	TVLDQQQTPSR	99.7%	66.8	25	51.5	2	0	0	1272.65	1129	1139
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	TVQLTSSELESTLETLK	99.7%	96.4	25	85.8	2	0	0	1878.99	656	672
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	VFNDTCR	99.6%	39.8	25	34.8	1	0	0	911.40	108	114
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	VIEPQYFGLAYLFR	99.7%	75.4	25	75.2	2	0	0	1715.92	1210	1223
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	41	46	90	0.09%	33.4%	VYLQNEYK	99.5%	38.1	25	31.2	2	0	0	1056.54	171	178
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	8	8	13	0.01%	14.6%	FLPEFPSCSLLK	98.6%	33.4	25	21.1	1	0	0	1437.74	257	268
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	8	8	13	0.01%	14.6%	GTAAILEYLR	99.7%	72.9	25	51.2	2	0	0	1106.62	588	597

Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	8	8	13	0.01%	14.6%	LQTINLSFNR	99.7%	57.2	25	50.8	2	0	0	1205.66	497	506
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	8	8	13	0.01%	14.6%	NLSEVPQCVWR	98.3%	32.6	25	31.9	1	0	0	1387.68	47	57
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	8	8	13	0.01%	14.6%	QATLIPDEVFDAVK	99.7%	42.9	25	35.7	2	0	0	1545.82	410	423
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	8	8	13	0.01%	14.6%	SNIVTSINFSK	99.7%	58.5	25	51	1	0	0	1209.65	424	434
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	8	8	13	0.01%	14.6%	SVPDEIILLR	99.7%	64.6	25	44.8	2	0	0	1154.68	303	312
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	8	8	13	0.01%	14.6%	TLLLDGNPFR	99.7%	68.3	25	59.6	2	0	0	1145.63	569	578
Leucine-rich repeat-containing protein 47	LRRC47	LRC47_HUMAN	63.5	100.0%	3	3	5	0.01%	7.0%	ELLLTGPGLEER	99.7%	57	25	50.7	2	0	0	1326.73	23	34
Leucine-rich repeat-containing protein 47	LRRC47	LRC47_HUMAN	63.5	100.0%	3	3	5	0.01%	7.0%	NALGPGLSPELGPLPALR	99.7%	48.5	25	48.5	2	0	0	1772.01	85	102
Leucine-rich repeat-containing protein 47	LRRC47	LRC47_HUMAN	63.5	100.0%	3	3	5	0.01%	7.0%	TAATLATHELR	99.7%	58.6	25	51	1	0	0	1183.64	371	381
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	23	26	48	0.05%	23.3%	CEFAVGYQR	99.7%	48	25	42.9	2	0	0	1129.51	70	78
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	23	26	48	0.05%	23.3%	ELAVEGMHR	99.7%	44.9	25	30.6	2	0	0	1057.51	837	845
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	23	26	48	0.05%	23.3%	ELMGEEILGASLSAPLTSYK	99.7%	62.4	25	62.4	4	0	0	2125.07	351	370
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	23	26	48	0.05%	23.3%	EVWDYVFFK	99.7%	47	25	42.8	2	0	0	1232.60	633	641
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	23	26	48	0.05%	23.3%	FASEAEDKIR	99.7%	67.5	25	56.2	2	0	0	1165.58	1040	1049
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	23	26	48	0.05%	23.3%	FDDPLLGPR	99.7%	58.3	25	45.9	2	0	0	1029.54	1118	1126
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	23	26	48	0.05%	23.3%	GFYEGIMLVDGFK	99.7%	69.6	25	64	4	0	0	1475.72	471	483
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	23	26	48	0.05%	23.3%	GTGVVTSVPSDSPDDIAALR	99.7%	72.4	25	72.4	2	0	0	1956.99	385	404
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	23	26	48	0.05%	23.3%	ILDLQLEFDEK	99.7%	93.2	25	92.3	2	0	0	1362.72	1007	1017
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	23	26	48	0.05%	23.3%	MIDAGDALIYMEPEK	99.7%	85.4	25	79.7	3	0	0	1695.80	498	512
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	23	26	48	0.05%	23.3%	QGDNCDSIIR	98.4%	32.7	25	25.9	2	0	0	1177.53	1089	1098
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	23	26	48	0.05%	23.3%	QTGEGVGPQEYTLLK	99.7%	69.8	25	61.8	2	0	0	1619.83	254	268
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	23	26	48	0.05%	23.3%	SFITTDVNPYYDSFVR	99.7%	84.3	25	84.3	2	0	0	1923.91	204	219
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	23	26	48	0.05%	23.3%	STGNFLTLTQAIDK	99.7%	87.7	25	76.8	2	0	0	1508.80	720	733
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	23	26	48	0.05%	23.3%	TGFFEFQAAK	99.7%	50.3	25	49.3	1	0	0	1145.56	823	832
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	23	26	48	0.05%	23.3%	TPISEHAVFNVDLMSK	99.7%	42.8	25	42.8	1	0	0	1803.89	1139	1154
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	23	26	48	0.05%	23.3%	VDIGDTIIYLVH	99.7%	60.8	25	60.8	2	0	0	1357.74	1165	1176
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	23	26	48	0.05%	23.3%	VFASELNAGIIK	99.7%	102	25	91.5	2	0	0	1261.72	796	807
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	23	26	48	0.05%	23.3%	VFEVNASNLEK	99.7%	59.9	25	54.8	2	0	0	1249.64	29	39
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	23	26	48	0.05%	23.3%	VIASELGSMPELK	99.7%	66.5	25	53.2	2	0	0	1389.73	971	983
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	23	26	48	0.05%	23.3%	VIASELGSMPELKK	99.7%	50.7	25	34	2	0	0	1501.83	971	984
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	23	26	48	0.05%	23.3%	VIYVLPMLTIK	99.7%	50.3	25	50.3	2	0	0	1289.79	371	381
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	23	26	48	0.05%	23.3%	VLEPYPSK	99.0%	35	25	23.5	1	0	0	932.51	271	278
Leukotriene A-4 hydrolase	LTA4H	LKHA4_HUMAN	69.3	99.9%	2	2	3	0.00%	3.8%	SAYEFSETESMLK	99.6%	39.9	25	39.9	1	0	0	1537.67	231	243
Leukotriene A-4 hydrolase	LTA4H	LKHA4_HUMAN	69.3	99.9%	2	2	3	0.00%	3.8%	TFGETHPFTK	99.7%	53.2	25	48.5	2	0	0	1164.57	356	365
Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	DBT	ODB2_HUMAN	53.5	99.8%	2	2	4	0.00%	4.8%	LSFMPFFLK	98.9%	34.3	25	26.9	2	0	0	1129.61	305	313
Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	DBT	ODB2_HUMAN	53.5	99.8%	2	2	4	0.00%	4.8%	SYLENPAFMLLDLK	99.7%	71.4	25	65	2	0	0	1653.86	469	482
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	5	5	8	0.01%	2.2%	EIFVDFAPFLSR	95.5%	28.3	25	28.3	1	0	0	1440.75	1813	1824
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	5	5	8	0.01%	2.2%	LSSAIAFTYNPR	99.3%	36.7	25	32.4	1	0	0	1339.70	413	424
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	5	5	8	0.01%	2.2%	SAAAIALPPIAK	99.7%	40.4	25	38.8	2	0	0	1122.69	213	224
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	5	5	8	0.01%	2.2%	SPVDIVTGGISPVR	99.7%	64.6	25	64.6	2	0	0	1396.78	1488	1501
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	5	5	8	0.01%	2.2%	YGPDAFFNFPGK	99.7%	53	25	48.1	2	0	0	1359.64	201	212
LisH domain and HEAT repeat-containing protein KIAA1468	KIAA1468	K1468_HUMAN	134.6	100.0%	2	2	2	0.00%	2.1%	ALNFLVNEFLLK	95.1%	28	25	28	1	0	0	1420.82	258	269
LisH domain and HEAT repeat-containing protein KIAA1468	KIAA1468	K1468_HUMAN	134.6	100.0%	2	2	2	0.00%	2.1%	SSPEIQEPIKPLEK	99.5%	38	25	28.6	1	0	0	1594.87	243	256
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	21	27	148	0.15%	62.0%	DLADELALVDVIEDK	99.7%	111	25	107	1	0	0	1657.85	43	57
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	21	27	148	0.15%	62.0%	DQLIYNLLK	99.7%	61.9	25	46.5	5	0	0	1119.64	6	14
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	21	27	148	0.15%	62.0%	DQLIYNLLKEEQTPQNK	99.7%	92.9	25	90.5	2	2	0	2074.08	6	22
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	21	27	148	0.15%	62.0%	DYNVTANSK	99.7%	59	25	54.8	8	0	0	1011.47	82	90
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	21	27	148	0.15%	62.0%	EVHKQVVESAYEVIK	98.8%	26.9	25	22	0	1	0	1757.94	229	243
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	21	27	148	0.15%	62.0%	FIIPNVVK	99.6%	38.9	25	18.8	5	0	0	929.58	119	126
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	21	27	148	0.15%	62.0%	GEMMDLQHGSLFLR	99.7%	74.9	25	74.9	6	6	0	1633.78	60	73
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	21	27	148	0.15%	62.0%	GYTSWAIGLSVADLAESIMK	99.7%	52.8	25	52.8	1	0	0	2128.06	246	265

L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	21	27	148	0.15%	62.0%	ITVVGVGAVGMACAISILMK	99.7%	41.8	25	34.7	3	0	0	2006.08	23	42
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	21	27	148	0.15%	62.0%	IVSGKDYNVTANSK	99.7%	88.8	25	88.7	4	3	0	1495.78	77	90
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	21	27	148	0.15%	62.0%	KSADTLWGIQK	99.7%	33.2	25	24.6	0	2	0	1246.68	318	328
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	21	27	148	0.15%	62.0%	LKGEMMDLQHGSLFLR	98.1%	25.3	25	25.3	0	1	0	1906.95	58	73
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	21	27	148	0.15%	62.0%	LLIVSNPVDILTYVAWK	99.7%	120	25	0	6	2	0	1944.12	133	149
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	21	27	148	0.15%	62.0%	LVIITAGAR	99.7%	72.8	25	53.3	21	0	0	913.58	91	99
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	21	27	148	0.15%	62.0%	QVVESAYEVIK	99.7%	71.7	25	64.3	12	0	0	1264.68	233	243
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	21	27	148	0.15%	62.0%	RVHPVSTMIK	99.7%	43.7	25	33.6	2	0	0	1167.67	269	278
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	21	27	148	0.15%	62.0%	SADTLWGIQK	99.7%	69	25	58.8	8	0	0	1118.58	319	328
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	21	27	148	0.15%	62.0%	TLHPDLGTDK	99.6%	39.7	25	39.7	2	0	0	1096.56	213	222
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	21	27	148	0.15%	62.0%	VIGSGCNLDSAR	99.7%	80.4	25	70.7	18	0	0	1248.60	158	169
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	21	27	148	0.15%	62.0%	VTLTSEEEAR	99.7%	73.1	25	64.2	25	0	0	1134.56	306	315
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	21	27	148	0.15%	62.0%	VTLTSEEEARLK	99.7%	51.8	25	42.5	2	0	0	1375.74	306	317
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	17	26	125	0.13%	53.6%	DYSVTANSK	97.1%	30.2	25	30.2	1	0	0	984.46	83	91
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	17	26	125	0.13%	53.6%	EKLIAPVAEEEATVPNNK	99.7%	108	25	105	2	0	0	1952.03	6	23
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	17	26	125	0.13%	53.6%	FIIPQIVK	99.7%	40.6	25	38.2	1	0	0	957.61	120	127
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	17	26	125	0.13%	53.6%	GEMMDLQHGSLFLQTPK	99.7%	72.9	25	69.3	5	6	0	1931.94	61	77
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	17	26	125	0.13%	53.6%	GLTSVINQK	99.7%	73.5	25	57.5	7	0	0	959.55	300	308
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	17	26	125	0.13%	53.6%	GMYGIENEVFLSLPCILNAR	95.0%	27.9	25	27.5	1	0	0	2312.14	280	299
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	17	26	125	0.13%	53.6%	HRVIGSGCNLDSAR	99.7%	59.1	25	59.1	0	2	0	1541.76	157	170
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	17	26	125	0.13%	53.6%	ITVVGVGQVGMACAISILGK	99.7%	130	25	130	12	6	0	1973.09	24	43
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	17	26	125	0.13%	53.6%	IVADKDYSVTANSK	99.7%	88.1	25	81.2	11	2	0	1510.77	78	91
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	17	26	125	0.13%	53.6%	IVVVTAGVR	99.7%	81.3	25	63.4	9	0	0	913.58	92	100
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	17	26	125	0.13%	53.6%	KSADTLWDIQK	99.7%	58.9	25	51.8	2	0	0	1304.68	319	329
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	17	26	125	0.13%	53.6%	LIAPVAEEEATVPNNK	99.7%	90.9	25	90	14	2	0	1694.90	8	23
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	17	26	125	0.13%	53.6%	LKDDEVAQLK	99.7%	60.8	25	48.9	2	0	0	1158.64	309	318
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	17	26	125	0.13%	53.6%	MVVESAYEVIK	99.7%	96.9	25	91.7	27	0	0	1267.66	234	244
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	17	26	125	0.13%	53.6%	SADTLWDIQK	99.7%	81	25	64.3	9	0	0	1176.59	320	329
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	17	26	125	0.13%	53.6%	SADTLWDIQKDLK	99.7%	59.7	25	40	2	0	0	1532.80	320	332
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	17	26	125	0.13%	53.6%	SLADELALVDVLEDK	99.7%	67.5	25	51.8	2	0	0	1629.86	44	58
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	17	26	125	0.13%	53.6%	VIGSGCNLDSAR	99.7%	80.4	25	70.7	18	0	0	1248.60	159	170
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	7	7	13	0.01%	8.8%	DIIALNPLYR	99.7%	60	25	51.9	2	0	0	1187.68	302	311
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	7	7	13	0.01%	8.8%	FSVGGMTDVAEIK	99.7%	82.3	25	75.6	1	0	0	1353.67	547	559
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	7	7	13	0.01%	8.8%	ILEFIAVSQLR	99.7%	60	25	54.5	3	0	0	1288.76	501	511
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	7	7	13	0.01%	8.8%	LAQPYVGVFLK	99.7%	47.2	25	47.2	2	0	0	1234.72	159	169
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	7	7	13	0.01%	8.8%	LGLLDNHSSEFNVTR	95.0%	21.8	25	21.8	0	1	0	1701.86	445	459
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	7	7	13	0.01%	8.8%	LSSDVLTLLIK	99.7%	84.4	25	68.1	2	0	0	1201.74	691	701
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	7	7	13	0.01%	8.8%	TENPLILIDEVDK	99.7%	54.9	25	54.9	2	0	0	1498.80	582	594
Long-chain fatty acid transport protein 4	SLC27A4	S27A4_HUMAN	72.1	99.9%	2	2	6	0.01%	3.1%	ILSFVYPIR	99.7%	43.7	25	24.1	2	0	0	1107.66	409	417
Long-chain fatty acid transport protein 4	SLC27A4	S27A4_HUMAN	72.1	99.9%	2	2	6	0.01%	3.1%	TVPILFASTVR	99.7%	59.6	25	58.2	4	0	0	1203.71	75	85
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	8	8	16	0.02%	13.9%	AKPVNSKPDSAYR	98.9%	34.2	25	31.6	2	0	0	1432.75	57	69
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	8	8	16	0.02%	13.9%	IGYSSPQTLADQSSK	99.7%	78.7	25	77.2	2	0	0	1581.78	349	363
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	8	8	16	0.02%	13.9%	LKDIVSLVPR	99.7%	45.2	25	41	2	0	0	1139.71	221	230
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	8	8	16	0.02%	13.9%	LLLCGGAPLSATTQR	99.7%	90.7	25	72.7	2	0	0	1557.84	447	461
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	8	8	16	0.02%	13.9%	LQAGEYVSLGK	99.7%	40.2	25	38.7	2	0	0	1164.63	586	596
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	8	8	16	0.02%	13.9%	LSPEPWTPETGLVTDAFK	99.7%	63.5	25	60.9	2	0	0	1988.00	682	699
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	8	8	16	0.02%	13.9%	THYQADIER	96.1%	28.9	25	28.9	2	0	0	1132.54	707	715
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	8	8	16	0.02%	13.9%	VSEMSSFQR	99.7%	69.8	25	69.3	2	0	0	1086.49	398	406
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	8	8	18	0.02%	21.8%	GSIFVVFDSIESAK	99.7%	83	25	68.9	2	0	0	1498.78	152	165
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	8	8	18	0.02%	21.8%	GSIFVVFDSIESAKK	99.7%	62.9	25	62.4	2	0	0	1626.87	152	166
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	8	8	18	0.02%	21.8%	IIEDQQESLNK	99.7%	88.8	25	76.2	3	0	0	1316.67	318	328

Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	8	8	18	0.02%	21.8%	KFVETPGQK	99.1%	35.5	25	33.2	2	0	0	1033.57	166	174
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	8	8	18	0.02%	21.8%	LDEGWVPLEIMIK	99.7%	54.2	25	48.5	2	0	0	1542.82	42	54
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	8	8	18	0.02%	21.8%	LTTDFNVIVEALSK	99.7%	112	25	109	4	0	0	1549.85	61	74
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	8	8	18	0.02%	21.8%	QKLEEDAEMK	95.8%	28.6	25	22.1	1	0	0	1236.58	215	224
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	8	8	18	0.02%	21.8%	SPSKPLPEVTDEYKNDVK	99.2%	28.5	25	27.8	0	2	0	2046.04	92	109
Lymphoid-specific helicase	HELLS	HELLS_HUMAN	97.1	100.0%	3	4	4	0.00%	3.7%	EVVVYAPLSK	99.7%	40.8	25	33	1	0	0	1104.63	465	474
Lymphoid-specific helicase	HELLS	HELLS_HUMAN	97.1	100.0%	3	4	4	0.00%	3.7%	IGQTKPVVVYR	99.5%	38.3	25	30.9	1	0	0	1259.75	711	721
Lymphoid-specific helicase	HELLS	HELLS_HUMAN	97.1	100.0%	3	4	4	0.00%	3.7%	MEQQQLEEQK	99.7%	43.5	25	35.8	2	0	0	1306.59	86	95
Lys-63-specific deubiquitinase BRCC36	BRCC3	BRCC3_HUMAN	36.1	100.0%	3	3	5	0.01%	10.8%	TVAEKVDAVR	99.7%	44.2	25	34.2	2	0	0	1087.61	61	70
Lys-63-specific deubiquitinase BRCC36	BRCC3	BRCC3_HUMAN	36.1	100.0%	3	3	5	0.01%	10.8%	VCLESAVELPK	99.7%	56.1	25	40.4	1	0	0	1244.66	227	237
Lys-63-specific deubiquitinase BRCC36	BRCC3	BRCC3_HUMAN	36.1	100.0%	3	3	5	0.01%	10.8%	VLYTCFQSIQAQK	99.7%	79.5	25	74.7	2	0	0	1585.80	168	180
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	6	6	11	0.01%	11.2%	IAPELYHK	98.1%	32	25	3.03	2	0	0	970.54	298	305
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	6	6	11	0.01%	11.2%	LPETNLFETEETRK	99.7%	36.4	25	34.3	0	2	0	1706.86	408	421
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	6	6	11	0.01%	11.2%	MLVVGGIDR	99.7%	56.2	25	49.9	2	0	0	959.53	306	314
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	6	6	11	0.01%	11.2%	RGDIIGVQGNPGK	99.7%	64.4	25	61.7	2	0	0	1310.72	178	190
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	6	6	11	0.01%	11.2%	SEEEFIHINNK	99.7%	54.8	25	50.5	1	0	0	1359.65	165	175
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	6	6	11	0.01%	11.2%	VAMFLTDSNNIK	99.7%	52.3	25	49.3	2	0	0	1352.69	554	565
Lysophosphatidylcholine acyltransferase 1	LPCAT1	PCAT1_HUMAN	59.2	100.0%	4	4	6	0.01%	9.7%	AAPASSAGASDAR	99.7%	75.9	25	75.9	2	0	0	1131.54	10	22
Lysophosphatidylcholine acyltransferase 1	LPCAT1	PCAT1_HUMAN	59.2	100.0%	4	4	6	0.01%	9.7%	ITFADFHR	99.4%	37.3	25	31.8	1	0	0	1006.51	471	478
Lysophosphatidylcholine acyltransferase 1	LPCAT1	PCAT1_HUMAN	59.2	100.0%	4	4	6	0.01%	9.7%	NPFVHELR	99.7%	52.8	25	41.7	2	0	0	1011.54	30	37
Lysophosphatidylcholine acyltransferase 1	LPCAT1	PCAT1_HUMAN	59.2	100.0%	4	4	6	0.01%	9.7%	TCLITFKPGAFIPGAPVQPVVLR	99.7%	42.5	25	42.5	0	1	0	2481.41	215	237
Lysosomal protective protein	CTSA	PPGB_HUMAN	54.5	100.0%	2	2	3	0.00%	5.0%	EFSHIAFLTIK	99.4%	37.2	25	24.8	1	0	0	1305.72	443	453
Lysosomal protective protein	CTSA	PPGB_HUMAN	54.5	100.0%	2	2	3	0.00%	5.0%	YGDSGEQIAGFVK	99.7%	72.6	25	68.2	2	0	0	1370.66	430	442
Macrophage migration inhibitory factor	MIF	MIF_HUMAN	12.5	99.8%	2	3	6	0.01%	17.4%	LLCGLLAER	99.7%	70.2	25	54.4	2	0	0	1044.59	79	87
Macrophage migration inhibitory factor	MIF	MIF_HUMAN	12.5	99.8%	2	3	6	0.01%	17.4%	PMFIVNTNVPR	99.7%	84.5	25	76.3	4	0	0	1287.69	2	12
Magnesium transporter protein 1	MAGT1	MAGT1_HUMAN	38.0	100.0%	4	4	7	0.01%	12.2%	GFSAEQIAR	99.5%	38.1	25	28.5	2	0	0	978.50	160	168
Magnesium transporter protein 1	MAGT1	MAGT1_HUMAN	38.0	100.0%	4	4	7	0.01%	12.2%	QADEEFQILANSWR	97.7%	31.1	25	27.9	1	0	0	1706.81	92	105
Magnesium transporter protein 1	MAGT1	MAGT1_HUMAN	38.0	100.0%	4	4	7	0.01%	12.2%	RGDTYELQVR	99.7%	41.3	25	34	2	0	0	1236.63	150	159
Magnesium transporter protein 1	MAGT1	MAGT1_HUMAN	38.0	100.0%	4	4	7	0.01%	12.2%	YSSAFTNR	99.7%	55	25	47.6	2	0	0	945.44	106	113
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	7	7	12	0.01%	29.0%	AGAGSATLSMAYAGAR	99.7%	85.9	25	85.9	1	0	0	1470.70	242	257
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	7	7	12	0.01%	29.0%	ANTFVAELK	99.7%	48	25	27.4	2	0	0	992.54	177	185
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	7	7	12	0.01%	29.0%	IFGVTTLDIVR	99.7%	54.7	25	44.4	2	0	0	1233.72	166	176
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	7	7	12	0.01%	29.0%	SQETECTYFSTPLLLGK	99.7%	58.7	25	58.7	2	0	0	1973.95	280	296
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	7	7	12	0.01%	29.0%	VAVLGASGGIGQPLSLLLK	99.7%	91.7	25	91.7	2	0	0	1793.09	27	45
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	7	7	12	0.01%	29.0%	VDFPQDQLTALTGR	99.7%	76.5	25	71.7	2	0	0	1560.80	216	229
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	7	7	12	0.01%	29.0%	VNVPVIGGHAGK	99.7%	45.5	25	45.5	1	0	0	1147.66	192	203
Malectin	MLEC	MLEC_HUMAN	32.2	100.0%	4	4	10	0.01%	18.5%	FAEVYFAQSQQK	99.7%	76.9	25	76.9	3	0	0	1445.71	127	138
Malectin	MLEC	MLEC_HUMAN	32.2	100.0%	4	4	10	0.01%	18.5%	LSVQGEVSTFTGK	99.7%	64.9	25	64.9	3	0	0	1352.71	178	190
Malectin	MLEC	MLEC_HUMAN	32.2	100.0%	4	4	10	0.01%	18.5%	SNPEDQILYQTER	99.7%	59.5	25	55.3	2	0	0	1592.76	91	103
Malectin	MLEC	MLEC_HUMAN	32.2	100.0%	4	4	10	0.01%	18.5%	VCALYIMAGTVDDVPK	99.7%	101	25	78.1	2	0	0	1751.87	205	220
Malonyl-CoA-acyl carrier protein transacylase, mitochondrial	MCAT	FABD_HUMAN	43.0	100.0%	3	3	5	0.01%	9.0%	LLAQQLVSPVK	99.7%	55.1	25	54.2	2	0	0	1195.74	315	325
Malonyl-CoA-acyl carrier protein transacylase, mitochondrial	MCAT	FABD_HUMAN	43.0	100.0%	3	3	5	0.01%	9.0%	LMEPAVEPLTQALK	98.1%	31.9	25	26.4	1	0	0	1539.85	273	286
Malonyl-CoA-acyl carrier protein transacylase, mitochondrial	MCAT	FABD_HUMAN	43.0	100.0%	3	3	5	0.01%	9.0%	VISGHQEALR	99.7%	42.4	25	38.7	2	0	0	1109.61	237	246
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	7	7	10	0.01%	18.8%	AVILIGGPQK	99.7%	47.5	25	47.5	2	0	0	995.63	4	13
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	7	7	10	0.01%	18.8%	GNVYIHPTAK	96.9%	29.9	25	29.9	1	0	0	1099.59	285	294
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	7	7	10	0.01%	18.8%	GVTVGEGVR	99.7%	46.4	25	30.7	2	0	0	873.48	310	318
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	7	7	10	0.01%	18.8%	LLPAITILGCR	97.5%	30.8	25	30.8	1	0	0	1226.73	380	390
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	7	7	10	0.01%	18.8%	SAGSALYASR	99.7%	47.8	25	36.8	2	0	0	982.50	250	259
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	7	7	10	0.01%	18.8%	VAPSAVLGPNVSIGK	99.7%	64.5	25	64	1	0	0	1408.82	295	309
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	7	7	10	0.01%	18.8%	VEGTPSDPNPNDPR	99.0%	35.1	25	27.2	1	0	0	1494.68	353	366
Mannose-1-phosphate guanyltransferase beta	GMPPB	GMPPB_HUMAN	39.8	100.0%	3	3	6	0.01%	13.6%	ALILVGGYGTR	99.7%	67.9	25	67.9	2	0	0	1119.65	3	13

Mannose-1-phosphate guanyltransferase beta	GMPPB	GMPPB_HUMAN	39.8	100.0%	3	3	6	0.01%	13.6%	ISMSHEEEPLGTAGPLALAR	99.7%	39.1	25	35.3	0	2	0	2095.05	75	94
Mannose-1-phosphate guanyltransferase beta	GMPPB	GMPPB_HUMAN	39.8	100.0%	3	3	6	0.01%	13.6%	LCSGPGIVGNVLVDPSAR	99.7%	79.3	25	79.3	2	0	0	1810.95	244	261
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	14	16	44	0.04%	19.4%	DLDELSRYPEDK	99.3%	36.6	25	34.4	2	0	0	1479.70	121	132
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	14	16	44	0.04%	19.4%	GDADQASNILASFGLSAR	99.7%	80.8	25	80.8	4	0	0	1792.88	103	120
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	14	16	44	0.04%	19.4%	GNLGAGNGNLQGPR	99.6%	39.2	25	39.2	2	0	0	1324.67	374	387
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	14	16	44	0.04%	19.4%	GPGPLQER	99.3%	36.8	25	30.2	1	0	0	853.45	256	263
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	14	16	44	0.04%	19.4%	GPLPLSSQHR	99.7%	41.5	25	34.6	4	0	0	1091.60	93	102
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	14	16	44	0.04%	19.4%	IGPYQPNVPVGIDYVIPK	99.7%	57.5	25	57.5	5	0	0	1969.08	781	798
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	14	16	44	0.04%	19.4%	ITPENLPQILLQLK	99.7%	70.4	25	67.5	2	0	0	1619.97	133	146
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	14	16	44	0.04%	19.4%	LCSLFYTNEEVAK	99.7%	68.7	25	62	4	0	0	1573.76	805	817
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	14	16	44	0.04%	19.4%	MDYEDDRLR	99.7%	49.1	25	41.7	2	0	0	1212.53	217	225
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	14	16	44	0.04%	19.4%	SFQQSSLSR	99.7%	72.7	25	48.1	2	0	0	1039.52	4	12
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	14	16	44	0.04%	19.4%	SQAFIEMETR	99.7%	59.9	25	55	5	0	0	1211.57	533	542
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	14	16	44	0.04%	19.4%	SQESGYYDR	99.5%	38.2	25	38.2	3	0	0	1104.46	208	216
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	14	16	44	0.04%	19.4%	TEEGPTLSYGR	99.7%	57.6	25	49.6	4	0	0	1209.57	150	160
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	14	16	44	0.04%	19.4%	VVHIMDFQR	99.5%	38.6	25	29.3	4	0	0	1160.59	399	407
MAX gene-associated protein	MGA	MGAP_HUMAN	331.8	100.0%	4	4	6	0.01%	1.9%	ISNPSAFSIVPR	99.7%	65.7	25	55.3	2	0	0	1287.71	2208	2219
MAX gene-associated protein	MGA	MGAP_HUMAN	331.8	100.0%	4	4	6	0.01%	1.9%	VANPSSDADGQSLK	95.5%	28.3	25	21.7	1	0	0	1388.67	2957	2970
MAX gene-associated protein	MGA	MGAP_HUMAN	331.8	100.0%	4	4	6	0.01%	1.9%	VLQSEGEAVDPEANVIK	99.7%	80.3	25	80.3	2	0	0	1797.92	1954	1970
MAX gene-associated protein	MGA	MGAP_HUMAN	331.8	100.0%	4	4	6	0.01%	1.9%	VTLGPTQVFLANK	99.7%	40.5	25	39.3	1	0	0	1387.79	2672	2684
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	6	6	9	0.01%	5.3%	EVGNALLNVVLK	99.7%	47.8	25	35.8	2	0	0	1268.76	1121	1132
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	6	6	9	0.01%	5.3%	FLELLPVSK	95.4%	28.2	25	23.3	1	0	0	1045.63	974	982
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	6	6	9	0.01%	5.3%	FLTEVLLPIVK	99.7%	59.3	25	53.1	2	0	0	1271.80	1230	1240
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	6	6	9	0.01%	5.3%	LFDLLYPEK	99.7%	43.4	25	37.4	2	0	0	1137.62	398	406
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	6	6	9	0.01%	5.3%	LITALGSSEVQPQFTR	99.3%	36.4	25	33.8	1	0	0	1746.94	652	667
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	6	6	9	0.01%	5.3%	SSVALAPALVETYSR	98.5%	33.1	25	25.8	1	0	0	1563.84	555	569
Melanoma-associated antigen D2	MAGED2	MAGD2_HUMAN	65.0	100.0%	4	4	6	0.01%	9.9%	EAPATQASSTTQLTDTQVLAAENK	97.5%	24.3	25	22.5	0	1	0	2475.22	77	100
Melanoma-associated antigen D2	MAGED2	MAGD2_HUMAN	65.0	100.0%	4	4	6	0.01%	9.9%	EYTDVYPEIIER	99.7%	64.9	25	63	2	0	0	1526.74	312	323
Melanoma-associated antigen D2	MAGED2	MAGD2_HUMAN	65.0	100.0%	4	4	6	0.01%	9.9%	LQSSQEPEAPPPR	99.7%	71.9	25	66.4	2	0	0	1435.72	262	274
Melanoma-associated antigen D2	MAGED2	MAGD2_HUMAN	65.0	100.0%	4	4	6	0.01%	9.9%	SSEAVIWEVLR	99.7%	42.2	25	3.93	1	0	0	1288.69	386	396
Melanoma-associated antigen G1	NDNL2	MAGG1_HUMAN	34.3	99.8%	2	2	3	0.00%	9.2%	GPGGSQGSQGPSPQGAR	99.7%	45.7	25	45.7	2	0	0	1524.72	53	69
Melanoma-associated antigen G1	NDNL2	MAGG1_HUMAN	34.3	99.8%	2	2	3	0.00%	9.2%	VSELVQFLLIK	99.7%	45.9	25	41.1	1	0	0	1288.79	89	99
Metaxin-1	MTX1	MTX1_HUMAN	51.5	100.0%	3	3	4	0.00%	9.7%	ISNPWQSPSGTLPALR	99.7%	59.9	25	58.9	2	0	0	1723.91	191	206
Metaxin-1	MTX1	MTX1_HUMAN	51.5	100.0%	3	3	4	0.00%	9.7%	QGADTLAFMSLLEEK	99.7%	49.7	25	49.7	1	0	0	1668.82	238	252
Metaxin-1	MTX1	MTX1_HUMAN	51.5	100.0%	3	3	4	0.00%	9.7%	QTPAGPETEEEPYR	99.7%	53.8	25	52.3	1	0	0	1603.72	403	416
Metaxin-2	MTX2	MTX2_HUMAN	29.8	100.0%	4	5	8	0.01%	20.2%	ANAEYMSPSGK	99.7%	51.6	25	51.6	3	0	0	1154.51	61	71
Metaxin-2	MTX2	MTX2_HUMAN	29.8	100.0%	4	5	8	0.01%	20.2%	LGTQPYFFNK	99.7%	48.7	25	45.4	2	0	0	1214.62	197	206
Metaxin-2	MTX2	MTX2_HUMAN	29.8	100.0%	4	5	8	0.01%	20.2%	NYSNLLAFCR	99.1%	35.1	25	34.5	1	0	0	1257.60	238	247
Metaxin-2	MTX2	MTX2_HUMAN	29.8	100.0%	4	5	8	0.01%	20.2%	VPFIHVGNQVVSELGPIVQFVK	99.7%	64.4	25	64.4	0	2	0	2406.35	72	93
Methionine adenosyltransferase 2 subunit beta	MAT2B	MAT2B_HUMAN	37.6	99.8%	2	2	3	0.00%	7.5%	AVLENNLGAAVLR	99.4%	37.2	25	37.2	1	0	0	1339.77	169	181
Methionine adenosyltransferase 2 subunit beta	MAT2B	MAT2B_HUMAN	37.6	99.8%	2	2	3	0.00%	7.5%	VLVTGATGLLGR	99.7%	65.6	25	50.8	2	0	0	1156.71	31	42
Methionine synthase	MTR	METH_HUMAN	140.5	99.8%	2	2	3	0.00%	1.8%	IPLLIGGATTSK	99.4%	37	25	37	2	0	0	1170.71	854	865
Methionine synthase	MTR	METH_HUMAN	140.5	99.8%	2	2	3	0.00%	1.8%	LADIEQSTGIR	99.7%	49.6	25	42.2	1	0	0	1202.64	1192	1202
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	29	61	0.06%	35.1%	ADKNEVAAEVAK	99.7%	66.1	25	44.1	2	0	0	1244.65	864	875
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	29	61	0.06%	35.1%	AEVLISTVGPEDCVVPFLTRPK	99.7%	50.8	25	50.8	0	2	0	2427.30	26	47
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	29	61	0.06%	35.1%	ALTHIDHSLSR	99.7%	33.5	25	31	2	2	0	1249.66	120	130
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	29	61	0.06%	35.1%	FFGGYVPEMVLTPDDQR	99.7%	72	25	72	4	0	0	1970.93	664	680
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	29	61	0.06%	35.1%	FVEGVCPFCGYEEAR	99.7%	64.4	25	64.4	1	0	0	1819.78	400	414
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	29	61	0.06%	35.1%	GFVLQDTVEQLR	99.7%	90.6	25	75.5	4	0	0	1404.75	377	388
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	29	61	0.06%	35.1%	GLESLPPLRPQQNPVLPVAGER	99.7%	35.1	25	33.9	0	2	0	2367.31	243	264
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	29	61	0.06%	35.1%	GVGVFGDMAQDTGIPADIWR	99.7%	92.1	25	92.1	3	0	0	2105.01	599	618

Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	29	61	0.06%	35.1%	ITQDIFQQLLK	99.7%	69.4	25	53.9	6	0	0	1346.77	365	375
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	29	61	0.06%	35.1%	ITQDIFQQLLKR	99.7%	47.4	25	35.3	2	0	0	1502.87	365	376
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	29	61	0.06%	35.1%	KGEDVLGSVR	99.7%	57.2	25	48.7	2	0	0	1059.58	109	118
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	29	61	0.06%	35.1%	LENDQIESLR	99.7%	84.4	25	70	2	0	0	1216.62	805	814
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	29	61	0.06%	35.1%	LFVSDGVPGCLPVLAAAGR	99.7%	86	25	84.5	2	0	0	1899.02	3	21
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	29	61	0.06%	35.1%	LINAVELK	99.7%	45.2	25	33.5	2	0	0	899.56	424	431
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	29	61	0.06%	35.1%	NNSELLNNLGNFINR	99.7%	112	25	109	2	0	0	1731.88	642	656
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	29	61	0.06%	35.1%	NPEQVDLYQFMAK	99.7%	75.7	25	75.7	4	0	0	1582.76	542	554
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	29	61	0.06%	35.1%	QLAVAEGKPPEAPK	99.7%	76.7	25	75.1	2	1	0	1434.80	882	895
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	29	61	0.06%	35.1%	QPQPSPAEGR	99.7%	41.8	25	31.8	2	0	0	1066.53	205	214
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	29	61	0.06%	35.1%	QQGVLALRPYLQK	99.7%	63.8	25	60.3	2	0	0	1513.89	192	204
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	29	61	0.06%	35.1%	RLEEWLGR	99.7%	43.3	25	25.7	2	0	0	1058.57	460	467
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	29	61	0.06%	35.1%	SCPVVQSSQHLFLDLPK	99.7%	78.8	25	78.8	2	2	0	1955.01	440	456
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	29	61	0.06%	35.1%	TLPGSDWTPNAQFITR	99.7%	76.1	25	72.5	2	0	0	1803.90	468	483
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	29	61	0.06%	35.1%	VPVLQLDSGNYLFSTSAICR	99.7%	153	25	153	2	0	0	2240.14	48	67
Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	MCCC1	MCCA_HUMAN	80.5	99.8%	2	2	2	0.00%	3.6%	ESLCQAALGLILK	99.7%	72.5	25	62.1	1	0	0	1415.79	506	518
Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	MCCC1	MCCA_HUMAN	80.5	99.8%	2	2	2	0.00%	3.6%	LIILENTIYLFSK	99.7%	49.5	25	49.5	1	0	0	1566.91	611	623
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	20	222	0.22%	37.7%	AHAAQVTCVAASPHK	99.7%	102	25	99.9	9	16	0	1547.77	165	179
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	20	222	0.22%	37.7%	AHAAQVTCVAASPHKDSVFLSCSEDNR	99.6%	31	25	31	0	1	0	2957.36	165	191
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	20	222	0.22%	37.7%	CWAGSLWLFK	99.7%	48.1	25	45	10	0	0	1267.63	53	62
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	20	222	0.22%	37.7%	DSVFLSCSEDNR	99.7%	80.9	25	74.3	15	0	0	1428.61	180	191
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	20	222	0.22%	37.7%	ETPPPLVPPAAR	99.7%	49.2	25	33.6	7	0	0	1244.70	4	15
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	20	222	0.22%	37.7%	EWNLPPNAPACMER	99.7%	70.7	25	70.7	19	0	0	1684.76	16	29
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	20	222	0.22%	37.7%	FCKYEHDDIVSTVSVLSSGTQAVSGSK	99.7%	87.7	25	87.7	0	2	0	2901.39	119	145
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	20	222	0.22%	37.7%	ILLWDTR	99.7%	53.3	25	48.5	22	0	0	916.53	192	198
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	20	222	0.22%	37.7%	KETPPPLVPPAAR	99.7%	51	25	44.7	3	2	0	1372.79	3	15
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	20	222	0.22%	37.7%	SDGALLLGASSLSGR	99.7%	126	25	121	38	1	0	1403.75	38	52
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	20	222	0.22%	37.7%	VWDLAQQVVLSSYR	99.7%	117	25	109	27	6	0	1663.88	151	164
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	20	222	0.22%	37.7%	YEHDDIVSTVSVLSSGTQAVSGSK	99.7%	134	25	134	11	12	0	2466.20	122	145
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	20	222	0.22%	37.7%	YRSDGALLLGASSLSGR	99.7%	106	25	100	9	12	0	1722.91	36	52
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	5	7	37	0.04%	31.2%	DRSDCLGEHLYVMVNAK	99.7%	46.3	25	46.3	0	2	0	2006.94	69	85
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	5	7	37	0.04%	31.2%	GLGTGTLYIAESR	99.7%	101	25	91	8	0	0	1337.71	31	43
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	5	7	37	0.04%	31.2%	LEGMLSQSVSSQYNMAGVR	99.7%	110	25	106	15	3	0	2072.97	188	206
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	5	7	37	0.04%	31.2%	QQPDTEAVLNGK	99.7%	61.2	25	56.3	4	0	0	1299.65	19	30
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	5	7	37	0.04%	31.2%	SFPPPGPAEGLLR	99.7%	45	25	39.8	5	0	0	1337.72	6	18
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	10	10	17	0.02%	30.1%	DLADVAAR	98.5%	33	25	13.4	2	0	0	830.44	102	109
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	10	10	17	0.02%	30.1%	EAEREGATEEAVR	99.7%	42.4	25	36.4	2	0	0	1446.68	110	122
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	10	10	17	0.02%	30.1%	EGATEEAVR	97.6%	31	25	29.4	1	0	0	961.46	114	122
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	10	10	17	0.02%	30.1%	EIIIEERPGQELTDVNGVR	99.7%	46.9	25	46.9	0	1	0	2167.14	294	312
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	10	10	17	0.02%	30.1%	GSLQILDQLLLPK	99.7%	69.3	25	48.2	2	0	0	1437.87	11	23
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	10	10	17	0.02%	30.1%	GVSAVVVGADR	99.7%	76.9	25	64.4	2	0	0	1029.57	239	249
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	10	10	17	0.02%	30.1%	TALTTTISSR	99.7%	68.3	25	59.8	2	0	0	1050.58	351	360
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	10	10	17	0.02%	30.1%	VGTYQLAIVAK	99.7%	87.3	25	81.1	2	0	0	1162.68	260	270
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	10	10	17	0.02%	30.1%	VICCTEDMLEK	99.5%	38.6	25	34.3	1	0	0	1397.61	125	135
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	10	10	17	0.02%	30.1%	YEAVGSVHQAWEAIR	99.7%	45.9	25	40.3	0	2	0	1715.85	27	41
Microsomal glutathione S-transferase 1	MGST1	MGST1_HUMAN	17.6	100.0%	3	5	14	0.01%	27.1%	IYHTIAYLTPLPQPNR	99.7%	41.1	25	41.1	2	0	0	1897.03	115	130
Microsomal glutathione S-transferase 1	MGST1	MGST1_HUMAN	17.6	100.0%	3	5	14	0.01%	27.1%	KVFANPEDCVAFGK	99.7%	54.7	25	47.3	2	1	0	1581.77	42	55
Microsomal glutathione S-transferase 1	MGST1	MGST1_HUMAN	17.6	100.0%	3	5	14	0.01%	27.1%	MMLMSTATAFYR	99.7%	78.8	25	73.3	9	0	0	1422.66	27	38
Microsomal glutathione S-transferase 3	MGST3	MGST3_HUMAN	16.5	99.8%	2	2	4	0.00%	18.4%	IASGLGLAWIVGR	99.7%	46.6	25	41.7	2	0	0	1312.77	85	97
Microsomal glutathione S-transferase 3	MGST3	MGST3_HUMAN	16.5	99.8%	2	2	4	0.00%	18.4%	VLYAYGYYTGEPSKR	99.2%	36.1	25	34.8	2	0	0	1766.87	98	112
Microtubule-associated protein 1B	MAP1B	MAP1B_HUMAN	270.6	100.0%	3	3	4	0.00%	1.4%	AAKPTTTPEVK	97.3%	30.4	25	30.4	1	0	0	1142.64	2299	2309

Microtubule-associated protein 1B	MAP1B	MAP1B_HUMAN	270.6	100.0%	3	3	4	0.00%	1.4%	AVLDALLEGK	99.7%	78.8	25	65.6	2	0	0	1028.60	2400	2409
Microtubule-associated protein 1B	MAP1B	MAP1B_HUMAN	270.6	100.0%	3	3	4	0.00%	1.4%	SVGNTIDPVILFQK	98.0%	31.7	25	23.1	1	0	0	1530.85	401	414
Microtubule-associated protein RP/EB family member 2	MAPRE2	MARE2_HUMAN	37.0	100.0%	3	3	4	0.00%	12.2%	FQDNLDFIQWFK	99.7%	43.4	25	31.4	1	0	0	1600.78	144	155
Microtubule-associated protein RP/EB family member 2	MAPRE2	MARE2_HUMAN	37.0	100.0%	3	3	4	0.00%	12.2%	LALEGVEKER	99.7%	58.4	25	37.6	2	0	0	1143.64	256	265
Microtubule-associated protein RP/EB family member 2	MAPRE2	MARE2_HUMAN	37.0	100.0%	3	3	4	0.00%	12.2%	SSPAAKPGSTPSRPSSAK	98.0%	25.1	25	13.3	0	1	0	1712.89	208	225
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	6	6	8	0.01%	1.4%	ALEFGEPVLLVGDTGCGK	99.7%	87.9	25	85.5	2	0	0	1861.94	1379	1396
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	6	6	8	0.01%	1.4%	APAVQDLLTR	99.7%	61.4	25	53	2	0	0	1083.62	3340	3349
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	6	6	8	0.01%	1.4%	GEPVLLVGETGTGK	99.7%	64.3	25	42	1	0	0	1356.74	670	683
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	6	6	8	0.01%	1.4%	LLEEAQLQDLEK	99.7%	69.5	25	66.8	1	0	0	1428.76	222	233
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	6	6	8	0.01%	1.4%	LNAALATPAK	99.7%	42.6	25	34.8	1	0	0	969.57	4206	4215
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	6	6	8	0.01%	1.4%	TSLVEYLAAVTGR	99.4%	37.7	25	32	1	0	0	1379.75	336	348
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	8	8	12	0.01%	10.6%	AMVEAVQLIADGK	99.7%	85.7	25	76.4	2	0	0	1344.72	197	209
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	8	8	12	0.01%	10.6%	DLGEEALNEYLK	99.7%	76.2	25	65.6	2	0	0	1393.68	904	915
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	8	8	12	0.01%	10.6%	EESFGPIMVISK	99.7%	47.9	25	46.1	1	0	0	1336.68	824	835
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	8	8	12	0.01%	10.6%	FLFPEGIK	94.9%	27.8	25	13.8	1	0	0	950.53	189	196
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	8	8	12	0.01%	10.6%	GVINIIPGSGGIAGQR	99.7%	43.9	25	43.9	2	0	0	1508.85	642	657
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	8	8	12	0.01%	10.6%	LGFTGSTPIGK	99.7%	60	25	56	1	0	0	1077.59	667	677
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	8	8	12	0.01%	10.6%	SPLIIFNDCELDK	99.7%	58	25	52.5	2	0	0	1563.77	699	711
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	8	8	12	0.01%	10.6%	VVGVFTVPDKDGK	99.7%	46.3	25	39.2	1	0	0	1360.75	48	60
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	37	0.04%	53.2%	AVIGMTAGATGAFVGTPAEVALIR	99.7%	115	25	115	4	2	0	2289.23	123	146
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	37	0.04%	53.2%	AVVVNAAQLASYSQSK	99.7%	128	25	121	2	0	0	1635.87	191	206
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	37	0.04%	53.2%	EEGVLTLWR	99.6%	39	25	30	2	0	0	1102.59	174	182
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	37	0.04%	53.2%	FLFGGLAGMGATVFVQPLDLVK	97.6%	31	25	31	1	0	0	2296.24	25	46
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	37	0.04%	53.2%	GIYTGLSAGLLR	99.7%	89.7	25	79.5	2	0	0	1220.70	79	90
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	37	0.04%	53.2%	ITREEGVLTLWR	99.7%	39.2	25	36.8	2	2	0	1472.82	171	182
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	37	0.04%	53.2%	LGIYTVLFER	99.7%	84.7	25	80.3	4	0	0	1210.68	99	108
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	37	0.04%	53.2%	LTGADGTPPGFLLK	99.7%	76.2	25	64.9	2	0	0	1386.76	109	122
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	37	0.04%	53.2%	MIDGKPEYK	99.2%	35.8	25	31.1	4	0	0	1096.53	252	260
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	37	0.04%	53.2%	MTADGRLPADQR	96.2%	29	25	18.4	2	0	0	1330.65	147	158
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	37	0.04%	53.2%	NGLDVLFK	99.7%	47.8	25	34.7	2	0	0	905.51	261	268
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	37	0.04%	53.2%	NVFNALIR	99.5%	37.8	25	25.1	2	0	0	946.55	163	170
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	37	0.04%	53.2%	TSFHALTSILK	99.7%	47.8	25	37	2	1	0	1217.69	63	73
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	37	0.04%	53.2%	YEGFFSLWK	99.6%	39	25	31.6	1	0	0	1176.57	272	280
Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20	MCAT_HUMAN	32.9	100.0%	6	6	11	0.01%	18.6%	EGITGLYR	99.7%	48.3	25	41.2	2	0	0	908.48	66	73
Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20	MCAT_HUMAN	32.9	100.0%	6	6	11	0.01%	18.6%	ELIRDEGVTSLYK	99.7%	43	25	39.4	2	0	0	1522.81	255	267
Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20	MCAT_HUMAN	32.9	100.0%	6	6	11	0.01%	18.6%	GTVLTLMR	99.7%	50.9	25	39.4	2	0	0	906.51	171	178
Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20	MCAT_HUMAN	32.9	100.0%	6	6	11	0.01%	18.6%	KLYQEFGIR	99.7%	47.5	25	42.1	2	0	0	1153.64	158	166
Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20	MCAT_HUMAN	32.9	100.0%	6	6	11	0.01%	18.6%	RVSELSAPR	97.1%	30.1	25	20.2	1	0	0	1014.57	203	211
Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20	MCAT_HUMAN	32.9	100.0%	6	6	11	0.01%	18.6%	YTGTLDCAK	99.7%	43.2	25	33.8	2	0	0	1028.47	149	157
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	15	29	0.03%	48.4%	FAIYETVR	99.5%	38.2	25	34.7	2	0	0	998.53	79	86
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	15	29	0.03%	48.4%	GALVTVGQLSCYDQAK	99.7%	91.7	25	91.7	2	0	0	1709.85	171	186
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	15	29	0.03%	48.4%	GEYQGVFHCAVETAK	99.7%	63	25	63	2	2	0	1695.78	232	246
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	15	29	0.03%	48.4%	GSQGPLPFHEK	99.7%	48.7	25	38.3	2	0	0	1196.61	92	102
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	15	29	0.03%	48.4%	LFSGATMASSR	99.7%	71	25	63.5	2	0	0	1143.55	160	170
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	15	29	0.03%	48.4%	LGPLAFYK	99.7%	52.1	25	39	2	0	0	908.52	247	254
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	15	29	0.03%	48.4%	NYAHALDGLYR	99.7%	47.2	25	47.2	2	1	0	1292.64	140	150
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	15	29	0.03%	48.4%	QMTYSLTR	99.7%	43.5	25	36.1	2	0	0	999.49	71	78
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	15	29	0.03%	48.4%	TDGILALYSGLSASLCR	99.7%	100	25	100	2	0	0	1796.92	54	70
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	15	29	0.03%	48.4%	VHLQTQQEVK	99.7%	44.9	25	41.6	2	2	0	1209.66	32	41
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	15	29	0.03%	48.4%	VLLGSVSGLAGGFVGTPADLVNVR	99.7%	73.3	25	73.3	2	2	0	2298.28	103	126
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	5	5	9	0.01%	21.7%	KLYPTVGKPSSS	99.7%	42.3	25	41.8	2	0	0	1263.69	155	166

Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	5	5	9	0.01%	21.7%	LYPTVGKPSSS	99.7%	40.6	25	29.1	1	0	0	1135.60	156	166
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	5	5	9	0.01%	21.7%	SVDFLLDSSLR	99.7%	78.7	25	52.5	2	0	0	1251.66	144	154
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	5	5	9	0.01%	21.7%	SVDFLLDSSLRK	99.7%	45.4	25	36.1	2	0	0	1379.75	144	155
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	5	5	9	0.01%	21.7%	YLGYANEVGEAFR	99.7%	75.3	25	71.7	2	0	0	1488.71	21	33
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	8	8	16	0.02%	25.1%	GAAVNLTLVTPEK	99.7%	84.2	25	79.1	2	0	0	1312.75	68	80
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	8	8	16	0.02%	25.1%	GLGATLLR	98.5%	33.1	25	6.31	2	0	0	800.50	189	196
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	8	8	16	0.02%	25.1%	GVNEDTYSGILDCAR	99.7%	72.7	25	72.7	2	0	0	1669.75	259	273
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	8	8	16	0.02%	25.1%	HEGPSAFLK	98.6%	33.2	25	30.1	2	0	0	985.51	278	286
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	8	8	16	0.02%	25.1%	IQLQDAGR	99.7%	48.8	25	27.7	2	0	0	900.49	129	136
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	8	8	16	0.02%	25.1%	LAANDFFR	99.7%	55.4	25	44.2	2	0	0	953.48	84	91
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	8	8	16	0.02%	25.1%	SEGYFGMYR	99.6%	38.9	25	38.9	2	0	0	1125.47	59	67
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	8	8	16	0.02%	25.1%	VYTSMSDCLIK	99.7%	43.8	25	38.4	2	0	0	1316.62	45	55
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	11	24	0.02%	29.7%	AQGPQQQPGSEGPSYAK	99.7%	74.8	25	74.7	6	0	0	1729.81	48	64
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	11	24	0.02%	29.7%	IPDEFDNDPILVQQLR	99.7%	81.9	25	73.2	2	0	0	1911.98	98	113
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	11	24	0.02%	29.7%	QNLFLGSLTSR	99.7%	59.5	25	46.2	2	0	0	1235.67	335	345
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	11	24	0.02%	29.7%	RAPDQAAEIGSR	99.7%	62.9	25	55.8	2	1	0	1270.65	32	43
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	11	24	0.02%	29.7%	SNKQNLFLGSLTSR	99.7%	72.1	25	72.1	2	0	0	1564.84	332	345
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	11	24	0.02%	29.7%	TIALNGVEDVR	99.7%	68.8	25	55	2	0	0	1186.64	285	295
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	11	24	0.02%	29.7%	TVLEHYALEDDPLAAFK	99.7%	64.7	25	59.6	2	2	0	1931.98	296	312
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	11	24	0.02%	29.7%	VLLDLSAFLK	99.7%	71.6	25	71.6	1	0	0	1118.68	275	284
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	11	24	0.02%	29.7%	VVVVDCKK	98.1%	32	25	31.9	2	0	0	946.54	244	251
Mitochondrial import receptor subunit TOM22 homolog	TOMM22	TOM22_HUMAN	15.5	99.8%	2	4	13	0.01%	16.2%	LQMEQQQQLQQR	99.7%	78.2	25	61.3	9	0	0	1557.78	106	117
Mitochondrial import receptor subunit TOM22 homolog	TOMM22	TOM22_HUMAN	15.5	99.8%	2	4	13	0.01%	16.2%	LWGLTEMFPER	99.7%	40.8	25	35.2	4	0	0	1378.68	48	58
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	7	10	18	0.02%	21.9%	ELFPIQMEGVK	99.7%	57	25	45.2	4	0	0	1290.68	92	102
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	7	10	18	0.02%	21.9%	FQCGFGLTIG	95.3%	28.1	25	20.7	1	0	0	1099.52	352	361
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	7	10	18	0.02%	21.9%	FVNWQVDGEYR	99.7%	52.4	25	48.6	2	0	0	1412.66	185	195
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	7	10	18	0.02%	21.9%	GSVDSNWIVGATLEK	99.7%	106	25	95.5	2	0	0	1575.80	316	330
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	7	10	18	0.02%	21.9%	MQDTSVSFGYQLDLPK	99.7%	98	25	98	4	0	0	1844.87	294	309
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	7	10	18	0.02%	21.9%	NKFQCGFGLTIG	99.7%	50.4	25	50.4	2	0	0	1341.66	350	361
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	7	10	18	0.02%	21.9%	RPGEEGTVMSLAGK	99.7%	61	25	49.2	2	1	0	1447.72	240	253
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	17	49	0.05%	23.4%	AAMDNSEIAGEKK	97.5%	30.7	25	30.7	2	0	0	1379.65	258	270
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	17	49	0.05%	23.4%	AVDEAADALLK	99.7%	65.3	25	46.5	4	0	0	1115.59	287	297
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	17	49	0.05%	23.4%	ELDSITPEVLPGWK	99.7%	70.1	25	65.5	4	0	0	1583.83	372	385
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	17	49	0.05%	23.4%	ERPPEEVAAR	99.7%	43.3	25	33.6	4	0	0	1153.60	196	205
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	17	49	0.05%	23.4%	EVAGAKPHITAAEGK	99.7%	57	25	51.7	1	1	0	1478.80	316	330
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	17	49	0.05%	23.4%	GVYSEETLR	99.7%	66.2	25	48.9	4	0	0	1053.52	624	632
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	17	49	0.05%	23.4%	LAQQEKQEQVK	96.3%	29.1	25	24.8	1	0	0	1328.72	206	216
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	17	49	0.05%	23.4%	LHNMIVDLDNVVK	99.7%	60.2	25	60.2	2	0	0	1509.81	331	343
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	17	49	0.05%	23.4%	LSEQELQFR	99.7%	70.4	25	45.5	4	0	0	1149.59	517	525
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	17	49	0.05%	23.4%	SEFEQNLSEK	99.7%	46.8	25	37.2	2	0	0	1210.56	507	516
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	17	49	0.05%	23.4%	TSSAETPTIPLGSAVEAIK	99.7%	102	25	94.9	4	0	0	1872.00	582	600
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	17	49	0.05%	23.4%	TVEGALKER	99.3%	36.8	25	28.1	2	0	0	1002.56	276	284
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	17	49	0.05%	23.4%	VAMIDETR	99.7%	46.7	25	40.2	4	0	0	934.47	645	652
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	17	49	0.05%	23.4%	VVSQYHELVVQAR	99.7%	84.8	25	78.4	3	3	0	1527.83	354	366
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	17	49	0.05%	23.4%	YSTSGSSGLTTGK	99.7%	79.4	25	77.1	4	0	0	1245.60	33	45
Mitochondrial inner membrane protein OXA1L	OXA1L	OXA1L_HUMAN	48.5	100.0%	6	7	13	0.01%	13.6%	ASSEMALYQK	99.7%	58.6	25	55	4	0	0	1127.54	198	207
Mitochondrial inner membrane protein OXA1L	OXA1L	OXA1L_HUMAN	48.5	100.0%	6	7	13	0.01%	13.6%	CLIFPLIVTGQR	99.7%	67.5	25	55.2	3	0	0	1416.80	153	164
Mitochondrial inner membrane protein OXA1L	OXA1L	OXA1L_HUMAN	48.5	100.0%	6	7	13	0.01%	13.6%	EGFLESFKK	95.3%	28.1	25	19.9	1	0	0	1084.57	359	367
Mitochondrial inner membrane protein OXA1L	OXA1L	OXA1L_HUMAN	48.5	100.0%	6	7	13	0.01%	13.6%	LAGDHIEYYK	99.7%	51.1	25	42.2	2	0	0	1208.59	188	197
Mitochondrial inner membrane protein OXA1L	OXA1L	OXA1L_HUMAN	48.5	100.0%	6	7	13	0.01%	13.6%	NQLELAAR	99.7%	45.6	25	19.1	2	0	0	914.51	387	394
Mitochondrial inner membrane protein OXA1L	OXA1L	OXA1L_HUMAN	48.5	100.0%	6	7	13	0.01%	13.6%	SKYPWHDTLG	99.6%	39.4	25	39.4	1	0	0	1203.58	426	435

Mitochondrial ornithine transporter 1	SLC25A15	ORNT1_HUMAN	32.7	100.0%	5	6	8	0.01%	15.9%	GLTDCCLK	96.1%	28.9	25	20.6	1	0	0	966.44	46	53
Mitochondrial ornithine transporter 1	SLC25A15	ORNT1_HUMAN	32.7	100.0%	5	6	8	0.01%	15.9%	IQVLSMSGK	98.2%	32.1	25	19.2	1	0	0	962.53	237	245
Mitochondrial ornithine transporter 1	SLC25A15	ORNT1_HUMAN	32.7	100.0%	5	6	8	0.01%	15.9%	LQTMYEMETSGK	99.7%	57.1	25	55.9	3	0	0	1417.63	134	145
Mitochondrial ornithine transporter 1	SLC25A15	ORNT1_HUMAN	32.7	100.0%	5	6	8	0.01%	15.9%	MQTFPDLYR	98.2%	32.2	25	18.5	1	0	0	1170.56	37	45
Mitochondrial ornithine transporter 1	SLC25A15	ORNT1_HUMAN	32.7	100.0%	5	6	8	0.01%	15.9%	SQNTVWSVIK	99.7%	60	25	49.1	2	0	0	1161.63	149	158
Mitochondrial pyruvate carrier 2	MPC2	MPC2_HUMAN	14.3	100.0%	2	2	5	0.01%	14.2%	TVFFWAPIMK	99.5%	38.6	25	25.4	3	0	0	1239.66	40	49
Mitochondrial pyruvate carrier 2	MPC2	MPC2_HUMAN	14.3	100.0%	2	2	5	0.01%	14.2%	YSLVIIPK	99.6%	39.2	25	39.2	2	0	0	932.58	85	92
Mitochondrial Rho GTPase 2	RHOT2	MIRO2_HUMAN	68.1	100.0%	5	5	9	0.01%	8.3%	ILLLGEAQVGK	99.7%	75.4	25	47.1	2	0	0	1140.70	7	17
Mitochondrial Rho GTPase 2	RHOT2	MIRO2_HUMAN	68.1	100.0%	5	5	9	0.01%	8.3%	NISELFYYAQK	98.2%	32.2	25	16.3	2	0	0	1375.69	154	164
Mitochondrial Rho GTPase 2	RHOT2	MIRO2_HUMAN	68.1	100.0%	5	5	9	0.01%	8.3%	SAFLQAFLGR	99.7%	70.5	25	56.5	2	0	0	1109.61	430	439
Mitochondrial Rho GTPase 2	RHOT2	MIRO2_HUMAN	68.1	100.0%	5	5	9	0.01%	8.3%	SFAHCASVYK	99.7%	40.4	25	36.1	1	0	0	1169.54	500	509
Mitochondrial Rho GTPase 2	RHOT2	MIRO2_HUMAN	68.1	100.0%	5	5	9	0.01%	8.3%	VPIILVGNK	99.7%	42	25	0	2	0	0	952.62	111	119
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	16	17	44	0.04%	46.4%	DSIIYLTADSPNVMTTFR	99.7%	67.8	25	64.8	7	0	0	2044.01	285	302
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	16	17	44	0.04%	46.4%	EVPEHITEEELK	99.7%	50.2	25	42.5	3	0	0	1452.72	107	118
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	16	17	44	0.04%	46.4%	LLETTEEDKQK	99.7%	62.6	25	55.4	4	0	0	1333.68	165	175
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	16	17	44	0.04%	46.4%	LLLTSTEK	98.9%	34.4	25	25.9	2	0	0	904.54	269	276
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	16	17	44	0.04%	46.4%	NESTPPSEELELDKWK	99.3%	36.4	25	32	1	0	0	1901.91	52	67
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	16	17	44	0.04%	46.4%	NFLFLR	98.1%	31.9	25	9.17	2	0	0	809.47	176	181
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	16	17	44	0.04%	46.4%	NLTLDQMIR	99.0%	35	25	26.7	1	0	0	1103.59	350	358
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	16	17	44	0.04%	46.4%	NMDIAMGWK	99.6%	39.2	25	30.6	2	0	0	1065.49	186	194
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	16	17	44	0.04%	46.4%	NNGNWQEALQFVPK	99.7%	52.3	25	46.7	2	0	0	1644.81	365	378
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	16	17	44	0.04%	46.4%	NVDPFHIYFCNLK	99.7%	40.3	25	40.3	2	0	0	1666.80	237	249
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	16	17	44	0.04%	46.4%	SMQPGTSLAK	99.7%	62.2	25	48	6	0	0	1019.52	316	325
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	16	17	44	0.04%	46.4%	SSVQEECVSTISSSKDEDPLAATR	99.7%	55.5	25	55.5	0	2	0	2596.20	72	95
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	16	17	44	0.04%	46.4%	TLMECVSNTAK	99.5%	38.6	25	34.8	2	0	0	1269.58	119	129
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	16	17	44	0.04%	46.4%	VYVIGSFVDK	99.7%	56.4	25	56.4	5	0	0	1126.61	306	315
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	16	17	44	0.04%	46.4%	YLQWEIGNK	99.7%	47	25	39.3	2	0	0	1150.59	341	349
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	16	17	44	0.04%	46.4%	YQEKWDK	98.5%	32.9	25	13.1	1	0	0	996.48	262	268
Mitochondrial ribonuclease P protein 3	KIAA0391	MRRP3_HUMAN	67.3	100.0%	4	4	9	0.01%	7.7%	DVIDGGDQYRK	99.7%	52.5	25	52.5	2	0	0	1265.61	375	385
Mitochondrial ribonuclease P protein 3	KIAA0391	MRRP3_HUMAN	67.3	100.0%	4	4	9	0.01%	7.7%	EALLLLEDIKK	99.7%	55.2	25	50.5	2	0	0	1284.78	228	238
Mitochondrial ribonuclease P protein 3	KIAA0391	MRRP3_HUMAN	67.3	100.0%	4	4	9	0.01%	7.7%	ESQLLLNVVSQLAK	99.7%	68.1	25	65.7	3	0	0	1541.89	422	435
Mitochondrial ribonuclease P protein 3	KIAA0391	MRRP3_HUMAN	67.3	100.0%	4	4	9	0.01%	7.7%	LLDILSYLR	99.7%	53.1	25	53.1	2	0	0	1105.66	301	309
Mitochondrial thiamine pyrophosphate carrier	SLC25A19	TPC_HUMAN	35.5	100.0%	3	3	4	0.00%	10.0%	ALISPFDVIK	95.9%	28.7	25	23.5	1	0	0	1102.65	31	40
Mitochondrial thiamine pyrophosphate carrier	SLC25A19	TPC_HUMAN	35.5	100.0%	3	3	4	0.00%	10.0%	QILQEEGPTAFWK	99.0%	34.8	25	28.2	1	0	0	1546.79	68	80
Mitochondrial thiamine pyrophosphate carrier	SLC25A19	TPC_HUMAN	35.5	100.0%	3	3	4	0.00%	10.0%	SEGPQVFYK	99.7%	50.8	25	41.1	2	0	0	1054.52	168	176
Mitogen-activated protein kinase kinase kinase 7	MAP3K7	M3K7_HUMAN	67.2	100.0%	2	2	2	0.00%	5.3%	MITTSGPTSEKPTR	99.7%	45	25	43.1	1	0	0	1521.76	464	477
Mitogen-activated protein kinase kinase kinase 7	MAP3K7	M3K7_HUMAN	67.2	100.0%	2	2	2	0.00%	5.3%	SIQDLTVTGTEPGQVSSR	99.7%	66.8	25	61.7	1	0	0	1874.95	439	456
Mitotic checkpoint protein BUB3	BUB3	BUB3_HUMAN	37.2	100.0%	4	4	6	0.01%	15.5%	LNQPPEDGISSVK	99.7%	45.3	25	45.3	1	0	0	1383.71	9	21
Mitotic checkpoint protein BUB3	BUB3	BUB3_HUMAN	37.2	100.0%	4	4	6	0.01%	15.5%	QGYVLSSIEGR	99.7%	87	25	81.1	1	0	0	1208.63	192	202
Mitotic checkpoint protein BUB3	BUB3	BUB3_HUMAN	37.2	100.0%	4	4	6	0.01%	15.5%	TPCNAGTFSQPEK	99.7%	72.8	25	68	2	0	0	1436.65	127	139
Mitotic checkpoint protein BUB3	BUB3	BUB3_HUMAN	37.2	100.0%	4	4	6	0.01%	15.5%	VAVEYLDPSPEVQK	99.7%	52.5	25	45.5	2	0	0	1573.81	203	216
Mitotic spindle assembly checkpoint protein MAD2A	MAD2L1	MD2L1_HUMAN	23.5	100.0%	3	3	4	0.00%	13.2%	GIYPSETFTR	97.9%	31.5	25	27.3	1	0	0	1170.58	36	45
Mitotic spindle assembly checkpoint protein MAD2A	MAD2L1	MD2L1_HUMAN	23.5	100.0%	3	3	4	0.00%	13.2%	SFTTTIHK	99.6%	38.8	25	18.6	1	0	0	934.50	185	192
Mitotic spindle assembly checkpoint protein MAD2A	MAD2L1	MD2L1_HUMAN	23.5	100.0%	3	3	4	0.00%	13.2%	WQFDIECDK	99.5%	38.7	25	38.7	2	0	0	1240.53	100	108
MKI67 FHA domain-interacting nucleolar phosphoprotein	NIFK	MK67I_HUMAN	34.2	100.0%	3	3	5	0.01%	14.0%	GIDYDFPSLILQK	99.7%	77.4	25	75.4	2	0	0	1508.80	180	192
MKI67 FHA domain-interacting nucleolar phosphoprotein	NIFK	MK67I_HUMAN	34.2	100.0%	3	3	5	0.01%	14.0%	GYAFVEFESEDVAK	99.7%	66.3	25	65.7	1	0	0	1590.73	87	100
MKI67 FHA domain-interacting nucleolar phosphoprotein	NIFK	MK67I_HUMAN	34.2	100.0%	3	3	5	0.01%	14.0%	IVAETMNNYLFGER	99.7%	76.8	25	75.3	2	0	0	1656.81	101	114
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	6	6	10	0.01%	6.4%	EDLILSLR	99.7%	49.3	25	16.5	2	0	0	958.56	239	246
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	6	6	10	0.01%	6.4%	FAEFLLPLLIEK	99.7%	72.1	25	65.7	3	0	0	1432.85	255	266
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	6	6	10	0.01%	6.4%	GLSHVLNR	98.0%	31.7	25	27	1	0	0	895.51	894	901
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	6	6	10	0.01%	6.4%	LLQAAAGASAR	99.7%	80.6	25	78.2	2	0	0	1028.58	374	384

MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	6	6	10	0.01%	6.4%	LPTPVLLPYKPQVIR	98.9%	27.4	25	27.4	0	1	0	1734.07	984	998
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	6	6	10	0.01%	6.4%	NVEIPQLNQLMR	99.7%	41.8	25	37.8	1	0	0	1454.78	728	739
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	8	10	20	0.02%	29.5%	AYLEPEHTK	96.0%	28.8	25	23	1	0	0	1087.54	24	32
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	8	10	20	0.02%	29.5%	CTAPQYVDFVMSSVQK	99.7%	70.6	25	66.1	3	1	0	1859.87	105	120
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	8	10	20	0.02%	29.5%	EFNLLDPK	95.5%	28.4	25	13.1	1	0	0	975.51	188	195
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	8	10	20	0.02%	29.5%	EFPSSFESLVR	99.7%	72.1	25	71.6	4	0	0	1297.64	135	145
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	8	10	20	0.02%	29.5%	ELVVLPR	99.7%	41.3	25	8.59	3	0	0	825.52	42	48
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	8	10	20	0.02%	29.5%	ITDFQFK	99.6%	39.8	25	15.3	2	0	0	898.47	35	41
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	8	10	20	0.02%	29.5%	KAYLEPEHTK	98.8%	26.9	25	26.9	0	1	0	1215.64	23	32
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	8	10	20	0.02%	29.5%	LVTDEDVFPTK	99.7%	81.1	25	71.7	4	0	0	1263.65	121	131
Monocarboxylate transporter 1	SLC16A1	MOT1_HUMAN	53.9	100.0%	3	3	10	0.01%	8.2%	DLHDANTDLIGR	99.7%	56	25	46.7	6	0	0	1339.66	225	236
Monocarboxylate transporter 1	SLC16A1	MOT1_HUMAN	53.9	100.0%	3	3	10	0.01%	8.2%	ESKEEETSIDVAGKPNEVTK	99.7%	50.8	25	50.8	0	3	0	2190.08	460	479
Monocarboxylate transporter 1	SLC16A1	MOT1_HUMAN	53.9	100.0%	3	3	10	0.01%	8.2%	LNDMYGDYK	97.0%	30	25	30	1	0	0	1118.48	412	420
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	27	53	0.05%	28.4%	AEIDLVCELAK	99.7%	82.6	25	73.1	2	0	0	1260.65	808	818
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	27	53	0.05%	28.4%	ASGLVPNVVVLVATVR	99.7%	56.3	25	56.3	2	1	0	1593.97	730	745
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	27	53	0.05%	28.4%	AVIELLEK	99.7%	51.7	25	24.5	2	0	0	914.56	206	213
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	27	53	0.05%	28.4%	DFILPISDVR	99.7%	54.6	25	44.7	2	0	0	1174.65	926	935
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	27	53	0.05%	28.4%	DIELSPEAQAK	99.7%	69	25	56.9	2	0	0	1200.61	881	891
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	27	53	0.05%	28.4%	DVDGVTDINLGK	99.7%	65.8	25	58.2	2	0	0	1245.63	178	189
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	27	53	0.05%	28.4%	EFSEIQLAR	99.7%	66.3	25	35	3	0	0	1092.57	531	539
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	27	53	0.05%	28.4%	EIGLLADEIEIYGK	99.7%	102	25	99	3	0	0	1562.83	380	393
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	27	53	0.05%	28.4%	EVLSLLQEK	99.7%	50.2	25	42.7	2	0	0	1058.61	84	92
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	27	53	0.05%	28.4%	FQFLYDVQVPIVDK	99.7%	94.7	25	94.5	2	0	0	1710.91	855	868
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	27	53	0.05%	28.4%	GDAHECFVSPVAK	99.7%	36.2	25	36.2	0	2	0	1416.66	193	205
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	27	53	0.05%	28.4%	ILHENTQTDK	99.7%	46.2	25	42.7	2	1	0	1198.61	507	516
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	27	53	0.05%	28.4%	IQNMVSSGR	99.7%	47.5	25	41.4	2	0	0	991.50	327	335
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	27	53	0.05%	28.4%	KITIGQGNTEK	99.7%	48.8	25	37.8	2	0	0	1188.66	586	596
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	27	53	0.05%	28.4%	LDIDPSTITWQR	99.7%	73	25	63.2	2	0	0	1444.74	564	575
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	27	53	0.05%	28.4%	LQPLSPVPSDIEISR	99.7%	60.2	25	59.2	2	0	0	1650.91	353	367
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	27	53	0.05%	28.4%	LVPLVNGVR	99.7%	53	25	53	2	0	0	966.61	522	530
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	27	53	0.05%	28.4%	MHGGGPSVTAGVPLKK	99.2%	28.5	25	28.5	0	2	0	1535.84	749	764
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	27	53	0.05%	28.4%	SGQPVTADDLGVTGALTVLMK	99.7%	101	25	98.8	4	0	0	2073.09	639	659
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	27	53	0.05%	28.4%	TDPSTLTEEEVSK	99.7%	79.4	25	70.1	2	0	0	1435.68	548	560
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	27	53	0.05%	28.4%	TIAQAVYGAK	99.7%	57.9	25	45.3	3	0	0	1021.57	871	880
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	27	53	0.05%	28.4%	VLNALKPEK	97.9%	31.5	25	29.5	1	0	0	1011.62	169	177
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	27	53	0.05%	28.4%	YVLVAGITPTPLGEGK	99.7%	100	25	99.1	3	0	0	1614.91	414	429
Motile sperm domain-containing protein 2	MOSPD2	MSPD2_HUMAN	59.7	100.0%	5	5	8	0.01%	10.0%	EISVNDLNESSIPR	99.7%	95.7	25	86.2	1	0	0	1572.79	74	87
Motile sperm domain-containing protein 2	MOSPD2	MSPD2_HUMAN	59.7	100.0%	5	5	8	0.01%	10.0%	KLEDQVQR	97.1%	30.2	25	11.5	1	0	0	1015.55	483	490
Motile sperm domain-containing protein 2	MOSPD2	MSPD2_HUMAN	59.7	100.0%	5	5	8	0.01%	10.0%	LIAFWLER	99.7%	55.3	25	44	2	0	0	1047.60	128	135
Motile sperm domain-containing protein 2	MOSPD2	MSPD2_HUMAN	59.7	100.0%	5	5	8	0.01%	10.0%	TLIVLTNVTK	99.7%	48.2	25	48.2	2	0	0	1101.69	348	357
Motile sperm domain-containing protein 2	MOSPD2	MSPD2_HUMAN	59.7	100.0%	5	5	8	0.01%	10.0%	TWLGPEAVSLLK	99.7%	43.5	25	20	2	0	0	1313.75	200	211
mRNA export factor	RAE1	RAE1L_HUMAN	41.0	100.0%	6	6	10	0.01%	20.1%	CWEVQDSGQTIPK	99.7%	65.8	25	64.7	2	0	0	1547.72	68	80
mRNA export factor	RAE1	RAE1L_HUMAN	41.0	100.0%	6	6	10	0.01%	20.1%	FSFWDKDAR	98.7%	33.8	25	27.6	2	0	0	1171.55	297	305
mRNA export factor	RAE1	RAE1L_HUMAN	41.0	100.0%	6	6	10	0.01%	20.1%	GLIVYQLENQPSEFR	99.7%	78.6	25	76.5	1	0	0	1792.92	191	205
mRNA export factor	RAE1	RAE1L_HUMAN	41.0	100.0%	6	6	10	0.01%	20.1%	NAAEELKPR	99.7%	43.3	25	34.4	2	0	0	1027.55	357	365
mRNA export factor	RAE1	RAE1L_HUMAN	41.0	100.0%	6	6	10	0.01%	20.1%	QNKPTGFALGSIEGR	97.8%	24.7	25	24.7	0	1	0	1574.83	225	239
mRNA export factor	RAE1	RAE1L_HUMAN	41.0	100.0%	6	6	10	0.01%	20.1%	SSNPMMVLQLPER	99.7%	46.7	25	41.6	2	0	0	1501.75	160	172
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	8	10	15	0.02%	36.8%	EGDVLTPEQAR	95.5%	28.3	25	8.91	1	0	0	1214.60	178	188
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	8	10	15	0.02%	36.8%	GEVGLLFTNR	99.7%	66	25	59.6	2	0	0	1105.60	98	107
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	8	10	15	0.02%	36.8%	GVVTLLSDYEVCK	99.7%	94.8	25	90.9	2	0	0	1482.75	165	177
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	8	10	15	0.02%	36.8%	QNLIEELRK	97.0%	30	25	11.3	1	0	0	1142.65	24	32

mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	8	10	15	0.02%	36.8%	SPSDEYKDNLHQVSK	99.7%	38.3	25	38.3	1	2	0	1746.83	80	94
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	8	10	15	0.02%	36.8%	TKEEVNEWFTK	99.7%	46.2	25	41.9	1	0	0	1410.69	108	118
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	8	10	15	0.02%	36.8%	YLFIFSVANMR	99.7%	58.2	25	51.6	4	0	0	1360.71	39	49
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	8	10	15	0.02%	36.8%	YTEMDYAR	99.6%	39.5	25	38.2	1	0	0	1064.44	119	126
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	10	10	17	0.02%	29.2%	ACGNFGIPCELR	99.7%	52.9	25	51	2	0	0	1393.64	287	298
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	10	10	17	0.02%	29.2%	ASILNTWISLK	99.7%	77	25	68.7	2	0	0	1245.72	404	414
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	10	10	17	0.02%	29.2%	DQITAGNAAR	98.5%	32.9	25	23.5	2	0	0	1016.51	37	46
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	10	10	17	0.02%	29.2%	EIVLADVIDNDSWR	99.7%	119	25	111	2	0	0	1644.82	202	215
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	10	10	17	0.02%	29.2%	EVTPEGLQMVK	99.1%	35.1	25	26	2	0	0	1230.64	236	246
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	10	10	17	0.02%	29.2%	IATGSFLKR	99.7%	67.8	25	58.8	2	0	0	992.59	103	111
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	10	10	17	0.02%	29.2%	ITSCIFQLLQEAGIK	99.7%	81.9	25	77	1	0	0	1720.93	60	74
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	10	10	17	0.02%	29.2%	TKEVYELLDSPGK	99.7%	87.9	25	78.1	2	0	0	1478.77	18	30
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	10	10	17	0.02%	29.2%	VTSAHKGPDETLR	99.3%	36.5	25	31.4	1	0	0	1410.73	299	311
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	10	10	17	0.02%	29.2%	VVVLMGSTSDLGHCEK	99.7%	78.2	25	76.9	1	0	0	1731.84	268	283
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	18	18	36	0.04%	14.3%	ALVDILSEVSK	99.7%	82.7	25	72.9	2	0	0	1173.67	180	190
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	18	18	36	0.04%	14.3%	ATLQEILPEVLK	99.7%	51.5	25	46.1	2	0	0	1353.80	191	202
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	18	18	36	0.04%	14.3%	EIPSATQSPISK	99.7%	45	25	37.9	2	0	0	1257.67	1156	1167
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	18	18	36	0.04%	14.3%	ELEAHSAEAR	99.5%	38.2	25	36.2	1	0	0	1112.53	582	591
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	18	18	36	0.04%	14.3%	EQLHLVMQGDVIR	99.1%	35.3	25	28.5	1	0	0	1553.81	319	331
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	18	18	36	0.04%	14.3%	EVVEQGLLK	99.7%	45	25	35.8	3	0	0	1014.58	287	295
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	18	18	36	0.04%	14.3%	GNTAEGCVHETQEK	99.7%	49.5	25	49.5	2	0	0	1559.68	936	949
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	18	18	36	0.04%	14.3%	HQACLLLQK	98.0%	31.8	25	27.2	2	0	0	1110.61	1028	1036
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	18	18	36	0.04%	14.3%	KPTSQIPETK	98.4%	32.8	25	31.4	1	0	0	1128.63	489	498
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	18	18	36	0.04%	14.3%	LLEYLR	96.6%	29.4	25	17.9	2	0	0	806.48	57	62
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	18	18	36	0.04%	14.3%	LLGAALPLLTK	99.7%	59.9	25	59.9	4	0	0	1109.73	308	318
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	18	18	36	0.04%	14.3%	LPAIALDLLR	99.7%	77.5	25	71.3	2	0	0	1094.69	264	273
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	18	18	36	0.04%	14.3%	LVGSVNLFSDENVPR	99.7%	92.6	25	87	2	0	0	1645.85	232	246
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	18	18	36	0.04%	14.3%	QLMGQVLAK	99.7%	44.7	25	31.5	1	0	0	987.57	1054	1062
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	18	18	36	0.04%	14.3%	SPAPGAPTR	97.9%	31.6	25	24.6	2	0	0	853.45	1232	1240
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	18	18	36	0.04%	14.3%	SPLSALAR	99.7%	51.6	25	26.6	2	0	0	814.48	1290	1297
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	18	18	36	0.04%	14.3%	SPSLLQSGAK	99.2%	36	25	22.5	1	0	0	987.55	1308	1317
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	18	18	36	0.04%	14.3%	VYSTALSSFLTK	99.7%	76.6	25	75	4	0	0	1316.71	977	988
Myosin light polypeptide 6	MYL6	MYL6_HUMAN	16.9	100.0%	4	5	9	0.01%	27.2%	ALGQNPTNAEVLK	99.7%	51.4	25	49.2	3	0	0	1354.73	38	50
Myosin light polypeptide 6	MYL6	MYL6_HUMAN	16.9	100.0%	4	5	9	0.01%	27.2%	EAFQLFDR	99.3%	36.7	25	28.3	1	0	0	1025.51	14	21
Myosin light polypeptide 6	MYL6	MYL6_HUMAN	16.9	100.0%	4	5	9	0.01%	27.2%	HVLVTLGEK	95.3%	28.2	25	28.2	1	0	0	995.59	111	119
Myosin light polypeptide 6	MYL6	MYL6_HUMAN	16.9	100.0%	4	5	9	0.01%	27.2%	ILYSQCGDVMR	99.7%	58.8	25	58.8	4	0	0	1357.62	27	37
Myosin-10	MYH10	MYH10_HUMAN	229.0	100.0%	3	3	5	0.01%	1.9%	ALELDPNLYR	99.6%	39.4	25	37.6	2	0	0	1203.64	753	762
Myosin-10	MYH10	MYH10_HUMAN	229.0	100.0%	3	3	5	0.01%	1.9%	QLLQANPILESFGNAK	99.7%	48.2	25	48.2	2	0	0	1742.94	217	232
Myosin-10	MYH10	MYH10_HUMAN	229.0	100.0%	3	3	5	0.01%	1.9%	SDLLLEGFNNYR	99.6%	40	25	40	1	0	0	1440.71	297	308
Myosin-9	MYH9	MYH9_HUMAN	226.5	100.0%	5	5	7	0.01%	3.2%	ALELDSNLYR	99.7%	51.2	25	44.4	1	0	0	1193.62	746	755
Myosin-9	MYH9	MYH9_HUMAN	226.5	100.0%	5	5	7	0.01%	3.2%	EQADFAIEALAK	99.3%	36.4	25	0	1	0	0	1305.67	408	419
Myosin-9	MYH9	MYH9_HUMAN	226.5	100.0%	5	5	7	0.01%	3.2%	QLLQANPILEAFGNAK	99.7%	66.3	25	66.3	2	0	0	1726.95	210	225
Myosin-9	MYH9	MYH9_HUMAN	226.5	100.0%	5	5	7	0.01%	3.2%	TDLLLEPYNK	99.7%	40.4	25	34.8	1	0	0	1205.64	290	299
Myosin-9	MYH9	MYH9_HUMAN	226.5	100.0%	5	5	7	0.01%	3.2%	VISGVLQLGNIVFK	99.7%	47.3	25	47.3	2	0	0	1486.90	342	355
N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	DDAH2	DDAH2_HUMAN	29.6	99.8%	2	2	3	0.00%	9.1%	GGGDLPNSQEALQK	99.6%	39	25	39	1	0	0	1413.70	238	251
N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	DDAH2	DDAH2_HUMAN	29.6	99.8%	2	2	3	0.00%	9.1%	TVVAGSSDAAQK	99.4%	37.7	25	26.1	2	0	0	1133.58	183	194
N-acetylserotonin O-methyltransferase-like protein	ASMTL	ASML_HUMAN	68.9	99.8%	2	2	3	0.00%	3.4%	LLELIEGFMLSK	99.6%	40	25	40	1	0	0	1392.78	288	299
N-acetylserotonin O-methyltransferase-like protein	ASMTL	ASML_HUMAN	68.9	99.8%	2	2	3	0.00%	3.4%	VVLASASPR	99.7%	45.7	25	30.4	2	0	0	899.53	15	23
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	11	11	19	0.02%	12.1%	AGFVPVYLR	99.4%	37.1	25	26.6	1	0	0	1021.58	726	734
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	11	11	19	0.02%	12.1%	AIEEQMVAAK	99.7%	41.3	25	37	2	0	0	1105.56	913	922
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	11	11	19	0.02%	12.1%	ASEVFLQR	99.7%	64	25	44	2	0	0	949.51	521	528

N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	11	11	19	0.02%	12.1%	EELEALFLPYDLK	99.7%	44.6	25	42	2	0	0	1579.83	811	823
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	11	11	19	0.02%	12.1%	ILIENGVAER	99.7%	58.9	25	49.8	2	0	0	1113.63	12	21
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	11	11	19	0.02%	12.1%	IVSGCPLPEACELYYVNR	99.4%	37.7	25	37.7	1	0	0	2140.02	495	512
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	11	11	19	0.02%	12.1%	LDYLGVSYGLTPR	99.7%	70.6	25	61.4	2	0	0	1453.77	706	718
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	11	11	19	0.02%	12.1%	QQSAQSQVSTTAENK	99.7%	71.4	25	65.6	2	0	0	1606.77	433	447
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	11	11	19	0.02%	12.1%	QSILNSLSR	98.4%	32.7	25	29.5	1	0	0	1017.57	588	596
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	11	11	19	0.02%	12.1%	SLFVVVGDR	99.7%	53.6	25	43.1	2	0	0	991.56	24	32
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	11	11	19	0.02%	12.1%	TEAHQDVVGR	99.7%	42.7	25	42.7	2	0	0	1111.55	173	182
N-acetyltransferase 14	NAT14	NAT14_HUMAN	21.7	100.0%	3	3	5	0.01%	19.4%	APSHLSVR	96.7%	29.6	25	23.8	1	0	0	866.48	2	9
N-acetyltransferase 14	NAT14	NAT14_HUMAN	21.7	100.0%	3	3	5	0.01%	19.4%	AWAGGMGEPR	99.7%	41	25	40.8	2	0	0	1031.47	153	162
N-acetyltransferase 14	NAT14	NAT14_HUMAN	21.7	100.0%	3	3	5	0.01%	19.4%	GSGDVCGVLALAPGTNAGDGAR	99.7%	85.4	25	85.4	2	0	0	2014.96	103	124
N-acylneuraminate cytidylyltransferase	CMAS	NEUA_HUMAN	48.4	100.0%	3	3	4	0.00%	8.8%	EVTEPLNLNPAK	97.0%	30	25	26.6	1	0	0	1324.71	189	200
N-acylneuraminate cytidylyltransferase	CMAS	NEUA_HUMAN	48.4	100.0%	3	3	4	0.00%	8.8%	GAATSVSNPR	99.7%	41.6	25	29	2	0	0	959.49	7	16
N-acylneuraminate cytidylyltransferase	CMAS	NEUA_HUMAN	48.4	100.0%	3	3	4	0.00%	8.8%	VGLSGAPADACSTAQK	99.7%	45.8	25	45.8	1	0	0	1532.74	384	399
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	7	7	9	0.01%	7.3%	AQYPIADLVK	96.2%	29	25	19	1	0	0	1117.63	940	949
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	7	7	9	0.01%	7.3%	AVVLAANHFGR	99.7%	41.5	25	41.5	2	0	0	1154.64	203	213
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	7	7	9	0.01%	7.3%	FFTGQITAAGK	99.7%	43.8	25	35.7	1	0	0	1140.60	214	224
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	7	7	9	0.01%	7.3%	GITHIGYTDLPSR	95.5%	28.3	25	28.3	1	0	0	1429.74	367	379
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	7	7	9	0.01%	7.3%	SLGAEPLEVDLK	99.2%	36.2	25	30.6	1	0	0	1270.69	268	279
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	7	7	9	0.01%	7.3%	TVAELEAEK	97.8%	31.4	25	22.3	1	0	0	989.52	454	462
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	7	7	9	0.01%	7.3%	VALSPAGVQNLVK	99.7%	44.3	25	42.9	2	0	0	1295.77	72	84
NAD(P)H-hydrate epimerase	APOA1BP	NNRE_HUMAN	31.7	99.8%	2	2	3	0.00%	10.4%	GNAGGIQPDLLISLTAPK	99.7%	47.8	25	47.8	1	0	0	1764.99	228	245
NAD(P)H-hydrate epimerase	APOA1BP	NNRE_HUMAN	31.7	99.8%	2	2	3	0.00%	10.4%	LFGYEPTIYYPK	99.7%	48.2	25	38.3	2	0	0	1490.76	133	144
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	9	9	14	0.01%	21.1%	CEVLQYSAR	99.7%	41	25	34	1	0	0	1125.54	253	261
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	9	9	14	0.01%	21.1%	FYDDPR	96.6%	29.5	25	29.5	2	0	0	812.36	117	122
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	9	9	14	0.01%	21.1%	ITSAYLQDIENAYK	99.7%	72.6	25	68.5	2	0	0	1628.82	229	242
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	9	9	14	0.01%	21.1%	KQCVDHYNEVK	99.7%	40	25	33	1	0	0	1419.67	181	191
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	9	9	14	0.01%	21.1%	LQSWLYSSR	99.7%	50.7	25	41.7	2	0	0	1139.58	131	139
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	9	9	14	0.01%	21.1%	QCVDHYNEVK	97.2%	30.3	25	27.5	2	0	0	1291.57	182	191
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	9	9	14	0.01%	21.1%	TLYHLR	95.4%	28.2	25	9.11	1	0	0	802.46	290	295
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	9	9	14	0.01%	21.1%	VVEDIEYLK	99.7%	54.2	25	53.2	2	0	0	1107.59	269	277
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	9	9	14	0.01%	21.1%	YGMWHFLLGDK	96.0%	28.8	25	26.7	1	0	0	1382.66	38	48
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	100.0%	4	5	10	0.01%	33.8%	FNVTGTPEQYVPYSTTR	99.7%	53.5	25	47.4	1	0	0	1959.94	115	131
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	100.0%	4	5	10	0.01%	33.8%	GLQQITGHGGLR	99.7%	73.3	25	63.9	5	1	0	1236.68	10	21
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	100.0%	4	5	10	0.01%	33.8%	VGTLVGEDK	99.7%	61.1	25	37.1	2	0	0	917.49	35	43
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	100.0%	4	5	10	0.01%	33.8%	YYEDNKQFFGR	99.2%	36	25	36	1	0	0	1466.67	48	58
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	NDUAD_HUMAN	16.7	100.0%	3	4	11	0.01%	20.8%	ENLEEEAIIMK	99.7%	73.8	25	57.1	4	0	0	1318.66	89	99
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	NDUAD_HUMAN	16.7	100.0%	3	4	11	0.01%	20.8%	LQIEDFEAR	99.7%	50.3	25	39.9	4	0	0	1120.56	60	68
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	NDUAD_HUMAN	16.7	100.0%	3	4	11	0.01%	20.8%	VGESVFHTTR	99.7%	74.6	25	62.8	3	0	0	1132.57	106	115
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	NDUFA4	NDUA4_HUMAN	9.4	100.0%	2	2	3	0.00%	22.2%	FYSVNVDYSK	99.7%	59	25	47.7	2	0	0	1221.58	64	73
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	NDUFA4	NDUA4_HUMAN	9.4	100.0%	2	2	3	0.00%	22.2%	LGPNDQYK	99.2%	36.2	25	32.4	1	0	0	934.46	56	63
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	NDUA5_HUMAN	13.5	100.0%	4	5	9	0.01%	44.0%	ILDVLEEIPK	99.7%	71.2	25	71.2	2	0	0	1168.68	31	40
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	NDUA5_HUMAN	13.5	100.0%	4	5	9	0.01%	44.0%	KYTEQITNEK	99.7%	48.7	25	42.3	2	0	0	1253.64	46	55
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	NDUA5_HUMAN	13.5	100.0%	4	5	9	0.01%	44.0%	LWEPLVEEPPADQWK	99.2%	36	25	35.7	2	0	0	1836.92	99	113
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	NDUA5_HUMAN	13.5	100.0%	4	5	9	0.01%	44.0%	TTGLVGLAVCNTPHER	99.7%	59.6	25	59.6	2	1	0	1724.88	8	23
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	NDUFA6	NDUA6_HUMAN	17.9	100.0%	3	3	8	0.01%	18.8%	FFHETEAPRPK	99.7%	42.7	25	41.6	3	0	0	1358.69	132	142
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	NDUFA6	NDUA6_HUMAN	17.9	100.0%	3	3	8	0.01%	18.8%	GKIELEETIK	99.1%	35.3	25	16.5	1	0	0	1159.66	112	121
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	NDUFA6	NDUA6_HUMAN	17.9	100.0%	3	3	8	0.01%	18.8%	VVDLLVIK	99.7%	52.5	25	51.3	4	0	0	898.60	104	111
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	10	11	19	0.02%	32.1%	DAFPEAIIVKPSDIFGR	99.7%	45.4	25	45.4	2	0	0	1875.00	193	209
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	10	11	19	0.02%	32.1%	FGPIPLGSLGWK	99.7%	44.9	25	36.6	2	0	0	1271.71	223	234
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	10	11	19	0.02%	32.1%	MGSQVIIPYR	99.7%	53.4	25	49	4	0	0	1179.62	76	85

NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	10	11	19	0.02%	32.1%	NFDFEDVFVK	99.7%	55.8	25	34.5	2	0	0	1259.59	138	147
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	10	11	19	0.02%	32.1%	QPVYVVDVSK	99.7%	44.6	25	41.5	2	0	0	1133.62	238	247
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	10	11	19	0.02%	32.1%	SFAFVGPSR	99.7%	49.2	25	38.6	2	0	0	967.50	262	270
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	10	11	19	0.02%	32.1%	SSVSGIVATVFGATGFLGR	99.7%	81	25	81	1	0	0	1825.98	49	67
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	10	11	19	0.02%	32.1%	VFEISPFEPWITR	99.7%	66.3	25	62.5	2	0	0	1620.84	304	316
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	10	11	19	0.02%	32.1%	WLSAEIEDVKPAK	95.2%	21.9	25	20.5	0	1	0	1485.79	361	373
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	10	11	19	0.02%	32.1%	YVVNHLGR	98.7%	33.5	25	22.5	1	0	0	957.53	68	75
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3	NDUFB3	NDUB3_HUMAN	11.4	99.8%	2	2	2	0.00%	21.4%	IEGTPLETIQK	96.8%	29.7	25	24.1	1	0	0	1228.68	24	34
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3	NDUFB3	NDUB3_HUMAN	11.4	99.8%	2	2	2	0.00%	21.4%	SVSFSDVFFK	99.4%	37.4	25	31.3	1	0	0	1162.58	60	69
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	NDUFB4	NDUB4_HUMAN	15.2	100.0%	4	4	7	0.01%	41.1%	EYLLQYNDPNRR	98.1%	25.2	25	23	0	1	0	1580.78	46	57
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	NDUFB4	NDUB4_HUMAN	15.2	100.0%	4	4	7	0.01%	41.1%	GLIENPALLR	99.7%	72	25	60.2	2	0	0	1095.65	58	67
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	NDUFB4	NDUB4_HUMAN	15.2	100.0%	4	4	7	0.01%	41.1%	TINVYPNFRPTPK	99.7%	48.3	25	48.3	2	0	0	1546.84	73	85
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	NDUFB4	NDUB4_HUMAN	15.2	100.0%	4	4	7	0.01%	41.1%	TLPETLDPAEYNISPETR	99.7%	60.2	25	58.2	2	0	0	2046.00	13	30
NADH dehydrogenase [ubiquinone] 1 subunit C2	NDUFC2	NDUC2_HUMAN	14.2	99.9%	2	2	4	0.00%	14.3%	DREMFGYMK	97.0%	29.9	25	22.5	1	0	0	1176.52	86	94
NADH dehydrogenase [ubiquinone] 1 subunit C2	NDUFC2	NDUC2_HUMAN	14.2	99.9%	2	2	4	0.00%	14.3%	EDYLYAVR	99.7%	40.7	25	33.3	3	0	0	1028.50	78	85
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	5	5	10	0.01%	11.9%	EAYEAGLIGK	99.7%	57.4	25	50.9	2	0	0	1050.55	175	184
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	5	5	10	0.01%	11.9%	GGAGFPTGLK	98.4%	32.7	25	25.3	2	0	0	904.49	89	98
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	5	5	10	0.01%	11.9%	GGTWFAGFGR	99.7%	57.5	25	48.8	2	0	0	1055.51	258	267
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	5	5	10	0.01%	11.9%	GPDWILGEIK	99.7%	57	25	52.9	2	0	0	1127.61	72	81
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	5	5	10	0.01%	11.9%	NACGSGYDFDVFVVR	99.7%	87.3	25	87.1	2	0	0	1705.76	185	199
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	4	4	5	0.01%	10.8%	GEFGVYLVSDGSSRPYR	95.2%	28	25	28	1	0	0	1888.92	405	421
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	4	4	5	0.01%	10.8%	IIAQCLNK	97.4%	30.6	25	22.3	1	0	0	959.53	343	350
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	4	4	5	0.01%	10.8%	MFEFYER	99.6%	39	25	31.1	2	0	0	1021.44	210	216
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	4	4	5	0.01%	10.8%	NITLNFGPQHPAAHGVLR	99.7%	32.9	25	29.6	0	1	0	1942.04	79	96
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	15	0.02%	39.0%	AANWYER	99.7%	42.6	25	42.6	2	0	0	909.42	162	168
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	15	0.02%	39.0%	DFPLSGYVELR	99.7%	66.3	25	54.2	2	0	0	1295.66	201	211
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	15	0.02%	39.0%	ESAGADTRPTVRPR	99.3%	28.9	25	26.6	0	1	0	1512.79	37	50
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	15	0.02%	39.0%	ILTDYGFEGHPFR	99.7%	71.5	25	71.5	2	0	0	1551.76	187	199
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	15	0.02%	39.0%	QLSAFGEYVAEILPK	99.7%	74.6	25	74.6	2	0	0	1664.89	57	71
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	15	0.02%	39.0%	SLVDLTAVDVPTR	99.7%	77.8	25	75.7	2	0	0	1385.76	110	122
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	15	0.02%	39.0%	TYTDELTPIESAVSVFK	99.7%	40.7	25	37.4	2	0	0	1899.96	145	161
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	15	0.02%	39.0%	VVAEPVELAQEFR	99.7%	52.5	25	52.5	2	0	0	1486.79	219	231
NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	NDUFS4	NDUS4_HUMAN	20.1	99.9%	2	2	2	0.00%	10.9%	EDAVSFAEK	99.4%	37.6	25	31.9	1	0	0	995.47	132	140
NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	NDUFS4	NDUS4_HUMAN	20.1	99.9%	2	2	2	0.00%	10.9%	SYGANFSWNK	98.3%	32.5	25	32.5	1	0	0	1173.53	159	168
NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	NDUFS6	NDUS6_HUMAN	13.7	99.8%	2	2	4	0.00%	21.8%	TGTCGYCGLQFR	99.7%	41.5	25	41.5	2	0	0	1419.61	109	120
NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	NDUFS6	NDUS6_HUMAN	13.7	99.8%	2	2	4	0.00%	21.8%	VIACDGGGGALGHPK	99.7%	68.7	25	57.7	2	0	0	1408.70	84	98
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	NDUS7_HUMAN	23.6	100.0%	4	6	19	0.02%	15.5%	KVYDQMPEPR	98.2%	32.3	25	30	1	0	0	1278.61	136	145
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	NDUS7_HUMAN	23.6	100.0%	4	6	19	0.02%	15.5%	LDDLVNWAR	99.7%	76.7	25	64.3	4	0	0	1101.57	67	75
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	NDUS7_HUMAN	23.6	100.0%	4	6	19	0.02%	15.5%	QSDVMIVAGTLTNK	99.7%	132	25	120	8	0	0	1476.77	116	129
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	NDUS7_HUMAN	23.6	100.0%	4	6	19	0.02%	15.5%	VYDQMPEPR	99.7%	59.1	25	59.1	6	0	0	1134.52	137	145
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	NDUS8_HUMAN	23.7	100.0%	5	5	11	0.01%	29.0%	EPATINYPFEK	97.9%	31.5	25	31.5	1	0	0	1308.65	78	88
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	NDUS8_HUMAN	23.7	100.0%	5	5	11	0.01%	29.0%	GLGMTLSYLFR	99.7%	53	25	48.1	2	0	0	1257.67	67	77
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	NDUS8_HUMAN	23.7	100.0%	5	5	11	0.01%	29.0%	LCEAICPAQAITIEAEPR	99.7%	87.2	25	82.2	2	0	0	2042.00	116	133
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	NDUS8_HUMAN	23.7	100.0%	5	5	11	0.01%	29.0%	TLLWTELFR	99.7%	68.2	25	63.6	2	0	0	1178.66	58	66
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	NDUS8_HUMAN	23.7	100.0%	5	5	11	0.01%	29.0%	YVNMQDPEMDMK	99.7%	63.7	25	57.1	4	0	0	1548.60	38	49
NADH-cytochrome b5 reductase 3	CYB5R3	NB5R3_HUMAN	34.2	99.8%	2	2	3	0.00%	9.3%	SVGMIAGGTGITPMLQVIR	99.7%	62.2	25	60	2	0	0	1901.04	174	192
NADH-cytochrome b5 reductase 3	CYB5R3	NB5R3_HUMAN	34.2	99.8%	2	2	3	0.00%	9.3%	VYFKDTHPK	95.2%	28	25	28	1	0	0	1134.59	112	120
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	19	22	32	0.03%	30.7%	ALSEIAGMTLPYDTLDQVR	99.7%	72.1	25	72.1	2	0	0	2093.06	625	643
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	19	22	32	0.03%	30.7%	FASEIAGVDDLGTTGR	99.7%	122	25	116	2	0	0	1608.79	185	200
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	19	22	32	0.03%	30.7%	FAYDGLKR	98.3%	32.3	25	24.8	1	0	0	969.52	292	299
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	19	22	32	0.03%	30.7%	FEAPLFNAR	99.7%	57	25	51.5	2	0	0	1064.55	409	417

NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	19	22	32	0.03%	30.7%	GLLTYTSWEDALSR	99.7%	102	25	101	2	0	0	1611.80	312	325
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	19	22	32	0.03%	30.7%	GWNILTNSEK	99.7%	45.5	25	36	2	0	0	1161.59	99	108
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	19	22	32	0.03%	30.7%	ILQDIASGSHPFSQVLK	99.7%	53.9	25	53.9	1	1	0	1840.00	451	467
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	19	22	32	0.03%	30.7%	LEEVSPNLVR	95.0%	27.9	25	0.9	1	0	0	1155.64	646	655
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	19	22	32	0.03%	30.7%	LSVAGNCR	96.2%	29	25	20.5	1	0	0	876.44	69	76
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	19	22	32	0.03%	30.7%	LTEPMVR	98.3%	32.3	25	15.6	1	0	0	845.46	302	308
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	19	22	32	0.03%	30.7%	LVNQQLLADPLVPPQLTIK	99.4%	37.2	25	36.1	1	0	0	2100.24	674	692
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	19	22	32	0.03%	30.7%	NDGAAILAAVSSIAQK	99.7%	120	25	116	2	0	0	1528.83	484	499
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	19	22	32	0.03%	30.7%	SATYVNTEGR	99.7%	60	25	51	2	0	0	1097.52	593	602
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	19	22	32	0.03%	30.7%	VAGMLQSFQGK	99.7%	66.6	25	55.6	2	0	0	1181.60	326	336
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	19	22	32	0.03%	30.7%	VAVTPPGLAR	99.1%	35.1	25	27.7	2	0	0	980.59	608	617
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	19	22	32	0.03%	30.7%	VGMQIPR	99.6%	39.2	25	21.9	3	0	0	800.44	56	62
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	19	22	32	0.03%	30.7%	VLFLLGADGGCITR	99.7%	96.7	25	88.2	2	0	0	1491.80	544	557
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	19	22	32	0.03%	30.7%	VMNILHR	99.3%	36.5	25	21.3	1	0	0	882.50	512	518
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	19	22	32	0.03%	30.7%	VVAACAMPVMK	97.9%	31.5	25	26.2	1	0	0	1176.59	88	98
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	8	9	15	0.02%	31.1%	AMIENFNAK	99.7%	41.7	25	31.9	3	0	0	1037.51	97	105
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	8	9	15	0.02%	31.1%	DLTQMADELRR	97.2%	30.3	25	27.9	1	0	0	1347.67	150	160
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	8	9	15	0.02%	31.1%	HVVLGAIENK	99.7%	43.3	25	40.5	2	0	0	1079.62	170	179
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	8	9	15	0.02%	31.1%	HVVLGAIENKVESK	97.0%	23.5	25	23.5	0	2	0	1522.86	170	183
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	8	9	15	0.02%	31.1%	MEEDPDDVPHGHITSLAVK	99.7%	52.3	25	48.3	0	2	0	2089.99	60	78
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	8	9	15	0.02%	31.1%	YVSLHVR	99.6%	40	25	32.5	1	0	0	873.49	106	112
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	8	9	15	0.02%	31.1%	YYADGEDAYAMK	99.7%	58.9	25	58.9	2	0	0	1396.57	137	148
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	8	9	15	0.02%	31.1%	YYADGEDAYAMKR	99.7%	55.3	25	55.3	2	0	0	1568.67	137	149
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	28	52	0.05%	25.2%	AIELATTLDESLTNR	99.7%	97.5	25	78	2	0	0	1646.86	783	797
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	28	52	0.05%	25.2%	ALKPANMLER	99.7%	53.7	25	35	2	0	0	1142.64	267	276
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	28	52	0.05%	25.2%	DLSLLQIQMR	99.7%	80.1	25	63.8	4	0	0	1216.67	119	128
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	28	52	0.05%	25.2%	EALEHLCTYEK	99.7%	56	25	40.3	2	0	0	1392.65	208	218
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	28	52	0.05%	25.2%	EEAYELVR	99.3%	36.4	25	24	1	0	0	1008.50	63	70
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	28	52	0.05%	25.2%	FAEHGETLAMK	99.7%	47	25	39.7	4	2	0	1233.59	42	52
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	28	52	0.05%	25.2%	FKECLDK	98.2%	32.2	25	16.6	2	0	0	939.46	306	312
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	28	52	0.05%	25.2%	FLLMLQSVK	99.7%	54.3	25	41.8	2	0	0	1094.63	688	696
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	28	52	0.05%	25.2%	GCPPVFNTLR	99.0%	34.9	25	26.2	2	0	0	1160.59	321	330
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	28	52	0.05%	25.2%	IAIEIYLK	99.7%	41.6	25	33	2	0	0	962.59	560	567
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	28	52	0.05%	25.2%	ILEEFRK	99.7%	41.3	25	35.7	2	0	0	934.54	170	176
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	28	52	0.05%	25.2%	IYEEAWTK	99.4%	37.4	25	26.3	2	0	0	1039.51	279	286
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	28	52	0.05%	25.2%	KEEAYELVR	99.7%	61.6	25	50	2	0	0	1136.59	62	70
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	28	52	0.05%	25.2%	LEDAADVYR	99.7%	73.4	25	72.8	2	0	0	1051.51	240	248
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	28	52	0.05%	25.2%	LFGATNPK	97.7%	31.2	25	10.5	2	0	0	847.47	741	748
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	28	52	0.05%	25.2%	LFNTAVCESK	99.7%	50.6	25	41	1	0	0	1168.57	715	724
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	28	52	0.05%	25.2%	LPLNFLSGEK	96.4%	29.2	25	23.9	2	0	0	1117.63	296	305
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	28	52	0.05%	25.2%	MVYYLDPSSQK	99.7%	50.7	25	48.7	3	0	0	1330.63	771	781
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	28	52	0.05%	25.2%	NFNETFLKR	99.3%	36.7	25	22.9	2	0	0	1168.61	749	757
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	28	52	0.05%	25.2%	NPENWAYYK	99.5%	38.1	25	29.2	2	0	0	1184.54	254	262
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	28	52	0.05%	25.2%	RLPLNFLSGEK	99.7%	50.5	25	47	2	0	0	1273.73	295	305
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	28	52	0.05%	25.2%	VAIIEELVVGYETSLK	99.7%	71.3	25	71.3	3	0	0	1762.98	339	354
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	28	52	0.05%	25.2%	VETPLEEAIK	99.1%	35.5	25	24.2	1	0	0	1128.61	650	659
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	28	52	0.05%	25.2%	WDKDNLQILR	99.7%	35.8	25	20.3	0	1	0	1300.70	109	118
N-alpha-acetyltransferase 20	NAA20	NAA20_HUMAN	20.4	100.0%	4	6	9	0.01%	21.9%	AFTCDDLFR	99.5%	38.4	25	34	1	0	0	1144.51	6	14
N-alpha-acetyltransferase 20	NAA20	NAA20_HUMAN	20.4	100.0%	4	6	9	0.01%	21.9%	LMELLEEISER	99.7%	64.2	25	58.6	3	0	0	1361.70	92	102
N-alpha-acetyltransferase 20	NAA20	NAA20_HUMAN	20.4	100.0%	4	6	9	0.01%	21.9%	QLGYSVYR	99.5%	38.2	25	22.7	2	0	0	985.51	125	132
N-alpha-acetyltransferase 20	NAA20	NAA20_HUMAN	20.4	100.0%	4	6	9	0.01%	21.9%	VSNQVAVNMYK	99.7%	58.5	25	46.8	3	0	0	1268.63	114	124

N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	16	29	0.03%	16.6%	DIQYPFLGPVPTR	99.7%	63.8	25	53.3	2	0	0	1502.80	748	760
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	16	29	0.03%	16.6%	DTSEYIIQAYK	99.7%	69	25	65.3	2	0	0	1330.65	576	586
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	16	29	0.03%	16.6%	FINQLLGVVPLSTPTEDK	99.7%	60.3	25	57.5	2	0	0	1971.08	384	401
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	16	29	0.03%	16.6%	IPEFIAFR	99.7%	49.5	25	32.5	2	0	0	992.56	593	600
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	16	29	0.03%	16.6%	LALPADIR	97.0%	30	25	20.5	1	0	0	868.53	402	409
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	16	29	0.03%	16.6%	LISGLPSLNHPVEPK	99.7%	61.5	25	50.5	2	0	0	1600.91	696	710
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	16	29	0.03%	16.6%	LLLQQLEATLETGK	99.7%	68.8	25	68.8	1	0	0	1556.89	729	742
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	16	29	0.03%	16.6%	LLLQQLEATLETGKR	99.7%	38.5	25	27.6	0	2	0	1712.99	729	743
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	16	29	0.03%	16.6%	LNNSLHFAQVR	99.7%	31.8	25	25.5	0	2	0	1298.70	603	613
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	16	29	0.03%	16.6%	LSLEEETLWLR	99.7%	54.8	25	49.6	2	0	0	1388.74	678	688
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	16	29	0.03%	16.6%	LTSEIQSR	99.6%	40	25	24.7	2	0	0	933.50	224	231
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	16	29	0.03%	16.6%	SLLDQLKDVFSK	99.7%	79.2	25	66.6	2	0	0	1392.77	807	818
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	16	29	0.03%	16.6%	TMFLPLAER	99.7%	40.9	25	33.5	3	0	0	1093.57	171	179
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	16	29	0.03%	16.6%	VFVDLLPATQCTK	99.7%	52.3	25	46.5	2	0	0	1491.79	371	383
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	16	29	0.03%	16.6%	YQEALDVIR	99.7%	66.4	25	48.3	2	0	0	1106.58	209	217
Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACA	NACAM_HUMAN	205.4	100.0%	3	3	6	0.01%	2.0%	IEDLSQQAQLAAAEK	99.7%	113	25	106	2	0	0	1614.83	1991	2005
Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACA	NACAM_HUMAN	205.4	100.0%	3	3	6	0.01%	2.0%	NILFVITKPDVYK	99.7%	63.5	25	63.5	2	0	0	1549.90	1964	1976
Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACA	NACAM_HUMAN	205.4	100.0%	3	3	6	0.01%	2.0%	SPASDTYIVFGEAK	99.7%	83	25	79.5	2	0	0	1484.73	1977	1990
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	10	10	14	0.01%	9.8%	AAEDLFVNIR	99.7%	77.3	25	57.8	2	0	0	1147.61	306	315
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	10	10	14	0.01%	9.8%	ASLGLADHR	99.7%	86.4	25	76.2	2	0	0	939.50	502	510
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	10	10	14	0.01%	9.8%	DEIIWLLR	98.5%	33	25	16.7	2	0	0	1057.60	380	387
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	10	10	14	0.01%	9.8%	ELATVLSDQPGLLGPK	99.7%	69.3	25	69.3	2	0	0	1637.91	352	367
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	10	10	14	0.01%	9.8%	EYLTSHLEIR	99.2%	36.2	25	33.2	1	0	0	1260.66	706	715
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	10	10	14	0.01%	9.8%	LQAYTSVSK	97.2%	30.2	25	27.4	1	0	0	996.54	493	501
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	10	10	14	0.01%	9.8%	LVVENVDVLTQMR	99.7%	59.5	25	58.9	1	0	0	1531.82	869	881
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	10	10	14	0.01%	9.8%	MFQQCLELPSQSR	96.8%	29.7	25	21.3	1	0	0	1623.76	552	564
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	10	10	14	0.01%	9.8%	NNNQQLAQLQK	99.7%	46	25	38.7	1	0	0	1298.68	71	81
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	10	10	14	0.01%	9.8%	QVEDGEVFDFR	99.3%	36.3	25	36.1	1	0	0	1340.61	474	484
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	7	7	12	0.01%	15.4%	DAAAVGNHVAK	99.7%	54.6	25	33.8	2	0	0	1052.55	353	363
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	7	7	12	0.01%	15.4%	EGQGNLPVR	98.7%	33.8	25	27.3	1	0	0	969.51	318	326
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	7	7	12	0.01%	15.4%	FTVVVATQLPESTSLR	99.7%	77.6	25	77.6	1	0	0	1747.96	123	138
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	7	7	12	0.01%	15.4%	GTIPDMIADSGK	99.4%	37.7	25	34.8	2	0	0	1204.59	327	338
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	7	7	12	0.01%	15.4%	LLCSNSAFLR	99.7%	50.1	25	36.5	2	0	0	1180.61	382	391
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	7	7	12	0.01%	15.4%	TYGLVGYMR	99.7%	45.4	25	39.9	2	0	0	1059.53	155	163
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	7	7	12	0.01%	15.4%	YPGVSNYQVEEDIGK	99.7%	65.1	25	65.1	2	0	0	1697.80	442	456
Negative elongation factor B	NELFB	NELFB_HUMAN	65.7	99.8%	2	2	3	0.00%	4.0%	ALEPTGQSGEAVK	99.7%	44.3	25	37	1	0	0	1286.66	526	538
Negative elongation factor B	NELFB	NELFB_HUMAN	65.7	99.8%	2	2	3	0.00%	4.0%	DSPDLLLLLR	99.7%	46.3	25	20.8	2	0	0	1154.68	334	343
Neuroblastoma-amplified sequence	NBAS	NBAS_HUMAN	268.6	100.0%	3	3	4	0.00%	1.2%	AEEIEHYAR	96.7%	29.6	25	18.6	2	0	0	1117.53	850	858
Neuroblastoma-amplified sequence	NBAS	NBAS_HUMAN	268.6	100.0%	3	3	4	0.00%	1.2%	CSGALTVSSVK	96.3%	29.1	25	19.7	1	0	0	1108.57	406	416
Neuroblastoma-amplified sequence	NBAS	NBAS_HUMAN	268.6	100.0%	3	3	4	0.00%	1.2%	LLGLAELLR	99.7%	50	25	21.9	1	0	0	997.64	1262	1270
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	6	6	10	0.01%	8.5%	ATLEMVNHEK	99.7%	50.1	25	43.4	2	0	0	1171.58	159	168
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	6	6	10	0.01%	8.5%	EIEAEIQALR	99.7%	80.2	25	57.6	2	0	0	1171.63	128	137
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	6	6	10	0.01%	8.5%	EYQDLLNVK	99.7%	49.3	25	38.5	6	0	0	1121.58	383	391
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	6	6	10	0.01%	8.5%	LLEGEETR	99.1%	35.2	25	18.8	2	0	0	946.48	404	411
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	6	6	10	0.01%	8.5%	LRDDTEAAIR	99.7%	62.6	25	43.6	2	0	0	1159.61	195	204
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	6	6	10	0.01%	8.5%	SIELESVR	96.5%	29.4	25	15.9	1	0	0	932.50	328	335
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	6	6	10	0.01%	8.5%	VEEHEETFEEK	99.5%	38	25	33	1	0	0	1405.61	883	893
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	6	6	10	0.01%	8.5%	VQSLQDEVAFLR	99.7%	80	25	67.6	2	0	0	1404.75	224	235
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	36	0.04%	19.6%	EVLDSFLDLAR	99.7%	83.5	25	75.1	8	0	0	1277.67	179	189
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	36	0.04%	19.6%	GPAGDATVASEK	99.7%	68	25	55.6	4	0	0	1102.54	526	537
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	36	0.04%	19.6%	GPAGDATVASEKESVM	99.7%	85.9	25	85.9	2	0	0	1564.72	526	541

Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	36	0.04%	19.6%	IVEMEDVGLLFAR	99.7%	78.5	25	73.2	4	0	0	1491.79	289	301
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	36	0.04%	19.6%	LGPEGELLIR	99.7%	79	25	63.2	2	0	0	1096.64	248	257
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	36	0.04%	19.6%	LSAFVFPGELLLR	99.7%	73.8	25	65.1	2	0	0	1461.85	86	98
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	36	0.04%	19.6%	NIFPSNLVSAAFR	99.7%	70.7	25	64.5	5	0	0	1435.77	190	202
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	36	0.04%	19.6%	SELPLDPLPVPTEEGNPLLK	99.7%	64.9	25	64.9	5	0	0	2158.16	503	522
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	36	0.04%	19.6%	STEPELIQVK	99.7%	62.8	25	55.7	4	0	0	1143.63	493	502
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	6	6	8	0.01%	9.1%	EGLGLDVER	99.2%	36	25	29.1	1	0	0	987.51	589	597
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	6	6	8	0.01%	9.1%	GAVEDVISR	99.7%	54.8	25	40	2	0	0	945.50	525	533
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	6	6	8	0.01%	9.1%	LLTDGYACEVR	99.7%	47.8	25	39.3	1	0	0	1296.63	235	245
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	6	6	8	0.01%	9.1%	SESHTDLTFSR	99.7%	33.4	25	27.1	0	1	0	1279.59	616	626
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	6	6	8	0.01%	9.1%	SGEGIREPISVK	98.3%	32.5	25	16.8	1	0	0	1271.70	572	583
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	6	6	8	0.01%	9.1%	TNPEYIYAPLK	99.7%	43.3	25	43.3	2	0	0	1308.68	212	222
NHP2-like protein 1	NHP2L1	NH2L1_HUMAN	14.2	99.7%	2	2	3	0.00%	18.0%	AYPLADAHLTK	94.7%	27.6	25	25.3	1	0	0	1199.64	10	20
NHP2-like protein 1	NHP2L1	NH2L1_HUMAN	14.2	99.7%	2	2	3	0.00%	18.0%	QQIQSIQQSIER	99.7%	65.7	25	63.4	2	0	0	1457.77	114	125
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	7	7	12	0.01%	13.5%	DPEFVFYDQLK	99.7%	53.2	25	48.3	2	0	0	1400.67	501	511
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	7	7	12	0.01%	13.5%	ELETVAAHQFPEVR	99.7%	70.1	25	60.8	2	0	0	1625.83	340	353
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	7	7	12	0.01%	13.5%	GSSLHLHVSKPPR	99.3%	28.9	25	28.9	0	2	0	1414.79	317	329
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	7	7	12	0.01%	13.5%	IIAEALTR	99.7%	56.7	25	24.1	2	0	0	886.54	417	424
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	7	7	12	0.01%	13.5%	NAVLNTEAR	99.7%	47.6	25	40.1	1	0	0	987.52	65	73
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	7	7	12	0.01%	13.5%	QSAGAVVIILPR	99.7%	66	25	42	1	0	0	1223.75	103	114
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	7	7	12	0.01%	13.5%	TMAAEVLSR	98.1%	32	25	28.2	2	0	0	977.51	74	82
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	15	18	28	0.03%	38.3%	DLLNCSFK	98.9%	34.3	25	31.3	1	0	0	996.48	393	400
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	15	18	28	0.03%	38.3%	DVYKEHFQDDVFNEK	99.7%	58.9	25	55.9	1	2	0	1912.87	85	99
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	15	18	28	0.03%	38.3%	EHFQDDVFNEK	99.6%	39	25	36.9	1	0	0	1407.62	89	99
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	15	18	28	0.03%	38.3%	GTDTVAGLALIK	99.7%	85.6	25	56.7	2	0	0	1158.67	217	228
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	15	18	28	0.03%	38.3%	GVSSQETAGIGASAHLVNFK	99.7%	86.4	25	86.4	1	2	0	1973.01	197	216
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	15	18	28	0.03%	38.3%	GWNYILEK	98.2%	32.1	25	23.2	2	0	0	1022.53	100	107
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	15	18	28	0.03%	38.3%	KFPVTENSK	99.5%	37.7	25	21.9	2	0	0	1049.56	331	339
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	15	18	28	0.03%	38.3%	MWSIENIAFGSGGGLLQK	99.7%	48.7	25	48.7	0	1	0	1907.97	372	389
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	15	18	28	0.03%	38.3%	SYSFDEIRK	98.7%	33.8	25	22.8	1	0	0	1144.56	470	478
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	15	18	28	0.03%	38.3%	TPAGNFVTLEEGKGDLEEYGQDLLHTVFK	99.7%	80	25	80	0	2	0	3207.58	435	463
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	15	18	28	0.03%	38.3%	VIQGDGVDINTLQEIVEGMK	99.7%	132	25	132	4	0	0	2158.11	350	369
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	15	18	28	0.03%	38.3%	VKYEETVFYGLQYILNK	99.7%	53.1	25	42.9	0	2	0	2107.11	52	68
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	15	18	28	0.03%	38.3%	VYSYFECR	99.2%	35.6	25	34.4	1	0	0	1123.49	33	40
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	15	18	28	0.03%	38.3%	YEETVFYGLQYILNK	99.7%	90.5	25	89.1	1	0	0	1879.95	54	68
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	15	18	28	0.03%	38.3%	YLLETSGNLDGLEYK	99.7%	104	25	98.8	2	0	0	1714.85	175	189
Nodal modulator 1	NOMO1	NOMO1_HUMAN	134.3	100.0%	3	3	3	0.00%	3.3%	DGENYVVLLDSTLPR	96.8%	29.8	25	29	1	0	0	1690.86	1106	1120
Nodal modulator 1	NOMO1	NOMO1_HUMAN	134.3	100.0%	3	3	3	0.00%	3.3%	FLLFSSLVTK	98.6%	33.5	25	33.5	1	0	0	1154.68	235	244
Nodal modulator 1	NOMO1	NOMO1_HUMAN	134.3	100.0%	3	3	3	0.00%	3.3%	SSIDSEPALVLGPLK	99.5%	38.4	25	38.4	1	0	0	1525.85	686	700
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	21	61	0.06%	30.1%	AAPGAEFAPNKR	99.7%	61.3	25	49.5	5	0	0	1228.64	457	468
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	21	61	0.06%	30.1%	AGEVFIHK	99.7%	53.4	25	34.9	6	0	0	900.49	100	107
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	21	61	0.06%	30.1%	AVVIVDDR	99.7%	41.8	25	36.5	2	0	0	886.50	177	184
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	21	61	0.06%	30.1%	DKGFGFIR	97.2%	30.3	25	17.7	1	0	0	939.50	108	115
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	21	61	0.06%	30.1%	EKLEMEMEAAR	99.7%	51.1	25	37.1	4	0	0	1336.62	294	304
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	21	61	0.06%	30.1%	FACHSASLTVR	99.7%	65.7	25	60.9	4	5	0	1248.62	143	153
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	21	61	0.06%	30.1%	FAQPGSFEYEYAMR	99.7%	66.7	25	64.1	5	0	0	1711.74	257	270
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	21	61	0.06%	30.1%	FGQAATMEGIGAIGGTPPAFNR	99.7%	42.2	25	42.2	1	1	0	2179.06	435	456
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	21	61	0.06%	30.1%	GIVEFSGKPAAR	99.7%	64.3	25	62.6	6	1	0	1231.68	191	202
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	21	61	0.06%	30.1%	MEELHNQEVQK	99.7%	71.8	25	18	5	0	0	1384.65	326	336
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	21	61	0.06%	30.1%	MGQMAMGGAMGINNR	99.7%	80.6	25	32.3	7	0	0	1586.65	384	398
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	21	61	0.06%	30.1%	RMEELHNQEVQK	99.6%	30.8	25	26.6	0	3	0	1540.75	325	336

Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	21	61	0.06%	30.1%	VELDNMPLR	99.7%	70.8	25	46.7	5	0	0	1086.56	127	135
Nuclear autoantigenic sperm protein	NASP	NASP_HUMAN	85.2	100.0%	3	3	5	0.01%	3.7%	EAQLYAAQAHLK	99.7%	52.3	25	44.6	2	0	0	1342.71	536	547
Nuclear autoantigenic sperm protein	NASP	NASP_HUMAN	85.2	100.0%	3	3	5	0.01%	3.7%	MAVLNEQVK	99.6%	39.4	25	32.7	1	0	0	1031.56	618	626
Nuclear autoantigenic sperm protein	NASP	NASP_HUMAN	85.2	100.0%	3	3	5	0.01%	3.7%	SIEVIENR	98.9%	34.5	25	26.1	2	0	0	959.52	610	617
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	9	9	17	0.02%	12.0%	ANNYNEAVYLVR	99.7%	57.2	25	48.4	2	0	0	1425.71	118	129
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	9	9	17	0.02%	12.0%	ATNDEIFSILK	99.7%	58.6	25	51.9	4	0	0	1250.66	512	522
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	9	9	17	0.02%	12.0%	DGVLEEQIER	96.5%	29.3	25	13.9	1	0	0	1187.59	685	694
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	9	9	17	0.02%	12.0%	IFANTESYLK	99.7%	50.5	25	35.4	2	0	0	1185.62	195	204
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	9	9	17	0.02%	12.0%	LDTMNTTCVDR	98.5%	33	25	32.8	1	0	0	1341.58	402	412
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	9	9	17	0.02%	12.0%	NLFLVIFQR	99.7%	61.9	25	59.7	3	0	0	1149.68	708	716
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	9	9	17	0.02%	12.0%	NYNFGGEFVEAMIR	99.7%	84.2	25	82.4	2	0	0	1646.76	97	110
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	9	9	17	0.02%	12.0%	SFSHSFSALAK	99.7%	50.1	25	35.9	1	0	0	1181.59	558	568
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	9	9	17	0.02%	12.0%	VMFEVWR	97.1%	30.1	25	28.5	1	0	0	966.49	589	595
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	7	7	11	0.01%	4.0%	AVQAQGGESQQEAQR	99.7%	54	25	54	2	0	0	1586.75	1574	1588
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	7	7	11	0.01%	4.0%	DSAQTSVTQAQR	99.7%	59.2	25	50.2	2	0	0	1291.62	632	643
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	7	7	11	0.01%	4.0%	HQVEQLSSSLK	99.7%	52.8	25	48	1	0	0	1255.66	551	561
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	7	7	11	0.01%	4.0%	LADDLSTLQEK	99.7%	53.5	25	44.9	2	0	0	1232.64	898	908
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	7	7	11	0.01%	4.0%	LLQAETASNSAR	99.7%	80.9	25	68.3	1	0	0	1260.65	1271	1282
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	7	7	11	0.01%	4.0%	SLEAQVAHADQQLR	99.7%	45	25	43.6	1	0	0	1565.80	1682	1695
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	7	7	11	0.01%	4.0%	YVQELAAVR	99.7%	50	25	40.8	2	0	0	1048.58	1476	1484
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	12	12	18	0.02%	14.7%	AGMTEEAQR	99.7%	45.5	25	31.8	1	0	0	992.45	356	364
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	12	12	18	0.02%	14.7%	AIYAALSGNLK	99.7%	72.6	25	56	2	0	0	1120.64	426	436
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	12	12	18	0.02%	14.7%	EADLDVATITK	99.7%	73	25	65.3	2	0	0	1175.62	627	637
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	12	12	18	0.02%	14.7%	EYLGANWTLEK	99.7%	56	25	43.3	1	0	0	1323.66	481	491
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	12	12	18	0.02%	14.7%	GHLDALTADVK	99.7%	55.9	25	49.7	2	0	0	1139.61	804	814
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	12	12	18	0.02%	14.7%	IDVIDWLVFDPAQR	99.7%	63	25	63	1	0	0	1686.89	672	685
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	12	12	18	0.02%	14.7%	LYLVFSK	95.0%	27.9	25	12.3	1	0	0	869.51	888	894
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	12	12	18	0.02%	14.7%	SGFGEISSPVIR	99.1%	35.4	25	25.7	2	0	0	1248.66	4	15
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	12	12	18	0.02%	14.7%	TVVEALFQR	99.7%	66.3	25	65.6	2	0	0	1062.59	251	259
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	12	12	18	0.02%	14.7%	VFEELQATDK	99.7%	63.9	25	53.3	2	0	0	1179.59	492	501
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	12	12	18	0.02%	14.7%	VLEENQEHYHIVQK	95.6%	22.2	25	22.2	0	1	0	1765.89	504	517
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	12	12	18	0.02%	14.7%	VLLQASQDENFGNTTPR	99.7%	90.6	25	90.6	1	0	0	1889.94	32	48
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	19	32	0.03%	18.3%	AAFLQYCR	99.7%	59.9	25	40.5	2	0	0	1028.50	524	531
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	19	32	0.03%	18.3%	DGIQLSEYLPEVK	99.7%	44.5	25	34.2	2	0	0	1490.77	1111	1123
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	19	32	0.03%	18.3%	DLLQADQLGSLK	99.7%	77.2	25	63	2	0	0	1300.71	1124	1135
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	19	32	0.03%	18.3%	DMLQAASHYR	99.7%	45.5	25	40.8	3	0	0	1191.56	734	743
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	19	32	0.03%	18.3%	ENITDAIWGSESNYEAIK	99.2%	36.1	25	36.1	1	0	0	2039.96	318	335
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	19	32	0.03%	18.3%	EYEIPSNLTPADVFFR	99.3%	36.6	25	36.6	2	0	0	1897.93	676	691
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	19	32	0.03%	18.3%	GLPLGSAVSSPVLFSPVGR	99.7%	88.3	25	88.3	2	0	0	1840.03	36	54
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	19	32	0.03%	18.3%	HAYSWDINR	99.7%	41	25	32	2	0	0	1161.54	306	314
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	19	32	0.03%	18.3%	IEEMAEQER	99.7%	75.6	25	41.8	1	0	0	1150.50	992	1000
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	19	32	0.03%	18.3%	LLLCEHAEK	99.7%	52.5	25	51.7	2	0	0	1112.58	638	646
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	19	32	0.03%	18.3%	LSAAIVLK	99.2%	35.7	25	15.8	1	0	0	814.54	647	654
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	19	32	0.03%	18.3%	NETIAQEDKIK	99.7%	59	25	43.5	2	0	0	1288.67	510	520
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	19	32	0.03%	18.3%	NSGLVSITSR	99.7%	78.4	25	72.7	1	0	0	1033.56	467	476
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	19	32	0.03%	18.3%	SNPYFEFVLK	99.7%	44	25	43.2	2	0	0	1243.64	1136	1145
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	19	32	0.03%	18.3%	SSFYSLTSSNISK	99.7%	106	25	90.4	2	0	0	1420.70	284	296
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	19	32	0.03%	18.3%	TFGSSLPVK	99.7%	41.1	25	31.7	2	0	0	935.52	83	91
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	19	32	0.03%	18.3%	VAYPQADSNLR	99.7%	66.2	25	59.2	2	0	0	1233.62	788	798
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	19	32	0.03%	18.3%	YMTQFADQNFSDFLFR	99.7%	59.1	25	59.1	1	0	0	2029.91	888	903
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	9	9	18	0.02%	7.1%	CYLVTGEGQK	97.5%	30.7	25	24	1	0	0	1154.55	916	925

Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	9	9	18	0.02%	7.1%	DLLILQQLLMR	99.7%	65.3	25	63	3	0	0	1355.81	733	743
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	9	9	18	0.02%	7.1%	EFTVCSIGTANAVAGAVK	99.7%	72.1	25	71.3	2	0	0	1794.91	61	78
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	9	9	18	0.02%	7.1%	LLSTYLER	99.7%	52.7	25	36.2	2	0	0	994.56	1291	1298
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	9	9	18	0.02%	7.1%	LLTGWMPTAIR	97.7%	31.2	25	30.6	2	0	0	1258.70	266	276
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	9	9	18	0.02%	7.1%	LPLTPVFEGLAFK	99.3%	36.4	25	36.3	1	0	0	1431.82	1237	1249
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	9	9	18	0.02%	7.1%	QLVVVLCER	99.7%	43.6	25	40.5	1	0	0	1115.62	1036	1044
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	9	9	18	0.02%	7.1%	SFVELSGAER	99.7%	68.3	25	61.5	3	0	0	1094.55	44	53
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	9	9	18	0.02%	7.1%	TAPLLLSYYLIK	99.7%	56	25	53	3	0	0	1394.83	766	777
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	27	0.03%	9.9%	AQIEQVIANCEHK	99.7%	66.4	25	61.4	2	0	0	1539.76	1207	1219
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	27	0.03%	9.9%	ASTEGVAIQGQQGTR	99.7%	67.5	25	67.2	2	0	0	1502.76	70	84
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	27	0.03%	9.9%	DACDGHEIGR	99.7%	46.9	25	46.9	2	0	0	1129.47	1484	1493
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	27	0.03%	9.9%	DLPSADSVQYR	99.7%	47.5	25	36.9	2	0	0	1250.60	572	582
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	27	0.03%	9.9%	EDTLLLIGHLER	99.7%	47.6	25	39.5	1	0	0	1408.78	244	255
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	27	0.03%	9.9%	ENLFMDLLR	99.7%	50.4	25	33.3	1	0	0	1150.59	860	868
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	27	0.03%	9.9%	FTDELMEQGLTYK	99.7%	44.8	25	41.8	2	0	0	1590.74	173	185
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	27	0.03%	9.9%	IQQGALELLR	99.7%	70.3	25	63.3	2	0	0	1140.67	1566	1575
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	27	0.03%	9.9%	LLDIEGLYSK	99.7%	47.4	25	41.9	1	0	0	1150.64	1979	1988
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	27	0.03%	9.9%	LPGLQATVR	99.3%	36.4	25	33.7	1	0	0	954.57	322	330
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	27	0.03%	9.9%	LTAPEDVFSK	99.7%	42.8	25	42.8	2	0	0	1106.57	1452	1461
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	27	0.03%	9.9%	MLALALLDR	99.7%	48.9	25	40.2	2	0	0	1031.59	1494	1502
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	27	0.03%	9.9%	QCLGLLSR	96.7%	29.6	25	19.5	1	0	0	946.51	1714	1721
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	27	0.03%	9.9%	QYIATIHSR	99.7%	46.1	25	29.8	1	0	0	1088.58	305	313
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	27	0.03%	9.9%	SVSGFLHFDTATK	99.7%	47.8	25	41.7	1	0	0	1409.71	1165	1177
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	27	0.03%	9.9%	TLQSLLTPQPPLLK	99.3%	36.7	25	31.7	1	0	0	1548.94	1535	1548
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	27	0.03%	9.9%	VLTLVSQIDVNNEFEK	99.7%	93.5	25	91.6	2	0	0	1847.98	186	201
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	27	0.03%	9.9%	YSFIQALVR	99.7%	67.8	25	57.1	1	0	0	1096.61	1993	2001
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	10	11	17	0.02%	19.4%	DAAFATLVSDR	99.7%	81.4	25	70.2	2	0	0	1165.58	495	505
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	10	11	17	0.02%	19.4%	DVDVYSQILR	99.7%	82.1	25	69.1	2	0	0	1207.63	60	69
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	10	11	17	0.02%	19.4%	EADASPASAGICR	99.7%	64.2	25	64	2	0	0	1304.59	219	231
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	10	11	17	0.02%	19.4%	FADAASLLLSLMTSR	99.7%	59.5	25	51.2	2	0	0	1595.85	553	567
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	10	11	17	0.02%	19.4%	IPLNTEQK	95.1%	28	25	12.5	1	0	0	942.53	442	449
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	10	11	17	0.02%	19.4%	LGSALSWSIR	99.7%	99.1	25	78.1	2	0	0	1089.61	483	492
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	10	11	17	0.02%	19.4%	SEMVPSCPFIYIIR	98.9%	34.3	25	31.1	1	0	0	1727.85	45	58
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	10	11	17	0.02%	19.4%	TMPILSPGNTQTLTELELK	99.7%	53.9	25	53.9	3	0	0	2086.11	239	257
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	10	11	17	0.02%	19.4%	VSLELHIER	97.3%	30.5	25	30.5	1	0	0	1095.62	433	441
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	10	11	17	0.02%	19.4%	YLQDSTFATSPHLESLLK	99.7%	67.3	25	66	1	0	0	2050.05	268	285
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	45	0.05%	28.3%	AFDIIER	99.2%	35.9	25	24.1	1	0	0	863.46	710	716
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	45	0.05%	28.3%	AQHQLGEFK	99.7%	44.1	25	38.1	1	0	0	1057.54	341	349
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	45	0.05%	28.3%	AVYCIIGR	99.7%	45.5	25	38.2	2	0	0	951.51	389	396
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	45	0.05%	28.3%	CGDLLAASQVVNR	99.7%	86.6	25	74.6	2	0	0	1402.71	328	340
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	45	0.05%	28.3%	CVSELVIESR	99.7%	44.1	25	17.5	2	0	0	1191.60	569	578
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	45	0.05%	28.3%	DNALLSAIEESR	99.7%	100	25	97	2	0	0	1317.66	107	118
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	45	0.05%	28.3%	EALQYFYFLR	99.7%	44.5	25	31.1	5	0	0	1349.69	546	555
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	45	0.05%	28.3%	ESMLVEWEQVK	99.7%	49.9	25	34.2	2	0	0	1377.67	131	141
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	45	0.05%	28.3%	FTSDTKPIINK	99.7%	60.2	25	43.5	2	0	0	1263.69	601	611
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	45	0.05%	28.3%	GLDISHISQR	99.7%	63.3	25	57.8	2	0	0	1125.60	68	77
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	45	0.05%	28.3%	LLMLYTR	99.7%	43	25	41.6	2	0	0	909.52	531	537
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	45	0.05%	28.3%	LLSPVVPQISAPQSNK	99.7%	61.7	25	61.7	2	0	0	1677.95	645	660
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	45	0.05%	28.3%	LTLSQFQK	99.7%	50.1	25	45.3	3	0	0	964.55	435	442
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	45	0.05%	28.3%	LVPLNQESVEER	99.7%	56.2	25	49.7	3	0	0	1412.74	719	730
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	45	0.05%	28.3%	NLQEIQQAGER	99.7%	65.6	25	36.4	2	0	0	1285.65	32	42

Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	45	0.05%	28.3%	NMALSIAER	99.5%	37.8	25	29.6	1	0	0	1004.52	665	673
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	45	0.05%	28.3%	QALAYLEQSYK	99.7%	53	25	50	2	0	0	1313.67	257	267
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	45	0.05%	28.3%	QMTDVLLTPATDALK	99.7%	64.4	25	49.7	2	0	0	1616.86	229	243
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	45	0.05%	28.3%	SSGQSAQLLSHEPGDPPCLR	99.7%	41.8	25	33.4	0	1	0	2136.01	505	524
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	45	0.05%	28.3%	TLITFAGMIPYR	99.7%	72	25	63.8	5	0	0	1382.75	791	802
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	45	0.05%	28.3%	TWFQEYMNSK	98.7%	33.8	25	33.8	1	0	0	1333.59	350	359
Nuclear pore complex protein Nup98-Nup96	NUP98	NUP98_HUMAN	197.6	100.0%	3	3	8	0.01%	1.9%	LALLLSQFVGSQSVR	99.7%	87.5	25	87.5	6	0	0	1617.93	1358	1372
Nuclear pore complex protein Nup98-Nup96	NUP98	NUP98_HUMAN	197.6	100.0%	3	3	8	0.01%	1.9%	SITADPLDYR	98.3%	32.6	25	25.5	1	0	0	1150.57	1514	1523
Nuclear pore complex protein Nup98-Nup96	NUP98	NUP98_HUMAN	197.6	100.0%	3	3	8	0.01%	1.9%	SLVGGLLQSK	99.7%	42.7	25	41.6	1	0	0	1001.60	1043	1052
Nuclear pore membrane glycoprotein 210	NUP210	PO210_HUMAN	205.1	100.0%	4	4	5	0.01%	2.9%	AVDPTSGQLYGLAR	99.7%	43.3	25	33.1	1	0	0	1447.75	1259	1272
Nuclear pore membrane glycoprotein 210	NUP210	PO210_HUMAN	205.1	100.0%	4	4	5	0.01%	2.9%	GVAIGQTSLTASVTNK	99.7%	68.2	25	68.2	1	0	0	1546.84	1048	1063
Nuclear pore membrane glycoprotein 210	NUP210	PO210_HUMAN	205.1	100.0%	4	4	5	0.01%	2.9%	TVSVGLTLLR	99.7%	49.5	25	39.6	2	0	0	1058.66	1448	1457
Nuclear pore membrane glycoprotein 210	NUP210	PO210_HUMAN	205.1	100.0%	4	4	5	0.01%	2.9%	VFGAPEVLENLEVK	99.7%	63.6	25	59.6	1	0	0	1543.84	1711	1724
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	9	10	15	0.02%	16.8%	AQFFVEDASTASALK	99.7%	109	25	104	2	0	0	1584.79	159	173
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	9	10	15	0.02%	16.8%	AWLLSMIQSK	99.7%	67.8	25	49.3	2	0	0	1176.64	133	142
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	9	10	15	0.02%	16.8%	DQSTYISAIR	99.7%	56.5	25	35.2	1	0	0	1153.58	333	342
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	9	10	15	0.02%	16.8%	GSYFGTENLK	99.7%	44	25	29.6	2	0	0	1115.54	375	384
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	9	10	15	0.02%	16.8%	IIEENIPELLSLNLSNNR	99.7%	48.5	25	48.5	1	0	0	2081.12	259	276
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	9	10	15	0.02%	16.8%	ILNLSGNELK	99.7%	53.7	25	38.7	2	0	0	1100.63	295	304
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	9	10	15	0.02%	16.8%	LDDMSSIVQK	99.7%	44.3	25	33.3	3	0	0	1151.56	280	289
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	9	10	15	0.02%	16.8%	LNVVAFLNELPK	99.7%	91.4	25	85.2	1	0	0	1356.79	460	471
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	9	10	15	0.02%	16.8%	SAQAFTHLK	99.3%	36.8	25	29.5	1	0	0	1002.54	599	607
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	7	8	17	0.02%	27.2%	EDVFVHQTAIK	99.7%	51.1	25	47.2	1	0	0	1286.67	82	92
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	7	8	17	0.02%	27.2%	GAEAANVTGPGGVPVQGSK	99.7%	127	25	127	2	0	0	1695.87	119	137
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	7	8	17	0.02%	27.2%	NDTKEDVFVHQTAIK	99.7%	85.9	25	79.8	2	3	0	1744.89	78	92
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	7	8	17	0.02%	27.2%	NEGSESAPEGQAQQR	99.7%	71.5	25	68.3	2	0	0	1587.70	171	185
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	7	8	17	0.02%	27.2%	NGYGFINR	99.7%	60	25	50.3	4	0	0	940.46	70	77
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	7	8	17	0.02%	27.2%	NYQQNYQNSESGEKNEGSESAPEGQAQQR	99.7%	87.4	25	87.4	0	1	0	3257.40	157	185
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	7	8	17	0.02%	27.2%	SVGDGETVEFDVVEGEK	99.7%	82.3	25	71.7	2	0	0	1795.82	102	118
Nucleolar and coiled-body phosphoprotein 1	NOLC1	NOLC1_HUMAN	73.6	100.0%	3	3	6	0.01%	5.0%	DNQLSEVANK	99.7%	45.6	25	36.3	1	0	0	1117.55	24	33
Nucleolar and coiled-body phosphoprotein 1	NOLC1	NOLC1_HUMAN	73.6	100.0%	3	3	6	0.01%	5.0%	VAGGAAPSKPASAK	99.2%	36.2	25	36.2	4	0	0	1211.67	497	510
Nucleolar and coiled-body phosphoprotein 1	NOLC1	NOLC1_HUMAN	73.6	100.0%	3	3	6	0.01%	5.0%	VREEEIEVDSR	99.7%	43.2	25	30.5	1	0	0	1360.67	628	638
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	13	26	0.03%	15.6%	DLIGCLQK	99.6%	39.4	25	26.8	1	0	0	946.50	214	221
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	13	26	0.03%	15.6%	DREIQLEISGK	99.7%	60.4	25	54.4	2	0	0	1287.69	627	637
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	13	26	0.03%	15.6%	EEGTPLTLYYSHWR	99.7%	52	25	49.9	1	0	0	1751.84	610	623
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	13	26	0.03%	15.6%	LFHEVVQAFR	99.7%	42.4	25	38.2	2	2	0	1245.67	169	178
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	13	26	0.03%	15.6%	LSNVNLQEK	99.7%	45.1	25	39.4	2	0	0	1044.57	508	516
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	13	26	0.03%	15.6%	MLQPSSSPLWGK	99.7%	55.2	25	37.5	4	0	0	1330.68	234	245
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	13	26	0.03%	15.6%	NSVPVTVAMVER	99.7%	48.7	25	43.3	2	0	0	1301.69	145	156
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	13	26	0.03%	15.6%	QVQQLLGK	99.7%	44.2	25	34.8	2	0	0	913.55	569	576
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	13	26	0.03%	15.6%	SPDKPGGSPSASR	99.0%	27.7	25	27.5	0	2	0	1242.61	49	61
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	13	26	0.03%	15.6%	VLAFLVLSR	99.7%	71.2	25	71.2	4	0	0	1017.65	311	319
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	13	26	0.03%	15.6%	VQENSAYICSR	99.7%	75.5	25	73	2	0	0	1326.61	577	587
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	7	7	13	0.01%	10.1%	DLSSSEPVHAK	99.7%	65.3	25	57.9	2	0	0	1169.58	113	123
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	7	7	13	0.01%	10.1%	FLQGDSFLNEDLNQLIK	99.7%	66.6	25	66.6	2	0	0	1994.02	761	777
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	7	7	13	0.01%	10.1%	FYLENLEQMVK	99.7%	60.6	25	50.8	2	0	0	1413.71	307	317
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	7	7	13	0.01%	10.1%	IRPLTEAEK	97.0%	30	25	23.1	2	0	0	1056.60	275	283
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	7	7	13	0.01%	10.1%	LGQASLGVIK	99.7%	72.1	25	35.2	2	0	0	985.60	394	403
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	7	7	13	0.01%	10.1%	NYEVRPEMLK	97.3%	30.4	25	22.7	1	0	0	1278.65	413	422
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	7	7	13	0.01%	10.1%	SPLLPAVLEGLAK	99.7%	58.6	25	58.6	2	0	0	1307.79	512	524
Nucleolar complex protein 4 homolog	NOC4L	NOC4L_HUMAN	58.5	100.0%	4	5	7	0.01%	8.0%	LFGALLER	99.7%	57.5	25	32.4	2	0	0	918.54	56	63

Nucleolar complex protein 4 homolog	NOC4L	NOC4L_HUMAN	58.5	100.0%	4	5	7	0.01%	8.0%	LGELLGHPSFQVK	99.7%	44.1	25	38.7	1	1	0	1424.79	103	115
Nucleolar complex protein 4 homolog	NOC4L	NOC4L_HUMAN	58.5	100.0%	4	5	7	0.01%	8.0%	REPTVSSFYVK	98.7%	33.8	25	25.9	1	0	0	1312.69	222	232
Nucleolar complex protein 4 homolog	NOC4L	NOC4L_HUMAN	58.5	100.0%	4	5	7	0.01%	8.0%	RLEAVLASR	99.7%	45.5	25	29	2	0	0	1014.61	17	25
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	6	6	9	0.01%	9.8%	ADVDVQPYAFTTK	99.7%	81.5	25	81.5	2	0	0	1454.72	191	203
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	6	6	9	0.01%	9.8%	FTQQNYHDR	99.7%	40.8	25	39.9	2	0	0	1208.54	53	61
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	6	6	9	0.01%	9.8%	IAELSEDDQK	99.7%	55.8	25	51.5	1	0	0	1147.55	296	305
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	6	6	9	0.01%	9.8%	LALGQINIAK	99.7%	50.7	25	46.5	1	0	0	1040.65	94	103
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	6	6	9	0.01%	9.8%	LSQILTDFPK	99.7%	55.3	25	45.5	2	0	0	1161.65	62	71
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	6	6	9	0.01%	9.8%	QSLEYLEQVR	99.7%	48.2	25	32.5	1	0	0	1264.65	146	155
Nucleolar MIF4G domain-containing protein 1	NOM1	NOM1_HUMAN	96.3	99.9%	2	2	2	0.00%	3.0%	DGLDYILGALESGK	99.7%	80	25	75.7	1	0	0	1450.74	214	227
Nucleolar MIF4G domain-containing protein 1	NOM1	NOM1_HUMAN	96.3	99.9%	2	2	2	0.00%	3.0%	TYNPFYAFLASK	99.7%	44.4	25	44.4	1	0	0	1421.71	702	713
Nucleolar pre-ribosomal-associated protein 1	URB1	NPA1P_HUMAN	254.4	100.0%	2	2	3	0.00%	1.2%	ILLTLVANPYSYTDK	99.7%	50.7	25	50.7	2	0	0	1710.93	703	717
Nucleolar pre-ribosomal-associated protein 1	URB1	NPA1P_HUMAN	254.4	100.0%	2	2	3	0.00%	1.2%	ISTINILLSTLK	99.7%	41.5	25	38.1	1	0	0	1315.82	237	248
Nucleolar protein 16	NOP16	NOP16_HUMAN	21.2	100.0%	4	5	8	0.01%	24.2%	AMEVDIEERPK	99.7%	44.1	25	44.1	1	0	0	1316.65	75	85
Nucleolar protein 16	NOP16	NOP16_HUMAN	21.2	100.0%	4	5	8	0.01%	24.2%	DEKNYYQDTPK	99.7%	44	25	44	2	0	0	1400.63	136	146
Nucleolar protein 16	NOP16	NOP16_HUMAN	21.2	100.0%	4	5	8	0.01%	24.2%	FGYSVNR	97.9%	31.4	25	24.8	2	0	0	842.42	13	19
Nucleolar protein 16	NOP16	NOP16_HUMAN	21.2	100.0%	4	5	8	0.01%	24.2%	QNLAEMGLAVDPNR	99.7%	63.8	25	62.8	3	0	0	1543.75	51	64
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	10	14	0.01%	18.5%	EAMVQAEEAAAEITR	99.7%	102	25	85.2	1	0	0	1618.77	423	437
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	10	14	0.01%	18.5%	ELNEDKLEK	95.0%	27.9	25	14.4	1	0	0	1117.57	222	230
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	10	14	0.01%	18.5%	IDCFSEVPTSVFGEK	99.7%	48.4	25	48.4	1	0	0	1714.80	382	396
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	10	14	0.01%	18.5%	IINDNATYCR	99.7%	59.6	25	59.6	2	0	0	1239.58	203	212
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	10	14	0.01%	18.5%	LIAHAGSLTNLAK	99.7%	60.9	25	60.8	1	0	0	1308.76	308	320
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	10	14	0.01%	18.5%	MSQVAPSLSALIGEAVGAR	99.7%	58.8	25	58.2	2	0	0	1872.98	289	307
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	10	14	0.01%	18.5%	VLLGVGDPK	99.7%	44.9	25	38.4	2	0	0	897.54	91	99
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	10	14	0.01%	18.5%	VVSLSEYR	99.7%	52	25	43.9	2	0	0	952.51	271	278
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	10	14	0.01%	18.5%	YGLIFHSTFIGR	98.8%	26.9	25	26.9	0	2	0	1410.75	348	359
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	8	9	16	0.02%	18.9%	EAHEPLAVADAK	99.5%	37.8	25	31.2	2	0	0	1250.64	82	93
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	8	9	16	0.02%	18.9%	HAASTVQILGAEK	99.7%	69.8	25	69.5	2	0	0	1324.72	311	323
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	8	9	16	0.02%	18.9%	IISDNLTYCK	99.7%	44.8	25	44.8	2	0	0	1226.61	197	206
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	8	9	16	0.02%	18.9%	LIAHAGSLLNLAK	99.7%	56.6	25	56.6	1	2	0	1320.80	298	310
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	8	9	16	0.02%	18.9%	LSELLPEEVEAEVK	99.7%	58.5	25	55.8	2	0	0	1584.84	222	235
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	8	9	16	0.02%	18.9%	SQMDGLIPGVEPR	99.7%	49	25	49	2	0	0	1414.70	121	133
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	8	9	16	0.02%	18.9%	TQLYEYLQNR	99.7%	46.7	25	46.7	2	0	0	1327.66	269	278
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	8	9	16	0.02%	18.9%	TYDPSGDSTLPTCSK	99.7%	60.4	25	60.4	1	0	0	1628.71	427	441
Nucleolar protein 9	NOP9	NOP9_HUMAN	69.4	100.0%	3	3	6	0.01%	6.5%	GSSVDGSPLLLFLR	99.7%	63.1	25	48.5	2	0	0	1460.81	311	324
Nucleolar protein 9	NOP9	NOP9_HUMAN	69.4	100.0%	3	3	6	0.01%	6.5%	TLLQVLGGTILESER	99.7%	79.1	25	79.1	2	0	0	1628.92	209	223
Nucleolar protein 9	NOP9	NOP9_HUMAN	69.4	100.0%	3	3	6	0.01%	6.5%	VLDAIWSGAALR	99.3%	36.8	25	17.9	2	0	0	1271.71	564	575
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	AAVIGDVIR	99.7%	66.9	25	52.3	6	0	0	913.55	424	432
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	APQVLVLAPTR	99.7%	69	25	69	7	0	0	1164.71	260	270
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	DFSDITKK	99.6%	39.7	25	27.9	2	0	0	953.49	279	286
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	DVESYIHR	99.7%	42.9	25	34.7	2	0	0	1018.50	517	524
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	EAQELSQNSAIK	99.7%	56.9	25	44.4	6	0	0	1317.66	450	461
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	EEYQLVQVEQK	99.7%	77	25	68.4	2	0	0	1392.70	545	555
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	EGAFSNFPISEETIK	99.7%	75.1	25	75.1	8	0	0	1668.81	185	199
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	ELKEQLGEEIDSK	99.7%	55.6	25	49.3	2	1	0	1517.77	656	668
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	EQLGEEIDSK	96.5%	29.4	25	29.4	1	0	0	1147.55	659	668
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	GAVEALAAALAHISGATSVDQR	99.6%	31.2	25	31.2	0	2	0	2108.11	606	627
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	GRAPQVLVLAPTR	99.7%	62.4	25	62.4	2	0	0	1377.83	258	270
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	GVTFLFPIQAK	99.7%	65.5	25	35.2	2	0	0	1220.70	205	215
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	IGVPSATEIIK	99.7%	47.6	25	42	3	0	0	1127.67	563	573
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	KAEPSEVDMNSPK	99.7%	49.6	25	42	3	0	0	1431.68	61	73

Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	LGVCFDVPTASVTEIQEK	99.7%	87.8	25	83.7	3	0	0	1992.99	679	696
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	LHGELQDR	98.8%	34	25	26.3	1	0	0	967.50	248	255
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	LLDSVPPTAISHFK	99.6%	38.9	25	33.5	1	1	0	1524.84	582	595
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	LSVACFYGGTPYGGQFER	99.7%	79.2	25	79.2	2	0	0	2008.92	287	304
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	NEEPSEEEIDAPKPK	99.5%	30	25	25.4	0	2	0	1711.80	117	131
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	NGIDILVGTPGR	99.7%	99.1	25	88.9	3	0	0	1211.67	307	318
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	NGSFGVLVATNVAAR	99.7%	95.1	25	94.2	2	0	0	1475.80	485	499
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	QDAQSLHGDIPQK	99.7%	69.4	25	61.3	2	0	0	1436.71	462	474
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	SDAGLESDTAMK	99.7%	62.8	25	62.8	3	0	0	1240.54	7	18
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	STYEQVDLIGK	99.7%	74.4	25	62.4	2	0	0	1252.64	392	402
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	STYEQVDLIGKK	99.7%	70.6	25	52.1	2	0	0	1380.74	392	403
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	TAITVEHLAIK	99.7%	78.9	25	74.2	4	0	0	1195.70	407	417
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	TFSFAIPLIEK	99.7%	59.7	25	57.2	2	0	0	1265.71	237	247
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	TIIFCETKK	97.4%	30.5	25	15.4	2	0	0	1139.61	441	449
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	83	0.08%	42.1%	WQLSVATEQPELEGPR	99.7%	72.1	25	72.1	2	0	0	1839.92	703	718
Nucleolar transcription factor 1	UBTF	UBF1_HUMAN	89.4	99.8%	2	2	2	0.00%	3.4%	FLESLPEEEQQR	99.7%	42.6	25	35.3	1	0	0	1504.73	361	372
Nucleolar transcription factor 1	UBTF	UBF1_HUMAN	89.4	99.8%	2	2	2	0.00%	3.4%	TLTELILDAQEHVK	99.7%	58.1	25	58.1	1	0	0	1609.88	84	97
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	31	167	0.17%	33.4%	ALELTGLK	99.7%	55.8	25	35.4	5	0	0	844.51	363	370
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	31	167	0.17%	33.4%	ALVATPGKK	97.4%	30.5	25	25.8	2	0	0	884.56	117	125
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	31	167	0.17%	33.4%	EAMEDGEIDGNK	99.7%	40.1	25	40.1	2	0	0	1323.54	628	639
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	31	167	0.17%	33.4%	EAMEDGEIDGNKVTLDWAKPK	99.7%	52.5	25	52.5	0	3	0	2362.12	628	648
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	31	167	0.17%	33.4%	ESFDGSVR	97.0%	30.1	25	21.8	2	0	0	896.41	590	597
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	31	167	0.17%	33.4%	EVFEDAAEIR	99.7%	68.8	25	53.4	8	0	0	1178.57	411	420
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	31	167	0.17%	33.4%	FGYVDFESAEDLEK	99.7%	106	25	99.9	8	0	0	1648.74	349	362
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	31	167	0.17%	33.4%	GFGFVDFNSEEDAK	99.7%	84.3	25	84.3	14	0	0	1561.68	611	624
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	31	167	0.17%	33.4%	GIAYIEFK	99.7%	53.9	25	41	8	0	0	940.51	430	437
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	31	167	0.17%	33.4%	GLSEDTTEETLK	99.7%	80.8	25	77.8	6	0	0	1322.63	578	589
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	31	167	0.17%	33.4%	GLSEDTTEETLKESFDGSVR	99.7%	121	25	117	4	5	0	2200.03	578	597
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	31	167	0.17%	33.4%	GYAFIEFASFEDAK	99.7%	106	25	98.2	12	0	0	1594.74	524	537
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	31	167	0.17%	33.4%	KFGYVDFESAEDLEK	99.7%	85.9	25	79.6	3	1	0	1776.83	348	362
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	31	167	0.17%	33.4%	LELQGPR	99.7%	44.3	25	29.5	9	0	0	812.46	555	561
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	31	167	0.17%	33.4%	NDLAVVDVR	99.7%	84.6	25	73.4	12	0	0	1000.54	334	342
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	31	167	0.17%	33.4%	SISLYYTGEK	99.7%	67.4	25	56.2	10	0	0	1160.58	458	467
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	31	167	0.17%	33.4%	TEADAEKTFEEK	99.7%	75.4	25	67.1	9	1	0	1397.64	438	449
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	31	167	0.17%	33.4%	TGISDVFAK	99.7%	70.5	25	53.1	12	0	0	937.50	325	333
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	31	167	0.17%	33.4%	TLVLSNLSYSATEETLQEVFEK	99.7%	135	25	135	3	1	0	2501.27	487	508
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	31	167	0.17%	33.4%	VAVATPAKK	98.1%	32	25	20.3	2	0	0	884.56	72	80
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	31	167	0.17%	33.4%	VEGTEPTTAFNLFVGNLNFNK	99.7%	104	25	104	7	1	0	2312.16	298	318
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	31	167	0.17%	33.4%	VFGNEIK	99.7%	43.9	25	13.9	6	0	0	806.44	371	377
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	31	167	0.17%	33.4%	VFGNEIKLEKPK	99.3%	28.8	25	28.8	0	1	0	1401.81	371	382
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	31	167	0.17%	33.4%	VTLDWAKPK	99.7%	53.7	25	51.1	2	0	0	1057.60	640	648
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	31	167	0.17%	33.4%	VTQDELKEVFEDAAEIR	99.7%	78.5	25	75.1	2	6	0	1991.99	404	420
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	7	11	51	0.05%	29.3%	DELHIVEAEAMNYEGSPIK	99.7%	35	25	35	0	1	0	2161.01	55	73
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	7	11	51	0.05%	29.3%	GPSSVEDIK	99.7%	63.1	25	53	10	0	0	931.47	240	248
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	7	11	51	0.05%	29.3%	GPSSVEDIKAK	99.7%	85	25	71.5	12	0	0	1130.61	240	250
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	7	11	51	0.05%	29.3%	LLSISGKR	99.7%	56.9	25	46.7	5	0	0	873.55	135	142
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	7	11	51	0.05%	29.3%	MSVQPTVSLGGFEITPPVVLR	99.7%	89.4	25	89.4	8	1	0	2227.22	81	101
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	7	11	51	0.05%	29.3%	MTDQEAIQDLWQWR	99.7%	74.4	25	74.2	6	0	0	1819.84	278	291
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	7	11	51	0.05%	29.3%	VDNDENEHQLSLR	99.7%	69.2	25	67	7	1	0	1568.73	33	45
Nucleoporin NDC1	NDC1	NDC1_HUMAN	76.3	100.0%	2	2	3	0.00%	3.3%	LILYQEAAATNGR	99.7%	45.9	25	45.9	1	0	0	1419.76	380	392
Nucleoporin NDC1	NDC1	NDC1_HUMAN	76.3	100.0%	2	2	3	0.00%	3.3%	VLIMYFFSK	99.7%	40.5	25	31.5	2	0	0	1147.62	537	545

Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	2	2	2	0.00%	1.7%	ALLLVPASVNCLR	99.7%	40.6	25	40.6	1	0	0	1425.82	1142	1154
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	2	2	2	0.00%	1.7%	VQRPPSAASAAPSSSK	99.5%	37.8	25	37.8	1	0	0	1540.81	1518	1533
Nucleoside diphosphate kinase 6	NME6	NDK6_HUMAN	21.1	100.0%	3	3	4	0.00%	18.3%	GSFGLTDTR	99.7%	67.9	25	56.4	1	0	0	953.47	117	125
Nucleoside diphosphate kinase 6	NME6	NDK6_HUMAN	21.1	100.0%	3	3	4	0.00%	18.3%	LVEFMASGPIR	99.7%	50.1	25	46.8	1	0	0	1235.65	72	82
Nucleoside diphosphate kinase 6	NME6	NDK6_HUMAN	21.1	100.0%	3	3	4	0.00%	18.3%	NTTHGSDSVVSASR	99.7%	56.4	25	51.3	2	0	0	1417.67	126	139
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	11	33	0.03%	46.7%	DRPFFAGLVK	99.7%	52.2	25	31.4	2	0	0	1149.64	57	66
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	11	33	0.03%	46.7%	GDFCIQVGR	99.7%	59.7	25	50.4	4	0	0	1051.50	106	114
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	11	33	0.03%	46.7%	GLVGEIIK	99.7%	42.4	25	32	3	0	0	828.52	19	26
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	11	33	0.03%	46.7%	GLVGEIIKR	99.7%	53.3	25	50.1	4	0	0	984.62	19	27
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	11	33	0.03%	46.7%	NIIHGSDSVESAEK	98.7%	26.6	25	26.6	0	2	0	1485.72	115	128
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	11	33	0.03%	46.7%	TFIAIKPDGVQR	99.7%	58.3	25	57.6	4	1	0	1344.76	7	18
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	11	33	0.03%	46.7%	VMLGETNPADSKPGTIR	99.7%	58	25	55.2	8	5	0	1785.92	89	105
Nucleoside diphosphate kinase, mitochondrial	NME4	NDKM_HUMAN	20.7	100.0%	3	3	5	0.01%	23.0%	AMIGHTDSAEAAPGTIR	98.6%	26.3	25	24.9	0	1	0	1713.82	122	138
Nucleoside diphosphate kinase, mitochondrial	NME4	NDKM_HUMAN	20.7	100.0%	3	3	5	0.01%	23.0%	NVIHASDSVEGAQR	99.5%	30.1	25	27.3	0	2	0	1482.73	148	161
Nucleoside diphosphate kinase, mitochondrial	NME4	NDKM_HUMAN	20.7	100.0%	3	3	5	0.01%	23.0%	TLVAVKPDGVQR	99.7%	42	25	41.5	2	0	0	1282.75	40	51
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	4	4	11	0.01%	17.1%	FYEEVHDLER	99.7%	43.5	25	38	6	0	0	1336.62	95	104
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	4	4	11	0.01%	17.1%	GIPEFWLTVFK	99.7%	63.1	25	63.1	4	0	0	1336.73	166	176
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	4	4	11	0.01%	17.1%	LDGLVETPTGYIESLPR	99.7%	66.5	25	64.1	2	0	0	1859.98	56	72
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	4	4	11	0.01%	17.1%	NVDLLSDMVQEHDEPILK	98.6%	26.2	25	23.4	0	2	0	2095.04	177	194
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	4	4	11	0.01%	17.1%	YAVLYQPLFDK	99.7%	48.7	25	48.7	3	0	0	1356.72	106	116
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	7	7	15	0.02%	20.3%	AAATAEEPDPK	99.7%	40.6	25	35.2	2	0	0	1099.53	147	157
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	7	7	15	0.02%	20.3%	FYEEVHDLER	99.7%	43.5	25	38	6	0	0	1336.62	84	93
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	7	7	15	0.02%	20.3%	GIPEFWFTIFR	99.2%	36.2	25	36.2	1	0	0	1412.74	158	168
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	7	7	15	0.02%	20.3%	LTDQVMQNPR	99.7%	72.6	25	63	3	0	0	1201.60	27	36
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	7	7	15	0.02%	20.3%	QVPNESFFNFFNPLK	99.7%	47.6	25	39.3	1	0	0	1827.91	283	297
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	7	7	15	0.02%	20.3%	VLAALQER	99.7%	46	25	36	1	0	0	899.53	37	44
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	7	7	15	0.02%	20.3%	YAALYQPLFDK	98.3%	32.5	25	32.1	1	0	0	1328.69	95	105
Oligosaccharyltransferase complex subunit OSTC	OSTC	OSTC_HUMAN	16.8	99.8%	2	2	7	0.01%	14.1%	MKLPGYLMG	99.7%	41.3	25	25.2	2	0	0	1025.52	141	149
Oligosaccharyltransferase complex subunit OSTC	OSTC	OSTC_HUMAN	16.8	99.8%	2	2	7	0.01%	14.1%	VPFLVLECPNLK	99.7%	73.8	25	69.4	5	0	0	1428.79	7	18
Origin recognition complex subunit 3	ORC3	ORC3_HUMAN	82.3	100.0%	5	6	9	0.01%	9.0%	AVSELELLGFIKPTK	98.3%	32.5	25	32.5	1	0	0	1644.96	683	697
Origin recognition complex subunit 3	ORC3	ORC3_HUMAN	82.3	100.0%	5	6	9	0.01%	9.0%	ENVVNFIDCLVR	99.7%	50.1	25	50.1	1	0	0	1477.75	553	564
Origin recognition complex subunit 3	ORC3	ORC3_HUMAN	82.3	100.0%	5	6	9	0.01%	9.0%	QVALLTNER	99.5%	38.3	25	27.1	1	0	0	1043.58	384	392
Origin recognition complex subunit 3	ORC3	ORC3_HUMAN	82.3	100.0%	5	6	9	0.01%	9.0%	SKEEESVHVTQR	99.7%	74.6	25	69.4	2	2	0	1428.71	164	175
Origin recognition complex subunit 3	ORC3	ORC3_HUMAN	82.3	100.0%	5	6	9	0.01%	9.0%	TTSSQWQSPPVVVILK	99.7%	49.6	25	49.6	2	0	0	1769.98	205	220
Origin recognition complex subunit 4	ORC4	ORC4_HUMAN	50.4	100.0%	3	3	3	0.00%	8.7%	LDILELLEK	99.7%	49.2	25	43.9	1	0	0	1085.65	196	204
Origin recognition complex subunit 4	ORC4	ORC4_HUMAN	50.4	100.0%	3	3	3	0.00%	8.7%	LLLDNTQIMNALQK	99.7%	85.1	25	79.3	1	0	0	1614.89	404	417
Origin recognition complex subunit 4	ORC4	ORC4_HUMAN	50.4	100.0%	3	3	3	0.00%	8.7%	QSPHSNLFGVQVQYK	99.7%	36.9	25	36.9	0	1	0	1731.88	31	45
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	7	7	11	0.01%	16.8%	AMQTVYLR	97.6%	30.9	25	15.3	1	0	0	981.52	264	271
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	7	7	11	0.01%	16.8%	EISSSQWEK	99.7%	47.5	25	36.7	2	0	0	1093.52	272	280
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	7	7	11	0.01%	16.8%	ESQVSILQSLFGER	99.7%	81.7	25	80.8	2	0	0	1592.83	12	25
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	7	7	11	0.01%	16.8%	LLAILYSIVDSR	99.7%	50.6	25	50.6	1	0	0	1362.80	362	373
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	7	7	11	0.01%	16.8%	LLLEQILNK	99.7%	49.3	25	37.3	2	0	0	1083.68	71	79
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	7	7	11	0.01%	16.8%	LQKDDTDPGQLK	97.4%	30.6	25	22.7	2	0	0	1357.70	281	292
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	7	7	11	0.01%	16.8%	TYVTQTLLK	99.4%	37.1	25	33.7	1	0	0	1066.61	44	52
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	25	60	0.06%	49.7%	AFYNNVLGEYEEYITK	99.7%	71	25	64.6	2	0	0	1952.93	114	129
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	25	60	0.06%	49.7%	DNGLLAKPTHGDIIR	99.7%	55.6	25	55.6	0	2	0	1619.89	399	413
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	25	60	0.06%	49.7%	EDELRESIEIINK	99.7%	74.1	25	54	2	0	0	1587.82	422	434
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	25	60	0.06%	49.7%	FAPPLVIKEDELR	99.7%	64.2	25	61.5	2	1	0	1526.86	414	426
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	25	60	0.06%	49.7%	GIYLWDVEGR	99.7%	62.2	25	48.7	3	0	0	1207.61	67	76
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	25	60	0.06%	49.7%	GIYLWDVEGRK	99.7%	49.5	25	41.8	2	0	0	1335.71	67	77
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	25	60	0.06%	49.7%	GKGLLNAIVIK	98.3%	32.3	25	32.3	1	0	0	1125.74	373	383

Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	25	60	0.06%	49.7%	GLLNAIVIK	99.7%	60.6	25	52.2	6	0	0	940.62	375	383
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	25	60	0.06%	49.7%	HQVLFIADEIQTGLAR	99.7%	44.5	25	35.3	0	2	0	1810.98	256	271
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	25	60	0.06%	49.7%	IVFAAGNFWGR	99.7%	73	25	68.5	5	0	0	1237.65	170	180
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	25	60	0.06%	49.7%	KTVQGPPTSDDIFER	99.7%	64	25	64	0	2	0	1689.84	32	46
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	25	60	0.06%	49.7%	KWGYTVK	95.3%	28.1	25	17.5	1	0	0	881.49	155	161
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	25	60	0.06%	49.7%	LPSDVVTAVR	99.7%	75.2	25	62.8	6	0	0	1056.60	363	372
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	25	60	0.06%	49.7%	NELMKLPSDVVTAVR	99.7%	55.7	25	50	1	2	0	1687.90	358	372
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	25	60	0.06%	49.7%	SQVDKLTLTSR	99.7%	62.8	25	56.7	5	2	0	1247.70	103	113
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	25	60	0.06%	49.7%	TVQGPPTSDDIFER	99.7%	86.6	25	74.8	2	0	0	1561.75	33	46
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	25	60	0.06%	49.7%	VAIAALEVLEEENLAENADK	99.7%	107	25	103	2	0	0	2141.10	332	351
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	25	60	0.06%	49.7%	VLPMNTGVEAGETACK	99.7%	109	25	106	4	0	0	1676.80	136	151
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	25	60	0.06%	49.7%	WLAVDYENVRPDIVLLGK	99.7%	42.4	25	42.4	2	1	0	2100.15	275	292
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	25	60	0.06%	49.7%	YGAHNYHPLPVALER	99.7%	59.3	25	55.7	2	0	0	1736.89	50	64
Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	CPOX	HEM6_HUMAN	50.2	99.8%	2	3	6	0.01%	4.9%	FGLFTPGSR	99.7%	47.7	25	40.9	2	0	0	981.52	405	413
Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	CPOX	HEM6_HUMAN	50.2	99.8%	2	3	6	0.01%	4.9%	IESILMSLPLTAR	99.7%	65.8	25	65.8	4	0	0	1459.82	414	426
Oxysterol-binding protein-related protein 8	OSBPL8	OSBL8_HUMAN	101.2	99.8%	2	2	5	0.01%	3.4%	GEAVGSITQPLPSSYLIIR	99.7%	48.9	25	48.9	1	0	0	2001.10	228	246
Oxysterol-binding protein-related protein 8	OSBPL8	OSBL8_HUMAN	101.2	99.8%	2	2	5	0.01%	3.4%	VVLPTFILEPR	99.7%	44.6	25	44.6	4	0	0	1283.77	423	433
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	14	25	0.03%	31.7%	CQIIYPR	98.7%	33.6	25	20	2	0	0	949.49	341	347
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	14	25	0.03%	31.7%	ELEMIGFIENNVSK	99.7%	112	25	104	2	0	0	1622.81	355	368
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	14	25	0.03%	31.7%	HSNVVILTTSNITEK	99.7%	44.8	25	44.8	0	2	0	1655.90	290	304
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	14	25	0.03%	31.7%	IDVAFVDR	99.7%	52	25	28.7	2	0	0	934.50	305	312
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	14	25	0.03%	31.7%	IYLSCLEELMK	99.7%	55.6	25	45	2	0	0	1398.70	330	340
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	14	25	0.03%	31.7%	LSLLLNDISR	99.7%	65.3	25	44.7	2	0	0	1143.67	369	378
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	14	25	0.03%	31.7%	NVNSNLITWNR	99.7%	53.5	25	52.9	1	0	0	1330.69	163	173
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	14	25	0.03%	31.7%	QQLLTLR	99.7%	46.5	25	25	2	0	0	871.54	348	354
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	14	25	0.03%	31.7%	QYIGPPSAAAIFK	99.7%	65.7	25	53.2	2	0	0	1362.74	317	329
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	14	25	0.03%	31.7%	VVLLHGPPGTGK	99.7%	65.5	25	56.9	2	0	0	1174.69	174	185
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	14	25	0.03%	31.7%	VVNAVLTQIDQIKR	99.7%	84.4	25	84.4	2	2	0	1596.94	276	289
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	14	25	0.03%	31.7%	YGQLIEINSHSLFSK	99.7%	80.9	25	79.5	1	1	0	1735.90	206	220
Paired amphipathic helix protein Sin3a	SIN3A	SIN3A_HUMAN	145.2	100.0%	2	2	2	0.00%	1.5%	SAEAYENFLR	99.7%	51.7	25	40.2	1	0	0	1199.57	476	485
Paired amphipathic helix protein Sin3a	SIN3A	SIN3A_HUMAN	145.2	100.0%	2	2	2	0.00%	1.5%	SLLESTYQR	98.6%	33.4	25	22.7	1	0	0	1096.56	1044	1052
Pantothenate kinase 4	PANK4	PANK4_HUMAN	86.0	100.0%	5	5	8	0.01%	8.3%	AVASQPDSVDAAER	99.7%	74.9	25	73.3	2	0	0	1415.68	463	476
Pantothenate kinase 4	PANK4	PANK4_HUMAN	86.0	100.0%	5	5	8	0.01%	8.3%	GLLAGNVFDWGAK	99.7%	47	25	42.1	1	0	0	1347.71	560	572
Pantothenate kinase 4	PANK4	PANK4_HUMAN	86.0	100.0%	5	5	8	0.01%	8.3%	LLLVQTGSSSPCLDLSR	99.7%	48.6	25	48.6	1	0	0	1845.97	688	704
Pantothenate kinase 4	PANK4	PANK4_HUMAN	86.0	100.0%	5	5	8	0.01%	8.3%	VIQATGGGAYK	99.7%	42.7	25	29.2	1	0	0	1064.57	119	129
Pantothenate kinase 4	PANK4	PANK4_HUMAN	86.0	100.0%	5	5	8	0.01%	8.3%	VYFGGFFIR	99.7%	43.8	25	39	3	0	0	1105.58	319	327
Parafibromin	CDC73	CDC73_HUMAN	60.6	99.8%	2	2	4	0.00%	3.8%	NIFAILQSVK	99.7%	40.3	25	40.3	2	0	0	1132.67	248	257
Parafibromin	CDC73	CDC73_HUMAN	60.6	99.8%	2	2	4	0.00%	3.8%	SAPLEIGLQR	99.7%	58.2	25	51.2	2	0	0	1083.62	111	120
PAX3- and PAX7-binding protein 1	PAXBP1	PAXB1_HUMAN	104.8	99.8%	2	2	2	0.00%	2.5%	LEGSSGGIGER	98.2%	32.2	25	15.8	1	0	0	1061.52	430	440
PAX3- and PAX7-binding protein 1	PAXBP1	PAXB1_HUMAN	104.8	99.8%	2	2	2	0.00%	2.5%	LQLLTWTPLEAK	98.8%	34	25	29	1	0	0	1412.82	632	643
PCI domain-containing protein 2	PCID2	PCID2_HUMAN	46.0	100.0%	5	5	11	0.01%	14.5%	AIDSSNLKDDYSTAQR	99.7%	36.9	25	33.5	0	1	0	1783.85	194	209
PCI domain-containing protein 2	PCID2	PCID2_HUMAN	46.0	100.0%	5	5	11	0.01%	14.5%	CGIFLILEK	99.7%	43.6	25	23.4	2	0	0	1092.61	308	316
PCI domain-containing protein 2	PCID2	PCID2_HUMAN	46.0	100.0%	5	5	11	0.01%	14.5%	CQTVIVQSFLR	99.7%	51.9	25	34.9	2	0	0	1350.72	83	93
PCI domain-containing protein 2	PCID2	PCID2_HUMAN	46.0	100.0%	5	5	11	0.01%	14.5%	DGASCAELVSFK	99.7%	71.1	25	69	2	0	0	1283.59	21	32
PCI domain-containing protein 2	PCID2	PCID2_HUMAN	46.0	100.0%	5	5	11	0.01%	14.5%	MILIYLLPVK	99.7%	72.8	25	72.8	4	0	0	1202.76	250	259
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	6	6	12	0.01%	9.4%	FIGPDQHR	99.7%	46.2	25	35.6	2	0	0	969.49	447	454
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	6	6	12	0.01%	9.4%	SAYESQPIR	99.5%	37.8	25	24.2	2	0	0	1050.52	557	565
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	6	6	12	0.01%	9.4%	SELLNELMDSAK	99.7%	72.9	25	69	2	0	0	1349.66	608	619
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	6	6	12	0.01%	9.4%	SPALQVLR	99.7%	64.5	25	58.3	2	0	0	883.54	351	358
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	6	6	12	0.01%	9.4%	VEGTDVTGIEEVVIPK	99.7%	103	25	94.6	2	0	0	1684.90	46	61
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	6	6	12	0.01%	9.4%	VMSDFAINQEQK	99.7%	99.7	25	97	2	0	0	1409.67	649	660

Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	11	14	26	0.03%	65.5%	ALSTGEKGFGYK	99.3%	36.9	25	32.1	2	0	0	1257.65	38	49
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	11	14	26	0.03%	65.5%	EGMNIVEAMER	99.7%	44.5	25	44.5	3	0	0	1278.58	134	144
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	11	14	26	0.03%	65.5%	IIPGFMCQGGDFTR	99.7%	48.4	25	45.3	3	0	0	1598.75	56	69
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	11	14	26	0.03%	65.5%	ITIADCGQLE	99.7%	48.2	25	38.2	2	0	0	1119.54	156	165
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	11	14	26	0.03%	65.5%	KITIADCGQLE	99.7%	72.4	25	57.5	2	0	0	1247.63	155	165
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	11	14	26	0.03%	65.5%	SIYGEKFEDENFILK	99.7%	70.1	25	59.3	2	0	0	1831.91	77	91
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	11	14	26	0.03%	65.5%	TEWLDGKHVVFGK	97.1%	23.8	25	20.2	0	2	0	1515.80	119	131
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	11	14	26	0.03%	65.5%	VKEGMNIVEAMER	99.7%	69.6	25	69.6	2	2	0	1505.75	132	144
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	11	14	26	0.03%	65.5%	VNPTVFFDIAVDGEPLGR	99.7%	74.6	25	74.6	2	0	0	1946.00	2	19
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	11	14	26	0.03%	65.5%	VSFELFADK	99.7%	55.6	25	50.4	2	0	0	1055.54	20	28
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	11	14	26	0.03%	65.5%	VSFELFADKVPK	99.7%	67.8	25	60	2	0	0	1379.76	20	31
Peptidyl-prolyl cis-trans isomerase B	PPIB	PPIB_HUMAN	23.7	100.0%	2	2	3	0.00%	12.0%	DTNGSQFFITTVK	99.7%	53.3	25	42.8	2	0	0	1457.73	146	158
Peptidyl-prolyl cis-trans isomerase B	PPIB	PPIB_HUMAN	23.7	100.0%	2	2	3	0.00%	12.0%	SIYGERFPDENFK	99.4%	37	25	35.6	1	0	0	1601.76	117	129
Peptidyl-prolyl cis-trans isomerase FKBP1A	FKBP1A	FKB1A_HUMAN	12.0	99.8%	2	2	3	0.00%	25.0%	GVQVETISPGDGR	99.7%	49.6	25	43.8	2	0	0	1314.67	2	14
Peptidyl-prolyl cis-trans isomerase FKBP1A	FKBP1A	FKB1A_HUMAN	12.0	99.8%	2	2	3	0.00%	25.0%	GWEEGVAQMSVGQR	98.8%	34.2	25	34.2	1	0	0	1533.71	59	72
Peptidyl-prolyl cis-trans isomerase H	PPIH	PPIH_HUMAN	19.2	99.8%	2	2	4	0.00%	13.0%	IIDGLLVMR	99.5%	38.2	25	24.8	2	0	0	1029.61	144	152
Peptidyl-prolyl cis-trans isomerase H	PPIH	PPIH_HUMAN	19.2	99.8%	2	2	4	0.00%	13.0%	KIENVPTGPNNKPK	99.7%	35.6	25	35.6	0	2	0	1535.85	153	166
Peptidyl-tRNA hydrolase ICT1, mitochondrial	ICT1	ICT1_HUMAN	23.6	99.8%	2	2	3	0.00%	8.7%	NLADCLQK	96.9%	29.9	25	20.5	1	0	0	961.48	146	153
Peptidyl-tRNA hydrolase ICT1, mitochondrial	ICT1	ICT1_HUMAN	23.6	99.8%	2	2	3	0.00%	8.7%	QADSDIPLDR	99.7%	51.5	25	40.1	2	0	0	1129.55	67	76
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	33	0.03%	52.8%	ADEGISFR	99.7%	50.8	25	38.6	2	0	0	894.43	121	128
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	33	0.03%	52.8%	ATAVMPDGQFK	99.7%	44.8	25	44.5	4	0	0	1180.57	17	27
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	33	0.03%	52.8%	ATAVMPDGQFKDISLSDYK	99.7%	38.3	25	36.2	1	3	0	2086.02	17	35
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	33	0.03%	52.8%	DISLSDYKGK	99.7%	48	25	42.4	2	0	0	1125.58	28	37
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	33	0.03%	52.8%	GLFIIDDKGILR	99.7%	56.6	25	56.6	4	2	0	1359.80	129	140
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	33	0.03%	52.8%	IGHPAPNFK	99.7%	40.5	25	37.8	1	0	0	980.53	8	16
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	33	0.03%	52.8%	LVQAFQFTDK	99.7%	65.6	25	55.8	2	0	0	1196.63	159	168
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	33	0.03%	52.8%	QGGLGPMNIPLVSDPK	99.7%	60	25	56	2	0	0	1638.85	94	109
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	33	0.03%	52.8%	QGGLGPMNIPLVSDPKR	99.2%	28.7	25	28.7	1	2	0	1794.95	94	110
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	33	0.03%	52.8%	QITVNDLPVGR	99.7%	78.2	25	70.6	3	0	0	1211.67	141	151
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	33	0.03%	52.8%	SVDETLR	99.5%	37.8	25	23.5	2	0	0	819.42	152	158
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	33	0.03%	52.8%	TIAQDYGVLK	99.7%	64.4	25	54.4	2	0	0	1107.60	111	120
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	5	5	8	0.01%	21.7%	ATAVVDGAFK	99.7%	56.8	25	50.2	2	0	0	978.53	17	26
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	5	5	8	0.01%	21.7%	ATAVVDGAFKEVK	99.7%	62.5	25	52.2	2	0	0	1334.73	17	29
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	5	5	8	0.01%	21.7%	IGKPAPDFK	99.7%	42.6	25	33.2	1	0	0	972.55	8	16
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	5	5	8	0.01%	21.7%	LSEDYGVLK	99.7%	56.9	25	47.3	2	0	0	1023.54	111	119
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	5	5	8	0.01%	21.7%	QITVNDLPVGR	99.7%	78.2	25	70.6	3	0	0	1211.67	140	150
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	5	5	8	0.01%	21.7%	RLSEDYGVLK	99.7%	51	25	34.7	1	0	0	1179.64	110	119
Peroxiredoxin-4	PRDX4	PRDX4_HUMAN	30.5	99.9%	2	2	3	0.00%	15.9%	DYGVYLEDSGHTLR	99.7%	88.4	25	88.4	1	0	0	1624.76	187	200
Peroxiredoxin-4	PRDX4	PRDX4_HUMAN	30.5	99.9%	2	2	3	0.00%	15.9%	GLFIIDDKGILR	99.7%	56.6	25	56.6	4	2	0	1359.80	201	212
Peroxiredoxin-4	PRDX4	PRDX4_HUMAN	30.5	99.9%	2	2	3	0.00%	15.9%	LVQAFQYTDK	98.4%	32.6	25	32.6	2	0	0	1212.63	231	240
Peroxiredoxin-4	PRDX4	PRDX4_HUMAN	30.5	99.9%	2	2	3	0.00%	15.9%	SVDETLR	99.5%	37.8	25	23.5	2	0	0	819.42	224	230
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	11	11	22	0.02%	53.1%	DFTPVCTTELGR	99.7%	73.3	25	72.2	4	0	0	1395.66	42	53
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	11	11	22	0.02%	53.1%	DGDSVMVLPTIPEEEAK	99.2%	36	25	23.5	2	0	0	1845.88	183	199
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	11	11	22	0.02%	53.1%	DINAYNCEEPTEK	99.7%	74.3	25	74.3	2	0	0	1582.67	85	97
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	11	11	22	0.02%	53.1%	ELAILLGMLDPAEKDEK	97.7%	31.1	25	25.2	1	0	0	1885.00	109	125
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	11	11	22	0.02%	53.1%	LPFPIIDDR	99.7%	58.9	25	46.2	2	0	0	1085.60	98	106
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	11	11	22	0.02%	53.1%	LPFPIIDDRNR	98.0%	25.1	25	21.1	0	1	0	1355.74	98	108
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	11	11	22	0.02%	53.1%	LSILYPATTGR	99.7%	61.8	25	43.4	2	0	0	1191.67	145	155
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	11	11	22	0.02%	53.1%	NFDEILR	99.7%	46.4	25	22.5	2	0	0	906.47	156	162
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	11	11	22	0.02%	53.1%	PGGLLLGDVAPNFEANTTVGR	99.7%	85.6	25	84.4	2	0	0	2098.09	2	22
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	11	11	22	0.02%	53.1%	VVFVFGPDK	99.7%	51.3	25	49.7	2	0	0	1007.56	133	141

Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	11	11	22	0.02%	53.1%	VVFVFGPDKK	99.7%	47.4	25	43	2	0	0	1135.65	133	142
Peroxisomal 2,4-dienoyl-CoA reductase	DECR2	DECR2_HUMAN	30.8	100.0%	3	3	4	0.00%	10.6%	GQALQVHAGSAK	99.7%	60.3	25	40	2	0	0	1166.63	171	182
Peroxisomal 2,4-dienoyl-CoA reductase	DECR2	DECR2_HUMAN	30.8	100.0%	3	3	4	0.00%	10.6%	LGGPQASLSTK	99.7%	51	25	40.5	1	0	0	1058.58	220	230
Peroxisomal 2,4-dienoyl-CoA reductase	DECR2	DECR2_HUMAN	30.8	100.0%	3	3	4	0.00%	10.6%	VTASPLQR	97.8%	31.3	25	13.8	1	0	0	871.50	231	238
Peroxisomal biogenesis factor 3	PEX3	PEX3_HUMAN	42.1	99.8%	2	2	3	0.00%	5.6%	EAAEYIAQAR	99.7%	58.9	25	51.4	2	0	0	1121.56	44	53
Peroxisomal biogenesis factor 3	PEX3	PEX3_HUMAN	42.1	99.8%	2	2	3	0.00%	5.6%	HSLSLLDLEQK	99.7%	56.1	25	49.8	1	0	0	1282.70	198	208
Peroxisomal membrane protein 2	PXMP2	PXMP2_HUMAN	22.3	99.9%	2	2	3	0.00%	10.8%	LRAEAGLGALPR	99.7%	33.5	25	21	0	1	0	1223.72	8	19
Peroxisomal membrane protein 2	PXMP2	PXMP2_HUMAN	22.3	99.9%	2	2	3	0.00%	10.8%	SLDVGGPLR	97.0%	30	25	23.7	2	0	0	913.51	66	74
Peroxisomal membrane protein PMP34	SLC25A17	PM34_HUMAN	34.6	100.0%	4	4	6	0.01%	17.3%	AIATTVTYPLQTVQSILR	99.7%	52.4	25	52.4	2	0	0	1975.12	214	231
Peroxisomal membrane protein PMP34	SLC25A17	PM34_HUMAN	34.6	100.0%	4	4	6	0.01%	17.3%	LSSLDVFIIGAVAK	99.7%	83.9	25	83.9	1	0	0	1432.84	200	213
Peroxisomal membrane protein PMP34	SLC25A17	PM34_HUMAN	34.6	100.0%	4	4	6	0.01%	17.3%	LTAATFTVMGLK	99.7%	43.6	25	43.6	2	0	0	1268.69	291	302
Peroxisomal membrane protein PMP34	SLC25A17	PM34_HUMAN	34.6	100.0%	4	4	6	0.01%	17.3%	NILYLLHQR	98.1%	31.9	25	31.9	1	0	0	1169.68	249	257
Peroxisomal multifunctional enzyme type 2	HSD17B4	DHB4_HUMAN	79.7	99.8%	2	2	2	0.00%	3.7%	IDVVVNNAGILR	99.0%	34.9	25	32.1	1	0	0	1282.75	93	104
Peroxisomal multifunctional enzyme type 2	HSD17B4	DHB4_HUMAN	79.7	99.8%	2	2	2	0.00%	3.7%	LGLLGLANSLAIEGR	98.9%	34.5	25	34.5	1	0	0	1496.88	169	183
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	8	14	0.01%	9.4%	EALAFIIR	97.0%	30	25	20.5	2	0	0	932.56	341	348
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	8	14	0.01%	9.4%	GSATNYITR	99.7%	67	25	55.5	2	0	0	982.50	12	20
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	8	14	0.01%	9.4%	LAALEEQR	99.7%	58.9	25	48	2	0	0	929.51	496	503
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	8	14	0.01%	9.4%	LAQEEESEAK	98.5%	32.9	25	31.8	1	0	0	1133.53	524	533
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	8	14	0.01%	9.4%	LAQEEESEAKR	99.7%	46.9	25	40.7	2	1	0	1289.63	524	534
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	8	14	0.01%	9.4%	LEGQAQAEAK	99.7%	57.2	25	43.7	2	0	0	1044.53	250	259
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	8	14	0.01%	9.4%	LQLSLADFR	99.7%	65.7	25	59.9	2	0	0	1062.59	27	35
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	10	12	17	0.02%	22.2%	DQHDTFFLR	99.7%	45.8	25	34.5	1	0	0	1178.56	272	280
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	10	12	17	0.02%	22.2%	DQHDTFFLRDPAEALQLPMDYVQR	99.7%	46.6	25	46.2	0	1	0	2905.39	272	295
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	10	12	17	0.02%	22.2%	FKPAYNPYTEPSMEVFSYHQGLK	99.7%	57.1	25	55.3	0	1	0	2733.30	405	427
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	10	12	17	0.02%	22.2%	HWELTAEGEEIAR	98.8%	34	25	34	1	0	0	1540.74	60	72
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	10	12	17	0.02%	22.2%	KPFTPVK	94.6%	27.6	25	11.3	1	0	0	816.50	343	349
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	10	12	17	0.02%	22.2%	LGITQLR	99.7%	56.8	25	35.9	2	0	0	800.50	398	404
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	10	12	17	0.02%	22.2%	SLQALGEVIEAELR	99.7%	114	25	107	2	1	0	1527.84	43	56
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	10	12	17	0.02%	22.2%	THSQGGYGSQGYK	99.7%	64	25	64	2	0	0	1369.61	299	311
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	10	12	17	0.02%	22.2%	VVDSMEDEVQR	99.7%	84.1	25	84.1	4	0	0	1306.59	128	138
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	10	12	17	0.02%	22.2%	VVDSMEDEVQRR	96.1%	22.7	25	22.7	0	1	0	1462.70	128	139
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	11	11	24	0.02%	19.5%	ASEGPAFFPGR	99.7%	77.4	25	58.1	2	0	0	1135.55	537	547
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	11	11	24	0.02%	19.5%	DLLFQALGR	99.7%	66.3	25	43.1	4	0	0	1032.58	9	17
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	11	11	24	0.02%	19.5%	DRYDSFIELQEK	99.7%	49.3	25	40.2	1	0	0	1542.74	134	145
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	11	11	24	0.02%	19.5%	ETPENLAK	97.4%	30.6	25	18.1	1	0	0	901.46	322	329
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	11	11	24	0.02%	19.5%	LFEISDIVIK	99.7%	61.2	25	44.1	4	0	0	1176.69	474	483
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	11	11	24	0.02%	19.5%	LGVLHPDVITK	99.7%	44.1	25	44.1	2	0	0	1191.71	561	571
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	11	11	24	0.02%	19.5%	LIITEETAK	99.4%	37.4	25	28.5	2	0	0	1017.58	108	116
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	11	11	24	0.02%	19.5%	NIFIECTGTDFTK	99.7%	103	25	98.7	2	0	0	1545.73	250	262
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	11	11	24	0.02%	19.5%	TTLLPGLLK	98.1%	32.1	25	32.1	2	0	0	955.62	452	460
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	11	11	24	0.02%	19.5%	TYTIANQFPLNK	99.7%	54.5	25	51.1	2	0	0	1409.74	384	395
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	11	11	24	0.02%	19.5%	YDLLCLEGLVR	99.7%	63.3	25	57.1	2	0	0	1350.71	72	82
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	81	0.08%	36.5%	EKGSSASLVLK	99.7%	41.8	25	32.9	1	0	0	1118.64	294	304
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	81	0.08%	36.5%	FACFER	97.9%	31.4	25	29.8	2	0	0	829.37	235	240
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	81	0.08%	36.5%	FGFYEVFK	99.3%	36.7	25	27.7	4	0	0	1036.51	138	145
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	81	0.08%	36.5%	GIFNGFSVTLK	99.7%	80.3	25	72.3	6	0	0	1182.65	102	112
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	81	0.08%	36.5%	GIFNGFSVTLKEDGVR	99.7%	77.2	25	72.2	1	0	0	1738.91	102	117
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	81	0.08%	36.5%	GSSASLVLK	99.7%	43.3	25	30.6	3	0	0	861.50	296	304
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	81	0.08%	36.5%	GSSASLVLKR	99.7%	61.1	25	44.1	5	0	0	1017.61	296	305
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	81	0.08%	36.5%	GVAPLWMR	99.7%	56.5	25	27	12	0	0	929.50	219	226
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	81	0.08%	36.5%	GWAPTFLGYSMQGLCK	99.7%	80.2	25	80.2	7	0	0	1831.85	122	137

Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	81	0.08%	36.5%	IQTQPGYANTLR	99.7%	80.1	25	64.7	14	0	0	1361.72	190	201
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	81	0.08%	36.5%	LPRPPPPEMPESLK	99.7%	36.8	25	36.8	0	1	0	1587.86	342	355
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	81	0.08%	36.5%	MQVDPQK	99.5%	37.9	25	24.9	1	0	0	845.42	93	99
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	81	0.08%	36.5%	MQVDPQKYK	99.7%	48.6	25	33.9	5	0	0	1136.58	93	101
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	81	0.08%	36.5%	MYKEEGLK	99.7%	48.5	25	34	8	0	0	997.50	207	214
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	81	0.08%	36.5%	TVEALYK	97.2%	30.3	25	18.9	2	0	0	823.46	241	247
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	81	0.08%	36.5%	VLYSNMLGEENTYLWR	99.7%	111	25	111	9	0	0	2003.95	146	161
Phosphatidylethanolamine-binding protein 1	PEBP1	PEBP1_HUMAN	21.1	99.8%	2	2	2	0.00%	18.2%	GNDISSGTVLSDYVGSGPPK	99.7%	87.3	25	79.3	1	0	0	1949.95	94	113
Phosphatidylethanolamine-binding protein 1	PEBP1	PEBP1_HUMAN	21.1	99.8%	2	2	2	0.00%	18.2%	LYTLVLTDPDAPSR	99.6%	39.8	25	39.8	1	0	0	1560.83	63	76
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	7	8	13	0.01%	38.8%	AATALLEAGLAR	99.7%	77.4	25	63.2	2	0	0	1156.67	2	13
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	7	8	13	0.01%	38.8%	GVITMNEEYETR	99.7%	76.2	25	73.2	4	0	0	1441.66	67	78
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	7	8	13	0.01%	38.8%	IDPTVLLGALPLR	99.7%	71	25	71	2	0	0	1377.85	41	53
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	7	8	13	0.01%	38.8%	LGVEQLR	99.7%	47.2	25	17.2	2	0	0	814.48	90	96
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	7	8	13	0.01%	38.8%	LSTVDMTGIPTLDNLQK	99.7%	42.4	25	33.6	1	0	0	1845.96	97	113
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	7	8	13	0.01%	38.8%	QLVQDENVR	98.5%	33.2	25	25.9	1	0	0	1100.57	58	66
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	7	8	13	0.01%	38.8%	WSPEEAVR	95.8%	28.5	25	28.5	1	0	0	973.47	153	160
Phosphatidylinositide phosphatase SAC1	SACM1L	SAC1_HUMAN	67.0	100.0%	3	3	6	0.01%	4.9%	ELSAQPEVHR	99.7%	53.9	25	40.2	2	0	0	1165.60	175	184
Phosphatidylinositide phosphatase SAC1	SACM1L	SAC1_HUMAN	67.0	100.0%	3	3	6	0.01%	4.9%	LEEQDEFEK	98.0%	31.8	25	17	2	0	0	1166.52	424	432
Phosphatidylinositide phosphatase SAC1	SACM1L	SAC1_HUMAN	67.0	100.0%	3	3	6	0.01%	4.9%	TNVIQSLLAR	99.7%	61.1	25	54.6	2	0	0	1114.66	396	405
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	100.0%	8	9	28	0.03%	13.6%	ALYSTAMESIQGGAAR	99.7%	99.5	25	99.5	3	0	0	1625.80	352	367
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	100.0%	8	9	28	0.03%	13.6%	DCLVLESFK	99.7%	56.8	25	42	2	0	0	1110.55	305	313
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	100.0%	8	9	28	0.03%	13.6%	FYGLYCVQSGGK	99.7%	57.6	25	43.4	4	0	0	1378.65	220	231
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	100.0%	8	9	28	0.03%	13.6%	GVDASGETTYK	99.7%	63.8	25	60.4	2	0	0	1127.52	62	72
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	100.0%	8	9	28	0.03%	13.6%	GVDASGETTYKK	99.7%	59.8	25	49.5	7	0	0	1255.62	62	73
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	100.0%	8	9	28	0.03%	13.6%	LLPGYYMNLNQNPR	99.7%	45.1	25	29	2	0	0	1692.85	201	214
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	100.0%	8	9	28	0.03%	13.6%	QAQGAQSTSDEKRPVGQK	99.7%	48.2	25	47.5	0	5	0	1914.96	334	351
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	100.0%	8	9	28	0.03%	13.6%	VVVMNNILPR	99.7%	60.5	25	49.3	3	0	0	1154.67	235	244
Phosphatidylserine decarboxylase proenzyme	PISD	PISD_HUMAN	46.7	99.8%	2	2	3	0.00%	5.1%	GVTYSLESFLGPR	99.7%	76.3	25	66.8	2	0	0	1425.74	210	222
Phosphatidylserine decarboxylase proenzyme	PISD	PISD_HUMAN	46.7	99.8%	2	2	3	0.00%	5.1%	ILNFGQVK	97.5%	30.8	25	11	1	0	0	918.54	194	201
Phosphatidylserine synthase 1	PTDSS1	PTSS1_HUMAN	55.5	99.8%	2	2	4	0.00%	5.7%	AVLQFTPASWTYVR	99.7%	53.3	25	51.2	2	0	0	1638.86	263	276
Phosphatidylserine synthase 1	PTDSS1	PTSS1_HUMAN	55.5	99.8%	2	2	4	0.00%	5.7%	ILFIGGITAPTVR	99.7%	54.1	25	49.4	2	0	0	1357.82	324	336
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	6	6	11	0.01%	12.4%	AFVRPSGTEDVVR	99.7%	60.8	25	52.8	0	2	0	1432.75	493	505
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	6	6	11	0.01%	12.4%	EAVNLQQDAFVVIGR	99.7%	52.1	25	41.2	1	0	0	1658.89	113	127
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	6	6	11	0.01%	12.4%	LNHLCGADFVK	97.8%	31.2	25	20.6	1	0	0	1273.64	245	255
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	6	6	11	0.01%	12.4%	MGLLAVLR	99.7%	74	25	54.3	4	0	0	872.54	42	49
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	6	6	11	0.01%	12.4%	VDCANGIGALK	99.7%	62.4	25	53.5	1	0	0	1117.57	210	220
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	6	6	11	0.01%	12.4%	VISTTDAER	95.6%	28.4	25	24.2	2	0	0	991.51	461	469
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	21	47	0.05%	35.0%	AIDTTQLFSLPK	99.7%	77.7	25	70.7	2	0	0	1333.74	589	600
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	21	47	0.05%	35.0%	DEAGHFLWPGFGENAR	99.7%	38.4	25	34.2	0	2	0	1802.82	538	553
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	21	47	0.05%	35.0%	DFVEHSAR	96.1%	28.9	25	24.1	1	0	0	960.45	46	53
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	21	47	0.05%	35.0%	DFWEQEVR	97.4%	30.6	25	19.3	1	0	0	1108.51	601	608
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	21	47	0.05%	35.0%	EGALDLSGLR	96.6%	29.5	25	22.6	2	0	0	1030.55	579	588
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	21	47	0.05%	35.0%	EIISFGSGYGGNSLLGK	99.7%	118	25	116	3	0	0	1698.87	245	261
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	21	47	0.05%	35.0%	ETPIGLVPK	97.7%	31.1	25	31.1	1	0	0	953.57	570	578
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	21	47	0.05%	35.0%	EVLAELEALER	99.7%	81	25	67.4	2	0	0	1271.68	625	635
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	21	47	0.05%	35.0%	GQLGNWMSPADFQR	99.7%	79.8	25	79.8	3	0	0	1606.74	129	142
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	21	47	0.05%	35.0%	GVPLVYEAFNWR	99.7%	65	25	58.3	2	0	0	1450.75	458	469
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	21	47	0.05%	35.0%	LGTPVLQALGDGDFVK	99.7%	110	25	102	6	0	0	1629.89	194	209
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	21	47	0.05%	35.0%	SYLTEQVNQDLPK	99.7%	108	25	104	2	0	0	1534.77	612	624
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	21	47	0.05%	35.0%	TLIGHVPDQR	99.6%	39.2	25	22.7	3	0	0	1135.62	235	244
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	21	47	0.05%	35.0%	TMYVLPFSMGPVGSPLSR	99.7%	86.6	25	69.1	8	0	0	1954.98	156	173

Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	21	47	0.05%	35.0%	TVIVTPSQR	97.2%	30.3	25	21.5	1	0	0	1000.58	109	117
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	21	47	0.05%	35.0%	VECVGDDIAWMR	99.4%	37	25	37	2	0	0	1466.64	323	334
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	21	47	0.05%	35.0%	VLDWICR	99.7%	47.2	25	42.5	2	0	0	961.49	554	560
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	21	47	0.05%	35.0%	VLSGDLGQLPTGIR	99.7%	108	25	100	2	0	0	1425.81	32	45
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	21	47	0.05%	35.0%	YNNCWLAR	97.5%	30.7	25	24.7	2	0	0	1096.50	89	96
Phosphoglycerate kinase 1	PGK1	PGK1_HUMAN	44.6	100.0%	4	4	6	0.01%	10.8%	DCVGPEVEK	97.7%	31.1	25	21.6	1	0	0	1032.47	98	106
Phosphoglycerate kinase 1	PGK1	PGK1_HUMAN	44.6	100.0%	4	4	6	0.01%	10.8%	FHVEEEGKGK	94.6%	27.6	25	20.9	1	0	0	1159.57	124	133
Phosphoglycerate kinase 1	PGK1	PGK1_HUMAN	44.6	100.0%	4	4	6	0.01%	10.8%	LGDVYVNDAFGTAHR	99.7%	66.6	25	53.7	0	2	0	1634.79	157	171
Phosphoglycerate kinase 1	PGK1	PGK1_HUMAN	44.6	100.0%	4	4	6	0.01%	10.8%	VLPGVDALSNI	99.7%	48.8	25	48.8	2	0	0	1097.62	407	417
Phosphoglycerate mutase 1	PGAM1	PGAM1_HUMAN	28.8	100.0%	4	4	8	0.01%	17.7%	ALPFWNEEIVPQIK	99.7%	40.6	25	40.6	2	0	0	1683.91	163	176
Phosphoglycerate mutase 1	PGAM1	PGAM1_HUMAN	28.8	100.0%	4	4	8	0.01%	17.7%	AMEAVAAQGK	99.7%	49.2	25	38.8	2	0	0	975.49	242	251
Phosphoglycerate mutase 1	PGAM1	PGAM1_HUMAN	28.8	100.0%	4	4	8	0.01%	17.7%	HYGGLTGLNK	99.7%	40.1	25	30.6	2	0	0	1059.56	91	100
Phosphoglycerate mutase 1	PGAM1	PGAM1_HUMAN	28.8	100.0%	4	4	8	0.01%	17.7%	VLIAAHGNSLR	99.7%	51.4	25	47.3	2	0	0	1150.67	181	191
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	8	10	19	0.02%	29.9%	AVEMAAQR	99.7%	55.3	25	31.7	2	0	0	875.44	221	228
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	8	10	19	0.02%	29.9%	AVVVGFDPHFSYMK	99.7%	56.4	25	56.4	4	1	0	1596.79	167	180
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	8	10	19	0.02%	29.9%	FIAGTGCLVR	99.7%	49.3	25	27.3	2	0	0	1093.58	211	220
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	8	10	19	0.02%	29.9%	FIFDCVSQEYGINPER	99.7%	77.3	25	70.9	2	0	0	1973.91	239	254
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	8	10	19	0.02%	29.9%	GETAVPGAPEALR	99.7%	61	25	43.5	2	0	0	1267.66	42	54
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	8	10	19	0.02%	29.9%	LGFITNNSSK	99.7%	47.1	25	34.1	2	0	0	1080.57	63	72
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	8	10	19	0.02%	29.9%	QADIIGKPSR	99.7%	47	25	27.9	2	0	0	1084.61	229	238
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	8	10	19	0.02%	29.9%	TILTLTGVSTLGDVK	99.7%	89.5	25	89.5	2	0	0	1517.88	276	290
Phosphoinositide 3-kinase regulatory subunit 4	PIK3R4	PI3R4_HUMAN	153.1	100.0%	5	5	7	0.01%	4.3%	FLELVQLK	99.5%	38.4	25	25.7	2	0	0	989.60	496	503
Phosphoinositide 3-kinase regulatory subunit 4	PIK3R4	PI3R4_HUMAN	153.1	100.0%	5	5	7	0.01%	4.3%	GVIDLAALGITGR	99.6%	40	25	40	1	0	0	1255.74	817	829
Phosphoinositide 3-kinase regulatory subunit 4	PIK3R4	PI3R4_HUMAN	153.1	100.0%	5	5	7	0.01%	4.3%	LSVEILLDR	99.7%	48.6	25	4.96	1	0	0	1057.63	409	417
Phosphoinositide 3-kinase regulatory subunit 4	PIK3R4	PI3R4_HUMAN	153.1	100.0%	5	5	7	0.01%	4.3%	VFAIQDPTLPLTSYK	96.6%	29.5	25	29.5	1	0	0	1692.92	54	68
Phosphoinositide 3-kinase regulatory subunit 4	PIK3R4	PI3R4_HUMAN	153.1	100.0%	5	5	7	0.01%	4.3%	VVTLLSDPENIVK	99.7%	51.7	25	43.1	2	0	0	1426.82	541	553
Phosphomannomutase 2	PMM2	PMM2_HUMAN	28.1	99.8%	2	2	4	0.00%	8.9%	IGVVGGSDFEK	99.7%	48.5	25	48.5	2	0	0	1107.57	41	51
Phosphomannomutase 2	PMM2	PMM2_HUMAN	28.1	99.8%	2	2	4	0.00%	8.9%	NGMLNVSPIGR	99.4%	37	25	34.7	2	0	0	1173.60	124	134
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	6	12	0.01%	32.0%	AGLTHIITMDLHQK	99.7%	52.6	25	0	0	2	0	1577.85	125	138
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	6	12	0.01%	32.0%	EIQGFFSFPVDNLR	99.7%	75.9	25	75.9	4	0	0	1668.84	139	152
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	6	12	0.01%	32.0%	EKPPITVVGDVGGR	99.7%	53.3	25	53.3	2	2	0	1423.79	237	250
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	6	12	0.01%	32.0%	GQDIFIIQTIPR	99.7%	95	25	86.1	2	0	0	1400.79	57	68
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	6	12	0.01%	32.0%	IYVMATHGILSAEAPR	99.6%	31.1	25	24.8	0	1	0	1744.91	280	295
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	6	12	0.01%	32.0%	NATVHPGLELPLMMAK	99.0%	27.5	25	27.5	0	1	0	1753.90	221	236
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	6	12	0.01%	32.0%	NIIGVIPYFPYSK	99.7%	62.1	25	61.2	2	0	0	1510.83	91	103
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	6	12	0.01%	32.0%	VFSANSTAACTELAK	99.7%	81.6	25	77.3	2	0	0	1569.76	10	24
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	11	19	36	0.04%	40.4%	AGLTHLITMDLHQK	99.7%	52.6	25	0	0	2	0	1577.85	137	150
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	11	19	36	0.04%	40.4%	EIQGFFNIPVDNLR	99.7%	66.8	25	53.2	2	0	0	1661.86	151	164
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	11	19	36	0.04%	40.4%	EKPPITVVGDVGGR	99.7%	53.3	25	53.3	2	2	0	1423.79	250	263
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	11	19	36	0.04%	40.4%	GGLVLFSANSNSSCMELSK	99.7%	116	25	116	2	0	0	2016.94	18	36
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	11	19	36	0.04%	40.4%	IFVMATHGLLSSDAPR	99.7%	97.2	25	86.3	4	4	0	1714.89	293	308
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	11	19	36	0.04%	40.4%	IHNGESMSYLFR	99.2%	28.7	25	14.3	0	1	0	1453.69	352	363
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	11	19	36	0.04%	40.4%	LLASMMCK	99.7%	54.6	25	43.6	5	0	0	953.46	129	136
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	11	19	36	0.04%	40.4%	SIIGVIPYFPYSK	99.7%	59.2	25	48.3	2	0	0	1483.82	103	115
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	11	19	36	0.04%	40.4%	SVAAIHPSLEIPMLIPK	99.6%	31	25	31	2	2	0	1816.04	233	249
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	11	19	36	0.04%	40.4%	TVDISMILSEAIR	99.7%	68.2	25	49.7	4	0	0	1447.78	338	350
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	11	19	36	0.04%	40.4%	VQVYQEPNR	99.7%	49.6	25	36	2	0	0	1132.57	49	57
Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform	PHKA1	KPB1_HUMAN	137.3	100.0%	3	3	4	0.00%	2.7%	AALEALDELDLFGVK	99.7%	42.2	25	42.2	1	0	0	1603.86	207	221
Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform	PHKA1	KPB1_HUMAN	137.3	100.0%	3	3	4	0.00%	2.7%	AYELEQSVVK	99.2%	36	25	32.8	1	0	0	1165.61	74	83
Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform	PHKA1	KPB1_HUMAN	137.3	100.0%	3	3	4	0.00%	2.7%	RLDGALNR	96.9%	29.8	25	0	2	0	0	914.52	1059	1066
Phosphoserine aminotransferase	PSAT1	SERC_HUMAN	40.4	100.0%	5	5	8	0.01%	13.8%	ALELNMLSLK	99.7%	64	25	55	2	0	0	1131.64	324	333

Phosphoserine aminotransferase	PSAT1	SERC_HUMAN	40.4	100.0%	5	5	8	0.01%	13.8%	ASLYNAVTIEDVQK	99.7%	106	25	96.7	2	0	0	1550.81	343	356
Phosphoserine aminotransferase	PSAT1	SERC_HUMAN	40.4	100.0%	5	5	8	0.01%	13.8%	ELLAVPDNYK	98.5%	33.1	25	27.7	1	0	0	1161.62	62	71
Phosphoserine aminotransferase	PSAT1	SERC_HUMAN	40.4	100.0%	5	5	8	0.01%	13.8%	FGTINIVHPK	99.7%	60.8	25	58.4	2	0	0	1125.64	118	127
Phosphoserine aminotransferase	PSAT1	SERC_HUMAN	40.4	100.0%	5	5	8	0.01%	13.8%	FLEMHQL	94.7%	27.7	25	15.9	1	0	0	917.46	364	370
Plasminogen activator inhibitor 1 RNA-binding protein	SERBP1	PAIRB_HUMAN	45.0	100.0%	3	3	7	0.01%	9.1%	EETQPPVALKK	98.6%	33.5	25	25.1	2	0	0	1239.69	93	103
Plasminogen activator inhibitor 1 RNA-binding protein	SERBP1	PAIRB_HUMAN	45.0	100.0%	3	3	7	0.01%	9.1%	SAAQAAAQTNSNAAGK	99.7%	108	25	98.2	4	0	0	1460.71	53	68
Plasminogen activator inhibitor 1 RNA-binding protein	SERBP1	PAIRB_HUMAN	45.0	100.0%	3	3	7	0.01%	9.1%	SSFSHYSGLK	98.9%	34.5	25	23.1	1	0	0	1112.54	202	211
Plastin-3	PLS3	PLST_HUMAN	70.8	100.0%	4	4	6	0.01%	6.8%	ALENDPDCR	94.9%	27.8	25	27.8	1	0	0	1089.46	136	144
Plastin-3	PLS3	PLST_HUMAN	70.8	100.0%	4	4	6	0.01%	6.8%	ANDDIIVNWVNR	99.7%	54	25	44.3	2	0	0	1428.72	519	530
Plastin-3	PLS3	PLST_HUMAN	70.8	100.0%	4	4	6	0.01%	6.8%	INNFSADIKDSK	99.7%	63.2	25	53.7	2	0	0	1351.69	289	300
Plastin-3	PLS3	PLST_HUMAN	70.8	100.0%	4	4	6	0.01%	6.8%	STSIQSFKDK	97.5%	30.8	25	30.1	1	0	0	1140.59	538	547
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	AELELELGR	99.7%	53.2	25	14.7	1	0	0	1029.56	2079	2087
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	ALQALEELR	98.9%	34.4	25	26.7	1	0	0	1042.59	1671	1679
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	APVPASELLASGVLSR	99.7%	68.2	25	68.2	2	0	0	1566.89	3447	3462
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	AVVQLKPR	94.7%	27.6	25	13	1	0	0	910.58	927	934
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	ELIPTEEALR	99.3%	36.4	25	30.7	1	0	0	1170.64	3926	3935
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	GLLSAEVAR	98.5%	32.9	25	10.7	2	0	0	915.53	3850	3858
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	GTQGAEEVLR	97.7%	31.2	25	17.7	1	0	0	1059.54	1234	1243
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	IIITVVEEQEQK	99.7%	65.4	25	60.1	2	0	0	1428.79	3095	3106
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	LAAIGEATR	99.7%	52.7	25	27.3	2	0	0	901.51	1976	1984
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	LAQGHTTVDELAR	98.0%	25	25	16.4	0	1	0	1410.73	2809	2821
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	LLDAQLATGGIVDPR	96.5%	29.3	25	24.1	1	0	0	1538.85	3936	3950
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	LLDAQLSTGGIVDPSK	99.7%	90.1	25	86.4	2	0	0	1613.87	3270	3285
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	LLEAAAQSTK	99.4%	37.5	25	27.2	2	0	0	1031.57	4600	4609
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	LQAEEVAQQK	99.7%	56.9	25	41.8	2	0	0	1143.60	1783	1792
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	LQEAGILSAEELQR	99.7%	68.9	25	67.5	1	0	0	1556.83	2795	2808
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	LQLEACETR	98.9%	34.4	25	26.5	1	0	0	1119.55	1131	1139
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	LSVAAQEAAR	99.7%	60.5	25	45.8	2	0	0	1015.55	2420	2429
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	LSVYAALQR	99.7%	59.5	25	48.9	2	0	0	1020.58	2847	2855
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	LTVDEAVR	99.6%	39.5	25	24	1	0	0	902.49	3213	3220
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	NLLDEELQR	99.3%	36.5	25	23.1	1	0	0	1129.58	2340	2348
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	QVEEEILALK	94.7%	27.7	25	18	1	0	0	1171.66	2059	2068
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	SIQEELQQLR	99.7%	45.1	25	25.3	1	0	0	1243.66	1554	1563
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	SLVPAAELLESR	99.7%	47	25	35.7	2	0	0	1284.72	3116	3127
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	SQVEEELFSVR	99.7%	45.6	25	42.4	1	0	0	1322.66	2361	2371
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	SSIAGLLLK	99.3%	36.8	25	23.1	1	0	0	901.57	2833	2841
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	TPVEVPVGGFK	97.9%	31.6	25	31.6	1	0	0	1129.63	3374	3384
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	VLADPSDDTK	97.2%	30.3	25	23.3	1	0	0	1060.52	2979	2988
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	VLALPEPSPAAPTLR	97.1%	30.1	25	30.1	1	0	0	1531.88	1187	1201
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	VPDVQDGVR	95.5%	28.3	25	28.2	1	0	0	984.51	402	410
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	VPLDVACAR	98.9%	34.3	25	29.8	2	0	0	1000.52	3289	3297
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	VPVDVAYR	99.7%	49.8	25	39	2	0	0	918.50	2961	2968
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	VQSGSESVIQEYVDLR	99.7%	72.2	25	66.2	1	0	0	1808.90	1442	1457
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	33	33	45	0.05%	7.6%	VTLVQTLEIQR	99.7%	43	25	34.5	1	0	0	1299.76	2565	2575
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	99.8%	2	3	5	0.01%	5.6%	ASVHTLSGHTNAVATVR	99.7%	47.9	25	44.8	0	2	0	1720.91	321	337
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	99.8%	2	3	5	0.01%	5.6%	GPQNATDSYVHK	99.7%	39.3	25	39.3	1	2	0	1316.62	69	80
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	7	7	17	0.02%	8.8%	AEPVEVVAPR	97.1%	30.1	25	26.6	1	0	0	1066.59	487	496
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	7	7	17	0.02%	8.8%	KPPLLNNADSVQAK	99.7%	56.2	25	47	1	0	0	1494.83	748	761
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	7	7	17	0.02%	8.8%	QQVPSGESAILDR	99.7%	64.4	25	55.4	2	0	0	1399.72	270	282
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	7	7	17	0.02%	8.8%	TLGDFAAEYAK	99.7%	57.5	25	52.4	3	0	0	1185.58	109	119
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	7	7	17	0.02%	8.8%	TTNFAGILSQGLR	99.7%	80.7	25	68.8	4	0	0	1377.75	866	878

Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	7	7	17	0.02%	8.8%	VFSATLGLVDIVK	99.7%	77.1	25	60.5	4	0	0	1361.80	552	564
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	7	7	17	0.02%	8.8%	VVSEDFLQDVSASTK	99.7%	110	25	102	2	0	0	1624.81	453	467
Poly(A) RNA polymerase, mitochondrial	MTPAP	PAPD1_HUMAN	66.2	100.0%	3	3	6	0.01%	5.2%	NVSQSQLQK	99.2%	35.7	25	22.9	2	0	0	1031.55	489	497
Poly(A) RNA polymerase, mitochondrial	MTPAP	PAPD1_HUMAN	66.2	100.0%	3	3	6	0.01%	5.2%	SPPILPTLDSLK	97.5%	30.7	25	30.7	2	0	0	1280.75	392	403
Poly(A) RNA polymerase, mitochondrial	MTPAP	PAPD1_HUMAN	66.2	100.0%	3	3	6	0.01%	5.2%	TVLIHCPEK	98.2%	32.3	25	26.6	2	0	0	1096.58	77	85
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	8	17	0.02%	26.4%	AITIAGVPQSVTECVK	99.7%	63.5	25	60	2	0	0	1672.89	145	160
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	8	17	0.02%	26.4%	ESTGAQVQVAGDMLPNSTER	99.7%	88.8	25	88.5	3	0	0	2089.98	125	144
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	8	17	0.02%	26.4%	IANPVEGSSGR	99.7%	64.6	25	54.2	2	0	0	1086.55	315	325
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	8	17	0.02%	26.4%	IITLTGPTNAIFK	99.7%	61.9	25	55.1	2	0	0	1388.82	58	70
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	8	17	0.02%	26.4%	INISEGNCPER	99.7%	58.6	25	56.9	5	0	0	1288.60	47	57
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	8	17	0.02%	26.4%	LVVPATQCGSLIGK	98.9%	34.4	25	28	1	0	0	1442.80	102	115
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	8	17	0.02%	26.4%	QGANINEIR	99.7%	59.8	25	55.3	2	0	0	1014.53	298	306
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	20	0.02%	23.3%	AITIAGIPQSIIECVK	99.7%	75.7	25	75.7	6	0	0	1712.96	145	160
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	20	0.02%	23.3%	ESTGAQVQVAGDMLPNSTER	99.7%	88.8	25	88.5	3	0	0	2089.98	125	144
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	20	0.02%	23.3%	IANPVEGSTDR	99.7%	50.8	25	49.9	4	0	0	1158.58	323	333
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	20	0.02%	23.3%	IITLAGPTNAIFK	99.7%	61.7	25	61.7	6	0	0	1358.80	58	70
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	20	0.02%	23.3%	INISEGNCPER	99.7%	58.6	25	56.9	5	0	0	1288.60	47	57
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	20	0.02%	23.3%	LVVPASQCGSLIGK	99.7%	71.3	25	71.3	4	0	0	1428.79	102	115
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	17	0.02%	16.8%	GYGFIEYEK	99.7%	57.4	25	52.3	1	0	0	1105.52	268	276
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	17	0.02%	16.8%	KQESTVMVLR	99.7%	48	25	40.3	3	0	0	1190.66	458	467
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	17	0.02%	16.8%	KVVAEVYDQER	99.7%	61.5	25	58.9	1	0	0	1335.69	541	551
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	17	0.02%	16.8%	LGLPPLTPEQQEALQK	99.7%	51.2	25	49.2	2	0	0	1761.97	54	69
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	17	0.02%	16.8%	QGEEEDAEIIVK	99.7%	70.2	25	58.6	2	0	0	1359.66	503	514
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	17	0.02%	16.8%	SIDMSWDSVTMK	99.7%	54.9	25	54.9	2	0	0	1399.62	157	168
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	17	0.02%	16.8%	VVAEVYDQER	99.7%	70.3	25	66.3	2	0	0	1207.60	542	551
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	17	0.02%	16.8%	VYVGSIYYELGEDTIR	99.7%	79.4	25	79.4	2	0	0	1876.93	131	146
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	17	0.02%	16.8%	YAMEQSIK	99.6%	39.5	25	29.4	2	0	0	969.47	73	80
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	24	33	107	0.11%	35.7%	AKEFTNVYIK	99.7%	47.3	25	42.3	2	0	0	1212.66	187	196
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	24	33	107	0.11%	35.7%	ALDTMNFDVIK	99.7%	82.9	25	74.8	7	0	0	1266.64	68	78
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	24	33	107	0.11%	35.7%	ALYDTFSAFGNILSCK	99.7%	91.7	25	90.9	8	0	0	1806.87	114	129
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	24	33	107	0.11%	35.7%	EFSPFGTITSAK	99.7%	56.2	25	42.6	6	0	0	1284.65	313	324
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	24	33	107	0.11%	35.7%	EFTNVYIK	99.1%	35.2	25	22.4	1	0	0	1013.53	189	196
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	24	33	107	0.11%	35.7%	FGPALSVK	99.7%	51	25	14.4	6	0	0	818.48	214	221
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	24	33	107	0.11%	35.7%	FSPAGPILSIR	99.7%	53.9	25	53.9	7	0	0	1157.67	31	41
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	24	33	107	0.11%	35.7%	GFGFVCFSSPEEATK	99.7%	92.1	25	92.1	6	0	0	1662.75	334	348
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	24	33	107	0.11%	35.7%	GFGFVSFER	99.7%	65.4	25	48.3	8	0	0	1045.51	232	240
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	24	33	107	0.11%	35.7%	GYGFVHFETQEAAER	99.7%	87.5	25	86.5	2	4	0	1740.80	139	153
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	24	33	107	0.11%	35.7%	IMWSQR	98.4%	32.7	25	0	1	0	0	820.41	84	89
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	24	33	107	0.11%	35.7%	IVATKPLYVALAQR	99.7%	85.7	25	85.7	4	4	0	1542.94	357	370
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	24	33	107	0.11%	35.7%	KEFSPFGTITSAK	99.7%	85.1	25	84.6	2	2	0	1412.74	312	324
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	24	33	107	0.11%	35.7%	LFPLIQAMHPTLAGK	99.7%	63.9	25	63.3	2	1	0	1636.92	566	580
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	24	33	107	0.11%	35.7%	MNGMLLNDR	99.7%	41.3	25	32.8	1	0	0	1063.50	158	166
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	24	33	107	0.11%	35.7%	MNGMLLNDRK	99.7%	40.3	25	33	1	0	0	1191.60	158	167
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	24	33	107	0.11%	35.7%	NLDDGIDDER	99.7%	64.1	25	50	2	0	0	1161.50	300	309
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	24	33	107	0.11%	35.7%	NLDDGIDDERLR	99.7%	58.4	25	51	3	1	0	1430.69	300	311
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	24	33	107	0.11%	35.7%	QAHLTNQYMQR	99.7%	65.2	25	62.7	4	2	0	1405.66	375	385
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	24	33	107	0.11%	35.7%	SGVGNIFIK	99.7%	63.1	25	38.6	7	0	0	934.54	96	104
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	24	33	107	0.11%	35.7%	SKVDEAVAVLQAHQAK	99.7%	101	25	97.2	1	2	0	1693.92	605	620
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	24	33	107	0.11%	35.7%	SLGYAYVNFQQPADAER	99.7%	90.6	25	90.6	5	0	0	1928.91	51	67
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	24	33	107	0.11%	35.7%	VDEAVAVLQAHQAK	99.7%	81.9	25	81.9	1	0	0	1478.80	607	620
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	24	33	107	0.11%	35.7%	YQGVNLYVK	99.7%	50.7	25	43	4	0	0	1083.58	291	299

Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	5	5	9	0.01%	22.4%	AKEFTNVYIK	99.7%	47.3	25	42.3	2	0	0	1212.66	187	196
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	5	5	9	0.01%	22.4%	ALDTMNFDVIK	99.7%	82.9	25	74.8	7	0	0	1266.64	68	78
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	5	5	9	0.01%	22.4%	ALYDTFSAFGNILSCK	99.7%	91.7	25	90.9	8	0	0	1806.87	114	129
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	5	5	9	0.01%	22.4%	AVEEMNGKEISGK	95.3%	28.2	25	25.4	1	0	0	1407.68	247	259
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	5	5	9	0.01%	22.4%	EFSPFGSITSAK	99.7%	62.7	25	61.5	2	0	0	1270.63	313	324
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	5	5	9	0.01%	22.4%	EFTNVYIK	99.1%	35.2	25	22.4	1	0	0	1013.53	189	196
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	5	5	9	0.01%	22.4%	FSPAGPVLSIR	99.7%	55.9	25	48.6	2	0	0	1143.65	31	41
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	5	5	9	0.01%	22.4%	GFGFVCFSSPEEATK	99.7%	92.1	25	92.1	6	0	0	1662.75	334	348
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	5	5	9	0.01%	22.4%	IMWSQR	98.4%	32.7	25	0	1	0	0	820.41	84	89
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	5	5	9	0.01%	22.4%	IVGSKPLYVALAQR	99.1%	28	25	6.4	0	2	0	1514.91	357	370
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	5	5	9	0.01%	22.4%	MNGMLLNDR	99.7%	41.3	25	32.8	1	0	0	1063.50	158	166
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	5	5	9	0.01%	22.4%	MNGMLLNDRK	99.7%	40.3	25	33	1	0	0	1191.60	158	167
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	5	5	9	0.01%	22.4%	SLGYAYVNFQQPADAER	99.7%	90.6	25	90.6	5	0	0	1928.91	51	67
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	5	5	9	0.01%	22.4%	YQGVNLYIK	99.7%	52.2	25	40.9	2	0	0	1097.60	291	299
Polycomb protein EED	EED	EED_HUMAN	50.2	99.9%	2	2	2	0.00%	5.4%	DPNLLLSVSK	96.0%	28.8	25	28.8	1	0	0	1085.62	202	211
Polycomb protein EED	EED	EED_HUMAN	50.2	99.9%	2	2	2	0.00%	5.4%	EGDPLVFATVGSNR	99.7%	53.4	25	52.5	1	0	0	1461.73	107	120
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	4	4	8	0.01%	12.5%	GVVLFPWQAR	97.3%	30.5	25	23.1	2	0	0	1172.66	92	101
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	4	4	8	0.01%	12.5%	IFSLSGTLETVR	99.7%	93.3	25	76.3	2	0	0	1322.73	286	297
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	4	4	8	0.01%	12.5%	LENLDSDVVQLR	99.7%	78.1	25	73.7	2	0	0	1400.74	269	280
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	4	4	8	0.01%	12.5%	VLETVGVFEVPK	99.7%	86.3	25	76.5	2	0	0	1316.75	61	72
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	7	8	12	0.01%	18.5%	GQPIYIQFSNHK	99.2%	35.9	25	32.2	1	0	0	1431.74	123	134
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	7	8	12	0.01%	18.5%	HQNVQLPR	99.5%	38	25	33.7	2	0	0	991.54	411	418
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	7	8	12	0.01%	18.5%	IAIPGLAGAGNSVLLVSNLNPER	99.7%	92	25	92	2	0	0	2275.28	326	348
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	7	8	12	0.01%	18.5%	KLPIDVTEGEVISLGLPFGK	99.7%	32.1	25	32.1	0	2	0	2112.20	65	84
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	7	8	12	0.01%	18.5%	LSLDGQNIYNACCTLR	99.7%	41.1	25	41.1	1	0	0	1897.89	239	254
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	7	8	12	0.01%	18.5%	VLFSSNGGVVK	99.7%	44.4	25	39.4	1	0	0	1106.62	472	482
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	7	8	12	0.01%	18.5%	VTNLLMLK	99.7%	57.4	25	0	3	0	0	947.56	85	92
Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	FIP1_HUMAN	66.5	100.0%	3	3	3	0.00%	7.9%	MGLEVIPVTSTTNK	97.6%	30.9	25	27.3	1	0	0	1489.79	197	210
Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	FIP1_HUMAN	66.5	100.0%	3	3	3	0.00%	7.9%	TGAPQYGSYGTAPVNLNIK	99.7%	60.4	25	56.5	1	0	0	1950.99	105	123
Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	FIP1_HUMAN	66.5	100.0%	3	3	3	0.00%	7.9%	TGNSEKETALPSTK	97.0%	30	25	22.2	1	0	0	1462.74	241	254
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	5	7	23	0.02%	48.0%	GTAYVVYEDIFDAK	99.7%	58.4	25	55.4	4	0	0	1590.77	58	71
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	5	7	23	0.02%	48.0%	ITAEEMYDIFGK	99.7%	83.7	25	76	8	0	0	1432.67	30	41
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	5	7	23	0.02%	48.0%	NACDHLSGFNVCNR	99.7%	62.3	25	62.3	3	3	0	1663.71	72	85
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	5	7	23	0.02%	48.0%	YGINTDPPK	95.6%	28.4	25	28.4	1	0	0	1004.50	117	125
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	5	7	23	0.02%	48.0%	YLVVLYYNANR	99.7%	86.5	25	84.3	4	0	0	1387.74	86	96
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	9	11	22	0.02%	23.8%	ATVLTTER	99.7%	42.6	25	36.1	2	0	0	890.49	180	187
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	9	11	22	0.02%	23.8%	FIASTGMDR	99.7%	53.5	25	39.2	4	0	0	997.48	489	497
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	9	11	22	0.02%	23.8%	ILTGGADKNVVVFDK	99.7%	86.8	25	84.8	2	2	0	1575.87	237	251
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	9	11	22	0.02%	23.8%	IWSVPNASCVQVVR	99.7%	67.3	25	58.7	2	0	0	1614.84	290	303
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	9	11	22	0.02%	23.8%	KVTSVVFHPSQDLVFSASPDATIR	99.7%	90.4	25	90.4	0	2	0	2601.37	266	289
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	9	11	22	0.02%	23.8%	QELSHALYQHDAACR	99.7%	64.4	25	64.4	0	2	0	1798.83	101	115
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	9	11	22	0.02%	23.8%	SSEQILATLK	99.7%	58.2	25	38.6	2	0	0	1089.62	252	261
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	9	11	22	0.02%	23.8%	TLQLDNNFEVK	99.7%	43.9	25	36.8	2	0	0	1320.68	429	439
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	9	11	22	0.02%	23.8%	TVPEELVKPEELSK	99.7%	78.8	25	72.9	2	0	0	1597.87	193	206
Pre-mRNA-processing factor 40 homolog A	PRPF40A	PR40A_HUMAN	108.8	99.8%	2	2	2	0.00%	2.8%	FTNMLGQPGSTALDLFK	96.5%	29.3	25	21.3	1	0	0	1855.93	646	662
Pre-mRNA-processing factor 40 homolog A	PRPF40A	PR40A_HUMAN	108.8	99.8%	2	2	2	0.00%	2.8%	STTLDAGNIK	96.4%	29.3	25	20.6	1	0	0	1019.54	709	718
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	18	20	38	0.04%	20.6%	AAELETDIR	99.7%	63.1	25	31.2	2	0	0	1017.52	379	387
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	18	20	38	0.04%	20.6%	AAVELEEPEDAR	99.7%	67	25	66.3	2	0	0	1328.63	409	420
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	18	20	38	0.04%	20.6%	AEVLWLMGAK	99.7%	64.3	25	56.7	2	0	0	1117.61	607	616
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	18	20	38	0.04%	20.6%	AGSVATCQAVMR	99.7%	45.1	25	34.9	4	0	0	1250.60	516	527
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	18	20	38	0.04%	20.6%	AIYAYALQVFPSK	99.7%	43.9	25	38.9	2	0	0	1470.80	561	573

Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	18	20	38	0.04%	20.6%	AVIGIGIEEEDRK	99.7%	73.8	25	73.8	2	0	0	1428.77	528	540
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	18	20	38	0.04%	20.6%	AVVAQAVR	99.4%	37	25	31.6	2	0	0	813.49	360	367
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	18	20	38	0.04%	20.6%	ESLEALLQR	99.7%	54.9	25	33.8	2	0	0	1058.58	591	599
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	18	20	38	0.04%	20.6%	HIWITAAK	99.7%	42.8	25	29.8	1	0	0	939.54	465	472
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	18	20	38	0.04%	20.6%	HYEDFPK	98.0%	31.7	25	28.4	2	0	0	935.43	704	710
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	18	20	38	0.04%	20.6%	IDSDLGDAWAFFYK	99.7%	99.7	25	99.7	2	0	0	1647.77	870	883
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	18	20	38	0.04%	20.6%	IQQQFSDLKR	99.7%	32.5	25	25.7	1	2	0	1262.69	138	147
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	18	20	38	0.04%	20.6%	LEEANGNTQMVEK	99.7%	56.9	25	49.2	1	0	0	1478.68	473	485
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	18	20	38	0.04%	20.6%	LESENDEYER	99.7%	53.6	25	53.6	2	0	0	1283.54	651	660
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	18	20	38	0.04%	20.6%	LEWVQDNIR	99.7%	47.1	25	32.4	2	0	0	1172.61	684	692
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	18	20	38	0.04%	20.6%	LSQVSDSVSGQTVVDPK	99.7%	107	25	96.4	3	0	0	1745.89	255	271
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	18	20	38	0.04%	20.6%	NPGLWLESVR	99.7%	55.2	25	48.4	2	0	0	1170.63	776	785
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	18	20	38	0.04%	20.6%	WLAGDVPAAR	99.7%	40.7	25	40.7	2	0	0	1055.56	619	628
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	AISAANLHLR	99.7%	52.9	25	42.4	2	0	0	1065.62	2077	2086
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	ALDIPLVK	99.7%	40.9	25	37.4	2	0	0	868.55	421	428
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	ANPALYVLR	99.7%	40.3	25	32.9	2	0	0	1016.59	1736	1744
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	AQIAGYLYGVSPPDNPQVK	99.7%	59.1	25	56.9	2	0	0	2017.04	2122	2140
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	DNPNLLFNMCGFECR	98.2%	32.2	25	32.2	1	0	0	1886.80	1181	1195
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	EAVVNTQELLDLLVK	99.7%	52.9	25	50.5	1	0	0	1683.95	1276	1290
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	EQSQLTATQTR	99.7%	55.5	25	34.5	2	0	0	1262.63	2035	2045
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	FGDLILK	99.7%	41.4	25	25.6	1	0	0	805.48	1902	1908
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	FGNAFHLCR	99.4%	37.3	25	27.3	1	0	0	1121.53	540	548
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	FICISDLR	99.4%	37	25	29.1	2	0	0	1023.53	2114	2121
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	FNTGPVGK	98.3%	32.4	25	16	1	0	0	819.44	616	623
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	GSELQLPFQACLK	99.7%	54.3	25	44.6	2	0	0	1490.77	1886	1898
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	GYLPSHYER	99.1%	35.1	25	34.3	1	0	0	1121.54	2250	2258
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	IDLTLLNR	99.7%	58.2	25	37.1	2	0	0	957.57	988	995
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	ISLIQIFR	99.7%	64.1	25	60.7	3	0	0	989.61	1571	1578
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	LIVDHNIADYMTAK	99.7%	64.3	25	61.9	1	0	0	1603.82	999	1012
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	LLILALER	99.7%	59.4	25	59.4	2	0	0	940.62	838	845
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	QILMASGSTTFTK	99.7%	64.3	25	62	3	0	0	1384.71	1246	1258
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	QQIAEIEK	94.6%	27.6	25	17.5	1	0	0	958.52	2024	2031
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	QTDVGITHFR	99.7%	56.4	25	40.4	2	0	0	1173.60	1345	1354
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	RALDIPLVK	98.6%	33.3	25	28.7	1	0	0	1024.65	420	428
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	SLPVEEQPK	98.0%	31.8	25	20.9	1	0	0	1026.55	1851	1859
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	TIIITCSFTPGSCTLTAYK	99.7%	52	25	52	1	0	0	2134.06	2211	2229
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	TISSYTAFSR	99.7%	41.9	25	37.6	2	0	0	1132.56	1926	1935
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	TSYEEFTHK	98.7%	33.7	25	29.5	1	0	0	1141.52	1202	1210
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	VQMLLSDR	98.8%	34.1	25	14	1	0	0	961.51	2259	2266
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	YIQPWESEFIDSQR	99.7%	42.6	25	42.6	1	0	0	1797.84	1371	1384
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	YWIDIQLR	98.6%	33.2	25	28.6	1	0	0	1106.60	1660	1667
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	29	30	45	0.05%	12.7%	YYVLNALK	98.5%	32.9	25	30.3	2	0	0	983.56	453	460
Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16	DHX38	PRP16_HUMAN	140.5	99.8%	2	2	4	0.00%	1.9%	DATSDLAIIAR	99.7%	51.2	25	35.7	2	0	0	1145.62	435	445
Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16	DHX38	PRP16_HUMAN	140.5	99.8%	2	2	4	0.00%	1.9%	SLNTDVLFGLLR	99.7%	75.9	25	64.3	2	0	0	1347.76	658	669
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	7	7	11	0.01%	12.3%	AAQEFFQR	98.5%	33	25	22.6	1	0	0	996.49	222	229
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	7	7	11	0.01%	12.3%	DLSIEEYIR	97.2%	30.3	25	20.5	1	0	0	1137.58	246	254
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	7	7	11	0.01%	12.3%	DSPPEVAGAR	96.7%	29.6	25	24.5	1	0	0	998.49	543	552
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	7	7	11	0.01%	12.3%	IVVEFSSPNVAK	99.7%	53.2	25	41.6	2	0	0	1289.71	127	138
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	7	7	11	0.01%	12.3%	SSQDFQPR	99.7%	41.5	25	32	2	0	0	964.45	512	519
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	7	7	11	0.01%	12.3%	TVLQQVIEDGSK	99.7%	65.7	25	59.9	2	0	0	1316.71	100	111
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	7	7	11	0.01%	12.3%	VGLAALIIQDFK	99.7%	67.7	25	67.7	2	0	0	1287.77	427	438

Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	19	0.02%	28.5%	APILIATDVASR	99.7%	74.9	25	74.9	8	0	0	1226.71	469	480
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	19	0.02%	28.5%	APLPDLYPFGTMR	99.5%	37.8	25	37.3	1	0	0	1477.75	69	81
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	19	0.02%	28.5%	DMVGIAQTGSGK	99.7%	69.1	25	61.5	2	0	0	1179.57	210	221
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	19	0.02%	28.5%	DWVLNEFR	99.7%	46.8	25	41.1	1	0	0	1078.53	458	465
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	19	0.02%	28.5%	ELAQQVQQVADDYGK	99.7%	107	25	100	2	0	0	1691.82	255	269
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	19	0.02%	28.5%	GDGPICLVLAPTR	99.7%	58.5	25	55.9	2	0	0	1368.73	242	254
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	19	0.02%	28.5%	GLDVEDVK	99.4%	37.1	25	29.1	2	0	0	874.45	481	488
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	19	0.02%	28.5%	GTAYTFFTPGNLK	99.7%	62.9	25	57.4	2	0	0	1416.72	516	528
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	19	0.02%	28.5%	GVEICIATPGR	99.7%	69.2	25	47.1	2	0	0	1172.61	294	304
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	19	0.02%	28.5%	IVDQIRPDR	98.3%	32.4	25	16.6	1	0	0	1111.62	342	350
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	19	0.02%	28.5%	LIDFLESGK	99.7%	51	25	42.8	1	0	0	1021.56	305	313
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	19	0.02%	28.5%	LMQLVDHR	96.6%	29.5	25	18.6	1	0	0	1027.54	548	555
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	19	0.02%	28.5%	MLDMGFEPQIR	99.7%	72.6	25	66.6	7	0	0	1336.64	330	340
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	19	0.02%	28.5%	NFYVEHPEVAR	99.7%	41.8	25	32.7	2	0	0	1360.66	133	143
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	19	0.02%	28.5%	QLAEDFLR	99.7%	55.3	25	26.5	2	0	0	991.52	365	372
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	19	0.02%	28.5%	QTLMWSATWPK	99.7%	64.8	25	58.6	2	0	0	1348.67	351	361
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	19	0.02%	28.5%	SSQSSSQQFSGIGR	99.7%	117	25	110	2	0	0	1455.68	671	684
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	19	0.02%	28.5%	STCIYGGAPK	99.7%	59.5	25	48.8	4	0	0	1053.50	275	284
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	19	0.02%	28.5%	VLEEANQAINPK	99.7%	69.4	25	66.5	3	0	0	1325.71	536	547
Probable ATP-dependent RNA helicase DDX20	DDX20	DDX20_HUMAN	92.2	99.8%	2	2	3	0.00%	2.3%	TAQDLSSPR	99.7%	41.9	25	32.6	2	0	0	974.49	42	50
Probable ATP-dependent RNA helicase DDX20	DDX20	DDX20_HUMAN	92.2	99.8%	2	2	3	0.00%	2.3%	VLISTDLTSR	99.3%	36.4	25	31.4	1	0	0	1104.63	362	371
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	3	3	5	0.01%	4.2%	ELGIQVHSVTR	99.5%	37.9	25	27.6	2	0	0	1238.69	300	310
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	3	3	5	0.01%	4.2%	IFVNSNTDVAPFLR	99.7%	56.4	25	49	2	0	0	1592.84	423	436
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	3	3	5	0.01%	4.2%	VLVLVPTR	96.7%	29.6	25	29.6	1	0	0	896.59	292	299
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	6	6	9	0.01%	13.1%	GSFADLGLEPR	99.7%	45.7	25	37.2	1	0	0	1161.59	126	136
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	6	6	9	0.01%	13.1%	LLGQPSLDSLPIPAPR	99.7%	43.9	25	43.9	2	0	0	1673.96	190	205
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	6	6	9	0.01%	13.1%	SPDEPLPVVR	99.7%	40.8	25	40.8	2	0	0	1108.60	28	37
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	6	6	9	0.01%	13.1%	TLSYLLPLLQR	99.7%	44.9	25	44.9	1	0	0	1316.79	179	189
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	6	6	9	0.01%	13.1%	VAELVHILK	99.3%	36.4	25	36.4	1	0	0	1021.64	378	386
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	6	6	9	0.01%	13.1%	VASPDAVTTITSSK	99.7%	50.5	25	43.6	2	0	0	1376.73	344	357
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	8	8	10	0.01%	14.5%	DVLVATDVASK	99.7%	60.2	25	45	2	0	0	1117.61	484	494
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	8	8	10	0.01%	14.5%	GVEAVAIHGGKDQEER	99.7%	34.3	25	34.3	0	1	0	1694.85	456	471
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	8	8	10	0.01%	14.5%	ILESVAEGR	99.5%	37.9	25	13.7	2	0	0	973.53	116	124
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	8	8	10	0.01%	14.5%	LLQEDSSPLLR	96.1%	28.9	25	24.8	1	0	0	1270.70	283	293
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	8	8	10	0.01%	14.5%	MVYLLECLQK	99.5%	38.3	25	33.3	1	0	0	1296.67	421	430
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	8	8	10	0.01%	14.5%	SALVKPVTINVGR	99.7%	33.2	25	33.2	0	1	0	1353.82	388	400
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	8	8	10	0.01%	14.5%	TPPPVLIFAEK	98.6%	33.3	25	33.3	1	0	0	1211.70	431	441
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	8	8	10	0.01%	14.5%	YLALDEADR	98.1%	32	25	24.7	1	0	0	1065.52	340	348
Probable ATP-dependent RNA helicase DDX46	DDX46	DDX46_HUMAN	117.4	100.0%	3	3	4	0.00%	3.0%	LLVATSVAAR	99.7%	55.2	25	42.7	2	0	0	1000.61	672	681
Probable ATP-dependent RNA helicase DDX46	DDX46	DDX46_HUMAN	117.4	100.0%	3	3	4	0.00%	3.0%	NFYVEVPELAK	99.7%	41.8	25	41.3	1	0	0	1308.68	334	344
Probable ATP-dependent RNA helicase DDX46	DDX46	DDX46_HUMAN	117.4	100.0%	3	3	4	0.00%	3.0%	TIAFLLPMFR	99.7%	42	25	40.3	1	0	0	1208.69	423	432
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	6	6	10	0.01%	16.0%	IQIEAIPLALQGR	99.7%	86.8	25	80.5	2	0	0	1421.85	50	62
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	6	6	10	0.01%	16.0%	KPHIIIATPGR	99.7%	35.4	25	35.4	0	1	0	1202.74	142	152
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	6	6	10	0.01%	16.0%	LIDHLENTK	99.7%	45	25	37.8	2	0	0	1082.58	153	161
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	6	6	10	0.01%	16.0%	LQQYYIFIPSK	99.7%	57.9	25	36	2	0	0	1399.76	238	248
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	6	6	10	0.01%	16.0%	SILLATDVASR	99.5%	37.8	25	29	1	0	0	1145.65	315	325
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	6	6	10	0.01%	16.0%	TGAFALPILNALLETPQR	99.7%	54.2	25	54.2	2	0	0	1925.09	75	92
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	21	22	61	0.06%	37.0%	APILIATDVASR	99.7%	74.9	25	74.9	8	0	0	1226.71	392	403
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	21	22	61	0.06%	37.0%	DGWPAMGIHGDK	99.7%	49.9	25	44.2	2	0	0	1283.58	364	375
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	21	22	61	0.06%	37.0%	DWVLNEFK	98.5%	33	25	28	1	0	0	1050.53	381	388
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	21	22	61	0.06%	37.0%	ELAQQVQQVAAEYCR	99.7%	92.8	25	92.8	3	0	0	1792.86	178	192

Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	21	22	61	0.06%	37.0%	FVINYDYPNSSEDYIHR	99.7%	31.9	25	29.4	0	2	0	2131.97	412	428
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	21	22	61	0.06%	37.0%	GDGPICLVLAPTR	99.7%	58.5	25	55.9	2	0	0	1368.73	165	177
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	21	22	61	0.06%	37.0%	GLDVEDVK	99.4%	37.1	25	29.1	2	0	0	874.45	404	411
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	21	22	61	0.06%	37.0%	GVEICIATPGR	99.7%	69.2	25	47.1	2	0	0	1172.61	217	227
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	21	22	61	0.06%	37.0%	IVDQIRPDR	98.3%	32.4	25	16.6	1	0	0	1111.62	265	273
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	21	22	61	0.06%	37.0%	LIDFLECGK	99.7%	58.8	25	58.8	4	0	0	1094.56	228	236
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	21	22	61	0.06%	37.0%	LLQLVEDR	99.7%	65.6	25	48.1	4	0	0	985.57	471	478
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	21	22	61	0.06%	37.0%	LMEEIMSEK	98.1%	32	25	24.7	1	0	0	1109.52	332	340
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	21	22	61	0.06%	37.0%	MLDMGFEPQIR	99.7%	72.6	25	66.6	7	0	0	1336.64	253	263
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	21	22	61	0.06%	37.0%	NFYQEHPDLAR	99.7%	55.7	25	43.1	2	0	0	1389.65	57	67
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	21	22	61	0.06%	37.0%	QTLMWSATWPK	99.7%	64.8	25	58.6	2	0	0	1348.67	274	284
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	21	22	61	0.06%	37.0%	QVSDLISVLR	99.7%	61	25	44.5	4	0	0	1129.66	452	461
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	21	22	61	0.06%	37.0%	STCIYGGAPK	99.7%	59.5	25	48.8	4	0	0	1053.50	198	207
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	21	22	61	0.06%	37.0%	TAQEVETYR	99.7%	66.4	25	57.4	2	0	0	1096.53	69	77
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	21	22	61	0.06%	37.0%	TGTAYTFFTPNNIK	99.7%	73.9	25	64.7	4	0	0	1574.79	438	451
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	21	22	61	0.06%	37.0%	TIVFVETKR	99.7%	49.2	25	49.2	2	0	0	1092.64	344	352
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	21	22	61	0.06%	37.0%	TTYLVLDEADR	99.7%	80.9	25	74.9	2	0	0	1295.65	242	252
Probable ATP-dependent RNA helicase DDX52	DDX52	DDX52_HUMAN	67.5	100.0%	5	6	8	0.01%	9.4%	DNTVHSFR	96.9%	29.8	25	19	1	0	0	975.46	452	459
Probable ATP-dependent RNA helicase DDX52	DDX52	DDX52_HUMAN	67.5	100.0%	5	6	8	0.01%	9.4%	ELASQIHR	99.7%	40.3	25	28.2	2	0	0	953.52	245	252
Probable ATP-dependent RNA helicase DDX52	DDX52	DDX52_HUMAN	67.5	100.0%	5	6	8	0.01%	9.4%	ELLASAPTGSGK	99.0%	35	25	35	1	0	0	1130.61	204	215
Probable ATP-dependent RNA helicase DDX52	DDX52	DDX52_HUMAN	67.5	100.0%	5	6	8	0.01%	9.4%	GFNPPVLVFVQSIER	99.7%	56.5	25	56.5	2	0	0	1701.93	410	424
Probable ATP-dependent RNA helicase DDX52	DDX52	DDX52_HUMAN	67.5	100.0%	5	6	8	0.01%	9.4%	TLAFSIPILMQLK	99.7%	63.1	25	58.5	2	0	0	1474.87	216	228
Probable ATP-dependent RNA helicase DHX36	DHX36	DHX36_HUMAN	114.8	100.0%	3	3	6	0.01%	3.6%	ASLLDDYQLPEILR	99.7%	82.9	25	73.9	2	0	0	1645.88	620	633
Probable ATP-dependent RNA helicase DHX36	DHX36	DHX36_HUMAN	114.8	100.0%	3	3	6	0.01%	3.6%	LGGIAYFLSR	99.7%	72.6	25	68.9	2	0	0	1096.62	648	657
Probable ATP-dependent RNA helicase DHX36	DHX36	DHX36_HUMAN	114.8	100.0%	3	3	6	0.01%	3.6%	NLQSDVLMTVVK	99.7%	59.9	25	48.8	2	0	0	1346.73	340	351
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	3	3	5	0.01%	2.0%	IAVNIALER	99.7%	54.9	25	51.1	1	0	0	998.60	47	55
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	3	3	5	0.01%	2.0%	LAAIAVAER	98.7%	33.6	25	18.5	2	0	0	913.55	251	259
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	3	3	5	0.01%	2.0%	LSQSLGLVSK	99.0%	34.8	25	23	2	0	0	1031.61	81	90
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	8	8	11	0.01%	7.7%	DLEDESTPIVK	97.8%	31.3	25	21.6	1	0	0	1245.62	940	950
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	8	8	11	0.01%	7.7%	DSPTLSNSGIR	99.7%	40.7	25	34.2	2	0	0	1146.58	898	908
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	8	8	11	0.01%	7.7%	GFQEDSEIR	98.6%	33.3	25	13.5	1	0	0	1080.50	208	216
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	8	8	11	0.01%	7.7%	LGDASIAAPFTSK	99.7%	49.2	25	49.2	2	0	0	1277.67	951	963
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	8	8	11	0.01%	7.7%	LGSTDLCYIAAVK	99.7%	44.4	25	43.7	1	0	0	1410.73	642	654
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	8	8	11	0.01%	7.7%	SIDGSIVLPLAR	99.7%	41.9	25	37.5	2	0	0	1240.73	786	797
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	8	8	11	0.01%	7.7%	SPQENLVPCDVLLLR	94.7%	27.6	25	27.6	1	0	0	1752.93	328	342
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	8	8	11	0.01%	7.7%	VLDLQADSR	99.3%	36.3	25	30	1	0	0	1016.54	372	380
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	5	6	12	0.01%	7.3%	IMDLIGIQTK	99.7%	53.7	25	31.8	3	0	0	1131.64	123	132
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	5	6	12	0.01%	7.3%	LTEYPLVINTLK	99.7%	56.5	25	56.5	2	0	0	1403.81	92	103
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	5	6	12	0.01%	7.3%	TEMGLYYSYFK	99.7%	59.4	25	59.4	2	0	0	1401.64	62	72
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	5	6	12	0.01%	7.3%	TPLCNLLVK	99.7%	50.5	25	45.6	3	0	0	1057.61	644	652
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	5	6	12	0.01%	7.3%	VLEVVKE	99.5%	37.9	25	7.43	2	0	0	815.49	669	675
Probable cytosolic iron-sulfur protein assembly protein CIAO1	CIAO1	CIAO1_HUMAN	37.8	100.0%	4	5	7	0.01%	14.5%	EPGLLASCSDDGEVAFWK	99.7%	73.6	25	73.6	1	0	0	1980.90	315	332
Probable cytosolic iron-sulfur protein assembly protein CIAO1	CIAO1	CIAO1_HUMAN	37.8	100.0%	4	5	7	0.01%	14.5%	IWGTEGDSWICK	97.9%	31.6	25	30.7	1	0	0	1451.66	42	53
Probable cytosolic iron-sulfur protein assembly protein CIAO1	CIAO1	CIAO1_HUMAN	37.8	100.0%	4	5	7	0.01%	14.5%	MKDSLVLLGR	99.7%	75.4	25	66.5	3	0	0	1131.66	1	10
Probable cytosolic iron-sulfur protein assembly protein CIAO1	CIAO1	CIAO1_HUMAN	37.8	100.0%	4	5	7	0.01%	14.5%	SVLSEGHQR	99.7%	43.7	25	36.1	2	0	0	1012.52	54	62
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	7	8	12	0.01%	22.7%	LLHGFNAEGIHFS	98.8%	27	25	27	0	1	0	1441.72	301	313
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	7	8	12	0.01%	22.7%	LQVLVGDVLK	99.7%	55.3	25	24.7	2	0	0	1083.68	107	116
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	7	8	12	0.01%	22.7%	LSINTQLLAR	99.7%	75.2	25	57.4	2	0	0	1128.67	175	184
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	7	8	12	0.01%	22.7%	LVAELHKR	99.7%	54.1	25	31.6	1	0	0	965.59	90	97
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	7	8	12	0.01%	22.7%	NPLIINSIIDK	99.7%	70.6	25	70.6	2	0	0	1239.73	41	51
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	7	8	12	0.01%	22.7%	SMDIDDFIR	99.7%	41.7	25	32.7	2	0	0	1111.51	292	300

Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	7	8	12	0.01%	22.7%	SSAVQQLLEK	99.7%	51.5	25	36.3	2	0	0	1102.61	244	253
Probable glutamate--tRNA ligase, mitochondrial	EARS2	SYEM_HUMAN	58.7	100.0%	3	3	5	0.01%	5.5%	GGPAGPYQQSQR	99.7%	51.1	25	50.3	2	0	0	1245.60	109	120
Probable glutamate--tRNA ligase, mitochondrial	EARS2	SYEM_HUMAN	58.7	100.0%	3	3	5	0.01%	5.5%	NMSQEQVAQK	99.7%	54.9	25	54.5	2	0	0	1162.55	169	178
Probable glutamate--tRNA ligase, mitochondrial	EARS2	SYEM_HUMAN	58.7	100.0%	3	3	5	0.01%	5.5%	VLGLLER	98.3%	32.5	25	22.5	1	0	0	799.50	449	455
Probable histidine--tRNA ligase, mitochondrial	HARS2	SYHM_HUMAN	56.9	99.8%	2	2	3	0.00%	4.0%	ESPTIVQGR	99.7%	43.8	25	36.7	2	0	0	986.53	160	168
Probable histidine--tRNA ligase, mitochondrial	HARS2	SYHM_HUMAN	56.9	99.8%	2	2	3	0.00%	4.0%	LIAELWDSGIK	99.7%	49.4	25	43.8	1	0	0	1244.69	428	438
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	9	10	18	0.02%	10.2%	EEVDLTGSVPVHAK	99.7%	58.7	25	48.4	1	0	0	1480.76	615	628
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	9	10	18	0.02%	10.2%	FYVLSMFPYPSGK	99.7%	77.9	25	77.9	3	0	0	1535.76	84	96
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	9	10	18	0.02%	10.2%	IPVPQQVAR	98.7%	33.8	25	28.9	2	0	0	1007.60	853	861
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	9	10	18	0.02%	10.2%	LLAQGLIK	99.5%	38	25	0	2	0	0	855.57	593	600
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	9	10	18	0.02%	10.2%	LPSGQYLQR	99.7%	66.6	25	56	2	0	0	1061.57	606	614
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	9	10	18	0.02%	10.2%	QDAFLALTQK	99.7%	50.5	25	28.8	2	0	0	1134.62	420	429
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	9	10	18	0.02%	10.2%	TALINFLVQD	99.7%	57.6	25	56.6	2	0	0	1133.62	894	903
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	9	10	18	0.02%	10.2%	TDALPGVLR	99.7%	54.5	25	42.9	2	0	0	941.54	682	690
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	9	10	18	0.02%	10.2%	VYTISDTIAR	99.7%	47.6	25	37.1	2	0	0	1138.61	104	113
Probable proline--tRNA ligase, mitochondrial	PARS2	SYPM_HUMAN	53.3	100.0%	3	3	6	0.01%	7.4%	DGVMDLLTPVQTV	99.4%	37.1	25	37.1	2	0	0	1387.71	463	475
Probable proline--tRNA ligase, mitochondrial	PARS2	SYPM_HUMAN	53.3	100.0%	3	3	6	0.01%	7.4%	FGYPFVIIAGK	99.7%	41	25	30.4	2	0	0	1211.68	428	438
Probable proline--tRNA ligase, mitochondrial	PARS2	SYPM_HUMAN	53.3	100.0%	3	3	6	0.01%	7.4%	QLPFLLYQVTR	99.7%	45.5	25	45	2	0	0	1377.79	176	186
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	7	7	11	0.01%	24.2%	AVDPEDDFQR	99.7%	61	25	61	2	0	0	1191.53	95	104
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	7	7	11	0.01%	24.2%	ELQDAFSR	97.7%	31.1	25	24.7	1	0	0	965.47	22	29
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	7	7	11	0.01%	24.2%	ESYDDVSSFR	99.7%	84.8	25	84.8	2	0	0	1204.51	263	272
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	7	7	11	0.01%	24.2%	GLLKPGLNVVLEGPK	98.0%	31.6	25	31.6	1	0	0	1533.94	30	44
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	7	7	11	0.01%	24.2%	QAQAAVLAVLPR	99.7%	80.5	25	80.5	2	0	0	1236.74	111	122
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	7	7	11	0.01%	24.2%	RPTDYFAEMAK	99.4%	37.7	25	27.9	1	0	0	1328.63	132	142
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	7	7	11	0.01%	24.2%	VQTEVLQK	96.9%	29.9	25	0	2	0	0	944.54	180	187
Probable serine carboxypeptidase CPVL	CPVL	CPVL_HUMAN	54.2	100.0%	3	3	8	0.01%	6.7%	FLSLPEVR	98.1%	31.9	25	27	2	0	0	960.55	332	339
Probable serine carboxypeptidase CPVL	CPVL	CPVL_HUMAN	54.2	100.0%	3	3	8	0.01%	6.7%	NNDFYVTGESYAGK	99.7%	102	25	102	4	0	0	1564.69	195	208
Probable serine carboxypeptidase CPVL	CPVL	CPVL_HUMAN	54.2	100.0%	3	3	8	0.01%	6.7%	SDSEVAGYIR	99.7%	73.3	25	54.1	2	0	0	1096.53	424	433
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	6	7	10	0.01%	24.2%	GPGMGAPLVSVAVVAR	99.7%	41.8	25	33.7	1	0	0	1480.83	79	94
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	6	7	10	0.01%	24.2%	ISNDPSPGYNIEQMAK	99.2%	36.1	25	36.1	2	0	0	1779.82	170	185
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	6	7	10	0.01%	24.2%	LVELPYTVK	99.0%	34.7	25	29.5	2	0	0	1061.62	190	198
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	6	7	10	0.01%	24.2%	PAVLGFEGSANK	99.7%	80	25	78.6	2	0	0	1189.62	2	13
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	6	7	10	0.01%	24.2%	TPLSDSGVTQR	99.7%	58.8	25	44.8	2	0	0	1160.59	313	323
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	6	7	10	0.01%	24.2%	TYVTPPGTGFLPGDTAR	99.7%	67.6	25	67.5	1	0	0	1749.88	31	47
Probable tRNA pseudouridine synthase 1	TRUB1	TRUB1_HUMAN	37.3	100.0%	3	3	5	0.01%	9.5%	AAAAVVAAAAR	99.7%	58.4	25	58.2	1	0	0	941.55	39	49
Probable tRNA pseudouridine synthase 1	TRUB1	TRUB1_HUMAN	37.3	100.0%	3	3	5	0.01%	9.5%	GPTSAELLNR	99.7%	50	25	42.3	2	0	0	1057.56	79	88
Probable tRNA pseudouridine synthase 1	TRUB1	TRUB1_HUMAN	37.3	100.0%	3	3	5	0.01%	9.5%	GVLVVGIGSGTK	99.7%	81.2	25	74.2	2	0	0	1086.65	126	137
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	16	17	23	0.02%	6.5%	EIYTNLGPR	99.2%	36	25	31.5	1	0	0	1062.56	795	803
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	16	17	23	0.02%	6.5%	ELLAFQTSEK	99.7%	48.5	25	39.5	2	0	0	1165.61	1436	1445
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	16	17	23	0.02%	6.5%	EYNIGVLR	96.7%	29.5	25	20.5	1	0	0	963.53	1638	1645
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	16	17	23	0.02%	6.5%	FLFTTGFHTK	99.7%	51.4	25	40.7	1	0	0	1198.63	2051	2060
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	16	17	23	0.02%	6.5%	FNDYFEFPR	99.7%	48.9	25	41.4	1	0	0	1234.55	1812	1820
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	16	17	23	0.02%	6.5%	FSEYLLECPSAEVR	96.6%	29.5	25	29.5	1	0	0	1699.80	2100	2113
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	16	17	23	0.02%	6.5%	GDLLEGANAYHCEK	99.7%	48.1	25	48.1	1	0	0	1576.71	1760	1773
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	16	17	23	0.02%	6.5%	LLLTAIGYGHVR	99.7%	73.6	25	73.6	2	0	0	1312.77	1157	1168
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	16	17	23	0.02%	6.5%	LPPVLAIQLK	99.7%	40.7	25	35.5	1	0	0	1091.72	1789	1798
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	16	17	23	0.02%	6.5%	LQYYVPR	95.7%	28.5	25	22.8	1	0	0	938.51	1659	1665
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	16	17	23	0.02%	6.5%	LYSVVSQLIR	99.7%	67.3	25	48.5	2	0	0	1177.69	2228	2237
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	16	17	23	0.02%	6.5%	MNALNEVNK	99.6%	38.9	25	25.9	1	0	0	1048.51	352	360
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	16	17	23	0.02%	6.5%	SGGLPLVLSMLTR	99.7%	58.5	25	58.5	3	0	0	1343.77	1120	1132
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	16	17	23	0.02%	6.5%	VISSVSYYTHR	98.6%	33.3	25	33.3	1	0	0	1311.67	361	371

Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	16	17	23	0.02%	6.5%	VLGGSFADQK	99.7%	48.3	25	41.1	2	0	0	1021.53	1713	1722
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	16	17	23	0.02%	6.5%	VVIQSNDDIASR	99.7%	57	25	57	2	0	0	1316.68	777	788
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	100.0%	3	3	4	0.00%	5.4%	FLGSGGFIGYAPNLSK	99.7%	69.3	25	64.2	1	0	0	1627.85	151	166
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	100.0%	3	3	4	0.00%	5.4%	FLLEYIAPMTEK	99.7%	54.6	25	54.6	2	0	0	1454.76	615	626
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	100.0%	3	3	4	0.00%	5.4%	SEDYVDIVQGR	99.7%	47.8	25	43.1	1	0	0	1280.61	431	441
Profilin-1	PFN1	PROF1_HUMAN	15.1	100.0%	2	3	8	0.01%	20.0%	DSLLQDGEFSMDLR	99.7%	94.4	25	94.4	4	0	0	1625.75	76	89
Profilin-1	PFN1	PROF1_HUMAN	15.1	100.0%	2	3	8	0.01%	20.0%	STGGAPTFNVTVTK	99.7%	44	25	43.1	4	0	0	1379.72	92	105
Profilin-2	PFN2	PROF2_HUMAN	15.0	100.0%	3	3	7	0.01%	29.3%	DSLYVDGDCTMDIR	98.6%	33.2	25	33.2	1	0	0	1675.69	76	89
Profilin-2	PFN2	PROF2_HUMAN	15.0	100.0%	3	3	7	0.01%	29.3%	EGFFTNGLTLGAK	99.7%	52	25	52	2	0	0	1354.70	57	69
Profilin-2	PFN2	PROF2_HUMAN	15.0	100.0%	3	3	7	0.01%	29.3%	SQGGEPTYNVAVGR	99.7%	59.3	25	59.3	4	0	0	1434.70	92	105
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	12	12	25	0.03%	15.4%	DLQQSIAR	98.6%	33.4	25	16.8	1	0	0	930.50	708	715
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	12	12	25	0.03%	15.4%	ELPELLQR	99.7%	54.7	25	42.3	2	0	0	997.57	439	446
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	12	12	25	0.03%	15.4%	ETVLSALSR	99.7%	56.9	25	42.1	2	0	0	975.55	165	173
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	12	12	25	0.03%	15.4%	FYNELTEILVR	99.7%	79.6	25	72.2	4	0	0	1396.75	676	686
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	12	12	25	0.03%	15.4%	LANQAADYFGDAFK	99.7%	94.1	25	94.1	2	0	0	1530.72	216	229
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	12	12	25	0.03%	15.4%	NIQVSHQEFSK	99.7%	48.2	25	47.7	3	0	0	1316.66	628	638
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	12	12	25	0.03%	15.4%	SLLSNLDEVKK	99.7%	58.9	25	38.9	2	0	0	1245.71	554	564
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	12	12	25	0.03%	15.4%	STPVNVPISQK	98.4%	32.7	25	30.3	2	0	0	1169.65	340	350
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	12	12	25	0.03%	15.4%	SVIEQGGIQTVDQLIK	99.7%	118	25	110	3	0	0	1727.95	423	438
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	12	12	25	0.03%	15.4%	TMQGSEVVNVLK	99.7%	47.2	25	38.7	1	0	0	1320.68	542	553
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	12	12	25	0.03%	15.4%	TPSNELYKPLR	97.8%	24.7	25	24.7	0	1	0	1317.72	479	489
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	12	12	25	0.03%	15.4%	TSEVDLAKPLVK	99.7%	50	25	41	2	0	0	1299.75	12	23
Programmed cell death protein 10	PDCD10	PDC10_HUMAN	24.7	100.0%	5	5	9	0.01%	21.2%	AEKENPGLTQDIIMK	97.1%	30.1	25	24.5	1	0	0	1686.87	51	65
Programmed cell death protein 10	PDCD10	PDC10_HUMAN	24.7	100.0%	5	5	9	0.01%	21.2%	AINVFVSANR	99.7%	49.2	25	40	2	0	0	1090.60	187	196
Programmed cell death protein 10	PDCD10	PDC10_HUMAN	24.7	100.0%	5	5	9	0.01%	21.2%	ENPGLTQDIIMK	98.2%	32.2	25	24.8	2	0	0	1358.70	54	65
Programmed cell death protein 10	PDCD10	PDC10_HUMAN	24.7	100.0%	5	5	9	0.01%	21.2%	IPDEINDR	99.7%	55.5	25	46.6	2	0	0	971.48	117	124
Programmed cell death protein 10	PDCD10	PDC10_HUMAN	24.7	100.0%	5	5	9	0.01%	21.2%	SVEVNFTESLLR	99.7%	77.8	25	69.7	2	0	0	1393.73	71	82
Programmed cell death protein 6	PDCD6	PDCD6_HUMAN	21.9	100.0%	5	6	11	0.01%	28.3%	AGVNFSEFTGVWK	99.7%	61.1	25	55.4	2	0	0	1441.71	78	90
Programmed cell death protein 6	PDCD6	PDCD6_HUMAN	21.9	100.0%	5	6	11	0.01%	28.3%	LSDQFHDILIR	99.7%	45.4	25	36.5	2	1	0	1356.73	126	136
Programmed cell death protein 6	PDCD6	PDCD6_HUMAN	21.9	100.0%	5	6	11	0.01%	28.3%	QALSGFGYR	99.7%	68.9	25	60.6	2	0	0	998.51	117	125
Programmed cell death protein 6	PDCD6	PDCD6_HUMAN	21.9	100.0%	5	6	11	0.01%	28.3%	SIISMFDRENK	99.7%	51.2	25	46.9	2	0	0	1339.67	67	77
Programmed cell death protein 6	PDCD6	PDCD6_HUMAN	21.9	100.0%	5	6	11	0.01%	28.3%	YITDWQNVFR	99.7%	52	25	46.5	2	0	0	1341.66	91	100
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	79	0.08%	57.0%	AAELIANSLATAGDGLIELR	99.7%	108	25	86.6	8	4	0	1998.09	220	239
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	79	0.08%	57.0%	AAIISAEGDSK	99.7%	81.2	25	73	7	0	0	1061.55	209	219
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	79	0.08%	57.0%	DLQNVNITLR	99.7%	73.9	25	59.8	4	0	0	1185.66	84	93
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	79	0.08%	57.0%	EFTEAVEAK	99.7%	66.6	25	46.7	4	0	0	1023.50	178	186
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	79	0.08%	57.0%	FDAGELITQR	99.7%	78.9	25	69	13	0	0	1149.59	134	143
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	79	0.08%	57.0%	FVVEKAEQQK	99.2%	35.8	25	28.2	1	0	0	1205.65	198	207
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	79	0.08%	57.0%	IFTSIGEDYDER	99.7%	94.2	25	86.3	7	0	0	1444.66	106	117
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	79	0.08%	57.0%	ILFRPVASQLPR	99.7%	56	25	50.7	4	6	0	1396.84	94	105
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	79	0.08%	57.0%	KAAIISAEGDSK	99.7%	45.7	25	42.1	2	0	0	1189.64	208	219
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	79	0.08%	57.0%	KLEAAEDIAYQLSR	99.7%	110	25	104	4	0	0	1606.84	240	253
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	79	0.08%	57.0%	LEAAEDIAYQLSR	99.7%	67.8	25	58.5	3	0	0	1478.75	241	253
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	79	0.08%	57.0%	NITYLPAGQSVLLQLPQ	99.7%	55	25	54.7	3	0	0	1855.03	256	272
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	79	0.08%	57.0%	NVPVITGSK	96.4%	29.2	25	29.2	1	0	0	914.53	75	83
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	79	0.08%	57.0%	QVSDDLTER	99.7%	60	25	50.5	4	0	0	1062.51	149	157
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	79	0.08%	57.0%	VLPSITTEILK	99.7%	62.8	25	51	4	0	0	1213.74	118	128
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	20	29	78	0.08%	67.2%	AQFLVEK	99.7%	41.9	25	23	2	0	0	834.47	210	216
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	20	29	78	0.08%	67.2%	AQVSLLIR	99.7%	45.2	25	32.9	4	0	0	899.57	158	165
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	20	29	78	0.08%	67.2%	AQVSLLIRR	99.7%	53.3	25	48.7	2	0	0	1055.67	158	166
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	20	29	78	0.08%	67.2%	DLAGRLPAGPR	99.6%	39.3	25	36.1	2	0	0	1122.64	7	17

Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	20	29	78	0.08%	67.2%	DLQMVNISLR	99.7%	74	25	57.4	4	0	0	1188.64	98	107
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	20	29	78	0.08%	67.2%	ESVFTVEGGHR	99.7%	89.8	25	70.9	2	2	0	1217.59	38	48
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	20	29	78	0.08%	67.2%	EYTAAVEAK	99.7%	42	25	39.5	2	0	0	981.49	192	200
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	20	29	78	0.08%	67.2%	FNASQLITQR	99.7%	72.3	25	62.2	8	0	0	1177.63	148	157
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	20	29	78	0.08%	67.2%	IGGVQQDTILAEGLHFR	99.7%	74.6	25	74.6	2	2	0	1853.99	55	71
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	20	29	78	0.08%	67.2%	IPWFQYPIIYDIR	99.7%	66.2	25	63.4	3	1	0	1723.92	72	84
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	20	29	78	0.08%	67.2%	IVQAEGEAEAAK	99.7%	90.4	25	78.1	2	0	0	1215.62	225	236
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	20	29	78	0.08%	67.2%	IYLTADNLVLNLQDESFTR	99.7%	71.1	25	71.1	2	0	0	2225.15	271	289
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	20	29	78	0.08%	67.2%	LGLDYEER	99.7%	62.4	25	50.9	9	0	0	994.48	124	131
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	20	29	78	0.08%	67.2%	LLLGAGAVAYGVR	99.7%	96	25	76.3	9	0	0	1259.75	25	37
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	20	29	78	0.08%	67.2%	MLGEALSK	99.7%	45.8	25	23	3	0	0	864.45	237	244
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	20	29	78	0.08%	67.2%	MLGEALSKNPGYIK	99.7%	45.4	25	45	2	0	0	1536.81	237	250
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	20	29	78	0.08%	67.2%	QKIVQAEGEAEAAK	99.7%	72.9	25	61.3	2	1	0	1471.78	223	236
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	20	29	78	0.08%	67.2%	QVAQQEAQR	99.1%	35.2	25	29.4	2	0	0	1057.54	201	209
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	20	29	78	0.08%	67.2%	VLPSIVNEVLK	99.5%	38.7	25	31.7	3	0	0	1210.74	132	142
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	20	29	78	0.08%	67.2%	VLSRPNAQELPSMYQR	99.7%	43	25	41.1	3	4	0	1888.97	108	123
Prolactin-inducible protein	PIP	PIP_HUMAN	16.6	100.0%	5	5	12	0.01%	43.8%	ELGICPDDAAVIPIK	99.0%	34.7	25	34	1	0	0	1610.85	119	133
Prolactin-inducible protein	PIP	PIP_HUMAN	16.6	100.0%	5	5	12	0.01%	43.8%	FYTIEILKVE	99.6%	39.1	25	27.1	6	0	0	1254.70	137	146
Prolactin-inducible protein	PIP	PIP_HUMAN	16.6	100.0%	5	5	12	0.01%	43.8%	TVQIAAVVDVIR	99.7%	59.9	25	52.8	2	0	0	1283.77	107	118
Prolactin-inducible protein	PIP	PIP_HUMAN	16.6	100.0%	5	5	12	0.01%	43.8%	TYLISSIPLQGAFNYK	96.2%	29	25	29	1	0	0	1814.97	70	85
Prolactin-inducible protein	PIP	PIP_HUMAN	16.6	100.0%	5	5	12	0.01%	43.8%	YTACLCDDNPK	99.6%	39	25	39	2	0	0	1356.56	86	96
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	11	14	32	0.03%	52.5%	AEDNADTLALVFEAPNQEK	99.7%	122	25	122	2	0	0	2074.99	92	110
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	11	14	32	0.03%	52.5%	ATPLSSTVTLSMSADVPLVVEYK	96.1%	28.9	25	20.8	1	0	0	2424.26	218	240
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	11	14	32	0.03%	52.5%	DLSHIGDAVVISCAK	99.7%	70.7	25	65.9	2	2	0	1584.81	150	164
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	11	14	32	0.03%	52.5%	FSASGELGNGNIK	99.7%	102	25	96.7	4	0	0	1293.64	169	181
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	11	14	32	0.03%	52.5%	IADMGHLK	99.7%	53.7	25	49.3	3	0	0	884.47	241	248
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	11	14	32	0.03%	52.5%	LMDLDVEQLGIPEQEYSCVVK	95.3%	28.1	25	28.1	1	0	0	2465.19	118	138
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	11	14	32	0.03%	52.5%	LVQGSILK	99.4%	37.4	25	11.1	2	0	0	857.55	6	13
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	11	14	32	0.03%	52.5%	LVQGSILKK	99.7%	42.2	25	3.85	2	0	0	985.64	6	14
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	11	14	32	0.03%	52.5%	MPSGEFAR	99.7%	41.7	25	34.9	4	0	0	894.41	139	146
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	11	14	32	0.03%	52.5%	NLAMGVNLTSMSK	99.7%	118	25	112	6	0	0	1365.69	65	77
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	11	14	32	0.03%	52.5%	SEGFDTYR	99.7%	51.9	25	43.3	3	0	0	974.42	54	61
Prolyl 3-hydroxylase 1	LEPRE1	P3H1_HUMAN	83.4	100.0%	3	3	5	0.01%	4.8%	DLSFFGGLLR	99.7%	64.7	25	47.7	2	0	0	1124.61	106	115
Prolyl 3-hydroxylase 1	LEPRE1	P3H1_HUMAN	83.4	100.0%	3	3	5	0.01%	4.8%	LTNVAATSGDGYR	99.7%	76.6	25	75.4	2	0	0	1324.65	489	501
Prolyl 3-hydroxylase 1	LEPRE1	P3H1_HUMAN	83.4	100.0%	3	3	5	0.01%	4.8%	TVTAEVQPQCGR	99.7%	47.4	25	42.4	1	0	0	1345.65	636	647
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	6	6	11	0.01%	13.7%	DPEGFVGHPVNAFK	99.7%	46.4	25	35.9	2	0	0	1513.74	73	86
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	6	6	11	0.01%	13.7%	GVAVDYLPER	99.7%	60.9	25	57	2	0	0	1118.58	277	286
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	6	6	11	0.01%	13.7%	HAACPVLVGNK	99.7%	48.8	25	39.5	2	0	0	1165.61	500	510
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	6	6	11	0.01%	13.7%	LLELDPEHQR	97.8%	31.4	25	31.4	2	0	0	1249.65	231	240
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	6	6	11	0.01%	13.7%	LQDTYNLDTDTISK	99.7%	80.9	25	76.6	2	0	0	1626.79	137	150
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	6	6	11	0.01%	13.7%	SAWLSGYENPVVSR	99.7%	86.6	25	86.6	1	0	0	1564.78	383	396
Prostaglandin E synthase 3	PTGES3	TEBP_HUMAN	18.7	99.8%	2	2	4	0.00%	14.4%	KGESGQSWPR	99.7%	45.1	25	41.6	2	0	0	1131.55	79	88
Prostaglandin E synthase 3	PTGES3	TEBP_HUMAN	18.7	99.8%	2	2	4	0.00%	14.4%	LTFSCLGGSDNFK	99.7%	62.1	25	62.1	2	0	0	1445.67	36	48
Proteasomal ATPase-associated factor 1	PAAF1	PAAF1_HUMAN	42.2	100.0%	2	2	6	0.01%	5.6%	FLAPYTTFSR	99.4%	37.7	25	33.3	2	0	0	1202.62	80	89
Proteasomal ATPase-associated factor 1	PAAF1	PAAF1_HUMAN	42.2	100.0%	2	2	6	0.01%	5.6%	SGAPVLSLLSVR	99.7%	74	25	67.4	4	0	0	1198.72	321	332
Proteasomal ubiquitin receptor ADRM1	ADRM1	ADRM1_HUMAN	42.2	99.8%	2	2	4	0.00%	5.9%	SQSAAVTPSSTTSSTR	99.7%	88.6	25	85.2	2	0	0	1567.76	211	226
Proteasomal ubiquitin receptor ADRM1	ADRM1	ADRM1_HUMAN	42.2	99.8%	2	2	4	0.00%	5.9%	VPQCPSGR	99.4%	37.4	25	35.5	2	0	0	900.44	85	92
Proteasome activator complex subunit 3	PSME3	PSME3_HUMAN	29.5	100.0%	6	6	8	0.01%	29.9%	ITSEAEDLVANFFPK	99.7%	74.3	25	71.5	2	0	0	1680.85	22	36
Proteasome activator complex subunit 3	PSME3	PSME3_HUMAN	29.5	100.0%	6	6	8	0.01%	29.9%	MWVQLLIPR	95.1%	27.9	25	15.6	1	0	0	1171.67	138	146
Proteasome activator complex subunit 3	PSME3	PSME3_HUMAN	29.5	100.0%	6	6	8	0.01%	29.9%	NQYVTLHDMILK	98.8%	34	25	30.5	1	0	0	1490.77	226	237
Proteasome activator complex subunit 3	PSME3	PSME3_HUMAN	29.5	100.0%	6	6	8	0.01%	29.9%	SNQQLVDIIEK	99.7%	49.2	25	46	1	0	0	1286.70	111	121

Proteasome activator complex subunit 3	PSME3	PSME3_HUMAN	29.5	100.0%	6	6	8	0.01%	29.9%	TVESEAASYLDQISR	99.7%	97.1	25	68.8	2	0	0	1668.81	167	181
Proteasome activator complex subunit 3	PSME3	PSME3_HUMAN	29.5	100.0%	6	6	8	0.01%	29.9%	TVTEIDEKEYISLR	99.7%	53.2	25	41	1	0	0	1695.88	205	218
Proteasome assembly chaperone 3	PSMG3	PSMG3_HUMAN	13.1	99.8%	2	2	4	0.00%	18.0%	AVLLAVAVK	99.7%	48.1	25	30.2	2	0	0	883.60	94	102
Proteasome assembly chaperone 3	PSMG3	PSMG3_HUMAN	13.1	99.8%	2	2	4	0.00%	18.0%	NLVAFVSQEAGNR	99.7%	99.6	25	81.2	2	0	0	1404.72	81	93
Proteasome subunit alpha type-3	PSMA3	PSA3_HUMAN	28.4	100.0%	3	3	7	0.01%	11.8%	CKDGVVFGVEK	99.6%	39.2	25	31.5	1	0	0	1237.62	42	52
Proteasome subunit alpha type-3	PSMA3	PSA3_HUMAN	28.4	100.0%	3	3	7	0.01%	11.8%	SNFGYNIPLK	99.7%	55.5	25	46.7	4	0	0	1152.60	101	110
Proteasome subunit alpha type-3	PSMA3	PSA3_HUMAN	28.4	100.0%	3	3	7	0.01%	11.8%	VFQVEYAMK	99.7%	51.6	25	47.7	2	0	0	1114.56	21	29
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	8	12	29	0.03%	29.5%	ATCIGNNSAAAVSMLK	99.7%	106	25	88.4	8	0	0	1607.79	161	176
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	8	12	29	0.03%	29.5%	LLDEVFFSEK	99.7%	67.2	25	57	4	0	0	1226.63	55	64
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	8	12	29	0.03%	29.5%	LSAEKVEIATLTR	99.7%	79	25	73.4	2	2	0	1430.82	206	218
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	8	12	29	0.03%	29.5%	QAYTQFGGK	99.7%	51.8	25	36.5	3	0	0	999.49	119	127
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	8	12	29	0.03%	29.5%	QDYKEGEMTLK	99.7%	49.7	25	40.7	4	1	0	1341.64	177	187
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	8	12	29	0.03%	29.5%	QKEVEQLIK	99.3%	36.6	25	23.9	1	0	0	1114.65	230	238
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	8	12	29	0.03%	29.5%	TTIFSPEGR	99.4%	37.5	25	29.6	2	0	0	1007.52	9	17
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	8	12	29	0.03%	29.5%	VEIATLTR	99.7%	64.1	25	40.6	2	0	0	902.53	211	218
Proteasome subunit alpha type-5	PSMA5	PSA5_HUMAN	26.4	100.0%	4	6	12	0.01%	22.4%	AIGSASEGAQSSLQEVYHK	99.7%	81	25	81	2	2	0	1961.96	169	187
Proteasome subunit alpha type-5	PSMA5	PSA5_HUMAN	26.4	100.0%	4	6	12	0.01%	22.4%	GVNTFSPEGR	99.7%	40.6	25	29.7	2	0	0	1063.52	11	20
Proteasome subunit alpha type-5	PSMA5	PSA5_HUMAN	26.4	100.0%	4	6	12	0.01%	22.4%	ITSPLMEPSSIEK	99.7%	79.4	25	74.3	4	0	0	1431.74	54	66
Proteasome subunit alpha type-5	PSMA5	PSA5_HUMAN	26.4	100.0%	4	6	12	0.01%	22.4%	LFQVEYAIEAIK	99.7%	73.6	25	65.2	2	0	0	1423.78	21	32
Proteasome subunit alpha type-6	PSMA6	PSA6_HUMAN	27.4	99.8%	2	2	3	0.00%	8.9%	AINQGGLTSVAVR	99.7%	82.1	25	73.4	2	0	0	1285.72	31	43
Proteasome subunit alpha type-6	PSMA6	PSA6_HUMAN	27.4	99.8%	2	2	3	0.00%	8.9%	LYQVEYAFK	99.4%	37.2	25	27.5	1	0	0	1160.60	22	30
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	6	7	13	0.01%	28.6%	ALLEVVQSGGK	99.7%	69.4	25	65.1	2	0	0	1100.63	194	204
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	6	7	13	0.01%	28.6%	ILNPEEIEK	98.1%	31.9	25	23.3	1	0	0	1084.59	219	227
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	6	7	13	0.01%	28.6%	LTVEDPVTVEYITR	99.7%	90.4	25	85.4	2	0	0	1634.86	96	109
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	6	7	13	0.01%	28.6%	LYQTDPSGTYHAWK	99.7%	41.8	25	34.5	2	0	0	1666.79	144	157
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	6	7	13	0.01%	28.6%	NIELAVMR	99.3%	36.6	25	27.1	4	0	0	961.51	205	212
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	6	7	13	0.01%	28.6%	NYTDEAIETDDLTIK	99.7%	107	25	96.9	2	0	0	1740.82	175	189
Proteasome subunit beta type-5	PSMB5	PSB5_HUMAN	28.5	100.0%	5	6	8	0.01%	22.4%	ATAGAYIASQTVK	99.7%	86.1	25	79.3	2	0	0	1280.68	79	91
Proteasome subunit beta type-5	PSMB5	PSB5_HUMAN	28.5	100.0%	5	6	8	0.01%	22.4%	DAYSGGAVNLYHVR	99.7%	40.3	25	40.3	1	0	0	1521.74	226	239
Proteasome subunit beta type-5	PSMB5	PSB5_HUMAN	28.5	100.0%	5	6	8	0.01%	22.4%	HGVIVAADSR	98.8%	34.1	25	33.4	2	0	0	1024.55	69	78
Proteasome subunit beta type-5	PSMB5	PSB5_HUMAN	28.5	100.0%	5	6	8	0.01%	22.4%	LLANMVYQYK	99.7%	41.9	25	41.9	2	0	0	1242.66	141	150
Proteasome subunit beta type-5	PSMB5	PSB5_HUMAN	28.5	100.0%	5	6	8	0.01%	22.4%	VSSDNVADLHEK	97.3%	30.4	25	26.3	1	0	0	1313.63	246	257
Proteasome subunit beta type-6	PSMB6	PSB6_HUMAN	25.4	100.0%	3	3	5	0.01%	13.0%	LAAIAESGVER	99.7%	66.3	25	50.3	2	0	0	1115.61	210	220
Proteasome subunit beta type-6	PSMB6	PSB6_HUMAN	25.4	100.0%	3	3	5	0.01%	13.0%	QVLLGDQIPK	99.5%	38.3	25	37.8	1	0	0	1110.65	221	230
Proteasome subunit beta type-6	PSMB6	PSB6_HUMAN	25.4	100.0%	3	3	5	0.01%	13.0%	TTTGSYIANR	99.7%	69.3	25	62.2	2	0	0	1083.54	54	63
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	31	0.03%	11.1%	AGEQLAPFLPQLVPR	98.5%	33	25	31.1	2	0	0	1635.92	1112	1126
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	31	0.03%	11.1%	AIACVVTACSAELEK	99.7%	88.9	25	86.2	2	0	0	1621.79	1591	1605
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	31	0.03%	11.1%	AQGAIAMASIAK	99.7%	48.8	25	40.1	2	0	0	1131.62	1545	1556
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	31	0.03%	11.1%	EGAVLKPELK	98.0%	31.7	25	20.4	1	0	0	1083.64	316	325
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	31	0.03%	11.1%	ESSCLALNDLLR	99.7%	40.8	25	31.8	1	0	0	1390.70	1180	1191
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	31	0.03%	11.1%	IVAISCAADILK	99.7%	75.9	25	68.1	2	0	0	1273.72	1633	1644
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	31	0.03%	11.1%	LCELIR	95.1%	28	25	9.48	1	0	0	803.44	1363	1368
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	31	0.03%	11.1%	LINEYKEDPK	95.1%	28	25	19.5	1	0	0	1248.65	405	414
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	31	0.03%	11.1%	LLLQGLMDSVEAK	99.7%	68	25	63.3	2	0	0	1416.78	880	892
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	31	0.03%	11.1%	LLSMAYSAVGK	99.7%	70.8	25	54.2	3	0	0	1139.61	415	425
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	31	0.03%	11.1%	LSSTQEGVR	99.0%	35	25	15.3	2	0	0	976.51	47	55
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	31	0.03%	11.1%	LYLQELITITQK	99.7%	71.6	25	71.6	2	0	0	1462.85	1523	1534
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	31	0.03%	11.1%	SASPFNLAEKPK	98.1%	32	25	26.8	1	0	0	1288.69	157	168
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	31	0.03%	11.1%	TEALSVIELLLK	99.7%	73.6	25	69.4	2	0	0	1328.80	1785	1796
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	31	0.03%	11.1%	TIAALLPCLLDK	99.7%	47.7	25	39	1	0	0	1327.77	1250	1261
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	31	0.03%	11.1%	TPDGQGLSTYK	99.4%	37	25	36.7	1	0	0	1166.57	1057	1067

Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	31	0.03%	11.1%	VYLGDIPLK	96.3%	29.2	25	28.1	1	0	0	1017.60	305	313
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	31	0.03%	11.1%	YLLLLAAGDPR	99.7%	61.7	25	61.7	4	0	0	1201.69	517	527
Protein arginine N-methyltransferase 1	PRMT1	ANM1_HUMAN	41.5	100.0%	4	4	6	0.01%	13.3%	ATLYVTAIEDR	99.7%	70.5	25	65.7	1	0	0	1251.66	186	196
Protein arginine N-methyltransferase 1	PRMT1	ANM1_HUMAN	41.5	100.0%	4	4	6	0.01%	13.3%	GKVEEVELPVEK	99.7%	48.5	25	46.5	1	0	0	1355.74	134	145
Protein arginine N-methyltransferase 1	PRMT1	ANM1_HUMAN	41.5	100.0%	4	4	6	0.01%	13.3%	QLVTNACLIK	99.5%	38.2	25	27.7	2	0	0	1159.65	234	243
Protein arginine N-methyltransferase 1	PRMT1	ANM1_HUMAN	41.5	100.0%	4	4	6	0.01%	13.3%	VEDLTFTSPFCLQVK	99.5%	38.2	25	38.2	2	0	0	1783.89	252	266
Protein arginine N-methyltransferase 3	PRMT3	ANM3_HUMAN	59.9	99.8%	2	2	4	0.00%	4.7%	AVIPEAVVEVLDPK	99.0%	34.8	25	28.9	2	0	0	1478.85	397	410
Protein arginine N-methyltransferase 3	PRMT3	ANM3_HUMAN	59.9	99.8%	2	2	4	0.00%	4.7%	VVFSTGPQSTK	99.5%	38.3	25	37.3	2	0	0	1150.61	467	477
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	AAILPTSIFLTNK	99.7%	106	25	106	33	0	0	1388.81	228	240
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	AAILPTSIFLTNKK	99.7%	66.8	25	66.8	5	6	0	1516.91	228	241
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	ADIIVSELLGSFADNELSPECLDGAQHFLK	99.7%	73.4	25	66.8	0	1	0	3288.61	429	458
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	DDGVSIPGEYTSFLAPISSSK	99.7%	100	25	97.4	13	0	0	2170.06	459	479
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	DDIIENAPTTHTEEYSGEEK	99.7%	79.6	25	79.6	3	3	0	2278.00	165	184
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	DLNCVPEIADTLGAVAK	99.7%	105	25	101	28	2	0	1785.91	19	35
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	DPEAQFEMPYVVR	99.7%	64.9	25	64.9	6	0	0	1580.74	493	505
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	DPIKYSQYQQAIYK	99.7%	73	25	71.2	2	2	0	1744.89	330	343
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	DPMIDNNR	99.7%	43	25	34.1	9	0	0	974.44	527	534
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	DRDPEAQFEMPYVVR	99.7%	70.6	25	69.3	3	5	0	1851.87	491	505
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	DTNVQVLMVLGAGR	99.7%	117	25	106	6	0	0	1472.79	355	368
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	DWNTLIVGK	99.7%	60.4	25	43.6	16	0	0	1045.57	77	85
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	EFCSYLQYLEYLSQNRPPPNAYELFAK	99.6%	30.8	25	30.8	0	1	0	3340.60	276	302
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	EFIQEPAK	99.7%	43.1	25	21.9	17	0	0	961.50	53	60
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	EGQTICVR	99.7%	42.8	25	36.4	24	0	0	962.47	594	601
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	EWVAPEK	99.0%	34.6	25	27.2	1	0	0	858.44	422	428
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	GPLVNASLR	99.7%	71	25	60.8	12	0	0	926.54	369	377
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	GYEDYLQSPLQPLMDNLESQTYEVFEKDPIK	99.7%	70.2	25	70.2	0	4	0	3705.75	303	333
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	IAVALEIGADLPSNHVIDR	99.7%	79.1	25	79.1	7	7	0	2003.09	202	220
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	IKLYAVEK	99.6%	40	25	21.9	6	0	0	963.59	386	393
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	KGFPVLSK	99.7%	55.5	25	31.4	14	0	0	875.54	241	248
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	KVWYEWAVTAPVCSAIHNPTGR	99.7%	69.6	25	69.6	0	2	0	2542.27	610	631
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	LSPWIRPDSK	98.8%	33.9	25	31.1	2	0	0	1198.66	86	95
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	QGFDFLCMPVFHPR	99.7%	62.9	25	62.9	12	19	0	1750.82	36	49
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	REFIQEPAK	99.7%	42.3	25	27.7	2	0	0	1117.60	52	60
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	SDLLLSGR	99.7%	46.8	25	36	6	0	0	860.48	69	76
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	SDLLLSGRDWNTLIVGK	99.7%	84	25	84	8	5	0	1887.03	69	85
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	TLCDYSKR	99.7%	55	25	38.1	5	0	0	1042.50	194	201
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	TWMWWHNFR	99.7%	48.7	25	38.4	10	6	0	1379.61	185	193
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	VPEEEKDTNVQVLMVLGAGR	99.7%	112	25	112	4	8	0	2184.13	349	368
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	VPLVAPEDLR	99.7%	54.4	25	53.1	16	0	0	1108.64	155	164
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	VPLVAPEDLRDDIIENAPTTHTEEYSGEEK	99.7%	94.4	25	94.4	0	2	0	3367.62	155	184
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	VWYEWAVTAPVCSAIHNPTGR	99.7%	74.9	25	74.9	2	2	0	2414.17	611	631
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	WLGEPIK	99.1%	35.4	25	22.5	3	0	0	842.48	221	227
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	35	57	369	0.37%	59.2%	YSQYQQAIYK	99.7%	68.5	25	68.5	19	0	0	1291.63	334	343
Protein CIP2A	KIAA1524	CIP2A_HUMAN	102.2	100.0%	5	5	7	0.01%	6.3%	ALALAQADR	99.7%	55.9	25	46.4	2	0	0	928.52	648	656
Protein CIP2A	KIAA1524	CIP2A_HUMAN	102.2	100.0%	5	5	7	0.01%	6.3%	DGVPGLNIEELIEK	98.7%	33.8	25	26.4	1	0	0	1525.81	590	603
Protein CIP2A	KIAA1524	CIP2A_HUMAN	102.2	100.0%	5	5	7	0.01%	6.3%	LITPLAFALTSDNR	99.7%	96.7	25	96.7	2	0	0	1531.85	509	522
Protein CIP2A	KIAA1524	CIP2A_HUMAN	102.2	100.0%	5	5	7	0.01%	6.3%	SEANATQLLR	99.7%	56.1	25	37.5	1	0	0	1102.59	22	31
Protein CIP2A	KIAA1524	CIP2A_HUMAN	102.2	100.0%	5	5	7	0.01%	6.3%	SLLLTVSQYK	99.7%	59.8	25	59.8	1	0	0	1151.67	9	18
Protein CMSS1	CMSS1	CMS1_HUMAN	31.9	100.0%	5	5	10	0.01%	15.8%	ANDLTHSLSSYLK	99.7%	67	25	62.3	2	0	0	1448.74	125	137
Protein CMSS1	CMSS1	CMS1_HUMAN	31.9	100.0%	5	5	10	0.01%	15.8%	FLVFDWNWR	99.7%	41.4	25	38	2	0	0	1282.64	232	240
Protein CMSS1	CMSS1	CMS1_HUMAN	31.9	100.0%	5	5	10	0.01%	15.8%	QGGLNLSPLK	99.7%	54.7	25	40.2	2	0	0	1026.59	222	231

Protein CMSS1	CMSS1	CMS1_HUMAN	31.9	100.0%	5	5	10	0.01%	15.8%	RVVHLGVGTPGR	99.7%	36	25	36	0	2	0	1247.73	204	215
Protein CMSS1	CMSS1	CMS1_HUMAN	31.9	100.0%	5	5	10	0.01%	15.8%	VVHLGVGTPGR	99.7%	63.5	25	60.2	2	0	0	1091.63	205	215
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	4	5	7	0.01%	8.8%	LLASANLEEVTMK	99.7%	104	25	96.9	2	0	0	1418.76	332	344
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	4	5	7	0.01%	8.8%	SGVNSELVK	99.7%	40.8	25	22.2	1	0	0	932.50	169	177
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	4	5	7	0.01%	8.8%	SGVNSELVKR	99.7%	87.6	25	76	2	0	0	1088.61	169	178
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	4	5	7	0.01%	8.8%	SICEVLDLER	99.7%	58.2	25	48.2	2	0	0	1233.61	159	168
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	4	4	7	0.01%	3.4%	DMPLLSCLESLR	98.6%	33.2	25	31.6	1	0	0	1433.71	158	169
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	4	4	7	0.01%	3.4%	ELGEYFLFDPK	99.7%	40.9	25	40.9	3	0	0	1357.67	1117	1127
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	4	4	7	0.01%	3.4%	LNAILFK	94.9%	27.8	25	14	1	0	0	818.51	937	943
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	4	4	7	0.01%	3.4%	TAQNLSIFLGSFR	99.7%	83.8	25	83.8	2	0	0	1453.78	856	868
Protein diaphanous homolog 3	DIAPH3	DIAP3_HUMAN	136.9	100.0%	4	4	4	0.00%	3.8%	FFCIVEGLR	99.7%	45.2	25	39	1	0	0	1140.59	323	331
Protein diaphanous homolog 3	DIAPH3	DIAP3_HUMAN	136.9	100.0%	4	4	4	0.00%	3.8%	INELQAELQAFK	99.7%	84.2	25	72.3	1	0	0	1403.75	537	548
Protein diaphanous homolog 3	DIAPH3	DIAP3_HUMAN	136.9	100.0%	4	4	4	0.00%	3.8%	LAESMIQNLIK	99.7%	48.2	25	41	1	0	0	1259.70	749	759
Protein diaphanous homolog 3	DIAPH3	DIAP3_HUMAN	136.9	100.0%	4	4	4	0.00%	3.8%	NESVPEVEALLAR	99.7%	55.7	25	51.2	1	0	0	1426.75	1177	1189
Protein disulfide-isomerase A6	PDIA6	PDIA6_HUMAN	48.1	100.0%	3	3	4	0.00%	8.6%	GESPVDYDGGR	99.7%	59.7	25	50.9	1	0	0	1151.50	246	256
Protein disulfide-isomerase A6	PDIA6	PDIA6_HUMAN	48.1	100.0%	3	3	4	0.00%	8.6%	GSFSEQGINEFLR	99.7%	66.3	25	50.5	1	0	0	1483.72	374	386
Protein disulfide-isomerase A6	PDIA6	PDIA6_HUMAN	48.1	100.0%	3	3	4	0.00%	8.6%	TGEAIVDAALSALR	99.7%	87.1	25	82.5	2	0	0	1386.76	119	132
Protein DJ-1	PARK7	PARK7_HUMAN	19.9	100.0%	3	4	7	0.01%	24.3%	DVVICPDASLEDAKK	99.5%	38.5	25	38.5	1	0	0	1659.83	49	63
Protein DJ-1	PARK7	PARK7_HUMAN	19.9	100.0%	3	4	7	0.01%	24.3%	GAEEMETVIPVDVMR	99.7%	65.1	25	56	2	0	0	1675.80	13	27
Protein DJ-1	PARK7	PARK7_HUMAN	19.9	100.0%	3	4	7	0.01%	24.3%	VTVAGLAGKDPVQCSR	99.7%	64.7	25	64.7	2	2	0	1657.87	33	48
Protein FAM127A	FAM127A	F127A_HUMAN	13.2	99.8%	2	2	3	0.00%	14.2%	ESPLLNDYR	99.5%	38.5	25	38.5	2	0	0	1106.55	87	95
Protein FAM127A	FAM127A	F127A_HUMAN	13.2	99.8%	2	2	3	0.00%	14.2%	VTFLITR	99.6%	39.2	25	32.5	1	0	0	849.52	65	71
Protein FAM207A	FAM207A	F207A_HUMAN	25.5	99.8%	2	2	4	0.00%	11.3%	DALPELLGLEAGSR	99.7%	41.1	25	41.1	2	0	0	1440.77	149	162
Protein FAM207A	FAM207A	F207A_HUMAN	25.5	99.8%	2	2	4	0.00%	11.3%	DWAFINTNIFAR	99.7%	58.6	25	54.7	2	0	0	1467.74	44	55
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	8	8	21	0.02%	7.1%	ADLTALFLPR	99.7%	63.7	25	54.7	4	0	0	1116.64	875	884
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	8	8	21	0.02%	7.1%	AVQGAQQPSLYQIR	99.7%	68.9	25	61.2	4	0	0	1558.83	1047	1060
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	8	8	21	0.02%	7.1%	GAQATLSSTTK	99.7%	41.6	25	40.4	2	0	0	1064.56	661	671
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	8	8	21	0.02%	7.1%	GLDIYVWR	99.0%	35	25	26.5	1	0	0	1021.55	653	660
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	8	8	21	0.02%	7.1%	GVDLSGNDFK	95.7%	28.5	25	28.1	2	0	0	1051.51	12	21
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	8	8	21	0.02%	7.1%	LLQSLLDTR	99.7%	47.2	25	39.9	4	0	0	1058.62	765	773
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	8	8	21	0.02%	7.1%	VGLGLGYLELPQINYK	99.7%	52.8	25	52.8	2	0	0	1776.99	731	746
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	8	8	21	0.02%	7.1%	VPECLYTLPSLR	99.7%	55	25	53.7	2	0	0	1447.76	238	249
Protein FRG1	FRG1	FRG1_HUMAN	29.2	99.8%	2	2	3	0.00%	8.5%	CNEAGDIEAK	98.0%	31.7	25	21.4	1	0	0	1106.48	159	168
Protein FRG1	FRG1	FRG1_HUMAN	29.2	99.8%	2	2	3	0.00%	8.5%	MALLASNSCFIR	99.7%	53.8	25	46.8	2	0	0	1382.69	147	158
Protein jagunal homolog 1	JAGN1	JAGN1_HUMAN	21.1	100.0%	3	3	7	0.01%	16.9%	AAGTDGSDFQHR	99.7%	69.8	25	69.8	3	0	0	1261.56	9	20
Protein jagunal homolog 1	JAGN1	JAGN1_HUMAN	21.1	100.0%	3	3	7	0.01%	16.9%	LLDSWFTSTQEK	99.7%	64.4	25	64.4	2	0	0	1454.72	169	180
Protein jagunal homolog 1	JAGN1	JAGN1_HUMAN	21.1	100.0%	3	3	7	0.01%	16.9%	MSVGHLR	98.2%	32.2	25	21.5	2	0	0	799.42	55	61
Protein KRI1 homolog	KRI1	KRI1_HUMAN	82.6	100.0%	3	3	3	0.00%	5.3%	LLGPTVMLGGCEFSR	99.7%	48.9	25	48.9	1	0	0	1636.82	657	671
Protein KRI1 homolog	KRI1	KRI1_HUMAN	82.6	100.0%	3	3	3	0.00%	5.3%	LQETSSQSYVEEQK	99.7%	41.3	25	41.3	1	0	0	1655.78	145	158
Protein KRI1 homolog	KRI1	KRI1_HUMAN	82.6	100.0%	3	3	3	0.00%	5.3%	VNAAFAAR	99.5%	37.9	25	32.4	1	0	0	819.45	12	19
Protein KTI12 homolog	KTI12	KTI12_HUMAN	38.6	100.0%	3	3	4	0.00%	7.9%	FEAPDSR	98.8%	34.1	25	28.7	1	0	0	821.38	216	222
Protein KTI12 homolog	KTI12	KTI12_HUMAN	38.6	100.0%	3	3	4	0.00%	7.9%	PLVVFCGLPYSGK	99.7%	50.4	25	47.4	2	0	0	1436.76	2	14
Protein KTI12 homolog	KTI12	KTI12_HUMAN	38.6	100.0%	3	3	4	0.00%	7.9%	YELYCLAR	98.9%	34.5	25	31.5	1	0	0	1087.52	89	96
Protein lin-28 homolog B	LIN28B	LN28B_HUMAN	27.1	99.8%	2	2	4	0.00%	9.2%	MGFGFISMINR	99.7%	52.7	25	52.7	2	0	0	1272.62	41	51
Protein lin-28 homolog B	LIN28B	LN28B_HUMAN	27.1	99.8%	2	2	4	0.00%	9.2%	NVAQPPASSQGR	98.6%	33.2	25	33.2	2	0	0	1211.61	168	179
Protein LSM12 homolog	LSM12	LSM12_HUMAN	21.7	99.8%	2	2	3	0.00%	11.3%	EGSALSHVR	99.3%	36.6	25	22.8	1	0	0	955.50	155	163
Protein LSM12 homolog	LSM12	LSM12_HUMAN	21.7	99.8%	2	2	3	0.00%	11.3%	LQGEVVAFDYQSK	99.7%	87.3	25	86.4	2	0	0	1483.74	25	37
Protein mago nashi homolog 2	MAGOHB	MGN2_HUMAN	17.3	99.8%	2	2	4	0.00%	14.2%	IGSLIDVNQSK	99.7%	67.8	25	52.9	2	0	0	1173.65	106	116
Protein mago nashi homolog 2	MAGOHB	MGN2_HUMAN	17.3	99.8%	2	2	4	0.00%	14.2%	VFYYLVQDLK	99.7%	49.5	25	41.4	2	0	0	1287.70	123	132
Protein MON2 homolog	MON2	MON2_HUMAN	190.5	99.7%	2	2	4	0.00%	1.2%	LQLLLLNPLK	99.7%	42.6	25	42.6	3	0	0	1164.77	862	871
Protein MON2 homolog	MON2	MON2_HUMAN	190.5	99.7%	2	2	4	0.00%	1.2%	YLLQPLGDFSR	94.5%	27.5	25	21	1	0	0	1308.69	1132	1142

Protein NipSnap homolog 1	NIPSNAP1	NIPS1_HUMAN	33.3	100.0%	4	5	9	0.01%	16.2%	DAHSTLLSK	99.1%	35.5	25	28	1	0	0	971.52	57	65
Protein NipSnap homolog 1	NIPSNAP1	NIPS1_HUMAN	33.3	100.0%	4	5	9	0.01%	16.2%	FSGGYPALMDCMNK	97.2%	30.2	25	30.2	2	0	0	1590.68	128	141
Protein NipSnap homolog 1	NIPSNAP1	NIPS1_HUMAN	33.3	100.0%	4	5	9	0.01%	16.2%	GWDENVYYTVPLVR	99.7%	58.7	25	57.4	2	0	0	1710.85	255	268
Protein NipSnap homolog 1	NIPSNAP1	NIPS1_HUMAN	33.3	100.0%	4	5	9	0.01%	16.2%	MGPNIYELR	99.7%	56.6	25	43	4	0	0	1092.55	180	188
Protein NipSnap homolog 2	GBAS	NIPS2_HUMAN	33.7	100.0%	3	3	6	0.01%	10.8%	ICQEVLPK	99.5%	38.1	25	19.5	2	0	0	986.53	92	99
Protein NipSnap homolog 2	GBAS	NIPS2_HUMAN	33.7	100.0%	3	3	6	0.01%	10.8%	SGPNIYELR	99.7%	73	25	62.6	2	0	0	1048.54	182	190
Protein NipSnap homolog 2	GBAS	NIPS2_HUMAN	33.7	100.0%	3	3	6	0.01%	10.8%	YEGGYPALTEVMNK	99.7%	47	25	47	2	0	0	1587.74	130	143
Protein odr-4 homolog	ODR4	ODR4_HUMAN	51.1	100.0%	4	4	7	0.01%	10.6%	AFVSGLLIGQCSSQK	99.7%	55.4	25	50.6	2	0	0	1594.83	24	38
Protein odr-4 homolog	ODR4	ODR4_HUMAN	51.1	100.0%	4	4	7	0.01%	10.6%	DYVILATR	99.7%	41.5	25	35.4	2	0	0	950.53	39	46
Protein odr-4 homolog	ODR4	ODR4_HUMAN	51.1	100.0%	4	4	7	0.01%	10.6%	GNTQATSHSFDVR	99.7%	57.7	25	56.7	1	0	0	1419.66	243	255
Protein odr-4 homolog	ODR4	ODR4_HUMAN	51.1	100.0%	4	4	7	0.01%	10.6%	VLTQLLLNSDHR	99.7%	63.9	25	58.6	2	0	0	1408.79	256	267
Protein pelota homolog	PELO	PELO_HUMAN	43.4	100.0%	5	6	9	0.01%	12.7%	FYEQVVQAIQR	99.7%	57.4	25	49.5	2	0	0	1380.73	185	195
Protein pelota homolog	PELO	PELO_HUMAN	43.4	100.0%	5	6	9	0.01%	12.7%	KQWDSVVLER	99.7%	43	25	36.1	1	0	0	1259.67	115	124
Protein pelota homolog	PELO	PELO_HUMAN	43.4	100.0%	5	6	9	0.01%	12.7%	KVQTESSTGSVGSNR	99.7%	105	25	96.6	2	1	0	1536.76	46	60
Protein pelota homolog	PELO	PELO_HUMAN	43.4	100.0%	5	6	9	0.01%	12.7%	LVDSVKENAGTVR	98.1%	31.9	25	26.3	1	0	0	1387.75	332	344
Protein pelota homolog	PELO	PELO_HUMAN	43.4	100.0%	5	6	9	0.01%	12.7%	VQTESSTGSVGSNR	99.7%	77.4	25	71.8	2	0	0	1408.67	47	60
Protein phosphatase 1B	PPM1B	PPM1B_HUMAN	52.6	100.0%	6	8	17	0.02%	14.4%	HIYFINCGDSR	99.6%	38.9	25	38.9	1	0	0	1381.63	143	153
Protein phosphatase 1B	PPM1B	PPM1B_HUMAN	52.6	100.0%	6	8	17	0.02%	14.4%	IQNAGGSVMIQR	99.7%	78.7	25	63.3	5	0	0	1273.67	180	191
Protein phosphatase 1B	PPM1B	PPM1B_HUMAN	52.6	100.0%	6	8	17	0.02%	14.4%	NVIEAVYSR	99.7%	55.6	25	51.3	4	0	0	1050.56	361	369
Protein phosphatase 1B	PPM1B	PPM1B_HUMAN	52.6	100.0%	6	8	17	0.02%	14.4%	QLLEEMLTSYR	99.6%	39.6	25	34.8	2	0	0	1382.70	409	419
Protein phosphatase 1B	PPM1B	PPM1B_HUMAN	52.6	100.0%	6	8	17	0.02%	14.4%	SGSALELSVENVK	99.7%	78.3	25	71.2	1	0	0	1332.70	91	103
Protein phosphatase 1B	PPM1B	PPM1B_HUMAN	52.6	100.0%	6	8	17	0.02%	14.4%	SGSTAVGVMISPK	99.7%	46	25	43	4	0	0	1249.65	130	142
Protein phosphatase 1F	PPM1F	PPM1F_HUMAN	49.8	99.8%	2	2	3	0.00%	6.8%	HVSLPSFNQLFGLSDPVNR	99.1%	28	25	28	0	1	0	2127.10	173	191
Protein phosphatase 1F	PPM1F	PPM1F_HUMAN	49.8	99.8%	2	2	3	0.00%	6.8%	YAAVHVHTNAAR	99.7%	32.6	25	31.2	0	2	0	1309.68	208	219
Protein RCC2	RCC2	RCC2_HUMAN	56.1	99.8%	2	2	3	0.00%	5.8%	AGGAAVVITEPEHTKER	99.7%	43.9	25	43.9	0	2	0	1764.92	78	94
Protein RCC2	RCC2	RCC2_HUMAN	56.1	99.8%	2	2	3	0.00%	5.8%	LGHAEQKDEMVPR	99.5%	30.2	25	29.4	0	1	0	1525.74	362	374
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	8	8	13	0.01%	5.0%	AIFENTLSTYPK	99.7%	46.3	25	46	2	0	0	1383.72	1782	1793
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	8	8	13	0.01%	5.0%	FAQLEFQLGDAER	99.7%	40.2	25	40	1	0	0	1523.75	1767	1779
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	8	8	13	0.01%	5.0%	IPLLLTSLSFK	99.7%	50.1	25	50.1	3	0	0	1231.77	1178	1188
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	8	8	13	0.01%	5.0%	LGPSVVGLAR	99.7%	64.2	25	53.2	2	0	0	968.59	1343	1352
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	8	8	13	0.01%	5.0%	LKDGVLAYAR	97.4%	30.6	25	22.4	1	0	0	1105.64	386	395
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	8	8	13	0.01%	5.0%	TTEPGVTGLLLAVEGPAAK	99.7%	82.7	25	81.5	2	0	0	1824.01	982	1000
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	8	8	13	0.01%	5.0%	VLCLSQSEGR	95.4%	28.2	25	20.9	1	0	0	1148.57	692	701
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	8	8	13	0.01%	5.0%	VLLCDPEAK	99.7%	40.2	25	34.7	1	0	0	1044.54	507	515
Protein S100-A8	S100A8	S10A8_HUMAN	10.8	100.0%	3	3	8	0.01%	46.2%	ALNSIIDVYHK	99.7%	47.5	25	40.9	2	0	0	1272.69	8	18
Protein S100-A8	S100A8	S10A8_HUMAN	10.8	100.0%	3	3	8	0.01%	46.2%	ELDINTDGAVNFQEFLILVIK	99.7%	66.6	25	66.6	3	0	0	2391.28	57	77
Protein S100-A8	S100A8	S10A8_HUMAN	10.8	100.0%	3	3	8	0.01%	46.2%	LLETECPQYIR	99.7%	61.6	25	53.3	3	0	0	1421.71	37	47
Protein SAAL1	SAAL1	SAAL1_HUMAN	53.6	100.0%	4	4	8	0.01%	9.7%	KPENSAESNTEETKR	99.7%	59.1	25	59.1	0	3	0	1719.81	369	383
Protein SAAL1	SAAL1	SAAL1_HUMAN	53.6	100.0%	4	4	8	0.01%	9.7%	LVPCILEAAK	97.9%	31.5	25	26	1	0	0	1113.63	245	254
Protein SAAL1	SAAL1	SAAL1_HUMAN	53.6	100.0%	4	4	8	0.01%	9.7%	VDLPLIDSLIR	99.7%	61.6	25	58.1	2	0	0	1253.75	348	358
Protein SAAL1	SAAL1	SAAL1_HUMAN	53.6	100.0%	4	4	8	0.01%	9.7%	VLQNMEQCQK	99.7%	50	25	39.7	2	0	0	1277.60	359	368
Protein SCO2 homolog, mitochondrial	SCO2	SCO2_HUMAN	29.8	100.0%	3	3	5	0.01%	14.3%	QGPAETGGQGQPQGPGLR	97.5%	30.8	25	30.8	2	0	0	1734.85	41	58
Protein SCO2 homolog, mitochondrial	SCO2	SCO2_HUMAN	29.8	100.0%	3	3	5	0.01%	14.3%	QVAQASHSYR	99.4%	37.4	25	35.6	1	0	0	1146.56	197	206
Protein SCO2 homolog, mitochondrial	SCO2	SCO2_HUMAN	29.8	100.0%	3	3	5	0.01%	14.3%	SAEQISDSVR	99.7%	61.3	25	34.4	2	0	0	1091.53	246	255
Protein SEC13 homolog	SEC13	SEC13_HUMAN	35.5	100.0%	3	3	5	0.01%	12.1%	FASGGCDNLIK	99.7%	47	25	36.5	2	0	0	1181.56	182	192
Protein SEC13 homolog	SEC13	SEC13_HUMAN	35.5	100.0%	3	3	5	0.01%	12.1%	NGGQILIADLR	99.7%	63.9	25	48.1	2	0	0	1169.66	44	54
Protein SEC13 homolog	SEC13	SEC13_HUMAN	35.5	100.0%	3	3	5	0.01%	12.1%	VFIWTCDDASSNTWSPK	99.7%	67.7	25	67.7	1	0	0	2013.90	240	256
Protein SET	SET	SET_HUMAN	33.5	100.0%	4	4	7	0.01%	16.6%	EFHLNESGDPSSK	99.7%	44.7	25	43.3	2	0	0	1446.65	155	167
Protein SET	SET	SET_HUMAN	33.5	100.0%	4	4	7	0.01%	16.6%	IDFYFDENPYFENK	99.7%	55.5	25	55.5	2	0	0	1840.81	137	150
Protein SET	SET	SET_HUMAN	33.5	100.0%	4	4	7	0.01%	16.6%	LNEQASEEILK	99.6%	39.4	25	23.2	1	0	0	1273.66	58	68
Protein SET	SET	SET_HUMAN	33.5	100.0%	4	4	7	0.01%	16.6%	VEVTEFEDIK	99.7%	73	25	65.9	2	0	0	1208.60	123	132

Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	6	7	12	0.01%	10.6%	DVLLDVAYAYGK	99.7%	86	25	81.7	2	0	0	1326.69	293	304
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	6	7	12	0.01%	10.6%	ELQSVEQEVR	99.7%	57.6	25	42.6	1	0	0	1216.62	164	173
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	6	7	12	0.01%	10.6%	LLGSLYALGIPK	99.7%	67.4	25	67.4	2	0	0	1244.76	149	160
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	6	7	12	0.01%	10.6%	LSFHQTQVSQR	99.7%	60.9	25	50.8	2	0	0	1330.69	305	315
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	6	7	12	0.01%	10.6%	LSHLLSEKPEDK	99.7%	46.5	25	41.5	1	0	0	1395.75	107	118
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	6	7	12	0.01%	10.6%	VLVMLAAQSR	99.7%	83.4	25	82.1	4	0	0	1087.63	261	270
Protein TFG	TFG	TFG_HUMAN	43.4	99.8%	2	2	3	0.00%	4.8%	AQLGEDIRR	95.9%	28.7	25	22.9	1	0	0	1057.58	15	23
Protein TFG	TFG	TFG_HUMAN	43.4	99.8%	2	2	3	0.00%	4.8%	LLSNDEVTIK	99.3%	36.4	25	22.4	2	0	0	1131.63	48	57
Protein transport protein Sec23A	SEC23A	SC23A_HUMAN	86.2	100.0%	3	3	4	0.00%	4.6%	AVLNPLCQVDYR	99.2%	35.9	25	32.2	2	0	0	1447.74	68	79
Protein transport protein Sec23A	SEC23A	SC23A_HUMAN	86.2	100.0%	3	3	4	0.00%	4.6%	FSWNVWPSSR	97.4%	30.6	25	22	1	0	0	1265.61	19	28
Protein transport protein Sec23A	SEC23A	SC23A_HUMAN	86.2	100.0%	3	3	4	0.00%	4.6%	MVVPVAALFTPLK	99.7%	70.4	25	70.4	1	0	0	1385.82	34	46
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	6	15	0.02%	10.9%	AFSPTTVNTGR	99.7%	58.2	25	41.8	4	0	0	1150.59	195	205
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	6	15	0.02%	10.9%	ETSMVHELNR	98.5%	33	25	18.6	1	0	0	1231.57	406	415
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	6	15	0.02%	10.9%	GQYNTYPIK	99.7%	52.6	25	36.6	4	0	0	1083.55	274	282
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	6	15	0.02%	10.9%	IIEVGDTPK	99.7%	52.3	25	41.8	4	0	0	971.54	99	107
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	6	15	0.02%	10.9%	IIEVGDTPKDR	99.3%	36.5	25	23.9	1	0	0	1242.67	99	109
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	6	15	0.02%	10.9%	TWIEVSGSSAK	99.7%	44.9	25	28.2	1	0	0	1164.59	378	388
Protein transport protein Sec61 subunit beta	SEC61B	SC61B_HUMAN	10.0	99.8%	2	3	5	0.01%	21.9%	FYTEDSPGLK	99.2%	35.8	25	29.6	2	0	0	1156.55	58	67
Protein transport protein Sec61 subunit beta	SEC61B	SC61B_HUMAN	10.0	99.8%	2	3	5	0.01%	21.9%	TTSAGTGGMWR	99.7%	50.2	25	38.7	3	0	0	1124.52	47	57
Protein tyrosine phosphatase type IVA 1	PTP4A1	TP4A1_HUMAN	19.8	99.8%	2	2	4	0.00%	12.7%	FLITHNPTNATLNK	99.7%	66.2	25	66.1	2	0	0	1583.85	19	32
Protein tyrosine phosphatase type IVA 1	PTP4A1	TP4A1_HUMAN	19.8	99.8%	2	2	4	0.00%	12.7%	YGVTTIVR	99.7%	47	25	0	2	0	0	908.52	40	47
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	9	9	15	0.02%	11.1%	ALIPLALEGTDVGQTK	99.7%	113	25	113	3	0	0	1625.91	692	707
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	9	9	15	0.02%	11.1%	LDQAVLDLQR	99.7%	60.3	25	44.8	2	0	0	1170.65	108	117
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	9	9	15	0.02%	11.1%	LLVLYSGEDDELLQR	99.7%	83.4	25	65.7	2	0	0	1762.92	822	836
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	9	9	15	0.02%	11.1%	MSASILLSK	98.9%	34.5	25	24.7	1	0	0	965.53	369	377
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	9	9	15	0.02%	11.1%	NIGGQIQEK	97.3%	30.5	25	27.1	1	0	0	986.53	134	142
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	9	9	15	0.02%	11.1%	QFAEGSTLK	97.2%	30.2	25	20	1	0	0	980.50	517	525
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	9	9	15	0.02%	11.1%	TVATLSILGTR	99.7%	76.2	25	69.4	2	0	0	1131.67	230	240
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	9	9	15	0.02%	11.1%	VEQMFQILLDPEEK	99.7%	48.3	25	33.7	2	0	0	1718.87	153	166
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	9	9	15	0.02%	11.1%	VFLALVEEVEDR	99.5%	38.2	25	36.3	1	0	0	1418.75	670	681
Protein virilizer homolog	KIAA1429	VIR_HUMAN	202.0	100.0%	3	3	4	0.00%	2.0%	LLELILLDQTVR	99.7%	83.4	25	83.4	2	0	0	1425.87	534	545
Protein virilizer homolog	KIAA1429	VIR_HUMAN	202.0	100.0%	3	3	4	0.00%	2.0%	VVTAGSAILQK	95.6%	28.4	25	25.1	1	0	0	1086.65	546	556
Protein virilizer homolog	KIAA1429	VIR_HUMAN	202.0	100.0%	3	3	4	0.00%	2.0%	WVTALEEIPSLIIK	97.7%	31.1	25	31.1	1	0	0	1611.94	400	413
Protein YIF1A	YIF1A	YIF1A_HUMAN	32.0	99.8%	2	2	4	0.00%	9.2%	TAALGPDSMGGPVPR	99.7%	68.3	25	59.8	2	0	0	1441.71	251	265
Protein YIF1A	YIF1A	YIF1A_HUMAN	32.0	99.8%	2	2	4	0.00%	9.2%	YFFAVDTAYVAK	99.7%	64.6	25	55.1	2	0	0	1394.70	93	104
Pumilio homolog 1	PUM1	PUM1_HUMAN	126.5	100.0%	4	4	7	0.01%	4.3%	FFEFGSLEQK	99.7%	50.3	25	32	2	0	0	1231.60	905	914
Pumilio homolog 1	PUM1	PUM1_HUMAN	126.5	100.0%	4	4	7	0.01%	4.3%	GNVLVLSQHK	99.7%	43.1	25	37.5	2	0	0	1094.63	1067	1076
Pumilio homolog 1	PUM1	PUM1_HUMAN	126.5	100.0%	4	4	7	0.01%	4.3%	SASSASSLFSPSSTLFSSSR	99.7%	48.6	25	47.6	2	0	0	1992.95	797	816
Pumilio homolog 1	PUM1	PUM1_HUMAN	126.5	100.0%	4	4	7	0.01%	4.3%	YISAAPGAEAK	98.1%	31.9	25	28.4	1	0	0	1077.56	784	794
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	AFFESHPAPSAER	99.7%	42.4	25	42.4	3	2	0	1445.68	870	882
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	AGIISTVEVLK	99.7%	71.8	25	60.4	4	0	0	1129.68	628	638
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	ATFDISLVVPK	99.7%	72.3	25	61.5	2	0	0	1189.68	198	208
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	DAESIHQYLLQR	99.7%	68.7	25	63.8	2	0	0	1472.75	901	912
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	DVFSPIGER	98.1%	32	25	26.5	1	0	0	1019.52	681	689
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	DYFNVPYPLPK	99.7%	52.6	25	52.6	3	0	0	1352.69	294	304
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	ETALLIDPK	99.7%	51.9	25	41.1	2	0	0	999.57	328	336
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	FALEVAAK	99.7%	47.6	25	31.5	2	0	0	848.49	280	287
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	GMNMYLTK	98.4%	32.7	25	24.5	1	0	0	957.45	460	467
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	HGDGTTLDIMLK	99.7%	51.3	25	51.3	1	0	0	1316.65	754	765
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	IDFVGELNDK	99.7%	62.4	25	38.9	2	0	0	1149.58	146	155
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	IDFVGELNDKMK	99.5%	38.3	25	38.3	2	0	0	1424.71	146	157

Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	ILMDKPEMNVVLK	99.3%	36.8	25	29.9	2	0	0	1529.84	559	571
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	KPYPDDENLVEVK	99.7%	71.7	25	62.6	2	0	0	1545.78	222	234
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	LEAAAQVR	99.5%	38.7	25	25.4	2	0	0	857.48	80	87
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	LGLQNDLFSLAR	99.7%	92.6	25	79.9	4	0	0	1346.74	616	627
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	LNLGTVGFYR	99.7%	66.8	25	54.8	2	0	0	1139.62	581	590
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	LSVEGFAVDK	99.7%	42.2	25	27.6	3	0	0	1064.56	854	863
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	NVKPDQWVK	99.0%	34.9	25	21.1	2	0	0	1113.61	572	580
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	QILSADLR	99.7%	55.1	25	39.5	2	0	0	915.53	737	744
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	SKYTTPSGEVR	95.6%	28.4	25	24.7	1	0	0	1224.62	162	172
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	SPVYLTVLK	99.7%	49.7	25	45.1	2	0	0	1019.61	745	753
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	TIQQCCENILLNAAWLK	99.7%	67.3	25	67.3	2	0	0	2075.04	883	899
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	TQYSSAMLESLLPGIR	99.7%	60.3	25	49.6	4	0	0	1781.91	591	606
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	VALSNMNVIDR	99.7%	76.8	25	67.6	4	0	0	1231.65	211	221
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	VLGATLLPDLIQK	99.7%	90.8	25	90.8	4	0	0	1380.85	782	794
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	VTLSFPSTLQTGTGTLK	99.7%	72.2	25	72.2	2	0	0	1750.96	129	145
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	YAAVTQFEATDAR	99.7%	107	25	107	2	0	0	1442.69	173	185
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	YAAVTQFEATDARR	98.2%	25.3	25	16.6	0	1	0	1598.79	173	186
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	70	0.07%	34.4%	YQGGFLISR	99.7%	70.9	25	61.9	2	0	0	1040.55	842	850
Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial	CLPP	CLPP_HUMAN	30.2	100.0%	3	4	8	0.01%	12.3%	AYDIYSR	99.7%	42.2	25	24.5	2	0	0	887.43	72	78
Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial	CLPP	CLPP_HUMAN	30.2	100.0%	3	4	8	0.01%	12.3%	GQATDIAIQAEEIMK	99.7%	119	25	116	4	0	0	1617.82	186	200
Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial	CLPP	CLPP_HUMAN	30.2	100.0%	3	4	8	0.01%	12.3%	QSLQVIESAMER	99.7%	73.7	25	73.2	2	0	0	1390.70	215	226
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	AIFQQPPVGVR	99.7%	53.9	25	53.9	2	0	0	1211.69	715	725
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	AIVLAAIFR	99.7%	64.3	25	64.3	4	0	0	973.62	886	894
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	ATISLSDSDLLR	99.7%	79.3	25	75.5	2	0	0	1290.69	1116	1127
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	CNVIITQPR	99.7%	41.7	25	25	2	0	0	1100.59	484	492
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	DPFSSSLQNR	99.7%	54.2	25	48.9	2	0	0	1150.55	909	918
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	DVNTDFLLILLK	99.7%	76.9	25	48.9	3	0	0	1403.81	565	576
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	ENYLEENLLYAPSLR	99.7%	46.5	25	41.8	3	0	0	1823.92	959	973
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	EYLTTLGQR	99.7%	54.2	25	48.7	2	0	0	1080.57	865	873
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	GGALLFCTVGILLR	99.7%	47.4	25	39.4	1	0	0	1489.86	529	542
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	GSSFEMTDDDSAIR	99.7%	50.3	25	50.3	2	0	0	1530.64	224	237
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	GVLMAGLYPNLIQVR	99.7%	47.3	25	32.7	3	0	0	1643.93	1017	1031
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	IPQLLLER	99.7%	52.9	25	39	3	0	0	981.61	467	474
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	ISAVSVAQR	99.7%	64	25	28.5	2	0	0	930.54	494	502
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	LQEALGMHESK	99.7%	59.9	25	46.7	3	0	0	1242.61	688	698
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	LQSDDILPLGK	99.7%	46.3	25	28.7	2	0	0	1198.67	378	388
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	LSQSLLELWR	99.7%	62.5	25	58	2	0	0	1244.70	413	422
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	LVLMSATGDNER	99.7%	63.5	25	60.1	4	0	0	1305.65	587	598
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	MVPFQVPEILR	99.7%	40.3	25	37.6	1	0	0	1328.74	803	813
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	NLLNSVIGR	99.7%	55.7	25	43.4	2	0	0	985.58	55	63
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	NLMQFHTVGTK	99.7%	45.2	25	34.6	3	0	0	1275.65	264	274
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	NVGFQVR	97.5%	30.8	25	22.6	1	0	0	819.45	514	520
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	QAAAAACQLFK	99.6%	39.9	25	33.5	1	0	0	1178.60	112	122
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	RISAVSVAQR	99.7%	49.3	25	11.4	2	0	0	1086.64	493	502
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	SGNILLHK	99.6%	38.9	25	25	1	0	0	881.52	1052	1059
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	SVEVEGYGSK	99.7%	44.4	25	39.6	2	0	0	1054.51	96	105
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	VIQIATSSSTAK	99.7%	71.4	25	64.6	4	0	0	1205.67	252	263
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	27	32	61	0.06%	23.6%	VSCLETVWVSR	99.7%	79.3	25	75	2	0	0	1335.67	763	773
Putative deoxyribose-phosphate aldolase	DERA	DEOC_HUMAN	35.2	100.0%	5	5	11	0.01%	19.8%	ETVNATFPVAIVMLR	99.7%	56.7	25	51.4	2	0	0	1660.91	224	238
Putative deoxyribose-phosphate aldolase	DERA	DEOC_HUMAN	35.2	100.0%	5	5	11	0.01%	19.8%	EWQAAWLLK	95.8%	28.6	25	22.1	1	0	0	1144.62	41	49
Putative deoxyribose-phosphate aldolase	DERA	DEOC_HUMAN	35.2	100.0%	5	5	11	0.01%	19.8%	GTELDLSWISK	99.7%	48.2	25	35.5	2	0	0	1248.65	7	17

Putative deoxyribose-phosphate aldolase	DERA	DEOC_HUMAN	35.2	100.0%	5	5	11	0.01%	19.8%	IGASTLLSDIER	99.7%	75.5	25	66.8	4	0	0	1274.70	288	299
Putative deoxyribose-phosphate aldolase	DERA	DEOC_HUMAN	35.2	100.0%	5	5	11	0.01%	19.8%	TILATGELGTLTNVYK	99.7%	99.8	25	99.8	2	0	0	1693.94	189	204
Putative GTP-binding protein 6	GTPBP6	GTPB6_HUMAN	56.9	100.0%	2	2	3	0.00%	4.3%	ALTGDAAIQPR	99.7%	48.2	25	34.5	1	0	0	1112.61	313	323
Putative GTP-binding protein 6	GTPBP6	GTPB6_HUMAN	56.9	100.0%	2	2	3	0.00%	4.3%	DVSHPEAELQK	99.6%	39.9	25	39.9	2	0	0	1252.62	383	393
Putative mitochondrial import inner membrane translocase subunit Tim23B	TIMM23B	TI23B_HUMAN	21.9	100.0%	3	4	6	0.01%	16.0%	ETQNMAWSKPR	99.7%	45.5	25	36	2	0	0	1347.65	102	112
Putative mitochondrial import inner membrane translocase subunit Tim23B	TIMM23B	TI23B_HUMAN	21.9	100.0%	3	4	6	0.01%	16.0%	GAEDDLNTVAAGTMTGMLYK	97.0%	30	25	10.2	1	0	0	2073.95	150	169
Putative mitochondrial import inner membrane translocase subunit Tim23B	TIMM23B	TI23B_HUMAN	21.9	100.0%	3	4	6	0.01%	16.0%	NVQILNMVTR	99.7%	68.7	25	39.4	3	0	0	1187.66	113	122
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	8	11	20	0.02%	18.8%	ALDQSDNDMSAVYR	99.7%	85.5	25	83.4	4	0	0	1584.70	536	549
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	8	11	20	0.02%	18.8%	CDLFIQEGAR	99.7%	58.6	25	46.9	2	0	0	1208.57	303	312
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	8	11	20	0.02%	18.8%	DLTIPESSTVK	98.7%	33.6	25	19	1	0	0	1189.63	180	190
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	8	11	20	0.02%	18.8%	DLVLGPSGVLQGIRPGK	99.7%	67.2	25	67.2	2	1	0	1706.00	339	355
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	8	11	20	0.02%	18.8%	FQQAVDAVEEFLR	99.7%	77.2	25	70.4	2	0	0	1551.78	79	91
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	8	11	20	0.02%	18.8%	GLYEDCSSCFQAMGK	99.7%	80.1	25	80.1	4	0	0	1768.70	408	422
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	8	11	20	0.02%	18.8%	GMMAGPMAAFK	99.5%	38.2	25	20.7	2	0	0	1111.51	191	201
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	8	11	20	0.02%	18.8%	TSFFLGEVGNAAK	99.7%	91.3	25	85.8	2	0	0	1340.68	423	435
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	5	7	22	0.02%	6.5%	FTDILVR	99.7%	41.1	25	26.8	2	0	0	863.50	146	152
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	5	7	22	0.02%	6.5%	RVAAMSVAQR	98.7%	33.6	25	20.8	1	0	0	1088.60	195	204
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	5	7	22	0.02%	6.5%	SNLGSVVLQLK	99.7%	71.9	25	60.6	3	0	0	1157.69	505	515
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	5	7	22	0.02%	6.5%	TLATDILMGVLK	99.7%	97.3	25	82.1	11	0	0	1290.73	266	277
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	5	7	22	0.02%	6.5%	YGVIILDEAHER	99.7%	47.1	25	46	4	1	0	1414.73	254	265
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	29	0.03%	16.7%	DLAQALINR	99.6%	39	25	35.4	2	0	0	1013.57	323	331
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	29	0.03%	16.7%	ELLLSAIDSVNATSK	99.7%	134	25	127	4	0	0	1560.85	493	507
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	29	0.03%	16.7%	GADSELSTVPSVTK	99.2%	36.2	25	7.63	2	0	0	1390.71	656	669
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	29	0.03%	16.7%	GISAGAVQTAGK	99.7%	83.3	25	74.7	4	0	0	1059.58	80	91
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	29	0.03%	16.7%	IQDIVGILR	99.7%	65.8	25	51.6	2	0	0	1026.63	243	251
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	29	0.03%	16.7%	LGVTNTIISHYDGR	96.2%	22.8	25	19.5	0	1	0	1545.80	432	445
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	29	0.03%	16.7%	LVPTGLDFGQEGFTR	99.7%	82.3	25	75.8	4	0	0	1636.83	539	553
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	29	0.03%	16.7%	NTGVILANDANAER	99.7%	108	25	103	1	0	0	1457.73	408	421
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	29	0.03%	16.7%	SPEAKPLPGK	99.2%	35.8	25	30.8	2	0	0	1023.58	67	76
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	29	0.03%	16.7%	SVVGNLHR	99.5%	38.3	25	31.4	4	0	0	881.50	424	431
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	29	0.03%	16.7%	TQASSSFQDSSQPAGK	99.7%	78.8	25	68.4	3	0	0	1625.74	670	685
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	4	4	7	0.01%	4.6%	ISHLSGSGSGDER	99.5%	37.7	25	29.3	2	0	0	1301.61	204	216
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	4	4	7	0.01%	4.6%	QDGGTAPVASASPK	99.7%	44.6	25	35.7	2	0	0	1285.64	770	783
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	4	4	7	0.01%	4.6%	VAFVNFR	95.8%	28.6	25	22.2	1	0	0	852.47	217	223
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	4	4	7	0.01%	4.6%	VGAGAGAAPFR	99.7%	54.4	25	41.5	2	0	0	973.52	349	359
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	2	2	2	0.00%	6.4%	VEQLGAEGNVEESQK	99.7%	56.6	25	55	1	0	0	1616.78	140	154
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	2	2	2	0.00%	6.4%	VHELNEEIGK	99.7%	51.2	25	45.2	1	0	0	1167.60	126	135
Pyridoxal phosphate phosphatase	PDXP	PLPP_HUMAN	31.7	99.8%	2	2	3	0.00%	10.5%	LAGDPSAGDGAAPR	99.7%	71.1	25	60.4	2	0	0	1254.61	129	142
Pyridoxal phosphate phosphatase	PDXP	PLPP_HUMAN	31.7	99.8%	2	2	3	0.00%	10.5%	TPGTGSLAAAVETASGR	99.7%	52.4	25	52.4	1	0	0	1545.79	190	206
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	12	18	46	0.05%	42.6%	CMTNTPVVVR	99.7%	61.6	25	49.8	7	0	0	1192.58	120	129
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	12	18	46	0.05%	42.6%	EGATVYATGTHAQVEDGR	99.7%	64.1	25	61.3	1	4	0	1861.87	130	147
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	12	18	46	0.05%	42.6%	ELQSMADQEQVSPAAIK	99.7%	83.1	25	74.6	1	0	0	1860.90	267	283
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	12	18	46	0.05%	42.6%	ELQSMADQEQVSPAAIKK	99.7%	71.7	25	69.6	3	4	0	1973.00	267	284
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	12	18	46	0.05%	42.6%	GFTAAGVLAAHK	99.7%	66.6	25	58.2	4	0	0	1142.63	18	29
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	12	18	46	0.05%	42.6%	IMASSPDMDLATVSALR	99.7%	91.4	25	91.4	3	0	0	1777.88	30	46
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	12	18	46	0.05%	42.6%	IMASSPDMDLATVSALRK	99.7%	33.2	25	27.4	0	1	0	1937.97	30	47
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	12	18	46	0.05%	42.6%	LDSPAGTALSPSGHTK	99.7%	89.9	25	72.6	3	2	0	1538.78	292	307
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	12	18	46	0.05%	42.6%	LGAQALLGAAK	99.7%	94.4	25	86.4	6	0	0	1012.62	205	215
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	12	18	46	0.05%	42.6%	MLLHSEQHPGQLK	99.7%	33.7	25	33.6	0	4	0	1533.78	216	228
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	12	18	46	0.05%	42.6%	SLLINAVEASCIR	99.7%	93.6	25	86.4	4	0	0	1445.78	252	264
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	12	18	46	0.05%	42.6%	TILDKVK	99.6%	38.8	25	30.7	1	0	0	816.52	285	291

Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	12	18	46	0.05%	42.6%	VKLDSPAGTALSPSGHTK	99.7%	50.6	25	37	0	2	0	1765.94	290	307
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	13	17	36	0.04%	39.1%	ELQSMADQEK	99.7%	47.5	25	31.8	4	0	0	1194.53	267	276
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	13	17	36	0.04%	39.1%	GFTAAGILSAHK	99.7%	75	25	66.1	2	0	0	1172.64	18	29
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	13	17	36	0.04%	39.1%	IIASSPEMNLPTVSALR	99.7%	126	25	118	4	0	0	1798.97	30	46
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	13	17	36	0.04%	39.1%	ISPAALKK	99.7%	49	25	39.9	2	0	0	827.54	277	284
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	13	17	36	0.04%	39.1%	KLMAFQPAPK	99.7%	51.3	25	37.3	2	0	0	1130.64	107	116
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	13	17	36	0.04%	39.1%	LAIQLGAQALLGAAK	99.7%	95.4	25	95.4	2	0	0	1437.88	201	215
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	13	17	36	0.04%	39.1%	LESPTVSTLTPSSPGK	99.7%	50.6	25	37.6	2	0	0	1600.84	292	307
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	13	17	36	0.04%	39.1%	LMAFQPAPK	99.7%	56.2	25	47.9	4	0	0	1002.54	108	116
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	13	17	36	0.04%	39.1%	MGVNLTR	99.7%	43.8	25	12	2	0	0	806.42	48	54
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	13	17	36	0.04%	39.1%	MLLDSEQHPCQLK	99.7%	58.7	25	52.8	2	0	0	1598.77	216	228
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	13	17	36	0.04%	39.1%	SLLINAVEASCIR	99.7%	93.6	25	86.4	4	0	0	1445.78	252	264
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	13	17	36	0.04%	39.1%	TRELQSMADQEK	99.7%	52.5	25	44.2	4	0	0	1451.68	265	276
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	13	17	36	0.04%	39.1%	VKLESPTVSTLTPSSPGK	99.7%	78.7	25	70.9	2	0	0	1828.01	290	307
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	6	10	18	0.02%	24.8%	AATMSAVEAATCR	99.7%	56.4	25	45.7	4	0	0	1338.61	255	267
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	6	10	18	0.02%	24.8%	IAAQTLLGTAK	99.7%	81.6	25	80.9	2	0	0	1086.65	208	218
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	6	10	18	0.02%	24.8%	MAGAIAQGLIR	99.7%	67.4	25	60.9	4	0	0	1116.62	19	29
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	6	10	18	0.02%	24.8%	MGMPSSLAHR	99.7%	45.3	25	34.8	3	0	0	1086.52	198	207
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	6	10	18	0.02%	24.8%	RVGFVGAGR	99.1%	35.2	25	32.6	1	0	0	918.53	10	18
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	6	10	18	0.02%	24.8%	VEAQHILASAPTDR	99.7%	76.8	25	76.8	2	2	0	1507.79	33	46
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	8	8	13	0.01%	9.3%	AEAEAQAEELSFPR	99.7%	117	25	114	2	0	0	1547.73	929	942
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	8	8	13	0.01%	9.3%	DAHQSLLATR	99.7%	55	25	47.5	2	0	0	1111.59	572	581
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	8	8	13	0.01%	9.3%	DFTATFGPLDSLNTR	99.7%	53.8	25	43.8	2	0	0	1654.81	1022	1036
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	8	8	13	0.01%	9.3%	FIGPSPEVVR	97.4%	30.5	25	28.3	1	0	0	1100.61	138	147
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	8	8	13	0.01%	9.3%	GANAVGYTNYPDNVVFK	99.7%	66.5	25	53	2	0	0	1828.89	645	661
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	8	8	13	0.01%	9.3%	QVGYENAGTVEFLVDR	99.7%	52.6	25	47	1	0	0	1796.88	301	316
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	8	8	13	0.01%	9.3%	TSTAPAASPNVR	99.7%	41.8	25	25.3	2	0	0	1171.61	19	30
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	8	8	13	0.01%	9.3%	VVEIAPAAHLDPQLR	95.9%	28.7	25	28.7	1	0	0	1628.91	274	288
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	14	16	44	0.04%	29.5%	AAASTDYYK	99.7%	44	25	44	2	0	0	989.46	236	244
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	14	16	44	0.04%	29.5%	AAASTDYYKR	99.7%	51.2	25	40.5	2	0	0	1145.56	236	245
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	14	16	44	0.04%	29.5%	AHGFTFTR	99.2%	36.1	25	26.3	2	0	0	936.47	120	127
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	14	16	44	0.04%	29.5%	EILAELTGR	99.7%	62.4	25	52	3	0	0	1001.56	133	141
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	14	16	44	0.04%	29.5%	GANQWIK	98.2%	32.1	25	18.6	2	0	0	816.44	379	385
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	14	16	44	0.04%	29.5%	GDFIPGLR	96.5%	29.3	25	16.2	1	0	0	874.48	246	253
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	14	16	44	0.04%	29.5%	GPILMELQTYR	99.7%	67.1	25	67.1	4	0	0	1320.70	278	288
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	14	16	44	0.04%	29.5%	LEEGPPVTTVLTR	99.7%	93.6	25	85.8	5	0	0	1411.78	46	58
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	14	16	44	0.04%	29.5%	LPCIFICENNR	99.7%	60.2	25	57.6	3	0	0	1435.68	216	226
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	14	16	44	0.04%	29.5%	RGDFIPGLR	99.7%	42.2	25	29.5	2	0	0	1030.58	245	253
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	14	16	44	0.04%	29.5%	SKSDPIMLLK	98.1%	32	25	26.2	2	0	0	1147.64	312	321
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	14	16	44	0.04%	29.5%	TREEIQEVR	99.5%	38.5	25	12.6	4	0	0	1159.61	303	311
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	14	16	44	0.04%	29.5%	VDGMDILCVR	99.7%	67.1	25	60.3	4	0	0	1177.57	254	263
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	14	16	44	0.04%	29.5%	YGMGTSVER	99.7%	53.7	25	48.1	8	0	0	999.46	227	235
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	10	14	31	0.03%	34.8%	DAINQGMDEELERDEK	98.6%	33.2	25	33.2	1	0	0	1891.83	37	52
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	10	14	31	0.03%	34.8%	DFLIPIGK	99.7%	51.5	25	31.4	2	0	0	902.53	220	227
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	10	14	31	0.03%	34.8%	DIIFAIKK	98.8%	34	25	22.1	2	0	0	947.59	348	355
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	10	14	31	0.03%	34.8%	EGVECEVINMR	99.7%	58.4	25	56	4	0	0	1335.60	259	269
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	10	14	31	0.03%	34.8%	ILEDNSIPQVK	99.7%	77.2	25	64	2	0	0	1255.69	337	347
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	10	14	31	0.03%	34.8%	IMEGPAFNFLDAPAVR	99.7%	101	25	93.3	5	0	0	1747.88	309	324
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	10	14	31	0.03%	34.8%	TYYMSGGLQPVPIVFR	99.7%	95.8	25	87.1	6	0	0	1827.95	130	145
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	10	14	31	0.03%	34.8%	VFLLGEEVAQYDGAYK	99.7%	117	25	117	3	0	0	1801.90	53	68
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	10	14	31	0.03%	34.8%	VTGADVPMPYAK	99.7%	60.5	25	55.9	4	0	0	1264.62	325	336

Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	10	14	31	0.03%	34.8%	VVSPWNSEDAK	99.7%	44.3	25	24	2	0	0	1231.60	174	184
Pyruvate dehydrogenase protein X component, mitochondrial	PDHX	ODPX_HUMAN	54.1	100.0%	4	4	6	0.01%	8.6%	GIQEIADSVK	99.7%	53	25	45.4	1	0	0	1059.57	385	394
Pyruvate dehydrogenase protein X component, mitochondrial	PDHX	ODPX_HUMAN	54.1	100.0%	4	4	6	0.01%	8.6%	HSLDASQGTATGPR	99.7%	70.3	25	62.4	2	0	0	1397.68	195	208
Pyruvate dehydrogenase protein X component, mitochondrial	PDHX	ODPX_HUMAN	54.1	100.0%	4	4	6	0.01%	8.6%	LTEDEEGNAK	99.1%	35.2	25	13.3	1	0	0	1105.50	451	460
Pyruvate dehydrogenase protein X component, mitochondrial	PDHX	ODPX_HUMAN	54.1	100.0%	4	4	6	0.01%	8.6%	VVDDELATR	99.7%	45.4	25	39.5	2	0	0	1017.52	477	485
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	AEGSDVANAVLDGADCIMLSGETAK	99.7%	83.4	25	78.6	4	1	0	2494.14	343	367
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	AGKPVICATQMLESMIK	99.7%	48.5	25	47.7	0	4	0	1876.97	320	336
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	CCSGAIIVLTK	99.7%	76.1	25	71	4	0	0	1221.63	423	433
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	CDENILWLDYK	99.7%	76	25	72.5	2	0	0	1468.68	152	162
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	DPVQEAWAEDVDLR	99.7%	101	25	98.1	2	0	0	1642.77	476	489
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	EAEAAIYHLQLFEELRR	99.7%	45.3	25	45.3	0	2	0	2088.09	384	400
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	FDEILEASDGIMVAR	99.7%	95.2	25	95.2	2	0	0	1665.82	280	294
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	FGVEQDVDMVFASFIR	99.7%	120	25	120	13	3	0	1859.90	231	246
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	GADFLVTEVENGGSLGSK	99.7%	151	25	149	6	0	0	1779.88	189	206
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	GADFLVTEVENGGSLGSKK	99.2%	28.4	25	21.6	0	1	0	1907.97	189	207
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	GDLGIEIPAEK	99.7%	56.5	25	38.1	15	0	0	1141.61	295	305
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	GDYPLEAVR	99.7%	59.1	25	50.6	17	0	0	1019.52	368	376
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	GIFPVLCK	95.1%	28	25	13.4	1	0	0	933.52	468	475
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	GIFPVLCKDPVQEAWAEDVDLR	99.7%	55.2	25	54.5	0	2	0	2557.28	468	489
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	GSGTAEVELK	99.7%	65.7	25	42.2	4	0	0	990.51	126	135
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	GSGTAEVELKK	99.7%	66.4	25	47.2	17	0	0	1118.61	126	136
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	GVNLPGAAVDLPAVSEK	99.7%	116	25	108	2	0	0	1636.89	208	224
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	ITLDNAYMEK	99.7%	68.7	25	64.4	8	0	0	1197.58	142	151
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	IYVDDGLISLQVK	99.7%	108	25	108	12	0	0	1462.82	174	186
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	LAPITSDPTEATAVGAVEASFK	99.7%	143	25	143	7	4	0	2175.12	401	422
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	LDIDSPPITAR	99.7%	69	25	62.7	17	0	0	1197.65	33	43
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	LNFSHGTHEYHAETIK	99.7%	43.3	25	43.3	0	2	0	1883.90	74	89
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	MQHLIAR	99.7%	41.2	25	28.7	10	0	0	868.48	377	383
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	NTGIICTIGPASR	99.7%	96.1	25	96	15	0	0	1359.71	44	56
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	RFDEILEASDGIMVAR	99.7%	82.2	25	77.7	5	5	0	1821.92	279	294
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	SVETLKEMIK	99.7%	51	25	40.7	6	0	0	1177.65	57	66
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	TATESFASDPILYRPVAVALDTK	99.7%	46.8	25	46.8	1	6	0	2465.29	93	115
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	28	42	211	0.21%	63.3%	VNFAMNVGK	99.7%	62.3	25	52	11	0	0	979.50	490	498
Queuine tRNA-ribosyltransferase subunit QTRTD1	QTRTD1	QTRD1_HUMAN	46.7	100.0%	4	4	6	0.01%	11.1%	GVDLFESFFPYQVTER	99.7%	49.2	25	49.2	1	0	0	1933.93	267	282
Queuine tRNA-ribosyltransferase subunit QTRTD1	QTRTD1	QTRD1_HUMAN	46.7	100.0%	4	4	6	0.01%	11.1%	LQEESEVLQK	99.7%	47.9	25	33.5	2	0	0	1202.63	177	186
Queuine tRNA-ribosyltransferase subunit QTRTD1	QTRTD1	QTRD1_HUMAN	46.7	100.0%	4	4	6	0.01%	11.1%	SLLFLDNCLR	99.7%	41.7	25	32.8	2	0	0	1250.66	167	176
Queuine tRNA-ribosyltransferase subunit QTRTD1	QTRTD1	QTRD1_HUMAN	46.7	100.0%	4	4	6	0.01%	11.1%	SVSVWSVAGR	99.7%	58.5	25	51.1	1	0	0	1047.56	112	121
Rab3 GTPase-activating protein non-catalytic subunit	RAB3GAP2	RBGPR_HUMAN	156.0	100.0%	4	4	5	0.01%	3.2%	VAQFLVIYAPR	99.7%	51	25	51	1	0	0	1276.74	461	471
Rab3 GTPase-activating protein non-catalytic subunit	RAB3GAP2	RBGPR_HUMAN	156.0	100.0%	4	4	5	0.01%	3.2%	VILLDVAR	95.3%	28.1	25	14.1	1	0	0	898.57	408	415
Rab3 GTPase-activating protein non-catalytic subunit	RAB3GAP2	RBGPR_HUMAN	156.0	100.0%	4	4	5	0.01%	3.2%	VSSLQAEPLPR	99.7%	42.2	25	34.6	1	0	0	1196.66	914	924
Rab3 GTPase-activating protein non-catalytic subunit	RAB3GAP2	RBGPR_HUMAN	156.0	100.0%	4	4	5	0.01%	3.2%	VVSAAVQAQHSATK	99.7%	66	25	64.7	2	0	0	1396.75	1220	1233
Rac GTPase-activating protein 1	RACGAP1	RGAP1_HUMAN	71.0	100.0%	3	3	4	0.00%	5.4%	NLFEQLVR	95.4%	28.2	25	16.6	1	0	0	1018.57	10	17
Rac GTPase-activating protein 1	RACGAP1	RGAP1_HUMAN	71.0	100.0%	3	3	4	0.00%	5.4%	SIGSAVDQGNESIVAK	99.7%	52.6	25	47.2	1	0	0	1574.80	203	218
Rac GTPase-activating protein 1	RACGAP1	RGAP1_HUMAN	71.0	100.0%	3	3	4	0.00%	5.4%	TPSSSSLSQR	99.7%	51.2	25	51.2	2	0	0	1049.52	588	597
Ragulator complex protein LAMTOR1	LAMTOR1	LTOR1_HUMAN	17.7	99.8%	2	2	4	0.00%	16.1%	IAAYAYSALSQIR	99.7%	67.7	25	54.9	2	0	0	1426.77	135	147
Ragulator complex protein LAMTOR1	LAMTOR1	LTOR1_HUMAN	17.7	99.8%	2	2	4	0.00%	16.1%	TDEQALLSSILAK	99.7%	90.4	25	84.8	2	0	0	1388.76	48	60
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	17	18	47	0.05%	34.8%	AFNSSSFNSNTFLTR	99.7%	96.7	25	88.9	3	0	0	1692.80	501	515
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	17	18	47	0.05%	34.8%	EIEDFDSLEALR	99.7%	66.6	25	54.9	2	0	0	1436.69	44	55
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	17	18	47	0.05%	34.8%	GAVAIADAIR	99.7%	83.7	25	66.7	4	0	0	956.55	280	289
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	17	18	47	0.05%	34.8%	GAVAMAETLK	99.7%	48.3	25	23.5	4	0	0	990.53	252	261
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	17	18	47	0.05%	34.8%	ILAAALTECHR	99.7%	56	25	50.9	2	0	0	1254.66	161	171

Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	17	18	47	0.05%	34.8%	LENDGATALAEAFR	99.7%	66.1	25	62.4	2	0	0	1477.73	192	205
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	17	18	47	0.05%	34.8%	LLVHMGLLK	98.0%	31.8	25	31.8	2	0	0	1023.64	516	524
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	17	18	47	0.05%	34.8%	LNNCGMGIGGGK	99.7%	50.7	25	50.7	2	0	0	1177.55	149	160
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	17	18	47	0.05%	34.8%	LNTAEDAKDVIK	99.7%	62.9	25	49.5	2	0	0	1316.71	32	43
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	17	18	47	0.05%	34.8%	MAVQDAVDALMQK	99.7%	66.6	25	66.6	4	0	0	1435.69	488	500
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	17	18	47	0.05%	34.8%	QVEVINFGDCLVR	99.7%	78.6	25	78.3	4	0	0	1548.78	265	277
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	17	18	47	0.05%	34.8%	SSACFTLQELK	99.7%	54	25	46.6	2	0	0	1283.63	138	148
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	17	18	47	0.05%	34.8%	SSAQGKPLALK	99.2%	35.8	25	24.5	3	0	0	1099.65	173	183
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	17	18	47	0.05%	34.8%	SSVLIAQQTDTSDPEK	99.7%	127	25	126	2	0	0	1718.84	453	468
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	17	18	47	0.05%	34.8%	TQVAGGQLSFK	99.7%	62.3	25	54.3	4	0	0	1135.61	16	26
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	17	18	47	0.05%	34.8%	VINLNDNTFTEK	99.7%	64.5	25	56.6	3	0	0	1407.71	240	251
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	17	18	47	0.05%	34.8%	VSSVFKDEATVR	99.7%	78.8	25	69.2	2	0	0	1337.71	476	487
Ran-specific GTPase-activating protein	RANBP1	RANG_HUMAN	23.3	100.0%	3	3	5	0.01%	15.4%	FASENDLPEWK	96.6%	29.5	25	24	1	0	0	1335.62	58	68
Ran-specific GTPase-activating protein	RANBP1	RANG_HUMAN	23.3	100.0%	3	3	5	0.01%	15.4%	FLNAENAQK	99.7%	55.6	25	38.1	2	0	0	1034.53	142	150
Ran-specific GTPase-activating protein	RANBP1	RANG_HUMAN	23.3	100.0%	3	3	5	0.01%	15.4%	TLEEDEEELFK	99.7%	80.4	25	74.2	2	0	0	1381.64	40	50
Ras GTPase-activating protein-binding protein 1	G3BP1	G3BP1_HUMAN	52.2	100.0%	3	3	5	0.01%	9.7%	EAGEQGDIEPR	99.7%	75.5	25	70.7	2	0	0	1200.55	321	331
Ras GTPase-activating protein-binding protein 1	G3BP1	G3BP1_HUMAN	52.2	100.0%	3	3	5	0.01%	9.7%	FMQTFVLAPEGSVANK	99.7%	74.8	25	69.8	2	0	0	1738.88	108	123
Ras GTPase-activating protein-binding protein 1	G3BP1	G3BP1_HUMAN	52.2	100.0%	3	3	5	0.01%	9.7%	SSSPAPADIAQTVQEDLR	99.7%	70.2	25	70.2	1	0	0	1884.93	230	247
Ras GTPase-activating protein-binding protein 2	G3BP2	G3BP2_HUMAN	54.1	99.8%	2	3	3	0.00%	5.0%	TEELKPQVEEK	99.7%	42.7	25	20.7	1	0	0	1329.69	206	216
Ras GTPase-activating protein-binding protein 2	G3BP2	G3BP2_HUMAN	54.1	99.8%	2	3	3	0.00%	5.0%	VEAKPEVQSQPPR	98.7%	26.6	25	26.6	1	1	0	1464.78	278	290
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	15	15	24	0.02%	10.6%	ALESGDVNTVWK	97.5%	30.7	25	25.8	1	0	0	1318.66	466	477
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	15	15	24	0.02%	10.6%	ALQSPALGLR	99.7%	40.6	25	29.5	2	0	0	1025.61	327	336
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	15	15	24	0.02%	10.6%	ATFYGEQVDYYK	99.7%	50.4	25	49.5	1	0	0	1483.67	1517	1528
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	15	15	24	0.02%	10.6%	ATGLHFR	96.6%	29.5	25	13.3	1	0	0	801.44	105	111
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	15	15	24	0.02%	10.6%	EEIQSSISGVTAAYNR	99.7%	75	25	75	1	0	0	1724.84	723	738
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	15	15	24	0.02%	10.6%	GVLLEIEDLQVNQFK	99.0%	35.1	25	35.1	1	0	0	1744.95	1572	1586
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	15	15	24	0.02%	10.6%	ILAIGLINEALDEGDAQK	99.7%	88.4	25	88.1	4	0	0	1883.01	539	556
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	15	15	24	0.02%	10.6%	ITLQDVVSHSK	99.4%	37.4	25	33.4	1	0	0	1226.67	925	935
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	15	15	24	0.02%	10.6%	LAAVALINAAIQK	99.7%	76.4	25	56.9	4	0	0	1295.80	389	401
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	15	15	24	0.02%	10.6%	LIFQMPQNK	97.1%	30.1	25	16.8	1	0	0	1118.60	989	997
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	15	15	24	0.02%	10.6%	LIVDVIR	95.5%	28.3	25	0	1	0	0	827.54	1391	1397
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	15	15	24	0.02%	10.6%	LQQTYAALNSK	99.7%	60.1	25	50.2	2	0	0	1236.66	1506	1516
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	15	15	24	0.02%	10.6%	TLINAEDPPMVVVR	99.7%	68.1	25	68.1	1	0	0	1553.84	857	870
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	15	15	24	0.02%	10.6%	TLQALQIPAAK	99.7%	57	25	50.6	2	0	0	1153.69	557	567
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	15	15	24	0.02%	10.6%	YGIQMPAFSK	97.7%	31.1	25	20.4	1	0	0	1141.57	192	201
Ras suppressor protein 1	RSU1	RSU1_HUMAN	31.5	99.9%	2	2	3	0.00%	8.7%	LQILSLR	94.5%	27.5	25	18.5	1	0	0	842.55	159	165
Ras suppressor protein 1	RSU1	RSU1_HUMAN	31.5	99.9%	2	2	3	0.00%	8.7%	LTVLPPELGNLDLTGQK	98.2%	32.2	25	32.2	2	0	0	1808.02	192	208
Ras-related protein Rab-10	RAB10	RAB10_HUMAN	22.5	100.0%	4	4	5	0.01%	25.5%	AFLTLAEDILR	99.7%	61.4	25	51.7	1	0	0	1261.72	162	172
Ras-related protein Rab-10	RAB10	RAB10_HUMAN	22.5	100.0%	4	4	5	0.01%	25.5%	ANINIEK	99.7%	41.6	25	23	1	0	0	801.45	155	161
Ras-related protein Rab-10	RAB10	RAB10_HUMAN	22.5	100.0%	4	4	5	0.01%	25.5%	FHTITTSYYR	99.2%	35.8	25	27.4	1	0	0	1288.63	71	80
Ras-related protein Rab-10	RAB10	RAB10_HUMAN	22.5	100.0%	4	4	5	0.01%	25.5%	LQIWDTAGQER	99.7%	61.2	25	0	6	0	0	1316.66	60	70
Ras-related protein Rab-10	RAB10	RAB10_HUMAN	22.5	100.0%	4	4	5	0.01%	25.5%	NIDEHANEDVER	99.7%	47.3	25	47.3	2	0	0	1440.64	106	117
Ras-related protein Rab-13	RAB13	RAB13_HUMAN	22.8	100.0%	3	4	6	0.01%	16.7%	SIKENASAGVER	99.7%	55.3	25	38.3	2	0	0	1260.65	105	116
Ras-related protein Rab-13	RAB13	RAB13_HUMAN	22.8	100.0%	3	4	6	0.01%	16.7%	SSMNVDEAFSSLAR	99.7%	105	25	101	2	0	0	1513.70	154	167
Ras-related protein Rab-13	RAB13	RAB13_HUMAN	22.8	100.0%	3	4	6	0.01%	16.7%	TITTAYYR	99.7%	41.8	25	31	2	0	0	988.51	72	79
Ras-related protein Rab-18	RAB18	RAB18_HUMAN	23.0	100.0%	4	4	7	0.01%	24.3%	GAQGVILVYDVTR	98.7%	33.5	25	27.8	2	0	0	1390.77	80	92
Ras-related protein Rab-18	RAB18	RAB18_HUMAN	23.0	100.0%	4	4	7	0.01%	24.3%	IIQTPGLWESENQNK	99.7%	47.7	25	40.7	2	0	0	1756.89	169	183
Ras-related protein Rab-18	RAB18	RAB18_HUMAN	23.0	100.0%	4	4	7	0.01%	24.3%	ILIIGESGVGK	99.7%	61	25	31	2	0	0	1085.66	11	21
Ras-related protein Rab-18	RAB18	RAB18_HUMAN	23.0	100.0%	4	4	7	0.01%	24.3%	LAIWDTAGQER	99.7%	62	25	53.6	1	0	0	1259.64	59	69
Ras-related protein Rab-1A	RAB1A	RAB1A_HUMAN	22.7	99.8%	2	2	4	0.00%	31.2%	EFADSLGIPFLETSAK	99.7%	59.4	25	52.7	2	0	0	1724.87	141	156
Ras-related protein Rab-1A	RAB1A	RAB1A_HUMAN	22.7	99.8%	2	2	4	0.00%	31.2%	LQIWDTAGQER	99.7%	61.2	25	0	6	0	0	1316.66	62	72

Ras-related protein Rab-1A	RAB1A	RAB1A_HUMAN	22.7	99.8%	2	2	4	0.00%	31.2%	MGPGATAGGAEK	99.5%	38.4	25	30.2	2	0	0	1046.49	176	187
Ras-related protein Rab-1A	RAB1A	RAB1A_HUMAN	22.7	99.8%	2	2	4	0.00%	31.2%	NATNVEQSFMTMAAEIK	99.7%	43.3	25	43.3	2	0	0	1916.87	157	173
Ras-related protein Rab-1A	RAB1A	RAB1A_HUMAN	22.7	99.8%	2	2	4	0.00%	31.2%	QWLQEIDR	99.7%	47.4	25	28	2	0	0	1087.55	104	111
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	5	8	19	0.02%	33.3%	EFADSLGIPFLETSAK	99.7%	59.4	25	52.7	2	0	0	1724.87	138	153
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	5	8	19	0.02%	33.3%	LQIWDTAGQER	99.7%	61.2	25	0	6	0	0	1316.66	59	69
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	5	8	19	0.02%	33.3%	MGPGAASGGERPNLK	99.7%	72.8	25	71.9	4	3	0	1457.72	173	187
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	5	8	19	0.02%	33.3%	NATNVEQAFMTMAAEIK	99.7%	89.8	25	14.6	2	0	0	1900.88	154	170
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	5	8	19	0.02%	33.3%	QWLQEIDR	99.7%	47.4	25	28	2	0	0	1087.55	101	108
Ras-related protein Rab-32	RAB32	RAB32_HUMAN	25.0	100.0%	4	4	6	0.01%	24.9%	AGGGAGDPGLGAAAAPAPETR	97.0%	30.1	25	21.8	1	0	0	1763.87	2	22
Ras-related protein Rab-32	RAB32	RAB32_HUMAN	25.0	100.0%	4	4	6	0.01%	24.9%	DNINIEEAAR	99.7%	72.7	25	63.2	2	0	0	1144.56	177	186
Ras-related protein Rab-32	RAB32	RAB32_HUMAN	25.0	100.0%	4	4	6	0.01%	24.9%	DSSQSPSQVDQFCK	99.7%	58.5	25	58.5	1	0	0	1612.69	150	163
Ras-related protein Rab-32	RAB32	RAB32_HUMAN	25.0	100.0%	4	4	6	0.01%	24.9%	LQLWDIAGQER	99.7%	61.9	25	47.5	2	0	0	1328.70	77	87
Ras-related protein Rab-39B	RAB39B	RB39B_HUMAN	24.6	99.8%	2	2	3	0.00%	20.2%	FAQVSDPTVGVDFFSR	99.7%	64.4	25	64.4	2	0	0	1771.87	33	48
Ras-related protein Rab-39B	RAB39B	RB39B_HUMAN	24.6	99.8%	2	2	3	0.00%	20.2%	LQIWDTAGQER	99.7%	61.2	25	0	6	0	0	1316.66	60	70
Ras-related protein Rab-39B	RAB39B	RB39B_HUMAN	24.6	99.8%	2	2	3	0.00%	20.2%	SGFVPNVVHSSEEVVK	97.2%	30.3	25	30	1	0	0	1713.88	191	206
Ras-related protein Rab-6A	RAB6A	RAB6A_HUMAN	23.6	100.0%	4	6	11	0.01%	28.8%	ELNVMFIETSAK	99.7%	81.6	25	74.7	4	0	0	1381.70	147	158
Ras-related protein Rab-6A	RAB6A	RAB6A_HUMAN	23.6	100.0%	4	6	11	0.01%	28.8%	GSDVIIMLVGNK	99.7%	77.7	25	66.2	2	0	0	1245.69	116	127
Ras-related protein Rab-6A	RAB6A	RAB6A_HUMAN	23.6	100.0%	4	6	11	0.01%	28.8%	LQLWDTAGQER	99.7%	61.2	25	0	6	0	0	1316.66	64	74
Ras-related protein Rab-6A	RAB6A	RAB6A_HUMAN	23.6	100.0%	4	6	11	0.01%	28.8%	LVFLGEQSVGK	99.7%	64	25	51.6	2	0	0	1176.66	16	26
Ras-related protein Rab-6A	RAB6A	RAB6A_HUMAN	23.6	100.0%	4	6	11	0.01%	28.8%	VAAALPGMESTQDR	99.7%	46.4	25	46.4	3	0	0	1445.71	170	183
Ras-related protein Rab-7a	RAB7A	RAB7A_HUMAN	23.5	100.0%	2	2	4	0.00%	13.0%	DPENFPFVVLGNK	97.8%	31.3	25	31.3	2	0	0	1475.75	114	126
Ras-related protein Rab-7a	RAB7A	RAB7A_HUMAN	23.5	100.0%	2	2	4	0.00%	13.0%	EAINVEQAFQTIAR	99.7%	71.1	25	68.4	2	0	0	1589.83	158	171
Ras-related protein Rab-9A	RAB9A	RAB9A_HUMAN	22.8	100.0%	3	3	5	0.01%	18.9%	DATNVAAAFEEAVR	99.7%	72.9	25	69.7	2	0	0	1463.71	157	170
Ras-related protein Rab-9A	RAB9A	RAB9A_HUMAN	22.8	100.0%	3	3	5	0.01%	18.9%	DNGDYPYFETSAK	99.7%	50.4	25	49.6	1	0	0	1506.64	144	156
Ras-related protein Rab-9A	RAB9A	RAB9A_HUMAN	22.8	100.0%	3	3	5	0.01%	18.9%	VILLGDGGVGK	99.7%	54.9	25	21.8	2	0	0	1027.61	10	20
Ras-related protein Rap-2c	RAP2C	RAP2C_HUMAN	20.7	99.8%	2	2	4	0.00%	19.7%	ALAQEWGCPFMETSAK	99.4%	37.2	25	37.2	2	0	0	1825.82	133	148
Ras-related protein Rap-2c	RAP2C	RAP2C_HUMAN	20.7	99.8%	2	2	4	0.00%	19.7%	VPLILVGNK	99.7%	42	25	0	2	0	0	952.62	109	117
Ras-related protein Rap-2c	RAP2C	RAP2C_HUMAN	20.7	99.8%	2	2	4	0.00%	19.7%	VVVLGSGGVGK	99.7%	61.2	25	41.4	2	0	0	971.59	6	16
Ras-related protein R-Ras2	RRAS2	RRAS2_HUMAN	23.4	100.0%	2	2	4	0.00%	11.3%	LVVVGGGGVGK	99.6%	39.1	25	38	2	0	0	941.58	17	27
Ras-related protein R-Ras2	RRAS2	RRAS2_HUMAN	23.4	100.0%	2	2	4	0.00%	11.3%	QVTQEEGQQLAR	99.7%	68.6	25	58.7	2	0	0	1386.70	136	147
Regulation of nuclear pre-mRNA domain-containing protein 1A	RPRD1A	RPR1A_HUMAN	35.7	100.0%	6	6	10	0.01%	23.4%	ALQDLENAASGDAAVHQR	99.7%	66.6	25	66.6	1	0	0	1865.91	169	186
Regulation of nuclear pre-mRNA domain-containing protein 1A	RPRD1A	RPR1A_HUMAN	35.7	100.0%	6	6	10	0.01%	23.4%	DFAPVIVEAFK	99.7%	57	25	47.8	2	0	0	1235.67	80	90
Regulation of nuclear pre-mRNA domain-containing protein 1A	RPRD1A	RPR1A_HUMAN	35.7	100.0%	6	6	10	0.01%	23.4%	IQSLPDLSR	98.8%	34.1	25	23.8	1	0	0	1028.57	283	291
Regulation of nuclear pre-mRNA domain-containing protein 1A	RPRD1A	RPR1A_HUMAN	35.7	100.0%	6	6	10	0.01%	23.4%	LTFLYLANDVIQNSK	99.7%	77.6	25	77.6	2	0	0	1738.94	57	71
Regulation of nuclear pre-mRNA domain-containing protein 1A	RPRD1A	RPR1A_HUMAN	35.7	100.0%	6	6	10	0.01%	23.4%	SVYENDVLEQLK	99.7%	55.7	25	48.9	2	0	0	1436.73	115	126
Regulation of nuclear pre-mRNA domain-containing protein 1A	RPRD1A	RPR1A_HUMAN	35.7	100.0%	6	6	10	0.01%	23.4%	VLSIWEER	99.7%	48.8	25	40.6	2	0	0	1031.55	107	114
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	12	12	19	0.02%	13.0%	ADSVVVLLCR	99.7%	52.2	25	46.7	2	0	0	1131.62	201	210
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	12	12	19	0.02%	13.0%	AGLSQSLFER	99.7%	77.4	25	56.6	2	0	0	1107.58	689	698
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	12	12	19	0.02%	13.0%	AYQHGGVTGLSQY	97.5%	30.8	25	30.8	1	0	0	1380.65	1117	1129
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	12	12	19	0.02%	13.0%	EKDFIILSCVR	99.7%	58.3	25	57.8	1	0	0	1379.74	844	854
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	12	12	19	0.02%	13.0%	IAYFTLPK	99.0%	34.8	25	29.3	2	0	0	952.55	342	349
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	12	12	19	0.02%	13.0%	LKESQTQDNITVR	99.0%	27.5	25	24.5	0	1	0	1531.81	320	332
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	12	12	19	0.02%	13.0%	LMQGDEICLR	99.7%	51.6	25	35.9	2	0	0	1234.59	367	376
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	12	12	19	0.02%	13.0%	LYQEVEIASVDAFQGR	99.7%	74	25	64	2	0	0	1824.91	828	843
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	12	12	19	0.02%	13.0%	SQIDVALSQDSTYQGER	99.7%	82.3	25	77.2	1	0	0	1896.89	1100	1116
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	12	12	19	0.02%	13.0%	TVTSATIVYHLAR	99.7%	92.8	25	85.2	2	0	0	1431.80	510	522
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	12	12	19	0.02%	13.0%	YEDAYQYQNIFGPLVK	99.7%	91	25	91	2	0	0	1947.95	296	311
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	12	12	19	0.02%	13.0%	YGVIIVGNPK	99.7%	59.5	25	59.5	1	0	0	1059.62	879	888
Regulator of nonsense transcripts 3B	UPF3B	REN3B_HUMAN	57.8	100.0%	4	4	6	0.01%	9.9%	FLESYATDNEK	99.7%	48.8	25	40.1	2	0	0	1316.60	163	173
Regulator of nonsense transcripts 3B	UPF3B	REN3B_HUMAN	57.8	100.0%	4	4	6	0.01%	9.9%	KAESTESIGSSEK	99.1%	35.5	25	29.5	2	0	0	1352.65	406	418
Regulator of nonsense transcripts 3B	UPF3B	REN3B_HUMAN	57.8	100.0%	4	4	6	0.01%	9.9%	MTSTPETLLEEIEAK	99.6%	39.4	25	39.4	1	0	0	1691.84	174	188

Regulator of nonsense transcripts 3B	UPF3B	REN3B_HUMAN	57.8	100.0%	4	4	6	0.01%	9.9%	NQEDIILFR	99.7%	53.3	25	43.2	1	0	0	1147.61	103	111
Regulatory-associated protein of mTOR	RPTOR	RPTOR_HUMAN	149.0	100.0%	3	3	5	0.01%	2.6%	LDDQIFLNR	99.7%	59.4	25	52	2	0	0	1133.60	1013	1021
Regulatory-associated protein of mTOR	RPTOR	RPTOR_HUMAN	149.0	100.0%	3	3	5	0.01%	2.6%	MPESVNVLQIVK	99.0%	35	25	24.6	1	0	0	1356.76	1243	1254
Regulatory-associated protein of mTOR	RPTOR	RPTOR_HUMAN	149.0	100.0%	3	3	5	0.01%	2.6%	SLIVAGLGDGSIR	99.7%	71.2	25	60.2	2	0	0	1257.72	1179	1191
Replication factor C subunit 1	RFC1	RFC1_HUMAN	128.3	99.9%	2	2	3	0.00%	2.2%	AALLSGPPGVGK	98.4%	32.8	25	31.6	1	0	0	1066.63	646	657
Replication factor C subunit 1	RFC1	RFC1_HUMAN	128.3	99.9%	2	2	3	0.00%	2.2%	AIVAESLNNTSIK	99.7%	53.4	25	47.2	2	0	0	1359.75	688	700
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	12	14	26	0.03%	42.4%	APGSAGHYELPWVEK	99.7%	45.9	25	45.9	2	2	0	1640.81	27	41
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	12	14	26	0.03%	42.4%	DAMLELNASNDR	99.7%	76.4	25	76	2	0	0	1348.62	100	111
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	12	14	26	0.03%	42.4%	EGNVPNIIIAGPPGTGK	99.7%	84.2	25	82.2	2	0	0	1633.89	66	82
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	12	14	26	0.03%	42.4%	FALACNASDK	99.7%	44.6	25	36.9	2	0	0	1096.51	167	176
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	12	14	26	0.03%	42.4%	FALACNASDKIIEPIQSR	99.7%	63.5	25	62.8	0	2	0	2033.05	167	184
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	12	14	26	0.03%	42.4%	IAEGVNSLLQMAGLLAR	99.7%	70.4	25	62.2	4	0	0	1755.98	327	343
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	12	14	26	0.03%	42.4%	IIILDEADSMTDGAQQALRR	98.7%	26.5	25	25.5	0	1	0	2232.13	137	156
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	12	14	26	0.03%	42.4%	LNEIVGNEDTVSR	99.7%	84.8	25	84.8	2	0	0	1445.72	47	59
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	12	14	26	0.03%	42.4%	LTDAQILTR	99.7%	77.4	25	67.5	2	0	0	1030.59	193	201
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	12	14	26	0.03%	42.4%	TFQMAEYLK	97.1%	30.1	25	25.3	1	0	0	1130.56	305	313
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	12	14	26	0.03%	42.4%	TTSILCLAR	99.7%	50.4	25	34.5	2	0	0	1034.57	83	91
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	12	14	26	0.03%	42.4%	VCDEPHPLLVK	99.7%	47.3	25	34.8	2	0	0	1306.68	254	264
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	12	13	23	0.02%	32.3%	AIYHLEAFVAK	99.7%	52.5	25	36.9	2	0	0	1261.69	328	338
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	12	13	23	0.02%	32.3%	ALLMCEACR	99.7%	46.2	25	46.2	3	0	0	1123.51	226	234
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	12	13	23	0.02%	32.3%	EGLNLPSQLAHR	99.7%	42.7	25	35.4	2	0	0	1334.72	203	214
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	12	13	23	0.02%	32.3%	ELYGVGVEK	95.5%	28.4	25	17.5	1	0	0	993.53	58	66
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	12	13	23	0.02%	32.3%	ETANAIVSQQTPQR	99.7%	97.1	25	87.9	2	0	0	1542.79	257	270
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	12	13	23	0.02%	32.3%	IEHQTITTPSK	99.7%	43.8	25	39.8	1	0	0	1254.67	69	79
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	12	13	23	0.02%	32.3%	IEHQTITTPSKK	97.9%	31.5	25	31.5	2	0	0	1382.76	69	80
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	12	13	23	0.02%	32.3%	LDYHKEQAAQLR	99.7%	32.5	25	31.8	0	2	0	1471.77	16	27
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	12	13	23	0.02%	32.3%	LILCCNSTSK	99.7%	41.5	25	41.5	2	0	0	1195.58	161	170
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	12	13	23	0.02%	32.3%	TVAQSQQLETNSQR	99.7%	119	25	111	2	0	0	1589.79	114	127
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	12	13	23	0.02%	32.3%	VVLLTEVDK	99.5%	37.8	25	37.8	2	0	0	1015.60	131	139
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	12	13	23	0.02%	32.3%	VVLLTEVDKLTK	99.7%	71.5	25	71.5	2	0	0	1357.83	131	142
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	18	0.02%	28.1%	AITFLQSATR	99.7%	76.2	25	62.2	2	0	0	1107.62	241	250
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	18	0.02%	28.1%	ELFGPELFR	99.7%	60.2	25	41.8	2	0	0	1107.58	94	102
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	18	0.02%	28.1%	GTSISTKPPLTK	99.7%	42.2	25	21.8	2	0	0	1229.71	7	18
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	18	0.02%	28.1%	ISDEGIAYLVK	99.7%	85.6	25	77.8	2	0	0	1207.66	222	232
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	18	0.02%	28.1%	SLEGADLPNLLFYGPPGTGK	99.7%	60.4	25	60.4	2	0	0	2046.05	65	84
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	18	0.02%	28.1%	TSTILAAAR	99.7%	66.8	25	53.7	2	0	0	903.53	85	93
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	18	0.02%	28.1%	VITDIAGVIPAEK	99.7%	83.9	25	73.9	2	0	0	1325.77	261	273
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	18	0.02%	28.1%	VLELNASDER	99.7%	66.2	25	58.4	2	0	0	1145.58	105	114
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	18	0.02%	28.1%	VSEGDLRK	99.7%	40.9	25	21.4	2	0	0	903.49	233	240
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	13	26	0.03%	35.9%	ALNILQSTNMAFGK	99.7%	84.1	25	68.2	4	0	0	1507.79	216	229
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	13	26	0.03%	35.9%	ALVTLSSGDMR	99.7%	75.2	25	66.5	3	0	0	1149.59	204	214
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	13	26	0.03%	35.9%	FCLICNYLSK	99.7%	59.2	25	59.2	2	0	0	1317.63	151	160
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	13	26	0.03%	35.9%	FGPLTPELMVPR	99.7%	52.9	25	51.6	3	0	0	1356.73	174	185
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	13	26	0.03%	35.9%	GPILSFASTR	99.7%	64.3	25	64.2	4	0	0	1048.58	103	112
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	13	26	0.03%	35.9%	IQLSSLIAAFQVTR	99.7%	94	25	94	3	0	0	1546.90	320	333
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	13	26	0.03%	35.9%	LSVGTNEK	96.0%	28.8	25	21.4	1	0	0	847.45	312	319
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	13	26	0.03%	35.9%	LVILDEADAMTQDAQNALR	99.7%	70.8	25	70.8	1	0	0	2087.04	121	139
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	13	26	0.03%	35.9%	MADIEYR	99.7%	41.2	25	35.8	2	0	0	897.41	305	311
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	13	26	0.03%	35.9%	TSTILACAK	99.5%	38.2	25	38.2	2	0	0	964.51	67	75
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	13	26	0.03%	35.9%	VDFPSSVR	94.6%	27.5	25	13.3	1	0	0	906.47	291	298
Required for meiotic nuclear division protein 1 homolog	RMND1	RMND1_HUMAN	51.6	100.0%	4	4	7	0.01%	10.7%	DAANILVMGVENSAK	99.7%	78.2	25	78.1	2	0	0	1531.78	205	219

Required for meiotic nuclear division protein 1 homolog	RMND1	RMND1_HUMAN	51.6	100.0%	4	4	7	0.01%	10.7%	EGDPGTIFFFR	99.7%	59.9	25	55.3	2	0	0	1285.62	220	230
Required for meiotic nuclear division protein 1 homolog	RMND1	RMND1_HUMAN	51.6	100.0%	4	4	7	0.01%	10.7%	IGELFALR	99.7%	66.7	25	47.9	2	0	0	918.54	353	360
Required for meiotic nuclear division protein 1 homolog	RMND1	RMND1_HUMAN	51.6	100.0%	4	4	7	0.01%	10.7%	LNSELDLDDAILEK	99.7%	67.6	25	66.7	1	0	0	1587.81	289	302
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	7	13	0.01%	23.3%	AEELHYPLGER	99.7%	45.7	25	45.7	2	0	0	1313.65	25	35
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	7	13	0.01%	23.3%	EALLGVQEDVDEYVK	99.7%	99.6	25	99.6	3	0	0	1706.85	42	56
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	7	13	0.01%	23.3%	QLHDDYFYHDEL	99.7%	43.1	25	40.7	2	2	0	1594.68	306	317
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	7	13	0.01%	23.3%	VIDFDENTALDDAEEESFR	99.7%	85.3	25	85.3	1	0	0	2214.97	130	148
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	7	13	0.01%	23.3%	VIDFDENTALDDAEEESFRK	99.4%	29.5	25	26.4	0	1	0	2343.06	130	149
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	7	13	0.01%	23.3%	WDPTANEDPEWILVEK	99.7%	68.6	25	68.6	2	0	0	1941.92	217	232
Retinoid-inducible serine carboxypeptidase	SCPEP1	RISC_HUMAN	50.8	100.0%	3	3	4	0.00%	6.6%	DALSQLMNGPIR	99.4%	37.6	25	32.8	1	0	0	1314.68	307	318
Retinoid-inducible serine carboxypeptidase	SCPEP1	RISC_HUMAN	50.8	100.0%	3	3	4	0.00%	6.6%	NLAFYWILK	96.5%	29.4	25	16.8	2	0	0	1167.66	420	428
Retinoid-inducible serine carboxypeptidase	SCPEP1	RISC_HUMAN	50.8	100.0%	3	3	4	0.00%	6.6%	SLETSAFVK	96.3%	29.1	25	18.5	1	0	0	981.53	408	416
Rho-related GTP-binding protein RhoG	RHOG	RHOG_HUMAN	21.3	100.0%	4	4	4	0.00%	28.3%	AVLNPTPIKR	96.8%	29.7	25	17.3	1	0	0	1108.68	175	184
Rho-related GTP-binding protein RhoG	RHOG	RHOG_HUMAN	21.3	100.0%	4	4	4	0.00%	28.3%	CVVVGDGAVGK	97.9%	31.6	25	24.1	1	0	0	1060.55	6	16
Rho-related GTP-binding protein RhoG	RHOG	RHOG_HUMAN	21.3	100.0%	4	4	4	0.00%	28.3%	EYIPTVFDNYSAQSAVDGR	99.7%	60.5	25	60.5	1	0	0	2131.99	31	49
Rho-related GTP-binding protein RhoG	RHOG	RHOG_HUMAN	21.3	100.0%	4	4	4	0.00%	28.3%	TCLLICYTTNAFPK	98.7%	33.6	25	33.6	1	0	0	1701.83	17	30
Ribonuclease P protein subunit p14	RPP14	RPP14_HUMAN	13.7	100.0%	4	4	5	0.01%	33.9%	ICSSGLVK	96.5%	29.4	25	17.4	1	0	0	863.47	77	84
Ribonuclease P protein subunit p14	RPP14	RPP14_HUMAN	13.7	100.0%	4	4	5	0.01%	33.9%	NPSEYHYMK	95.6%	28.4	25	28.4	1	0	0	1168.51	15	23
Ribonuclease P protein subunit p14	RPP14	RPP14_HUMAN	13.7	100.0%	4	4	5	0.01%	33.9%	PAPAATYER	99.5%	38.3	25	31.2	2	0	0	975.49	2	10
Ribonuclease P protein subunit p14	RPP14	RPP14_HUMAN	13.7	100.0%	4	4	5	0.01%	33.9%	VIQVSPFLLALSGNSR	99.7%	58.7	25	46.1	1	0	0	1700.97	104	119
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	5	5	8	0.01%	26.8%	AVVLEYFTR	99.7%	51.3	25	47.8	2	0	0	1097.60	55	63
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	5	5	8	0.01%	26.8%	CPSYVGITGILLQETK	99.7%	42.6	25	42.6	1	0	0	1778.94	147	162
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	5	5	8	0.01%	26.8%	EANDSDVQPSGAQR	99.7%	54.9	25	48.1	2	0	0	1473.66	13	26
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	5	5	8	0.01%	26.8%	LFDIKPEQQR	98.9%	34.5	25	26.1	1	0	0	1273.69	86	95
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	5	5	8	0.01%	26.8%	SVIYHALSQK	99.7%	41.3	25	32.8	2	0	0	1145.63	3	12
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	7	8	23	0.02%	30.6%	AALLHGETR	99.7%	53.2	25	51.9	4	0	0	967.53	227	235
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	7	8	23	0.02%	30.6%	GLAFELVYSPAIK	99.7%	75	25	70.2	2	0	0	1407.79	149	161
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	7	8	23	0.02%	30.6%	KTAFGIISTVK	99.4%	37	25	37	2	0	0	1164.70	236	246
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	7	8	23	0.02%	30.6%	LYDVVAVFPK	99.7%	72.2	25	72.2	6	0	0	1150.65	99	108
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	7	8	23	0.02%	30.6%	NVIISSAAERPLEIR	95.0%	27.8	25	18.7	1	0	0	1667.94	184	198
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	7	8	23	0.02%	30.6%	RPPINVAIDR	99.7%	43.2	25	31	4	0	0	1150.67	139	148
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	7	8	23	0.02%	30.6%	YTISSALNLMQICK	99.7%	65.5	25	65.5	4	0	0	1657.83	168	181
Ribonuclease P protein subunit p38	RPP38	RPP38_HUMAN	31.8	100.0%	3	3	4	0.00%	10.6%	ELLLVLVCK	99.7%	52.7	25	52.7	2	0	0	1086.66	128	136
Ribonuclease P protein subunit p38	RPP38	RPP38_HUMAN	31.8	100.0%	3	3	4	0.00%	10.6%	QLAIGVNEVTR	97.7%	31.1	25	18.3	1	0	0	1199.67	112	122
Ribonuclease P protein subunit p38	RPP38	RPP38_HUMAN	31.8	100.0%	3	3	4	0.00%	10.6%	TSLNNPYIIR	99.7%	47.2	25	37.9	1	0	0	1190.65	23	32
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	6	6	11	0.01%	6.8%	AGPEGTSQEIPK	99.7%	61.2	25	48.6	2	0	0	1213.61	89	100
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	6	6	11	0.01%	6.8%	EMLGPVTFIWK	98.3%	32.5	25	24.6	1	0	0	1320.70	303	313
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	6	6	11	0.01%	6.8%	ISDQDLNR	99.5%	37.9	25	23.9	2	0	0	960.47	567	574
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	6	6	11	0.01%	6.8%	NQPTNVTLSSGFVADR	99.7%	90.5	25	90.5	2	0	0	1705.85	15	30
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	6	6	11	0.01%	6.8%	SSNSLVFQTLPR	99.7%	44	25	27.8	2	0	0	1348.72	126	137
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	6	6	11	0.01%	6.8%	YITASTFAQAR	99.7%	46.9	25	46.9	2	0	0	1228.63	101	111
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	7	9	16	0.02%	29.6%	IFSGSSHQDLSQK	99.7%	79.1	25	75.8	2	0	0	1433.70	6	18
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	7	9	16	0.02%	29.6%	MVLVGDVKDR	99.7%	69.2	25	64.4	4	0	0	1131.62	205	214
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	7	9	16	0.02%	29.6%	NCTIVSPDAGGAK	99.7%	66.4	25	55.2	2	0	0	1289.62	164	176
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	7	9	16	0.02%	29.6%	RVTSIADR	95.6%	28.4	25	19.5	1	0	0	917.52	177	184
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	7	9	16	0.02%	29.6%	VAILVDDMADTCGTICHAADK	98.6%	26.4	25	26.1	0	1	0	2292.03	215	235
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	7	9	16	0.02%	29.6%	VTAVIPCFPYAR	99.7%	46.5	25	43.3	2	0	0	1393.73	85	96
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	7	9	16	0.02%	29.6%	VYAILTHGIFSGPAISR	99.7%	102	25	102	2	2	0	1802.00	244	260
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	6	6	10	0.01%	9.1%	AWNNPSPR	99.5%	38.5	25	33.9	1	0	0	941.46	296	303
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	6	6	10	0.01%	9.1%	FVNLISER	99.7%	50.4	25	29.2	2	0	0	977.54	122	129
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	6	6	10	0.01%	9.1%	GCYFVLDWLQK	99.7%	62.8	25	56.6	2	0	0	1428.70	172	182

Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	6	6	10	0.01%	9.1%	LLDVTGGLGTDELR	99.7%	83.9	25	80.8	2	0	0	1458.78	99	112
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	6	6	10	0.01%	9.1%	SGNELPLAVASTADLIR	99.7%	115	25	109	2	0	0	1726.93	80	96
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	6	6	10	0.01%	9.1%	VECVLAELK	99.4%	37.5	25	22.7	1	0	0	1060.57	304	312
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	12	12	20	0.02%	24.3%	AAESETPGKSPEK	99.7%	50.2	25	45.3	2	0	0	1330.65	418	430
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	12	12	20	0.02%	24.3%	ATNESEDEIPQLVPIGK	99.7%	53.3	25	49.8	1	0	0	1839.93	357	373
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	12	12	20	0.02%	24.3%	AVDALLTHCK	98.3%	32.4	25	27.2	1	0	0	1127.59	39	48
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	12	12	20	0.02%	24.3%	EINDCIGGTVLNISK	99.7%	78.5	25	74.3	2	0	0	1632.83	193	207
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	12	12	20	0.02%	24.3%	LLPSLIGR	99.6%	39.1	25	28.4	2	0	0	868.56	164	171
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	12	12	20	0.02%	24.3%	LLSSFDFFLTDAR	99.7%	98.3	25	93.1	2	0	0	1531.78	148	160
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	12	12	20	0.02%	24.3%	LTLPHSIR	99.7%	41.7	25	41.7	2	0	0	936.56	82	89
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	12	12	20	0.02%	24.3%	RLLPSLIGR	95.0%	27.9	25	22.8	1	0	0	1024.66	163	171
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	12	12	20	0.02%	24.3%	TPANEKVEIQK	99.7%	49	25	39	2	0	0	1256.68	375	385
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	12	12	20	0.02%	24.3%	TVSQIISLQTLK	99.7%	74.9	25	74.9	2	0	0	1330.79	125	136
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	12	12	20	0.02%	24.3%	TVSQIISLQTLKK	99.7%	44.8	25	44.8	2	0	0	1458.89	125	137
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	12	12	20	0.02%	24.3%	VPVSVNLLSK	96.6%	29.5	25	24.6	1	0	0	1055.65	179	188
Ribosomal protein S6 kinase alpha-1	RPS6KA1	KS6A1_HUMAN	82.7	99.8%	2	2	2	0.00%	8.0%	DLKPENILLDEEGHIK	99.7%	44.3	25	44.3	0	2	0	1862.99	187	202
Ribosomal protein S6 kinase alpha-1	RPS6KA1	KS6A1_HUMAN	82.7	99.8%	2	2	2	0.00%	8.0%	EASFVLHTIGK	99.7%	46.2	25	44.9	1	0	0	1201.66	511	521
Ribosomal protein S6 kinase alpha-1	RPS6KA1	KS6A1_HUMAN	82.7	99.8%	2	2	2	0.00%	8.0%	ICDFGFAK	99.7%	51.9	25	0	2	0	0	957.45	555	562
Ribosomal protein S6 kinase alpha-1	RPS6KA1	KS6A1_HUMAN	82.7	99.8%	2	2	2	0.00%	8.0%	LGSGPDGAEEIKR	96.2%	29	25	20.4	1	0	0	1328.68	305	317
Ribosomal protein S6 kinase alpha-1	RPS6KA1	KS6A1_HUMAN	82.7	99.8%	2	2	2	0.00%	8.0%	YGQHPNIITLK	96.5%	29.4	25	24.4	1	0	0	1283.71	466	476
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	5	5	8	0.01%	8.0%	DLKPENILLDEEGHIK	99.7%	44.3	25	44.3	0	2	0	1862.99	193	208
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	5	5	8	0.01%	8.0%	ICDFGFAK	99.7%	51.9	25	0	2	0	0	957.45	559	566
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	5	5	8	0.01%	8.0%	LGAGPDGVEEIKR	98.4%	32.8	25	28.3	1	0	0	1340.72	311	323
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	5	5	8	0.01%	8.0%	PLAQLADPWQK	99.7%	44	25	44	2	0	0	1266.68	2	12
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	5	5	8	0.01%	8.0%	YGQHPNIITLK	96.5%	29.4	25	24.4	1	0	0	1283.71	470	480
Ribosomal RNA processing protein 1 homolog A	RRP1	RRP1_HUMAN	52.8	100.0%	3	3	6	0.01%	7.4%	LAGNEQVTR	99.7%	78.2	25	65.1	3	0	0	987.52	17	25
Ribosomal RNA processing protein 1 homolog A	RRP1	RRP1_HUMAN	52.8	100.0%	3	3	6	0.01%	7.4%	TKDSLVLNNITR	99.7%	67.3	25	59.2	1	0	0	1373.77	204	215
Ribosomal RNA processing protein 1 homolog A	RRP1	RRP1_HUMAN	52.8	100.0%	3	3	6	0.01%	7.4%	VGAEELTADQNLK	99.7%	65.1	25	55	2	0	0	1387.71	180	192
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	6	6	10	0.01%	9.6%	ELLADQNLK	99.7%	42.7	25	37.7	2	0	0	1043.57	183	191
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	6	6	10	0.01%	9.6%	ETGGFSQEELLK	99.7%	44.7	25	28.1	1	0	0	1337.66	42	53
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	6	6	10	0.01%	9.6%	GSPTGGAQLLK	97.0%	30	25	15.9	1	0	0	1028.57	512	522
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	6	6	10	0.01%	9.6%	SILVSPTGPSR	97.2%	30.3	25	16.8	2	0	0	1113.63	702	712
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	6	6	10	0.01%	9.6%	SSTATHPPGPAVQLNK	99.7%	50.2	25	47.8	2	0	0	1604.84	661	676
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	6	6	10	0.01%	9.6%	TPTSSPASSPLVAK	99.7%	61.8	25	61.2	2	0	0	1342.72	728	741
Ribosome biogenesis protein BRX1 homolog	BRIX1	BRX1_HUMAN	41.4	100.0%	3	3	5	0.01%	7.7%	FLVQNIHTLAELK	99.7%	75.8	25	66.5	2	0	0	1525.87	141	153
Ribosome biogenesis protein BRX1 homolog	BRIX1	BRX1_HUMAN	41.4	100.0%	3	3	5	0.01%	7.7%	FVLNLIK	98.0%	31.7	25	30.6	2	0	0	846.54	236	242
Ribosome biogenesis protein BRX1 homolog	BRIX1	BRX1_HUMAN	41.4	100.0%	3	3	5	0.01%	7.7%	HLMQDLR	95.4%	28.2	25	5.72	1	0	0	912.47	76	82
Ribosome production factor 2 homolog	RPF2	RPF2_HUMAN	35.6	100.0%	4	4	7	0.01%	12.7%	GPTVSNIR	99.3%	36.7	25	27.7	2	0	0	843.47	169	176
Ribosome production factor 2 homolog	RPF2	RPF2_HUMAN	35.6	100.0%	4	4	7	0.01%	12.7%	KPYGVLYK	98.7%	33.6	25	17	2	0	0	967.56	57	64
Ribosome production factor 2 homolog	RPF2	RPF2_HUMAN	35.6	100.0%	4	4	7	0.01%	12.7%	NISHDTFGTTYGR	99.7%	47.8	25	47.8	1	0	0	1468.68	253	265
Ribosome production factor 2 homolog	RPF2	RPF2_HUMAN	35.6	100.0%	4	4	7	0.01%	12.7%	THLASDDLYK	99.7%	44.3	25	41.7	2	0	0	1162.57	228	237
RING finger protein 219	RNF219	RN219_HUMAN	81.1	100.0%	4	4	6	0.01%	5.5%	FAVAALQSK	99.7%	41.3	25	23	1	0	0	934.54	217	225
RING finger protein 219	RNF219	RN219_HUMAN	81.1	100.0%	4	4	6	0.01%	5.5%	KIQSSLSSASPSK	99.7%	60.3	25	48	1	0	0	1319.72	710	722
RING finger protein 219	RNF219	RN219_HUMAN	81.1	100.0%	4	4	6	0.01%	5.5%	NLSLESQIK	99.7%	49.7	25	24.7	2	0	0	1031.57	117	125
RING finger protein 219	RNF219	RN219_HUMAN	81.1	100.0%	4	4	6	0.01%	5.5%	SLDLDGLSK	99.4%	37.5	25	18.4	2	0	0	947.50	561	569
RNA 3'-terminal phosphate cyclase	RTCA	RTCA_HUMAN	39.3	100.0%	5	5	15	0.02%	15.6%	AFVAGVLPFK	99.7%	60.2	25	49.8	4	0	0	1048.62	196	205
RNA 3'-terminal phosphate cyclase	RTCA	RTCA_HUMAN	39.3	100.0%	5	5	15	0.02%	15.6%	DLYVNIQPVQEPK	99.7%	60.9	25	60.9	2	0	0	1542.82	224	236
RNA 3'-terminal phosphate cyclase	RTCA	RTCA_HUMAN	39.3	100.0%	5	5	15	0.02%	15.6%	FGFIFNCDIK	99.7%	48.4	25	41.2	3	0	0	1260.61	147	156
RNA 3'-terminal phosphate cyclase	RTCA	RTCA_HUMAN	39.3	100.0%	5	5	15	0.02%	15.6%	QLNPINLTER	99.7%	58.5	25	44.9	2	0	0	1197.66	177	186
RNA 3'-terminal phosphate cyclase	RTCA	RTCA_HUMAN	39.3	100.0%	5	5	15	0.02%	15.6%	VSTALSCLLGLPLR	99.7%	42.6	25	42.6	4	0	0	1499.86	22	35
RNA binding protein fox-1 homolog 1	RBFOX1	RFOX1_HUMAN	42.8	99.8%	2	2	2	0.00%	4.8%	LHGTVVEGR	95.9%	28.7	25	23.6	1	0	0	967.53	176	184

RNA binding protein fox-1 homolog 1	RBFOX1	RFOX1_HUMAN	42.8	99.8%	2	2	2	0.00%	4.8%	RLHVSNIPFR	99.5%	30.3	25	30	0	1	0	1238.71	118	127
RNA methyltransferase-like protein 1	RNMTL1	RMTL1_HUMAN	47.0	100.0%	4	4	8	0.01%	11.0%	APSTWEESGLR	99.7%	64.4	25	58.5	2	0	0	1232.59	83	93
RNA methyltransferase-like protein 1	RNMTL1	RMTL1_HUMAN	47.0	100.0%	4	4	8	0.01%	11.0%	EKQPLEESASR	99.4%	37.6	25	34.1	2	0	0	1273.64	72	82
RNA methyltransferase-like protein 1	RNMTL1	RMTL1_HUMAN	47.0	100.0%	4	4	8	0.01%	11.0%	KAPSEASAQEQR	99.7%	65.5	25	58	2	0	0	1301.64	60	71
RNA methyltransferase-like protein 1	RNMTL1	RMTL1_HUMAN	47.0	100.0%	4	4	8	0.01%	11.0%	VVFPSGEVVEQK	99.7%	63.3	25	61.5	2	0	0	1317.70	40	51
RNA polymerase II-associated factor 1 homolog	PAF1	PAF1_HUMAN	60.0	100.0%	5	5	8	0.01%	11.7%	AGVQSGTNALLVVK	99.7%	83.9	25	77.4	2	0	0	1356.78	339	352
RNA polymerase II-associated factor 1 homolog	PAF1	PAF1_HUMAN	60.0	100.0%	5	5	8	0.01%	11.7%	EGDGVYYNELETR	99.7%	63.4	25	63.4	2	0	0	1544.69	317	329
RNA polymerase II-associated factor 1 homolog	PAF1	PAF1_HUMAN	60.0	100.0%	5	5	8	0.01%	11.7%	GYEENYFFIFR	98.5%	32.9	25	32.9	1	0	0	1484.68	306	316
RNA polymerase II-associated factor 1 homolog	PAF1	PAF1_HUMAN	60.0	100.0%	5	5	8	0.01%	11.7%	SISQHYSKPR	97.0%	23.6	25	17	0	1	0	1202.63	189	198
RNA polymerase II-associated factor 1 homolog	PAF1	PAF1_HUMAN	60.0	100.0%	5	5	8	0.01%	11.7%	VTPVEVMPVFPDFK	99.7%	44.5	25	37.3	2	0	0	1604.84	199	212
RNA pseudouridylate synthase domain-containing protein 3	RPUSD3	RUSD3_HUMAN	38.5	100.0%	4	4	7	0.01%	13.7%	DTPVELLAPLPPYFSR	99.3%	36.7	25	36.5	2	0	0	1814.97	326	341
RNA pseudouridylate synthase domain-containing protein 3	RPUSD3	RUSD3_HUMAN	38.5	100.0%	4	4	7	0.01%	13.7%	QVLDEALLR	99.5%	38.4	25	24.8	1	0	0	1056.60	288	296
RNA pseudouridylate synthase domain-containing protein 3	RPUSD3	RUSD3_HUMAN	38.5	100.0%	4	4	7	0.01%	13.7%	SGPLGDQPFAGLLPK	99.7%	59	25	59	2	0	0	1496.81	54	68
RNA pseudouridylate synthase domain-containing protein 3	RPUSD3	RUSD3_HUMAN	38.5	100.0%	4	4	7	0.01%	13.7%	TLQCLGLR	98.8%	34.1	25	11.8	2	0	0	960.53	342	349
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	12	13	21	0.02%	30.4%	AIKVEQATKPSFESGR	99.7%	62	25	62	0	2	0	1747.93	78	93
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	12	13	21	0.02%	30.4%	DSYESYGNSR	99.7%	65.8	25	65.3	1	0	0	1177.48	283	292
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	12	13	21	0.02%	30.4%	DVYLSPR	96.6%	29.4	25	25.4	1	0	0	849.45	204	210
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	12	13	21	0.02%	30.4%	DYGHSSSRDDYPSR	95.7%	22.4	25	22.4	0	1	0	1641.69	245	258
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	12	13	21	0.02%	30.4%	GFAFVTFESPADAK	99.7%	97.1	25	63.6	2	0	0	1486.72	50	63
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	12	13	21	0.02%	30.4%	GPPPSYGGSSR	99.7%	45.3	25	45.3	2	0	0	1061.50	299	309
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	12	13	21	0.02%	30.4%	GYSDRDGYGR	97.8%	31.4	25	29.5	1	0	0	1145.50	259	268
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	12	13	21	0.02%	30.4%	IVEVLLMK	99.7%	50.6	25	31.6	4	0	0	960.58	34	41
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	12	13	21	0.02%	30.4%	LFIGGLNTETNEK	99.7%	92	25	82.6	2	0	0	1435.74	10	22
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	12	13	21	0.02%	30.4%	RGPPPPPR	99.2%	36.2	25	31.2	1	0	0	873.51	94	101
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	12	13	21	0.02%	30.4%	VEQATKPSFESGR	99.7%	51.3	25	49.2	2	0	0	1435.72	81	93
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	12	13	21	0.02%	30.4%	YDDYSSSR	99.7%	43.1	25	43.1	2	0	0	992.40	310	317
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	AHLSENELEALEK	99.7%	72	25	72	2	0	0	1482.74	794	806
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	AQPGAAPGIYQQSAEASSSQGTAANSQSYTIMSPAVLK	99.7%	77.1	25	76.7	0	2	0	3783.81	499	536
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	ASNIVMLR	99.7%	71.3	25	53.8	2	0	0	903.51	127	134
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	CGVQNFK	99.7%	48.4	25	34	2	0	0	852.40	222	228
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	DGDYRDQDYR	99.2%	36.1	25	36.1	1	2	0	1302.53	99	108
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	DGLGSDNIGSR	99.7%	60.7	25	50	8	0	0	1090.51	854	864
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	EKYGIPEPPEPK	99.7%	41.4	25	33.3	2	0	0	1383.72	823	834
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	ESATADAGYAILEK	99.7%	117	25	112	9	0	0	1438.71	686	699
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	GDPTGAGPEASLEPGADSVSMQAFSR	99.7%	72.8	25	72.8	3	2	0	2550.14	473	498
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	GFAFVEFSHLQDATR	99.7%	114	25	114	6	6	0	1724.84	172	186
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	GLVAAYSGESDSEEEQER	99.7%	131	25	126	2	0	0	1955.85	727	744
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	GQLQSHGVQAR	99.7%	68.5	25	55.6	12	0	0	1180.62	147	157
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	GSSYGVTSTESYK	99.7%	64.2	25	64.2	2	0	0	1365.62	903	915
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	GSSYGVTSTESYKETLHK	98.5%	26.1	25	21.8	0	1	0	1973.95	903	920
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	HQQLSGLHK	97.8%	31.3	25	29.6	2	0	0	1047.57	777	785
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	INEDWLCNK	99.7%	63.5	25	41.7	6	0	0	1191.55	213	221
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	KQGIVTPIEAQTR	99.7%	47.7	25	47.7	1	0	0	1440.82	881	893
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	KYGGISTASVDFEQPTR	99.7%	108	25	108	2	2	0	1855.92	837	853
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	LACLLCR	99.7%	44.2	25	34.3	2	0	0	905.47	759	765
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	LDQQTLPLGGR	99.7%	78.8	25	73.1	6	0	0	1197.66	253	263
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	MLPQAATEDDIR	99.7%	68.5	25	64	8	0	0	1359.66	135	146
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	MLPQAATEDDIRGQLQSHGVQAR	94.8%	21.7	25	20.8	0	1	0	2521.26	135	157
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	MLQAMGWK	99.7%	40.6	25	36	4	0	0	996.46	865	872
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	NLNPHSTMDSILGALAPYAVLSSSNVR	99.7%	53.5	25	53.5	0	1	0	2827.44	306	332
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	NSFQPISSLR	99.7%	56	25	26.7	4	0	0	1148.61	671	680

RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	NSFQPISSLRDDER	97.2%	30.3	25	23.4	1	0	0	1663.80	671	684
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	QGIVTPIEAQTR	99.7%	56.4	25	43.2	4	0	0	1312.72	882	893
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	QNLEIHR	98.0%	31.8	25	21.4	1	0	0	909.49	786	792
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	RTYVPALEQSADGHK	99.7%	32.4	25	28.6	0	2	0	1671.85	613	627
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	SEAEQKLPLGTR	99.7%	76.1	25	61.4	11	1	0	1328.72	241	252
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	TINVEFAK	99.7%	44.5	25	32.3	2	0	0	921.50	376	383
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	TYVPALEQSADGHK	99.7%	71.2	25	68	2	0	0	1515.74	614	627
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	TYVPALEQSADGHKETGAPSK	99.7%	38	25	37	0	2	0	2186.07	614	634
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	VSMHYSDPKPK	99.7%	42.3	25	39.6	0	10	0	1304.63	202	212
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	WMEANQHSLNILGQK	99.7%	57.4	25	52.1	2	1	0	1768.88	187	201
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	YGGISTASVDFEQPTR	99.7%	94.2	25	94.2	3	0	0	1727.82	838	853
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	37	49	146	0.15%	43.3%	YGIPEPPEPK	97.5%	30.7	25	25.2	1	0	0	1126.58	825	834
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	11	22	0.02%	19.4%	AQPSASLGVGYR	95.0%	27.9	25	22.9	1	0	0	1205.63	251	262
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	11	22	0.02%	19.4%	AQPSVSLGAPYR	98.4%	32.7	25	21.6	1	0	0	1245.66	275	286
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	11	22	0.02%	19.4%	ASYDDPYKK	98.7%	33.8	25	20.6	1	0	0	1086.51	586	594
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	11	22	0.02%	19.4%	ASYVAPLTAQPATYR	99.7%	80.3	25	70.1	2	0	0	1608.84	224	238
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	11	22	0.02%	19.4%	IFVGNVSAACTSQELR	99.7%	131	25	131	4	0	0	1751.87	81	96
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	11	22	0.02%	19.4%	INVELSTK	99.3%	36.9	25	28.5	4	0	0	903.51	142	149
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	11	22	0.02%	19.4%	KGPGLAVQSGDK	99.7%	43.2	25	34.1	2	0	0	1156.63	153	164
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	11	22	0.02%	19.4%	TQPMTAQAASYR	99.7%	48.3	25	44.3	4	0	0	1340.63	263	274
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	11	22	0.02%	19.4%	TQSSASLAASYAAQQHPQAAASYR	99.7%	84.6	25	84.6	0	1	0	2465.18	518	541
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	11	22	0.02%	19.4%	YSGSYNDYLR	99.7%	62.8	25	62.8	2	0	0	1237.55	648	657
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	7	8	16	0.02%	10.1%	EKEELEEIR	99.7%	46.9	25	25.4	2	0	0	1174.60	539	547
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	7	8	16	0.02%	10.1%	FPVAPLIPYPLITK	99.7%	53.5	25	53.5	1	0	0	1568.95	248	261
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	7	8	16	0.02%	10.1%	GAIEVLIR	99.7%	42.7	25	25.1	4	0	0	870.54	209	216
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	7	8	16	0.02%	10.1%	LGASNSPGQPNSVK	99.7%	43.1	25	42	2	0	0	1355.69	672	685
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	7	8	16	0.02%	10.1%	LLAEGHPDPDAELQR	99.7%	59.3	25	55.9	2	1	0	1660.83	550	564
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	7	8	16	0.02%	10.1%	LLHDLQIGEK	99.2%	36.2	25	32.4	2	0	0	1165.66	146	155
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	7	8	16	0.02%	10.1%	LVPLDYGEDDKNATK	99.7%	46	25	43.9	2	0	0	1677.83	712	726
RNA-binding protein 26	RBM26	RBM26_HUMAN	113.6	100.0%	4	4	5	0.01%	4.4%	AEAEAAAVHGAR	99.7%	41.1	25	32.1	2	0	0	1152.58	936	947
RNA-binding protein 26	RBM26	RBM26_HUMAN	113.6	100.0%	4	4	5	0.01%	4.4%	AISSTEAVLNNR	98.7%	33.8	25	33.8	1	0	0	1274.67	586	597
RNA-binding protein 26	RBM26	RBM26_HUMAN	113.6	100.0%	4	4	5	0.01%	4.4%	EGSTQQLQTTSPK	99.7%	61.6	25	56.6	1	0	0	1404.70	606	618
RNA-binding protein 26	RBM26	RBM26_HUMAN	113.6	100.0%	4	4	5	0.01%	4.4%	LNEHFSR	95.7%	28.5	25	20.6	1	0	0	902.45	549	555
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	9	9	13	0.01%	13.4%	AAEGVSAADMAK	99.7%	62.3	25	59.9	2	0	0	1136.53	454	465
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	9	9	13	0.01%	13.4%	AEVEQVELPDGK	99.7%	52.7	25	47.6	1	0	0	1313.66	654	665
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	9	9	13	0.01%	13.4%	CLLAASPENEAGGLK	99.7%	50.5	25	44.7	1	0	0	1529.76	392	406
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	9	9	13	0.01%	13.4%	EITTFEGCK	99.7%	40.4	25	14.7	1	0	0	1084.50	64	72
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	9	9	13	0.01%	13.4%	FNQLVEQYK	99.3%	36.5	25	20.2	1	0	0	1168.60	730	738
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	9	9	13	0.01%	13.4%	LLLSATSGEK	98.7%	33.7	25	30.7	2	0	0	1018.58	506	515
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	9	9	13	0.01%	13.4%	QQLSSEQVSR	99.7%	52.1	25	48.8	2	0	0	1161.59	709	718
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	9	9	13	0.01%	13.4%	SEQLEELFSQVGPVK	99.7%	83.6	25	77.2	2	0	0	1689.87	17	31
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	9	9	13	0.01%	13.4%	TVAVDWAVAK	97.7%	31.1	25	18.1	1	0	0	1059.58	183	192
RNA-binding protein 39	RBM39	RBM39_HUMAN	59.4	100.0%	4	4	9	0.01%	10.0%	DLEEFFSTVGK	99.7%	66.4	25	59.8	3	0	0	1271.62	168	178
RNA-binding protein 39	RBM39	RBM39_HUMAN	59.4	100.0%	4	4	9	0.01%	10.0%	TDASSASSFLDSDELER	99.7%	70.4	25	70.4	1	0	0	1829.80	330	346
RNA-binding protein 39	RBM39	RBM39_HUMAN	59.4	100.0%	4	4	9	0.01%	10.0%	TGIDLGTTGR	99.7%	59	25	51.5	1	0	0	990.52	347	356
RNA-binding protein 39	RBM39	RBM39_HUMAN	59.4	100.0%	4	4	9	0.01%	10.0%	VLGVPIIVQASQAEK	99.7%	92.4	25	80.8	4	0	0	1551.91	218	232
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	8	9	14	0.01%	25.3%	AEDAVEAIR	99.7%	58.6	25	33.7	2	0	0	973.49	121	129
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	8	9	14	0.01%	25.3%	ATAPVPTVGEGYGYGHESELSQASAAAR	99.7%	35.1	25	35.1	0	1	0	2776.32	314	341
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	8	9	14	0.01%	25.3%	GLDNTEFQGK	99.7%	52.9	25	50.4	1	0	0	1108.53	130	139
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	8	9	14	0.01%	25.3%	GLDNTEFQGKR	99.5%	38.7	25	30.5	2	0	0	1264.63	130	140
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	8	9	14	0.01%	25.3%	LFIGNLPR	99.7%	51.6	25	16.5	2	0	0	929.56	4	11

RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	8	9	14	0.01%	25.3%	LHGVNINVEASK	99.7%	71.2	25	57.9	1	1	0	1280.70	60	71
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	8	9	14	0.01%	25.3%	VADLTEQYNEQYGAVR	99.7%	102	25	95.3	2	0	0	1855.88	183	198
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	8	9	14	0.01%	25.3%	VLECDIIK	99.6%	38.9	25	22.1	2	0	0	989.53	28	35
RNA-binding protein FUS	FUS	FUS_HUMAN	53.4	100.0%	3	4	7	0.01%	6.3%	AAIDWFDGKEFSGNPIK	99.7%	55.3	25	50.5	2	2	0	1894.93	349	365
RNA-binding protein FUS	FUS	FUS_HUMAN	53.4	100.0%	3	4	7	0.01%	6.3%	GEATVSFDDPPSAK	99.7%	107	25	99.3	2	0	0	1420.66	335	348
RNA-binding protein FUS	FUS	FUS_HUMAN	53.4	100.0%	3	4	7	0.01%	6.3%	LKGEATVSFDDPPSAK	99.7%	43.3	25	43.3	0	1	0	1661.84	333	348
RNA-binding protein Musashi homolog 1	MSI1	MSI1H_HUMAN	39.1	100.0%	4	5	6	0.01%	15.7%	EYFGQFGEVK	96.5%	29.4	25	29.4	1	0	0	1203.57	38	47
RNA-binding protein Musashi homolog 1	MSI1	MSI1H_HUMAN	39.1	100.0%	4	5	6	0.01%	15.7%	GFGFVTFESEDIVEK	98.8%	34	25	30.5	1	0	0	1703.82	151	165
RNA-binding protein Musashi homolog 1	MSI1	MSI1H_HUMAN	39.1	100.0%	4	5	6	0.01%	15.7%	GFGFVTFMDQAGVDK	99.7%	88	25	83.7	3	0	0	1618.76	62	76
RNA-binding protein Musashi homolog 1	MSI1	MSI1H_HUMAN	39.1	100.0%	4	5	6	0.01%	15.7%	SYTGLAPGYTYQFPEFR	99.7%	42.1	25	42.1	1	0	0	1996.94	231	247
RNA-binding protein PNO1	PNO1	PNO1_HUMAN	27.9	100.0%	3	4	6	0.01%	13.5%	AEEGFTQVTR	99.7%	51.6	25	38.4	2	0	0	1137.55	12	21
RNA-binding protein PNO1	PNO1	PNO1_HUMAN	27.9	100.0%	3	4	6	0.01%	13.5%	IFTPIVEHLGLQIR	99.6%	39.7	25	39.7	1	1	0	1635.96	95	108
RNA-binding protein PNO1	PNO1	PNO1_HUMAN	27.9	100.0%	3	4	6	0.01%	13.5%	MDTEEARPAK	96.3%	29.1	25	28.7	2	0	0	1147.54	47	56
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	4	4	8	0.01%	13.1%	GYAFVQYSNER	99.7%	76.8	25	69.3	2	0	0	1333.62	56	66
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	4	4	8	0.01%	13.1%	SNIDALLSR	99.7%	49.1	25	28.6	2	0	0	988.54	199	207
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	4	4	8	0.01%	13.1%	SSELQAIK	98.7%	33.5	25	14.9	1	0	0	875.48	184	191
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	4	4	8	0.01%	13.1%	VFIGNLNTALVK	99.7%	66.2	25	0	3	0	0	1288.76	23	34
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	12	15	27	0.03%	39.9%	ANCIDSTASAEAVFASEVK	99.7%	82.5	25	78.1	2	0	0	1969.92	266	284
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	12	15	27	0.03%	39.9%	ANCIDSTASAEAVFASEVKK	98.8%	27	25	27	0	2	0	2098.01	266	285
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	12	15	27	0.03%	39.9%	DHAVVVGVYRPPPK	99.6%	31.5	25	30	0	2	0	1533.85	305	318
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	12	15	27	0.03%	39.9%	GKEDALVTK	99.6%	39.8	25	29.1	1	0	0	960.54	101	109
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	12	15	27	0.03%	39.9%	HEGVFICR	99.7%	49	25	49	2	0	0	1017.49	93	100
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	12	15	27	0.03%	39.9%	IVALNAHTFLR	99.7%	58.5	25	54	2	2	0	1254.73	245	255
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	12	15	27	0.03%	39.9%	LAAAILGGVDQIHIKPGAK	99.7%	42.6	25	41.1	0	2	0	1872.11	144	162
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	12	15	27	0.03%	39.9%	NLVPGESVYGEK	96.2%	29	25	24.5	1	0	0	1291.65	110	121
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	12	15	27	0.03%	39.9%	NLVPGESVYGEKR	99.7%	50.9	25	42.2	2	1	0	1447.75	110	122
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	12	15	27	0.03%	39.9%	SGRDLINLAK	99.0%	34.8	25	19.9	2	0	0	1086.63	196	205
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	12	15	27	0.03%	39.9%	TNIIPVIEDAR	99.7%	55.2	25	0	2	0	0	1240.69	208	218
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	12	15	27	0.03%	39.9%	VSISEGDDKIEYR	99.7%	66.8	25	66.8	2	2	0	1510.74	123	135
RRP12-like protein	RRP12	RRP12_HUMAN	143.7	100.0%	4	4	6	0.01%	3.8%	EICAVLAAVTEVIR	99.7%	48.7	25	46.3	1	0	0	1543.85	123	136
RRP12-like protein	RRP12	RRP12_HUMAN	143.7	100.0%	4	4	6	0.01%	3.8%	RAVLETIR	97.6%	31	25	12.9	2	0	0	957.58	711	718
RRP12-like protein	RRP12	RRP12_HUMAN	143.7	100.0%	4	4	6	0.01%	3.8%	TYLTITDTQLVNSLLEK	99.7%	40	25	40	1	0	0	1952.06	719	735
RRP12-like protein	RRP12	RRP12_HUMAN	143.7	100.0%	4	4	6	0.01%	3.8%	VLATQPGPGR	99.1%	35.6	25	35.3	2	0	0	995.56	1129	1138
RUN and FYVE domain-containing protein 1	RUFY1	RUFY1_HUMAN	79.8	99.8%	2	2	3	0.00%	3.1%	AQNAESSLQQK	99.7%	55.5	25	48.7	1	0	0	1203.60	470	480
RUN and FYVE domain-containing protein 1	RUFY1	RUFY1_HUMAN	79.8	99.8%	2	2	3	0.00%	3.1%	SFFGPLELVEK	98.8%	34.1	25	33.2	2	0	0	1265.68	172	182
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	16	0.02%	19.3%	ALESSIAPIVIFASNR	99.7%	71.8	25	71.8	2	2	0	1687.94	318	333
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	16	0.02%	19.3%	AVLLAGPPGTGK	99.7%	42.6	25	35.1	2	0	0	1080.64	65	76
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	16	0.02%	19.3%	EACGVIVELIK	99.7%	42.7	25	28.6	2	0	0	1230.68	47	57
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	16	0.02%	19.3%	GLGLDESGLAK	99.6%	38.8	25	33.1	2	0	0	1059.57	23	33
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	16	0.02%	19.3%	LDPSIFESLQK	99.7%	40.9	25	27.6	2	0	0	1276.68	172	182
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	16	0.02%	19.3%	QAASGLVGQENAR	99.7%	81.1	25	72.3	2	0	0	1300.66	34	46
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	16	0.02%	19.3%	TALALAIAQELGSK	99.7%	108	25	108	2	0	0	1385.80	77	90
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	13	24	0.02%	31.7%	AAGVVLEMIR	99.7%	62.1	25	48.8	2	0	0	1058.60	55	64
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	13	24	0.02%	31.7%	ALESDMAPVLIMATNR	99.7%	72.4	25	66.6	2	0	0	1731.88	315	330
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	13	24	0.02%	31.7%	AVLIAGQPGTGK	99.7%	58.8	25	49.1	2	0	0	1111.65	72	83
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	13	24	0.02%	31.7%	DKVQAGDVITIDK	99.7%	83.1	25	68.9	2	0	0	1401.76	185	197
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	13	24	0.02%	31.7%	EVVHTVSLHEIDVINSR	99.7%	44.4	25	44.4	0	2	0	1947.03	237	253
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	13	24	0.02%	31.7%	FVQCPDGELQK	99.7%	60.8	25	52.6	2	0	0	1320.63	224	234
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	13	24	0.02%	31.7%	GTEVQVDDIKR	99.7%	61.8	25	43.4	2	0	0	1259.66	418	428
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	13	24	0.02%	31.7%	LLIVSTTPYSEK	99.7%	44.3	25	35.7	1	0	0	1350.75	354	365
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	13	24	0.02%	31.7%	LLIVSTTPYSEKDTK	99.7%	77.6	25	77.6	1	0	0	1694.92	354	368

RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	13	24	0.02%	31.7%	QASQGMVGQLAAR	99.7%	65.7	25	56.6	2	0	0	1316.67	41	53
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	13	24	0.02%	31.7%	TQGFLALFSGDTGEIK	99.7%	94.2	25	89.7	2	0	0	1683.86	254	269
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	13	24	0.02%	31.7%	TTEMETIYDLGTK	99.7%	82.8	25	78.1	4	0	0	1501.71	165	177
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	8	10	17	0.02%	21.5%	DLDLKKPIYQR	99.7%	53.5	25	48.4	1	0	0	1388.79	363	373
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	8	10	17	0.02%	21.5%	ELLEIVKK	99.5%	37.8	25	27.9	2	0	0	971.61	344	351
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	8	10	17	0.02%	21.5%	FVIGGPQGDAGLTGR	99.7%	106	25	101	2	0	0	1444.75	250	264
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	8	10	17	0.02%	21.5%	FVIGGPQGDAGLTGRK	97.7%	24.5	25	22	0	1	0	1572.85	250	265
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	8	10	17	0.02%	21.5%	NFDLRPGVIVR	97.4%	30.5	25	27.5	1	0	0	1285.74	352	362
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	8	10	17	0.02%	21.5%	TGMILLAGEITSR	99.7%	84.7	25	78.1	4	0	0	1361.75	62	74
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	8	10	17	0.02%	21.5%	TQVTVQYMQDR	99.7%	53.1	25	44	2	0	0	1368.66	182	192
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	8	10	17	0.02%	21.5%	YLDEDTIYHLQPSGR	99.7%	70.4	25	68.2	2	2	0	1806.87	235	249
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	23	32	67	0.07%	25.1%	AEIGIAMGSGTAVAK	99.7%	91.2	25	82.8	4	0	0	1391.72	713	727
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	23	32	67	0.07%	25.1%	AMGVVVATGVNTEIGK	99.7%	77.4	25	64.8	4	0	0	1545.83	219	234
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	23	32	67	0.07%	25.1%	ANACNSVIK	97.3%	30.4	25	15.1	2	0	0	976.49	468	476
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	23	32	67	0.07%	25.1%	EEMHLEDSANFIK	97.3%	30.4	25	30.2	1	0	0	1562.72	573	585
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	23	32	67	0.07%	25.1%	EFDELNPSAQR	99.7%	58.2	25	47.5	2	0	0	1305.61	656	666
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	23	32	67	0.07%	25.1%	EFTLEFSR	99.7%	41.9	25	30.3	2	0	0	1028.50	482	489
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	23	32	67	0.07%	25.1%	EWGSGSDTLR	99.7%	46.1	25	33.7	2	0	0	1107.51	550	559
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	23	32	67	0.07%	25.1%	GAPEGVIDR	98.8%	34.2	25	34	2	0	0	913.47	515	523
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	23	32	67	0.07%	25.1%	GTAVAICR	99.7%	42.2	25	21.6	2	0	0	847.45	629	636
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	23	32	67	0.07%	25.1%	HTDPVPDPR	94.8%	27.7	25	22.2	1	0	0	1033.51	190	198
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	23	32	67	0.07%	25.1%	IGIFGQDEDVTSK	99.7%	87.1	25	79.3	4	0	0	1408.70	638	650
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	23	32	67	0.07%	25.1%	IRDEMVATEQER	99.7%	54.2	25	45.1	3	2	0	1476.71	235	246
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	23	32	67	0.07%	25.1%	ISLPVILMDETLK	99.7%	78.4	25	69.1	6	0	0	1471.84	972	984
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	23	32	67	0.07%	25.1%	KAEIGIAMGSGTAVAK	97.3%	24	25	15.7	0	1	0	1503.82	712	727
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	23	32	67	0.07%	25.1%	LDEFGEQLSK	99.7%	53.7	25	37.6	4	0	0	1165.57	253	262
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	23	32	67	0.07%	25.1%	MNVFDTELK	99.7%	53.2	25	34.5	4	0	0	1112.53	452	460
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	23	32	67	0.07%	25.1%	NMLFSGTNIAAGK	99.7%	81.7	25	79.1	4	0	0	1323.67	206	218
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	23	32	67	0.07%	25.1%	SLPSVETLGCTSVICSDK	99.7%	86.4	25	86.4	2	0	0	1952.93	335	352
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	23	32	67	0.07%	25.1%	SMSVYCTPNKPSR	99.7%	45.3	25	42.7	2	0	0	1526.71	493	505
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	23	32	67	0.07%	25.1%	TGTLTTNQMSVCR	99.7%	55.3	25	49.5	3	0	0	1484.68	353	365
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	23	32	67	0.07%	25.1%	VDQSILTGESVSVIK	99.7%	80.3	25	69.8	4	0	0	1574.86	175	189
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	23	32	67	0.07%	25.1%	VGEATETALTCLVEK	99.7%	125	25	117	4	0	0	1620.82	437	451
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	23	32	67	0.07%	25.1%	VIMITGDNK	99.6%	39.1	25	16.6	2	0	0	990.53	620	628
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	19	55	0.06%	22.5%	DQIIDSLKR	99.7%	46.8	25	32.4	4	0	0	1087.61	80	88
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	19	55	0.06%	22.5%	EPAVLMGILGIYK	99.7%	67.1	25	67.1	2	0	0	1403.80	539	551
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	19	55	0.06%	22.5%	LGSSSLTNIPEEVR	99.7%	73.3	25	58.2	3	0	0	1501.79	288	301
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	19	55	0.06%	22.5%	LILPELGPVFK	99.7%	49.6	25	39.9	4	0	0	1225.76	408	418
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	19	55	0.06%	22.5%	LLLNVTPTVRPDADQMTK	95.2%	21.9	25	21.9	0	1	0	2012.08	306	323
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	19	55	0.06%	22.5%	LLTVQHPLEESR	99.7%	71	25	65.7	4	0	0	1421.77	101	112
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	19	55	0.06%	22.5%	LYDVETK	99.4%	37	25	28.8	3	0	0	867.45	149	155
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	19	55	0.06%	22.5%	MDLLLTK	96.8%	29.7	25	18.9	1	0	0	849.48	433	439
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	19	55	0.06%	22.5%	MVHGNITPENIILNK	99.3%	28.7	25	28.7	0	2	0	1692.91	174	188
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	19	55	0.06%	22.5%	NACLQTSSLAVR	99.7%	89.6	25	78.8	4	0	0	1319.67	494	505
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	19	55	0.06%	22.5%	NSVLPMVYR	98.8%	34.1	25	24.3	1	0	0	1078.57	447	455
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	19	55	0.06%	22.5%	QEVAVFVFDKK	99.7%	52.8	25	40.4	3	0	0	1309.72	59	69
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	19	55	0.06%	22.5%	SQQPLKPQVHTPVATVK	95.6%	22.2	25	22.2	0	1	0	1858.05	698	714
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	19	55	0.06%	22.5%	VNSLVCLGK	99.7%	48.1	25	42.8	4	0	0	989.54	506	514
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	19	55	0.06%	22.5%	VTADVTSAVMGNPVTR	99.7%	124	25	109	10	0	0	1633.82	15	30
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	19	55	0.06%	22.5%	VTNIGNQQIDK	99.7%	62.2	25	48.9	4	0	0	1229.65	637	647
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	19	55	0.06%	22.5%	YGLLQVSEGLSFLHSSVK	99.7%	54.4	25	54.4	2	2	0	1964.05	156	173

Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	7	8	14	0.01%	14.6%	FGQDIISPLLSVK	99.7%	80.5	25	76.5	3	0	0	1416.81	51	63
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	7	8	14	0.01%	14.6%	GTAAEMVAVK	99.7%	49.7	25	39.1	1	0	0	976.51	215	224
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	7	8	14	0.01%	14.6%	LTSAVSSLPELLEK	99.7%	84	25	60.7	4	0	0	1486.84	382	395
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	7	8	14	0.01%	14.6%	QQNLPVTR	98.6%	33.3	25	23	2	0	0	955.53	542	549
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	7	8	14	0.01%	14.6%	SLLDIISDPDAGTPEDK	99.7%	48.5	25	43.5	1	0	0	1785.88	437	453
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	7	8	14	0.01%	14.6%	SYDLTPVDKFWQK	99.7%	58.2	25	54.3	1	0	0	1626.82	316	328
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	7	8	14	0.01%	14.6%	VNLEESSGVENSPAGARPK	99.7%	94.9	25	94.9	1	1	0	1940.97	292	310
Sentrin-specific protease 3	SENP3	SENP3_HUMAN	65.0	100.0%	4	4	5	0.01%	7.7%	GLVLQLIQSYQR	99.7%	46.4	25	38.1	2	0	0	1417.82	358	369
Sentrin-specific protease 3	SENP3	SENP3_HUMAN	65.0	100.0%	4	4	5	0.01%	7.7%	LGLLGALMAEDGVR	99.5%	38.1	25	38.1	1	0	0	1414.77	197	210
Sentrin-specific protease 3	SENP3	SENP3_HUMAN	65.0	100.0%	4	4	5	0.01%	7.7%	STSLTFHWK	95.5%	28.3	25	18.3	1	0	0	1106.56	141	149
Sentrin-specific protease 3	SENP3	SENP3_HUMAN	65.0	100.0%	4	4	5	0.01%	7.7%	YLQAEAVKK	99.3%	36.8	25	26.5	1	0	0	1049.60	498	506
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	6	6	15	0.02%	11.9%	FINDQYEK	99.1%	35.1	25	25	1	0	0	1056.50	382	389
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	6	6	15	0.02%	11.9%	LEPKPQPPVAEATPR	99.7%	56.7	25	56.7	0	2	0	1629.90	223	237
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	6	6	15	0.02%	11.9%	QVENAGAIGPSR	99.7%	50	25	37.7	2	0	0	1198.62	118	129
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	6	6	15	0.02%	11.9%	VPEVPTAPATDAAPK	99.7%	57.5	25	48.8	4	0	0	1463.77	172	186
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	6	6	15	0.02%	11.9%	VVNIVPVIAK	99.7%	45.9	25	45.9	3	0	0	1051.69	436	445
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	6	6	15	0.02%	11.9%	YLQEEVNINR	99.7%	54	25	45.2	3	0	0	1277.65	390	399
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	11	12	19	0.02%	30.2%	AACFAIQK	99.7%	45.7	25	30.5	2	0	0	908.47	190	197
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	11	12	19	0.02%	30.2%	DHPALNYNIVSGPPSHK	99.5%	30	25	30	0	2	0	1845.92	76	92
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	11	12	19	0.02%	30.2%	ECINFASFNFLGLLDNPR	97.5%	30.8	25	30.8	1	0	0	2127.03	99	116
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	11	12	19	0.02%	30.2%	EQEIEDQKNPR	99.7%	50.3	25	47.4	2	0	0	1385.67	223	233
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	11	12	19	0.02%	30.2%	HNDMADLER	99.7%	51.3	25	51.3	3	0	0	1100.48	211	219
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	11	12	19	0.02%	30.2%	IFLEESLSFGVLGEHGR	99.7%	32.8	25	29.4	0	1	0	1889.98	271	287
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	11	12	19	0.02%	30.2%	RGDIVFVDR	98.6%	33.2	25	17	2	0	0	1076.58	181	189
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	11	12	19	0.02%	30.2%	SIALTQAR	97.5%	30.7	25	2.13	1	0	0	859.50	423	430
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	11	12	19	0.02%	30.2%	TEEAIIYSYGFATIASAIPAYSK	99.7%	52.5	25	52.5	1	0	0	2466.24	158	180
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	11	12	19	0.02%	30.2%	VVVTVEQTEEELER	99.7%	107	25	105	2	0	0	1659.84	446	459
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	11	12	19	0.02%	30.2%	YGVGTCGPR	99.7%	64.5	25	55.9	2	0	0	966.45	128	136
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	10	11	32	0.03%	40.7%	DAEDAVYGR	99.7%	44.2	25	38.9	2	0	0	995.44	66	74
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	10	11	32	0.03%	40.7%	DGTGVVEFVR	99.7%	56.5	25	39.5	5	0	0	1078.55	155	164
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	10	11	32	0.03%	40.7%	DGYDYDGYR	99.7%	44.1	25	44.1	2	0	0	1123.43	75	83
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	10	11	32	0.03%	40.7%	EAGDVCYADVYR	99.7%	66.9	25	66.9	3	0	0	1417.61	143	154
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	10	11	32	0.03%	40.7%	EDMTYAVR	98.6%	33.2	25	28.2	1	0	0	984.45	166	173
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	10	11	32	0.03%	40.7%	GGPPFAFVEFEDPR	99.7%	49.3	25	49.3	2	0	0	1564.74	52	65
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	10	11	32	0.03%	40.7%	IYVGNLPPDIR	99.7%	61.5	25	49.6	5	0	0	1256.70	18	28
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	10	11	32	0.03%	40.7%	KEDMTYAVR	99.7%	54	25	41.1	4	0	0	1112.54	165	173
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	10	11	32	0.03%	40.7%	LRVEFPR	98.6%	33.4	25	14.1	4	0	0	916.54	84	90
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	10	11	32	0.03%	40.7%	SHEGETAYIR	99.7%	48.2	25	44.8	6	0	0	1162.55	182	191
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	10	11	32	0.03%	40.7%	TKDIEDVFYK	99.7%	68.6	25	65.8	2	0	0	1257.64	29	38
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	8	9	16	0.02%	42.1%	AFGYYGPLR	99.7%	49.4	25	44	4	0	0	1043.53	29	37
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	8	9	16	0.02%	42.1%	DSCPLDCK	98.9%	34.3	25	34.3	2	0	0	994.40	4	11
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	8	9	16	0.02%	42.1%	NPPGFAFVEFEDPR	99.7%	46.8	25	46.8	1	0	0	1621.76	44	57
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	8	9	16	0.02%	42.1%	NRGPPPSWGR	99.6%	38.9	25	33	2	0	0	1123.58	89	98
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	8	9	16	0.02%	42.1%	VELSNGEKR	98.5%	33.1	25	16	1	0	0	1031.55	78	86
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	8	9	16	0.02%	42.1%	VRVELSNGEK	99.7%	48.2	25	36	2	0	0	1130.62	76	85
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	8	9	16	0.02%	42.1%	VYVGNLGNNGNK	99.7%	42.9	25	35.4	2	0	0	1248.63	12	23
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	8	9	16	0.02%	42.1%	VYVGNLGNNGNKTELER	99.7%	44.3	25	32.4	1	1	0	1876.95	12	28
Serine/arginine-rich splicing factor 5	SRSF5	SRSF5_HUMAN	31.3	100.0%	4	4	7	0.01%	18.0%	LIVENLSSR	99.7%	51.8	25	43	2	0	0	1030.59	110	118
Serine/arginine-rich splicing factor 5	SRSF5	SRSF5_HUMAN	31.3	100.0%	4	4	7	0.01%	18.0%	LNEGVVEFASYGDLK	99.7%	108	25	101	2	0	0	1640.82	144	158
Serine/arginine-rich splicing factor 5	SRSF5	SRSF5_HUMAN	31.3	100.0%	4	4	7	0.01%	18.0%	QAGEVTFADAHRPK	99.7%	39.5	25	37.4	0	1	0	1526.77	130	143
Serine/arginine-rich splicing factor 5	SRSF5	SRSF5_HUMAN	31.3	100.0%	4	4	7	0.01%	18.0%	VSWQDLKDFMR	99.7%	48.1	25	40.3	2	0	0	1424.70	119	129

Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	7	8	17	0.02%	31.2%	DGVGMVEYLR	99.7%	63.6	25	40.6	4	0	0	1138.56	145	154
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	7	8	17	0.02%	31.2%	EAGDVCYADVQK	99.7%	79	25	74.3	2	0	0	1354.59	133	144
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	7	8	17	0.02%	31.2%	EKDLEDLFYK	99.7%	46.2	25	36	2	0	0	1299.65	27	36
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	7	8	17	0.02%	31.2%	IYVGNLPTDVR	99.7%	54.9	25	40.3	2	0	0	1246.68	16	26
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	7	8	17	0.02%	31.2%	LRVEFPR	98.6%	33.4	25	14.1	4	0	0	916.54	82	88
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	7	8	17	0.02%	31.2%	NGYDYGQCR	99.7%	46.4	25	46.4	1	0	0	1132.45	73	81
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	7	8	17	0.02%	31.2%	SHEGETSYIR	99.7%	42.4	25	38.5	2	0	0	1178.54	172	181
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	15	17	31	0.03%	43.4%	AERDILVEADSLWVVK	99.5%	30.6	25	30.6	0	1	0	1843.00	136	151
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	15	17	31	0.03%	43.4%	AKDLILR	99.6%	40	25	24	2	0	0	828.53	353	359
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	15	17	31	0.03%	43.4%	DIKPDNLLLDSK	99.7%	42.6	25	35.2	2	0	0	1370.75	212	223
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	15	17	31	0.03%	43.4%	DILVEADSLWVVK	99.7%	90.5	25	88.9	4	0	0	1486.82	139	151
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	15	17	31	0.03%	43.4%	DTGHVYAMK	99.4%	37.3	25	28.2	2	0	0	1021.48	110	118
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	15	17	31	0.03%	43.4%	DWVFINYTYK	99.7%	54.6	25	0	4	0	0	1348.66	437	446
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	15	17	31	0.03%	43.4%	ERPAAISIEIK	99.4%	37.4	25	15.4	1	0	0	1226.71	392	402
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	15	17	31	0.03%	43.4%	FCCEWEHR	99.7%	41.2	25	41.2	2	0	0	1223.47	360	367
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	15	17	31	0.03%	43.4%	IGAPGVEEIK	99.7%	60.7	25	45.1	2	0	0	1012.57	368	377
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	15	17	31	0.03%	43.4%	LGLEDFESLK	99.7%	68.2	25	67.9	3	0	0	1150.60	84	93
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	15	17	31	0.03%	43.4%	LSDFGLCTGLK	99.7%	87.2	25	78.5	4	0	0	1210.61	228	238
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	15	17	31	0.03%	43.4%	LSDFGLCTGLKK	99.7%	66.8	25	60.7	4	1	0	1338.71	228	239
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	15	17	31	0.03%	43.4%	NLNHSLPSDFTFQNMNSK	99.1%	27.9	25	27.9	0	1	0	2093.97	248	265
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	15	17	31	0.03%	43.4%	QLAFSTVGTPDYIAPEVFMQTGYNK	99.7%	51	25	51	0	2	0	2777.35	277	301
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	15	17	31	0.03%	43.4%	RFEGLTAR	99.6%	39.3	25	32.5	2	0	0	949.52	447	454
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	15	17	31	0.03%	43.4%	SNSFFEGVDWEHIR	99.7%	36.3	25	36.3	0	1	0	1722.79	378	391
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	15	17	31	0.03%	43.4%	VMEEEGLKDEEK	99.7%	92.9	25	74.8	3	0	0	1435.66	51	62
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	15	17	31	0.03%	43.4%	VTLENFYSNLIAQHEER	99.7%	68.6	25	62	2	2	0	2063.02	25	41
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	15	17	31	0.03%	43.4%	VTLENFYSNLIAQHEEREMR	99.7%	34.1	25	33.5	0	1	0	2495.20	25	44
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	20	51	0.05%	33.8%	AKDLILR	99.6%	40	25	24	2	0	0	828.53	354	360
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	20	51	0.05%	33.8%	DIKPDNLLLDAK	99.7%	49.2	25	44	4	0	0	1354.76	213	224
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	20	51	0.05%	33.8%	DILVEADGAWVVK	99.7%	63.2	25	52.3	1	0	0	1414.76	140	152
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	20	51	0.05%	33.8%	DTGHIYAMK	99.7%	47.4	25	39	3	0	0	1035.49	111	119
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	20	51	0.05%	33.8%	DWVFLNYTYK	99.7%	54.6	25	0	4	0	0	1348.66	435	444
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	20	51	0.05%	33.8%	ERPAAIPIEIK	99.7%	50.1	25	39.1	5	0	0	1236.73	393	403
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	20	51	0.05%	33.8%	FCIDSENR	99.5%	38	25	36.9	4	0	0	1040.45	361	368
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	20	51	0.05%	33.8%	FEGLTQR	99.6%	39.7	25	25.9	2	0	0	850.44	446	452
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	20	51	0.05%	33.8%	GHPFFEGVDWEHIR	99.7%	42.1	25	42.1	0	1	0	1725.81	379	392
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	20	51	0.05%	33.8%	GSIPTYMK	95.7%	28.5	25	14	2	0	0	912.45	453	460
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	20	51	0.05%	33.8%	LGLDDFESLK	99.7%	57.9	25	57.9	5	0	0	1136.58	85	94
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	20	51	0.05%	33.8%	LSDFGLCTGLK	99.7%	87.2	25	78.5	4	0	0	1210.61	229	239
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	20	51	0.05%	33.8%	LSDFGLCTGLKK	99.7%	66.8	25	60.7	4	1	0	1338.71	229	240
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	20	51	0.05%	33.8%	LTLENFYSNLILQHEER	99.7%	52.4	25	52.4	2	2	0	2119.08	26	42
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	20	51	0.05%	33.8%	NLTHNPPSDFSFQNMNSK	99.7%	51.4	25	51.4	0	2	0	2093.93	249	266
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	20	51	0.05%	33.8%	RFEGLTQR	99.3%	36.6	25	22	3	0	0	1006.54	445	452
Serine/threonine-protein kinase D1	PRKD1	KPCD1_HUMAN	101.7	99.8%	2	2	4	0.00%	5.3%	EIPLSEILSLEPVK	99.7%	43.6	25	43.6	2	0	0	1566.90	465	478
Serine/threonine-protein kinase D1	PRKD1	KPCD1_HUMAN	101.7	99.8%	2	2	4	0.00%	5.3%	FLITQILVALR	99.7%	68.4	25	68.4	2	0	0	1286.82	685	695
Serine/threonine-protein kinase D1	PRKD1	KPCD1_HUMAN	101.7	99.8%	2	2	4	0.00%	5.3%	LCDFGFAR	99.7%	48.8	25	36.8	2	0	0	985.46	725	732
Serine/threonine-protein kinase D1	PRKD1	KPCD1_HUMAN	101.7	99.8%	2	2	4	0.00%	5.3%	SVVGTPAYLAPEVLR	99.7%	81.2	25	75.5	2	0	0	1571.88	742	756
Serine/threonine-protein kinase D2	PRKD2	KPCD2_HUMAN	96.8	100.0%	3	3	5	0.01%	3.3%	FLITQILVALR	99.7%	68.4	25	68.4	2	0	0	1286.82	653	663
Serine/threonine-protein kinase D2	PRKD2	KPCD2_HUMAN	96.8	100.0%	3	3	5	0.01%	3.3%	LCDFGFAR	99.7%	48.8	25	36.8	2	0	0	985.46	693	700
Serine/threonine-protein kinase D2	PRKD2	KPCD2_HUMAN	96.8	100.0%	3	3	5	0.01%	3.3%	NEVAILQSLR	99.7%	73	25	64.4	1	0	0	1142.65	597	606
Serine/threonine-protein kinase D3	PRKD3	KPCD3_HUMAN	100.5	99.8%	2	3	4	0.00%	4.9%	FMVTQILVALR	99.7%	71.2	25	65.6	3	0	0	1290.76	678	688
Serine/threonine-protein kinase D3	PRKD3	KPCD3_HUMAN	100.5	99.8%	2	3	4	0.00%	4.9%	LCDFGFAR	99.7%	48.8	25	36.8	2	0	0	985.46	718	725

Serine/threonine-protein kinase D3	PRKD3	KPCD3_HUMAN	100.5	99.8%	2	3	4	0.00%	4.9%	SVVGTPAYLAPEVLR	99.7%	81.2	25	75.5	2	0	0	1571.88	735	749
Serine/threonine-protein kinase D3	PRKD3	KPCD3_HUMAN	100.5	99.8%	2	3	4	0.00%	4.9%	YITHESDDAR	97.5%	30.7	25	23	1	0	0	1206.54	852	861
Serine/threonine-protein kinase MST4	MST4	MST4_HUMAN	46.5	100.0%	5	5	9	0.01%	15.4%	AANVLLSEQGDVK	99.7%	81.2	25	81.2	3	0	0	1343.72	147	159
Serine/threonine-protein kinase MST4	MST4	MST4_HUMAN	46.5	100.0%	5	5	9	0.01%	15.4%	ADIWSLGITAIELAK	99.7%	90.1	25	79.5	2	0	0	1600.89	200	214
Serine/threonine-protein kinase MST4	MST4	MST4_HUMAN	46.5	100.0%	5	5	9	0.01%	15.4%	AGPFDEFQIATMLK	99.7%	49.9	25	47.4	1	0	0	1567.78	113	126
Serine/threonine-protein kinase MST4	MST4	MST4_HUMAN	46.5	100.0%	5	5	9	0.01%	15.4%	SIAVAEAACPGITDK	99.7%	58.7	25	58.7	1	0	0	1502.75	384	398
Serine/threonine-protein kinase MST4	MST4	MST4_HUMAN	46.5	100.0%	5	5	9	0.01%	15.4%	VLFLIPK	99.0%	35.1	25	35.1	2	0	0	829.55	227	233
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	5	5	11	0.01%	2.4%	DASAVSLSESK	99.7%	60.1	25	50.9	2	0	0	1093.54	911	921
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	5	5	11	0.01%	2.4%	STAMDTLSSLVFQLGK	98.7%	33.5	25	33.5	1	0	0	1697.88	1171	1186
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	5	5	11	0.01%	2.4%	TLDQSPELR	98.7%	33.7	25	24.8	1	0	0	1058.55	1162	1170
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	5	5	11	0.01%	2.4%	TLVLLLGVDPSR	99.7%	62.2	25	48.8	4	0	0	1282.77	1672	1683
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	5	5	11	0.01%	2.4%	VLGLLGALDPYK	99.7%	43.2	25	43.2	3	0	0	1258.74	887	898
Serine/threonine-protein kinase Nek7	NEK7	NEK7_HUMAN	34.6	99.8%	2	2	2	0.00%	5.3%	GQFSEVYR	99.7%	41.7	25	35.8	1	0	0	985.47	43	50
Serine/threonine-protein kinase Nek7	NEK7	NEK7_HUMAN	34.6	99.8%	2	2	2	0.00%	5.3%	LGDLGLGR	99.4%	37.2	25	7.34	1	0	0	800.46	177	184
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	5	5	9	0.01%	11.4%	EVLEGLEYLHK	99.2%	36.2	25	27	1	0	0	1329.71	129	139
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	5	5	9	0.01%	11.4%	IPISLVLR	99.7%	49	25	49	2	0	0	910.61	432	439
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	5	5	9	0.01%	11.4%	LLSGGSVLDIIK	99.7%	81	25	65.7	2	0	0	1214.74	94	105
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	5	5	9	0.01%	11.4%	SGVLDESTIATILR	99.7%	81.9	25	76.6	2	0	0	1474.81	115	128
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	5	5	9	0.01%	11.4%	TAQALSSGSGSQETK	99.7%	65	25	61.3	2	0	0	1451.70	417	431
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	28	122	0.12%	39.3%	AMEIASQR	99.7%	52.2	25	37.7	6	0	0	905.45	402	409
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	28	122	0.12%	39.3%	ATVEQVLDPR	99.7%	64.4	25	54.3	10	0	0	1127.61	156	165
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	28	122	0.12%	39.3%	DCANVNDFFMR	99.7%	77.2	25	77.2	9	0	0	1388.57	360	370
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	28	122	0.12%	39.3%	DKYVSGEFR	98.8%	33.9	25	15.8	2	0	0	1100.54	221	229
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	28	122	0.12%	39.3%	DMDIIMK	98.8%	34	25	22.9	2	0	0	865.42	443	449
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	28	122	0.12%	39.3%	EANVYHASTANGESR	99.7%	87.1	25	86.8	6	0	0	1605.73	191	205
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	28	122	0.12%	39.3%	ELFEFVTDPSITHENMDAYLSK	98.9%	27.3	25	27.3	0	3	0	2602.20	380	401
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	28	122	0.12%	39.3%	ELYLQVIQYMR	99.7%	81.5	25	72.3	13	0	0	1455.77	302	312
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	28	122	0.12%	39.3%	GIITEINGCISTGK	99.7%	71	25	66	3	0	0	1462.76	177	190
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	28	122	0.12%	39.3%	GYVWNGGSNPQANR	99.7%	72.1	25	69.4	2	0	0	1519.70	82	95
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	28	122	0.12%	39.3%	HSVAVMTVR	99.7%	52.6	25	35.8	5	0	0	999.54	371	379
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	28	122	0.12%	39.3%	INLDKLNVTDSVINK	99.7%	103	25	103	6	7	0	1685.94	120	134
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	28	122	0.12%	39.3%	LNTAEIPCPEPIMLR	99.7%	62	25	47.4	8	0	0	1753.90	257	271
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	28	122	0.12%	39.3%	LNVTDSVINK	99.7%	71.6	25	53.5	7	0	0	1102.61	125	134
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	28	122	0.12%	39.3%	NVQLSESK	94.7%	27.7	25	17.2	1	0	0	904.47	292	299
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	28	122	0.12%	39.3%	NYERDMDIIMK	95.8%	28.6	25	16.5	2	0	0	1459.66	439	449
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	28	122	0.12%	39.3%	SSQDHVDEEVFKR	99.7%	56.4	25	55.2	4	5	0	1575.74	415	427
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	28	122	0.12%	39.3%	TSILVFK	99.2%	35.8	25	28.6	4	0	0	807.50	212	218
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	28	122	0.12%	39.3%	TSILVFKDR	99.7%	51.1	25	47	2	0	0	1078.63	212	220
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	28	122	0.12%	39.3%	VPALLENQVEER	99.7%	87.3	25	87.3	10	0	0	1396.74	482	493
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	28	122	0.12%	39.3%	VVPGQFDDADSSDSENR	99.7%	85.8	25	85.8	4	0	0	1837.78	11	27
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	28	122	0.12%	39.3%	YVSGEFR	99.2%	36.2	25	29.4	1	0	0	857.42	223	229
Serine/threonine-protein kinase ULK3	ULK3	ULK3_HUMAN	53.4	99.8%	2	2	2	0.00%	5.1%	ASVENLLTEIEILK	96.6%	29.5	25	25.4	1	0	0	1571.89	54	67
Serine/threonine-protein kinase ULK3	ULK3	ULK3_HUMAN	53.4	99.8%	2	2	2	0.00%	5.1%	ATALVVQAVK	99.7%	41.7	25	28.7	1	0	0	999.62	284	293
Serine/threonine-protein kinase VRK1	VRK1	VRK1_HUMAN	45.5	100.0%	3	3	4	0.00%	5.8%	KTVLQLSLR	99.7%	57	25	52	1	0	0	1057.67	152	160
Serine/threonine-protein kinase VRK1	VRK1	VRK1_HUMAN	45.5	100.0%	3	3	4	0.00%	5.8%	TVLQLSLR	99.7%	42.5	25	22.9	1	0	0	929.58	153	160
Serine/threonine-protein kinase VRK1	VRK1	VRK1_HUMAN	45.5	100.0%	3	3	4	0.00%	5.8%	VEPSDNGPLFTELK	99.7%	44.2	25	41.5	2	0	0	1545.78	72	85
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	5	5	9	0.01%	9.6%	ESSLTEPVIVGLLK	99.7%	61.6	25	61.3	2	0	0	1484.86	354	367
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	5	5	9	0.01%	9.6%	FLESPDFQPNIAK	99.7%	70.6	25	59.3	2	0	0	1505.76	220	232
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	5	5	9	0.01%	9.6%	TVETEAVQMLK	99.7%	48.6	25	39.8	2	0	0	1248.65	550	560
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	5	5	9	0.01%	9.6%	VLPIMFPALYR	99.7%	48.4	25	48.4	2	0	0	1319.75	442	452
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	5	5	9	0.01%	9.6%	YSGGPQIVK	95.5%	28.3	25	20.2	1	0	0	948.52	74	82

Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	8	9	14	0.01%	15.4%	ELVSDANQHVK	99.7%	45.2	25	36.4	2	0	0	1239.63	332	342
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	8	9	14	0.01%	15.4%	LAGGDWFTSR	97.9%	31.6	25	0.43	1	0	0	1109.54	135	144
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	8	9	14	0.01%	15.4%	LSTIALALGVER	99.7%	65.6	25	64.4	2	0	0	1242.74	35	46
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	8	9	14	0.01%	15.4%	LTQDQDVDVK	99.7%	68.1	25	61	2	0	0	1160.58	567	576
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	8	9	14	0.01%	15.4%	MAGDPVANVR	99.7%	69.9	25	61.1	4	0	0	1045.51	528	537
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	8	9	14	0.01%	15.4%	VLAMSGDPNYLHR	99.7%	31.8	25	30.6	0	1	0	1488.73	486	498
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	8	9	14	0.01%	15.4%	YFAQEALTVLSLA	94.7%	27.6	25	27.6	1	0	0	1425.76	577	589
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	8	9	14	0.01%	15.4%	YMVADKFTELQK	98.5%	33.1	25	31.6	1	0	0	1472.75	261	272
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	PPP2R1B	2AAB_HUMAN	66.2	99.8%	2	2	2	0.00%	5.5%	ELVSDTNQHVK	99.7%	48.3	25	38.8	1	0	0	1269.64	344	354
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	PPP2R1B	2AAB_HUMAN	66.2	99.8%	2	2	2	0.00%	5.5%	LSTIALALGVER	99.7%	65.6	25	64.4	2	0	0	1242.74	47	58
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	PPP2R1B	2AAB_HUMAN	66.2	99.8%	2	2	2	0.00%	5.5%	MAGDQVANVR	99.7%	50.2	25	42.2	1	0	0	1060.52	540	549
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	7	8	15	0.02%	29.2%	APLDLDKYVEIAR	99.7%	61.6	25	57.3	2	2	0	1502.82	2	14
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	7	8	15	0.02%	29.2%	GAGWLFGAK	99.7%	55.9	25	36.7	2	0	0	906.48	211	219
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	7	8	15	0.02%	29.2%	LVTVWSAPNYCYR	99.7%	42.7	25	42.7	2	0	0	1628.79	252	264
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	7	8	15	0.02%	29.2%	QITQVYGFYDECQTK	99.7%	72.2	25	72.2	2	0	0	1879.85	118	132
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	7	8	15	0.02%	29.2%	TGGQVPDTNYIFMGDFVDR	99.7%	57.6	25	51.2	2	0	0	2131.98	67	85
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	7	8	15	0.02%	29.2%	VTNEFVHINNLK	99.7%	72.6	25	72.6	2	0	0	1427.76	220	231
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	7	8	15	0.02%	29.2%	YGNANAWR	99.7%	63.9	25	55.2	1	0	0	951.44	133	140
Serine/threonine-protein phosphatase 6 regulatory subunit 3	PPP6R3	PP6R3_HUMAN	97.7	100.0%	3	3	4	0.00%	3.6%	GPNSALVQQLIK	99.7%	44.2	25	37.3	1	0	0	1267.74	475	486
Serine/threonine-protein phosphatase 6 regulatory subunit 3	PPP6R3	PP6R3_HUMAN	97.7	100.0%	3	3	4	0.00%	3.6%	IANCIVHSTDK	97.2%	30.3	25	30.3	1	0	0	1257.63	464	474
Serine/threonine-protein phosphatase 6 regulatory subunit 3	PPP6R3	PP6R3_HUMAN	97.7	100.0%	3	3	4	0.00%	3.6%	VLSILISR	99.7%	53.8	25	53.8	2	0	0	900.59	127	134
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	6	6	20	0.02%	21.1%	AIETTDIISR	99.7%	70.8	25	59	5	0	0	1118.61	153	162
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	6	6	20	0.02%	21.1%	ALQFPPEGWLR	97.6%	31	25	24.3	1	0	0	1313.70	241	251
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	6	6	20	0.02%	21.1%	EQAELTGLR	99.7%	50.7	25	35.8	6	0	0	1016.54	126	134
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	6	6	20	0.02%	21.1%	NVESGEEELASK	99.7%	71.3	25	67.7	4	0	0	1291.60	77	88
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	6	6	20	0.02%	21.1%	TLGDTGFMPPDK	99.7%	48.6	25	41	2	0	0	1278.60	274	285
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	6	6	20	0.02%	21.1%	VSTDLLR	99.5%	38.6	25	23.5	2	0	0	803.46	170	176
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	PP1G_HUMAN	37.0	100.0%	5	6	8	0.01%	21.4%	EIFLSQPILLELEAPLK	99.7%	40.7	25	40.7	1	0	0	1953.13	44	60
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	PP1G_HUMAN	37.0	100.0%	5	6	8	0.01%	21.4%	IKYPENFFLLR	97.8%	24.7	25	24	1	2	0	1439.80	112	122
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	PP1G_HUMAN	37.0	100.0%	5	6	8	0.01%	21.4%	NVQLQENEIR	99.7%	58.2	25	51.8	2	0	0	1242.64	27	36
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	PP1G_HUMAN	37.0	100.0%	5	6	8	0.01%	21.4%	QSLETICLLLAYK	97.7%	31	25	26.7	1	0	0	1551.85	99	111
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	PP1G_HUMAN	37.0	100.0%	5	6	8	0.01%	21.4%	TFTDCFNCLPIAAIVDEK	99.3%	36.3	25	27.5	1	0	0	2113.99	151	168
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	9	10	14	0.01%	34.3%	EFLVAGGEDFK	99.1%	35.5	25	35.5	1	0	0	1211.59	236	246
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	9	10	14	0.01%	34.3%	FSPDGELYASGSEDGTLR	99.7%	65.2	25	60.6	1	0	0	1900.86	273	290
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	9	10	14	0.01%	34.3%	IYDLNKPEAEPK	99.7%	51.2	25	47.9	2	1	0	1416.74	126	137
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	9	10	14	0.01%	34.3%	LWDHATMTEVK	99.3%	36.5	25	36.5	1	0	0	1330.65	168	178
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	9	10	14	0.01%	34.3%	LWQTVVGK	99.3%	36.6	25	28.1	1	0	0	930.54	291	298
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	9	10	14	0.01%	34.3%	QGDTGDWIGTFLGHK	99.7%	48.8	25	47.8	0	2	0	1631.78	45	59
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	9	10	14	0.01%	34.3%	SIAFHSAVSLDPIK	99.7%	46.2	25	46.2	1	0	0	1484.81	205	218
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	9	10	14	0.01%	34.3%	TVDFTQDSNYLLTGGQDK	99.7%	108	25	108	2	0	0	2001.94	105	122
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	9	10	14	0.01%	34.3%	YDYNSGEELESYK	99.7%	76.8	25	76.8	2	0	0	1596.67	250	262
Serpin B12	SERPINB12	SPB12_HUMAN	46.3	100.0%	2	2	4	0.00%	5.9%	ADLTGISPSPNLYLSK	99.4%	37.5	25	25.1	3	0	0	1675.89	328	343
Serpin B12	SERPINB12	SPB12_HUMAN	46.3	100.0%	2	2	4	0.00%	5.9%	IGFIEEVK	98.0%	31.8	25	22.5	1	0	0	934.52	232	239
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	8	8	19	0.02%	24.9%	DTQSGSLLFIGR	99.7%	85.1	25	71.6	5	0	0	1293.68	394	405
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	8	8	19	0.02%	24.9%	GVVEVTHDLQK	99.7%	57.5	25	42.8	2	0	0	1224.66	309	319
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	8	8	19	0.02%	24.9%	HLAGLGLTEAIDKNK	99.7%	64.6	25	64.6	0	2	0	1579.88	320	334
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	8	8	19	0.02%	24.9%	KPAAAAAPGTAEK	99.7%	56.7	25	51.5	2	0	0	1182.65	23	35
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	8	8	19	0.02%	24.9%	LFYADHPFIFLVR	99.7%	51.6	25	51.6	2	0	0	1637.88	381	393
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	8	8	19	0.02%	24.9%	LYGPSSVSFADDFVR	99.7%	85.9	25	80.9	2	0	0	1659.80	134	148
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	8	8	19	0.02%	24.9%	SAGLAFSLYQAMAK	99.7%	71.9	25	67.2	2	0	0	1457.75	47	60
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	8	8	19	0.02%	24.9%	SYTVGVMMMHR	99.7%	41.6	25	41.6	2	0	0	1311.60	229	239

Serrate RNA effector molecule homolog	SRRT	SRRT_HUMAN	100.7	100.0%	5	5	8	0.01%	5.7%	ESLSEEEAQK	99.7%	66.9	25	61.2	2	0	0	1149.53	678	687
Serrate RNA effector molecule homolog	SRRT	SRRT_HUMAN	100.7	100.0%	5	5	8	0.01%	5.7%	LRECELSPGVNR	97.1%	30.1	25	30.1	1	0	0	1429.72	487	498
Serrate RNA effector molecule homolog	SRRT	SRRT_HUMAN	100.7	100.0%	5	5	8	0.01%	5.7%	LTPLLSVR	96.1%	28.9	25	24.3	1	0	0	898.57	670	677
Serrate RNA effector molecule homolog	SRRT	SRRT_HUMAN	100.7	100.0%	5	5	8	0.01%	5.7%	MEGGTENDLR	99.7%	53.8	25	39.5	2	0	0	1121.49	257	266
Serrate RNA effector molecule homolog	SRRT	SRRT_HUMAN	100.7	100.0%	5	5	8	0.01%	5.7%	VALSEPQPER	99.7%	47.5	25	41.4	2	0	0	1125.59	450	459
Serum albumin	ALB	ALBU_HUMAN	69.4	100.0%	3	3	6	0.01%	6.1%	KVPQVSTPTLVEVSR	97.2%	23.9	25	23.9	0	1	0	1639.94	438	452
Serum albumin	ALB	ALBU_HUMAN	69.4	100.0%	3	3	6	0.01%	6.1%	LVNEVTEFAK	99.7%	51.3	25	39.3	3	0	0	1149.62	66	75
Serum albumin	ALB	ALBU_HUMAN	69.4	100.0%	3	3	6	0.01%	6.1%	YICENQDSISSK	99.3%	36.3	25	32.5	2	0	0	1443.64	287	298
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	9	10	17	0.02%	25.5%	ASSTCPLTFENVK	99.7%	58.5	25	54.2	2	0	0	1453.70	257	269
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	9	10	17	0.02%	25.5%	ATYLPQLTTEK	99.7%	51.5	25	47.4	2	0	0	1264.68	160	170
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	9	10	17	0.02%	25.5%	FAQEQIAPLVSTMDENSK	99.7%	48.7	25	48.7	1	0	0	2007.97	71	88
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	9	10	17	0.02%	25.5%	FAQEQIAPLVSTMDENSKMEK	95.3%	22	25	22	0	1	0	2428.14	71	91
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	9	10	17	0.02%	25.5%	GITSFLVDR	97.0%	29.9	25	17.5	1	0	0	1007.55	231	239
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	9	10	17	0.02%	25.5%	IGTIYEGASNIQLNTIAK	99.7%	120	25	113	2	0	0	1906.03	409	426
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	9	10	17	0.02%	25.5%	LLEAGKPFIK	99.7%	44.8	25	27.7	2	0	0	1115.68	356	365
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	9	10	17	0.02%	25.5%	VPEANILGQIGHGYK	99.7%	77	25	74.2	2	2	0	1595.85	270	284
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	9	10	17	0.02%	25.5%	YYASEIAGQTTSK	99.7%	110	25	100	2	0	0	1418.68	372	384
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	18	42	0.04%	43.2%	AKYIYDSAFHPDTGEK	99.7%	63.6	25	62	2	2	0	1841.87	71	86
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	18	42	0.04%	43.2%	ANHFFTVTDPR	99.7%	40.1	25	37.6	2	1	0	1304.64	25	35
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	18	42	0.04%	43.2%	FVPFAAVAAANCINIPLMR	99.7%	43.3	25	41.1	1	0	0	2075.09	179	197
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	18	42	0.04%	43.2%	HVSPLIGR	99.6%	38.8	25	35	2	0	0	878.52	171	178
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	18	42	0.04%	43.2%	IQESHPELR	99.7%	58	25	43.8	2	0	0	1108.57	306	314
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	18	42	0.04%	43.2%	IQESHPELRR	99.7%	33.8	25	26.8	0	2	0	1264.68	306	315
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	18	42	0.04%	43.2%	NILLTNEQLESAR	99.7%	107	25	97.4	3	0	0	1500.80	36	48
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	18	42	0.04%	43.2%	NILLTNEQLESARK	99.7%	77.9	25	73.3	2	0	0	1628.90	36	49
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	18	42	0.04%	43.2%	QAITQVVVSR	99.7%	95.6	25	91.7	3	0	0	1100.64	224	233
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	18	42	0.04%	43.2%	QGIVPPGLTENELWR	99.7%	70.3	25	67.1	4	0	0	1708.90	56	70
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	18	42	0.04%	43.2%	SSMSVTSLEAELQAK	99.7%	88.1	25	88.1	6	0	0	1596.78	291	305
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	18	42	0.04%	43.2%	VGIPVTDENGNR	99.7%	72.8	25	72.8	2	0	0	1270.64	203	214
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	18	42	0.04%	43.2%	WDQSTFIGR	99.7%	68.6	25	0	2	0	0	1109.54	16	24
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	18	42	0.04%	43.2%	YIYDSAFHPDTGEK	99.7%	76.3	25	73.2	4	2	0	1642.74	73	86
Sideroflexin-2	SFXN2	SFXN2_HUMAN	36.2	100.0%	4	4	7	0.01%	15.8%	AAAIGITQVVISR	99.7%	86.1	25	72.3	2	0	0	1298.78	220	232
Sideroflexin-2	SFXN2	SFXN2_HUMAN	36.2	100.0%	4	4	7	0.01%	15.8%	MGVVPPGTQVEQLLYAK	99.6%	38.9	25	34.9	2	0	0	1829.98	55	71
Sideroflexin-2	SFXN2	SFXN2_HUMAN	36.2	100.0%	4	4	7	0.01%	15.8%	NAASPTSVR	94.8%	27.7	25	22.7	1	0	0	902.47	136	144
Sideroflexin-2	SFXN2	SFXN2_HUMAN	36.2	100.0%	4	4	7	0.01%	15.8%	YGELEPYVYFNK	99.7%	79.4	25	68.8	2	0	0	1521.73	309	320
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	100.0%	6	6	8	0.01%	21.7%	DAVPAFIEPNVR	99.7%	51	25	49	2	0	0	1327.70	19	30
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	100.0%	6	6	8	0.01%	21.7%	GIAVMDKEGNVLGHSR	98.9%	27.1	25	27.1	0	1	0	1682.86	224	239
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	100.0%	6	6	8	0.01%	21.7%	IQEAWKR	99.4%	37.2	25	24.8	1	0	0	930.52	85	91
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	100.0%	6	6	8	0.01%	21.7%	IQSPTEETEIFYHR	99.7%	33.3	25	33.3	0	1	0	1749.84	322	335
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	100.0%	6	6	8	0.01%	21.7%	SLATVHPDSSNLIPK	99.2%	36	25	32	2	0	0	1578.85	92	106
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	100.0%	6	6	8	0.01%	21.7%	SYTCKPLER	96.2%	29	25	23.6	1	0	0	1153.57	156	164
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	6	9	17	0.02%	30.7%	EIPIVHR	97.6%	30.9	25	19.6	1	0	0	863.51	91	97
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	6	9	17	0.02%	30.7%	GDLLFLTNR	99.7%	53.1	25	29.8	2	0	0	1048.58	64	72
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	6	9	17	0.02%	30.7%	GDLLFLTNRVEDPIR	99.7%	36.6	25	36.5	0	1	0	1757.95	64	78
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	6	9	17	0.02%	30.7%	GDNNAVDDRGLYK	99.7%	44.6	25	44.6	2	1	0	1436.68	115	127
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	6	9	17	0.02%	30.7%	MLSLDFLDDVRR	99.3%	29.1	25	29.1	2	2	0	1495.76	1	12
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	6	9	17	0.02%	30.7%	VGEIVVFR	99.7%	68	25	61.7	6	0	0	918.54	79	86
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	8	15	0.02%	35.4%	FDDKYTLK	99.6%	39.8	25	30.7	2	0	0	1029.53	166	173
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	8	15	0.02%	35.4%	FFDHSGTLVMDAYEPEISR	99.7%	35.9	25	35.9	0	2	0	2230.01	196	214
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	8	15	0.02%	35.4%	IDDKPVKIDK	99.7%	45.7	25	31.2	2	0	0	1170.67	41	50
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	8	15	0.02%	35.4%	IDKWDGSAVK	99.7%	52.7	25	36.5	2	0	0	1118.58	48	57

Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	8	15	0.02%	35.4%	LHDSLAIER	99.7%	42.4	25	35.8	1	0	0	1053.57	215	223
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	8	15	0.02%	35.4%	SGLLDKWK	99.7%	58.7	25	38.4	2	0	0	946.54	33	40
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	8	15	0.02%	35.4%	SIFLVAHR	99.6%	39.5	25	30.4	2	0	0	942.55	138	145
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	8	15	0.02%	35.4%	YVENFGLIDGR	99.7%	68.5	25	61.6	2	0	0	1282.64	74	84
Signal peptidase complex subunit 3	SPCS3	SPCS3_HUMAN	20.3	100.0%	4	4	12	0.01%	21.7%	MNTVLSR	99.0%	35.1	25	12	2	0	0	820.43	1	7
Signal peptidase complex subunit 3	SPCS3	SPCS3_HUMAN	20.3	100.0%	4	4	12	0.01%	21.7%	NNALNQVVLWDK	99.7%	62.7	25	48.9	2	0	0	1413.75	97	108
Signal peptidase complex subunit 3	SPCS3	SPCS3_HUMAN	20.3	100.0%	4	4	12	0.01%	21.7%	NVEDFTGPR	99.7%	55.4	25	51.5	4	0	0	1034.49	50	58
Signal peptidase complex subunit 3	SPCS3	SPCS3_HUMAN	20.3	100.0%	4	4	12	0.01%	21.7%	YFFFDDGNGLK	99.7%	44.6	25	40.3	4	0	0	1322.61	127	137
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	8	9	14	0.01%	47.1%	EVNKFQMAYSNLLR	99.7%	41.7	25	39.9	2	1	0	1712.88	75	88
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	8	9	14	0.01%	47.1%	FQMAYSNLLR	99.7%	61.5	25	48	2	0	0	1242.63	79	88
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	8	9	14	0.01%	47.1%	GTVEGFEPADNK	99.7%	56.1	25	56.1	2	0	0	1263.59	44	55
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	8	9	14	0.01%	47.1%	GTVEGFEPADNKCLLR	99.2%	28.3	25	13.1	0	1	0	1805.89	44	59
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	8	9	14	0.01%	47.1%	ISTVVSSK	98.1%	31.9	25	26.4	1	0	0	820.48	67	74
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	8	9	14	0.01%	47.1%	KISTVVSSK	97.5%	30.7	25	23.8	1	0	0	948.57	66	74
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	8	9	14	0.01%	47.1%	TSGSVYITLKK	99.7%	56.2	25	56.2	2	0	0	1196.69	22	32
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	8	9	14	0.01%	47.1%	VLLESEQFLTELTR	99.7%	107	25	99.6	2	0	0	1677.91	2	15
Signal recognition particle 19 kDa protein	SRP19	SRP19_HUMAN	16.2	100.0%	3	3	4	0.00%	19.4%	SVMLYAAEMIPK	99.7%	47.8	25	40.4	1	0	0	1384.69	103	114
Signal recognition particle 19 kDa protein	SRP19	SRP19_HUMAN	16.2	100.0%	3	3	4	0.00%	19.4%	TGGADQSLQQGEGSK	99.7%	58.5	25	55.1	2	0	0	1462.68	122	136
Signal recognition particle 19 kDa protein	SRP19	SRP19_HUMAN	16.2	100.0%	3	3	4	0.00%	19.4%	TGGADQSLQQGEGSKK	94.7%	21.6	25	21.6	0	1	0	1590.77	122	137
Signal recognition particle 9 kDa protein	SRP9	SRP09_HUMAN	10.1	100.0%	3	4	8	0.01%	34.9%	LYLADPMK	99.4%	37.4	25	19.2	3	0	0	966.50	17	24
Signal recognition particle 9 kDa protein	SRP9	SRP09_HUMAN	10.1	100.0%	3	4	8	0.01%	34.9%	PQYQTWEEFSR	99.7%	57.6	25	54.8	2	0	0	1470.66	2	12
Signal recognition particle 9 kDa protein	SRP9	SRP09_HUMAN	10.1	100.0%	3	4	8	0.01%	34.9%	VTDDLVCLVYK	99.7%	72.9	25	65.6	3	0	0	1324.68	42	52
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	6	8	11	0.01%	10.3%	AGAVEQLR	99.7%	41	25	24.8	2	0	0	843.47	459	466
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	6	8	11	0.01%	10.3%	ALADHSMAQTPR	99.7%	47.7	25	39.4	1	1	0	1297.63	569	580
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	6	8	11	0.01%	10.3%	DAAGIAMEAIAFAR	99.7%	98.1	25	87.2	2	0	0	1406.71	497	510
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	6	8	11	0.01%	10.3%	GGNNSFTHEALTLK	99.5%	38.7	25	28.9	1	0	0	1488.74	42	55
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	6	8	11	0.01%	10.3%	MLDFFTIFSK	99.7%	46.7	25	41.7	3	0	0	1248.63	1	10
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	6	8	11	0.01%	10.3%	TMVQLFEK	98.3%	32.3	25	28.6	1	0	0	995.52	485	492
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	26	0.03%	50.9%	AIVFVVDSAAFQR	99.7%	72.1	25	72.1	4	0	0	1422.77	138	150
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	26	0.03%	50.9%	AVLLVGLCDSGK	99.7%	81.1	25	70.3	2	0	0	1231.67	66	77
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	26	0.03%	50.9%	DTQTSITDSCAVYR	99.7%	99.5	25	99.5	2	0	0	1616.72	91	104
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	26	0.03%	50.9%	GDVGSADIQDLEK	99.7%	91.6	25	76.3	3	0	0	1346.64	253	265
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	26	0.03%	50.9%	GNSLTLIDLPGHESLR	99.7%	50.5	25	50.5	2	2	0	1721.92	110	125
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	26	0.03%	50.9%	LIQQQLEK	99.7%	43.4	25	19.2	2	0	0	999.58	192	199
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	26	0.03%	50.9%	LLTGLYR	98.8%	34.2	25	11.8	1	0	0	835.50	84	90
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	26	0.03%	50.9%	LQFLER	99.5%	38.7	25	0	2	0	0	805.46	126	131
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	26	0.03%	50.9%	NTPSFLIACNK	99.7%	55.3	25	48.6	2	0	0	1264.64	171	181
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	26	0.03%	50.9%	SAAPSTLDSSSTAPAQLGK	99.7%	94.2	25	94.2	2	0	0	1788.90	209	227
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	26	0.03%	50.9%	VADGGGAGGTFQPYLDTLR	99.7%	84.8	25	84.8	2	0	0	1894.93	9	27
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	10	11	18	0.02%	21.1%	AAIEAFNK	96.0%	28.8	25	18.3	1	0	0	863.46	206	213
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	10	11	18	0.02%	21.1%	ALLQQQPEDDSKR	99.5%	30.6	25	25.8	0	1	0	1527.78	405	417
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	10	11	18	0.02%	21.1%	DLPDVQELITQVR	99.7%	59.5	25	55.2	2	0	0	1525.82	509	521
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	10	11	18	0.02%	21.1%	EFGDSLSLEILQIIK	95.8%	28.6	25	25.1	1	0	0	1704.94	53	67
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	10	11	18	0.02%	21.1%	FETFCLDPSLVTK	99.7%	76.6	25	73.2	2	0	0	1556.77	558	570
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	10	11	18	0.02%	21.1%	LASAFTEEQAVLYNQR	99.7%	104	25	95	2	0	0	1839.92	221	236
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	10	11	18	0.02%	21.1%	LEALITQTR	99.5%	37.9	25	23.5	1	0	0	1044.60	278	286
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	10	11	18	0.02%	21.1%	LFESMLSECR	99.7%	61.7	25	57.2	3	0	0	1271.58	336	345
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	10	11	18	0.02%	21.1%	QVPGGGGGGGSGGGGGSGGGGSGGGR	99.7%	71.5	25	71.5	2	0	0	1843.80	6	31
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	10	11	18	0.02%	21.1%	VEEISPNIR	99.7%	46	25	45.2	3	0	0	1056.57	237	245
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	7	7	9	0.01%	12.8%	AIELLQEFSDQHPENAAEIK	99.7%	35.1	25	35.1	0	1	0	2282.13	357	376
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	7	7	9	0.01%	12.8%	EALNVINTHTK	96.7%	29.6	25	20.9	1	0	0	1239.67	63	73

Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	7	7	9	0.01%	12.8%	SPAHLSLIR	99.7%	65.3	25	53.6	2	0	0	993.58	443	451
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	7	7	9	0.01%	12.8%	TEEALQLYNQIIK	99.7%	67.1	25	57.7	2	0	0	1562.84	242	254
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	7	7	9	0.01%	12.8%	TIESANQQTDKLK	99.7%	64.3	25	52.9	1	0	0	1475.77	100	112
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	7	7	9	0.01%	12.8%	VLANNSLSFEK	99.7%	57.5	25	46.3	1	0	0	1221.65	74	84
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	7	7	9	0.01%	12.8%	YDECLAVYR	99.7%	41.3	25	41.3	1	0	0	1188.54	125	133
Signal transducer and activator of transcription 3	STAT3	STAT3_HUMAN	88.1	100.0%	3	3	6	0.01%	6.5%	GLSIEQLTTLAEK	99.7%	91.8	25	82	2	0	0	1402.78	519	531
Signal transducer and activator of transcription 3	STAT3	STAT3_HUMAN	88.1	100.0%	3	3	6	0.01%	6.5%	LLQTAATAAQQGGQANHPTAAVVTEK	99.7%	93.1	25	93.1	0	2	0	2576.34	115	140
Signal transducer and activator of transcription 3	STAT3	STAT3_HUMAN	88.1	100.0%	3	3	6	0.01%	6.5%	TQIQSVEPYTK	99.7%	40.7	25	16.9	2	0	0	1293.67	632	642
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	4	4	8	0.01%	21.6%	DVAYQYVK	95.8%	28.6	25	22.4	1	0	0	985.50	96	103
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	4	4	8	0.01%	21.6%	DVAYQYVKK	98.2%	32.2	25	22.3	2	0	0	1113.59	96	104
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	4	4	8	0.01%	21.6%	SGDSEVYQLGDVSQK	99.7%	97.1	25	96.1	3	0	0	1611.75	67	81
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	4	4	8	0.01%	21.6%	VGQDPVLR	99.7%	59.6	25	54.2	2	0	0	883.50	39	46
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	10	10	19	0.02%	9.1%	DIFLFITR	98.1%	32	25	28.1	1	0	0	1024.58	115	122
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	10	10	19	0.02%	9.1%	DLALVNDQLLGFVR	99.7%	125	25	117	2	0	0	1572.87	391	404
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	10	10	19	0.02%	9.1%	EVQLAQIFEPLSR	99.7%	61.7	25	55.1	2	0	0	1529.83	751	763
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	10	10	19	0.02%	9.1%	IETDLPQIR	99.7%	51.1	25	38.1	2	0	0	1084.60	709	717
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	10	10	19	0.02%	9.1%	LLVACCLADIFR	99.7%	73.9	25	73.9	3	0	0	1450.75	88	99
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	10	10	19	0.02%	9.1%	LYTVCDVALCVINSK	99.7%	73.4	25	68.2	2	0	0	1754.88	1075	1089
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	10	10	19	0.02%	9.1%	NDDLNKPINK	99.6%	39.5	25	28.7	2	0	0	1170.61	1285	1294
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	10	10	19	0.02%	9.1%	SIEGTADDEEEGVSPDTAIR	99.7%	59.3	25	55.2	2	0	0	2090.94	638	657
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	10	10	19	0.02%	9.1%	SYISEETR	94.7%	27.6	25	11.3	1	0	0	984.46	1120	1127
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	10	10	19	0.02%	9.1%	TVTAAGAENIQQK	99.7%	109	25	96.5	2	0	0	1330.70	1240	1252
Small nuclear ribonucleoprotein E	SNRPE	RUXE_HUMAN	10.8	100.0%	2	3	4	0.00%	29.3%	IMLKGDNITLLQSVSN	97.5%	30.7	25	30.7	1	0	0	1761.94	77	92
Small nuclear ribonucleoprotein E	SNRPE	RUXE_HUMAN	10.8	100.0%	2	3	4	0.00%	29.3%	VMVQPINLIFR	99.7%	54.1	25	49	3	0	0	1345.77	13	23
Small nuclear ribonucleoprotein Sm D1	SNRPD1	SMD1_HUMAN	13.3	100.0%	4	6	18	0.02%	37.8%	EPVQLETLSIR	99.7%	60.1	25	37.8	2	0	0	1284.72	51	61
Small nuclear ribonucleoprotein Sm D1	SNRPD1	SMD1_HUMAN	13.3	100.0%	4	6	18	0.02%	37.8%	LSHETVTIELK	99.7%	55.1	25	44.2	6	2	0	1269.71	10	20
Small nuclear ribonucleoprotein Sm D1	SNRPD1	SMD1_HUMAN	13.3	100.0%	4	6	18	0.02%	37.8%	NGTQVHGTITGVDVSMNTHLK	99.7%	38.7	25	38.7	0	2	0	2209.10	21	41
Small nuclear ribonucleoprotein Sm D1	SNRPD1	SMD1_HUMAN	13.3	100.0%	4	6	18	0.02%	37.8%	NREPVQLETLSIR	99.7%	70.3	25	70.3	4	2	0	1554.86	49	61
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	7	9	17	0.02%	55.9%	EEEEFNTGPLSVLTQSVK	99.7%	62.5	25	62.5	2	0	0	2006.99	20	37
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	7	9	17	0.02%	55.9%	EMWTEVPK	98.3%	32.5	25	28.5	1	0	0	1019.49	72	79
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	7	9	17	0.02%	55.9%	GDSVIVVLR	99.7%	73.5	25	49.6	4	0	0	957.57	103	111
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	7	9	17	0.02%	55.9%	HCNMVLENVK	99.7%	59.3	25	55.4	4	0	0	1243.59	62	71
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	7	9	17	0.02%	55.9%	NNTQVLINCR	99.7%	73.7	25	62.6	2	0	0	1231.62	38	47
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	7	9	17	0.02%	55.9%	SEMTPEELQK	99.7%	49.3	25	40.8	3	0	0	1191.56	9	18
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	7	9	17	0.02%	55.9%	SEMTPEELQKR	99.7%	42.4	25	42.1	1	0	0	1347.66	9	19
Small nuclear ribonucleoprotein Sm D3	SNRPD3	SMD3_HUMAN	13.9	99.8%	2	3	5	0.01%	15.1%	FLILPDMLK	99.7%	40.1	25	18.9	4	0	0	1105.63	70	78
Small nuclear ribonucleoprotein Sm D3	SNRPD3	SMD3_HUMAN	13.9	99.8%	2	3	5	0.01%	15.1%	VAQLEQVYIR	99.7%	77.3	25	63.9	1	0	0	1218.68	55	64
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN	24.6	100.0%	4	5	14	0.01%	15.8%	GENLVSMTVEGPPPK	99.7%	76.2	25	59.4	4	0	0	1554.78	74	88
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN	24.6	100.0%	4	5	14	0.01%	15.8%	IFIGTFK	98.3%	32.4	25	18.1	2	0	0	825.49	26	32
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN	24.6	100.0%	4	5	14	0.01%	15.8%	MLQHIDYR	99.7%	50	25	47.6	1	0	0	1075.54	9	16
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN	24.6	100.0%	4	5	14	0.01%	15.8%	VLGLVLLR	99.7%	62	25	59.3	7	0	0	882.61	66	73
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	71	0.07%	28.5%	ADIGVAMGIAGSDVSK	99.7%	86.3	25	84.2	4	0	0	1490.75	728	743
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	71	0.07%	28.5%	AVAGDASESALLK	99.7%	96.3	25	89.5	5	0	0	1231.65	446	458
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	71	0.07%	28.5%	AVFQANQENLPILK	99.7%	70.1	25	50	2	0	0	1584.87	431	444
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	71	0.07%	28.5%	DGPNALTPPPTTPEWIK	99.4%	37.7	25	37.7	2	0	0	1833.94	75	91
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	71	0.07%	28.5%	GIVVYTGDR	99.7%	73.4	25	65.9	4	0	0	979.52	256	264
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	71	0.07%	28.5%	GVGIISEGNETVEDIAAR	99.7%	118	25	118	4	0	0	1829.92	630	647
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	71	0.07%	28.5%	IAGLCNR	99.0%	35.4	25.5	22.6	1	0	0	803.42	424	430
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	71	0.07%	28.5%	LIFDNLKK	99.1%	35.1	25	23.2	2	0	0	990.60	767	774
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	71	0.07%	28.5%	LIIVEGCQR	99.7%	56.5	25	50.4	5	0	0	1087.59	699	707
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	71	0.07%	28.5%	LNIPVSQVNPR	99.7%	62.2	25	55.9	6	0	0	1236.71	648	658

Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	71	0.07%	28.5%	LSLDELHR	99.7%	59.2	25	54.9	2	0	0	982.53	46	53
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	71	0.07%	28.5%	MSINAEEVVVGDLVEVK	99.7%	62.5	25	62.5	2	0	0	1846.95	178	194
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	71	0.07%	28.5%	NIAFFSTNCVEGTAR	99.7%	91.1	25	91.1	3	0	0	1686.79	241	255
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	71	0.07%	28.5%	NLEAVETLGSTSTICSDK	99.7%	57	25	57	2	0	0	1924.92	360	377
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	71	0.07%	28.5%	NMVPQQALVIR	99.7%	50.6	25	46	3	0	0	1284.71	163	173
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	71	0.07%	28.5%	NPNTSEPQHLLVMK	99.7%	58.1	25	52.6	4	0	0	1607.82	495	508
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	71	0.07%	28.5%	QGAIVAVTGDGVNDSPALK	99.7%	104	25	104	2	0	0	1811.95	708	726
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	71	0.07%	28.5%	QGAIVAVTGDGVNDSPALKK	99.7%	36.8	25	36.8	0	1	0	1940.05	708	727
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	71	0.07%	28.5%	SPDFTNENPLETR	99.7%	82.7	25	70.4	4	0	0	1519.70	228	240
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	71	0.07%	28.5%	TSATWLALSR	99.7%	78.7	25	66.6	4	0	0	1105.60	414	423
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	71	0.07%	28.5%	VDNSSLTGESEPQTR	99.7%	86.4	25	79.6	2	0	0	1619.75	213	227
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	71	0.07%	28.5%	VIMVTGDHPITAK	99.7%	71	25	71	3	0	0	1381.75	613	625
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	71	0.07%	28.5%	YGTDLSR	99.2%	36	25	22.9	2	0	0	811.39	55	61
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	71	0.07%	28.5%	YHTEIVFAR	99.7%	44	25	31	2	0	0	1135.59	684	692
Sodium/potassium-transporting ATPase subunit beta-3	ATP1B3	AT1B3_HUMAN	31.5	99.8%	2	2	3	0.00%	8.6%	LFIYNPTTGEFLGR	99.7%	65.2	25	65.2	2	0	0	1627.85	18	31
Sodium/potassium-transporting ATPase subunit beta-3	ATP1B3	AT1B3_HUMAN	31.5	99.8%	2	2	3	0.00%	8.6%	SLNQSLAEWK	99.1%	35.5	25	19.4	1	0	0	1175.61	8	17
Sorting and assembly machinery component 50 homolog	SAMM50	SAM50_HUMAN	52.0	100.0%	3	3	6	0.01%	8.1%	SSLSHAMVIDSR	99.7%	74.1	25	63.9	2	0	0	1302.65	256	267
Sorting and assembly machinery component 50 homolog	SAMM50	SAM50_HUMAN	52.0	100.0%	3	3	6	0.01%	8.1%	TKDDIIICEIGDVFK	99.7%	97.7	25	94.5	2	0	0	1765.90	58	72
Sorting and assembly machinery component 50 homolog	SAMM50	SAM50_HUMAN	52.0	100.0%	3	3	6	0.01%	8.1%	VTGQFPWSSLR	99.0%	34.7	25	21.3	2	0	0	1277.66	195	205
Sorting nexin-2	SNX2	SNX2_HUMAN	58.5	99.8%	2	2	4	0.00%	4.1%	ELSANTAAFAK	99.7%	53.3	25	36.6	2	0	0	1122.58	336	346
Sorting nexin-2	SNX2	SNX2_HUMAN	58.5	99.8%	2	2	4	0.00%	4.1%	QFLESSELPR	99.7%	48.2	25	34.9	2	0	0	1205.62	260	269
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	SPTN1_HUMAN	284.5	100.0%	8	8	10	0.01%	3.6%	DLASVQALLR	99.7%	65.6	25	49.6	1	0	0	1085.63	286	295
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	SPTN1_HUMAN	284.5	100.0%	8	8	10	0.01%	3.6%	DLTGVQNLR	97.9%	31.5	25	25.4	1	0	0	1015.55	1795	1803
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	SPTN1_HUMAN	284.5	100.0%	8	8	10	0.01%	3.6%	DVTGAEALLER	99.7%	64.5	25	52.6	1	0	0	1173.61	1370	1380
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	SPTN1_HUMAN	284.5	100.0%	8	8	10	0.01%	3.6%	ELPTAFDYVEFTR	99.4%	37	25	33	1	0	0	1587.77	2455	2467
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	SPTN1_HUMAN	284.5	100.0%	8	8	10	0.01%	3.6%	LFGAAEVQR	99.7%	49.7	25	24.5	2	0	0	990.54	251	259
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	SPTN1_HUMAN	284.5	100.0%	8	8	10	0.01%	3.6%	LGESQTLQQFSR	99.7%	72.5	25	69.5	1	0	0	1393.71	1547	1558
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	SPTN1_HUMAN	284.5	100.0%	8	8	10	0.01%	3.6%	LIQEQHPEEELIK	95.8%	28.6	25	28.6	1	0	0	1605.85	215	227
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	SPTN1_HUMAN	284.5	100.0%	8	8	10	0.01%	3.6%	SQLLGSAHEVQR	99.7%	68.1	25	53.2	2	0	0	1324.70	1226	1237
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	4	4	6	0.01%	2.0%	ALVADSHPESER	99.7%	47.5	25	44.1	1	0	0	1310.63	1657	1668
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	4	4	6	0.01%	2.0%	SQNIVTDSSSLSAEAIR	99.7%	103	25	102	2	0	0	1777.89	1548	1564
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	4	4	6	0.01%	2.0%	VLDNAIETEK	99.4%	37.1	25	30.3	1	0	0	1131.59	293	302
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	4	4	6	0.01%	2.0%	VQAVVAVAR	99.7%	58.1	25	32.7	2	0	0	912.56	478	486
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	5	5	10	0.01%	13.2%	AAFVLPEFAR	99.7%	48	25	44.2	2	0	0	1120.61	286	295
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	5	5	10	0.01%	13.2%	KVLIIGGGDGGVLR	99.7%	53.5	25	53.5	0	2	0	1353.82	96	109
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	5	5	10	0.01%	13.2%	VLIIGGGDGGVLR	99.7%	60.2	25	60.2	2	0	0	1225.73	97	109
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	5	5	10	0.01%	13.2%	YQDILVFR	99.7%	52.4	25	52.3	2	0	0	1053.57	48	55
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	5	5	10	0.01%	13.2%	YYNSDVHR	99.6%	39.8	25	39.8	2	0	0	1053.47	278	285
Sphingomyelin phosphodiesterase 4	SMPD4	NSMA3_HUMAN	93.4	100.0%	3	3	4	0.00%	2.9%	LAQLITQAK	99.4%	37.5	25	31.1	1	0	0	985.60	557	565
Sphingomyelin phosphodiesterase 4	SMPD4	NSMA3_HUMAN	93.4	100.0%	3	3	4	0.00%	2.9%	LFVGFLNR	99.7%	64.2	25	57.2	1	0	0	965.56	444	451
Sphingomyelin phosphodiesterase 4	SMPD4	NSMA3_HUMAN	93.4	100.0%	3	3	4	0.00%	2.9%	LSEAQLR	99.7%	44.3	25	10.5	2	0	0	816.46	632	638
Spindle and kinetochore-associated protein 1	SKA1	SKA1_HUMAN	29.5	99.8%	2	2	3	0.00%	8.2%	FIDEETKDTK	97.5%	30.8	25	17	1	0	0	1225.59	197	206
Spindle and kinetochore-associated protein 1	SKA1	SKA1_HUMAN	29.5	99.8%	2	2	3	0.00%	8.2%	LTYNQINDVIK	99.7%	76.7	25	63.7	2	0	0	1320.72	156	166
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	9	11	25	0.03%	46.2%	ADAGHAGVSANMMK	98.3%	25.6	25	0.76	0	1	0	1375.61	15	28
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	9	11	25	0.03%	46.2%	EGNGPVTQWK	99.4%	37	25	30.8	2	0	0	1115.55	64	73
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	9	11	25	0.03%	46.2%	GTVLDQVPVNPSLYLIK	99.7%	58	25	45.3	3	0	0	1856.05	74	90
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	9	11	25	0.03%	46.2%	IMPDSNDSPPAEREPGEVVDSLVGK	99.2%	28.5	25	27.6	0	2	0	2654.26	192	216
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	9	11	25	0.03%	46.2%	ISDAHLADTMIGK	99.7%	62.1	25	58.5	2	0	0	1371.69	123	135
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	9	11	25	0.03%	46.2%	SRADAGHAGVSANMMK	98.9%	27.4	25	27.4	0	1	0	1634.74	13	28
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	9	11	25	0.03%	46.2%	SSVGPSKPVSQPR	99.7%	77	25	60.3	4	4	0	1325.72	38	50
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	9	11	25	0.03%	46.2%	VSALEVLPDR	99.7%	75.6	25	63.5	4	0	0	1098.62	108	117

Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	9	11	25	0.03%	46.2%	YDGFDCVYGLELNKDER	99.5%	38.4	25	37.2	1	1	0	2092.93	91	107
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	26	28	72	0.07%	24.8%	AFAVVASALGIPSLLPFLK	98.9%	34.2	25	31.2	1	0	0	1914.15	631	649
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	26	28	72	0.07%	24.8%	AIGPHDVLATLLNNLK	97.3%	24	25	24	0	1	0	1688.97	1087	1102
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	26	28	72	0.07%	24.8%	AIVNVIGMHK	99.7%	43.3	25	38.4	4	0	0	1097.61	999	1008
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	26	28	72	0.07%	24.8%	DTPGHGSGWAETPR	94.5%	21.5	25	21.5	0	1	0	1467.66	302	315
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	26	28	72	0.07%	24.8%	EVMLILIR	99.7%	72.1	25	54.3	7	0	0	986.61	768	775
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	26	28	72	0.07%	24.8%	GGDSIGETPTPGASK	99.7%	52.7	25	52.7	4	0	0	1373.65	319	333
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	26	28	72	0.07%	24.8%	ICFELLELLK	99.7%	53.6	25	49.4	4	0	0	1277.72	1058	1067
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	26	28	72	0.07%	24.8%	ILVVIEPLLIDEDYYAR	99.7%	77.2	25	77.2	3	0	0	2034.12	574	590
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	26	28	72	0.07%	24.8%	IYNDDKNTYIR	99.7%	57	25	52.5	4	3	0	1414.70	1287	1297
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	26	28	72	0.07%	24.8%	IYNSIYIGSQDALIAHYPR	99.1%	28.1	25	25.6	0	1	0	2194.13	1268	1286
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	26	28	72	0.07%	24.8%	LLVDVDESTLSPEEQK	96.5%	29.3	25	24.7	1	0	0	1801.91	478	493
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	26	28	72	0.07%	24.8%	LLVDVDESTLSPEEQKER	99.7%	46.7	25	44.3	0	3	0	2087.05	478	495
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	26	28	72	0.07%	24.8%	MTPPIKDLLPR	98.3%	32.4	25	26.2	1	0	0	1296.73	1009	1019
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	26	28	72	0.07%	24.8%	QLVDTTVELANK	99.7%	92.9	25	81.3	4	0	0	1330.72	832	843
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	26	28	72	0.07%	24.8%	QQAADLISR	99.7%	51.4	25	41.7	4	0	0	1001.54	949	957
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	26	28	72	0.07%	24.8%	SLVEIIEHGLVDEQQK	99.7%	49.1	25	48.4	3	0	0	1836.97	685	700
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	26	28	72	0.07%	24.8%	TEILPPFFK	99.1%	35.3	25	21.8	3	0	0	1091.61	808	816
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	26	28	72	0.07%	24.8%	THEDIEAQIR	99.7%	58	25	52.1	3	0	0	1211.60	7	16
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	26	28	72	0.07%	24.8%	TMIISPER	99.1%	35.2	25	34.7	1	0	0	962.50	125	132
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	26	28	72	0.07%	24.8%	VGAAEIISR	99.7%	91.2	25	44	5	0	0	915.53	844	852
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	26	28	72	0.07%	24.8%	VLPPPAGYVPIR	97.9%	31.4	25	28.8	1	0	0	1278.76	414	425
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	26	28	72	0.07%	24.8%	VPELNVQNGVLK	99.7%	57.9	25	54.2	3	0	0	1309.75	1138	1149
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	26	28	72	0.07%	24.8%	VQENCIDLVGR	99.7%	74.5	25	68.8	4	0	0	1302.65	1031	1041
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	26	28	72	0.07%	24.8%	VVNGAAASQPPSKR	99.6%	39.6	25	39.6	1	0	0	1381.75	183	196
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	26	28	72	0.07%	24.8%	WDETPASQMGGSTPVLTPGK	99.7%	45.8	25	45.8	1	0	0	2074.98	338	357
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	26	28	72	0.07%	24.8%	WDQTADQTPGATPK	99.3%	36.2	25	36.2	1	0	0	1515.71	200	213
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	4	4	9	0.01%	4.7%	AAVLLEQER	99.7%	59.1	25	53.5	4	0	0	1028.57	184	192
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	4	4	9	0.01%	4.7%	KPGDLSDELR	99.7%	61	25	49.6	2	0	0	1129.59	605	614
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	4	4	9	0.01%	4.7%	VGEPVALSEEER	99.7%	79.2	25	71.5	2	0	0	1314.65	135	146
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	4	4	9	0.01%	4.7%	YGPPPSYPNLK	98.0%	31.8	25	29.7	1	0	0	1232.63	639	649
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	19	38	0.04%	16.4%	DYIVVGSDSGR	99.7%	68.1	25	60	1	0	0	1167.56	76	86
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	19	38	0.04%	16.4%	FGNICVVR	99.7%	56.3	25	43	2	0	0	964.50	1050	1057
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	19	38	0.04%	16.4%	FLAVGLVDNTVR	99.7%	88.4	25	80.2	4	0	0	1303.74	604	615
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	19	38	0.04%	16.4%	FSNTGEDWYVLVGVAK	99.7%	97.2	25	97.2	2	0	0	1784.89	896	911
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	19	38	0.04%	16.4%	ITLETDEDMVTEIR	99.7%	84	25	84	1	0	0	1680.80	313	326
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	19	38	0.04%	16.4%	IVILEYQPSK	99.7%	76.8	25	63.4	2	0	0	1189.68	87	96
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	19	38	0.04%	16.4%	LGAVFNQVAFPLQYTPR	99.7%	77.8	25	77.8	4	0	0	1921.03	770	786
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	19	38	0.04%	16.4%	MFLYNLTLQR	99.7%	68.3	25	64.5	2	0	0	1298.69	1	10
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	19	38	0.04%	16.4%	MQGQEAVLAMSSR	99.7%	60.2	25	56.6	4	0	0	1423.67	706	718
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	19	38	0.04%	16.4%	NENQLIIFADDTYPR	99.7%	98	25	98	2	1	0	1808.88	1017	1031
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	19	38	0.04%	16.4%	NFGDQPDIR	99.7%	47.5	25	39.5	2	0	0	1061.50	260	268
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	19	38	0.04%	16.4%	SVAGGFVYTYK	99.7%	56.2	25	46.3	1	0	0	1191.60	919	929
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	19	38	0.04%	16.4%	SWLSYSYQSR	99.7%	41.2	25	37.3	2	0	0	1276.60	719	728
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	19	38	0.04%	16.4%	TVLDPVTGDLSDTR	99.7%	109	25	109	4	0	0	1488.75	677	690
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	19	38	0.04%	16.4%	VIVSDVQESFIWVR	99.7%	78.7	25	70.6	2	0	0	1676.90	1000	1013
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	19	38	0.04%	16.4%	YFDTVPVAAAMCVLK	99.7%	52.5	25	50.8	2	0	0	1684.84	329	343
Splicing factor 45	RBM17	SPF45_HUMAN	45.0	99.9%	2	2	2	0.00%	5.7%	ACFYNLDKFR	99.7%	40.6	25	30.9	1	0	0	1333.64	384	393
Splicing factor 45	RBM17	SPF45_HUMAN	45.0	99.9%	2	2	2	0.00%	5.7%	IIVGDATEKDASK	99.7%	68.5	25	62.7	1	0	0	1346.72	277	289
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	5	5	10	0.01%	25.8%	AVIDLNNR	99.7%	49.8	25	37.9	2	0	0	914.51	126	133
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	5	5	10	0.01%	25.8%	GGFCNFMHLKPISR	99.7%	42.3	25	38.4	0	2	0	1663.82	166	179

Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	5	5	10	0.01%	25.8%	NPQNSSQSADGLR	99.7%	77.6	25	75.8	2	0	0	1373.64	54	66
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	5	5	10	0.01%	25.8%	QYEMGECTR	99.7%	47	25	36.5	2	0	0	1173.47	157	165
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	5	5	10	0.01%	25.8%	WFNGQPIHAELSPVTDFR	99.7%	32.2	25	32.2	0	2	0	2114.05	134	151
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	8	11	20	0.02%	24.8%	GAKEEHGGLIR	98.6%	33.2	25	27.8	2	0	0	1166.63	68	78
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	8	11	20	0.02%	24.8%	IFVEFTSVFDCQK	99.7%	68.2	25	67.6	2	0	0	1619.78	432	444
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	8	11	20	0.02%	24.8%	LFIGGLPNYLNDDQVK	99.7%	48.1	25	36.7	2	0	0	1805.94	261	276
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	8	11	20	0.02%	24.8%	LGGLTQAPGNPVLAVQINQDK	99.7%	87.4	25	87.4	2	2	0	2133.17	175	195
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	8	11	20	0.02%	24.8%	NFAFLEFR	99.7%	47.2	25	42	2	0	0	1043.53	196	203
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	8	11	20	0.02%	24.8%	SIEIPRPVDGVEVPGCGK	99.7%	73.1	25	66.3	2	2	0	1908.99	414	431
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	8	11	20	0.02%	24.8%	SVDETTQAMAFDGIIFQGQSLK	99.7%	69.6	25	69.6	2	0	0	2386.16	204	225
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	8	11	20	0.02%	24.8%	YCDPDSYHR	99.7%	55.8	25	49.8	2	0	0	1212.47	463	471
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	4	4	7	0.01%	7.8%	AELDDTPMR	99.7%	49.7	25	46.4	2	0	0	1063.47	350	358
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	4	4	7	0.01%	7.8%	AVVIVDDR	99.7%	41.8	25	36.5	2	0	0	886.50	400	407
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	4	4	7	0.01%	7.8%	FGQGGAGPVGGQGPR	99.7%	53.4	25	52.2	2	0	0	1341.67	667	681
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	4	4	7	0.01%	7.8%	GIVEFASKPAAR	97.6%	30.9	25	30.9	1	0	0	1245.70	414	425
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	4	4	7	0.01%	7.8%	YGEPGEVFINK	99.7%	56.8	25	54.6	2	0	0	1252.62	320	330
SRA stem-loop-interacting RNA-binding protein, mitochondrial	SLIRP	SLIRP_HUMAN	12.3	100.0%	3	3	5	0.01%	35.8%	GLGWVQFSSEEGLR	99.5%	38.2	25	38.2	2	0	0	1564.78	61	74
SRA stem-loop-interacting RNA-binding protein, mitochondrial	SLIRP	SLIRP_HUMAN	12.3	100.0%	3	3	5	0.01%	35.8%	IPWTAASSQLK	96.9%	29.9	25	20	1	0	0	1201.66	26	36
SRA stem-loop-interacting RNA-binding protein, mitochondrial	SLIRP	SLIRP_HUMAN	12.3	100.0%	3	3	5	0.01%	35.8%	NALQQENHIIDGVK	99.7%	75.1	25	75.1	2	0	0	1578.82	75	88
SRSF protein kinase 1	SRPK1	SRPK1_HUMAN	74.3	100.0%	2	2	6	0.01%	3.5%	HFTEDIQTR	99.7%	44.6	25	38.5	4	0	0	1146.55	507	515
SRSF protein kinase 1	SRPK1	SRPK1_HUMAN	74.3	100.0%	2	2	6	0.01%	3.5%	STAGNFLVNPLEPK	99.7%	57.8	25	38.3	2	0	0	1486.79	473	486
SRSF protein kinase 2	SRPK2	SRPK2_HUMAN	77.5	99.8%	2	2	3	0.00%	4.8%	AADLLVNPLDPR	99.7%	46	25	40.6	2	0	0	1293.72	508	519
SRSF protein kinase 2	SRPK2	SRPK2_HUMAN	77.5	99.8%	2	2	3	0.00%	4.8%	HFTEDIQTR	99.7%	44.6	25	38.5	4	0	0	1146.55	540	548
SRSF protein kinase 2	SRPK2	SRPK2_HUMAN	77.5	99.8%	2	2	3	0.00%	4.8%	TVSASSTGDLPK	99.3%	36.8	25	30.6	1	0	0	1162.60	492	503
Sterile alpha and TIR motif-containing protein 1	SARM1	SARM1_HUMAN	79.4	100.0%	2	2	3	0.00%	3.3%	IGLGVILNLAK	99.7%	49.9	25	49.9	2	0	0	1110.72	163	173
Sterile alpha and TIR motif-containing protein 1	SARM1	SARM1_HUMAN	79.4	100.0%	2	2	3	0.00%	3.3%	SNLADWLGSLDPR	99.7%	51.9	25	49.5	1	0	0	1443.72	485	497
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	10	10	18	0.02%	37.9%	AEQINQAAGEASAVLAK	99.7%	127	25	127	2	0	0	1670.87	234	250
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	10	10	18	0.02%	37.9%	APVPGTPDSLSSGSSR	99.7%	63.1	25	59.5	2	0	0	1514.74	322	337
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	10	10	18	0.02%	37.9%	ASYGVEDPEYAVTQLAQTTMR	99.7%	101	25	94.5	2	0	0	2330.10	115	135
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	10	10	18	0.02%	37.9%	ATVLESEGTR	99.7%	75.9	25	62.1	2	0	0	1062.54	202	211
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	10	10	18	0.02%	37.9%	DVQGTDASLDEELDRVK	99.7%	92.9	25	89.3	2	0	0	1889.91	338	354
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	10	10	18	0.02%	37.9%	ESAINVAEGK	98.0%	31.7	25	27.4	1	0	0	1017.52	212	221
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	10	10	18	0.02%	37.9%	ESAINVAEGKK	99.7%	52.4	25	44	2	0	0	1145.62	212	222
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	10	10	18	0.02%	37.9%	ILEPGLNILIPVLDR	99.7%	80.1	25	80.1	2	0	0	1675.02	58	72
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	10	10	18	0.02%	37.9%	NTVVLFVPQQEAWVVER	99.7%	48.8	25	40.7	2	0	0	2014.08	35	51
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	10	10	18	0.02%	37.9%	QAQILASEAEK	99.7%	45.9	25	40.1	1	0	0	1187.63	223	233
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	18	20	46	0.05%	36.1%	AQFEGIVTDLIR	99.7%	83.7	25	77	4	0	0	1361.74	349	360
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	18	20	46	0.05%	36.1%	ASNGDAWVEAHGK	99.7%	70.1	25	70.1	2	0	0	1341.62	147	159
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	18	20	46	0.05%	36.1%	DAGQISGLNVLR	99.7%	79.1	25	58.5	4	0	0	1242.68	207	218
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	18	20	46	0.05%	36.1%	ETGVDLTKDNMALQR	99.7%	62	25	60.8	1	0	0	1706.84	293	307
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	18	20	46	0.05%	36.1%	LLGQFTLIGIPPAPR	99.7%	49.1	25	49.1	3	0	0	1592.95	499	513
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	18	20	46	0.05%	36.1%	LYSPSQIGAFVLMK	99.7%	64.3	25	64.3	2	2	0	1569.83	160	173
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	18	20	46	0.05%	36.1%	MKETAENYLGHTAK	99.7%	70.2	25	63.4	1	0	0	1592.77	174	187
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	18	20	46	0.05%	36.1%	NAVITVPAYFNDSQR	99.7%	66.3	25	63.7	2	0	0	1694.85	188	202
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	18	20	46	0.05%	36.1%	QAASSLQQASLK	99.7%	93.1	25	84.7	4	0	0	1231.66	635	646
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	18	20	46	0.05%	36.1%	QAVTNPNNTFYATK	99.7%	90.5	25	89.8	2	0	0	1568.77	108	121
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	18	20	46	0.05%	36.1%	RYDDPEVQK	99.7%	44.8	25	38.3	2	0	0	1149.55	127	135
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	18	20	46	0.05%	36.1%	SDIGEVILVGGMTR	99.7%	79.7	25	74.9	4	0	0	1446.76	378	391
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	18	20	46	0.05%	36.1%	SQVFSTAADGQTQVEIK	99.7%	123	25	121	2	0	0	1808.90	469	485
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	18	20	46	0.05%	36.1%	STNGDTFLGGEDFDQALLR	99.7%	82.6	25	81.2	2	0	0	2055.96	266	284
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	18	20	46	0.05%	36.1%	TTPSVVAFTADGER	99.7%	113	25	110	2	0	0	1450.72	86	99

Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	18	20	46	0.05%	36.1%	VINEPTAAALAYGLDK	99.7%	112	25	104	3	0	0	1645.88	219	234
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	18	20	46	0.05%	36.1%	VLENAEGAR	99.7%	65.1	25	58.1	2	0	0	958.50	77	85
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	18	20	46	0.05%	36.1%	VQQTVQDLFGR	99.7%	74.5	25	68.8	2	0	0	1290.68	395	405
Striatin-interacting protein 1	STRIP1	STRP1_HUMAN	95.6	100.0%	4	4	6	0.01%	5.1%	FFNQNIMSYITAK	99.6%	39.3	25	39.3	1	0	0	1576.78	616	628
Striatin-interacting protein 1	STRIP1	STRP1_HUMAN	95.6	100.0%	4	4	6	0.01%	5.1%	ILLAAAPTSK	99.7%	49	25	35.8	2	0	0	984.61	527	536
Striatin-interacting protein 1	STRIP1	STRP1_HUMAN	95.6	100.0%	4	4	6	0.01%	5.1%	LLDGLEVTAR	99.7%	66.9	25	48.8	1	0	0	1086.62	129	138
Striatin-interacting protein 1	STRIP1	STRP1_HUMAN	95.6	100.0%	4	4	6	0.01%	5.1%	NLFSCINLLR	99.7%	40.7	25	16	2	0	0	1249.67	664	673
Stromal cell-derived factor 2-like protein 1	SDF2L1	SDF2L_HUMAN	23.6	100.0%	3	3	3	0.00%	20.4%	LTHVLTGK	99.2%	35.9	25	35.9	1	0	0	868.53	106	113
Stromal cell-derived factor 2-like protein 1	SDF2L1	SDF2L_HUMAN	23.6	100.0%	3	3	3	0.00%	20.4%	TGAELVTCGSVLK	99.7%	53	25	40.4	1	0	0	1334.70	31	43
Stromal cell-derived factor 2-like protein 1	SDF2L1	SDF2L_HUMAN	23.6	100.0%	3	3	3	0.00%	20.4%	YGSGSGQQSVTGVEASDDANSYWR	99.7%	79.6	25	79.6	1	0	0	2521.09	60	83
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	20	22	42	0.04%	17.9%	AEEDTQFNYHR	99.7%	45.9	25	34.6	2	0	0	1409.61	178	188
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	20	22	42	0.04%	17.9%	DLTLEENQVKK	94.9%	27.8	25	24.9	1	0	0	1316.71	364	374
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	20	22	42	0.04%	17.9%	FNACFESVATNIDEIYK	99.7%	47.6	25	47.6	1	0	0	2020.93	1070	1086
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	20	22	42	0.04%	17.9%	HLALNLQEK	99.2%	36	25	31.9	2	0	0	1065.61	726	734
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	20	22	42	0.04%	17.9%	IIDETMAQLQDLK	99.7%	58.9	25	53.1	2	0	0	1533.78	862	874
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	20	22	42	0.04%	17.9%	LGIQLDFEK	99.4%	37.7	25	26.2	1	0	0	1062.58	817	825
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	20	22	42	0.04%	17.9%	LNEQQSVLQR	99.7%	69.6	25	55.1	4	0	0	1214.65	1010	1019
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	20	22	42	0.04%	17.9%	LTEELKEQMK	97.2%	30.3	25	25.2	1	0	0	1248.65	681	690
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	20	22	42	0.04%	17.9%	LVIDVIR	96.9%	29.9	25	15.8	1	0	0	827.54	593	599
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	20	22	42	0.04%	17.9%	LYHNEVEIEK	99.2%	28.2	25	22.9	3	1	0	1273.64	228	237
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	20	22	42	0.04%	17.9%	NFLVFQGAVESIAMK	99.7%	69.6	25	67	5	0	0	1653.87	132	146
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	20	22	42	0.04%	17.9%	NMDAIIVDSEK	99.7%	42.2	25	35.8	1	0	0	1250.59	541	551
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	20	22	42	0.04%	17.9%	QIIGPFQR	97.3%	30.4	25	20.4	1	0	0	958.55	19	26
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	20	22	42	0.04%	17.9%	SGELAQEYDKR	99.7%	51.7	25	47.8	2	0	0	1295.62	161	171
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	20	22	42	0.04%	17.9%	SGVISGGASDLK	99.7%	52.8	25	36.2	4	0	0	1090.57	649	660
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	20	22	42	0.04%	17.9%	SNLMDAISFVLGEK	99.7%	45.2	25	43.3	1	0	0	1539.77	39	52
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	20	22	42	0.04%	17.9%	TALFEEISR	99.7%	61.8	25	57.6	4	0	0	1065.56	152	160
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	20	22	42	0.04%	17.9%	TVALDGTLFQK	99.7%	49	25	34	1	0	0	1192.66	638	648
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	20	22	42	0.04%	17.9%	VVQLHEYSEELEK	99.7%	58.3	25	52.6	2	0	0	1602.80	111	123
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	20	22	42	0.04%	17.9%	YSQSDLEQTK	99.7%	59.6	25	45.8	2	0	0	1198.56	714	723
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	ALNHEIEELEK	99.7%	44.6	25	40	2	0	0	1324.67	276	286
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	AMNVLTEAEER	99.7%	47.2	25	37.1	2	0	0	1278.60	987	997
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	ASNLQDLVYK	98.0%	31.7	25	22.8	1	0	0	1150.61	59	68
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	ASVSITFDNSDKK	99.7%	47.9	25	37.5	2	0	0	1411.71	77	89
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	DQEALEAVKR	99.7%	49.9	25	42.5	2	0	0	1158.61	447	456
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	DTSATTALELVAGER	99.7%	94.7	25	81.9	2	0	0	1533.78	534	548
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	EGMFNNANVLFK	97.1%	30.2	25	19.1	1	0	0	1383.67	1147	1158
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	EIEHLSR	98.8%	34.1	25	14.8	1	0	0	883.46	226	232
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	ENLTELSGGQR	99.7%	85.9	25	66.9	2	0	0	1203.60	1080	1090
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	FQELKDVQDELR	99.7%	61	25	51.3	2	0	0	1519.78	678	689
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	FVDGVSTVAR	99.7%	81.9	25	70.6	2	0	0	1050.56	1161	1170
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	GLVASLISVK	99.7%	65	25	63.2	2	0	0	986.62	524	533
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	IKELDHNISK	99.7%	47.5	25	41.9	2	0	0	1196.66	910	919
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	ILTTIEDLDQKK	99.7%	71	25	59.3	2	2	0	1416.79	1015	1026
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	ITDGLHALQEASNK	99.7%	64.7	25	49.8	2	0	0	1496.77	355	368
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	LKETYEALLAR	99.7%	56.3	25	47.6	2	0	0	1306.74	492	502
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	LYNVVVDTEVTGK	99.7%	105	25	97.4	2	0	0	1436.76	549	561
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	LYNVVVDTEVTGKK	98.2%	32.1	25	29	1	0	0	1564.86	549	562
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	QQLEAVNEAIK	99.7%	56.8	25	48.4	2	0	0	1242.67	838	848
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	SAEELKEMQDK	99.7%	46.7	25	36.5	2	0	0	1307.61	249	259
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	SIILEGFK	99.4%	37.1	25	31.1	1	0	0	906.53	5	12

Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	SLEDALAEAQR	99.7%	93.1	25	81	2	0	0	1202.60	298	308
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	SQAASILTK	99.2%	36.1	25	25.5	2	0	0	918.53	669	677
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	SQSAFDLKK	97.2%	30.3	25	30.3	1	0	0	1023.55	313	321
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	SSYLEYQK	99.7%	45	25	38.8	1	0	0	1017.49	215	222
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	TEEADLLQTK	99.7%	49.8	25	35.6	2	0	0	1147.58	723	732
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	TIEESEETLK	99.7%	52.3	25	37.5	2	0	0	1178.58	751	760
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	TILEEEITPTIQK	99.7%	74.7	25	67.7	2	0	0	1514.83	197	209
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	TVTLGGDVFDPHGTLSGGAR	99.7%	42.1	25	42.1	0	2	0	1956.98	649	668
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	YLINGVNANNTR	99.7%	54.7	25	51.5	2	0	0	1348.70	115	126
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	32	56	0.06%	27.8%	YTIIPLNK	95.3%	28.2	25	21.9	1	0	0	961.57	573	580
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	AELGTDLLSQLSLEDQK	99.7%	60.5	25	54.2	2	0	0	1859.96	779	795
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	AILNGIDSINK	99.3%	36.5	25	30.2	2	0	0	1157.65	504	514
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	AKLDELSAK	98.4%	32.8	25	14	1	0	0	974.55	237	245
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	ALDQFVNFSEQK	99.7%	82.3	25	76.5	2	0	0	1425.70	986	997
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	ALEYTIYNQELNETR	99.7%	76.5	25	55.7	2	0	0	1856.90	222	236
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	DLEDTEANKEK	99.6%	38.9	25	35.5	2	0	0	1291.60	419	429
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	DLQDELAGNSEQR	99.7%	50.9	25	41.2	1	0	0	1474.68	311	323
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	DQTIVDPFSSK	99.7%	58.5	25	31.2	2	0	0	1236.61	16	26
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	DTAYPETNDAIPMISK	99.7%	41.3	25	41.3	3	0	0	1781.83	597	612
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	EENAEQQALAAK	99.7%	84.7	25	73	2	0	0	1301.63	475	486
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	ELGSLPQEAFEK	99.7%	55.5	25	35.2	2	0	0	1347.68	945	956
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	GALTGGYYDTR	99.7%	77.6	25	69.6	2	0	0	1173.55	662	672
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	GSQFTSKEER	99.7%	51.1	25	43.3	2	0	0	1168.56	382	391
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	INQMATAPDSQR	99.7%	69.4	25	62.4	4	0	0	1347.63	144	155
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	KAEEELGELEAK	99.7%	76	25	62.8	2	0	0	1345.68	684	695
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	KEESISLMK	99.7%	41.2	25	28.7	1	0	0	1064.57	172	180
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	KYEAIQLTFK	98.5%	33	25	33	2	0	0	1240.69	1025	1034
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	LALLHEGTGPR	99.7%	53.9	25	51.5	2	0	0	1163.65	62	72
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	LFYHIVDSDEVSTK	99.7%	56.7	25	48.3	2	1	0	1652.82	558	571
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	MNLPGEVTFLPLNK	99.7%	89.6	25	79.2	4	0	0	1588.84	579	592
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	NDVMNLLESAGFSR	99.7%	98.9	25	93.9	4	0	0	1568.74	119	132
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	NFSEVFQK	96.2%	29	25	13.6	2	0	0	998.49	1039	1046
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	QKELAETEPK	96.9%	29.9	25	19.3	2	0	0	1172.62	341	350
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	QVIIQGFR	99.7%	58.2	25	45	2	0	0	960.56	5	12
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	SEDLDNSIDKTEAGIK	99.7%	77.4	25	72	2	0	0	1734.84	880	895
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	SIMELMNVLELR	99.7%	60.1	25	42.7	6	0	0	1447.76	1013	1024
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	SLDQAINDK	99.5%	38.7	25	31.1	2	0	0	1003.51	401	409
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	SMEVSTQLAR	99.7%	53.6	25	48.6	4	0	0	1137.56	635	644
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	VDALNDEIR	99.7%	61	25	38.6	1	0	0	1044.53	797	805
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	VETYLNENLR	99.7%	53.2	25	20.6	2	0	0	1250.64	828	837
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	38	72	0.07%	29.7%	VSHIDVITAEMAK	99.7%	58.7	25	51.5	2	0	0	1413.74	1195	1207
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	15	16	24	0.02%	13.3%	DTLVADNLDQATR	99.7%	74.4	25	67.1	2	0	0	1431.71	714	726
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	15	16	24	0.02%	13.3%	FTASIQR	96.5%	29.4	25	19	2	0	0	822.45	821	827
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	15	16	24	0.02%	13.3%	FTQLDLEDVQVR	99.7%	83.7	25	77.9	2	0	0	1462.75	390	401
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	15	16	24	0.02%	13.3%	LIEQEEYLNVQVK	99.7%	84.8	25	69.3	1	0	0	1604.85	828	840
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	15	16	24	0.02%	13.3%	LLEENVSAFK	99.7%	48	25	37.7	1	0	0	1149.62	858	867
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	15	16	24	0.02%	13.3%	LTQEETNFK	99.7%	48.2	25	44.9	2	0	0	1109.55	565	573
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	15	16	24	0.02%	13.3%	NTNAAEESLPEIQK	99.7%	65.4	25	64.6	1	0	0	1543.76	975	988
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	15	16	24	0.02%	13.3%	QAFYFALR	99.7%	42.2	25	26	1	0	0	1015.54	706	713
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	15	16	24	0.02%	13.3%	QLDECASAITK	99.7%	45.7	25	44.4	1	0	0	1235.59	912	922
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	15	16	24	0.02%	13.3%	QNIGVATFIGLDK	99.5%	38.2	25	38.2	2	0	0	1375.76	661	673

Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	15	16	24	0.02%	13.3%	SNNIINETTTR	99.7%	59.9	25	52.9	2	0	0	1262.63	435	445
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	15	16	24	0.02%	13.3%	TEYDAVAEK	98.5%	33	25	26.7	1	0	0	1025.48	868	876
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	15	16	24	0.02%	13.3%	VIQENEHALQK	99.7%	82.9	25	79.6	2	0	0	1308.69	999	1009
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	15	16	24	0.02%	13.3%	VLDAIIQEK	99.7%	47	25	31.6	2	0	0	1028.60	599	607
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	15	16	24	0.02%	13.3%	VVTLQGQIIEQSGTMTGGGSK	99.7%	92.9	25	92.9	2	0	0	2107.07	737	757
Structural maintenance of chromosomes protein 6	SMC6	SMC6_HUMAN	126.3	100.0%	3	3	5	0.01%	2.8%	GIETVLLIK	97.2%	30.3	25	22.1	2	0	0	985.63	607	615
Structural maintenance of chromosomes protein 6	SMC6	SMC6_HUMAN	126.3	100.0%	3	3	5	0.01%	2.8%	IEAENKYDAIK	99.3%	36.8	25	26.5	1	0	0	1293.67	774	784
Structural maintenance of chromosomes protein 6	SMC6	SMC6_HUMAN	126.3	100.0%	3	3	5	0.01%	2.8%	SATGSVVSTR	98.8%	34.2	25	26.8	2	0	0	964.51	158	167
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	SDHB	SDHB_HUMAN	31.6	100.0%	3	3	6	0.01%	11.8%	IKNEVDSTLTFR	99.7%	48.4	25	42	2	0	0	1422.76	79	90
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	SDHB	SDHB_HUMAN	31.6	100.0%	3	3	6	0.01%	11.8%	LQDPFSLYR	99.5%	38.7	25	31.4	2	0	0	1138.59	234	242
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	SDHB	SDHB_HUMAN	31.6	100.0%	3	3	6	0.01%	11.8%	YLGPAVLMQAYR	99.7%	43.4	25	42.9	2	0	0	1381.73	206	217
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	8	11	20	0.02%	27.7%	GGQTHLGLPVFNTVK	99.7%	68.7	25	66.1	2	2	0	1567.86	91	105
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	8	11	20	0.02%	27.7%	IGIMPGHIHK	99.6%	39.8	25	31.8	1	0	0	1102.62	183	192
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	8	11	20	0.02%	27.7%	IICQGFTGK	99.7%	43	25	36.8	2	0	0	1023.53	58	66
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	8	11	20	0.02%	27.7%	LIGPNCPGVINPGECK	99.7%	80.8	25	74.2	2	0	0	1724.85	167	182
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	8	11	20	0.02%	27.7%	LVGGTTPGK	99.7%	41.5	25	32.3	2	0	0	829.48	82	90
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	8	11	20	0.02%	27.7%	MGHAGAIIAGGK	99.7%	76.1	25	73.6	4	0	0	1098.57	297	308
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	8	11	20	0.02%	27.7%	QGTFHSQQALEYGTK	99.7%	51.6	25	48	2	2	0	1694.81	67	81
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	8	11	20	0.02%	27.7%	QHLYVDKNTK	99.7%	40.1	25	27.9	1	0	0	1245.66	48	57
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	12	24	0.02%	25.3%	CDVIAQGIVMAVK	99.7%	105	25	87.6	2	0	0	1403.74	384	396
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	12	24	0.02%	25.3%	DLEIKIPVVVR	99.7%	44.1	25	44.1	2	1	0	1280.79	397	407
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	12	24	0.02%	25.3%	EQALQLAQK	99.7%	51.1	25	43.9	4	0	0	1028.57	217	225
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	12	24	0.02%	25.3%	ICNQVLVCER	99.7%	67.8	25	56.1	2	0	0	1290.63	151	160
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	12	24	0.02%	25.3%	ILACDDLDEAAR	99.7%	73.8	25	64.2	2	0	0	1361.64	427	438
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	12	24	0.02%	25.3%	INFDSNSAYR	99.7%	66.1	25	60	2	0	0	1186.55	275	284
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	12	24	0.02%	25.3%	IVFSPEEAK	97.5%	30.8	25	21.4	1	0	0	1019.54	121	129
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	12	24	0.02%	25.3%	LSEIVTLAK	99.7%	57.1	25	38.8	2	0	0	973.59	443	451
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	12	24	0.02%	25.3%	LYSLFLK	99.4%	37.1	25	24.1	2	0	0	883.53	243	249
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	12	24	0.02%	25.3%	MGFPPNIVESAAENMVK	99.7%	74.3	25	63.1	2	0	0	1833.89	226	242
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	12	24	0.02%	25.3%	SPDEAYAIAK	99.7%	71.8	25	64.5	2	0	0	1064.53	79	88
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	15	40	0.04%	29.2%	EAQVYQAFK	98.2%	32.3	25	25.5	4	0	0	1083.55	339	347
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	15	40	0.04%	29.2%	ELELKVPLVVR	97.3%	30.5	25	24.2	1	1	0	1294.81	382	392
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	15	40	0.04%	29.2%	ETYLAILMDR	99.7%	52.8	25	52.8	4	0	0	1240.62	151	160
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	15	40	0.04%	29.2%	FFVADTANEALEAAK	99.7%	120	25	111	4	0	0	1596.79	59	73
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	15	40	0.04%	29.2%	ILNNSGLPITSAIDLEDAAK	99.7%	74.5	25	74.5	4	0	0	2055.10	404	423
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	15	40	0.04%	29.2%	INFDDNAEFR	99.7%	71.1	25	65.3	4	0	0	1240.56	260	269
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	15	40	0.04%	29.2%	LEGTNVQEAQK	99.7%	71.2	25	59	2	0	0	1216.62	393	403
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	15	40	0.04%	29.2%	LYNLFLK	99.7%	41.5	25	30.5	3	0	0	910.54	228	234
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	15	40	0.04%	29.2%	MAENLGFVGPLK	99.7%	84.2	25	71.8	6	0	0	1275.68	207	218
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	15	40	0.04%	29.2%	QMIGYNLATK	99.7%	50.8	25	36.7	3	0	0	1138.59	119	128
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	15	40	0.04%	29.2%	VMVAEALDISR	99.7%	93.6	25	79.4	4	0	0	1203.64	140	150
SUMO-activating enzyme subunit 1	SAE1	SAE1_HUMAN	38.5	100.0%	2	2	4	0.00%	6.1%	NLILAGVK	96.3%	29.1	25	16.4	2	0	0	827.54	54	61
SUMO-activating enzyme subunit 1	SAE1	SAE1_HUMAN	38.5	100.0%	2	2	4	0.00%	6.1%	VSQGVEDGPDTKR	99.7%	42.9	25	42.6	2	0	0	1387.68	184	196
SUMO-activating enzyme subunit 2	UBA2	SAE2_HUMAN	71.2	100.0%	2	2	4	0.00%	4.2%	QFILVMNALDNR	99.7%	52	25	41.9	2	0	0	1433.76	108	119
SUMO-activating enzyme subunit 2	UBA2	SAE2_HUMAN	71.2	100.0%	2	2	4	0.00%	4.2%	VLVVGAGGIGCELLK	99.7%	107	25	98.9	2	0	0	1484.85	20	34
SUN domain-containing protein 2	SUN2	SUN2_HUMAN	80.3	100.0%	6	6	11	0.01%	10.9%	AEHQQDSEDLFKK	99.6%	30.9	25	30.9	0	1	0	1574.74	364	376
SUN domain-containing protein 2	SUN2	SUN2_HUMAN	80.3	100.0%	6	6	11	0.01%	10.9%	DSSPHFQAEQR	99.7%	44	25	37.3	2	0	0	1301.59	265	275
SUN domain-containing protein 2	SUN2	SUN2_HUMAN	80.3	100.0%	6	6	11	0.01%	10.9%	IGLADYALESGGASVISTR	99.7%	115	25	112	2	0	0	1879.98	544	562
SUN domain-containing protein 2	SUN2	SUN2_HUMAN	80.3	100.0%	6	6	11	0.01%	10.9%	ILTHVAEMQGK	99.7%	55.8	25	51.3	2	0	0	1242.65	492	502
SUN domain-containing protein 2	SUN2	SUN2_HUMAN	80.3	100.0%	6	6	11	0.01%	10.9%	LTTAASLLDVFVLTR	99.7%	77.9	25	77.9	2	0	0	1619.94	191	205
SUN domain-containing protein 2	SUN2	SUN2_HUMAN	80.3	100.0%	6	6	11	0.01%	10.9%	RPDEGWEAR	98.6%	33.5	25	30.1	2	0	0	1115.52	256	264

Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	18	20	40	0.04%	20.0%	AIGNTELENK	99.7%	46.5	25	37.2	2	0	0	1088.56	1013	1022
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	18	20	40	0.04%	20.0%	ALFATETFAMGINMPAR	99.7%	41.6	25	40.3	3	0	0	1872.90	478	494
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	18	20	40	0.04%	20.0%	EIEEYIHKPK	99.7%	41.5	25	21.3	1	0	0	1285.68	639	648
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	18	20	40	0.04%	20.0%	ETIEILFSEGLIK	99.7%	43.8	25	43.7	1	0	0	1491.83	465	477
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	18	20	40	0.04%	20.0%	EYPFILDAFQR	99.7%	54	25	44.8	4	0	0	1398.71	135	145
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	18	20	40	0.04%	20.0%	GIVILMVDEK	99.7%	76.8	25	73.6	4	0	0	1132.63	533	542
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	18	20	40	0.04%	20.0%	IEESITEDLSLADLMPR	99.1%	35.2	25	35.2	2	0	0	1931.96	82	98
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	18	20	40	0.04%	20.0%	IVIPNEESVVIYYK	99.7%	42.7	25	41.3	2	0	0	1665.91	615	628
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	18	20	40	0.04%	20.0%	KAQIAIDIK	99.3%	36.7	25	17.9	1	0	0	999.62	825	833
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	18	20	40	0.04%	20.0%	LDFNTDEEKK	97.6%	31	25	17.7	1	0	0	1238.59	409	418
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	18	20	40	0.04%	20.0%	LGFATSSDVIEMK	99.7%	74.4	25	55.5	4	0	0	1397.70	861	873
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	18	20	40	0.04%	20.0%	LTEQLAGPLR	99.7%	79.7	25	69.8	2	0	0	1097.63	924	933
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	18	20	40	0.04%	20.0%	MTDVFEGSIIR	99.7%	68.1	25	64.7	2	0	0	1283.63	985	995
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	18	20	40	0.04%	20.0%	NFQPVIIFSFSK	99.7%	52.4	25	51.4	4	0	0	1426.77	385	396
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	18	20	40	0.04%	20.0%	SFYQFQHYR	99.6%	39.1	25	35.8	2	0	0	1275.59	588	596
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	18	20	40	0.04%	20.0%	TVCAEYAIALALR	99.7%	67.2	25	62.2	2	0	0	1450.77	168	180
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	18	20	40	0.04%	20.0%	TVLQMDELK	99.2%	35.9	25	25	1	0	0	1076.57	844	852
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	18	20	40	0.04%	20.0%	YCLPFLQPGR	99.6%	39.1	25	39.1	2	0	0	1250.64	649	658
Suppressor of SWI4 1 homolog	PPAN	SSF1_HUMAN	53.2	100.0%	3	3	5	0.01%	7.2%	LPGGPTLTFQVK	99.7%	67.2	25	59.9	2	0	0	1257.72	102	113
Suppressor of SWI4 1 homolog	PPAN	SSF1_HUMAN	53.2	100.0%	3	3	5	0.01%	7.2%	TETNVYFK	99.1%	35.5	25	27.4	1	0	0	1001.49	91	98
Suppressor of SWI4 1 homolog	PPAN	SSF1_HUMAN	53.2	100.0%	3	3	5	0.01%	7.2%	VGGSDEEASGIPSR	99.7%	62.7	25	61	2	0	0	1360.63	356	369
Surfeit locus protein 4	SURF4	SURF4_HUMAN	30.4	100.0%	4	4	7	0.01%	17.5%	LCLISTFLEDGIR	99.7%	86.4	25	78.9	2	0	0	1536.81	31	43
Surfeit locus protein 4	SURF4	SURF4_HUMAN	30.4	100.0%	4	4	7	0.01%	17.5%	NLALGGGLLLLLAESR	99.7%	72.1	25	72.1	2	0	0	1609.96	120	135
Surfeit locus protein 4	SURF4	SURF4_HUMAN	30.4	100.0%	4	4	7	0.01%	17.5%	QYLPHVAR	97.8%	31.2	25	16.9	1	0	0	983.54	23	30
Surfeit locus protein 4	SURF4	SURF4_HUMAN	30.4	100.0%	4	4	7	0.01%	17.5%	SMFAGVPTMR	99.0%	34.8	25	33.6	2	0	0	1112.52	140	149
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	7	7	9	0.01%	8.2%	APSSLSDAVPQR	99.7%	56.3	25	49	1	0	0	1227.63	570	581
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	7	7	9	0.01%	8.2%	ATTGTQTLLSSGTR	99.7%	52.3	25	30.3	1	0	0	1393.73	696	709
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	7	7	9	0.01%	8.2%	FGIEIIK	99.7%	41	25	22	1	0	0	819.50	328	334
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	7	7	9	0.01%	8.2%	SLALLGQTFSLASSFR	99.7%	92.1	25	92.1	1	0	0	1697.92	479	494
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	7	7	9	0.01%	8.2%	SVTPLLMACNAYELSVK	99.2%	35.7	25	35.7	1	0	0	1895.96	439	455
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	7	7	9	0.01%	8.2%	VDNEFLNMLLDK	99.7%	49.4	25	43.7	2	0	0	1450.72	398	409
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	7	7	9	0.01%	8.2%	YSLSGSVAHSR	99.7%	78.6	25	72.9	2	0	0	1163.58	63	73
Survival motor neuron protein	SMN1	SMN_HUMAN	31.8	100.0%	4	4	7	0.01%	17.0%	ETCVVVYTGYGNR	99.7%	43.4	25	43.4	1	0	0	1517.71	121	133
Survival motor neuron protein	SMN1	SMN_HUMAN	31.8	100.0%	4	4	7	0.01%	17.0%	GTGQSDDSDIWDDTALIK	99.7%	70.4	25	66.8	2	0	0	1936.88	24	41
Survival motor neuron protein	SMN1	SMN_HUMAN	31.8	100.0%	4	4	7	0.01%	17.0%	LGPGKPGLK	99.4%	36.9	25	32.9	2	0	0	866.55	205	213
Survival motor neuron protein	SMN1	SMN_HUMAN	31.8	100.0%	4	4	7	0.01%	17.0%	NTAASLQQWK	99.7%	40.9	25	35.1	2	0	0	1146.59	84	93
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H box 1	SMARCAD1	SMRCD_HUMAN	117.4	99.8%	2	2	2	0.00%	2.1%	QEQLYLGLFNR	98.3%	32.5	25	31.8	1	0	0	1380.73	747	757
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H box 1	SMARCAD1	SMRCD_HUMAN	117.4	99.8%	2	2	2	0.00%	2.1%	VLGCILSELK	98.1%	31.9	25	27.4	1	0	0	1131.64	858	867
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	20	22	40	0.04%	20.7%	CNELQDIEK	99.7%	51	25	34.3	2	0	0	1148.53	891	899
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	20	22	40	0.04%	20.7%	CNTLITLIER	99.7%	55.8	25	44.3	1	0	0	1232.67	1001	1010
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	20	22	40	0.04%	20.7%	DFNQFIK	98.6%	33.4	25	11.1	2	0	0	911.46	849	855
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	20	22	40	0.04%	20.7%	DIDILNSAGK	99.7%	52.8	25	32.4	2	0	0	1045.55	431	440
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	20	22	40	0.04%	20.7%	ESEITDEDIDGILER	99.7%	78.8	25	78.8	2	0	0	1733.81	666	680
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	20	22	40	0.04%	20.7%	IMAQIER	98.9%	34.5	25	12.6	2	0	0	876.46	900	906
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	20	22	40	0.04%	20.7%	LDGQTPHDER	99.7%	61.4	25	59.8	2	0	0	1167.54	529	538
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	20	22	40	0.04%	20.7%	LDSIVIQQGR	99.7%	68.5	25	57.2	2	0	0	1128.64	627	636
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	20	22	40	0.04%	20.7%	LLNILMQLR	99.7%	72.6	25	61.1	5	0	0	1113.68	446	454
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	20	22	40	0.04%	20.7%	LLTQGFTNWNK	99.7%	48.3	25	44.8	1	0	0	1321.69	837	847
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	20	22	40	0.04%	20.7%	NPELPNAAQAQK	99.7%	54.2	25	48.1	2	0	0	1280.66	803	814
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	20	22	40	0.04%	20.7%	QNLLSVGDYR	99.7%	69.9	25	48.3	2	0	0	1164.60	133	142
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	20	22	40	0.04%	20.7%	QTELFAHFIQPAAQK	99.7%	49.8	25	44.9	1	0	0	1728.91	98	112

SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	20	22	40	0.04%	20.7%	SVCLIGDKEQR	99.7%	55.3	25	30	2	0	0	1304.66	257	267
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	20	22	40	0.04%	20.7%	TEQEEDEELLTESSK	99.7%	67.4	25	67.4	1	0	0	1766.78	146	160
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	20	22	40	0.04%	20.7%	TLQTISLLGYMK	99.7%	63.8	25	63.8	2	0	0	1383.76	212	223
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	20	22	40	0.04%	20.7%	TPEEVIEYSAVFWER	99.7%	55.8	25	53.9	2	0	0	1854.89	876	890
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	20	22	40	0.04%	20.7%	VLDILEDYCMWR	99.6%	38.9	25	38.9	1	0	0	1612.75	511	522
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	20	22	40	0.04%	20.7%	VLIFSQMTR	99.7%	60.2	25	55.3	4	0	0	1094.60	502	510
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	20	22	40	0.04%	20.7%	YLVIDEAHR	99.7%	49.3	25	45.9	2	0	0	1115.58	304	312
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	SMARCD2	SMRD2_HUMAN	58.9	100.0%	3	3	5	0.01%	8.1%	AEGDSAGTAGTPGGTPAGDK	99.7%	51.1	25	51.1	1	0	0	1716.77	207	226
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	SMARCD2	SMRD2_HUMAN	58.9	100.0%	3	3	5	0.01%	8.1%	IITDVIGNPEEERR	99.7%	32.1	25	30.2	0	2	0	1640.86	481	494
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	SMARCD2	SMRD2_HUMAN	58.9	100.0%	3	3	5	0.01%	8.1%	LLGVHTQTR	99.7%	44.8	25	33.2	2	0	0	1024.59	320	328
Symplekin	SYMPK	SYMPK_HUMAN	141.2	100.0%	9	10	16	0.02%	8.8%	AEVLSFILEDVR	99.7%	64.8	25	58.5	1	0	0	1390.76	602	613
Symplekin	SYMPK	SYMPK_HUMAN	141.2	100.0%	9	10	16	0.02%	8.8%	ETAAGGLTLKEER	99.7%	43.5	25	37.2	1	0	0	1374.72	1230	1242
Symplekin	SYMPK	SYMPK_HUMAN	141.2	100.0%	9	10	16	0.02%	8.8%	FVEGLIVTLSPR	99.7%	44.7	25	31.4	1	0	0	1330.77	186	197
Symplekin	SYMPK	SYMPK_HUMAN	141.2	100.0%	9	10	16	0.02%	8.8%	LGGFVMNILSR	99.7%	70.8	25	56.6	2	0	0	1206.67	1012	1022
Symplekin	SYMPK	SYMPK_HUMAN	141.2	100.0%	9	10	16	0.02%	8.8%	LLSGLQEKPDQK	99.7%	44.3	25	32.3	1	0	0	1355.75	649	660
Symplekin	SYMPK	SYMPK_HUMAN	141.2	100.0%	9	10	16	0.02%	8.8%	MADSEIPR	96.2%	29	25	28.6	1	0	0	934.43	198	205
Symplekin	SYMPK	SYMPK_HUMAN	141.2	100.0%	9	10	16	0.02%	8.8%	TVIQSLTMYPR	99.7%	49	25	40	3	0	0	1324.69	1001	1011
Symplekin	SYMPK	SYMPK_HUMAN	141.2	100.0%	9	10	16	0.02%	8.8%	VVDLLNQAALITNDSK	99.7%	58.4	25	58.4	2	0	0	1713.94	36	51
Symplekin	SYMPK	SYMPK_HUMAN	141.2	100.0%	9	10	16	0.02%	8.8%	VVLEAPLITESALEVVR	99.7%	96.3	25	96.3	4	0	0	1838.06	667	683
Synembryn-A	RIC8A	RIC8A_HUMAN	59.7	100.0%	4	4	4	0.00%	7.5%	ASINPVTGR	95.4%	28.2	25	16.2	1	0	0	914.51	451	459
Synembryn-A	RIC8A	RIC8A_HUMAN	59.7	100.0%	4	4	4	0.00%	7.5%	LLFLLTALR	99.7%	48.4	25	48.4	1	0	0	1059.69	167	175
Synembryn-A	RIC8A	RIC8A_HUMAN	59.7	100.0%	4	4	4	0.00%	7.5%	VIWLQSVR	98.0%	31.7	25	18.5	1	0	0	1000.59	64	71
Synembryn-A	RIC8A	RIC8A_HUMAN	59.7	100.0%	4	4	4	0.00%	7.5%	YTGYGNAAGLLAAR	99.7%	93.6	25	92.8	1	0	0	1397.72	410	423
Syntaxin-18	STX18	STX18_HUMAN	38.7	100.0%	3	3	5	0.01%	10.1%	LIGEMNSLFDEVR	99.7%	43.7	25	43.7	2	0	0	1522.76	242	254
Syntaxin-18	STX18	STX18_HUMAN	38.7	100.0%	3	3	5	0.01%	10.1%	LSKLEPEPNTK	98.4%	32.7	25	30.7	1	0	0	1255.69	166	176
Syntaxin-18	STX18	STX18_HUMAN	38.7	100.0%	3	3	5	0.01%	10.1%	TCSEAIQQLR	99.7%	56.2	25	34.7	2	0	0	1205.59	106	115
Syntaxin-binding protein 2	STXBP2	STXB2_HUMAN	66.5	100.0%	3	3	6	0.01%	6.4%	ADTPSLGEGPEK	99.4%	36.9	25	29.1	2	0	0	1200.57	214	225
Syntaxin-binding protein 2	STXBP2	STXB2_HUMAN	66.5	100.0%	3	3	6	0.01%	6.4%	LIVPVLLDAAVPAYDK	99.7%	52	25	52	2	0	0	1696.99	388	403
Syntaxin-binding protein 2	STXBP2	STXB2_HUMAN	66.5	100.0%	3	3	6	0.01%	6.4%	YETTGLSEAR	99.7%	49.2	25	41.8	2	0	0	1126.54	266	275
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	6	7	12	0.01%	15.2%	FGGNPGGFGNQGGFGNSR	99.7%	115	25	109	2	0	0	1726.77	276	293
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	6	7	12	0.01%	15.2%	FTEYETQVK	99.7%	45.5	25	33.7	2	0	0	1144.55	152	160
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	6	7	12	0.01%	15.2%	GISVHISNAEPK	99.7%	55.4	25	51.3	2	0	0	1251.67	252	263
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	6	7	12	0.01%	15.2%	KMDETDASSAVK	99.7%	68.5	25	57.5	3	0	0	1281.60	84	95
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	6	7	12	0.01%	15.2%	MDETDASSAVK	99.7%	48.3	25	48.3	1	0	0	1153.50	85	95
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	6	7	12	0.01%	15.2%	TSDLIVLGLPWK	99.7%	90.9	25	81.6	2	0	0	1341.78	103	114
Target of EGR1 protein 1	TOE1	TOE1_HUMAN	56.5	100.0%	4	4	6	0.01%	8.6%	ALLNLPGTQTSGEAK	99.7%	53.9	25	48.6	2	0	0	1499.81	348	362
Target of EGR1 protein 1	TOE1	TOE1_HUMAN	56.5	100.0%	4	4	6	0.01%	8.6%	SILSLGLACFK	99.6%	39	25	39	2	0	0	1208.67	96	106
Target of EGR1 protein 1	TOE1	TOE1_HUMAN	56.5	100.0%	4	4	6	0.01%	8.6%	SLLNQCIEER	99.4%	37.4	25	28.4	1	0	0	1261.62	75	84
Target of EGR1 protein 1	TOE1	TOE1_HUMAN	56.5	100.0%	4	4	6	0.01%	8.6%	YAAEFHAR	96.8%	29.7	25	25.6	1	0	0	964.46	231	238
TATA-binding protein-associated factor 172	BTAF1	BTAF1_HUMAN	206.9	100.0%	3	3	5	0.01%	1.9%	IAAGQAVEAIVK	99.7%	72.3	25	65.2	2	0	0	1169.69	60	71
TATA-binding protein-associated factor 172	BTAF1	BTAF1_HUMAN	206.9	100.0%	3	3	5	0.01%	1.9%	LFILLDTGTTPVTR	99.7%	65.5	25	60.3	2	0	0	1546.88	9	22
TATA-binding protein-associated factor 172	BTAF1	BTAF1_HUMAN	206.9	100.0%	3	3	5	0.01%	1.9%	LLCVFALDR	99.7%	41.7	25	35.8	1	0	0	1106.60	346	354
TBC1 domain family member 15	TBC1D15	TBC15_HUMAN	79.5	100.0%	3	3	3	0.00%	4.3%	EFSFLDILR	99.7%	46.3	25	31.2	1	0	0	1139.61	539	547
TBC1 domain family member 15	TBC1D15	TBC15_HUMAN	79.5	100.0%	3	3	3	0.00%	4.3%	TQLIQLSTLLR	99.7%	67.7	25	63.8	1	0	0	1285.78	497	507
TBC1 domain family member 15	TBC1D15	TBC15_HUMAN	79.5	100.0%	3	3	3	0.00%	4.3%	VTNYIFDSLR	99.7%	50	25	32.6	1	0	0	1227.64	253	262
TBC1 domain family member 4	TBC1D4	TBCD4_HUMAN	146.6	100.0%	2	2	2	0.00%	2.2%	IQALESNLENLLTR	99.7%	91.1	25	87.2	1	0	0	1613.89	1227	1240
TBC1 domain family member 4	TBC1D4	TBCD4_HUMAN	146.6	100.0%	2	2	2	0.00%	2.2%	LLPADALVNCDLLLR	99.7%	46.3	25	46.3	1	0	0	1695.95	1268	1282
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	AFHNEAQVNPER	99.7%	62.9	25	62.9	4	4	0	1411.67	469	480
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	AFHNEAQVNPERK	99.7%	49.3	25	46	4	3	0	1539.77	469	481
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	DCLINAAK	99.7%	51	25	34.3	3	0	0	904.46	146	153
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	DDKHGSYEDAVHSGALND	99.7%	56	25	56	1	2	0	1929.82	539	556

T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	EQLAIAEFAR	99.7%	68.3	25	56.1	13	0	0	1147.61	434	443
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	EVGDGTTSVVIIAAELLK	99.7%	86.1	25	84	3	0	0	1815.01	85	102
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	FATEAAITILR	99.7%	89.5	25	68.9	15	0	0	1205.69	516	526
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	GANDFMCDEMER	99.7%	83.8	25	83.8	8	0	0	1474.54	379	390
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	HGSYEDAVHSGALND	99.7%	86.9	25	86	2	0	0	1571.67	542	556
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	IACLDFSLQK	99.7%	76.9	25	70.9	4	0	0	1194.62	234	243
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	ICDDELILIK	99.7%	62.2	25	52.2	6	0	0	1231.66	356	365
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	IHPTSVISGYR	96.9%	29.9	25	27.6	1	0	0	1229.66	112	122
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	ILATGANVILTTGGIDDMCLK	99.7%	125	25	112	4	0	0	2192.13	278	298
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	LGVQVVITDPEK	99.7%	86.6	25	82.8	2	0	0	1297.74	248	259
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	LGVQVVITDPEKLDQIR	99.7%	59.4	25	59.4	2	4	0	1923.09	248	264
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	LLEVEHPAAK	99.7%	64.1	25	55.8	9	0	0	1106.62	64	73
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	MLVDDIGDVTITNDGATILK	99.7%	142	25	136	5	0	0	2120.08	44	63
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	QAGVFEPTIVK	99.7%	48.9	25	35.4	3	0	0	1188.66	500	510
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	SLHDALCVVK	99.7%	45.1	25	41.6	3	0	0	1141.60	391	400
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	SLHDALCVVKR	99.6%	31.5	25	21.8	0	1	0	1297.70	391	401
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	SLLVIPNTLAVNAAQDSTDLVAK	99.7%	85.6	25	85.6	8	2	0	2353.30	444	466
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	SQNVMAAASIANIVK	99.7%	129	25	123	5	0	0	1516.82	19	33
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	SSLGPVGLDK	99.7%	66	25	30.5	3	0	0	972.54	34	43
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	SVVPGGGAVEAALSIYLENYATSMGSR	96.2%	22.8	25	22.8	0	1	0	2699.33	407	433
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	TSASIILR	99.7%	61.6	25	48.9	2	0	0	860.52	371	378
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	VLCELADLQDK	99.7%	59.3	25	51.9	2	0	0	1303.66	74	84
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	VLCELADLQDKEVGDGTTSVVIIAAELLK	99.7%	66.2	25	66.2	0	2	0	3099.65	74	102
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	WIGLDLSNGKPR	99.7%	45.1	25	40.2	1	2	0	1355.74	485	496
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	YFVEAGAMAVR	99.7%	74.4	25	66.1	5	0	0	1213.60	299	309
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	30	41	144	0.14%	60.8%	YPVNSVNILK	99.7%	57.2	25	41.3	5	0	0	1146.65	190	199
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	19	26	43	0.04%	46.5%	AAHSEGNTTAGLDMR	99.7%	74.3	25	70.4	2	4	0	1530.70	467	481
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	19	26	43	0.04%	46.5%	AGADEERAETAR	99.7%	43.7	25	36.8	2	0	0	1275.59	14	25
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	19	26	43	0.04%	46.5%	DASLMVTNDGATILK	99.7%	80.7	25	72.7	1	0	0	1548.79	58	72
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	19	26	43	0.04%	46.5%	EAESLIAK	98.2%	32.2	25	16.6	1	0	0	860.47	112	119
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	19	26	43	0.04%	46.5%	EALLSSAVDHGSDEVK	99.7%	84.3	25	79.5	2	2	0	1656.81	139	154
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	19	26	43	0.04%	46.5%	EAVAMESYAK	98.2%	32.3	25	31.4	2	0	0	1098.51	432	441
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	19	26	43	0.04%	46.5%	EGTIGDMAILGITESFQVK	99.7%	88.8	25	88.8	1	0	0	2009.03	482	500
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	19	26	43	0.04%	46.5%	GATQQILDEAER	99.7%	104	25	98	2	0	0	1330.66	377	388
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	19	26	43	0.04%	46.5%	HGINCFINR	99.7%	47.6	25	39.2	2	0	0	1130.55	285	293
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	19	26	43	0.04%	46.5%	ILIANTGMDTDKIK	99.7%	86.7	25	73.1	4	1	0	1532.84	237	250
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	19	26	43	0.04%	46.5%	LALVTGGEIASTFDHPELVK	98.6%	26.5	25	26.5	0	1	0	2097.12	323	342
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	19	26	43	0.04%	46.5%	LAVEAVLR	99.7%	50.5	25	14.9	1	0	0	870.54	182	189
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	19	26	43	0.04%	46.5%	LKGSGNLEAIHIIK	99.7%	33.4	25	30.5	0	2	0	1492.88	190	203
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	19	26	43	0.04%	46.5%	LTSFIGAIAIGDLVK	99.7%	116	25	107	1	0	0	1517.89	26	40
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	19	26	43	0.04%	46.5%	MLPTIIADNAGYDSADLVAQLR	99.7%	130	25	130	3	2	0	2347.20	445	466
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	19	26	43	0.04%	46.5%	VAEIEHAEK	99.7%	44.5	25	42.1	2	0	0	1025.53	264	272
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	19	26	43	0.04%	46.5%	VAEIEHAEKEK	99.7%	58.1	25	48	2	0	0	1282.66	264	274
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	19	26	43	0.04%	46.5%	VLVDMSR	99.5%	38	25	21.5	2	0	0	819.44	83	89
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	19	26	43	0.04%	46.5%	VQDDEVGDGTTSVTVLAAELLR	99.7%	133	25	133	1	0	0	2288.16	90	111
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	22	30	98	0.10%	56.2%	AFADAMEVIPSTLAENAGLNPISTVTELR	99.7%	39.7	25	38.9	0	1	0	3030.55	453	481
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	22	30	98	0.10%	56.2%	ALIAGGGAPEIELALR	99.7%	101	25	101	11	0	0	1550.89	420	435
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	22	30	98	0.10%	56.2%	AQDIEAGDGTTSVVIIAGSLLDSCTK	99.7%	148	25	148	2	2	0	2621.30	97	122
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	22	30	98	0.10%	56.2%	AYILNLVK	99.7%	52.9	25	47.2	2	0	0	933.58	281	288
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	22	30	98	0.10%	56.2%	DALSDLALHFLNK	99.7%	97.6	25	85.2	10	2	0	1456.78	307	319
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	22	30	98	0.10%	56.2%	DIEREDIEFICK	99.7%	57.1	25	57.1	2	1	0	1566.75	327	338

T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	22	30	98	0.10%	56.2%	FSNISAAK	99.7%	45.4	25	35.9	2	0	0	837.45	35	42
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	22	30	98	0.10%	56.2%	GAYQDRDKPAQIR	99.7%	37.9	25	33.3	0	2	0	1517.78	22	34
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	22	30	98	0.10%	56.2%	GIHPTIISESFQK	99.7%	40.1	25	35.5	0	2	0	1456.78	127	139
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	22	30	98	0.10%	56.2%	IDDVVNTR	99.7%	55.1	25	48.5	2	0	0	931.48	532	539
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	22	30	98	0.10%	56.2%	IGLIQFCLSAPK	99.7%	70.7	25	63.2	8	0	0	1346.75	246	257
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	22	30	98	0.10%	56.2%	KTGCNVLLIQK	99.7%	41.4	25	23	1	0	0	1273.73	292	302
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	22	30	98	0.10%	56.2%	LGGTIDDCELVEGLVLTQK	99.7%	108	25	107	2	2	0	2060.06	214	232
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	22	30	98	0.10%	56.2%	LVIEEAER	99.7%	57.8	25	52.1	4	0	0	958.52	396	403
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	22	30	98	0.10%	56.2%	MIQDGKGDVTITNDGATILK	99.7%	61.9	25	57.7	2	4	0	2106.08	60	79
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	22	30	98	0.10%	56.2%	MLVELSK	98.7%	33.6	25	9.45	2	0	0	835.46	90	96
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	22	30	98	0.10%	56.2%	QMQVLHPAAR	99.7%	46.7	25	41.7	3	0	0	1150.62	80	89
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	22	30	98	0.10%	56.2%	SIHDALCVIR	99.7%	61.6	25	0	5	0	0	1183.63	404	413
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	22	30	98	0.10%	56.2%	TDMDNQIVVSDYAQMDR	99.7%	108	25	108	2	0	0	2032.86	258	274
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	22	30	98	0.10%	56.2%	TGCNVLLIQK	99.7%	53.5	25	35.7	7	0	0	1145.63	293	302
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	22	30	98	0.10%	56.2%	TLSGMESYCVR	99.7%	71	25	66.4	8	0	0	1318.58	442	452
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	22	30	98	0.10%	56.2%	VIDPATATSVDLR	99.7%	87.4	25	77.1	8	0	0	1357.73	194	206
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	22	30	98	0.10%	56.2%	VVSQYSSLLSPMSVNAVMK	99.7%	116	25	114	4	0	0	2072.04	175	193
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	AVTIFIR	99.7%	47.8	25	21.9	5	0	0	819.51	382	388
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	CPTLEQYAMR	99.7%	56.1	25	51.7	3	0	0	1268.58	440	449
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	DKMLVIEQCK	99.7%	55.9	25	51.2	2	0	0	1279.64	369	378
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	DTEPLIQTAK	99.7%	40.1	25	38.1	2	0	0	1115.59	161	170
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	DVDFELIK	99.0%	34.8	25	15.6	2	0	0	978.51	203	210
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	DVDFELIKVEGK	99.7%	70.2	25	62.1	2	0	0	1391.74	203	214
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	EKFEEMIQQIK	99.7%	59.7	25	50.2	2	0	0	1438.72	283	293
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	EMNPALGIDCLHK	99.7%	80.8	25	72.2	4	3	0	1513.71	484	496
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	FEEMIQQIK	99.7%	52	25	36.8	4	0	0	1165.59	285	293
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	FSELTAEK	99.7%	61.1	25	50.1	2	0	0	924.47	345	352
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	GVIVDKDFSHPQMPK	99.7%	34.3	25	34.3	0	4	0	1713.86	227	241
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	HKLDVTSVEDYK	94.6%	21.5	25	16.8	0	1	0	1433.73	264	275
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	IADGYEQAAR	99.7%	87.3	25	79.2	9	0	0	1093.53	133	142
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	IAILTCPFEPPKPK	99.7%	40.9	25	40.9	2	0	0	1610.90	248	261
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	IDDIRKPGESEE	97.3%	30.5	25	28.9	1	0	0	1387.67	530	541
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	ISDSVLVDIK	99.7%	50.8	25	39.9	2	0	0	1088.62	151	160
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	ISDSVLVDIKDTEPLIQTAK	98.5%	26.1	25	26.1	0	1	0	2185.20	151	170
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	KQQISLATQMVR	99.7%	72.2	25	72.2	3	4	0	1402.78	514	525
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	LDVTSVEDYK	99.7%	76.7	25	70.5	2	0	0	1168.57	266	275
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	LGFAGLVQEISFGTTK	99.7%	114	25	114	8	0	0	1667.90	353	368
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	LMGLEALK	99.5%	38.5	25	24.9	3	0	0	874.51	28	35
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	LMVELSK	99.7%	44.4	25	13.7	4	0	0	835.46	90	96
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	MIIEEAKR	99.7%	59.2	25	43.1	4	0	0	989.54	393	400
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	QQHVIETLIGK	99.5%	30.1	25	30.1	2	2	0	1265.72	503	513
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	QQISLATQMVR	99.7%	54.9	25	45.1	4	0	0	1274.69	515	525
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	RDVDFELIK	99.7%	44.2	25	7.96	2	0	0	1134.62	202	210
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	SLHDALCVIR	99.7%	61.6	25	0	5	0	0	1183.63	401	410
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	TSLGPNGLDK	99.7%	67.2	25	61.5	2	0	0	1001.53	50	59
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	VAIEHLDK	99.7%	53.9	25	34.1	2	0	0	924.52	143	150
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	44	104	0.10%	48.4%	WVGGPEIELIAIATGGR	99.7%	97.8	25	95.6	6	0	0	1738.95	324	340
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	21	26	66	0.07%	45.7%	ALEIIPR	99.7%	53.5	25	43.1	4	0	0	811.50	441	447
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	21	26	66	0.07%	45.7%	ATISNDGATILK	99.7%	53.5	25	39.3	2	0	0	1203.66	56	67
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	21	26	66	0.07%	45.7%	CQVFEETQIGGER	99.7%	82	25	69.6	2	0	0	1552.71	345	357
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	21	26	66	0.07%	45.7%	GGAEQFMEETER	99.7%	72.6	25	72.3	4	0	0	1383.58	376	387

T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	21	26	66	0.07%	45.7%	IALLNVELELK	99.7%	64.1	25	55.2	2	0	0	1254.77	237	247
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	21	26	66	0.07%	45.7%	INALTAASEAACLIVSVDETIK	99.7%	102	25	102	1	4	0	2289.20	500	521
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	21	26	66	0.07%	45.7%	INALTAASEAACLIVSVDETIKNPR	99.7%	77.8	25	77.8	0	2	0	2656.40	500	524
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	21	26	66	0.07%	45.7%	LLDVVHPAAK	99.7%	57.3	25	48.3	5	0	0	1062.63	68	77
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	21	26	66	0.07%	45.7%	LPIGDVATQYFADR	99.7%	103	25	99.8	3	0	0	1565.80	293	306
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	21	26	66	0.07%	45.7%	LPIGDVATQYFADRDMFCAGR	99.6%	30.8	25	30.8	0	1	0	2403.12	293	313
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	21	26	66	0.07%	45.7%	MVVDAVMMLDDLLQLK	99.7%	98.3	25	57.6	6	0	0	1849.95	178	193
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	21	26	66	0.07%	45.7%	QLCDNAGFDATNILNK	99.7%	87.8	25	76.5	2	0	0	1793.85	448	463
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	21	26	66	0.07%	45.7%	QQLLIGAYAK	98.5%	32.9	25	20.4	1	0	0	1104.64	431	440
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	21	26	66	0.07%	45.7%	SLHDAIMIVR	99.7%	45	25	39.5	1	0	0	1170.63	388	397
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	21	26	66	0.07%	45.7%	SQDAEVGDGTTSVTLLAAEFLK	99.7%	143	25	143	2	1	0	2252.13	85	106
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	21	26	66	0.07%	45.7%	TATQLAVNK	99.7%	85	25	73	4	0	0	945.54	127	135
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	21	26	66	0.07%	45.7%	TCTFILR	99.7%	45.1	25	19.3	4	0	0	910.48	369	375
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	21	26	66	0.07%	45.7%	TFSYAGFEMQPK	99.7%	78.7	25	74	6	0	0	1405.65	219	230
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	21	26	66	0.07%	45.7%	VPEEDLKR	99.7%	62.4	25	52.5	4	0	0	985.53	314	321
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	21	26	66	0.07%	45.7%	VQGGALEDSQLVAGVAFK	99.7%	105	25	105	2	0	0	1788.95	200	217
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	21	26	66	0.07%	45.7%	YNFFTGCPK	99.7%	50	25	39.9	3	0	0	1133.51	358	366
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	ACTILLR	99.7%	53.3	25	34.9	2	0	0	846.49	371	377
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	ALDDMISTLK	99.7%	84.2	25	73.2	5	0	0	1106.58	129	138
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	ALDDMISTLKK	99.7%	48.7	25	37.7	4	0	0	1234.67	129	139
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	AMTGVEQWPYR	99.7%	60.8	25	59.9	4	0	0	1337.63	428	438
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	ANITAIRR	99.6%	39.2	25	25.7	2	0	0	914.55	307	314
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	AVAQALEVIPR	99.7%	96.2	25	75.9	16	0	0	1166.69	439	449
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	EILSEVER	99.7%	62.2	25	20.1	5	0	0	974.52	382	389
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	EIQVQHPAAK	99.7%	55.8	25	44	10	0	0	1120.61	69	78
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	ELGIWEPLAVK	99.7%	54.2	25	48.5	4	0	0	1254.71	492	502
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	GESQTDIEITR	99.5%	38.7	25	20.2	1	0	0	1248.61	250	260
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	GISDLAQHYLMR	99.7%	82.6	25	77.4	14	1	0	1403.71	295	306
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	IDDIVSGHK	99.7%	45.5	25	34	6	0	0	983.52	519	527
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	IDDIVSGHKK	99.2%	36	25	26.4	3	0	0	1111.61	519	528
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	IGDEYFTFITDCK	99.7%	82.9	25	79.3	2	0	0	1608.73	355	367
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	IGDEYFTFITDCKDPK	97.6%	24.3	25	24.3	0	1	0	1948.90	355	370
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	IPGGIIEDSCVLR	99.7%	90.8	25	80.9	6	0	0	1428.75	204	216
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	IVLLDSSLEYK	99.7%	79.2	25	72.9	7	0	0	1279.71	238	248
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	IVLLDSSLEYKK	99.7%	67.8	25	64.4	3	0	0	1407.81	238	249
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	KGESQTDIEITR	99.7%	96.1	25	62.5	2	2	0	1376.70	249	260
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	MLLDPMGGIVMTNDGNAILR	99.7%	93.2	25	93.2	16	2	0	2179.06	49	68
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	MVQFEENGR	99.7%	46.8	25	44.5	2	0	0	1109.50	182	190
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	MVQFEENGRK	99.7%	40.5	25	26.5	2	0	0	1237.60	182	191
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	NLQDAMQVCR	99.7%	74.7	25	63.5	12	0	0	1234.57	390	399
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	NVLLDPQLVPGGGASEMAVAHALTEK	98.9%	27.1	25	21	0	2	0	2617.37	400	425
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	SMIEISR	99.7%	43	25	22.8	2	0	0	835.43	79	85
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	TAVETAVLLLR	99.7%	107	25	92.7	6	0	0	1185.72	508	518
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	TLIQNCGASTIR	99.7%	73.3	25	62.1	4	0	0	1333.69	450	461
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	VQSGNINAAK	99.7%	42.5	25	29.8	1	0	0	1001.54	22	31
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	38	155	0.16%	49.7%	WSSLACNIALDAVK	99.7%	94.7	25	83.7	6	0	0	1547.79	168	181
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	10	10	17	0.02%	20.6%	AIADTGANVVVTGGK	99.7%	79.1	25	72.3	2	0	0	1372.74	282	296
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	10	10	17	0.02%	20.6%	APGFAQMLK	98.0%	31.7	25	19.5	1	0	0	962.51	8	16
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	10	10	17	0.02%	20.6%	AVDDGVNTFK	99.7%	66.7	25	57.4	2	0	0	1065.52	391	400
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	10	10	17	0.02%	20.6%	DIDEVSSLLR	99.7%	57.5	25	33.1	2	0	0	1146.60	156	165
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	10	10	17	0.02%	20.6%	ETEGDVTSVK	99.6%	39.4	25	36	1	0	0	1064.51	226	235

T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	10	10	17	0.02%	20.6%	FAEAFEAIPR	99.7%	81.6	25	71.4	2	0	0	1150.59	441	450
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	10	10	17	0.02%	20.6%	IAVYSCPFDGMITETK	99.7%	54.4	25	54.4	2	0	0	1831.86	239	254
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	10	10	17	0.02%	20.6%	LFVTNDAATILR	99.7%	100	25	88.2	2	0	0	1333.75	63	74
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	10	10	17	0.02%	20.6%	LVPGGGATEIELAK	99.6%	38.8	25	27.3	2	0	0	1354.76	408	421
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	10	10	17	0.02%	20.6%	YNIMLVR	99.7%	41.7	25	35	1	0	0	908.50	308	314
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	28	108	0.11%	47.1%	ALQFLEEVK	99.7%	55.7	25	49.8	2	0	0	1076.60	130	138
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	28	108	0.11%	47.1%	AQAALAVNISAAR	99.7%	98.5	25	93.4	8	0	0	1255.71	16	28
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	28	108	0.11%	47.1%	AQLGVQAFADALLIIPK	99.7%	85.1	25	84.4	7	0	0	1768.04	433	449
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	28	108	0.11%	47.1%	DGNVLLHEMQIQHPTASLIAK	99.7%	38.3	25	38.3	0	2	0	2331.21	59	79
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	28	108	0.11%	47.1%	EGIVALRR	97.5%	30.8	25	12.6	2	0	0	913.56	308	315
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	28	108	0.11%	47.1%	EMDRETLIDVAR	99.7%	51.7	25	40.1	2	4	0	1447.72	142	153
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	28	108	0.11%	47.1%	ETLIDVAR	99.7%	56	25	50	2	0	0	916.51	146	153
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	28	108	0.11%	47.1%	GFVVINQK	99.7%	42.2	25	27.5	2	0	0	904.53	288	295
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	28	108	0.11%	47.1%	GIDPFSLDALSK	99.7%	90.5	25	34.7	10	0	0	1262.66	296	307
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	28	108	0.11%	47.1%	GLQDVLR	99.7%	40.7	25	15.2	2	0	0	800.46	29	35
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	28	108	0.11%	47.1%	GLVLDHGAR	99.7%	55.7	25	44.4	12	0	0	937.52	209	217
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	28	108	0.11%	47.1%	HKSETDTSLIR	96.4%	23	25	15.8	0	2	0	1286.67	198	208
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	28	108	0.11%	47.1%	HTLTQIK	95.3%	28.1	25	13.5	2	0	0	840.49	382	388
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	28	108	0.11%	47.1%	IITEGFEAAK	99.7%	65.1	25	37.9	6	0	0	1078.58	118	127
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	28	108	0.11%	47.1%	MLVSGAGDIK	99.7%	64.8	25	39.6	7	0	0	990.53	46	55
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	28	108	0.11%	47.1%	NAIDDGCVVPGAGAVEVAMAEALIK	99.7%	40.4	25	35.5	0	1	0	2470.23	400	424
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	28	108	0.11%	47.1%	QADLYISEGLHPR	99.7%	66.1	25	61.3	6	3	0	1498.77	105	117
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	28	108	0.11%	47.1%	SETDTSLIR	99.7%	62.6	25	48.9	5	0	0	1021.52	200	208
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	28	108	0.11%	47.1%	TEVNSGFFYK	99.7%	58.8	25	54.8	2	0	0	1191.57	242	251
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	28	108	0.11%	47.1%	VATAQDDITGDGTTSNVLIIGELLK	99.7%	83.5	25	83.5	3	3	0	2544.34	80	104
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	28	108	0.11%	47.1%	VCGDSDKGFVVINQK	99.7%	71.2	25	71.2	2	2	0	1665.83	281	295
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	28	108	0.11%	47.1%	VLAQNSGFDLQETLVK	99.7%	104	25	104	9	0	0	1761.94	450	465
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	11	11	24	0.02%	6.7%	GATALEMGMPLLLQK	99.7%	44.2	25	32.2	1	0	0	1604.84	203	217
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	11	11	24	0.02%	6.7%	IGISDISSLSEK	99.7%	65.4	25	59.4	2	0	0	1248.67	1700	1711
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	11	11	24	0.02%	6.7%	ITSELSEANALELLSK	99.7%	70.7	25	70.7	4	0	0	1717.92	88	103
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	11	11	24	0.02%	6.7%	LIAEQTLQENLIEK	99.7%	114	25	109	2	0	0	1641.91	1468	1481
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	11	11	24	0.02%	6.7%	LIEQAPIQMGEEAVR	98.2%	32.2	25	32.2	1	0	0	1683.87	169	183
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	11	11	24	0.02%	6.7%	LVIPLVVHSAQK	99.0%	35	25	35	2	0	0	1303.81	187	198
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	11	11	24	0.02%	6.7%	LVSDIIDPVALEIPLSK	99.7%	73.2	25	73.2	3	0	0	1822.06	2399	2415
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	11	11	24	0.02%	6.7%	SLIDNFALNPDILCSAK	99.7%	60.5	25	60.3	4	0	0	1890.96	299	315
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	11	11	24	0.02%	6.7%	TIGDLSTLTASEIK	99.7%	89.2	25	88	1	0	0	1448.78	2329	2342
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	11	11	24	0.02%	6.7%	TLGETSANAETEQNKK	99.7%	59.8	25	59.8	2	0	0	1720.83	1489	1504
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	11	11	24	0.02%	6.7%	YAEYSFTSLPVPESNLR	99.7%	46.7	25	46.7	2	0	0	1972.97	1659	1675
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	6	6	9	0.01%	8.1%	LAAVQLLQFLAPK	99.7%	72.1	25	61.2	2	0	0	1411.87	116	128
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	6	6	9	0.01%	8.1%	LLLQHAPLR	99.7%	49.5	25	38.9	2	0	0	1060.66	866	874
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	6	6	9	0.01%	8.1%	LQNATPTNFK	99.7%	44.6	25	37.6	1	0	0	1133.60	25	34
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	6	6	9	0.01%	8.1%	SQNFDILQSAISK	99.7%	101	25	95.9	2	0	0	1450.75	747	759
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	6	6	9	0.01%	8.1%	VGPEELPVVGQLLR	98.7%	33.6	25	30.1	1	0	0	1505.87	852	865
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	6	6	9	0.01%	8.1%	VLDILLEQYPALITGR	99.7%	77	25	77	1	0	0	1814.04	163	178
Tetratricopeptide repeat protein 19, mitochondrial	TTC19	TTC19_HUMAN	42.5	99.8%	2	2	3	0.00%	5.5%	GQLENAEQLFK	99.7%	40.6	25	21.4	1	0	0	1276.65	150	160
Tetratricopeptide repeat protein 19, mitochondrial	TTC19	TTC19_HUMAN	42.5	99.8%	2	2	3	0.00%	5.5%	LASIYAAQNR	99.7%	78.2	25	61.5	2	0	0	1106.60	185	194
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	8	8	13	0.01%	6.9%	AALVDYLDGK	98.5%	32.9	25	32.9	1	0	0	1064.56	682	691
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	8	8	13	0.01%	6.9%	AILLLQTAEDQDTYNVAIR	99.7%	49.9	25	49.1	1	0	0	2147.13	1006	1024
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	8	8	13	0.01%	6.9%	ASELNPESIYSVFK	99.7%	49.5	25	49.5	2	0	0	1583.80	624	637
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	8	8	13	0.01%	6.9%	DDYELIDVLVNNAK	96.6%	29.5	25	24.2	1	0	0	1620.81	1534	1547
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	8	8	13	0.01%	6.9%	LSDYDSSEEAIR	99.7%	63.7	25	59.9	2	0	0	1384.62	363	374

Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	8	8	13	0.01%	6.9%	SNPDQPAVILLLR	99.7%	51.5	25	51.5	2	0	0	1435.83	1355	1367
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	8	8	13	0.01%	6.9%	TLDQISDADNIPGLLVLK	99.7%	71.1	25	68.3	2	0	0	1925.06	375	392
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	8	8	13	0.01%	6.9%	VVAQYAQR	99.4%	37.5	25	29.1	2	0	0	934.51	1202	1209
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	30	0.03%	28.0%	HEDMTLLVR	98.9%	34.5	25	29.4	3	0	0	1129.57	355	363
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	30	0.03%	28.0%	IHSDTFASGGER	99.7%	74.5	25	62.9	3	0	0	1276.59	337	348
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	30	0.03%	28.0%	LSQLGLDAGK	99.7%	60.1	25	43.4	2	0	0	1001.56	218	227
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	30	0.03%	28.0%	NFGYPLGEMSQPTPSPAPAAGGR	99.7%	59.2	25	59.2	1	0	0	2318.09	364	386
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	30	0.03%	28.0%	QTSLDAVAQAVVDR	99.7%	102	25	93.5	4	0	0	1472.77	320	333
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	30	0.03%	28.0%	QVGIICGQESTR	99.7%	41.9	25	39	2	0	0	1347.67	230	241
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	30	0.03%	28.0%	SFLESIDDALAEK	99.7%	82	25	73.8	4	0	0	1437.71	116	128
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	30	0.03%	28.0%	VLLQAFDVVER	99.7%	82.1	25	72.2	4	0	0	1288.73	105	115
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	30	0.03%	28.0%	VTNFVAQR	99.7%	64.7	25	46.3	3	0	0	934.51	76	83
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	30	0.03%	28.0%	VYPVSVPYSSAQSTSK	99.7%	70.7	25	68.4	2	0	0	1699.85	387	402
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	30	0.03%	28.0%	YGYTDIDLLSAAK	99.7%	99	25	98.6	2	0	0	1429.72	250	262
TGF-beta-activated kinase 1 and MAP3K7-binding protein 2	TAB2	TAB2_HUMAN	76.5	99.8%	2	2	2	0.00%	3.2%	AIGNNSATSPR	98.1%	32	25	23.6	1	0	0	1087.55	442	452
TGF-beta-activated kinase 1 and MAP3K7-binding protein 2	TAB2	TAB2_HUMAN	76.5	99.8%	2	2	2	0.00%	3.2%	GTSSLSQQTPR	96.0%	28.8	25	21.2	1	0	0	1161.59	163	173
Thioredoxin	TXN	THIO_HUMAN	11.7	100.0%	4	4	6	0.01%	31.4%	EKLEATINELV	99.7%	50.3	25	50.3	2	0	0	1258.69	95	105
Thioredoxin	TXN	THIO_HUMAN	11.7	100.0%	4	4	6	0.01%	31.4%	TAFQEALDAAGDK	99.7%	76.2	25	73.2	1	0	0	1336.64	9	21
Thioredoxin	TXN	THIO_HUMAN	11.7	100.0%	4	4	6	0.01%	31.4%	VGEFSGANK	99.7%	59.2	25	50.2	2	0	0	908.45	86	94
Thioredoxin	TXN	THIO_HUMAN	11.7	100.0%	4	4	6	0.01%	31.4%	VGEFSGANKEK	99.7%	51	25	41.2	1	0	0	1165.58	86	96
Thioredoxin domain-containing protein 5	TXNDC5	TXND5_HUMAN	47.6	99.8%	2	2	3	0.00%	4.4%	GYPTLLWFR	98.7%	33.6	25	29	2	0	0	1152.62	261	269
Thioredoxin domain-containing protein 5	TXNDC5	TXND5_HUMAN	47.6	99.8%	2	2	3	0.00%	4.4%	IAEVDCTAER	99.7%	46	25	41.4	1	0	0	1163.54	376	385
Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3	PRDX3_HUMAN	27.7	99.8%	2	2	6	0.01%	10.2%	DYGVLLEGSGLALR	99.7%	50.4	25	42.8	2	0	0	1462.79	171	184
Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3	PRDX3_HUMAN	27.7	99.8%	2	2	6	0.01%	10.2%	GLFIIDPNGVIK	99.7%	58	25	46.8	4	0	0	1285.75	185	196
THO complex subunit 1	THOC1	THOC1_HUMAN	75.7	99.8%	2	2	2	0.00%	3.4%	ILMGNEELTR	99.7%	52.2	25	36.5	1	0	0	1175.61	431	440
THO complex subunit 1	THOC1	THOC1_HUMAN	75.7	99.8%	2	2	2	0.00%	3.4%	SLPEYLENMVIK	98.0%	31.7	25	26.3	1	0	0	1435.75	517	528
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	10	10	22	0.02%	6.8%	AEGGYFGQIR	99.7%	49.8	25	41.2	2	0	0	1097.54	711	720
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	10	10	22	0.02%	6.8%	FLCCMLETVTR	99.7%	58.6	25	52.6	2	0	0	1429.66	1042	1052
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	10	10	22	0.02%	6.8%	FVELVHQQK	99.7%	41.1	25	41.1	2	0	0	1127.62	999	1007
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	10	10	22	0.02%	6.8%	GEFLHLCR	99.6%	39.4	25	31.1	2	0	0	1031.51	22	29
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	10	10	22	0.02%	6.8%	LDPETLESLGLIK	99.7%	54.4	25	42.5	2	0	0	1427.80	127	139
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	10	10	22	0.02%	6.8%	LGLLEALLK	99.7%	55.7	25	48.2	4	0	0	969.63	346	354
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	10	10	22	0.02%	6.8%	LIALAICK	97.0%	30	25	20.9	1	0	0	901.55	378	385
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	10	10	22	0.02%	6.8%	TPNFSTLLCYDR	99.7%	49.6	25	49.6	2	0	0	1486.70	1008	1019
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	10	10	22	0.02%	6.8%	VFSDIIYTVASCTENEASR	99.7%	75.8	25	75.8	2	0	0	2162.01	1020	1038
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	10	10	22	0.02%	6.8%	VLNLGQALER	99.7%	55.8	25	44.8	3	0	0	1112.64	1137	1146
THO complex subunit 3	THOC3	THOC3_HUMAN	38.8	100.0%	3	5	9	0.01%	8.6%	TASVFLLEKDR	99.7%	53.2	25	50.1	2	1	0	1278.71	78	88
THO complex subunit 3	THOC3	THOC3_HUMAN	38.8	100.0%	3	5	9	0.01%	8.6%	TLSFSHDGK	99.5%	37.9	25	29.1	2	0	0	991.48	271	279
THO complex subunit 3	THOC3	THOC3_HUMAN	38.8	100.0%	3	5	9	0.01%	8.6%	YVLGMQELFR	99.7%	63.3	25	61	4	0	0	1255.65	34	43
THO complex subunit 4	ALYREF	THOC4_HUMAN	26.9	100.0%	3	5	11	0.01%	15.2%	MDMSLDDIIK	99.7%	48.7	25	43	1	0	0	1180.56	5	14
THO complex subunit 4	ALYREF	THOC4_HUMAN	26.9	100.0%	3	5	11	0.01%	15.2%	QQLSAEELDAQLDAYNAR	99.7%	111	25	110	3	2	0	2034.97	236	253
THO complex subunit 4	ALYREF	THOC4_HUMAN	26.9	100.0%	3	5	11	0.01%	15.2%	SLGTADVHFER	99.7%	65.7	25	55.1	4	1	0	1231.61	145	155
THO complex subunit 6 homolog	THOC6	THOC6_HUMAN	37.5	100.0%	3	3	5	0.01%	11.4%	AVPLAVPLGQTEVFQALQR	99.7%	68	25	68	2	0	0	2037.15	4	22
THO complex subunit 6 homolog	THOC6	THOC6_HUMAN	37.5	100.0%	3	3	5	0.01%	11.4%	VDVFTNLGYR	99.7%	70.1	25	58.6	2	0	0	1183.61	326	335
THO complex subunit 6 homolog	THOC6	THOC6_HUMAN	37.5	100.0%	3	3	5	0.01%	11.4%	VLTAAGNSCR	99.7%	42.3	25	33.9	1	0	0	1048.52	316	325
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	7	7	12	0.01%	11.6%	AELNPWPEYIYTR	99.7%	47.8	25	44.2	1	0	0	1651.81	45	57
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	7	7	12	0.01%	11.6%	FLGDIEVWDQAEK	99.7%	40.3	25	31.9	1	0	0	1549.75	505	517
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	7	7	12	0.01%	11.6%	GAYIYNALIEFIR	99.7%	62.8	25	60.6	2	0	0	1542.83	349	361
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	7	7	12	0.01%	11.6%	GFQEVVTPNIFNSR	99.7%	67.8	25	63.1	2	0	0	1607.82	368	381
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	7	7	12	0.01%	11.6%	NELSGALTGLTR	99.7%	79.2	25	60.2	2	0	0	1231.66	443	454
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	7	7	12	0.01%	11.6%	TVYSVFGFSFK	99.6%	38.9	25	38.9	2	0	0	1281.65	485	495

Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	7	7	12	0.01%	11.6%	WPFWLSPR	98.8%	34.2	25	23.6	2	0	0	1088.57	612	619
Threonine--tRNA ligase, mitochondrial	TARS2	SYTM_HUMAN	81.0	100.0%	4	4	8	0.01%	5.6%	LADFGALHR	99.7%	67	25	53.3	2	0	0	999.54	430	438
Threonine--tRNA ligase, mitochondrial	TARS2	SYTM_HUMAN	81.0	100.0%	4	4	8	0.01%	5.6%	LVELQNTR	99.6%	39	25	30.2	2	0	0	972.55	703	710
Threonine--tRNA ligase, mitochondrial	TARS2	SYTM_HUMAN	81.0	100.0%	4	4	8	0.01%	5.6%	VSGISFPTTELLR	99.6%	39.9	25	35.8	2	0	0	1419.78	276	288
Threonine--tRNA ligase, mitochondrial	TARS2	SYTM_HUMAN	81.0	100.0%	4	4	8	0.01%	5.6%	VYNALVAFIR	99.7%	68.8	25	60.8	2	0	0	1165.67	331	340
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	5	6	10	0.01%	11.4%	AANNIASLLTK	99.7%	61.3	25	52.4	2	0	0	1115.64	359	369
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	5	6	10	0.01%	11.4%	AAVYVLIR	99.1%	35.2	25	23	2	0	0	904.56	477	484
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	5	6	10	0.01%	11.4%	AVLLTQDTK	94.8%	27.7	25	17.9	1	0	0	988.57	441	449
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	5	6	10	0.01%	11.4%	TGSVDIIVTDLPFGK	99.7%	53	25	53	2	0	0	1561.85	397	411
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	5	6	10	0.01%	11.4%	TPQAFVHPSEQDGER	99.7%	42.1	25	42.1	1	2	0	1697.79	485	499
Thymidine kinase, cytosolic	TK1	KITH_HUMAN	25.5	100.0%	3	4	5	0.01%	15.8%	GQIQVILGPMFSGK	99.5%	38.5	25	38.5	2	0	0	1474.81	19	32
Thymidine kinase, cytosolic	TK1	KITH_HUMAN	25.5	100.0%	3	4	5	0.01%	15.8%	TVIVAALDGTFQR	99.7%	86.6	25	80.4	2	0	0	1390.77	118	130
Thymidine kinase, cytosolic	TK1	KITH_HUMAN	25.5	100.0%	3	4	5	0.01%	15.8%	YSSSFCTHDR	99.3%	36.4	25	36.4	1	0	0	1259.51	61	70
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	7	8	20	0.02%	8.3%	ASAVSELSPR	99.7%	64.2	25	58.6	4	0	0	1016.54	236	245
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	7	8	20	0.02%	8.3%	EESAASGGAAYTK	99.7%	56.4	25	56.4	3	0	0	1241.56	334	346
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	7	8	20	0.02%	8.3%	EQTFSGGTSQDTK	99.7%	49.3	25	48.1	2	0	0	1385.62	203	215
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	7	8	20	0.02%	8.3%	GSFSDTGLGDGK	99.7%	60.9	25	59.2	4	0	0	1140.52	376	387
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	7	8	20	0.02%	8.3%	SIFQHIQSAQSQR	99.7%	73.4	25	62.4	3	1	0	1529.78	609	621
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	7	8	20	0.02%	8.3%	SPLQSVVVR	99.7%	46.5	25	35.1	2	0	0	984.58	253	261
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	7	8	20	0.02%	8.3%	YKDDPVDLR	96.2%	29	25	14.8	1	0	0	1120.56	710	718
Thyroid transcription factor 1-associated protein 26	CCDC59	TAP26_HUMAN	28.7	99.8%	2	2	3	0.00%	7.9%	GEGVSTVGYR	99.7%	47.1	25	25.8	2	0	0	1024.51	19	28
Thyroid transcription factor 1-associated protein 26	CCDC59	TAP26_HUMAN	28.7	99.8%	2	2	3	0.00%	7.9%	HLYLAEEER	99.6%	39	25	24.7	1	0	0	1159.57	95	103
Torsin-1A-interacting protein 1	TOR1AIP1	TOIP1_HUMAN	66.2	99.9%	2	2	4	0.00%	4.3%	SELGNQSPSTSSR	98.9%	34.3	25	34.3	1	0	0	1349.63	309	321
Torsin-1A-interacting protein 1	TOR1AIP1	TOIP1_HUMAN	66.2	99.9%	2	2	4	0.00%	4.3%	SQPAILLLTAAR	99.7%	78.9	25	78.9	3	0	0	1253.76	405	416
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	5	6	9	0.01%	22.5%	ATTPADGEEPAPEAEALAAAR	99.7%	101	25	101	2	1	0	2037.97	6	26
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	5	6	9	0.01%	22.5%	FLSGLELVK	99.7%	51	25	38.2	2	0	0	1005.60	32	40
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	5	6	9	0.01%	22.5%	GVDLYVLEK	99.7%	53.9	25	33.7	1	0	0	1035.57	197	205
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	5	6	9	0.01%	22.5%	TIGQVLAR	99.7%	46.1	25	12.4	1	0	0	857.52	145	152
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	5	6	9	0.01%	22.5%	TPQGLSNLAK	99.7%	45.3	25	37.4	2	0	0	1028.57	135	144
TraB domain-containing protein	TRABD	TRABD_HUMAN	42.3	99.8%	2	2	4	0.00%	5.9%	AIAALSFWQK	99.7%	56.8	25	44.4	2	0	0	1134.63	200	209
TraB domain-containing protein	TRABD	TRABD_HUMAN	42.3	99.8%	2	2	4	0.00%	5.9%	TVTQLVAEDGSR	99.7%	71.1	25	58	2	0	0	1275.65	63	74
Trafficking protein particle complex subunit 1	TRAPPC1	TPPC1_HUMAN	16.8	100.0%	3	3	5	0.01%	19.3%	DGFLAFQTSR	99.7%	49.8	25	43.8	2	0	0	1141.56	59	68
Trafficking protein particle complex subunit 1	TRAPPC1	TPPC1_HUMAN	16.8	100.0%	3	3	5	0.01%	19.3%	SRLDSYVR	98.1%	31.9	25	23.3	2	0	0	995.53	128	135
Trafficking protein particle complex subunit 1	TRAPPC1	TPPC1_HUMAN	16.8	100.0%	3	3	5	0.01%	19.3%	TVHNLYLFDR	99.6%	38.8	25	25.6	1	0	0	1277.66	2	11
Trafficking protein particle complex subunit 5	TRAPPC5	TPPC5_HUMAN	20.8	99.8%	2	2	4	0.00%	11.7%	EADKLEQANDDAR	99.5%	38.3	25	37.1	2	0	0	1474.68	101	113
Trafficking protein particle complex subunit 5	TRAPPC5	TPPC5_HUMAN	20.8	99.8%	2	2	4	0.00%	11.7%	VLGALLFVK	98.3%	32.5	25	30.9	2	0	0	959.63	82	90
Transaldolase	TALDO1	TALDO_HUMAN	37.5	99.9%	2	2	3	0.00%	7.1%	ALAGCDFLTISPK	99.7%	65.1	25	65.1	1	0	0	1392.72	246	258
Transaldolase	TALDO1	TALDO_HUMAN	37.5	99.9%	2	2	3	0.00%	7.1%	LLGELLQDNAK	99.7%	69.9	25	69.9	2	0	0	1213.68	259	269
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	8	8	14	0.01%	5.5%	AVATYHANTER	99.7%	46	25	38.2	2	0	0	1232.60	503	513
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	8	8	14	0.01%	5.5%	DTALETALNAK	99.7%	68.9	25	54	2	0	0	1146.60	427	437
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	8	8	14	0.01%	5.5%	ELPEYYELIR	99.7%	54.3	25	51.7	2	0	0	1324.68	1493	1502
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	8	8	14	0.01%	5.5%	GLDPVEILQER	99.7%	60.9	25	54.6	2	0	0	1268.68	360	370
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	8	8	14	0.01%	5.5%	IQELENLPGSLAGDLR	99.7%	51.7	25	47.3	2	0	0	1724.92	382	397
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	8	8	14	0.01%	5.5%	LCTVNSVEEK	99.3%	36.3	25	24	1	0	0	1178.57	1204	1213
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	8	8	14	0.01%	5.5%	LLLTGTPLQNK	99.4%	37	25	0	2	0	0	1197.72	907	917
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	8	8	14	0.01%	5.5%	VIQAGMFDQK	99.7%	50.1	25	40.2	1	0	0	1136.58	1228	1237
Transcription elongation factor B polypeptide 1	TCEB1	ELOC_HUMAN	12.5	99.9%	2	2	2	0.00%	23.2%	LISSDGHEFIVK	98.1%	31.9	25	21.6	1	0	0	1344.72	21	32
Transcription elongation factor B polypeptide 1	TCEB1	ELOC_HUMAN	12.5	99.9%	2	2	2	0.00%	23.2%	TYGGCEGPDAMYVK	96.7%	29.6	25	29.6	1	0	0	1563.65	7	20
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	4	5	8	0.01%	15.4%	AEWQVYKEEISR	99.7%	52.2	25	50.8	2	2	0	1537.76	105	116
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	4	5	8	0.01%	15.4%	ELTLLGKPK	94.6%	27.6	25	27.6	1	0	0	998.62	148	156
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	4	5	8	0.01%	15.4%	EQLPIFK	98.5%	33	25	11.4	1	0	0	874.50	63	69

Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	4	5	8	0.01%	15.4%	SAYNVYVAER	99.7%	67.3	25	60.8	2	0	0	1171.57	160	169
Transcription initiation factor TFIID subunit 4	TAF4	TAF4_HUMAN	110.1	100.0%	3	3	8	0.01%	4.0%	ALSAVSAQAAAAQK	99.7%	92.2	25	74.6	3	0	0	1286.71	804	817
Transcription initiation factor TFIID subunit 4	TAF4	TAF4_HUMAN	110.1	100.0%	3	3	8	0.01%	4.0%	ELNSSPQPYLVPFLK	95.1%	28	25	27.8	1	0	0	1731.93	644	658
Transcription initiation factor TFIID subunit 4	TAF4	TAF4_HUMAN	110.1	100.0%	3	3	8	0.01%	4.0%	ILATNSELVGTLTR	99.7%	101	25	101	4	0	0	1487.84	852	865
Transcriptional activator protein Pur-alpha	PURA	PURA_HUMAN	34.9	100.0%	3	3	4	0.00%	8.7%	FFFDVGSNK	99.7%	68.4	25	67.6	2	0	0	1060.51	231	239
Transcriptional activator protein Pur-alpha	PURA	PURA_HUMAN	34.9	100.0%	3	3	4	0.00%	8.7%	IAEVGAGGNK	98.6%	33.5	25	16.6	1	0	0	915.49	88	97
Transcriptional activator protein Pur-alpha	PURA	PURA_HUMAN	34.9	100.0%	3	3	4	0.00%	8.7%	VSEVKPTYR	95.4%	28.2	25	21.9	1	0	0	1078.59	246	254
Transcriptional activator protein Pur-beta	PURB	PURB_HUMAN	33.2	100.0%	4	4	5	0.01%	14.4%	FFFDVGCNK	98.1%	31.9	25	31.9	1	0	0	1133.51	232	240
Transcriptional activator protein Pur-beta	PURB	PURB_HUMAN	33.2	100.0%	4	4	5	0.01%	14.4%	GGGEQETQELASK	99.7%	81.1	25	71.1	1	0	0	1333.62	25	37
Transcriptional activator protein Pur-beta	PURB	PURB_HUMAN	33.2	100.0%	4	4	5	0.01%	14.4%	GGGGGPCGFQPASR	99.1%	35.2	25	29	1	0	0	1304.58	11	24
Transcriptional activator protein Pur-beta	PURB	PURB_HUMAN	33.2	100.0%	4	4	5	0.01%	14.4%	VSEVKPSYR	99.7%	45.8	25	40.3	2	0	0	1064.57	247	255
Transducin beta-like protein 3	TBL3	TBL3_HUMAN	89.0	99.9%	2	2	3	0.00%	3.0%	LWALQDFSCLK	99.3%	36.9	25	35.7	1	0	0	1380.70	547	557
Transducin beta-like protein 3	TBL3	TBL3_HUMAN	89.0	99.9%	2	2	3	0.00%	3.0%	VNILEVASGAVLR	99.7%	86.2	25	86.2	2	0	0	1340.79	47	59
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	15	28	0.03%	22.9%	AFTYINLDK	99.7%	52.4	25	44.5	1	0	0	1084.57	478	486
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	15	28	0.03%	22.9%	AVLGTSNFK	98.8%	34	25	25.4	1	0	0	936.51	487	495
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	15	28	0.03%	22.9%	DSAQNSVIIVDK	99.7%	79.2	25	68.9	2	0	0	1288.67	194	205
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	15	28	0.03%	22.9%	ILNIFGVIK	99.7%	53.2	25	39	2	0	0	1016.65	386	394
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	15	28	0.03%	22.9%	LAQMFSDMVLK	96.7%	29.6	25	23.9	1	0	0	1282.65	429	439
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	15	28	0.03%	22.9%	LAVDEEENADNNTK	99.7%	95.6	25	70.3	2	0	0	1561.70	40	53
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	15	28	0.03%	22.9%	LLNENSYVPR	99.7%	70.8	25	57.7	2	0	0	1204.63	146	155
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	15	28	0.03%	22.9%	LTVSNVLK	97.4%	30.7	25	18.5	1	0	0	873.54	375	382
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	15	28	0.03%	22.9%	LVYLVENPGGYVAYSK	99.7%	75.5	25	75.5	2	0	0	1771.93	209	224
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	15	28	0.03%	22.9%	SAFSNLFGGEPLSYTR	99.7%	92.4	25	89.5	2	0	0	1745.85	7	22
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	15	28	0.03%	22.9%	SGVGTALLLK	99.7%	63.4	25	39.5	2	0	0	958.59	419	428
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	15	28	0.03%	22.9%	SSGLPNIPVQTISR	99.7%	65.7	25	59.1	2	0	0	1468.81	326	339
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	15	28	0.03%	22.9%	VEYHFLSPYVSPK	99.7%	33.7	25	33.1	0	2	0	1565.80	681	693
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	15	28	0.03%	22.9%	VSASPLLYTLIEK	99.7%	112	25	107	4	0	0	1433.83	496	508
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	15	28	0.03%	22.9%	YNSQLLSFVR	99.7%	74	25	74	2	0	0	1226.65	614	623
Transformer-2 protein homolog alpha	TRA2A	TRA2A_HUMAN	32.7	99.8%	2	2	5	0.01%	11.3%	GFAFVYFER	99.7%	67.4	25	48.1	3	0	0	1135.56	161	169
Transformer-2 protein homolog alpha	TRA2A	TRA2A_HUMAN	32.7	99.8%	2	2	5	0.01%	11.3%	RSPSPYYSR	94.7%	27.7	25	21.1	1	0	0	1112.55	259	267
Transformer-2 protein homolog alpha	TRA2A	TRA2A_HUMAN	32.7	99.8%	2	2	5	0.01%	11.3%	YGPLSGVNVVYDQR	99.7%	58.3	25	50.7	2	0	0	1566.79	142	155
Transformer-2 protein homolog beta	TRA2B	TRA2B_HUMAN	33.7	100.0%	3	3	3	0.00%	11.5%	GFAFVYFENVDDAK	99.7%	44	25	37	1	0	0	1621.75	160	173
Transformer-2 protein homolog beta	TRA2B	TRA2B_HUMAN	33.7	100.0%	3	3	3	0.00%	11.5%	GYDDRDYYSR	95.5%	28.3	25	28.3	1	0	0	1309.54	229	238
Transformer-2 protein homolog beta	TRA2B	TRA2B_HUMAN	33.7	100.0%	3	3	3	0.00%	11.5%	RSPSPYYSR	94.7%	27.7	25	21.1	1	0	0	1112.55	263	271
Transgelin-2	TAGLN2	TAGL2_HUMAN	22.4	100.0%	2	2	4	0.00%	12.6%	GASQAGMTGYGMPR	99.7%	50	25	50	2	0	0	1415.60	183	196
Transgelin-2	TAGLN2	TAGL2_HUMAN	22.4	100.0%	2	2	4	0.00%	12.6%	NFSDNQLQEGK	99.7%	61.6	25	52.5	2	0	0	1279.59	161	171
Transitional endoplasmic reticulum ATPase	VCP	TERA_HUMAN	89.3	100.0%	5	5	5	0.01%	7.9%	ESIESEIRR	96.0%	28.8	25	10.6	1	0	0	1118.58	701	709
Transitional endoplasmic reticulum ATPase	VCP	TERA_HUMAN	89.3	100.0%	5	5	5	0.01%	7.9%	GILLYGPPGTGK	99.7%	56.3	25	0	1	0	0	1172.67	240	251
Transitional endoplasmic reticulum ATPase	VCP	TERA_HUMAN	89.3	100.0%	5	5	5	0.01%	7.9%	IVSQLLTLMDGLK	98.8%	33.9	25	33.9	1	0	0	1430.83	324	336
Transitional endoplasmic reticulum ATPase	VCP	TERA_HUMAN	89.3	100.0%	5	5	5	0.01%	7.9%	LDQLIYIPLPDEK	99.3%	36.7	25	36.7	1	0	0	1556.86	639	651
Transitional endoplasmic reticulum ATPase	VCP	TERA_HUMAN	89.3	100.0%	5	5	5	0.01%	7.9%	NAPAIIFIDELDAIAPK	99.7%	42.5	25	39.2	1	0	0	1811.00	296	312
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	5	5	10	0.01%	18.4%	DGATILTHAYSR	99.7%	62.2	25	54	2	0	0	1304.66	121	132
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	5	5	10	0.01%	18.4%	DKGETIQGLR	99.7%	41.4	25	29.2	2	0	0	1116.60	37	46
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	5	5	10	0.01%	18.4%	FISLASLEYSDYSK	99.7%	102	25	93.6	2	0	0	1622.79	75	88
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	5	5	10	0.01%	18.4%	IGTNQMAVCAK	99.7%	42.8	25	34.2	2	0	0	1208.58	210	220
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	5	5	10	0.01%	18.4%	VLEAAVAAK	99.7%	52.4	25	33.1	2	0	0	871.52	137	145
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	6	6	10	0.01%	23.9%	AVTGTHTLALAAK	99.7%	74.2	25	70.4	2	0	0	1253.72	247	259
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	6	6	10	0.01%	23.9%	FVAPEEVLPFTEGDILEK	99.7%	56.9	25	55.2	2	0	0	2033.05	288	305
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	6	6	10	0.01%	23.9%	LMSELYHPDDHVL	99.7%	41.6	25	41.6	1	0	0	1568.74	339	351
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	6	6	10	0.01%	23.9%	MTAAQPSETTVGNMVR	99.7%	92.7	25	92.7	2	0	0	1724.79	68	83
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	6	6	10	0.01%	23.9%	SDESDQQESLHK	99.7%	59.2	25	54.8	2	0	0	1402.61	100	111

Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	6	6	10	0.01%	23.9%	WSNAGELMELIR	99.7%	53.3	25	48.4	1	0	0	1418.71	51	62
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	6	6	10	0.01%	12.8%	AELPPGPGAVGR	99.7%	41.7	25	32.9	1	0	0	1120.61	18	29
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	6	6	10	0.01%	12.8%	ASPSTAGETPSGVK	99.7%	80.8	25	72.3	2	0	0	1288.64	129	142
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	6	6	10	0.01%	12.8%	ASPSTAGETPSGVKR	99.7%	53.2	25	53.2	2	0	0	1444.74	129	143
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	6	6	10	0.01%	12.8%	LGLQYSQGLVSGSNAR	99.7%	87.7	25	86.3	2	0	0	1649.86	210	225
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	6	6	10	0.01%	12.8%	LPEYPQVDDLLLR	99.7%	41.4	25	41.4	1	0	0	1570.85	144	156
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	6	6	10	0.01%	12.8%	VGTAQLALVAR	99.7%	109	25	89.4	2	0	0	1098.66	418	428
Translation initiation factor eIF-2B subunit epsilon	EIF2B5	EI2BE_HUMAN	80.4	100.0%	4	4	9	0.01%	5.8%	GYNPAEVGAAGK	99.7%	66.9	25	54.1	2	0	0	1133.56	482	493
Translation initiation factor eIF-2B subunit epsilon	EIF2B5	EI2BE_HUMAN	80.4	100.0%	4	4	9	0.01%	5.8%	IITSELYR	99.7%	45.5	25	17.1	2	0	0	994.56	122	129
Translation initiation factor eIF-2B subunit epsilon	EIF2B5	EI2BE_HUMAN	80.4	100.0%	4	4	9	0.01%	5.8%	VFQNEVLGTLQR	99.7%	78.7	25	68.9	1	0	0	1403.76	552	563
Translation initiation factor eIF-2B subunit epsilon	EIF2B5	EI2BE_HUMAN	80.4	100.0%	4	4	9	0.01%	5.8%	YCALLLPLLK	99.7%	40.1	25	40.1	4	0	0	1203.72	617	626
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	5	5	7	0.01%	14.6%	DFIGVDSTGKR	99.7%	46.1	25	38.9	1	0	0	1194.61	156	166
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	5	5	7	0.01%	14.6%	KGQDSIEPVPGQK	99.7%	80.1	25	78.9	2	0	0	1382.73	134	146
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	5	5	7	0.01%	14.6%	LLSALCPEEPPVHSSAQIVSK	96.9%	23.4	25	23.4	0	1	0	2262.18	329	349
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	5	5	7	0.01%	14.6%	SELIPYLVR	99.4%	37.5	25	31.7	2	0	0	1089.63	226	234
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	5	5	7	0.01%	14.6%	VGFEEVIVVTTR	99.7%	64.1	25	64.1	1	0	0	1348.75	46	57
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	AALLETLSLLLAK	99.7%	77.7	25	77.7	3	0	0	1355.85	2324	2336
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	ADYTSHLR	99.7%	40.3	25	33.6	2	0	0	962.47	2184	2191
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	AGSVELLGAMAYCAPK	99.7%	78.8	25	74.7	2	0	0	1637.80	1515	1530
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	AIITALGVER	99.7%	63.7	25	48.4	1	0	0	1042.63	1872	1881
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	ALADENEFVR	99.7%	49	25	38.5	2	0	0	1163.57	1785	1794
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	ALGTLVSHVTLR	99.7%	52.9	25	52.9	2	1	0	1266.75	915	926
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	ALQAAIQQLAEAQPEATAK	99.7%	52.3	25	52.3	1	0	0	1952.04	69	87
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	ALVAVLLSR	99.7%	75.3	25	64.4	4	0	0	941.61	568	576
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	ASLLDPVPEVR	99.4%	37	25	32.4	2	0	0	1195.67	1664	1674
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	AVMSNLSAHGVK	99.7%	53.6	25	50.1	2	0	0	1213.64	1485	1496
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	DLAPYLPSVTPGLK	98.0%	31.8	25	29.3	1	0	0	1470.82	1650	1663
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	EDAGGMIQR	99.6%	39	25	28.2	1	0	0	976.45	1372	1380
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	FTPYVGPIIPCILK	97.2%	30.2	25	30.2	1	0	0	1617.91	1771	1784
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	GAAYGLAGLVK	99.7%	61.5	25	49.4	2	0	0	1019.59	1396	1406
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	GEPGAAPLSAPAFSLVFPFLK	98.4%	32.6	25	32.6	1	0	0	2116.15	966	986
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	GIKEEVQLTSK	99.4%	37.4	25	25.8	1	0	0	1231.69	819	829
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	GVTSILPVLR	99.3%	36.5	25	31.5	2	0	0	1054.66	2260	2269
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	HLDQIIPR	99.7%	43.7	25	36.4	2	0	0	991.57	705	712
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	ILPEIIPILEEGLR	99.7%	40.5	25	40.5	2	0	0	1604.96	1960	1973
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	LFCLTLHR	98.4%	32.6	25	23.5	2	0	0	1059.58	53	60
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	LLTWVIGTGSPR	99.7%	74.8	25	74.8	1	0	0	1299.74	1043	1054
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	LMDEAVLALR	99.7%	63.1	25	52.3	4	0	0	1146.62	314	323
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	LMPEIVATASK	97.2%	30.2	25	19.6	1	0	0	1159.64	1735	1745
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	LSVADSQAEAK	99.7%	62.6	25	50.9	2	0	0	1118.57	499	509
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	LYRPPPVLDALGR	99.7%	47	25	47	0	2	0	1466.85	1209	1221
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	NAPNDASYDAVR	99.7%	59	25	56.8	2	0	0	1292.59	1305	1316
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	NLLHSLQSSGIGSK	99.7%	50.6	25	49.7	2	1	0	1440.78	88	101
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	NPEILAIAPVLLDALTDPSR	99.7%	45.7	25	45.7	1	0	0	2118.18	1571	1590
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	QAAAIILNIYCSR	99.7%	57	25	57	1	0	0	1492.79	2169	2181
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	QAGAEALSQAVAR	99.7%	70.1	25	60.3	2	0	0	1271.67	1177	1189
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	QGEEVFQSLSK	98.3%	32.6	25	31.4	1	0	0	1251.62	2624	2634
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	QLSSCLPNIVPK	99.3%	36.5	25	35.1	2	0	0	1355.74	1531	1542
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	SALLDFYMK	99.7%	42.2	25	34.2	2	0	0	1087.55	221	229
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	SDTQLVVR	99.7%	50.7	25	4.51	2	0	0	917.51	1894	1901
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	SIIQSAQQDSIK	99.7%	48.2	25	37.9	1	0	0	1317.70	777	788

Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	VDENGPELLPR	99.7%	46	25	44.6	2	0	0	1238.64	1027	1037
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	VDIAPHVR	98.8%	34.1	25	30.5	2	0	0	906.52	1746	1753
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	VDPLFTELLNGIR	99.7%	44.2	25	42.8	1	0	0	1486.83	2381	2393
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	VLAFLSSVAGDALTR	99.7%	91.5	25	91.5	4	0	0	1519.85	2093	2107
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	VLAGLYMGR	99.7%	54.9	25	47.2	2	0	0	979.54	1885	1893
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	VLPLEALVTDAGEVTEAGK	99.7%	100	25	100	3	2	0	1912.03	617	635
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	VLQEALCVISGVPGLK	99.5%	37.9	25	35.3	1	0	0	1682.95	642	657
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	43	47	83	0.08%	19.6%	YLLDSCAPLLR	99.7%	60.8	25	59.3	2	0	0	1320.70	241	251
Translin-associated protein X	TSNAX	TSNAX_HUMAN	33.1	100.0%	3	4	6	0.01%	13.8%	DVNSSSPVMLAFK	99.7%	53	25	48.3	1	0	0	1394.70	28	40
Translin-associated protein X	TSNAX	TSNAX_HUMAN	33.1	100.0%	3	4	6	0.01%	13.8%	ITSAPDMEDILTESEIK	99.7%	59.8	25	59.8	1	0	0	1891.92	77	93
Translin-associated protein X	TSNAX	TSNAX_HUMAN	33.1	100.0%	3	4	6	0.01%	13.8%	SLISMDEINK	99.7%	43.9	25	29.3	4	0	0	1149.58	141	150
Translocation protein SEC63 homolog	SEC63	SEC63_HUMAN	88.0	100.0%	3	3	4	0.00%	3.8%	AYAALTDEESR	99.7%	60.9	25	46.2	1	0	0	1225.57	148	158
Translocation protein SEC63 homolog	SEC63	SEC63_HUMAN	88.0	100.0%	3	3	4	0.00%	3.8%	VLLLSHLAR	99.7%	53	25	53	2	0	0	1021.65	303	311
Translocation protein SEC63 homolog	SEC63	SEC63_HUMAN	88.0	100.0%	3	3	4	0.00%	3.8%	YSGDQILIR	99.7%	53.4	25	42.2	1	0	0	1064.57	218	226
Translocator protein	TSPO	TSPOA_HUMAN	18.8	99.8%	2	2	3	0.00%	9.5%	ELGGFTEK	99.7%	64.6	25	27.4	2	0	0	880.44	70	77
Translocator protein	TSPO	TSPOA_HUMAN	18.8	99.8%	2	2	3	0.00%	9.5%	FVHGEGLR	98.9%	34.6	25	27	1	0	0	914.48	25	32
Translocon-associated protein subunit alpha	SSR1	SSRA_HUMAN	32.2	99.8%	2	2	4	0.00%	9.1%	GEDFPANNIVK	99.7%	48.1	25	43.5	2	0	0	1203.60	92	102
Translocon-associated protein subunit alpha	SSR1	SSRA_HUMAN	32.2	99.8%	2	2	4	0.00%	9.1%	GTEDFIVESLDASFR	99.7%	70.5	25	70.5	2	0	0	1685.80	111	125
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	7	9	21	0.02%	38.2%	FFDEESYSLLR	99.7%	75.4	25	75.4	5	0	0	1405.66	106	116
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	7	9	21	0.02%	38.2%	FFDEESYSLLRK	99.7%	61.9	25	55.7	2	0	0	1533.76	106	117
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	7	9	21	0.02%	38.2%	NNEDISIIPPLFTVSVDHR	99.7%	44.2	25	43.6	2	2	0	2166.12	121	139
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	7	9	21	0.02%	38.2%	NRVQNMALYADVGGK	98.6%	26.4	25	23.3	0	1	0	1651.82	59	73
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	7	9	21	0.02%	38.2%	SAHAGTYEVR	99.3%	36.2	25	29.3	3	0	0	1090.53	96	105
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	7	9	21	0.02%	38.2%	VQNMALYADVGGK	99.7%	91.1	25	87.2	4	0	0	1365.68	61	73
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	7	9	21	0.02%	38.2%	YQVSWSLDHK	99.7%	43	25	25.2	2	0	0	1262.62	86	95
Transmembrane 9 superfamily member 3	TM9SF3	TM9S3_HUMAN	67.9	100.0%	3	3	7	0.01%	5.4%	NLSGQPNFPCR	95.5%	28.4	25	28.1	1	0	0	1289.61	419	429
Transmembrane 9 superfamily member 3	TM9SF3	TM9S3_HUMAN	67.9	100.0%	3	3	7	0.01%	5.4%	YFSLPFCVGSK	99.6%	39.7	25	25.6	3	0	0	1304.63	60	70
Transmembrane 9 superfamily member 3	TM9SF3	TM9S3_HUMAN	67.9	100.0%	3	3	7	0.01%	5.4%	YLDPSFFQHR	99.6%	39.5	25	33.1	3	0	0	1309.63	211	220
Transmembrane and coiled-coil domain-containing protein 1	TMCO1	TMCO1_HUMAN	21.2	100.0%	2	2	4	0.00%	11.7%	ILGLAPSR	99.2%	36.2	25	32.9	2	0	0	826.51	161	168
Transmembrane and coiled-coil domain-containing protein 1	TMCO1	TMCO1_HUMAN	21.2	100.0%	2	2	4	0.00%	11.7%	QAGGFLGPPPPSGK	99.7%	68.5	25	66.5	2	0	0	1309.69	173	186
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	7	10	16	0.02%	34.2%	DLLVTGAYEISDQSGGAGGLR	99.7%	83.8	25	83.8	2	0	0	2079.04	51	71
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	7	10	16	0.02%	34.2%	IPDQLVILDMK	99.7%	68.1	25	50.8	4	0	0	1284.72	117	127
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	7	10	16	0.02%	34.2%	ITDSAGHILYSK	99.7%	74.7	25	66.5	2	2	0	1304.68	76	87
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	7	10	16	0.02%	34.2%	ITDSAGHILYSKEDATK	99.7%	81.4	25	81.3	1	2	0	1848.93	76	92
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	7	10	16	0.02%	34.2%	LEDLSESIVNDFAYMK	97.6%	31	25	31	1	0	0	1889.88	154	169
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	7	10	16	0.02%	34.2%	NYEEIAK	94.8%	27.7	25	22.2	1	0	0	866.43	134	140
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	7	10	16	0.02%	34.2%	NYEEIAKVEK	99.4%	37.3	25	24.8	1	0	0	1222.63	134	143
Transmembrane emp24 domain-containing protein 2	TMED2	TMED2_HUMAN	22.8	100.0%	3	5	9	0.01%	16.9%	HEQEYMEVR	98.7%	33.6	25	33.6	1	0	0	1236.53	146	154
Transmembrane emp24 domain-containing protein 2	TMED2	TMED2_HUMAN	22.8	100.0%	3	5	9	0.01%	16.9%	IVMFTIDIGEAPK	99.7%	76	25	76	4	0	0	1433.77	105	117
Transmembrane emp24 domain-containing protein 2	TMED2	TMED2_HUMAN	22.8	100.0%	3	5	9	0.01%	16.9%	YTFAAHMDGTYK	99.7%	53.6	25	53.6	4	0	0	1420.62	80	91
Transmembrane protein 11, mitochondrial	TMEM11	TMM11_HUMAN	21.5	100.0%	4	5	9	0.01%	21.4%	KIYELYAV	97.9%	31.5	25	31.5	1	0	0	998.56	185	192
Transmembrane protein 11, mitochondrial	TMEM11	TMM11_HUMAN	21.5	100.0%	4	5	9	0.01%	21.4%	LPLHTLTSSTPVVLVR	99.7%	69.8	25	69.8	2	2	0	1733.03	146	161
Transmembrane protein 11, mitochondrial	TMEM11	TMM11_HUMAN	21.5	100.0%	4	5	9	0.01%	21.4%	YIVIEPTR	97.8%	31.4	25	22.6	2	0	0	990.56	59	66
Transmembrane protein 11, mitochondrial	TMEM11	TMM11_HUMAN	21.5	100.0%	4	5	9	0.01%	21.4%	YQVEYDAYK	99.7%	42.8	25	32.9	2	0	0	1178.54	134	142
Transmembrane protein 126A	TMEM126A	T126A_HUMAN	21.5	100.0%	5	5	9	0.01%	27.7%	ALQLSEPGKEIH	99.5%	38.6	25	38.6	2	0	0	1321.71	184	195
Transmembrane protein 126A	TMEM126A	T126A_HUMAN	21.5	100.0%	5	5	9	0.01%	27.7%	GNILSYWIR	99.0%	34.8	25	28.2	3	0	0	1121.61	142	150
Transmembrane protein 126A	TMEM126A	T126A_HUMAN	21.5	100.0%	5	5	9	0.01%	27.7%	KINQLPEAER	99.7%	43.6	25	20.1	2	0	0	1197.66	20	29
Transmembrane protein 126A	TMEM126A	T126A_HUMAN	21.5	100.0%	5	5	9	0.01%	27.7%	SNNKENITIVDISR	99.7%	51.1	25	50.3	1	0	0	1602.84	6	19
Transmembrane protein 126A	TMEM126A	T126A_HUMAN	21.5	100.0%	5	5	9	0.01%	27.7%	YQSALLPHK	99.3%	36.8	25	35.2	1	0	0	1056.58	133	141
Transmembrane protein 201	TMEM201	TM201_HUMAN	72.2	100.0%	3	3	5	0.01%	5.0%	ALLLSHQFK	99.7%	55.7	25	49.5	2	0	0	1056.62	184	192
Transmembrane protein 201	TMEM201	TM201_HUMAN	72.2	100.0%	3	3	5	0.01%	5.0%	EADQTHAQNFSSAVK	99.7%	65.9	25	63.9	1	0	0	1632.76	195	209

Transmembrane protein 201	TMEM201	TM201_HUMAN	72.2	100.0%	3	3	5	0.01%	5.0%	SPVQVILLR	99.7%	52.1	25	48.3	2	0	0	1024.65	210	218
Transmembrane protein 209	TMEM209	TM209_HUMAN	62.9	99.9%	2	2	2	0.00%	4.3%	FQYQLACR	99.1%	35.2	25	25.4	1	0	0	1085.52	289	296
Transmembrane protein 209	TMEM209	TM209_HUMAN	62.9	99.9%	2	2	2	0.00%	4.3%	SQAPCANKDEADLSSK	95.6%	28.4	25	28.4	1	0	0	1720.78	297	312
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	6	7	15	0.02%	22.7%	ALLANALTSALR	99.7%	102	25	97.6	4	0	0	1213.73	58	69
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	6	7	15	0.02%	22.7%	GSNSLPLLR	99.6%	39.7	25	32.5	2	0	0	956.55	135	143
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	6	7	15	0.02%	22.7%	LCLQSIAFISR	99.7%	69.4	25	60.7	2	0	0	1307.71	231	241
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	6	7	15	0.02%	22.7%	LDTAMWLSR	99.7%	79.7	25	60.4	3	0	0	1092.55	23	31
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	6	7	15	0.02%	22.7%	LSANQQNILK	99.6%	39.1	25	27	1	0	0	1128.64	149	158
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	6	7	15	0.02%	22.7%	SVLDKLSANQQNILK	99.7%	70.6	25	64	2	1	0	1670.94	144	158
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	11	12	22	0.02%	14.1%	ALVMLLEVR	99.7%	79.7	25	71	4	0	0	1059.62	246	254
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	11	12	22	0.02%	14.1%	ATVGILITTIASK	99.7%	111	25	111	2	0	0	1287.79	116	128
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	11	12	22	0.02%	14.1%	ESQSPDTTIQR	99.7%	58.8	25	50.4	2	0	0	1261.60	29	39
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	11	12	22	0.02%	14.1%	FSDQFPLPLK	99.7%	45.7	25	45.3	1	0	0	1191.64	880	889
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	11	12	22	0.02%	14.1%	GELQNWPDLLPK	99.7%	53.2	25	39.2	2	0	0	1409.74	129	140
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	11	12	22	0.02%	14.1%	QSSFALLGDLTK	99.7%	69.8	25	56	2	0	0	1279.69	693	704
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	11	12	22	0.02%	14.1%	SECLNNIGDSSPLIR	99.7%	61.8	25	58.8	2	0	0	1674.81	101	115
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	11	12	22	0.02%	14.1%	SITCWTLSR	99.7%	47.3	25	17.8	2	0	0	1123.56	464	472
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	11	12	22	0.02%	14.1%	SNILTLMYQCMQDK	99.7%	63.5	25	63.5	1	0	0	1744.81	674	687
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	11	12	22	0.02%	14.1%	TLLENTAITIGR	99.7%	78.7	25	61.8	2	0	0	1301.74	774	785
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	11	12	22	0.02%	14.1%	YSDIDIILLK	99.7%	70.5	25	64.6	2	0	0	1192.68	318	327
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	16	0.02%	13.4%	ASFWLGELQR	99.7%	43.4	25	35.6	2	0	0	1206.63	30	39
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	16	0.02%	13.4%	ETTVGAVTVTHK	99.7%	65.7	25	46.4	2	0	0	1242.67	882	893
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	16	0.02%	13.4%	GTALVLAR	99.7%	60.3	25	35.9	2	0	0	800.50	564	571
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	16	0.02%	13.4%	IFTELCETFLEK	99.7%	59.1	25	43.4	1	0	0	1529.76	298	309
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	16	0.02%	13.4%	IVCTPGQGLGDLR	99.7%	64	25	61.8	2	0	0	1385.72	310	322
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	16	0.02%	13.4%	LGEHLYK	99.7%	42.5	25	27.7	2	0	0	859.47	349	355
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	16	0.02%	13.4%	SLDSFLLSPEAAVGLLK	99.7%	86.6	25	86.6	1	0	0	1759.98	547	563
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	16	0.02%	13.4%	SVDPENNPTLVEVLEGVVR	99.7%	58.6	25	58.6	1	0	0	2066.08	450	468
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	16	0.02%	13.4%	TNDEVIHGIFK	99.7%	46.6	25	30.4	1	0	0	1272.66	356	366
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	16	0.02%	13.4%	VIQEIWPVLSETLNK	99.7%	46.6	25	46.6	2	0	0	1768.98	637	651
Treacle protein	TCOF1	TCOF_HUMAN	152.1	100.0%	2	2	2	0.00%	1.8%	GSLGQGTAPVLPGK	99.7%	53.1	25	42.7	1	0	0	1281.72	733	746
Treacle protein	TCOF1	TCOF_HUMAN	152.1	100.0%	2	2	2	0.00%	1.8%	TSQVGAASAPAK	97.5%	30.8	25	30.8	1	0	0	1087.57	368	379
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	10	13	27	0.03%	31.5%	FFVMTSLR	99.7%	55.1	25	23.1	4	0	0	1000.53	199	206
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	10	13	27	0.03%	31.5%	FGMFEFLSNHMR	99.7%	57.9	25	54.7	4	2	0	1531.68	102	113
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	10	13	27	0.03%	31.5%	FIHDQTSPNPK	99.7%	43.2	25	40.7	2	2	0	1283.64	150	160
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	10	13	27	0.03%	31.5%	GFFHGVR	97.2%	30.2	25	21.8	2	0	0	819.43	163	169
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	10	13	27	0.03%	31.5%	GLSSLLYGSIPK	99.7%	68.2	25	50.5	2	0	0	1234.70	86	97
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	10	13	27	0.03%	31.5%	GTYQGLTATVLK	99.7%	64.6	25	56.3	2	0	0	1251.69	179	190
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	10	13	27	0.03%	31.5%	MQGLEAHK	99.1%	35.4	25	22.8	1	0	0	913.46	248	255
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	10	13	27	0.03%	31.5%	NTWDCGLQILK	99.7%	53.2	25	43.6	2	0	0	1347.67	258	268
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	10	13	27	0.03%	31.5%	SHGVLGLYR	99.7%	41.9	25	41.9	2	0	0	1001.55	77	85
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	10	13	27	0.03%	31.5%	TQLQLDER	99.7%	52.1	25	33.7	2	0	0	1002.52	51	58
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	33	65	0.07%	40.4%	ADMVIEAVFEDLSLK	99.7%	112	25	104	4	0	0	1679.86	441	455
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	33	65	0.07%	40.4%	ALMGLYHGQVLCK	99.7%	49.7	25	45.5	2	0	0	1489.77	338	350
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	33	65	0.07%	40.4%	ALTSFER	99.4%	37.2	25	15.1	2	0	0	823.43	416	422
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	33	65	0.07%	40.4%	CLAPMMSEVIR	99.5%	38.3	25	31.6	2	0	0	1306.63	550	560
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	33	65	0.07%	40.4%	DATLTALDR	99.7%	68.7	25	19.5	2	0	0	975.51	391	399
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	33	65	0.07%	40.4%	DGPGFYTTR	99.7%	57.2	25	46.4	3	0	0	1013.47	541	549
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	33	65	0.07%	40.4%	DLNSDMDSILASLK	99.7%	101	25	94	2	0	0	1521.75	647	660
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	33	65	0.07%	40.4%	DSIFSNLTGQLDYQGFEK	99.7%	90.4	25	90.4	2	0	0	2061.98	423	440
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	33	65	0.07%	40.4%	DTSASAVAVGLK	99.7%	77.9	25	57.6	3	0	0	1118.61	520	531

Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	33	65	0.07%	40.4%	FGELVMTK	99.7%	48.6	25	27.5	2	0	0	940.48	327	334
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	33	65	0.07%	40.4%	FGGGNPELLTQMVSK	99.7%	84.6	25	75.9	4	0	0	1577.80	611	625
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	33	65	0.07%	40.4%	FVDLYGAQK	99.7%	42.6	25	37.8	1	0	0	1040.54	720	728
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	33	65	0.07%	40.4%	GFYIYQEGVK	99.7%	68.8	25	63	2	0	0	1203.60	635	644
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	33	65	0.07%	40.4%	KALTSFER	95.9%	28.7	25	15.3	2	0	0	951.53	415	422
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	33	65	0.07%	40.4%	LTAYAMTIPFVR	99.7%	53.9	25	53.9	6	0	0	1398.75	268	279
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	33	65	0.07%	40.4%	MGLVDQLVEPLGPGLKPPEER	99.7%	54.8	25	54.8	0	1	0	2290.21	215	235
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	33	65	0.07%	40.4%	MQLLEIITTEK	99.7%	73.5	25	64	6	0	0	1318.73	506	516
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	33	65	0.07%	40.4%	MVGVPAALDMMLTGR	99.7%	89.7	25	87	4	0	0	1561.79	191	205
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	33	65	0.07%	40.4%	SEVSSDEDIQFR	99.7%	86.5	25	86	2	0	0	1411.63	665	676
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	33	65	0.07%	40.4%	TGIEQGSDAGYLCESQK	99.7%	94	25	94	2	0	0	1842.82	310	326
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	33	65	0.07%	40.4%	THINYGVK	95.2%	28	25	21	1	0	0	931.50	39	46
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	33	65	0.07%	40.4%	TIEYLEEVAITFAK	99.7%	101	25	90.6	1	0	0	1626.86	236	249
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	33	65	0.07%	40.4%	TLQEVTQLSQEAQR	99.7%	97.4	25	89.8	2	1	0	1630.84	112	125
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	33	65	0.07%	40.4%	TVLGTPEVLLGALPGAGGTQR	99.7%	64.1	25	64.1	2	2	0	2007.12	167	187
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	33	65	0.07%	40.4%	VIGMHYFSPVDK	99.4%	37.3	25	31.1	2	0	0	1392.70	494	505
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	29	0.03%	37.6%	AALTGLLHR	99.7%	61.3	25	50.9	1	0	0	951.57	82	90
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	29	0.03%	37.6%	ALAMGYKPK	96.3%	29.1	25	29.1	2	0	0	994.54	326	334
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	29	0.03%	37.6%	AMDSDWFAENYMGR	99.7%	64.3	25	64.3	2	0	0	1692.68	392	405
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	29	0.03%	37.6%	DFMYVSQDPKDQLLLGPTYATPK	98.4%	25.9	25	24.7	0	1	0	2627.31	339	361
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	29	0.03%	37.6%	DLMPHDLAR	99.4%	37.6	25	33.3	1	0	0	1083.53	73	81
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	29	0.03%	37.6%	DNGIRPSSLEQMAK	99.7%	45.5	25	23.3	1	0	0	1545.77	278	291
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	29	0.03%	37.6%	DQLLLGPTYATPK	99.7%	69.2	25	69.2	1	0	0	1416.77	349	361
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	29	0.03%	37.6%	EAALGAGFSDK	99.7%	61.8	25	50.7	2	0	0	1065.52	118	128
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	29	0.03%	37.6%	EVVDYIIFGTVIQEVK	99.7%	78.4	25	77.9	3	0	0	1852.01	96	111
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	29	0.03%	37.6%	FNNWGGSLSLGHPFGATGCR	99.7%	62.7	25	62.7	0	2	0	2134.99	417	436
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	29	0.03%	37.6%	KLMLDLNK	99.7%	40.2	25	13.9	2	0	0	990.57	181	188
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	29	0.03%	37.6%	LAAAFAVSR	99.7%	73.1	25	56.9	2	0	0	905.52	230	238
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	29	0.03%	37.6%	LVMAAANR	99.7%	60	25.3	46.3	2	0	0	845.47	437	444
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	29	0.03%	37.6%	NVVVVDGVR	99.7%	57.7	25	51.2	2	0	0	956.55	53	61
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	29	0.03%	37.6%	TPFLLSGTSYK	99.7%	52.7	25	43.4	2	0	0	1213.65	62	72
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	29	0.03%	37.6%	TPFLLSGTSYKDLMPHDLAR	99.7%	40.5	25	40.5	0	1	0	2262.16	62	81
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	29	0.03%	37.6%	VGLPPLEK	99.3%	36.9	25	35.3	2	0	0	852.52	409	416
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	AAGFKDPLLASGTDGVGTK	99.7%	67.8	25	64.3	2	0	0	1804.94	481	499
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	AFAHITGGGLLENIPR	99.7%	70.6	25	62.7	2	2	0	1665.91	677	692
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	AIAFLQQPR	99.7%	44.8	25	27.8	4	0	0	1043.60	425	433
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	AVQEIMQEK	99.5%	38.6	25	30.5	3	0	0	1091.54	170	178
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	EHTLAWK	96.2%	29	25	17.9	1	0	0	884.46	14	20
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	ENLISALEEAKK	99.7%	66.8	25	52.5	4	0	0	1344.74	394	405
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	EQTEQILR	97.8%	31.3	25	21.9	1	0	0	1016.54	744	751
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	ESGVDIAAGNMLVK	99.7%	73.1	25	67.3	4	0	0	1403.72	439	452
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	FEGAIYR	95.0%	27.9	25	9.55	1	0	0	855.44	412	418
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	FEGAIYRK	99.5%	38.6	25	23.8	2	0	0	983.53	412	419
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	FGDPECQVILPLLK	99.7%	69.9	25	66.2	4	0	0	1628.87	293	306
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	GDTVATLSER	99.7%	45.6	25	16.5	2	0	0	1048.53	966	975
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	GVEITGFPEAQALGLEVFHAGTALK	99.7%	32.6	25	29.9	0	1	0	2555.35	351	375
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	HGIPTAQWK	97.5%	30.7	25	26.8	2	0	0	1037.55	117	125
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	IKDTVLQR	99.7%	55.9	25	27	3	0	0	972.58	250	257
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	ILSGPFVQK	99.5%	38.5	25	2.55	2	0	0	988.58	898	906
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	ISNTAISISDHTALAQFCK	99.7%	62.1	25	61.1	0	1	0	2077.04	45	63
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	IYSHSLLPVLR	99.7%	40.9	25	31.3	2	2	0	1297.76	661	671

Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	LDLSVTEAVVAGIAK	99.7%	105	25	89.7	2	0	0	1485.85	543	557
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	LGVDLDAQTWR	99.5%	37.8	25	32.5	1	0	0	1273.65	698	708
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	MLNIHPSLLPSFK	99.7%	54.8	25	43.3	4	0	0	1496.83	911	923
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	QVLVAPGNAGTACSEK	99.7%	70.1	25	69.3	4	0	0	1601.80	29	44
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	SAGVQCFGPTAEAAQLESSKR	99.7%	33.5	25	33.1	0	3	0	2194.06	88	108
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	TFNCGVGAVLVVSK	99.7%	98.6	25	98.5	2	0	0	1450.77	730	743
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	TVAPMPPAQDHKR	97.1%	30.1	25	23.4	1	0	0	1463.74	208	220
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	VDLGGFAGLFDLK	99.7%	91.2	25	87.8	3	0	0	1351.73	468	480
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	VLAVTAIR	99.7%	60.1	25	30.9	4	0	0	842.55	386	393
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	28	32	71	0.07%	33.5%	VLEFNCR	98.9%	34.2	25	32	2	0	0	937.46	286	292
Triosephosphate isomerase	TPI1	TPIS_HUMAN	30.8	100.0%	3	3	7	0.01%	13.3%	IAVAAQNCYK	95.4%	28.2	25	24.4	1	0	0	1137.57	97	106
Triosephosphate isomerase	TPI1	TPIS_HUMAN	30.8	100.0%	3	3	7	0.01%	13.3%	TATPQQAQEVHEK	99.7%	58	25	55.2	4	0	0	1466.72	213	225
Triosephosphate isomerase	TPI1	TPIS_HUMAN	30.8	100.0%	3	3	7	0.01%	13.3%	VVLAYEPVWAIGTGK	99.7%	63.2	25	60.7	2	0	0	1602.89	198	212
TRMT1-like protein	TRMT1L	TRM1L_HUMAN	81.7	99.8%	2	2	2	0.00%	3.7%	QLIFCTLAALAEER	99.7%	65.8	25	58.8	1	0	0	1634.86	261	274
TRMT1-like protein	TRMT1L	TRM1L_HUMAN	81.7	99.8%	2	2	2	0.00%	3.7%	SSYIAASTAKPPK	99.7%	66.8	25	66.8	1	0	0	1320.72	214	226
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	13	14	31	0.03%	18.1%	CYLLVHQAK	95.2%	28.1	25	21.3	1	0	0	1131.60	221	229
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	13	14	31	0.03%	18.1%	FYALDPSFPR	99.6%	39.8	25	35.3	2	0	0	1212.60	536	545
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	13	14	31	0.03%	18.1%	GAEQLAEGGR	99.7%	88.3	25	78.6	3	0	0	987.49	306	315
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	13	14	31	0.03%	18.1%	IITVSMEDVK	99.7%	58	25	48.3	4	0	0	1134.61	619	628
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	13	14	31	0.03%	18.1%	ILCDVPCSGDGTMR	99.7%	53.5	25	53.5	1	0	0	1580.69	265	278
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	13	14	31	0.03%	18.1%	ILLTQENPFFR	99.7%	85.3	25	72.9	4	0	0	1377.75	629	639
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	13	14	31	0.03%	18.1%	KLSSETYSQAK	99.7%	61.5	25	56.7	3	0	0	1241.64	640	650
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	13	14	31	0.03%	18.1%	LAQEGIYTLYPFINSR	99.7%	66.5	25	65.4	4	0	0	1884.99	603	618
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	13	14	31	0.03%	18.1%	LQAMHLER	99.7%	46.6	25	33.7	1	0	0	997.52	401	408
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	13	14	31	0.03%	18.1%	LSSETYSQAK	99.7%	63.7	25	56.6	2	0	0	1113.54	641	650
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	13	14	31	0.03%	18.1%	MMGLEVLGEK	98.9%	34.3	25	34.3	2	0	0	1106.56	701	710
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	13	14	31	0.03%	18.1%	NNSGEEFDCAFR	99.7%	74.7	25	74.7	2	0	0	1445.58	591	602
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	13	14	31	0.03%	18.1%	SEGALELADVSNELPGLK	99.7%	98.9	25	89.4	2	0	0	1841.95	339	356
tRNA pseudouridine synthase A, mitochondrial	PUS1	TRUA_HUMAN	47.5	99.8%	2	2	3	0.00%	5.2%	APGLGLVLER	99.7%	49.7	25	47.8	1	0	0	1024.62	328	337
tRNA pseudouridine synthase A, mitochondrial	PUS1	TRUA_HUMAN	47.5	99.8%	2	2	3	0.00%	5.2%	TIEDDLVSALVR	99.7%	63.5	25	56.9	2	0	0	1330.72	111	122
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	8	9	15	0.02%	20.4%	GFVPNMQVEGVFYVNDALEK	99.7%	44.5	25	43.8	1	0	0	2256.10	25	44
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	8	9	15	0.02%	20.4%	GGGVGGFLPAMK	99.7%	48.1	25	32.6	2	0	0	1090.57	56	67
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	8	9	15	0.02%	20.4%	GQVCVMIHSGSR	99.7%	76.2	25	76.2	2	0	0	1330.64	252	263
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	8	9	15	0.02%	20.4%	LMFEELR	99.4%	37.6	25	33.8	2	0	0	937.48	45	51
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	8	9	15	0.02%	20.4%	LVMEEAPESYK	99.7%	50.5	25	50.5	1	0	0	1311.61	466	476
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	8	9	15	0.02%	20.4%	NLDFQDVLDKLADMGIAIR	99.5%	30.5	25	30.5	0	1	0	2163.11	442	460
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	8	9	15	0.02%	20.4%	SYNDELQFLEK	99.7%	63.9	25	32.8	2	0	0	1385.66	4	14
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	8	9	15	0.02%	20.4%	VEQHVVDGKER	99.7%	49.4	25	44.8	2	2	0	1295.67	358	368
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	66.7%	AFVHWYVGEGMEEGEFSEAR	99.7%	56.5	25	56.5	2	4	0	2330.02	403	422
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	66.7%	AFVHWYVGEGMEEGEFSEAREDMAALEK	99.7%	55	25	55	0	3	0	3217.42	403	430
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	66.7%	AVCMLSNTTAIAEAWAR	99.7%	128	25	123	22	9	0	1864.90	374	390
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	66.7%	AVFVDLEPTVIDEVR	99.7%	114	25	113	45	6	0	1701.91	65	79
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	66.7%	AYHEQLSVAEITNACFEPANQMVK	99.7%	66.2	25	66.2	0	8	0	2766.29	281	304
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	66.7%	DVNAAIATIK	99.7%	81.2	25	63.7	19	0	0	1015.58	327	336
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	66.7%	EDMAALEK	99.7%	54	25	30.2	4	0	0	906.42	423	430
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	66.7%	EIIDLVLDR	99.7%	79.4	25	75.7	37	0	0	1085.62	113	121
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	66.7%	FDGALNVDLTEFQTNLVPYPR	99.7%	125	25	125	15	2	0	2409.21	244	264
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	66.7%	FDLMYAK	99.7%	46.3	25	30.9	6	0	0	903.43	395	401
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	66.7%	IHFPLATYAPVISAEK	99.7%	103	25	92	6	8	0	1756.96	265	280
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	66.7%	LADQCTGLQGFLVFHSFGGGTGSGFTSLLMER	99.7%	107	25	107	0	25	0	3406.62	125	156
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	66.7%	LDHKFDLMYAK	99.7%	47.6	25	29.7	9	8	0	1380.70	391	401

Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	66.7%	LIGQIVSSITASLR	99.7%	91	25	85.1	4	0	0	1457.87	230	243
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	66.7%	LSVDYGKK	99.7%	54.2	25	44.5	13	0	0	909.50	157	164
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	66.7%	NLDIERPTYTNLNR	99.7%	71.3	25	69.4	12	11	0	1718.88	216	229
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	66.7%	QLFHPEQLITGK	99.7%	60	25	0	4	4	0	1410.77	85	96
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	66.7%	QLFHPEQLITGKEDAANNYAR	99.7%	85.9	25	85.9	2	6	0	2415.21	85	105
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	66.7%	RNLDIERPTYTNLNR	98.9%	27.2	25	27.2	0	2	0	1874.98	215	229
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	66.7%	TIGGGDDSFNTFFSETGAGK	99.7%	116	25	116	27	0	0	2007.89	41	60
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	66.7%	TIQFVDWCPTGFK	99.7%	67.8	25	64	15	0	0	1598.77	340	352
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	66.7%	VGINYQPPTVVPGGDLAK	99.7%	71	25	71	21	0	0	1824.99	353	370
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	66.7%	YMACCLLYR	99.7%	51.1	25	50.1	24	0	0	1249.55	312	320
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	44	404	0.41%	66.7%	AFVHWYVGEGMEEGEFSEAR	99.7%	56.5	25	56.5	2	4	0	2330.02	403	422
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	44	404	0.41%	66.7%	AFVHWYVGEGMEEGEFSEAREDMAALEK	99.7%	55	25	55	0	3	0	3217.42	403	430
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	44	404	0.41%	66.7%	AVCMLSNTTAIAEAWAR	99.7%	128	25	123	22	9	0	1864.90	374	390
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	44	404	0.41%	66.7%	AVFVDLEPTVIDEVR	99.7%	114	25	113	45	6	0	1701.91	65	79
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	44	404	0.41%	66.7%	AYHEQLSVAEITNACFEPANQMVK	99.7%	66.2	25	66.2	0	8	0	2766.29	281	304
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	44	404	0.41%	66.7%	DVNAAIATIK	99.7%	81.2	25	63.7	19	0	0	1015.58	327	336
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	44	404	0.41%	66.7%	EDMAALEK	99.7%	54	25	30.2	4	0	0	906.42	423	430
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	44	404	0.41%	66.7%	EIIDLVLDR	99.7%	79.4	25	75.7	37	0	0	1085.62	113	121
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	44	404	0.41%	66.7%	FDGALNVDLTEFQTNLVPYPR	99.7%	125	25	125	15	2	0	2409.21	244	264
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	44	404	0.41%	66.7%	FDLMYAK	99.7%	46.3	25	30.9	6	0	0	903.43	395	401
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	44	404	0.41%	66.7%	IHFPLATYAPVISAEK	99.7%	103	25	92	6	8	0	1756.96	265	280
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	44	404	0.41%	66.7%	LADQCTGLQGFLVFHSFGGGTGSGFTSLLMER	99.7%	107	25	107	0	25	0	3406.62	125	156
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	44	404	0.41%	66.7%	LDHKFDLMYAK	99.7%	47.6	25	29.7	9	8	0	1380.70	391	401
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	44	404	0.41%	66.7%	LISQIVSSITASLR	99.7%	108	25	108	16	3	0	1487.88	230	243
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	44	404	0.41%	66.7%	LSVDYGKK	99.7%	54.2	25	44.5	13	0	0	909.50	157	164
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	44	404	0.41%	66.7%	NLDIERPTYTNLNR	99.7%	71.3	25	69.4	12	11	0	1718.88	216	229
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	44	404	0.41%	66.7%	QLFHPEQLITGK	99.7%	60	25	0	4	4	0	1410.77	85	96
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	44	404	0.41%	66.7%	QLFHPEQLITGKEDAANNYAR	99.7%	85.9	25	85.9	2	6	0	2415.21	85	105
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	44	404	0.41%	66.7%	RNLDIERPTYTNLNR	98.9%	27.2	25	27.2	0	2	0	1874.98	215	229
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	44	404	0.41%	66.7%	SIQFVDWCPTGFK	99.7%	88.8	25	88.1	20	0	0	1584.75	340	352
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	44	404	0.41%	66.7%	SIQFVDWCPTGFKVGINYQPPTVVPGGDLAK	99.7%	35.4	25	35.4	0	1	0	3390.72	340	370
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	44	404	0.41%	66.7%	TIGGGDDSFNTFFSETGAGK	99.7%	116	25	116	27	0	0	2007.89	41	60
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	44	404	0.41%	66.7%	VGINYQPPTVVPGGDLAK	99.7%	71	25	71	21	0	0	1824.99	353	370
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	44	404	0.41%	66.7%	YMACCLLYR	99.7%	51.1	25	50.1	24	0	0	1249.55	312	320
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	67.0%	AFVHWYVGEGMEEGEFSEAR	99.7%	56.5	25	56.5	2	4	0	2330.02	403	422
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	67.0%	AFVHWYVGEGMEEGEFSEAREDMAALEK	99.7%	55	25	55	0	3	0	3217.42	403	430
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	67.0%	AVCMLSNTTAVAEAWAR	99.7%	85.4	25	83.9	3	4	0	1866.88	374	390
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	67.0%	AVFVDLEPTVIDEVR	99.7%	114	25	113	45	6	0	1701.91	65	79
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	67.0%	AYHEQLTVAEITNACFEPANQMVK	99.0%	27.4	25	25.4	0	2	0	2780.30	281	304
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	67.0%	DVNAAIATIK	99.7%	81.2	25	63.7	19	0	0	1015.58	327	336
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	67.0%	EDMAALEK	99.7%	54	25	30.2	4	0	0	906.42	423	430
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	67.0%	EIIDLVLDR	99.7%	79.4	25	75.7	37	0	0	1085.62	113	121
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	67.0%	FDGALNVDLTEFQTNLVPYPR	99.7%	125	25	125	15	2	0	2409.21	244	264
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	67.0%	FDLMYAK	99.7%	46.3	25	30.9	6	0	0	903.43	395	401
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	67.0%	IHFPLATYAPVISAEK	99.7%	103	25	92	6	8	0	1756.96	265	280
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	67.0%	LADQCTGLQGFLVFHSFGGGTGSGFTSLLMER	99.7%	107	25	107	0	25	0	3406.62	125	156
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	67.0%	LDHKFDLMYAK	99.7%	47.6	25	29.7	9	8	0	1380.70	391	401
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	67.0%	LISQIVSSITASLR	99.7%	108	25	108	16	3	0	1487.88	230	243
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	67.0%	LSVDYGKK	99.7%	54.2	25	44.5	13	0	0	909.50	157	164
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	67.0%	NLDIERPTYTNLNR	99.7%	71.3	25	69.4	12	11	0	1718.88	216	229
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	67.0%	QLFHPEQLITGK	99.7%	60	25	0	4	4	0	1410.77	85	96

Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	67.0%	QLFHPEQLITGKEDAANNYAR	99.7%	85.9	25	85.9	2	6	0	2415.21	85	105
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	67.0%	RNLDIERPTYTNLNR	98.9%	27.2	25	27.2	0	2	0	1874.98	215	229
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	67.0%	TIGGGDDSFNTFFSETGAGK	99.7%	116	25	116	27	0	0	2007.89	41	60
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	67.0%	TIQFVDWCPTGFK	99.7%	67.8	25	64	15	0	0	1598.77	340	352
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	67.0%	VGINYQPPTVVPGGDLAK	99.7%	71	25	71	21	0	0	1824.99	353	370
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	67.0%	YMACCLLYR	99.7%	51.1	25	50.1	24	0	0	1249.55	312	320
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	AILVDLEPGTMDSVR	99.7%	101	25	96.4	41	0	0	1615.84	63	77
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	ALTVPELTQQVFDAK	99.7%	65.8	25	65.8	19	4	0	1659.90	283	297
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	110	25	0	0	8	0	3311.53	123	154
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	EIVHIQAGQCGNQIGAK	99.7%	94.9	25	0	4	4	0	1822.92	3	19
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	EVDEQMLNVQNK	99.7%	88.3	25	87.6	17	0	0	1462.68	325	336
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	FPGQLNADLR	99.7%	61.5	25	40.7	15	0	0	1130.60	242	251
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	FPGQLNADLRK	99.7%	44.2	25	33	8	4	0	1258.69	242	252
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	FWEVISDEHGIDPTGTYHGDSDLQLDR	99.7%	87.5	25	43.9	0	4	0	3102.41	20	46
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	GHYTEGAELVDSVLDVVR	99.7%	129	25	126	4	5	0	1958.98	104	121
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	GHYTEGAELVDSVLDVVRK	99.7%	122	25	107	2	3	0	2087.08	104	122
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	IMNTFSVVPSPK	99.7%	92.9	25	80.4	28	0	0	1335.70	163	174
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	IREEYPDR	99.5%	38.7	25	25.2	5	0	0	1077.53	155	162
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	ISEQFTAMFR	99.7%	94.3	25	90.7	24	0	0	1229.60	381	390
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	ISVYYNEATGGK	99.7%	82.6	25	82.6	24	0	0	1301.64	47	58
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	KEAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	93	25	0	0	2	0	3439.63	122	154
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	KLAVNMVPFPR	99.7%	75.3	25	75	7	4	0	1271.73	252	262
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	LAVNMVPFPR	99.7%	84.4	25	72.5	30	0	0	1143.63	253	262
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	LHFFMPGFAPLTSR	99.7%	73.7	25	63.7	19	15	0	1620.84	263	276
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	LTTPTYGDLNHLVSATMSGVTTCLR	99.7%	66.9	25	66	2	18	0	2708.34	217	241
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	MAVTFIGNSTAIQELFK	99.7%	138	25	131	21	3	0	1885.97	363	379
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	MAVTFIGNSTAIQELFKR	99.7%	108	25	108	7	10	0	2026.08	363	380
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	MREIVHIQAGQCGNQIGAK	99.7%	69.9	25	0	0	12	0	2126.06	1	19
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	MSMKEVDEQMLNVQNK	99.7%	57.9	25	31.2	6	21	0	1955.89	321	336
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	NMMAACDPR	99.7%	48.6	25	48.6	14	0	0	1065.43	298	306
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	NSSYFVEWIPNNVK	99.7%	81	25	69.5	11	0	0	1696.83	337	350
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	RISEQFTAMFR	99.7%	60.3	25	53.7	2	0	0	1385.70	380	390
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	SGPFGQIFRPDNFVFGQSGAGNNWAK	99.7%	83.5	25	82.6	1	10	0	2798.34	78	103
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	TAVCDIPPR	99.7%	57.6	25	50.2	34	0	0	1028.52	351	359
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	29	60	482	0.48%	74.3%	YLTVAAVFR	99.7%	88.6	25	84.4	10	0	0	1039.59	310	318
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	AILVDLEPGTMDSVR	99.7%	101	25	96.4	41	0	0	1615.84	63	77
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	ALTVPELTQQMFDSK	99.7%	98.8	25	41.9	8	0	0	1707.86	283	297
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	EIVHIQAGQCGNQIGAK	99.7%	94.9	25	0	4	4	0	1822.92	3	19
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	ESESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	48.3	25	48.3	0	2	0	3343.52	123	154
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	EVDEQMLNVQNK	99.7%	88.3	25	87.6	17	0	0	1462.68	325	336
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	FPGQLNADLR	99.7%	61.5	25	40.7	15	0	0	1130.60	242	251
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	FPGQLNADLRK	99.7%	44.2	25	33	8	4	0	1258.69	242	252
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	GHYTEGAELVDSVLDVVR	99.7%	129	25	126	4	5	0	1958.98	104	121
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	GHYTEGAELVDSVLDVVRK	99.7%	122	25	107	2	3	0	2087.08	104	122
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	IMNTFSVMPSPK	99.7%	86.9	25	79.8	13	0	0	1351.67	163	174
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	INVYYNEATGNK	99.7%	73.1	25	68.8	4	0	0	1385.67	47	58
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	IREEYPDR	99.5%	38.7	25	25.2	5	0	0	1077.53	155	162
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	ISEQFTAMFR	99.7%	94.3	25	90.7	24	0	0	1229.60	381	390
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	KLAVNMVPFPR	99.7%	75.3	25	75	7	4	0	1271.73	252	262
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	LAVNMVPFPR	99.7%	84.4	25	72.5	30	0	0	1143.63	253	262
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	LHFFMPGFAPLTSR	99.7%	73.7	25	63.7	19	15	0	1620.84	263	276

Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	LTTPTYGDLNHLVSATMSGVTTCLR	99.7%	66.9	25	66	2	18	0	2708.34	217	241
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	MREIVHIQAGQCGNQIGAK	99.7%	69.9	25	0	0	12	0	2126.06	1	19
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	MSATFIGNSTAIQELFK	99.7%	125	25	0	9	0	0	1873.94	363	379
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	MSATFIGNSTAIQELFKR	99.7%	70.7	25	0	2	8	0	2014.04	363	380
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	MSMKEVDEQMLNVQNK	99.7%	57.9	25	31.2	6	21	0	1955.89	321	336
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	NMMAACDPR	99.7%	48.6	25	48.6	14	0	0	1065.43	298	306
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	NSSYFVEWIPNNVK	99.7%	81	25	69.5	11	0	0	1696.83	337	350
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	RISEQFTAMFR	99.7%	60.3	25	53.7	2	0	0	1385.70	380	390
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	SGPFGQIFRPDNFVFGQSGAGNNWAK	99.7%	83.5	25	82.6	1	10	0	2798.34	78	103
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	TAVCDIPPR	99.7%	57.6	25	50.2	34	0	0	1028.52	351	359
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	31	0.03%	68.1%	YLTVAAIFR	99.7%	73.6	25	60.9	4	0	0	1053.61	310	318
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	5	17	0.02%	68.0%	ALTVPELTQQMFDAK	99.7%	94.5	25	37.9	15	1	0	1707.86	283	297
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	5	17	0.02%	68.0%	AVLVDLEPGTMDSVR	99.7%	102	25	79.5	17	0	0	1601.82	63	77
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	5	17	0.02%	68.0%	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	110	25	0	0	8	0	3311.53	123	154
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	5	17	0.02%	68.0%	EIVHLQAGQCGNQIGAK	99.7%	94.9	25	0	4	4	0	1822.92	3	19
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	5	17	0.02%	68.0%	FPGQLNADLR	99.7%	61.5	25	40.7	15	0	0	1130.60	242	251
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	5	17	0.02%	68.0%	FPGQLNADLRK	99.7%	44.2	25	33	8	4	0	1258.69	242	252
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	5	17	0.02%	68.0%	FWEVISDEHGIDPTGTYHGDSDLQLER	99.7%	80.5	25	78.7	0	2	0	3116.42	20	46
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	5	17	0.02%	68.0%	GHYTEGAELVDAVLDVVR	99.7%	56.8	25	53.2	0	2	0	1942.99	104	121
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	5	17	0.02%	68.0%	IMNTFSVVPSPK	99.7%	92.9	25	80.4	28	0	0	1335.70	163	174
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	5	17	0.02%	68.0%	IREEFPDR	97.0%	29.9	25	15.7	2	0	0	1061.54	155	162
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	5	17	0.02%	68.0%	ISEQFTAMFR	99.7%	94.3	25	90.7	24	0	0	1229.60	381	390
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	5	17	0.02%	68.0%	KEAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	93	25	0	0	2	0	3439.63	122	154
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	5	17	0.02%	68.0%	KLAVNMVPFPR	99.7%	75.3	25	75	7	4	0	1271.73	252	262
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	5	17	0.02%	68.0%	LAVNMVPFPR	99.7%	84.4	25	72.5	30	0	0	1143.63	253	262
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	5	17	0.02%	68.0%	LHFFMPGFAPLTSR	99.7%	73.7	25	63.7	19	15	0	1620.84	263	276
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	5	17	0.02%	68.0%	LTTPTYGDLNHLVSATMSGVTTCLR	99.7%	66.9	25	66	2	18	0	2708.34	217	241
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	5	17	0.02%	68.0%	MAATFIGNSTAIQELFK	99.7%	98.4	25	0	9	0	0	1857.94	363	379
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	5	17	0.02%	68.0%	MAATFIGNSTAIQELFKR	99.7%	74.1	25	1.66	4	0	0	2014.04	363	380
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	5	17	0.02%	68.0%	MREIVHLQAGQCGNQIGAK	99.7%	69.9	25	0	0	12	0	2126.06	1	19
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	5	17	0.02%	68.0%	NMMAACDPR	99.7%	48.6	25	48.6	14	0	0	1065.43	298	306
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	5	17	0.02%	68.0%	NSSYFVEWIPNNVK	99.7%	81	25	69.5	11	0	0	1696.83	337	350
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	5	17	0.02%	68.0%	RISEQFTAMFR	99.7%	60.3	25	53.7	2	0	0	1385.70	380	390
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	5	17	0.02%	68.0%	SGPFGQIFRPDNFVFGQSGAGNNWAK	99.7%	83.5	25	82.6	1	10	0	2798.34	78	103
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	5	17	0.02%	68.0%	TAVCDIPPR	99.7%	57.6	25	50.2	34	0	0	1028.52	351	359
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	5	17	0.02%	68.0%	YLTVAAVFR	99.7%	88.6	25	84.4	10	0	0	1039.59	310	318
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	ALTVPELTQQMFDAK	99.7%	94.5	25	37.9	15	1	0	1707.86	283	297
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	AVLVDLEPGTMDSVR	99.7%	102	25	79.5	17	0	0	1601.82	63	77
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	110	25	0	0	8	0	3311.53	123	154
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	EIVHLQAGQCGNQIGAK	99.7%	94.9	25	0	4	4	0	1822.92	3	19
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	EVDEQMLNVQNK	99.7%	88.3	25	87.6	17	0	0	1462.68	325	336
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	FPGQLNADLR	99.7%	61.5	25	40.7	15	0	0	1130.60	242	251
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	FPGQLNADLRK	99.7%	44.2	25	33	8	4	0	1258.69	242	252
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	FWEVISDEHGIDPTGTYHGDSDLQLER	99.7%	80.5	25	78.7	0	2	0	3116.42	20	46
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	GHYTEGAELVDSVLDVVR	99.7%	129	25	126	4	5	0	1958.98	104	121
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	GHYTEGAELVDSVLDVVRK	99.7%	122	25	107	2	3	0	2087.08	104	122
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	IMNTFSVVPSPK	99.7%	92.9	25	80.4	28	0	0	1335.70	163	174
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	INVYYNEATGGK	99.7%	82.1	25	69.8	10	0	0	1328.65	47	58
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	IREEYPDR	99.5%	38.7	25	25.2	5	0	0	1077.53	155	162
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	ISEQFTAMFR	99.7%	94.3	25	90.7	24	0	0	1229.60	381	390
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	KEAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	93	25	0	0	2	0	3439.63	122	154

Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	KLAVNMVPFPR	99.7%	75.3	25	75	7	4	0	1271.73	252	262
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	LAVNMVPFPR	99.7%	84.4	25	72.5	30	0	0	1143.63	253	262
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	LHFFMPGFAPLTSR	99.7%	73.7	25	63.7	19	15	0	1620.84	263	276
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	LTTPTYGDLNHLVSATMSGVTTCLR	99.7%	66.9	25	66	2	18	0	2708.34	217	241
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	MREIVHLQAGQCGNQIGAK	99.7%	69.9	25	0	0	12	0	2126.06	1	19
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	MSATFIGNSTAIQELFK	99.7%	125	25	0	9	0	0	1873.94	363	379
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	MSATFIGNSTAIQELFKR	99.7%	70.7	25	0	2	8	0	2014.04	363	380
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	MSMKEVDEQMLNVQNK	99.7%	57.9	25	31.2	6	21	0	1955.89	321	336
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	NMMAACDPR	99.7%	48.6	25	48.6	14	0	0	1065.43	298	306
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	NSSYFVEWIPNNVK	99.7%	81	25	69.5	11	0	0	1696.83	337	350
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	RISEQFTAMFR	99.7%	60.3	25	53.7	2	0	0	1385.70	380	390
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	SGPFGQIFRPDNFVFGQSGAGNNWAK	99.7%	83.5	25	82.6	1	10	0	2798.34	78	103
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	TAVCDIPPR	99.7%	57.6	25	50.2	34	0	0	1028.52	351	359
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.06%	74.2%	YLTVAAVFR	99.7%	88.6	25	84.4	10	0	0	1039.59	310	318
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	4	8	0.01%	32.3%	AALVDLEPGTMDSVR	99.7%	66.7	25	62.7	3	0	0	1589.78	63	77
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	4	8	0.01%	32.3%	ALTVPELTQQMFDAR	99.7%	55.5	25	54.7	3	0	0	1719.87	283	297
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	4	8	0.01%	32.3%	FPGQLNADLR	99.7%	61.5	25	40.7	15	0	0	1130.60	242	251
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	4	8	0.01%	32.3%	FPGQLNADLRK	99.7%	44.2	25	33	8	4	0	1258.69	242	252
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	4	8	0.01%	32.3%	GHYTEGAELVDAVLDVVR	99.7%	56.8	25	53.2	0	2	0	1942.99	104	121
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	4	8	0.01%	32.3%	IMNTFSVMPSPK	99.7%	86.9	25	79.8	13	0	0	1351.67	163	174
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	4	8	0.01%	32.3%	IREEFPDR	97.0%	29.9	25	15.7	2	0	0	1061.54	155	162
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	4	8	0.01%	32.3%	KLAVNMVPFPR	99.7%	75.3	25	75	7	4	0	1271.73	252	262
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	4	8	0.01%	32.3%	LAVNMVPFPR	99.7%	84.4	25	72.5	30	0	0	1143.63	253	262
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	4	8	0.01%	32.3%	LHFFMPGFAPLTSR	99.7%	73.7	25	63.7	19	15	0	1620.84	263	276
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	4	8	0.01%	32.3%	MASTFIGNSTAIQELFK	99.7%	131	25	9.86	9	0	0	1873.94	363	379
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	4	8	0.01%	32.3%	MASTFIGNSTAIQELFKR	99.7%	33.8	25	0.78	1	1	0	2030.04	363	380
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	4	8	0.01%	32.3%	NMMAACDPR	99.7%	48.6	25	48.6	14	0	0	1065.43	298	306
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	4	8	0.01%	32.3%	NSSYFVEWIPNNVK	99.7%	81	25	69.5	11	0	0	1696.83	337	350
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	6	7	10	0.01%	15.5%	AVLLDLEPR	99.7%	42.2	25	35.3	2	0	0	1025.60	64	72
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	6	7	10	0.01%	15.5%	DVFFYQADDEHYIPR	99.7%	79.5	25	79.5	1	0	0	1914.87	49	63
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	6	7	10	0.01%	15.5%	KTTVLDVMR	99.7%	51.9	25	40.8	2	0	0	1062.60	287	295
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	6	7	10	0.01%	15.5%	LNDRYPK	96.8%	29.7	25	25.3	1	0	0	905.48	157	163
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	6	7	10	0.01%	15.5%	LTQNADCVVVLDNTALNR	99.7%	89.8	25	89.8	1	0	0	2016.02	195	212
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	6	7	10	0.01%	15.5%	VIHSILNSPYAK	99.7%	49.8	25	46.3	2	1	0	1341.75	73	84
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	12	13	19	0.02%	11.7%	AAMTSLMDLTLLLAR	97.3%	30.4	25	19.9	1	0	0	1651.88	874	888
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	12	13	19	0.02%	11.7%	DAAAVLVSR	99.7%	55.2	25	40.4	2	0	0	901.51	205	213
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	12	13	19	0.02%	11.7%	GACSVGTNVR	98.7%	33.6	25	27.8	1	0	0	1020.49	455	464
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	12	13	19	0.02%	11.7%	ILQIAESYLIVSDK	99.7%	89.2	25	88.7	2	0	0	1591.89	189	202
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	12	13	19	0.02%	11.7%	IMCCVAQQASEK	99.7%	47.3	25	47.3	2	0	0	1440.63	902	913
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	12	13	19	0.02%	11.7%	ITQLLGLPTYR	98.5%	33	25	33	2	0	0	1274.75	969	979
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	12	13	19	0.02%	11.7%	LDGNLLTQPGQAR	99.7%	58.1	25	48.8	2	0	0	1382.74	170	182
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	12	13	19	0.02%	11.7%	LPESNQTLLR	99.7%	46.3	25	36.1	1	0	0	1170.65	285	294
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	12	13	19	0.02%	11.7%	LQQVLTGLR	99.7%	72.1	25	45.2	2	0	0	1027.63	791	799
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	12	13	19	0.02%	11.7%	QAVCVLIEK	96.9%	29.9	25	16.2	1	0	0	1059.59	678	686
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	12	13	19	0.02%	11.7%	SDVASVNWSAPSQAFPR	99.7%	47.4	25	47.4	1	0	0	1818.88	952	968
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	12	13	19	0.02%	11.7%	VIEQLLVGLK	99.7%	64.5	25	64.5	2	0	0	1111.71	361	370
Tyrosine-protein kinase CSK	CSK	CSK_HUMAN	50.7	100.0%	3	3	4	0.00%	8.4%	EASSTQDTGKLPVK	99.7%	53.8	25	41.5	1	0	0	1460.76	338	351
Tyrosine-protein kinase CSK	CSK	CSK_HUMAN	50.7	100.0%	3	3	4	0.00%	8.4%	LLYPPETGLFLVR	99.6%	39.4	25	36.8	1	0	0	1517.87	95	107
Tyrosine-protein kinase CSK	CSK	CSK_HUMAN	50.7	100.0%	3	3	4	0.00%	8.4%	NVLVSEDNVAK	99.7%	45.8	25	39.5	2	0	0	1187.63	319	329
Tyrosine-protein kinase JAK1	JAK1	JAK1_HUMAN	133.3	100.0%	3	3	4	0.00%	3.1%	EISNLLVATK	95.0%	27.9	25	22.6	1	0	0	1087.64	550	559
Tyrosine-protein kinase JAK1	JAK1	JAK1_HUMAN	133.3	100.0%	3	3	4	0.00%	3.1%	NVLVESEHQVK	99.7%	44.8	25	44.8	2	0	0	1281.68	1008	1018

Tyrosine-protein kinase JAK1	JAK1	JAK1_HUMAN	133.3	100.0%	3	3	4	0.00%	3.1%	YDPEGDNTGEQVAVK	99.7%	57	25	55.3	1	0	0	1621.73	894	908
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	AFCEPGNVENNGVLSFIK	99.7%	61.2	25	55.9	2	0	0	1994.96	248	265
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	AMLESIGVPLEK	99.7%	82.8	25	71.4	4	0	0	1302.70	103	114
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	APWELLELR	99.7%	51.2	25	38.9	5	0	0	1126.63	85	93
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	DFAAEVVHPGDLK	99.7%	73.3	25	51.2	2	0	0	1397.71	298	310
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	EYTLDVYR	99.7%	50.4	25	44	2	0	0	1058.52	128	135
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	GQPDEELKPK	99.7%	40.2	25	37.6	2	0	0	1140.59	475	484
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	GTDYQLSK	99.7%	41.1	25	28	2	0	0	911.45	120	127
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	GVESQGMLLCASIEGINR	99.7%	89.9	25	89.6	4	0	0	1933.95	433	450
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	HPDADSLYVEK	99.7%	51.4	25	45.4	2	0	0	1273.61	381	391
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	HVLFPLK	99.1%	35.2	25	27.2	2	0	0	853.53	266	272
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	IDVGEAEPR	99.7%	72.1	25	57.5	2	0	0	985.50	392	400
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	IITVEKHPDADSLYVEK	98.4%	25.8	25	25.8	0	1	0	1957.03	375	391
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	ISEECIAQWK	99.7%	78.8	25	72.6	2	0	0	1263.60	497	506
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	KIFTFAEK	96.4%	29.3	25	10.4	1	0	0	983.56	190	197
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	KLASAAYPDPSK	99.7%	64.2	25	57.3	2	0	0	1247.66	335	346
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	LASAAYPDPSK	99.7%	73.5	25	64.4	2	0	0	1119.57	336	346
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	LLDPIREK	98.2%	32.3	25	15.1	3	0	0	983.59	320	327
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	LSSVVTQHDSK	99.7%	56.4	25	56.4	3	0	0	1200.62	136	146
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	LSSVVTQHDSKK	99.7%	61.6	25	56.8	2	2	0	1328.72	136	147
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	LVVVLCNLKPQK	99.7%	64	25	64	2	0	0	1410.85	419	430
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	MSSSEEESKIDLLDR	99.7%	31.9	25	26.1	0	1	0	1754.81	223	237
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	NLQEVLGEEK	99.7%	53.6	25	44.8	3	0	0	1158.60	17	26
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	NSEPEEVIPSR	99.7%	61.6	25	49.3	2	0	0	1256.61	357	367
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	NSVEVALNK	99.7%	73.1	25	51.1	2	0	0	973.53	311	319
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	QVEPLDPPAGSAPGEHVFVK	99.7%	37.3	25	37.3	2	2	0	2074.06	451	470
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	SEFVILR	99.7%	40.3	25	31	1	0	0	863.50	273	279
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	SEFVILRDEK	99.7%	51.9	25	39.8	2	0	0	1235.66	273	282
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	TVVSGLVQFVPK	99.7%	97.2	25	83.4	2	0	0	1273.75	401	412
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	TYTAYVDLEK	99.7%	49.3	25	42.1	2	0	0	1202.59	288	297
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	VDAQFGGIDQR	99.7%	85.6	25	72.3	2	0	0	1205.59	179	189
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	VHLMNPMVPGLTGSK	99.4%	36.9	25	36.9	1	0	0	1580.83	208	222
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	VSYYENVIK	99.7%	43	25	39.6	1	0	0	1114.58	94	102
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	33	37	74	0.07%	62.9%	YLPALGYSK	98.8%	33.9	25	19.1	2	0	0	1011.55	198	206
U1 small nuclear ribonucleoprotein A	SNRPA	SNRPA_HUMAN	31.3	99.9%	2	2	4	0.00%	6.4%	EVSSATNALR	99.7%	64.1	25	39.5	2	0	0	1047.54	61	70
U1 small nuclear ribonucleoprotein A	SNRPA	SNRPA_HUMAN	31.3	99.9%	2	2	4	0.00%	6.4%	GQAFVIFK	99.7%	48.4	25	39.4	2	0	0	909.52	53	60
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	6	6	11	0.01%	26.7%	GLLQSGQIPGR	99.7%	70.7	25	34.9	2	0	0	1125.64	222	232
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	6	6	11	0.01%	26.7%	KLDGFPLLR	99.7%	57	25	36.3	1	0	0	1058.64	56	64
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	6	6	11	0.01%	26.7%	LTAELIEQAAQYTNAVR	99.7%	84.9	25	81	2	0	0	1890.99	4	20
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	6	6	11	0.01%	26.7%	NAIANASTLAEVER	99.7%	103	25	97.4	2	0	0	1458.75	206	219
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	6	6	11	0.01%	26.7%	SLTYLSILR	99.7%	59.4	25	41.9	2	0	0	1065.63	114	122
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	6	6	11	0.01%	26.7%	TLLVNNNR	99.0%	34.7	25	14	2	0	0	943.53	68	75
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	26	82	0.08%	46.1%	ASEVMGPVEAAPEYR	99.7%	84.3	25	84.3	8	0	0	1605.76	77	91
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	26	82	0.08%	46.1%	ELGNSLDK	97.9%	31.5	25	9.98	1	0	0	875.45	141	148
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	26	82	0.08%	46.1%	IEEYISK	99.7%	41.4	25	26.7	2	0	0	881.46	67	73
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	26	82	0.08%	46.1%	IMGVAGGLTNLSK	99.7%	91.3	25	77.1	9	0	0	1260.70	231	243
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	26	82	0.08%	46.1%	IYEYVESR	99.7%	62.7	25	52.1	7	0	0	1058.52	204	211
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	26	82	0.08%	46.1%	LEEACDMALELNASK	99.7%	87.1	25	87.1	3	0	0	1709.77	187	201
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	26	82	0.08%	46.1%	LGLTEIR	99.7%	56.6	25	24	2	0	0	801.48	366	372
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	26	82	0.08%	46.1%	LGLTEIRK	99.7%	55.1	25	44.9	6	0	0	929.58	366	373
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	26	82	0.08%	46.1%	MFAEIMMK	98.5%	33	25	1.4	3	0	0	1016.46	59	66

U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	26	82	0.08%	46.1%	MPACNIMLLGAQR	99.7%	83.5	25	68.6	6	0	0	1490.73	244	256
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	26	82	0.08%	46.1%	MSFGEIEEDAYQEDLGFSLGHLGK	99.7%	44	25	43.6	0	2	0	2672.22	378	401
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	26	82	0.08%	46.1%	MSFIAPNLSIIIGASTAAK	99.7%	74.7	25	74.7	4	0	0	1921.05	212	230
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	26	82	0.08%	46.1%	QVKPLPAPLDGQR	99.7%	50.9	25	50.9	0	4	0	1418.81	339	351
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	26	82	0.08%	46.1%	SSGTASSVAFTPLQGLEIVNPQAAEK	99.7%	40.2	25	40.2	2	2	0	2602.34	445	470
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	26	82	0.08%	46.1%	VDSFHESTEGK	99.7%	65.5	25	65.5	6	0	0	1235.55	305	315
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	26	82	0.08%	46.1%	VGYELKDEIER	99.7%	78.5	25	54.4	6	3	0	1350.69	316	326
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	26	82	0.08%	46.1%	VIVDANNLTVEIENELNIIHK	99.7%	42.6	25	40.9	0	2	0	2390.29	92	112
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	26	82	0.08%	46.1%	YFSSMAEFLK	99.7%	59	25	52.8	4	0	0	1238.58	479	488
U4/U6 small nuclear ribonucleoprotein Prp4	PRPF4	PRP4_HUMAN	58.5	100.0%	2	2	3	0.00%	4.8%	ALGEPITLFGEGPAER	99.7%	80.3	25	80.3	2	0	0	1656.86	114	129
U4/U6 small nuclear ribonucleoprotein Prp4	PRPF4	PRP4_HUMAN	58.5	100.0%	2	2	3	0.00%	4.8%	FLGTTCYDR	98.9%	34.3	25	28	1	0	0	1132.51	337	345
U4/U6.U5 tri-snRNP-associated protein 1	SART1	SNUT1_HUMAN	90.3	100.0%	4	4	6	0.01%	6.5%	EAAGTTAAAGTGGATEQPPR	99.7%	56.7	25	56.7	2	0	0	1813.87	12	31
U4/U6.U5 tri-snRNP-associated protein 1	SART1	SNUT1_HUMAN	90.3	100.0%	4	4	6	0.01%	6.5%	LEQGGTADGLR	99.7%	61.8	25	49.4	2	0	0	1116.56	351	361
U4/U6.U5 tri-snRNP-associated protein 1	SART1	SNUT1_HUMAN	90.3	100.0%	4	4	6	0.01%	6.5%	LQAQSLSTVGPR	99.7%	87.7	25	87.6	1	0	0	1256.70	374	385
U4/U6.U5 tri-snRNP-associated protein 1	SART1	SNUT1_HUMAN	90.3	100.0%	4	4	6	0.01%	6.5%	QLQQLQQLR	99.7%	48.2	25	36.7	1	0	0	1154.66	511	519
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	AALETDENLLLCAPTGAGK	99.7%	87.3	25	83.1	2	0	0	1943.97	491	509
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	ANSNLVLQADR	99.7%	66.3	25	56.7	1	0	0	1200.63	15	25
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	DEPTGEVLSLVGK	99.7%	74.6	25	64	2	0	0	1343.71	34	46
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	DILCGAADEVLAVLK	99.7%	95.8	25	86	1	0	0	1586.85	130	144
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	DTLGLFLR	99.7%	57.3	25	29.8	2	0	0	934.54	746	753
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	EEGWWVVIGDAK	98.9%	34.2	25	21.5	1	0	0	1388.68	2061	2072
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	EGSASTEVLR	99.7%	42.4	25	30.6	2	0	0	1048.53	754	763
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	FQIMNEIVYEK	99.7%	72.8	25	58.5	4	0	0	1413.71	701	711
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	FYDDAIVSQK	99.7%	57.8	25	49.2	2	0	0	1185.58	275	284
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	GTQVYSPEK	96.2%	29	25	23.7	1	0	0	1008.50	830	838
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	HLILPEK	99.6%	39.6	25	24.5	2	0	0	849.52	1288	1294
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	IIYIAPMR	99.5%	38.5	25	26.1	4	0	0	992.56	538	545
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	IVALSSSLSNAK	99.7%	105	25	99.2	2	0	0	1189.68	1487	1498
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	KADEVLEILK	99.7%	59	25	48.1	2	0	0	1157.68	285	294
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	KPVIVFVPSR	99.7%	69.9	25	67.2	2	0	0	1141.71	1557	1566
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	LELSVHLQPITR	99.7%	44.8	25	44.8	1	2	0	1405.82	1184	1195
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	LIGLSATLPNYEDVATFLR	99.7%	45.4	25	45.4	1	0	0	2093.13	648	666
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	LTAIDILTTCAADIQR	99.7%	107	25	99.1	2	0	0	1774.94	1571	1586
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	LYDLNHNEIGELIR	99.7%	37.1	25	29.7	0	2	0	1698.88	1153	1166
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	MEADPELSK	96.3%	29.1	25	21.7	1	0	0	1019.47	350	358
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	MQLSAELQSDTEEILSK	99.7%	71.9	25	69.2	2	0	0	1937.94	1902	1918
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	NALLQLTDSQIADVAR	99.7%	108	25	103	2	0	0	1727.93	1994	2009
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	NIEMTQEDVR	99.7%	47	25	39	3	0	0	1250.57	638	647
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	NQVLVFVHSR	99.7%	66.6	25	62.4	2	0	0	1198.67	719	728
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	SGGPVVVLVQLER	99.7%	50.8	25	50.8	1	0	0	1352.79	2031	2043
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	SLVQEMVGSFGK	99.7%	97.1	25	91.4	5	0	0	1281.65	546	557
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	TNLLLQAHLSR	99.7%	71.8	25	68.6	2	0	0	1265.73	1891	1901
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	TNVALMCMLR	99.7%	70.1	25	60.6	1	0	0	1208.59	510	519
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	TYTQLVR	98.3%	32.5	25	18.7	1	0	0	880.49	604	610
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	VFSLSSEFK	99.7%	41.6	25	31.1	1	0	0	1043.54	1017	1025
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	VVLLTGETSTDLK	99.7%	106	25	97.9	2	0	0	1375.77	1405	1417
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	WLSCETQLPVSFR	99.7%	63.2	25	55.6	2	0	0	1622.80	1275	1287
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	YAQAGFEGFK	99.7%	61.4	25	60.4	2	0	0	1117.53	470	479
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	34	40	66	0.07%	18.4%	YVHLFPK	98.2%	32.1	25	23.1	1	0	0	903.51	1177	1183
Ubiquinol-cytochrome-c reductase complex assembly factor 1	UQCC1	UQCC1_HUMAN	34.6	100.0%	3	4	7	0.01%	10.4%	IIEAMGFTGPLK	99.7%	75	25	71.7	4	0	0	1276.70	96	107
Ubiquinol-cytochrome-c reductase complex assembly factor 1	UQCC1	UQCC1_HUMAN	34.6	100.0%	3	4	7	0.01%	10.4%	TDFEEFFLR	99.7%	70.2	25	62.8	2	0	0	1203.57	128	136

Ubiquinol-cytochrome-c reductase complex assembly factor 1	UQCC1	UQCC1_HUMAN	34.6	100.0%	3	4	7	0.01%	10.4%	VMGVNPYILK	99.0%	35	25	23	1	0	0	1133.64	189	198
Ubiquitin carboxyl-terminal hydrolase 15	USP15	UBP15_HUMAN	112.4	100.0%	3	3	6	0.01%	3.1%	FSYVTPR	99.4%	37.4	25	29.5	2	0	0	869.45	354	360
Ubiquitin carboxyl-terminal hydrolase 15	USP15	UBP15_HUMAN	112.4	100.0%	3	3	6	0.01%	3.1%	QDTFSGTGFFPLDR	99.7%	42.5	25	42.5	2	0	0	1587.74	933	946
Ubiquitin carboxyl-terminal hydrolase 15	USP15	UBP15_HUMAN	112.4	100.0%	3	3	6	0.01%	3.1%	VEVYLTELK	99.1%	35.5	25	35.5	2	0	0	1093.61	129	137
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	2	2	3	0.00%	0.9%	LVSIPELLSAVK	94.6%	27.6	25	27.6	1	0	0	1268.78	358	369
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	2	2	3	0.00%	0.9%	VLYNLEVLSSK	99.7%	64.6	25	62.1	2	0	0	1264.71	1174	1184
Ubiquitin conjugation factor E4 A	UBE4A	UBE4A_HUMAN	122.6	100.0%	4	4	5	0.01%	4.6%	DAQQSSSPAADNLR	99.7%	69.9	25	61	1	0	0	1459.68	545	558
Ubiquitin conjugation factor E4 A	UBE4A	UBE4A_HUMAN	122.6	100.0%	4	4	5	0.01%	4.6%	IFLITLDNSDPSLK	99.7%	95.1	25	84.8	2	0	0	1575.86	91	104
Ubiquitin conjugation factor E4 A	UBE4A	UBE4A_HUMAN	122.6	100.0%	4	4	5	0.01%	4.6%	LLTFNPTYCALK	98.3%	32.3	25	31.8	1	0	0	1440.76	457	468
Ubiquitin conjugation factor E4 A	UBE4A	UBE4A_HUMAN	122.6	100.0%	4	4	5	0.01%	4.6%	VFVEYIQPK	98.7%	33.8	25	28.6	1	0	0	1122.62	309	317
Ubiquitin conjugation factor E4 B	UBE4B	UBE4B_HUMAN	146.2	99.8%	2	2	4	0.00%	1.7%	ELFEEVISK	98.8%	34.1	25	28.3	2	0	0	1093.58	1181	1189
Ubiquitin conjugation factor E4 B	UBE4B	UBE4B_HUMAN	146.2	99.8%	2	2	4	0.00%	1.7%	YFSGPAITLENTR	99.7%	43.7	25	41.7	2	0	0	1468.74	611	623
Ubiquitin thioesterase OTUB1	OTUB1	OTUB1_HUMAN	31.3	100.0%	3	4	6	0.01%	12.5%	FFEHFIEGGR	99.7%	51.3	25	41.9	2	1	0	1238.60	189	198
Ubiquitin thioesterase OTUB1	OTUB1	OTUB1_HUMAN	31.3	100.0%	3	4	6	0.01%	12.5%	IQQEIAVQNPLVSER	99.7%	70.1	25	58.9	1	0	0	1723.93	37	51
Ubiquitin thioesterase OTUB1	OTUB1	OTUB1_HUMAN	31.3	100.0%	3	4	6	0.01%	12.5%	LLTSGYLQR	99.7%	62.3	25	53.2	2	0	0	1050.59	177	185
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	6	6	50	0.05%	50.6%	CCLTYCFNKPEDK	99.7%	55.6	25	55.6	4	0	0	1734.73	144	156
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	6	6	50	0.05%	50.6%	ECPSDECGAGVFMASHFDR	99.7%	32.2	25	32.2	0	3	0	2187.85	120	138
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	6	6	50	0.05%	50.6%	IQDKEGIPPDQQR	95.6%	28.4	25	28.4	1	0	0	1523.78	30	42
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	6	6	50	0.05%	50.6%	TITLEVEPSDTIENVK	99.7%	95.2	25	85.4	20	0	0	1787.93	12	27
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	6	6	50	0.05%	50.6%	TLSDYNIQK	99.7%	55.5	25	46.1	20	0	0	1081.55	55	63
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	6	6	50	0.05%	50.6%	YYKVDENGK	99.7%	41.2	25	27.8	2	0	0	1115.54	105	113
Ubiquitin-like modifier-activating enzyme 1	UBA1	UBA1_HUMAN	117.9	100.0%	4	4	7	0.01%	6.0%	AAVATFLQSVQVPEFTPK	99.4%	37.5	25	37.5	2	0	0	1933.04	785	802
Ubiquitin-like modifier-activating enzyme 1	UBA1	UBA1_HUMAN	117.9	100.0%	4	4	7	0.01%	6.0%	LAGTQPLEVLEAVQR	99.7%	89.1	25	89.1	2	0	0	1623.91	679	693
Ubiquitin-like modifier-activating enzyme 1	UBA1	UBA1_HUMAN	117.9	100.0%	4	4	7	0.01%	6.0%	LQTSSVLVSGLR	99.7%	62.6	25	60.6	1	0	0	1259.73	70	81
Ubiquitin-like modifier-activating enzyme 1	UBA1	UBA1_HUMAN	117.9	100.0%	4	4	7	0.01%	6.0%	SLVASLAEPDFVVTDFAK	99.7%	60.8	25	60.8	2	0	0	1909.00	305	322
UDP-glucose 6-dehydrogenase	UGDH	UGDH_HUMAN	55.0	100.0%	5	5	6	0.01%	12.3%	DVLNLVYLCEALNLPEVAR	99.7%	57.1	25	54.2	1	0	0	2201.16	280	298
UDP-glucose 6-dehydrogenase	UGDH	UGDH_HUMAN	55.0	100.0%	5	5	6	0.01%	12.3%	IAILGFAFK	99.6%	39.3	25	38	2	0	0	979.60	331	339
UDP-glucose 6-dehydrogenase	UGDH	UGDH_HUMAN	55.0	100.0%	5	5	6	0.01%	12.3%	LAANAFLAQR	99.7%	64.9	25	57.1	1	0	0	1074.61	221	230
UDP-glucose 6-dehydrogenase	UGDH	UGDH_HUMAN	55.0	100.0%	5	5	6	0.01%	12.3%	VLIGGDETPEGQR	99.7%	43	25	41.3	1	0	0	1370.69	178	190
UDP-glucose 6-dehydrogenase	UGDH	UGDH_HUMAN	55.0	100.0%	5	5	6	0.01%	12.3%	VTVVDVNESR	99.7%	54.6	25	45.3	1	0	0	1117.58	32	41
UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	OGT	OGT1_HUMAN	116.9	100.0%	5	5	6	0.01%	5.1%	DSGNIPEAIASYR	99.7%	46.5	25	46.5	1	0	0	1392.68	441	453
UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	OGT	OGT1_HUMAN	116.9	100.0%	5	5	6	0.01%	5.1%	EQGNIEEAVR	98.0%	31.7	25	31.7	1	0	0	1144.56	339	348
UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	OGT	OGT1_HUMAN	116.9	100.0%	5	5	6	0.01%	5.1%	IIFSPVAPK	98.8%	34.1	25	20.4	1	0	0	971.59	900	908
UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	OGT	OGT1_HUMAN	116.9	100.0%	5	5	6	0.01%	5.1%	LVSIVADQLEK	99.7%	62.7	25	48.3	2	0	0	1214.70	489	499
UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	OGT	OGT1_HUMAN	116.9	100.0%	5	5	6	0.01%	5.1%	VPNSVLWLLR	99.7%	42.9	25	42.9	1	0	0	1196.72	868	877
Uncharacterized protein C11orf84	C11orf84	CK084_HUMAN	41.0	100.0%	4	4	6	0.01%	15.0%	DREVAEGGLPR	99.7%	54.3	25	44.7	2	0	0	1198.62	295	305
Uncharacterized protein C11orf84	C11orf84	CK084_HUMAN	41.0	100.0%	4	4	6	0.01%	15.0%	GTLDLQVIR	98.6%	33.2	25	23.4	1	0	0	1014.59	319	327
Uncharacterized protein C11orf84	C11orf84	CK084_HUMAN	41.0	100.0%	4	4	6	0.01%	15.0%	MPAEIVVLLDSEDNPSLPK	99.7%	47	25	47	2	0	0	2067.07	171	189
Uncharacterized protein C11orf84	C11orf84	CK084_HUMAN	41.0	100.0%	4	4	6	0.01%	15.0%	SNILEAWSEGVALLQDVR	99.7%	99.1	25	52.8	1	0	0	2000.04	126	143
Uncharacterized protein C19orf52	C19orf52	CS052_HUMAN	29.2	100.0%	6	6	11	0.01%	27.7%	AEAGDAVVAKPGVWAR	99.7%	62.1	25	57.3	2	0	0	1596.85	15	30
Uncharacterized protein C19orf52	C19orf52	CS052_HUMAN	29.2	100.0%	6	6	11	0.01%	27.7%	ESEAFVQR	99.7%	48.4	25	36.4	2	0	0	965.47	105	112
Uncharacterized protein C19orf52	C19orf52	CS052_HUMAN	29.2	100.0%	6	6	11	0.01%	27.7%	LALSQAHSLVQAEAPR	99.7%	57.3	25	57.3	0	2	0	1690.92	245	260
Uncharacterized protein C19orf52	C19orf52	CS052_HUMAN	29.2	100.0%	6	6	11	0.01%	27.7%	VLDVGFVGR	99.7%	51.4	25	51.4	3	0	0	961.55	163	171
Uncharacterized protein C19orf52	C19orf52	CS052_HUMAN	29.2	100.0%	6	6	11	0.01%	27.7%	VVGPQQLHSETNER	99.7%	56.9	25	56.9	1	0	0	1593.80	198	211
Uncharacterized protein C19orf52	C19orf52	CS052_HUMAN	29.2	100.0%	6	6	11	0.01%	27.7%	WWVLGAWMR	96.7%	29.6	25	19.3	1	0	0	1204.61	172	180
Uncharacterized protein C2orf47, mitochondrial	C2orf47	CB047_HUMAN	32.5	100.0%	4	5	9	0.01%	16.8%	EFTQGVKPDWTIAR	99.7%	38.9	25	38.9	2	2	0	1647.85	270	283
Uncharacterized protein C2orf47, mitochondrial	C2orf47	CB047_HUMAN	32.5	100.0%	4	5	9	0.01%	16.8%	FDLLEELVAK	99.7%	55.6	25	51.2	2	0	0	1176.65	164	173
Uncharacterized protein C2orf47, mitochondrial	C2orf47	CB047_HUMAN	32.5	100.0%	4	5	9	0.01%	16.8%	MIVLGFSNPINWVR	99.7%	42.2	25	42.2	1	0	0	1645.89	110	123
Uncharacterized protein C2orf47, mitochondrial	C2orf47	CB047_HUMAN	32.5	100.0%	4	5	9	0.01%	16.8%	QLLSASYEFQR	99.7%	73.1	25	70.7	2	0	0	1341.68	259	269
Uncharacterized protein C7orf50	C7orf50	CG050_HUMAN	22.1	100.0%	4	4	6	0.01%	35.6%	ASAEGPLLGPEAAPSGEGAGSK	99.7%	72.2	25	72.2	2	0	0	1952.96	22	43
Uncharacterized protein C7orf50	C7orf50	CG050_HUMAN	22.1	100.0%	4	4	6	0.01%	35.6%	EAGLVAQHPPAR	99.7%	57.8	25	52.6	2	0	0	1245.67	84	95

Uncharacterized protein C7orf50	C7orf50	CG050_HUMAN	22.1	100.0%	4	4	6	0.01%	35.6%	ELDEEGSDPPLPGR	98.9%	34.2	25	34.2	1	0	0	1510.70	169	182
Uncharacterized protein C7orf50	C7orf50	CG050_HUMAN	22.1	100.0%	4	4	6	0.01%	35.6%	GEAVLRPGLDAEPELSPEEQR	99.7%	42.1	25	38.3	0	1	0	2292.15	44	64
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	9	9	17	0.02%	9.6%	EQLLQSNPVLEAFGNAK	99.7%	124	25	124	2	0	0	1857.97	140	156
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	9	9	17	0.02%	9.6%	IFLLTNNNLLLADQK	99.7%	86.3	25	86.3	2	0	0	1729.98	1007	1021
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	9	9	17	0.02%	9.6%	IIIAEVVNK	99.7%	54.7	25	40.8	2	0	0	998.62	987	995
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	9	9	17	0.02%	9.6%	LGNIEFKPESR	99.7%	41.9	25	32.4	1	0	0	1289.68	281	291
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	9	9	17	0.02%	9.6%	LVMSYVAAVCGK	99.7%	52.2	25	51.2	2	0	0	1297.66	120	131
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	9	9	17	0.02%	9.6%	SEVPLVDVTK	99.7%	46.7	25	41.1	2	0	0	1086.60	1027	1036
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	9	9	17	0.02%	9.6%	SSALVIQSYIR	99.7%	71.2	25	58	2	0	0	1236.69	752	762
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	9	9	17	0.02%	9.6%	VSTTLNVAQAYYAR	99.7%	79.3	25	73.7	2	0	0	1556.81	336	349
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	9	9	17	0.02%	9.6%	YNYLSLDSAK	99.7%	41.2	25	34.3	2	0	0	1173.58	232	241
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	10	10	18	0.02%	12.2%	DGTIDFTPGSELLITK	99.7%	69.3	25	69.3	2	0	0	1706.89	1032	1047
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	10	10	18	0.02%	12.2%	GEELLSPLNLEQAAYAR	99.7%	73.8	25	67.4	2	0	0	1873.97	362	378
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	10	10	18	0.02%	12.2%	KYEAFLQR	99.7%	47.7	25	40.4	1	0	0	1054.57	667	674
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	10	10	18	0.02%	12.2%	LGTDEISPR	99.7%	92	25	69.9	2	0	0	987.51	901	909
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	10	10	18	0.02%	12.2%	LLQFYAETCPAPER	99.7%	55.4	25	46.3	2	0	0	1694.82	153	166
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	10	10	18	0.02%	12.2%	LLQSNPVLEAFGNAK	99.7%	79.6	25	78	2	0	0	1600.87	174	188
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	10	10	18	0.02%	12.2%	QLLLTPNAVVIVEDAK	97.4%	30.5	25	22.4	1	0	0	1723.00	939	954
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	10	10	18	0.02%	12.2%	TSFLLNLR	99.7%	61.5	25	57.4	2	0	0	963.56	814	821
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	10	10	18	0.02%	12.2%	VLQALGSEPIQYAVPVVK	99.7%	62.5	25	62.5	2	0	0	1911.10	910	927
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	10	10	18	0.02%	12.2%	YLGLLENLR	99.7%	44.7	25	44.7	2	0	0	1090.63	648	656
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	8	8	12	0.01%	8.1%	IGELVGVLVNHFK	99.7%	48.6	25	48.6	2	0	0	1424.83	942	954
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	8	8	12	0.01%	8.1%	LFCWIVTR	99.4%	37.2	25	31.1	1	0	0	1094.58	351	358
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	8	8	12	0.01%	8.1%	NYDTTIHGK	95.4%	28.2	25	23.3	1	0	0	1048.51	367	375
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	8	8	12	0.01%	8.1%	SYIHEVAR	99.6%	39.3	25	34.5	2	0	0	974.51	738	745
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	8	8	12	0.01%	8.1%	TLFTLEELR	98.6%	33.2	25	25.4	2	0	0	1121.62	686	694
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	8	8	12	0.01%	8.1%	VIVQQPGER	98.4%	32.7	25	26.9	2	0	0	1025.57	191	199
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	8	8	12	0.01%	8.1%	VTDEMFLEALNSK	99.7%	59.9	25	41.5	1	0	0	1496.73	466	478
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	8	8	12	0.01%	8.1%	VVSIIAELLSTK	99.7%	98	25	98	1	0	0	1272.78	296	307
Unconventional myosin-Vb	MYO5B	MYO5B_HUMAN	213.7	100.0%	6	6	8	0.01%	3.7%	AGQVAYLEK	99.7%	45.8	25	32.6	1	0	0	978.53	750	758
Unconventional myosin-Vb	MYO5B	MYO5B_HUMAN	213.7	100.0%	6	6	8	0.01%	3.7%	EYSQLEQR	98.4%	32.8	25	8.42	1	0	0	1052.50	1073	1080
Unconventional myosin-Vb	MYO5B	MYO5B_HUMAN	213.7	100.0%	6	6	8	0.01%	3.7%	ILNLYTPLNEFEER	99.1%	35.5	25	34.8	2	0	0	1750.90	1775	1788
Unconventional myosin-Vb	MYO5B	MYO5B_HUMAN	213.7	100.0%	6	6	8	0.01%	3.7%	NDPQQLLLDAK	99.6%	39.7	25	21.1	1	0	0	1254.67	1805	1815
Unconventional myosin-Vb	MYO5B	MYO5B_HUMAN	213.7	100.0%	6	6	8	0.01%	3.7%	TIQAQLQER	99.7%	40	25	24.1	2	0	0	1086.59	1796	1804
Unconventional myosin-Vb	MYO5B	MYO5B_HUMAN	213.7	100.0%	6	6	8	0.01%	3.7%	YFATVGGSASETNIEEK	99.7%	55.5	25	55.5	1	0	0	1802.84	179	195
UPF0420 protein C16orf58	C16orf58	CP058_HUMAN	51.0	100.0%	2	2	4	0.00%	4.3%	AALTVHQAR	99.6%	40	25	39.3	2	0	0	966.55	212	220
UPF0420 protein C16orf58	C16orf58	CP058_HUMAN	51.0	100.0%	2	2	4	0.00%	4.3%	GEVLDPTAANR	99.7%	57.2	25	52.4	2	0	0	1142.58	303	313
UPF0428 protein CXorf56	CXorf56	CX056_HUMAN	25.6	99.8%	2	2	2	0.00%	11.3%	EVADSYAQNAK	99.7%	42.4	25	36.2	1	0	0	1195.56	173	183
UPF0428 protein CXorf56	CXorf56	CX056_HUMAN	25.6	99.8%	2	2	2	0.00%	11.3%	NAPVTFIVDGAVVK	99.7%	42	25	39.1	1	0	0	1429.81	108	121
UPF0488 protein C8orf33	C8orf33	CH033_HUMAN	25.0	100.0%	3	3	7	0.01%	15.3%	AAAYSAQVQPVDGATR	99.7%	65.5	25	62.3	2	0	0	1604.80	183	198
UPF0488 protein C8orf33	C8orf33	CH033_HUMAN	25.0	100.0%	3	3	7	0.01%	15.3%	LPGPVSSAR	99.7%	55.8	25	24.9	4	0	0	883.50	28	36
UPF0488 protein C8orf33	C8orf33	CH033_HUMAN	25.0	100.0%	3	3	7	0.01%	15.3%	QKEQAIGAIR	99.6%	39.2	25	26.5	1	0	0	1113.64	134	143
UPF0505 protein C16orf62	C16orf62	CP062_HUMAN	109.6	100.0%	3	3	3	0.00%	3.5%	EVNTVLADVIK	99.7%	47.1	25	40.9	1	0	0	1200.68	521	531
UPF0505 protein C16orf62	C16orf62	CP062_HUMAN	109.6	100.0%	3	3	3	0.00%	3.5%	FLPFLDMFQK	98.6%	33.3	25	20.9	1	0	0	1285.67	569	578
UPF0505 protein C16orf62	C16orf62	CP062_HUMAN	109.6	100.0%	3	3	3	0.00%	3.5%	FVLITDILDTFGK	99.7%	50.1	25	50.1	1	0	0	1481.83	231	243
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	10	10	18	0.02%	23.3%	AALGPLVTGLYDVQAFK	99.7%	76.1	25	76.1	2	0	0	1762.97	6	22
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	10	10	18	0.02%	23.3%	AAWEAYLSR	99.7%	66.2	25	40.3	2	0	0	1066.53	469	477
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	10	10	18	0.02%	23.3%	FGDFVLK	99.7%	40.2	25	28.9	2	0	0	825.45	23	29
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	10	10	18	0.02%	23.3%	IASWADLVNAHVVPGSGVVK	99.7%	47	25	46.8	0	2	0	2019.10	333	352
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	10	10	18	0.02%	23.3%	KVDAETVGR	99.7%	51	25	37.3	2	0	0	974.53	188	196
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	10	10	18	0.02%	23.3%	LHSVCTLSK	99.0%	35.1	25	31.5	2	0	0	1044.55	170	178

Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	10	10	18	0.02%	23.3%	MLEILEQQK	99.7%	45.5	25	31.9	2	0	0	1131.61	179	187
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	10	10	18	0.02%	23.3%	RGSDIIIVGR	99.7%	57	25	41.8	1	0	0	1085.64	442	451
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	10	10	18	0.02%	23.3%	SGLSSPIYIDLR	99.7%	60.9	25	50.6	2	0	0	1320.72	30	41
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	10	10	18	0.02%	23.3%	VTDAIVLLDR	99.7%	77	25	46.5	1	0	0	1114.65	146	155
Uridine-cytidine kinase 2	UCK2	UCK2_HUMAN	29.3	100.0%	5	5	9	0.01%	21.8%	IVQLLGQNEVDYR	99.7%	50.7	25	43.2	2	0	0	1546.82	40	52
Uridine-cytidine kinase 2	UCK2	UCK2_HUMAN	29.3	100.0%	5	5	9	0.01%	21.8%	LFVDTDADTR	99.7%	57.7	25	51.3	1	0	0	1152.55	153	162
Uridine-cytidine kinase 2	UCK2	UCK2_HUMAN	29.3	100.0%	5	5	9	0.01%	21.8%	QVVILSQDSFYR	99.7%	87.9	25	74.3	2	0	0	1454.76	55	66
Uridine-cytidine kinase 2	UCK2	UCK2_HUMAN	29.3	100.0%	5	5	9	0.01%	21.8%	TVQIPVYDFVSHSR	99.7%	41.4	25	38	2	0	0	1647.85	106	119
Uridine-cytidine kinase 2	UCK2	UCK2_HUMAN	29.3	100.0%	5	5	9	0.01%	21.8%	YADVIIPR	99.7%	42.2	25	39.9	2	0	0	946.54	203	210
Uridine-cytidine kinase-like 1	UCKL1	UCKL1_HUMAN	61.1	100.0%	3	3	3	0.00%	5.8%	EAFAIGLGGGSASGK	99.7%	40.7	25	38.1	1	0	0	1321.67	97	111
Uridine-cytidine kinase-like 1	UCKL1	UCKL1_HUMAN	61.1	100.0%	3	3	3	0.00%	5.8%	IITTAVDKR	95.7%	28.5	25	28.5	1	0	0	1016.61	503	511
Uridine-cytidine kinase-like 1	UCKL1	UCKL1_HUMAN	61.1	100.0%	3	3	3	0.00%	5.8%	LADIVVPR	99.7%	40.6	25	40.6	1	0	0	882.54	274	281
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	7	8	14	0.01%	29.4%	EITGIGPSTTTETETIAK	99.7%	73.5	25	73.5	2	0	0	1848.94	215	232
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	7	8	14	0.01%	29.4%	ELALPGELTQSR	99.7%	68.2	25	60.8	2	0	0	1313.71	94	105
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	7	8	14	0.01%	29.4%	FESPESQASAEQPEM	99.7%	75.9	25	75.9	2	0	0	1682.69	313	327
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	7	8	14	0.01%	29.4%	HYLFYDGESVSGK	99.7%	53	25	47.8	2	0	0	1501.70	39	51
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	7	8	14	0.01%	29.4%	LFLAGYDPTPTMR	99.7%	71.5	25	71.3	4	0	0	1497.74	250	262
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	7	8	14	0.01%	29.4%	QQEIILWR	98.9%	34.4	25	20.4	1	0	0	1085.61	289	296
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	7	8	14	0.01%	29.4%	YEIMDGAPVKGESIPIR	98.7%	26.5	25	26.5	0	1	0	1890.96	233	249
Vacuolar protein sorting-associated protein 29	VPS29	VPS29_HUMAN	20.5	100.0%	4	4	6	0.01%	22.0%	FEAFEHENK	96.6%	29.5	25	23.1	1	0	0	1150.52	119	127
Vacuolar protein sorting-associated protein 29	VPS29	VPS29_HUMAN	20.5	100.0%	4	4	6	0.01%	22.0%	GDFDENLNYPEQK	99.7%	58.6	25	58.6	1	0	0	1568.69	61	73
Vacuolar protein sorting-associated protein 29	VPS29	VPS29_HUMAN	20.5	100.0%	4	4	6	0.01%	22.0%	TLAGDVHIVR	99.7%	71.9	25	66.9	2	0	0	1080.62	51	60
Vacuolar protein sorting-associated protein 29	VPS29	VPS29_HUMAN	20.5	100.0%	4	4	6	0.01%	22.0%	VVTVGQFK	96.9%	29.9	25	21.4	2	0	0	877.51	74	81
Vacuolar protein sorting-associated protein 33B	VPS33B	VP33B_HUMAN	70.6	100.0%	2	2	3	0.00%	3.4%	FIFLTTAVTNSAR	99.7%	75.8	25	67.2	2	0	0	1440.78	595	607
Vacuolar protein sorting-associated protein 33B	VPS33B	VP33B_HUMAN	70.6	100.0%	2	2	3	0.00%	3.4%	IIEQVLER	98.9%	34.6	25	19.2	1	0	0	999.58	524	531
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	11	12	22	0.02%	17.7%	ACAELHQNVNVK	99.7%	58.3	25	51.2	1	0	0	1382.68	285	296
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	11	12	22	0.02%	17.7%	AELAELPLR	99.7%	41.6	25	29	2	0	0	1011.58	574	582
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	11	12	22	0.02%	17.7%	ENDAVTIQVLNQLIQK	99.7%	70	25	60.8	1	0	0	1826.00	734	749
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	11	12	22	0.02%	17.7%	ESPESEGPIYEGLIL	99.7%	42	25	41.8	2	0	0	1632.80	782	796
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	11	12	22	0.02%	17.7%	HASNMLGELR	99.7%	44.1	25	30.5	4	0	0	1143.56	45	54
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	11	12	22	0.02%	17.7%	ILVGTNLVR	99.7%	61.9	25	44.3	2	0	0	984.62	218	226
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	11	12	22	0.02%	17.7%	IPVDTYNNILTVLK	99.7%	77.3	25	70.1	3	0	0	1602.91	404	417
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	11	12	22	0.02%	17.7%	LFDIFSQQVATVIQSR	99.7%	85.9	25	68.8	1	0	0	1852.00	324	339
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	11	12	22	0.02%	17.7%	LNLEHIATSSAVSK	99.7%	62.4	25	54.9	2	0	0	1469.80	383	396
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	11	12	22	0.02%	17.7%	LSQLEGVNVER	99.7%	63	25	57.3	2	0	0	1243.66	227	237
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	11	12	22	0.02%	17.7%	SEDPDQQYLILNTAR	99.7%	87	25	77.1	2	0	0	1762.86	500	514
Vacuolar protein-sorting-associated protein 25	VPS25	VPS25_HUMAN	20.7	100.0%	2	2	2	0.00%	10.2%	AEIITVSDGR	99.7%	54.5	25	39.2	1	0	0	1060.56	162	171
Vacuolar protein-sorting-associated protein 25	VPS25	VPS25_HUMAN	20.7	100.0%	2	2	2	0.00%	10.2%	LIYQWVSR	98.7%	33.5	25	26.1	1	0	0	1064.59	110	117
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	14	14	21	0.02%	11.9%	ADYNLTR	99.1%	35.5	25	13.1	2	0	0	852.42	1123	1129
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	14	14	21	0.02%	11.9%	DINLDVNR	98.1%	32	25	10.6	1	0	0	958.50	935	942
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	14	14	21	0.02%	11.9%	DPGVITYDLPTPPGEK	99.7%	65	25	65	2	0	0	1698.86	274	289
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	14	14	21	0.02%	11.9%	EAFLQEVWK	99.7%	43.7	25	31.8	1	0	0	1149.59	410	418
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	14	14	21	0.02%	11.9%	EVYLHAIVR	97.0%	30	25	20.2	1	0	0	1099.63	848	856
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	14	14	21	0.02%	11.9%	ICLQPPPTSR	95.0%	27.9	25	19.1	1	0	0	1168.61	40	49
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	14	14	21	0.02%	11.9%	ILPEAHQR	98.3%	32.3	25	23.4	1	0	0	963.54	700	707
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	14	14	21	0.02%	11.9%	IQQQQPPPGEK	98.5%	33	25	28.2	1	0	0	1249.65	253	263
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	14	14	21	0.02%	11.9%	LHEEGIIYR	99.7%	48.4	25	41.5	2	0	0	1129.60	462	470
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	14	14	21	0.02%	11.9%	LQQTEAELR	99.7%	55.4	25	44.7	2	0	0	1087.57	1243	1251
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	14	14	21	0.02%	11.9%	LSAAVTEAFVR	99.7%	106	25	96.8	2	0	0	1163.64	451	461
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	14	14	21	0.02%	11.9%	SSAQDPQAVLGALGR	99.7%	91.5	25	84.5	2	0	0	1469.77	123	137
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	14	14	21	0.02%	11.9%	VPLEVQEADEAK	99.7%	64.9	25	64.9	2	0	0	1327.67	1231	1242

Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	14	14	21	0.02%	11.9%	YGEAGEGPGWGGAHPR	99.7%	33	25	33	0	1	0	1597.71	24	39
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	5	5	9	0.01%	8.8%	LESEGSPETLTNLR	99.7%	105	25	96.7	2	0	0	1545.78	133	146
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	5	5	9	0.01%	8.8%	LESEGSPETLTNLRK	99.7%	55.3	25	48	1	0	0	1673.87	133	147
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	5	5	9	0.01%	8.8%	LRLESEGSPETLTNLR	99.7%	35.6	25	32.7	0	2	0	1814.96	131	146
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	5	5	9	0.01%	8.8%	QVNITVQK	99.7%	54.6	25	40.2	2	0	0	929.54	77	84
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	5	5	9	0.01%	8.8%	VSQWWER	99.7%	40.6	25	30.4	2	0	0	990.48	86	92
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	5	5	17	0.02%	15.3%	FSHGTMPLR	97.9%	31.4	25	14.1	2	0	0	1061.52	151	159
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	5	5	17	0.02%	15.3%	LLETLFVHR	99.7%	61.1	25	37.5	3	0	0	1127.66	142	150
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	5	5	17	0.02%	15.3%	LPVGTTATLYFR	99.7%	70.6	25	70.6	4	0	0	1338.74	68	79
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	5	5	17	0.02%	15.3%	SLKDEDVLQK	99.7%	58.6	25	52.8	5	0	0	1174.63	58	67
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	5	5	17	0.02%	15.3%	YDFTSSR	97.4%	30.6	25	28.1	3	0	0	875.39	117	123
Vesicle-associated membrane protein-associated protein B/C	VAPB	VAPB_HUMAN	27.2	99.8%	2	2	3	0.00%	10.3%	GPFTDVVTTNLK	99.7%	50.8	25	44.9	2	0	0	1291.69	20	31
Vesicle-associated membrane protein-associated protein B/C	VAPB	VAPB_HUMAN	27.2	99.8%	2	2	3	0.00%	10.3%	SLSSSLDDTEVKK	99.7%	44.3	25	38	1	0	0	1408.72	156	168
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	20	21	38	0.04%	28.5%	AENSSLNLIGK	99.7%	85.7	25	67.4	2	0	0	1145.62	188	198
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	20	21	38	0.04%	28.5%	DFQSGQHVIVR	99.7%	55.8	25	51.4	1	0	0	1285.66	28	38
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	20	21	38	0.04%	28.5%	DIEAMDPSILK	99.7%	51	25	44.1	1	0	0	1231.62	151	161
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	20	21	38	0.04%	28.5%	GILLYGPPGCGK	99.7%	44.7	25	33.5	2	0	0	1231.65	255	266
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	20	21	38	0.04%	28.5%	GSMAGSTGVHDTVVNQLLSK	99.7%	36.3	25	32.7	0	1	0	2001.01	338	357
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	20	21	38	0.04%	28.5%	IAEESNFPFIK	99.7%	42	25	26.4	2	0	0	1294.67	556	566
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	20	21	38	0.04%	28.5%	KLLIIGTTSR	99.7%	47.2	25	35	2	0	0	1101.70	639	648
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	20	21	38	0.04%	28.5%	LLDYVPIGPR	99.7%	58.7	25	55.2	2	0	0	1142.66	608	617
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	20	21	38	0.04%	28.5%	LLIIGTTSR	99.7%	60	25	52.8	2	0	0	973.60	640	648
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	20	21	38	0.04%	28.5%	MEIGLPDEK	99.2%	36.2	25	29.8	1	0	0	1031.51	393	401
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	20	21	38	0.04%	28.5%	MIGFSETAK	97.7%	31.1	25	26.9	1	0	0	983.49	573	581
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	20	21	38	0.04%	28.5%	NFSGAELEGLVR	99.7%	83.2	25	64.9	2	0	0	1291.66	435	446
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	20	21	38	0.04%	28.5%	QSIINPDWNFEK	99.7%	60.9	25	57.9	2	0	0	1490.73	206	217
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	20	21	38	0.04%	28.5%	SIDSNPYDTDK	99.7%	46.2	25	46.2	2	0	0	1254.55	106	116
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	20	21	38	0.04%	28.5%	SQLSCVVVDDIER	99.7%	112	25	107	2	0	0	1519.74	595	607
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	20	21	38	0.04%	28.5%	TPLVSVLLEGPPHSGK	99.7%	74	25	69.7	2	2	0	1630.92	534	549
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	20	21	38	0.04%	28.5%	VLDDGELLVQQTK	99.7%	88.5	25	88.5	4	0	0	1457.78	517	529
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	20	21	38	0.04%	28.5%	VVNGPEILNK	99.7%	43.4	25	41.1	1	0	0	1082.62	284	293
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	20	21	38	0.04%	28.5%	YVGESEANIR	99.7%	44.3	25	39.2	2	0	0	1137.55	294	303
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	20	21	38	0.04%	28.5%	YVGESEANIRK	99.7%	57.1	25	55	2	0	0	1265.65	294	304
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	DGQVINETSQHHDDLE	99.7%	68.5	25	68.5	5	2	0	1836.80	451	466
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	DNLAEDIMR	99.7%	56.5	25	53.7	6	0	0	1076.50	176	184
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	EEAENTLQSFR	99.7%	72.4	25	65.1	3	0	0	1323.62	197	207
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	EEAENTLQSFRQDVDNASLAR	99.7%	44.1	25	44.1	0	2	0	2393.13	197	217
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	EKLQEEMLQR	99.7%	50.7	25	37.9	5	0	0	1319.66	187	196
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	EMEENFAVEAANYQDTIGR	99.7%	127	25	127	8	4	0	2186.97	346	364
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	ETNLDSLPLVDTHSK	99.7%	51.9	25	45	5	2	0	1668.84	425	439
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	ETNLDSLPLVDTHSKR	99.7%	58.5	25	55.5	2	3	0	1824.95	425	440
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	EYQDLLNVK	99.7%	49.3	25	38.5	6	0	0	1121.58	382	390
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	FADLSEAANR	99.7%	75	25	58.5	7	0	0	1093.53	295	304
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	FANYIDK	99.4%	37	25	28.2	2	0	0	870.44	114	120
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	FANYIDKVR	99.7%	67.8	25	59.2	4	0	0	1125.61	114	122
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	FLEQQNK	97.7%	31.2	25	9.59	1	0	0	906.47	123	129
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	ILLAELEQLK	99.7%	70.5	25	60.7	9	0	0	1169.71	130	139
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	ILLAELEQLKGQGK	99.7%	72	25	67.9	4	4	0	1539.91	130	143
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	ISLPLPNFSSLNLR	99.7%	63.9	25	52.7	5	2	0	1570.90	411	424
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	KLLEGEESR	99.7%	58.2	25	43.8	4	0	0	1060.56	402	410
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	KVESLQEEIAFLK	99.7%	116	25	108	4	2	0	1533.85	223	235

Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	LGDLYEEEMR	99.7%	63.3	25	63.3	4	0	0	1254.57	146	155
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	LLEGEESR	99.7%	65.3	25	49.4	4	0	0	932.47	403	410
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	LLQDSVDFSLADAINTEFK	99.7%	126	25	119	22	7	0	2126.07	79	97
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	LQDEIQNMK	99.7%	65.9	25	56	4	0	0	1118.55	365	373
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	LQDEIQNMKEEMAR	99.7%	87.7	25	82.1	12	10	0	1734.82	365	378
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	LQEEMLQR	99.7%	50	25	33	5	0	0	1046.53	189	196
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	LQEEMLQREEAENTLQSFR	99.7%	53.2	25	53.2	0	3	0	2367.12	189	207
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	MALDIEIATYR	99.7%	73.3	25	28.7	4	0	0	1295.67	391	401
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	MALDIEIATYRK	99.7%	32.7	25	21.9	0	2	0	1423.76	391	402
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	MFGGPGTASRPSSSR	99.7%	37.5	25	33.8	1	3	0	1510.71	14	28
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	NLQEAEEWYK	99.7%	64.1	25	61.3	4	0	0	1309.61	283	292
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	QDVDNASLAR	99.7%	80.1	25	70.6	7	0	0	1088.53	208	217
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	QMREMEENFAVEAANYQDTIGR	99.7%	70.2	25	70.2	0	2	0	2634.16	343	364
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	QQYESVAAK	99.7%	63.7	25	48	4	0	0	1023.51	274	282
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	QVDQLTNDK	99.7%	62.4	25	49.3	2	0	0	1060.53	160	168
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	QVDQLTNDKAR	99.7%	69.3	25	50.1	4	1	0	1287.67	160	170
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	QVQSLTCEVDALK	99.7%	78.3	25	71.2	4	0	0	1490.75	322	334
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	QVQSLTCEVDALKGTNESLER	99.7%	77.8	25	73.4	2	3	0	2377.17	322	342
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	RQVDQLTNDK	99.7%	59.3	25	49.5	2	1	0	1216.63	159	168
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	SLYASSPGGVYATR	99.7%	89.8	25	89.8	15	0	0	1428.71	51	64
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	SYVTTSTR	99.7%	46.6	25	36.3	3	0	0	914.46	29	36
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	TNEKVELQELNDR	99.7%	81.9	25	81.2	4	2	0	1587.80	101	113
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	TYSLGSALRPSTSR	99.7%	49.7	25	49.7	2	3	0	1495.79	37	50
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	VELQELNDR	99.7%	59.2	25	54.1	3	0	0	1115.57	105	113
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	VESLQEEIAFLK	99.7%	50	25	35	1	0	0	1405.76	224	235
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	44	74	263	0.26%	76.0%	VEVERDNLAEDIMR	99.7%	45	25	45	5	7	0	1688.83	171	184
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	7	8	15	0.02%	32.5%	GYGFGLIK	96.0%	28.8	25	21.9	1	0	0	854.48	21	28
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	7	8	15	0.02%	32.5%	KLETAVNLAWTAGNSNTR	99.7%	46.6	25	42.9	0	2	0	1946.01	201	218
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	7	8	15	0.02%	32.5%	LTFDSSFSPNTGK	99.7%	90	25	76.8	2	0	0	1400.67	97	109
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	7	8	15	0.02%	32.5%	LTFDSSFSPNTGKK	99.7%	80.3	25	80.3	2	1	0	1528.76	97	110
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	7	8	15	0.02%	32.5%	LTLSALLDGK	99.7%	78.5	25	0	13	0	0	1030.61	257	266
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	7	8	15	0.02%	32.5%	VTQSNFAVGYK	99.7%	79.3	25	69.9	1	0	0	1213.62	164	174
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	7	8	15	0.02%	32.5%	WNTDNTLGTEITVEDQLAR	99.7%	84.2	25	84.2	2	0	0	2176.05	75	93
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	7	8	15	0.02%	32.5%	YQIDPDACFSAK	99.7%	61.8	25	60.2	4	0	0	1414.63	225	236
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	9	11	43	0.04%	34.7%	GFGFGLVK	97.7%	31.1	25	22.2	2	0	0	824.47	32	39
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	9	11	43	0.04%	34.7%	LTFDTTFSPNTGK	99.7%	108	25	95.2	4	0	0	1428.70	108	120
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	9	11	43	0.04%	34.7%	LTFDTTFSPNTGKK	99.7%	71.2	25	71.2	4	1	0	1556.80	108	121
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	9	11	43	0.04%	34.7%	LTLSALVDGK	99.7%	83.8	25	74.1	8	0	0	1016.60	268	277
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	9	11	43	0.04%	34.7%	NNFAVGYR	99.7%	52.9	25	45.3	5	0	0	940.46	178	185
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	9	11	43	0.04%	34.7%	SCSGVEFSTSGSSNTDTGK	99.7%	125	25	125	4	0	0	1907.79	46	64
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	9	11	43	0.04%	34.7%	VNNSSLIGVGYTQTLRPGVK	99.7%	98.3	25	98.3	4	4	0	2103.16	248	267
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	9	11	43	0.04%	34.7%	WCEYGLTFTEK	99.7%	54.7	25	54.7	3	0	0	1433.64	75	85
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	9	11	43	0.04%	34.7%	YQLDPTASISAK	99.7%	77.6	25	68.8	4	0	0	1293.67	236	247
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	14	50	0.05%	41.7%	GYGFGMVK	99.4%	37.7	25	26.5	2	0	0	874.41	21	28
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	14	50	0.05%	41.7%	IETSINLAWTAGSNNTR	99.7%	106	25	106	4	0	0	1847.92	202	218
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	14	50	0.05%	41.7%	LSQNNFALGYK	99.7%	65.7	25	52.4	7	0	0	1254.65	164	174
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	14	50	0.05%	41.7%	LTLDTIFVPNTGK	99.7%	93.8	25	93.8	6	0	0	1418.79	97	109
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	14	50	0.05%	41.7%	LTLDTIFVPNTGKK	99.7%	60	25	60	2	2	0	1546.88	97	110
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	14	50	0.05%	41.7%	LTLSALIDGK	99.7%	78.5	25	0	13	0	0	1030.61	257	266
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	14	50	0.05%	41.7%	SCSGVEFSTSGHAYTDTGK	99.7%	88	25	88	2	2	0	1990.84	35	53
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	14	50	0.05%	41.7%	VCNYGLTFTQK	99.7%	66.4	25	57.1	4	0	0	1330.65	64	74

Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	14	50	0.05%	41.7%	VNNASLIGLGYTQTLRPGVK	99.7%	81.2	25	81.2	1	2	0	2101.18	237	256
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	14	50	0.05%	41.7%	YKVCNYGLTFTQK	99.7%	82.5	25	78.6	2	0	0	1621.80	62	74
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	14	50	0.05%	41.7%	YMLDCR	95.3%	28.1	25	26.5	1	0	0	873.36	225	230
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	7	9	17	0.02%	12.3%	EHMGDILYK	98.4%	32.6	25	25.1	1	0	0	1105.53	572	580
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	7	9	17	0.02%	12.3%	FTMVQVWPVR	99.7%	48.3	25	42.1	2	0	0	1262.67	203	212
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	7	9	17	0.02%	12.3%	GVNVSALSR	99.7%	61.7	25	42.6	3	0	0	902.51	121	129
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	7	9	17	0.02%	12.3%	LPANHPLLTGQR	99.7%	39.1	25	34.3	2	2	0	1316.74	221	232
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	7	9	17	0.02%	12.3%	TALVANTSNMPVAAR	99.7%	62.8	25	57.1	2	0	0	1515.79	309	323
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	7	9	17	0.02%	12.3%	TVISQSLSK	98.1%	32	25	24.6	2	0	0	962.55	257	265
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	7	9	17	0.02%	12.3%	VGHSELVGEIIR	99.7%	53.7	25	47	1	2	0	1308.73	45	56
V-type proton ATPase subunit d 1	ATP6V0D1	VA0D1_HUMAN	40.3	100.0%	3	3	6	0.01%	9.4%	LYPEGLAQLAR	99.7%	48.3	25	47	2	0	0	1230.68	247	257
V-type proton ATPase subunit d 1	ATP6V0D1	VA0D1_HUMAN	40.3	100.0%	3	3	6	0.01%	9.4%	NIVWIAECIAQR	99.7%	65.3	25	57.8	2	0	0	1472.77	328	339
V-type proton ATPase subunit d 1	ATP6V0D1	VA0D1_HUMAN	40.3	100.0%	3	3	6	0.01%	9.4%	NVADYYPEYK	99.7%	43.1	25	43.1	2	0	0	1261.57	266	275
V-type proton ATPase subunit H	ATP6V1H	VATH_HUMAN	55.9	100.0%	4	4	7	0.01%	12.6%	LLEVSDDPQVLAVAAHDVGEYVR	99.4%	29.9	25	29.9	0	2	0	2495.28	397	419
V-type proton ATPase subunit H	ATP6V1H	VATH_HUMAN	55.9	100.0%	4	4	7	0.01%	12.6%	QLQSEQPQTAAAR	99.7%	62.4	25	56	3	0	0	1427.72	470	482
V-type proton ATPase subunit H	ATP6V1H	VATH_HUMAN	55.9	100.0%	4	4	7	0.01%	12.6%	VSIFFDYAR	99.7%	59	25	51.3	1	0	0	1117.57	108	116
V-type proton ATPase subunit H	ATP6V1H	VATH_HUMAN	55.9	100.0%	4	4	7	0.01%	12.6%	YNIIPVLSDILQESVK	99.7%	82.5	25	72	1	0	0	1831.02	263	278
WASH complex subunit 7	KIAA1033	WASH7_HUMAN	136.4	100.0%	6	7	12	0.01%	6.0%	DLALFFSLNPIR	99.7%	59	25	57.4	2	0	0	1405.78	706	717
WASH complex subunit 7	KIAA1033	WASH7_HUMAN	136.4	100.0%	6	7	12	0.01%	6.0%	FLEEYTSQLR	99.7%	62.4	25	56.4	2	0	0	1285.64	34	43
WASH complex subunit 7	KIAA1033	WASH7_HUMAN	136.4	100.0%	6	7	12	0.01%	6.0%	LGEPSEIDQR	99.7%	58	25	51.9	1	0	0	1143.56	303	312
WASH complex subunit 7	KIAA1033	WASH7_HUMAN	136.4	100.0%	6	7	12	0.01%	6.0%	LLPYEQSSLLELIK	99.7%	46.1	25	46.1	2	0	0	1645.94	68	81
WASH complex subunit 7	KIAA1033	WASH7_HUMAN	136.4	100.0%	6	7	12	0.01%	6.0%	MLVDVFAPEFR	99.7%	60.1	25	55.1	4	0	0	1323.68	993	1003
WASH complex subunit 7	KIAA1033	WASH7_HUMAN	136.4	100.0%	6	7	12	0.01%	6.0%	YLYNLNNQIFIER	99.4%	37.2	25	37.2	1	0	0	1699.88	796	808
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	20	0.02%	19.3%	DYSGQGVVK	99.7%	43.3	25	29.6	2	0	0	952.47	397	405
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	20	0.02%	19.3%	FATASADGQIYIYDGK	99.7%	65.5	25	65.5	1	0	0	1719.82	204	219
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	20	0.02%	19.3%	IAVVGEGR	99.6%	39.7	25	25.8	2	0	0	800.46	117	124
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	20	0.02%	19.3%	LATGSDDNCAAFFEGPPFK	99.7%	82.6	25	79.3	2	0	0	2043.91	162	180
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	20	0.02%	19.3%	LYSILGTTLKDEGK	99.7%	82.9	25	67	2	1	0	1537.85	471	484
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	20	0.02%	19.3%	SIQCLTVHK	99.7%	43.8	25	34.5	2	0	0	1085.58	322	330
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	20	0.02%	19.3%	VFASLPQVER	99.7%	46.3	25	42.3	2	0	0	1145.63	8	17
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	20	0.02%	19.3%	YAPSGFYIASGDVSGK	99.7%	133	25	127	2	0	0	1618.77	66	81
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	20	0.02%	19.3%	YEYQPFAGK	98.3%	32.4	25	24.8	2	0	0	1102.52	96	104
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	20	0.02%	19.3%	YTSLMLR	99.3%	36.3	25	23.2	2	0	0	883.47	390	396
WD repeat-containing protein 5	WDR5	WDR5_HUMAN	36.6	100.0%	4	4	8	0.01%	15.0%	DGSLIVSSSYDGLCR	99.7%	96.1	25	94.3	2	0	0	1628.76	182	196
WD repeat-containing protein 5	WDR5	WDR5_HUMAN	36.6	100.0%	4	4	8	0.01%	15.0%	FTLAGHTK	96.6%	29.5	25	17.4	2	0	0	874.48	39	46
WD repeat-containing protein 5	WDR5	WDR5_HUMAN	36.6	100.0%	4	4	8	0.01%	15.0%	IWDTASGQCLK	99.7%	50.7	25	46.8	2	0	0	1278.61	197	207
WD repeat-containing protein 5	WDR5	WDR5_HUMAN	36.6	100.0%	4	4	8	0.01%	15.0%	TLPAHSDPVSAVHFNR	99.7%	52.6	25	50.3	0	2	0	1747.89	166	181
WD repeat-containing protein 82	WDR82	WDR82_HUMAN	35.1	100.0%	8	9	15	0.02%	29.1%	KYGVDLIR	99.1%	35.3	25	22	2	0	0	963.56	63	70
WD repeat-containing protein 82	WDR82	WDR82_HUMAN	35.1	100.0%	8	9	15	0.02%	29.1%	LILISTNGSFIR	99.7%	75.8	25	66.9	2	0	0	1333.78	208	219
WD repeat-containing protein 82	WDR82	WDR82_HUMAN	35.1	100.0%	8	9	15	0.02%	29.1%	MKLTDSVLR	95.3%	28.1	25	9.15	1	0	0	1078.59	1	9
WD repeat-containing protein 82	WDR82	WDR82_HUMAN	35.1	100.0%	8	9	15	0.02%	29.1%	SFDKGPFATFK	99.7%	52.5	25	43.6	2	0	0	1244.63	178	188
WD repeat-containing protein 82	WDR82	WDR82_HUMAN	35.1	100.0%	8	9	15	0.02%	29.1%	VVALSMSPVDDTFISGSLDK	99.7%	101	25	101	4	0	0	2097.04	110	129
WD repeat-containing protein 82	WDR82	WDR82_HUMAN	35.1	100.0%	8	9	15	0.02%	29.1%	YLSLHDNKYIR	95.6%	22.3	25	17.5	0	1	0	1421.75	91	101
WD repeat-containing protein 82	WDR82	WDR82_HUMAN	35.1	100.0%	8	9	15	0.02%	29.1%	YTHAANTVVYSSNK	99.7%	64.4	25	61.1	2	0	0	1554.75	71	84
WD repeat-containing protein 82	WDR82	WDR82_HUMAN	35.1	100.0%	8	9	15	0.02%	29.1%	YTHAANTVVYSSNKIDDTIR	99.7%	42.8	25	42.8	0	1	0	2268.13	71	90
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	46	0.05%	22.7%	AFREEAIK	99.0%	35	25	11.6	2	0	0	963.53	641	648
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	46	0.05%	22.7%	ALQEKVEIK	99.4%	37.3	25	17	2	0	0	1057.63	661	669
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	46	0.05%	22.7%	ANPQVGVAFPHIK	99.5%	37.9	25	29.6	3	0	0	1377.76	401	413
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	46	0.05%	22.7%	CFSVLGFCK	99.7%	55	25	54	2	0	0	1117.52	339	347
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	46	0.05%	22.7%	EDGSGDRGDGPFR	98.9%	27.2	25	27.2	0	1	0	1364.58	172	184
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	46	0.05%	22.7%	EEASGSSVTAEEAK	99.7%	111	25	111	4	0	0	1394.63	689	702

X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	46	0.05%	22.7%	EEASGSSVTAEEAKK	99.7%	89.6	25	73.9	5	0	0	1522.72	689	703
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	46	0.05%	22.7%	FFMGNQVLK	99.7%	43.3	25	34.9	2	0	0	1083.57	355	363
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	46	0.05%	22.7%	HIEIFTDLSSR	99.7%	49.8	25	39.2	2	0	0	1317.68	131	141
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	46	0.05%	22.7%	LFQCLLHR	99.4%	37.4	25	26.9	3	0	0	1086.59	490	497
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	46	0.05%	22.7%	LGGHGPSFPLK	99.7%	41.3	25	31.7	2	0	0	1109.61	185	195
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	46	0.05%	22.7%	LTIGSNLSIR	99.7%	58.2	25	46.6	2	0	0	1073.63	251	260
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	46	0.05%	22.7%	SQLDIIIHSLK	99.7%	55.5	25	43.6	2	0	0	1266.74	145	155
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	46	0.05%	22.7%	TDTLEDLFPTTK	99.7%	71.3	25	68.4	2	0	0	1380.69	470	481
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	46	0.05%	22.7%	TLFPLIEAK	99.7%	44.8	25	29	4	0	0	1031.61	535	543
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	46	0.05%	22.7%	VITMFVQR	99.7%	56.8	25	41.4	5	0	0	993.56	37	44
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	46	0.05%	22.7%	YGSDIVPFSK	99.7%	56.1	25	46	3	0	0	1112.56	316	325
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	17	19	36	0.04%	29.4%	DIISIAEDEDLR	99.7%	50.3	25	46	1	0	0	1388.69	219	230
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	17	19	36	0.04%	29.4%	DSLIFLVDASK	99.7%	87.7	25	73.4	6	0	0	1207.66	36	46
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	17	19	36	0.04%	29.4%	DTGIFLDLMHLK	99.7%	65.8	25	61.5	4	0	0	1402.74	195	206
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	17	19	36	0.04%	29.4%	EVAALCR	99.6%	39	25	23.5	1	0	0	818.42	393	399
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	17	19	36	0.04%	29.4%	IISSDRDLLAVVFYGTEK	99.6%	31.5	25	22.1	0	1	0	2026.09	75	92
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	17	19	36	0.04%	29.4%	ILELDQFK	98.5%	33	25	10.6	2	0	0	1005.56	116	123
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	17	19	36	0.04%	29.4%	ILELDQFKGQQGQK	99.7%	73.1	25	60.4	2	0	0	1631.88	116	129
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	17	19	36	0.04%	29.4%	IMATPEQVGK	99.7%	54.3	25	40.7	4	0	0	1089.56	452	461
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	17	19	36	0.04%	29.4%	IMLFTNEDNPHGNDSAK	99.7%	48.3	25	46.6	0	2	0	1902.87	166	182
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	17	19	36	0.04%	29.4%	KQELLEALTK	99.7%	49.9	25	30.3	2	0	0	1172.69	596	605
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	17	19	36	0.04%	29.4%	LGSLVDEFK	99.5%	38.4	25	31.2	1	0	0	1007.54	518	526
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	17	19	36	0.04%	29.4%	NIYVLQELDNPGAK	99.7%	135	25	130	2	0	0	1573.82	101	114
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	17	19	36	0.04%	29.4%	QELLEALTK	99.7%	41.2	25	26	2	0	0	1044.59	597	605
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	17	19	36	0.04%	29.4%	SDSFENPVLQQHFR	99.7%	51.4	25	45.9	0	2	0	1703.81	475	488
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	17	19	36	0.04%	29.4%	TFNTSTGGLLLPSDTK	99.7%	66.5	25	45.7	1	0	0	1651.85	302	317
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	17	19	36	0.04%	29.4%	TFNTSTGGLLLPSDTKR	99.7%	83.4	25	83.4	2	0	0	1807.96	302	318
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	17	19	36	0.04%	29.4%	VEYSEEELKTHISK	99.5%	30.4	25	26.1	0	1	0	1691.85	557	570
YEATS domain-containing protein 4	YEATS4	YETS4_HUMAN	26.5	100.0%	3	4	6	0.01%	16.7%	GVTIVKPIVYGNVAR	99.7%	44.2	25	43.6	1	2	0	1585.94	18	32
YEATS domain-containing protein 4	YEATS4	YETS4_HUMAN	26.5	100.0%	3	4	6	0.01%	16.7%	LFQSDTNAMLGK	99.7%	44.3	25	33.3	1	0	0	1324.66	120	131
YEATS domain-containing protein 4	YEATS4	YETS4_HUMAN	26.5	100.0%	3	4	6	0.01%	16.7%	MAEFGPDSGGR	99.7%	42.4	25	38.1	2	0	0	1139.48	5	15
YTH domain-containing family protein 2	YTHDF2	YTHD2_HUMAN	62.3	100.0%	3	3	7	0.01%	5.9%	LENNENKPVTNSR	99.7%	33	25	31.5	0	2	0	1514.76	515	527
YTH domain-containing family protein 2	YTHDF2	YTHD2_HUMAN	62.3	100.0%	3	3	7	0.01%	5.9%	LGSTEVASNVPK	99.7%	77.9	25	65.1	3	0	0	1201.64	194	205
YTH domain-containing family protein 2	YTHDF2	YTHD2_HUMAN	62.3	100.0%	3	3	7	0.01%	5.9%	SYSEDDIHR	99.7%	42.2	25	42.2	2	0	0	1121.49	417	425
Zinc finger CCCH domain-containing protein 8	ZC3H8	ZC3H8_HUMAN	33.6	99.8%	2	2	3	0.00%	7.9%	ELQQYIQAR	99.7%	60.2	25	47.1	2	0	0	1148.61	93	101
Zinc finger CCCH domain-containing protein 8	ZC3H8	ZC3H8_HUMAN	33.6	99.8%	2	2	3	0.00%	7.9%	EMANAAQPEESTKK	97.8%	31.2	25	30	1	0	0	1533.72	102	115
Zinc finger protein 768	ZNF768	ZN768_HUMAN	60.2	100.0%	2	2	4	0.00%	4.1%	AFSQSSDLIR	99.7%	44.5	25	24.9	2	0	0	1123.57	521	530
Zinc finger protein 768	ZNF768	ZN768_HUMAN	60.2	100.0%	2	2	4	0.00%	4.1%	FGQSSVLAIHAR	99.7%	61.3	25	56.4	2	0	0	1285.70	438	449

Table S-1-2. List of proteins identified in immunoprecipitation product of control vector (Replicate 2)

Protein name	Gene name	Accession number	M.W. (kDa)	Protein probability	No. of unique peptide	No. of unique spectra	No. of total spectra	Percentage of total spectra	Sequence coverage	Peptide sequence	Best peptide probability	Mascot			No. of spectra			Calculated +1H peptide mass (AMU)	Peptide index	
												ion score	identity score	delta ion score	+2H	+3H	+4H		start	stop
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	PDK1	PDK1_HUMAN	49.2	100.0%	5	5	7	0.01%	14.7%	AIYDFTDTVIR	99.7%	66.8	25	62.1	1	0	0	1313.67	134	144
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	PDK1	PDK1_HUMAN	49.2	100.0%	5	5	7	0.01%	14.7%	AVPLAGFGYGLPISR	99.7%	56.9	25	54.5	2	0	0	1517.85	349	363
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	PDK1	PDK1_HUMAN	49.2	100.0%	5	5	7	0.01%	14.7%	EISLLPDNLLR	99.7%	40.3	25	36.9	1	0	0	1282.74	93	103
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	PDK1	PDK1_HUMAN	49.2	100.0%	5	5	7	0.01%	14.7%	LYAQYFQGDLK	99.7%	47.4	25	38.5	2	0	0	1345.68	364	374
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	PDK1	PDK1_HUMAN	49.2	100.0%	5	5	7	0.01%	14.7%	LYSLEGYGTDAVIYIK	99.7%	40.1	25	40.1	1	0	0	1804.94	375	390
10 kDa heat shock protein, mitochondrial	HSPE1	CH10_HUMAN	10.9	100.0%	5	5	7	0.01%	51.0%	GGEIQPVSVK	99.7%	55.2	25	40.1	2	0	0	1013.56	57	66
10 kDa heat shock protein, mitochondrial	HSPE1	CH10_HUMAN	10.9	100.0%	5	5	7	0.01%	51.0%	GKGGEIQPVSVK	99.7%	40.5	25	40.5	1	0	0	1198.68	55	66
10 kDa heat shock protein, mitochondrial	HSPE1	CH10_HUMAN	10.9	100.0%	5	5	7	0.01%	51.0%	VGDKVLLPEYGGTK	96.3%	28.8	25	28.8	1	0	0	1475.81	67	80
10 kDa heat shock protein, mitochondrial	HSPE1	CH10_HUMAN	10.9	100.0%	5	5	7	0.01%	51.0%	VLQATVVAVGSGSK	99.7%	109	25	104	2	0	0	1315.76	41	54
10 kDa heat shock protein, mitochondrial	HSPE1	CH10_HUMAN	10.9	100.0%	5	5	7	0.01%	51.0%	VVLDDKDYFLFR	99.3%	35.9	25	35.9	1	0	0	1529.80	81	92
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	65	0.07%	32.2%	AFIPAIDSFGFETDLR	99.7%	95.7	25	95.6	4	0	0	1798.90	873	888
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	65	0.07%	32.2%	DSIVQGFQWGTR	99.7%	75.5	25	67.1	2	0	0	1393.69	764	775
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	65	0.07%	32.2%	EGPLCDELIR	99.7%	42.2	25	35.5	2	0	0	1201.59	776	785
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	65	0.07%	32.2%	FFDDPMLLELAK	99.7%	70.8	25	63.7	6	0	0	1438.73	952	963
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	65	0.07%	32.2%	GGGQIIPTAR	98.6%	32.8	25	23.9	5	0	0	969.55	804	813
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	65	0.07%	32.2%	GHVTQDAPIPGSPLYTIK	99.3%	29.8	25	24.6	0	2	0	1894.01	855	872
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	65	0.07%	32.2%	GLSEDVSISK	99.7%	56.2	25	42.9	2	0	0	1034.54	942	951
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	65	0.07%	32.2%	GNEEAQIFRPLK	99.7%	53.3	25	42.2	3	0	0	1401.75	570	581
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	65	0.07%	32.2%	IAVEPVNPSELPK	99.7%	62.6	25	59.7	3	0	0	1392.77	590	602
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	65	0.07%	32.2%	ILAQVVGDVDTSLPR	99.7%	62.6	25	59.3	1	0	0	1582.88	380	394
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	65	0.07%	32.2%	ILDAVVAQEPLHR	99.7%	59.1	25	58	2	2	0	1460.82	791	803
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	65	0.07%	32.2%	ITMIAEPLEK	99.7%	46	25	40.5	4	0	0	1144.63	685	694
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	65	0.07%	32.2%	IYADTFGDINYQEFAK	99.7%	117	25	116	2	0	0	1894.89	326	341
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	65	0.07%	32.2%	LGEFFQTK	99.7%	54.8	25	43.6	2	0	0	969.50	714	721
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	65	0.07%	32.2%	MYSTDDGVQFHAFGR	99.2%	29.3	25	29.3	0	2	0	1746.75	481	495
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	65	0.07%	32.2%	SFVEFILEPLYK	99.7%	67	25	55.6	4	0	0	1484.80	368	379
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	65	0.07%	32.2%	STPVTVVLPDTK	99.7%	67.5	25	62.5	3	0	0	1256.71	183	194
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	65	0.07%	32.2%	VADPVVTFCETVVETSSLK	99.7%	56	25	50.7	3	0	0	2081.05	655	673
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	65	0.07%	32.2%	VLGENYTLEDEEDSQICTVGR	99.7%	118	25	118	1	0	0	2427.10	509	529
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	65	0.07%	32.2%	VLSGTIHAGQPVK	99.7%	90.7	25	85.8	3	0	0	1306.75	496	508
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	65	0.07%	32.2%	VPAGNWVLIEGVDQPIVK	99.7%	61.7	25	61.7	2	0	0	1934.07	544	561
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	65	0.07%	32.2%	VVYSAFLMATPR	96.9%	29.6	25	23.3	1	0	0	1354.72	815	826
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	65	0.07%	32.2%	YDWDLLAAR	99.7%	63.6	25	56.3	3	0	0	1122.56	722	730
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	65	0.07%	32.2%	YHIEVNR	96.4%	29	25	15.1	1	0	0	930.48	537	543
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	7	7	12	0.01%	35.3%	DSTLIMQLLR	98.1%	31.5	25	20.3	2	0	0	1205.66	216	225
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	7	7	12	0.01%	35.3%	EAAENSLVAYK	99.7%	63.4	25	58.7	2	0	0	1194.60	143	153
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	7	7	12	0.01%	35.3%	HLIPAANTGESK	99.2%	35.3	25	26.1	1	0	0	1237.65	107	118
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	7	7	12	0.01%	35.3%	IISSIEQKEENK	99.7%	39.8	25	37.3	2	0	0	1417.75	62	73
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	7	7	12	0.01%	35.3%	LICCDILDVLDK	99.7%	69.5	25	63.3	2	0	0	1476.74	95	106
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	7	7	12	0.01%	35.3%	QMVETELK	95.3%	27.9	25	13.1	2	0	0	977.50	87	94
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	7	7	12	0.01%	35.3%	VAGMDVELTVEER	99.7%	89.8	25	75.7	2	0	0	1463.70	30	42
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	7	7	12	0.01%	35.3%	YLAEFATGNDRK	99.4%	36.6	25	30.5	1	0	0	1384.69	131	142
14-3-3 protein eta	YWHAH	1433F_HUMAN	28.2	100.0%	3	3	5	0.01%	18.7%	AVTELNEPLSNEDR	99.7%	51	25	45.9	1	0	0	1586.77	29	42
14-3-3 protein eta	YWHAH	1433F_HUMAN	28.2	100.0%	3	3	5	0.01%	18.7%	DSTLIMQLLR	98.1%	31.5	25	20.3	2	0	0	1205.66	218	227
14-3-3 protein eta	YWHAH	1433F_HUMAN	28.2	100.0%	3	3	5	0.01%	18.7%	NSVVEASEAAYK	99.7%	51	25	35.4	2	0	0	1267.62	144	155

14-3-3 protein eta	YWHAH	1433F_HUMAN	28.2	100.0%	3	3	5	0.01%	18.7%	YLAEVASGEK	99.7%	53.8	25	44.7	2	0	0	1066.54	133	142
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	3	3	8	0.01%	18.4%	AVTEQGAELSNEER	99.7%	101	25	92.2	4	0	0	1532.72	28	41
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	3	3	8	0.01%	18.4%	DSTLIMQLLR	98.1%	31.5	25	20.3	2	0	0	1205.66	213	222
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	3	3	8	0.01%	18.4%	YDDMATCMK	95.5%	28	25	28	1	0	0	1134.43	19	27
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	3	3	8	0.01%	18.4%	YLAEVACGDDRK	99.7%	50.9	25	48.5	3	0	0	1396.65	128	139
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	4	4	9	0.01%	22.0%	DSTLIMQLLR	98.1%	31.5	25	20.3	2	0	0	1205.66	213	222
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	4	4	9	0.01%	22.0%	GIVDQSQQAYQEAFEISK	99.7%	77.1	25	77.1	1	0	0	2040.99	140	157
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	4	4	9	0.01%	22.0%	SVTEQGAELSNEER	99.7%	96.8	25	96.8	2	0	0	1548.71	28	41
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	4	4	9	0.01%	22.0%	YLAEVAAGDDKK	99.7%	64.5	25	54.3	4	0	0	1279.65	128	139
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	5	5	8	0.01%	12.4%	AGQVFLEELGNHK	99.7%	98.6	25	88.8	2	0	0	1441.74	205	217
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	5	5	8	0.01%	12.4%	AIFTGYYGK	96.9%	29.5	25	20	1	0	0	1019.52	392	400
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	5	5	8	0.01%	12.4%	GAFSEEYKR	99.7%	56.1	25	44.2	2	0	0	1086.52	94	102
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	5	5	8	0.01%	12.4%	GEEVGELSR	99.5%	37.1	25	12.7	2	0	0	975.47	361	369
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	5	5	8	0.01%	12.4%	NQWQLSADDLKK	99.7%	39.8	25	33.1	1	0	0	1445.74	165	176
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	8	10	37	0.04%	26.7%	ALQSVGQIVGEVLK	99.7%	90	25	88.7	6	0	0	1440.84	49	62
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	8	10	37	0.04%	26.7%	AVASQLDCNFLK	99.7%	73.3	25	62.7	4	0	0	1365.68	186	197
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	8	10	37	0.04%	26.7%	EVIELPLTNPELFQR	99.7%	54.8	25	54.8	5	0	0	1797.97	147	161
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	8	10	37	0.04%	26.7%	HGEIDYEAIVK	99.7%	74.3	25	66.9	4	0	0	1273.64	323	333
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	8	10	37	0.04%	26.7%	KIHIDLPNEQAR	99.7%	43	25	40.6	0	2	0	1433.79	298	309
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	8	10	37	0.04%	26.7%	NVCTEAGMFAIR	99.7%	70.3	25	62	7	0	0	1384.63	345	356
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	8	10	37	0.04%	26.7%	VALDMTTLTIMR	99.7%	102	25	98.3	3	0	0	1364.73	98	109
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	8	10	37	0.04%	26.7%	VVSSSIVDKYIGESAR	99.7%	82.4	25	82.4	2	4	0	1709.91	198	213
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	16	32	0.03%	40.9%	AICTEAGLMALR	99.7%	70.1	25	57.2	2	0	0	1321.66	397	408
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	16	32	0.03%	40.9%	AVANQTSATFLR	99.7%	88.8	25	79	5	0	0	1278.68	238	249
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	16	32	0.03%	40.9%	GVILYGPPGTGK	99.7%	59.1	25	0	5	0	0	1158.65	221	232
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	16	32	0.03%	40.9%	IETLDPALIRPGR	99.7%	42.5	25	41.6	0	2	0	1450.84	334	346
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	16	32	0.03%	40.9%	IFQIHTSR	99.7%	45.1	25	27.6	2	0	0	1001.55	364	371
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	16	32	0.03%	40.9%	KIEFPLPDEK	99.7%	40.4	25	20.1	2	0	0	1215.66	350	359
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	16	32	0.03%	40.9%	KQEGTPEGLYL	99.7%	45.3	25	38.7	2	0	0	1234.63	430	440
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	16	32	0.03%	40.9%	KYEPPVPTR	99.5%	37.5	25	19.4	2	0	0	1086.59	24	32
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	16	32	0.03%	40.9%	LPLVTPHTQCR	99.7%	53.4	25	44.2	2	0	0	1321.70	49	59
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	16	32	0.03%	40.9%	MTLADDVTLDDLIMAK	99.7%	85.1	25	84.5	3	0	0	1764.88	372	387
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	16	32	0.03%	40.9%	TMLELLNQLDGFDSR	99.7%	107	25	99.2	4	0	0	1751.86	308	322
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	16	32	0.03%	40.9%	VAEEHAPSIVFIDEIDAIGTK	99.7%	67.2	25	67.2	0	2	0	2254.16	273	293
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	16	32	0.03%	40.9%	VAEEHAPSIVFIDEIDAIGTKR	99.7%	93.1	25	93.1	0	1	0	2410.26	273	294
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	16	32	0.03%	40.9%	VHAVIGVLMDDTDPLVTVMK	99.7%	50.7	25	43.9	0	1	0	2153.13	156	175
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	16	32	0.03%	40.9%	VVGSELIQK	99.7%	69.2	25	50.9	2	0	0	972.57	250	258
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	26	54	0.06%	51.5%	AMEVDERPTEQYSDIGGLDK	99.7%	38.3	25	38.3	0	1	0	2269.03	174	193
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	26	54	0.06%	51.5%	APSIIFIDELDAIGTK	99.7%	95	25	90.8	2	0	0	1702.93	279	294
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	26	54	0.06%	51.5%	AVCVEAGMIALR	99.7%	70.9	25	65.3	1	0	0	1289.67	398	409
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	26	54	0.06%	51.5%	CTDDFNGAQCK	99.3%	36	25	36	1	0	0	1315.50	387	397
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	26	54	0.06%	51.5%	DSYLILETLPTEYDSR	99.7%	77	25	77	4	0	0	1914.93	156	171
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	26	54	0.06%	51.5%	EKAPSIIFIDELDAIGTK	99.7%	38.9	25	38.9	0	2	0	1960.06	277	294
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	26	54	0.06%	51.5%	EKFENLGIQPPK	99.7%	40.4	25	32.5	2	0	0	1399.76	210	221
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	26	54	0.06%	51.5%	FENLGIQPPK	99.7%	62	25	37.4	2	0	0	1142.62	212	221
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	26	54	0.06%	51.5%	GVLMYGPPGTGK	99.7%	75.4	25	65.4	4	0	0	1192.60	222	233
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	26	54	0.06%	51.5%	KMNVSPDVNYEELAR	99.7%	62.7	25	57	1	4	0	1780.85	372	386
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	26	54	0.06%	51.5%	LAGPQLVQMFIGDGAK	99.7%	79.5	25	79.5	4	0	0	1644.88	251	266
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	26	54	0.06%	51.5%	LLDSEIK	97.7%	30.7	25	11.5	2	0	0	817.47	47	53
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	26	54	0.06%	51.5%	MSTEEIIQR	99.7%	60.9	25	44.2	4	0	0	1122.55	36	44
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	26	54	0.06%	51.5%	QIQELVEAIVLPMNHK	99.7%	56.6	25	56.6	0	3	0	1862.02	194	209

26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	26	54	0.06%	51.5%	QTYFLPVIGLVDAEK	99.7%	96.7	25	82	4	0	0	1692.92	130	144
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	26	54	0.06%	51.5%	TMLELLNQLDGFQPNTQVK	99.7%	100	25	100	4	0	0	2189.13	309	327
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	26	54	0.06%	51.5%	VDILDPALLR	99.7%	64.2	25	49.7	4	0	0	1124.67	335	344
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	26	54	0.06%	51.5%	VIAATNRVDILDPALLR	99.7%	79.9	25	79.9	1	2	0	1850.09	328	344
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	26	54	0.06%	51.5%	VTHELQAMKDK	99.7%	50	25	41.2	2	0	0	1299.67	62	72
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	18	35	0.04%	36.1%	ADTLDPALLRPGR	99.4%	36.8	25	34.7	2	0	0	1394.78	314	326
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	18	35	0.04%	36.1%	AVAHHTTAAFIR	99.7%	53	25	49.5	2	2	0	1294.70	218	229
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	18	35	0.04%	36.1%	EAVELPLTHFELYK	99.7%	59.2	25	56.2	2	0	0	1688.89	179	192
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	18	35	0.04%	36.1%	EFLHAQEEVKR	99.7%	55.7	25	38.8	2	0	0	1385.72	71	81
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	18	35	0.04%	36.1%	ELLKPNASVALHK	99.7%	55.2	25	55.2	0	2	0	1419.83	122	134
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	18	35	0.04%	36.1%	ENAPAIIFIDEIDAIATK	99.7%	82.9	25	82.9	3	1	0	1944.03	256	273
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	18	35	0.04%	36.1%	FDAQTGADREVQR	97.5%	30.4	25	26.2	2	0	0	1492.71	275	287
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	18	35	0.04%	36.1%	GVLMYGPPGCGK	99.7%	50.1	25	47.2	4	0	0	1251.59	201	212
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	18	35	0.04%	36.1%	ILLELLNQMDGFDQNVNVK	99.7%	110	25	110	4	2	0	2219.14	288	306
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	18	35	0.04%	36.1%	ILSTIDRELLKPNASVALHK	96.1%	23.2	25	23.2	0	1	0	2218.29	115	134
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	18	35	0.04%	36.1%	LIFSTITSK	99.7%	50.6	25	42	2	0	0	1009.59	343	351
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	18	35	0.04%	36.1%	RLIFSTITSK	99.6%	38.4	25	38.3	2	0	0	1165.69	342	351
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	18	35	0.04%	36.1%	VVGSEFVQK	99.7%	71.2	25	59.1	2	0	0	992.54	230	238
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	27	55	0.06%	57.7%	ACLIFFDEIDAIGGAR	99.7%	87.2	25	82.6	1	0	0	1767.87	269	284
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	27	55	0.06%	57.7%	ALDEGDIALLK	99.7%	67.8	25	57.3	2	0	0	1157.64	24	34
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	27	55	0.06%	57.7%	DIRFELLAR	99.6%	38.1	25	33.3	2	0	0	1132.65	367	375
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	27	55	0.06%	57.7%	FDDGAGGDNEVQR	99.7%	83.3	25	83.2	3	0	0	1379.58	285	297
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	27	55	0.06%	57.7%	FVNLGIEPPK	99.7%	59.3	25	35.9	4	0	0	1113.63	201	210
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	27	55	0.06%	57.7%	FVNLGIEPPKGVLLFGPPGTGK	99.3%	29.5	25	29.5	0	1	0	2237.27	201	222
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	27	55	0.06%	57.7%	FVVDLSDQVAPTDIEEGMR	99.7%	89.9	25	81.9	4	0	0	2121.02	121	139
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	27	55	0.06%	57.7%	GVLLFGPPGTGK	99.7%	72.3	25	67.9	4	0	0	1142.66	211	222
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	27	55	0.06%	57.7%	IATEKDFLEAVNK	99.7%	61.8	25	54.6	2	2	0	1477.79	403	415
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	27	55	0.06%	57.7%	IEFSLPDLEGR	99.7%	43.7	25	34.2	2	0	0	1275.66	341	351
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	27	55	0.06%	57.7%	IINADSEDPKYIINVK	99.7%	90.2	25	90.2	2	0	0	1831.98	101	116
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	27	55	0.06%	57.7%	KINELTGIK	99.7%	40.2	25	23.4	1	0	0	1015.61	58	66
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	27	55	0.06%	57.7%	LCPNSTGAEIR	99.7%	53.1	25	36.7	2	0	0	1217.59	376	386
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	27	55	0.06%	57.7%	LREVVETPLLHPER	99.7%	40.2	25	40.2	1	2	0	1687.95	187	200
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	27	55	0.06%	57.7%	PDYLGADQRK	99.7%	46.2	25	36.8	2	0	0	1162.59	2	11
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	27	55	0.06%	57.7%	QTLQSEQPLQVAR	99.7%	61.6	25	60.9	2	0	0	1497.80	85	97
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	27	55	0.06%	57.7%	QVEDDIQQLLK	99.7%	83.3	25	71.5	2	0	0	1328.71	47	57
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	27	55	0.06%	57.7%	SVCTEAGMFAIR	99.7%	68.2	25	68.2	5	0	0	1357.62	387	398
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	27	55	0.06%	57.7%	TDACFIR	99.7%	48.4	25	35.9	2	0	0	882.41	233	239
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	27	55	0.06%	57.7%	TMLELINQLDGFDPR	99.7%	82.7	25	82.7	3	0	0	1777.88	298	312
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	27	55	0.06%	57.7%	TYGQSTYSR	99.7%	53.5	25	41	2	0	0	1062.49	35	43
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	27	55	0.06%	57.7%	VIGSELVQK	99.7%	39.6	25	25.2	2	0	0	972.57	240	248
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	24	50	0.05%	50.7%	AVAHHTDCTFIR	99.7%	40.8	25	27.4	2	2	0	1427.68	202	213
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	24	50	0.05%	50.7%	EELQLLQEQGSYVGEVVR	99.7%	102	25	99.3	1	0	0	2076.06	61	78
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	24	50	0.05%	50.7%	EHAPSIIFMDEIDSIGSSR	99.7%	33.2	25	33.2	0	2	0	2120.00	240	258
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	24	50	0.05%	50.7%	ELFVMAR	99.6%	38.8	25	30.8	4	0	0	881.46	233	239
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	24	50	0.05%	50.7%	FVVDVDKNIDINDVTPNCR	99.7%	39.5	25	38.2	0	2	0	2233.09	95	113
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	24	50	0.05%	50.7%	GVCTEAGMYALR	99.7%	66.5	25	63.2	4	0	0	1327.61	361	372
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	24	50	0.05%	50.7%	GVLLYGPPGTGK	99.7%	59.1	25	0	5	0	0	1158.65	185	196
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	24	50	0.05%	50.7%	IAELMPGASGAEVK	99.7%	69.1	25	49.8	4	0	0	1388.71	347	360
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	24	50	0.05%	50.7%	IDILDSALLRPGR	99.7%	54.7	25	49.5	2	2	0	1438.84	298	310
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	24	50	0.05%	50.7%	IEELQLIVNDK	99.7%	95.8	25	86.6	2	0	0	1313.73	28	38
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	24	50	0.05%	50.7%	IEELQLIVNDKSQNLR	99.7%	49.7	25	49	0	1	0	1912.05	28	43

26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	24	50	0.05%	50.7%	LEGGSGGDSEVQR	99.7%	52.5	25	52.5	4	0	0	1290.59	259	271
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	24	50	0.05%	50.7%	TMLELLNQLDGFEATK	99.7%	122	25	119	5	0	0	1838.92	272	287
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	24	50	0.05%	50.7%	VALRNDSYTLHK	99.7%	37	25	20.2	0	2	0	1416.76	114	125
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	24	50	0.05%	50.7%	VPDSTYEMIGGLDK	99.7%	89.2	25	83.2	4	0	0	1540.72	143	156
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	24	50	0.05%	50.7%	VSGSELVQK	99.7%	62.7	25	35.5	2	0	0	946.52	214	222
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	25	30	58	0.06%	36.5%	AAVESLGFILFR	99.7%	84.6	25	80.7	9	0	0	1322.75	617	628
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	25	30	58	0.06%	36.5%	DNLEWLAR	99.7%	47.7	25	37.2	2	0	0	1016.52	388	395
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	25	30	58	0.06%	36.5%	DTSEDIEELVEPVAAHGPK	99.7%	80.4	25	80.3	2	2	0	2035.98	916	934
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	25	30	58	0.06%	36.5%	EAINLLEPMTNDPVNYVR	99.7%	79.1	25	79.1	4	0	0	2088.04	667	684
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	25	30	58	0.06%	36.5%	EALQLMATYLPK	99.7%	56.8	25	54.4	4	0	0	1377.74	418	429
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	25	30	58	0.06%	36.5%	FTATASLGVIHK	99.5%	31.5	25	28.5	0	2	0	1244.70	402	413
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	25	30	58	0.06%	36.5%	GLAVGIALVMYGR	99.7%	72.4	25	68.8	2	0	0	1335.75	547	559
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	25	30	58	0.06%	36.5%	LCMSLMQNK	96.7%	29.3	25	29.3	1	0	0	1156.52	183	191
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	25	30	58	0.06%	36.5%	LLHVAVSDVNDDVRR	99.7%	42.5	25	42.5	0	2	0	1707.91	602	616
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	25	30	58	0.06%	36.5%	MEEADALIESLCR	99.7%	102	25	91.5	4	0	0	1552.70	560	572
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	25	30	58	0.06%	36.5%	NAQAIEDMVGYAQETQHEK	96.6%	23.7	25	23.7	0	1	0	2161.98	525	543
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	25	30	58	0.06%	36.5%	NNNTDLMILK	98.4%	32.3	25	23.1	1	0	0	1175.61	345	354
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	25	30	58	0.06%	36.5%	QAIGIALETR	99.7%	54.4	25	32.2	1	0	0	1071.62	149	158
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	25	30	58	0.06%	36.5%	QDVYDLLK	99.7%	49	25	31.6	2	0	0	993.53	491	498
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	25	30	58	0.06%	36.5%	QFAALVASK	99.7%	47.6	25	32.8	2	0	0	934.54	58	66
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	25	30	58	0.06%	36.5%	RLDVFEK	96.1%	28.6	25	10.8	1	0	0	906.50	159	165
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	25	30	58	0.06%	36.5%	SNCKPSTFAYPAPLEVPK	99.3%	29.8	25	13.9	0	2	0	2006.01	804	821
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	25	30	58	0.06%	36.5%	TILESNDVPGMLAYSLK	99.7%	90.2	25	88.1	2	0	0	1850.96	166	182
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	25	30	58	0.06%	36.5%	TPEASPEPK	99.7%	39.7	25	39	2	0	0	955.47	311	319
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	25	30	58	0.06%	36.5%	TPEQCPSVVSLLSESYNPHVR	99.7%	65.9	25	65.9	0	2	0	2399.17	629	649
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	25	30	58	0.06%	36.5%	TVGTPIASVPGSTNTGTVPGSEKDSDSMETEEK	99.7%	50.3	25	50.3	0	1	0	3324.53	270	302
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	25	30	58	0.06%	36.5%	VINDKHDDVMAK	99.7%	45.9	25	40.7	2	0	0	1384.69	716	727
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	25	30	58	0.06%	36.5%	VSTAVLSITAK	99.7%	93.7	25	90.7	2	0	0	1089.65	828	838
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	25	30	58	0.06%	36.5%	YGAAMALGICCAGTGNK	99.7%	99.3	25	85.8	2	0	0	1714.77	650	666
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	25	30	58	0.06%	36.5%	YQPFKPLSIGGIIILK	99.2%	35.4	25	35.4	1	0	0	1787.08	900	915
26S proteasome non-ATPase regulatory subunit 10	PSMD10	PSD10_HUMAN	24.4	100.0%	3	3	5	0.01%	21.2%	ASTNIQDTEGNTPLHLACDEERVEEAK	99.7%	59.8	25	56.8	0	1	0	3027.40	163	189
26S proteasome non-ATPase regulatory subunit 10	PSMD10	PSD10_HUMAN	24.4	100.0%	3	3	5	0.01%	21.2%	LEELKESILADK	99.7%	64.7	25	51.7	2	0	0	1387.77	19	30
26S proteasome non-ATPase regulatory subunit 10	PSMD10	PSD10_HUMAN	24.4	100.0%	3	3	5	0.01%	21.2%	MIHILLYYK	99.7%	41.9	25	31.2	2	0	0	1193.68	154	162
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	6	6	10	0.01%	16.8%	EQSILELGSLLAK	99.7%	46.2	25	42.2	2	0	0	1400.80	47	59
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	6	6	10	0.01%	16.8%	LYDNLLEQNLIR	99.7%	59.6	25	55	2	0	0	1503.82	326	337
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	6	6	10	0.01%	16.8%	TGQAAELGGLLK	99.7%	54.2	25	47	1	0	0	1157.65	60	71
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	6	6	10	0.01%	16.8%	TYHALSNLPK	99.7%	39.9	25	30.9	2	0	0	1143.62	176	185
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	6	6	10	0.01%	16.8%	VQIEHISSLIK	99.7%	42.8	25	40	2	0	0	1266.74	345	355
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	6	6	10	0.01%	16.8%	YQEALHLGSQLLR	99.7%	35.4	25	32.7	0	1	0	1527.83	143	155
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	8	9	15	0.02%	23.7%	DLPVSEQQER	99.7%	53.6	25	51.8	2	0	0	1200.59	187	196
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	8	9	15	0.02%	23.7%	FLGCVDIKDLPVSEQQER	99.7%	38.2	25	38.2	0	1	0	2133.06	179	196
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	8	9	15	0.02%	23.7%	ITVNEVELLVMK	99.7%	104	25	104	2	0	0	1387.79	302	313
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	8	9	15	0.02%	23.7%	LNIGDLQVTK	99.7%	59.6	25	50.4	2	0	0	1100.63	123	132
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	8	9	15	0.02%	23.7%	QLTFEEIAK	99.5%	37.2	25	35.1	1	0	0	1078.58	290	298
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	8	9	15	0.02%	23.7%	QMTDPNVALTFLEK	99.7%	75.4	25	73.7	3	0	0	1606.81	86	99
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	8	9	15	0.02%	23.7%	TAWGQQPDLAANEAQLLR	99.7%	115	25	113	2	0	0	1982.01	253	270
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	8	9	15	0.02%	23.7%	VLDLQQIK	99.7%	57	25	31.8	2	0	0	956.58	340	347
26S proteasome non-ATPase regulatory subunit 14	PSMD14	PSDE_HUMAN	34.6	100.0%	4	5	11	0.01%	20.0%	AVAVVVDPIQSVK	99.7%	73.8	25	73.8	4	0	0	1324.78	140	152
26S proteasome non-ATPase regulatory subunit 14	PSMD14	PSDE_HUMAN	34.6	100.0%	4	5	11	0.01%	20.0%	AVEEEDKMTPEQLAIK	99.7%	64.4	25	64.4	3	0	0	1830.92	258	273
26S proteasome non-ATPase regulatory subunit 14	PSMD14	PSDE_HUMAN	34.6	100.0%	4	5	11	0.01%	20.0%	VIDVFAMPQSGTGVSVEAVDPVFQAK	99.5%	31.6	25	31.1	0	2	0	2707.37	69	94
26S proteasome non-ATPase regulatory subunit 14	PSMD14	PSDE_HUMAN	34.6	100.0%	4	5	11	0.01%	20.0%	VVIDAFR	99.6%	38	25	33.2	2	0	0	819.47	155	161

26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	APVQPQQSPAAAPGGTDEKPSGK	99.7%	69.4	25	69.4	0	2	0	2218.11	9	31
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	AVPLALALISVSNPR	99.7%	49.3	25	49.3	2	2	0	1520.92	689	703
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	CALGVFR	98.1%	31.5	25	24.3	2	0	0	822.43	251	257
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	DKAPVQPQQSPAAAPGGTDEKPSGK	99.7%	56.5	25	56.5	0	2	0	2461.23	7	31
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	DPNNLFMVR	99.7%	39.6	25	32.3	4	0	0	1121.54	755	763
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	DTSLYRPALEELRR	99.2%	29.2	25	24.2	0	2	0	1718.92	67	80
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	EDVLTLLLPVMGDSK	99.7%	109	25	99	5	0	0	1629.88	495	509
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	ELDIMEPK	99.7%	44.8	25	15.9	2	0	0	990.48	336	343
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	EPLLTLVK	99.0%	34.1	25	33.8	2	0	0	912.58	182	189
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	EWQELDDAEK	99.7%	52.6	25	43.1	2	0	0	1262.55	169	178
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	FAADIISVLAMTMSGER	99.7%	100	25	33.7	5	0	0	1827.90	121	137
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	FGGSGSQVDSAR	99.7%	119	25	102	4	0	0	1167.54	358	369
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	GTLTLCPYHSDR	99.7%	46.3	25	44.4	2	1	0	1419.67	774	785
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	LAQGLTHLGK	99.7%	50	25	49.5	2	0	0	1037.61	764	773
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	LGSIFGLGLAYAGSNR	99.7%	110	25	108	2	2	0	1595.85	479	494
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	LNILDTLSK	99.7%	47.9	25	24.1	2	0	0	1016.60	704	712
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	LVGSQEELASWGHEYVR	99.7%	45.3	25	42.2	0	2	0	1959.96	144	160
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	MLVTFDEELRPLPVSVR	99.7%	33.8	25	33.8	0	2	0	2001.08	829	845
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	QMAFMLGR	97.9%	31.2	25	21.5	1	0	0	953.47	293	300
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	SETELKDTYAR	95.5%	22.7	25	22.7	0	1	0	1312.64	546	556
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	SFANTLVDVCAYAGSGNVLK	99.7%	119	25	111	2	0	0	2086.03	589	608
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	SSTTSMTSVPKPLK	99.7%	69.9	25	61	4	0	0	1463.78	84	97
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	TITGFQTHTTPVLLAHGER	99.7%	47.7	25	47.7	0	2	0	2079.10	861	879
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	VGQAVDVVGQAGKPK	99.7%	88.4	25	77	3	0	0	1452.82	846	860
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	WLPLGLGLNHLGK	99.7%	56.6	25	56.6	2	0	0	1417.83	557	569
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	YGEPTLR	99.1%	34.8	25	30.6	2	0	0	835.43	681	687
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	27	35	70	0.07%	37.2%	YLYSSEDYIK	99.7%	44	25	37.1	2	0	0	1280.60	432	441
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	AIQLEYSEAR	99.7%	73.8	25	66.8	2	0	0	1179.60	297	306
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	AIQLEYSEARR	97.4%	30.2	25	12.8	2	0	0	1335.70	297	307
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	AIRDGVIEASINHEK	99.7%	36.7	25	30.7	0	2	0	1651.88	441	455
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	APQHTAVGFK	99.7%	45.2	25	35.5	2	0	0	1055.56	316	325
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	AVQGFFTSNNATR	99.7%	83.2	25	75.3	2	0	0	1412.69	116	128
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	DGVIEASINHEK	99.7%	52.5	25	32.8	2	0	0	1311.65	444	455
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	DLESAEERR	99.2%	35.2	25	21.8	1	0	0	1104.53	504	512
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	ELDTVTLEDIKEHVK	99.7%	97.5	25	92.8	2	2	0	1768.93	66	80
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	EMIDIYSTR	99.7%	54.5	25	42.5	4	0	0	1143.54	462	470
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	EPQLAFHQR	99.7%	51.1	25	36.9	2	0	0	1125.58	471	479
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	EQQDLEFAK	98.5%	32.5	25	26.9	1	0	0	1107.53	515	523
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	EREQQDLEFAK	99.7%	47.3	25	36.5	1	0	0	1392.68	513	523
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	FNQVLDQFGEK	99.7%	68.5	25	46.1	2	0	0	1324.65	375	385
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	FQADGTYTLIIR	99.7%	51	25	43.4	1	0	0	1397.74	386	397
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	HDADGQATLLNLLLR	99.7%	105	25	105	2	2	0	1649.90	242	256
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	ISDDLMQK	99.7%	59.3	25	28	4	0	0	949.47	187	194
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	ISFCLDIHNMSVK	99.7%	66.9	25	59.8	4	0	0	1563.77	480	492
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	ISLADIAQK	99.7%	76.1	25	32.5	2	0	0	958.56	417	425
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	LQLDSPEDAEFIVAK	99.7%	85.7	25	73.2	2	0	0	1674.86	426	440
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	MISLSYSR	99.7%	52.1	25	45.3	4	0	0	956.49	409	416
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	NYLHYSLYDQAEK	99.7%	81.6	25	69	2	2	0	1643.77	257	269
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	RALDLVAAK	96.3%	28.8	25	21.6	1	0	0	956.59	201	209
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	RLNHYVLYK	96.7%	23.8	25	18.7	0	1	0	1205.68	107	115
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	SLMPYFLLTQAVR	99.7%	86.7	25	69.3	6	0	0	1538.84	356	368

26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	SVFPEQANNNEWAR	99.7%	76.7	25	74.9	2	0	0	1661.77	274	287
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	VYEFLDKLDVVR	99.7%	78.5	25	70.8	2	2	0	1495.82	217	228
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	36	67	0.07%	50.6%	YLYYTGR	97.3%	30.1	25	20.9	1	0	0	935.46	288	294
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	4	7	19	0.02%	17.5%	AAAASAAEAGIATTGTEDSDDALLK	99.7%	161	25	161	2	4	0	2320.12	238	262
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	4	7	19	0.02%	17.5%	IIAFVGSPVEDNEKDLVK	99.7%	87.2	25	78.8	2	5	0	1973.06	109	126
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	4	7	19	0.02%	17.5%	ITFCTGIR	99.7%	57.4	25	46.8	2	0	0	967.50	84	91
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	4	7	19	0.02%	17.5%	LQAQQDAVNIVCHSK	99.7%	68.7	25	63.7	2	2	0	1710.86	26	40
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	41	0.04%	46.5%	DNNMAPYYEALCK	99.7%	45.8	25	34.5	2	0	0	1604.67	47	59
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	41	0.04%	46.5%	DWLFAPHYR	99.5%	37	25	27.4	2	0	0	1204.59	285	293
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	41	0.04%	46.5%	FLLSLPEHR	99.7%	40.6	25	36.8	2	0	0	1111.63	24	32
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	41	0.04%	46.5%	GAEILEVLHSLPAVR	99.7%	88.6	25	88.6	2	0	0	1603.92	243	257
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	41	0.04%	46.5%	GDAAVRDELMAAVR	99.7%	51.5	25	43.8	3	3	0	1473.75	33	46
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	41	0.04%	46.5%	IDKVNEIVETNRPDSK	99.7%	39.3	25	39.3	0	2	0	1856.97	347	362
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	41	0.04%	46.5%	IGLFYMDNDLITR	99.7%	95.5	25	94.4	4	0	0	1570.79	147	159
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	41	0.04%	46.5%	IHAYSQLLESYR	99.7%	50.3	25	38	2	2	0	1479.76	301	312
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	41	0.04%	46.5%	KGDLLLNR	99.7%	46.5	25	37.7	2	0	0	928.56	372	379
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	41	0.04%	46.5%	LDIVFYLLR	99.7%	81.4	25	61.1	2	0	0	1151.68	138	146
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	41	0.04%	46.5%	PLENLEEEGLPK	99.7%	79.1	25	79.1	2	0	0	1367.71	2	13
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	41	0.04%	46.5%	PLENLEEEGLPKNPDLR	99.7%	41.1	25	38.5	0	2	0	1963.01	2	18
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	41	0.04%	46.5%	QYLFSLYECR	99.7%	53.6	25	46.4	2	0	0	1378.65	258	267
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	41	0.04%	46.5%	SLDWQIDVDLLNK	99.7%	50.8	25	32.6	1	0	0	1558.81	60	72
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	41	0.04%	46.5%	SLIEEGGDWDRR	99.3%	35.9	25	34.3	1	0	0	1432.68	166	177
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	41	0.04%	46.5%	VNEIVETNRPDSK	99.7%	68.5	25	53.3	2	1	0	1500.77	350	362
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	41	0.04%	46.5%	VYQGLYCVAIR	99.7%	86.2	25	80.9	2	0	0	1341.70	182	192
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	6	6	12	0.01%	16.3%	DIQTNVYIK	99.7%	43.2	25	35.4	4	0	0	1093.59	219	227
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	6	6	12	0.01%	16.3%	ILFFNTPK	96.0%	28.5	25	13	1	0	0	979.56	290	297
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	6	6	12	0.01%	16.3%	ILFTEATR	99.7%	45.1	25	29.2	1	0	0	950.53	282	289
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	6	6	12	0.01%	16.3%	LVLLELNFLPTTGTK	99.7%	52.3	25	52.3	3	0	0	1658.97	121	135
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	6	6	12	0.01%	16.3%	QVIEYAR	94.6%	27.4	25	17.7	1	0	0	878.47	338	344
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	6	6	12	0.01%	16.3%	VAEFHTELER	99.7%	45.5	25	34.5	2	0	0	1230.61	205	214
28S ribosomal protein S10, mitochondrial	MRPS10	RT10_HUMAN	23.0	100.0%	4	5	10	0.01%	28.4%	AVLDSYEYFAVLAAK	99.7%	69.1	25	69.1	2	0	0	1659.86	86	100
28S ribosomal protein S10, mitochondrial	MRPS10	RT10_HUMAN	23.0	100.0%	4	5	10	0.01%	28.4%	DLTKPVVTISDEPDILYKR	99.7%	35.9	25	35.9	0	1	0	2202.20	57	75
28S ribosomal protein S10, mitochondrial	MRPS10	RT10_HUMAN	23.0	100.0%	4	5	10	0.01%	28.4%	FTLLQSVHIYK	99.7%	48.5	25	39.6	2	0	0	1348.76	118	128
28S ribosomal protein S10, mitochondrial	MRPS10	RT10_HUMAN	23.0	100.0%	4	5	10	0.01%	28.4%	NLPEGVAMEVTK	99.7%	54.7	25	42.9	5	0	0	1287.66	163	174
28S ribosomal protein S11, mitochondrial	MRPS11	RT11_HUMAN	20.6	100.0%	3	5	9	0.01%	14.4%	GTGIAAQTAGIAAAAR	99.7%	102	25	102	2	0	0	1399.77	123	138
28S ribosomal protein S11, mitochondrial	MRPS11	RT11_HUMAN	20.6	100.0%	3	5	9	0.01%	14.4%	KFEEIPIAHIK	99.7%	46.2	25	46.2	1	2	0	1324.76	79	89
28S ribosomal protein S11, mitochondrial	MRPS11	RT11_HUMAN	20.6	100.0%	3	5	9	0.01%	14.4%	KGTGIAAQTAGIAAAAR	99.7%	125	25	117	2	2	0	1527.86	122	138
28S ribosomal protein S12, mitochondrial	MRPS12	RT12_HUMAN	15.2	99.8%	2	2	5	0.01%	14.5%	GVVLCTFTR	99.4%	36.6	25	23.5	3	0	0	1052.56	60	68
28S ribosomal protein S12, mitochondrial	MRPS12	RT12_HUMAN	15.2	99.8%	2	2	5	0.01%	14.5%	LGPTEGRPQLK	99.6%	38.1	25	31.7	2	0	0	1195.68	49	59
28S ribosomal protein S14, mitochondrial	MRPS14	RT14_HUMAN	15.1	99.8%	2	3	9	0.01%	18.8%	ILQDVADEEIAALPR	99.7%	68.5	25	65.4	4	0	0	1652.89	66	80
28S ribosomal protein S14, mitochondrial	MRPS14	RT14_HUMAN	15.1	99.8%	2	3	9	0.01%	18.8%	MAYEYADER	99.7%	60.3	25	57.9	5	0	0	1147.47	43	51
28S ribosomal protein S15, mitochondrial	MRPS15	RT15_HUMAN	29.8	100.0%	4	4	8	0.01%	14.4%	DYQNVPGIEK	99.7%	40	25	33	1	0	0	1162.57	75	84
28S ribosomal protein S15, mitochondrial	MRPS15	RT15_HUMAN	29.8	100.0%	4	4	8	0.01%	14.4%	IVANPEDTR	96.0%	28.5	25	21.9	1	0	0	1014.52	115	123
28S ribosomal protein S15, mitochondrial	MRPS15	RT15_HUMAN	29.8	100.0%	4	4	8	0.01%	14.4%	NTNYDVFEK	99.7%	44.6	25	36.9	2	0	0	1129.52	172	180
28S ribosomal protein S15, mitochondrial	MRPS15	RT15_HUMAN	29.8	100.0%	4	4	8	0.01%	14.4%	YLLMSIDQR	99.7%	63.5	25	52.7	4	0	0	1138.59	155	163
28S ribosomal protein S16, mitochondrial	MRPS16	RT16_HUMAN	15.3	100.0%	3	3	5	0.01%	26.3%	AREVLLASQK	99.7%	41.3	25	29	2	0	0	1114.66	115	124
28S ribosomal protein S16, mitochondrial	MRPS16	RT16_HUMAN	15.3	100.0%	3	3	5	0.01%	26.3%	FVEQLGSYDPLPNSHGEK	99.7%	44.4	25	42	0	2	0	2016.97	47	64
28S ribosomal protein S16, mitochondrial	MRPS16	RT16_HUMAN	15.3	100.0%	3	3	5	0.01%	26.3%	LVALNLDR	99.4%	36.6	25	21	1	0	0	913.55	65	72
28S ribosomal protein S17, mitochondrial	MRPS17	RT17_HUMAN	14.5	100.0%	3	3	6	0.01%	44.6%	HELAEIVFK	99.7%	45.3	25	45.3	2	0	0	1085.60	79	87
28S ribosomal protein S17, mitochondrial	MRPS17	RT17_HUMAN	14.5	100.0%	3	3	6	0.01%	44.6%	TYFAHDALQQCTVGDIVLLR	99.7%	42.6	25	35.5	0	2	0	2320.18	48	67
28S ribosomal protein S17, mitochondrial	MRPS17	RT17_HUMAN	14.5	100.0%	3	3	6	0.01%	44.6%	VIDPVTGKPCAGTTYLESPLSSETTQLSK	99.7%	84.6	25	84.6	0	2	0	3079.55	91	119

28S ribosomal protein S18a, mitochondrial	MRPS18A	RT18A_HUMAN	22.2	100.0%	2	2	4	0.00%	13.8%	ESPNPPNPSGQCPICR	99.7%	54.2	25	54.2	2	0	0	1809.80	59	74
28S ribosomal protein S18a, mitochondrial	MRPS18A	RT18A_HUMAN	22.2	100.0%	2	2	4	0.00%	13.8%	WAPGSVKPIYK	97.2%	29.9	25	22.5	2	0	0	1245.70	154	164
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	5	6	11	0.01%	30.2%	APSEEDSLSSVPISPYKDEPWK	99.7%	47.2	25	47.2	0	2	0	2461.18	36	57
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	5	6	11	0.01%	30.2%	LYQGHLQEESGPPPESMPK	99.7%	60.4	25	50.8	0	3	0	2140.00	219	237
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	5	6	11	0.01%	30.2%	TPAEASSTGQTGPQSAL	99.7%	65.8	25	64.6	2	0	0	1602.76	242	258
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	5	6	11	0.01%	30.2%	VVGNPCPICR	99.7%	53.8	25	51.6	2	0	0	1171.57	100	109
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	5	6	11	0.01%	30.2%	YLESEEYQER	99.7%	50.9	25	50.9	2	0	0	1345.59	58	67
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	6	6	11	0.01%	17.2%	FMEPYIFGSR	99.7%	44.4	25	36.4	2	0	0	1246.59	101	110
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	6	6	11	0.01%	17.2%	GIILFISR	99.7%	63.6	25	51.1	2	0	0	918.58	140	147
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	6	6	11	0.01%	17.2%	HSDFFNVK	99.7%	45.3	25	29.8	2	0	0	993.48	69	76
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	6	6	11	0.01%	17.2%	LFQTAITR	99.7%	61.6	25	45.2	2	0	0	949.55	252	259
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	6	6	11	0.01%	17.2%	LLFGPTVR	98.5%	32.6	25	15.2	2	0	0	902.55	181	188
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	6	6	11	0.01%	17.2%	RQQVEALYR	99.2%	35.3	25	26.5	1	0	0	1162.63	264	272
28S ribosomal protein S21, mitochondrial	MRPS21	RT21_HUMAN	10.7	100.0%	3	5	12	0.01%	39.1%	ILTMDGLIEDIK	99.7%	54.4	25	39.3	4	0	0	1360.74	29	40
28S ribosomal protein S21, mitochondrial	MRPS21	RT21_HUMAN	10.7	100.0%	3	5	12	0.01%	39.1%	IYNMEMAR	99.7%	48.1	25	38.6	2	0	0	1027.47	63	70
28S ribosomal protein S21, mitochondrial	MRPS21	RT21_HUMAN	10.7	100.0%	3	5	12	0.01%	39.1%	TVMVQEGNVESAYR	99.7%	101	25	92	6	0	0	1598.75	11	24
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	15	25	0.03%	32.5%	DQAAEGINLIK	99.7%	64.1	25	56.3	2	0	0	1171.63	319	329
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	15	25	0.03%	32.5%	IDGLLIDQIQR	99.7%	73.5	25	57.8	2	0	0	1283.73	281	291
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	15	25	0.03%	32.5%	ILTPIIFKEENLR	99.7%	54.8	25	54	1	2	0	1585.93	204	216
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	15	25	0.03%	32.5%	KIDGLLIDQIQR	99.7%	81.6	25	74	2	2	0	1411.83	280	291
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	15	25	0.03%	32.5%	LMTQAQLEEATR	99.7%	95.6	25	88.8	4	0	0	1406.69	105	116
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	15	25	0.03%	32.5%	MIQVYFPK	99.7%	44.9	25	38.5	2	0	0	1025.55	192	199
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	15	25	0.03%	32.5%	TFKPAIQELKPPTYK	96.8%	24	25	24	0	1	0	1760.99	90	104
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	15	25	0.03%	32.5%	VPINDVLAEDK	99.7%	51	25	45.2	1	0	0	1212.65	136	146
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	15	25	0.03%	32.5%	VPINDVLAEDKILEGTETTK	98.5%	26.9	25	26.9	0	1	0	2185.16	136	155
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	15	25	0.03%	32.5%	YFGGMVWYFVNNK	99.6%	38.3	25	38.3	2	0	0	1624.76	267	279
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	15	25	0.03%	32.5%	YVFTDISYSIPHR	99.7%	62.8	25	62.8	2	1	0	1597.80	156	168
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	4	5	10	0.01%	23.7%	AFDLFNPNFK	99.7%	67.4	25	62.8	2	0	0	1212.60	84	93
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	4	5	10	0.01%	23.7%	ALLAEGVILR	99.7%	79.8	25	54.1	2	0	0	1054.66	124	133
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	4	5	10	0.01%	23.7%	LETVGSIFSR	99.7%	71.3	25	57.1	2	0	0	1108.60	6	15
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	4	5	10	0.01%	23.7%	LGETDEEKLFVETGK	99.7%	62.8	25	58.9	2	2	0	1694.85	109	123
28S ribosomal protein S24, mitochondrial	MRPS24	RT24_HUMAN	19.0	100.0%	3	3	5	0.01%	10.8%	LHLQTVPSK	99.7%	46.4	25	39.8	2	0	0	1022.60	153	161
28S ribosomal protein S24, mitochondrial	MRPS24	RT24_HUMAN	19.0	100.0%	3	3	5	0.01%	10.8%	TVEDVFLR	94.9%	27.6	25	20.3	1	0	0	978.53	86	93
28S ribosomal protein S24, mitochondrial	MRPS24	RT24_HUMAN	19.0	100.0%	3	3	5	0.01%	10.8%	TVEDVFLRK	99.4%	36.2	25	28.3	2	0	0	1106.62	86	94
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	6	9	18	0.02%	37.6%	FVFFNIPQIQYK	98.8%	33.4	25	32.7	1	0	0	1543.83	47	58
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	6	9	18	0.02%	37.6%	NMTPSPFLR	97.3%	30	25	6.28	1	0	0	1062.54	69	77
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	6	9	18	0.02%	37.6%	NPWVQIMMFK	99.7%	53.8	25	50.9	6	0	0	1325.64	59	68
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	6	9	18	0.02%	37.6%	TLQYLSQGNVVFK	99.7%	81.4	25	62.9	2	0	0	1496.81	12	24
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	6	9	18	0.02%	37.6%	TLQYLSQGNVVFKDSVK	99.7%	65.2	25	62.3	2	0	0	1926.03	12	28
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	6	9	18	0.02%	37.6%	VMTVNYNTHGELGEGAR	99.7%	59.8	25	59.8	2	4	0	1847.87	29	45
28S ribosomal protein S26, mitochondrial	MRPS26	RT26_HUMAN	24.2	100.0%	5	7	11	0.01%	20.0%	EGLVVRPQR	95.3%	27.9	25	13.6	1	0	0	1053.62	194	202
28S ribosomal protein S26, mitochondrial	MRPS26	RT26_HUMAN	24.2	100.0%	5	7	11	0.01%	20.0%	EREVLQLQEEVK	99.7%	49	25	37	1	0	0	1499.81	154	165
28S ribosomal protein S26, mitochondrial	MRPS26	RT26_HUMAN	24.2	100.0%	5	7	11	0.01%	20.0%	EVLQLQEEVK	99.7%	64.3	25	40.1	2	0	0	1214.66	156	165
28S ribosomal protein S26, mitochondrial	MRPS26	RT26_HUMAN	24.2	100.0%	5	7	11	0.01%	20.0%	KAEEVQAWAQR	99.7%	57.8	25	52.9	2	2	0	1315.68	142	152
28S ribosomal protein S26, mitochondrial	MRPS26	RT26_HUMAN	24.2	100.0%	5	7	11	0.01%	20.0%	MEFVSEVQR	99.7%	60	25	50.4	3	0	0	1124.54	72	80
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	8	8	23	0.02%	21.3%	EALDVLGAVLK	99.7%	91.3	25	85.3	4	0	0	1127.67	278	288
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	8	8	23	0.02%	21.3%	IESEGLLSLTTQLVK	99.7%	110	25	98.6	4	0	0	1630.93	347	361
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	8	8	23	0.02%	21.3%	KLPVSSLTISR	99.7%	53.2	25	41.6	4	0	0	1200.73	64	74
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	8	8	23	0.02%	21.3%	LIDNISSR	96.4%	29	25	11.3	1	0	0	917.51	75	82
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	8	8	23	0.02%	21.3%	LVEQLDIEETEQSK	99.7%	80.4	25	76.2	2	0	0	1660.83	313	326
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	8	8	23	0.02%	21.3%	NFGASLLLPGLK	99.7%	67.8	25	60.1	4	0	0	1229.73	203	214

28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	8	8	23	0.02%	21.3%	VAASPEDIK	99.0%	34	25	28.4	3	0	0	929.49	266	274
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	8	8	23	0.02%	21.3%	VELQQGLR	98.5%	32.5	25	22.1	1	0	0	942.54	234	241
28S ribosomal protein S28, mitochondrial	MRPS28	RT28_HUMAN	20.8	100.0%	3	4	13	0.01%	15.5%	AGGFASALER	99.7%	63.4	25	53.7	4	0	0	978.50	49	58
28S ribosomal protein S28, mitochondrial	MRPS28	RT28_HUMAN	20.8	100.0%	3	4	13	0.01%	15.5%	LLDLELTSR	99.7%	70.9	25	63.4	4	0	0	1059.60	144	152
28S ribosomal protein S28, mitochondrial	MRPS28	RT28_HUMAN	20.8	100.0%	3	4	13	0.01%	15.5%	NVESFASMLR	99.7%	65.4	25	55.6	5	0	0	1169.56	76	85
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	8	9	19	0.02%	25.9%	EGFDALDPFIPILVSNYNPK	99.7%	43.4	25	43.4	1	0	0	2249.15	332	351
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	8	9	19	0.02%	25.9%	ELLFLSNANPSLLER	99.7%	83.7	25	81.1	2	0	0	1715.93	379	393
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	8	9	19	0.02%	25.9%	FDQPLEASTWLK	99.7%	74.6	25	59.5	2	0	0	1434.73	178	189
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	8	9	19	0.02%	25.9%	GSPLGEVVEQGITR	99.7%	88.2	25	78.7	4	0	0	1441.76	219	232
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	8	9	19	0.02%	25.9%	KAYLPQELLGK	99.7%	41.3	25	41.3	2	0	0	1259.74	321	331
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	8	9	19	0.02%	25.9%	NATDAVGIVLK	99.7%	61.3	25	52.2	2	0	0	1100.63	235	245
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	8	9	19	0.02%	25.9%	NTSFAYPAIR	99.7%	54.4	25	39.3	2	0	0	1139.58	114	123
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	8	9	19	0.02%	25.9%	TFSEACLMVR	99.7%	61.8	25	60.5	4	0	0	1213.57	93	102
28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	5	6	11	0.01%	17.2%	EAPETDTSPSLWDVEFAK	99.7%	62.6	25	62.6	2	0	0	2021.93	267	284
28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	5	6	11	0.01%	17.2%	IQFDEGYDNYPGQEK	99.7%	85.4	25	85.4	2	0	0	1802.79	226	240
28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	5	6	11	0.01%	17.2%	ISFSNIISDMK	99.7%	72.6	25	63	4	0	0	1254.64	199	209
28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	5	6	11	0.01%	17.2%	SELLSQLQQHEEESR	97.2%	24.5	25	24.5	0	1	0	1812.87	175	189
28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	5	6	11	0.01%	17.2%	VELSTVNVR	99.7%	52.6	25	36.6	2	0	0	1016.57	108	116
28S ribosomal protein S33, mitochondrial	MRPS33	RT33_HUMAN	12.6	99.8%	2	2	3	0.00%	19.8%	LFGEVTRPTNSK	99.7%	47.9	25	38.1	2	0	0	1348.72	18	29
28S ribosomal protein S33, mitochondrial	MRPS33	RT33_HUMAN	12.6	99.8%	2	2	3	0.00%	19.8%	LFSELPLAK	99.7%	43.9	25	29	1	0	0	1017.60	36	44
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	4	5	8	0.01%	17.4%	AWGILTFK	99.7%	44.2	25	32.5	2	0	0	935.54	114	121
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	4	5	8	0.01%	17.4%	LLQLLGR	99.7%	42.7	25	14.2	2	0	0	812.54	64	70
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	4	5	8	0.01%	17.4%	LPLFGLGR	99.7%	41.2	25	39.5	2	0	0	872.54	71	78
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	4	5	8	0.01%	17.4%	NGDTSTEEPMLNVQR	99.6%	38.4	25	38.4	2	0	0	1706.77	181	195
28S ribosomal protein S35, mitochondrial	MRPS35	RT35_HUMAN	36.8	100.0%	4	5	8	0.01%	16.4%	LSSLNLDDHAK	99.7%	73.8	25	55	2	0	0	1212.62	177	187
28S ribosomal protein S35, mitochondrial	MRPS35	RT35_HUMAN	36.8	100.0%	4	5	8	0.01%	16.4%	NILETLLQMK	99.7%	74	25	60.4	2	0	0	1202.68	261	270
28S ribosomal protein S35, mitochondrial	MRPS35	RT35_HUMAN	36.8	100.0%	4	5	8	0.01%	16.4%	NMEINKEELLGTK	99.7%	47.2	25	32.4	1	0	0	1518.78	275	287
28S ribosomal protein S35, mitochondrial	MRPS35	RT35_HUMAN	36.8	100.0%	4	5	8	0.01%	16.4%	SVVSLKNEEENENSISQYK	99.7%	75.2	25	75.2	1	2	0	2197.06	295	313
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	6	9	16	0.02%	16.3%	GAAGFSIGK	98.3%	31.9	25	19.2	2	0	0	807.44	252	260
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	6	9	16	0.02%	16.3%	LTADELWK	99.7%	52.7	25	41	2	0	0	975.51	93	100
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	6	9	16	0.02%	16.3%	NGAVQTIAQR	99.7%	62	25	53	2	0	0	1057.57	151	160
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	6	9	16	0.02%	16.3%	VSGSINMLSLTQGLFR	99.7%	93.7	25	92.9	4	0	0	1722.92	336	351
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	6	9	16	0.02%	16.3%	YEDHTIFHDISLR	99.2%	29.4	25	20.5	1	2	0	1645.80	285	297
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	6	9	16	0.02%	16.3%	YGFLWPGLNVPLMK	99.7%	49.6	25	47.2	3	0	0	1634.88	137	150
28S ribosomal protein S6, mitochondrial	MRPS6	RT06_HUMAN	14.2	100.0%	3	3	5	0.01%	22.4%	AMQRPETAATLK	97.8%	30.9	25	20.4	1	0	0	1316.70	12	23
28S ribosomal protein S6, mitochondrial	MRPS6	RT06_HUMAN	14.2	100.0%	3	3	5	0.01%	22.4%	DLENLGER	99.0%	34.2	25	20.4	2	0	0	945.46	38	45
28S ribosomal protein S6, mitochondrial	MRPS6	RT06_HUMAN	14.2	100.0%	3	3	5	0.01%	22.4%	TIEALMDR	99.7%	43.1	25	35.8	2	0	0	964.48	25	32
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	5	5	9	0.01%	25.2%	LLEAFHNQGPVIK	99.7%	64.7	25	54.8	1	0	0	1465.82	209	221
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	5	5	9	0.01%	25.2%	NPYTIFHQALK	99.7%	47.3	25	37.9	1	0	0	1331.71	140	150
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	5	5	9	0.01%	25.2%	SLMIQTLEAVK	99.4%	36.8	25	28.6	1	0	0	1232.69	109	119
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	5	5	9	0.01%	25.2%	TSSVFEDPVISK	99.7%	54.1	25	50.7	4	0	0	1308.67	82	93
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	5	5	9	0.01%	25.2%	YHAASAEEQATIER	99.7%	62.2	25	58	2	0	0	1575.74	126	139
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	7	7	12	0.01%	22.0%	AIAYLFPSGLFEK	99.7%	51.3	25	48.8	2	0	0	1455.79	107	119
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	7	7	12	0.01%	22.0%	ALCSFVTEDEVEWMR	99.7%	115	25	115	1	0	0	1871.83	351	365
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	7	7	12	0.01%	22.0%	EQLMFPFHFVDR	94.9%	27.6	25	15.1	1	0	0	1565.76	311	322
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	7	7	12	0.01%	22.0%	ETYTEDFIKK	98.2%	31.8	25	23.1	2	0	0	1273.63	67	76
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	7	7	12	0.01%	22.0%	LLTSQCGAAEEEFVQR	99.7%	114	25	114	2	0	0	1837.88	228	243
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	7	7	12	0.01%	22.0%	LSDLDYMQFIR	99.7%	56.8	25	51	2	0	0	1416.68	213	223
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	7	7	12	0.01%	22.0%	QIEEFNIGKR	96.5%	29	25	16.5	2	0	0	1233.66	77	86
2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	GCAT	KBL_HUMAN	45.3	99.8%	2	2	8	0.01%	8.4%	ALGGASGGYTTGPGPLVSLLR	99.7%	74.9	25	74.3	4	0	0	1944.06	266	286
2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	GCAT	KBL_HUMAN	45.3	99.8%	2	2	8	0.01%	8.4%	GIFVIGFSYPVVPK	99.7%	60.5	25	60.5	4	0	0	1522.87	370	383

2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	COQ5	COQ5_HUMAN	37.1	100.0%	5	5	7	0.01%	19.6%	EYQNEEDSLGGSR	99.7%	70.2	25	70.2	1	0	0	1483.63	154	166
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	COQ5	COQ5_HUMAN	37.1	100.0%	5	5	7	0.01%	19.6%	FLCLEFSQVNNPLISR	99.5%	37.2	25	37.2	2	0	0	1937.00	242	257
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	COQ5	COQ5_HUMAN	37.1	100.0%	5	5	7	0.01%	19.6%	FLNYVQSQHQR	99.7%	41.7	25	35	1	0	0	1419.71	124	134
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	COQ5	COQ5_HUMAN	37.1	100.0%	5	5	7	0.01%	19.6%	NVTHIDQALQEAHR	99.7%	46.3	25	46.3	0	1	0	1631.82	221	234
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	COQ5	COQ5_HUMAN	37.1	100.0%	5	5	7	0.01%	19.6%	VYQVFESVAK	99.7%	70.2	25	64.4	2	0	0	1169.62	68	77
2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	BCKDHA	ODBA_HUMAN	50.5	99.8%	2	2	2	0.00%	5.8%	AVAENQPFLIEAMTYR	98.9%	34	25	31	1	0	0	1852.93	317	332
2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	BCKDHA	ODBA_HUMAN	50.5	99.8%	2	2	2	0.00%	5.8%	GPGYGIMSIR	99.7%	53	25	27.8	1	0	0	1050.54	288	297
2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	BCKDHB	ODBB_HUMAN	43.1	99.9%	2	2	3	0.00%	6.1%	LGVSCEVIDLR	99.7%	62.8	25	46.9	2	0	0	1260.66	295	305
2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	BCKDHB	ODBB_HUMAN	43.1	99.9%	2	2	3	0.00%	6.1%	SGDLFNCGSLTIR	99.7%	54.5	25	54.5	1	0	0	1439.69	171	183
39S ribosomal protein L10, mitochondrial	MRPL10	RM10_HUMAN	29.3	100.0%	2	2	3	0.00%	9.6%	EIAAVFQDNR	99.7%	61.1	25	55.6	2	0	0	1162.59	85	94
39S ribosomal protein L10, mitochondrial	MRPL10	RM10_HUMAN	29.3	100.0%	2	2	3	0.00%	9.6%	MIAVCQNVALSAEDK	99.7%	53.4	25	52.9	1	0	0	1664.80	95	109
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	6	7	24	0.02%	41.7%	AGLAMPGPPLGPVLGQR	99.7%	50.4	25	48.9	5	0	0	1630.91	26	42
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	6	7	24	0.02%	41.7%	AQDEAFALQDVPLSSVVR	99.7%	63.9	25	63.9	4	0	0	1945.00	125	142
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	6	7	24	0.02%	41.7%	DLSSEELAAFQK	99.7%	81.7	25	63	4	0	0	1337.66	158	169
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	6	7	24	0.02%	41.7%	EADLAAQEEAAKK	99.6%	37.9	25	29.6	4	0	0	1373.69	180	192
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	6	7	24	0.02%	41.7%	GVSINQFCK	99.7%	42.4	25	37	4	0	0	1052.52	43	51
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	6	7	24	0.02%	41.7%	IGQPTVSYFLK	99.7%	48.2	25	48.2	3	0	0	1252.69	82	92
39S ribosomal protein L12, mitochondrial	MRPL12	RM12_HUMAN	21.3	99.8%	2	2	4	0.00%	11.6%	KLVESLPQEIK	99.7%	54.9	25	48	2	0	0	1283.76	163	173
39S ribosomal protein L12, mitochondrial	MRPL12	RM12_HUMAN	21.3	99.8%	2	2	4	0.00%	11.6%	NYIQGINLVQAK	99.7%	80.3	25	67.9	2	0	0	1360.76	151	162
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	6	7	13	0.01%	33.7%	APQQWATFAR	99.7%	70.9	25	66.1	2	0	0	1175.60	7	16
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	6	7	13	0.01%	33.7%	LAAMASIR	99.6%	39.1	25	34.8	1	0	0	848.47	31	38
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	6	7	13	0.01%	33.7%	LAIYGMLPK	99.3%	35.7	25	24.7	2	0	0	1021.58	106	114
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	6	7	13	0.01%	33.7%	LWTPPEDYRL	99.3%	36.1	25	27.2	2	0	0	1289.65	169	178
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	6	7	13	0.01%	33.7%	NLVEELPQPR	99.7%	54.3	25	47.2	2	0	0	1194.65	140	149
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	6	7	13	0.01%	33.7%	VYSSHTGYPGGFR	99.7%	53.4	25	53.4	2	2	0	1427.67	76	88
39S ribosomal protein L14, mitochondrial	MRPL14	RM14_HUMAN	15.9	100.0%	3	4	9	0.01%	29.0%	FDSNNVVLIEDNGNPVGTR	99.7%	80.5	25	78.8	2	0	0	2060.00	100	118
39S ribosomal protein L14, mitochondrial	MRPL14	RM14_HUMAN	15.9	100.0%	3	4	9	0.01%	29.0%	VLAIAQNFV	99.7%	49.7	25	46.5	2	0	0	974.57	137	145
39S ribosomal protein L14, mitochondrial	MRPL14	RM14_HUMAN	15.9	100.0%	3	4	9	0.01%	29.0%	VVDNSALGNSPYHR	99.7%	66.6	25	54.1	4	1	0	1528.75	40	53
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	7	8	12	0.01%	31.8%	DYGVQLVEEGADTFTAK	99.7%	109	25	107	2	0	0	1842.88	135	151
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	7	8	12	0.01%	31.8%	GYLADPAKFPEAR	99.3%	35.6	25	32.9	1	1	0	1434.74	221	233
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	7	8	12	0.01%	31.8%	LGFEGGQTPFYIR	99.7%	51.6	25	43.2	2	0	0	1484.75	65	77
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	7	8	12	0.01%	31.8%	LQYLIDLGR	99.7%	48.5	25	48.1	2	0	0	1090.63	101	109
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	7	8	12	0.01%	31.8%	NGGVVTTAFYDPR	99.7%	55.8	25	55.8	1	0	0	1396.69	170	182
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	7	8	12	0.01%	31.8%	VDPSQPIDLTQLVNGR	99.7%	41.8	25	41.2	2	0	0	1751.93	110	125
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	7	8	12	0.01%	31.8%	VSLANLKPNPGSK	99.7%	47.6	25	47.6	1	0	0	1324.76	22	34
39S ribosomal protein L16, mitochondrial	MRPL16	RM16_HUMAN	28.5	100.0%	3	3	6	0.01%	12.4%	GAIDHYVTPVK	99.7%	63.6	25	50.3	2	0	0	1199.64	145	155
39S ribosomal protein L16, mitochondrial	MRPL16	RM16_HUMAN	28.5	100.0%	3	3	6	0.01%	12.4%	IATANMLGIR	99.7%	77.6	25	62.9	2	0	0	1059.60	218	227
39S ribosomal protein L16, mitochondrial	MRPL16	RM16_HUMAN	28.5	100.0%	3	3	6	0.01%	12.4%	VPAPFKPITR	99.7%	64	25	51.7	2	0	0	1125.68	124	133
39S ribosomal protein L18, mitochondrial	MRPL18	RM18_HUMAN	20.6	100.0%	4	4	7	0.01%	24.4%	LQSAMTEGGVVLREPQR	99.2%	29.4	25	28	0	2	0	1886.98	161	177
39S ribosomal protein L18, mitochondrial	MRPL18	RM18_HUMAN	20.6	100.0%	4	4	7	0.01%	24.4%	NLELLSVAR	99.7%	61.5	25	31.9	2	0	0	1014.59	55	63
39S ribosomal protein L18, mitochondrial	MRPL18	RM18_HUMAN	20.6	100.0%	4	4	7	0.01%	24.4%	NVVACESIGR	99.7%	48.6	25	45.7	2	0	0	1104.55	121	130
39S ribosomal protein L18, mitochondrial	MRPL18	RM18_HUMAN	20.6	100.0%	4	4	7	0.01%	24.4%	VVVSASTR	99.7%	44.8	25	35.5	1	0	0	818.47	101	108
39S ribosomal protein L19, mitochondrial	MRPL19	RM19_HUMAN	33.5	100.0%	3	3	5	0.01%	9.9%	FLSPEFIPR	98.8%	33.4	25	26.3	1	0	0	1105.60	75	83
39S ribosomal protein L19, mitochondrial	MRPL19	RM19_HUMAN	33.5	100.0%	3	3	5	0.01%	9.9%	GLGATFILR	99.7%	69.7	25	57.6	2	0	0	947.57	144	152
39S ribosomal protein L19, mitochondrial	MRPL19	RM19_HUMAN	33.5	100.0%	3	3	5	0.01%	9.9%	ISQFLGICIQR	99.7%	73.9	25	69.5	2	0	0	1334.73	130	140
39S ribosomal protein L2, mitochondrial	MRPL2	RM02_HUMAN	33.3	99.8%	2	2	4	0.00%	7.2%	AAGTCGVLLR	99.7%	49.6	25	40.3	2	0	0	1017.55	209	218
39S ribosomal protein L2, mitochondrial	MRPL2	RM02_HUMAN	33.3	99.8%	2	2	4	0.00%	7.2%	SADIALVAGGSR	99.7%	63.8	25	51.3	2	0	0	1116.60	136	147
39S ribosomal protein L20, mitochondrial	MRPL20	RM20_HUMAN	17.4	99.9%	2	2	3	0.00%	14.8%	ITAASQEHGLK	99.7%	45.3	25	43.6	1	0	0	1154.62	72	82
39S ribosomal protein L20, mitochondrial	MRPL20	RM20_HUMAN	17.4	99.9%	2	2	3	0.00%	14.8%	VLADLAIYEPK	99.7%	74.4	25	58.7	2	0	0	1231.69	101	111
39S ribosomal protein L21, mitochondrial	MRPL21	RM21_HUMAN	22.8	99.8%	2	2	7	0.01%	9.8%	IVTTPQTVLR	99.7%	48.5	25	35.5	3	0	0	1127.68	185	194
39S ribosomal protein L21, mitochondrial	MRPL21	RM21_HUMAN	22.8	99.8%	2	2	7	0.01%	9.8%	LFAVVHFASR	99.7%	68.8	25	58.6	4	0	0	1146.64	95	104

39S ribosomal protein L22, mitochondrial	MRPL22	RM22_HUMAN	23.6	100.0%	4	5	12	0.01%	21.4%	EVLLEAQDMAVR	99.7%	55	25	48.5	3	0	0	1389.70	113	124
39S ribosomal protein L22, mitochondrial	MRPL22	RM22_HUMAN	23.6	100.0%	4	5	12	0.01%	21.4%	EYIQQLR	99.6%	39	25	0	2	0	0	949.51	192	198
39S ribosomal protein L22, mitochondrial	MRPL22	RM22_HUMAN	23.6	100.0%	4	5	12	0.01%	21.4%	LVEGPPPPPEPPK	99.7%	47.3	25	45.5	4	0	0	1353.74	172	184
39S ribosomal protein L22, mitochondrial	MRPL22	RM22_HUMAN	23.6	100.0%	4	5	12	0.01%	21.4%	SNLYIAESTSGR	99.7%	82.8	25	82.8	3	0	0	1297.64	132	143
39S ribosomal protein L27, mitochondrial	MRPL27	RM27_HUMAN	16.1	99.8%	2	2	6	0.01%	14.2%	CLYALEEGIVR	99.7%	69.4	25	58	2	0	0	1322.68	88	98
39S ribosomal protein L27, mitochondrial	MRPL27	RM27_HUMAN	16.1	99.8%	2	2	6	0.01%	14.2%	NTEAVDLITR	99.7%	73.5	25	63.4	4	0	0	1131.60	110	119
39S ribosomal protein L33, mitochondrial	MRPL33	RM33_HUMAN	7.6	99.8%	2	3	3	0.00%	38.5%	LTLLHYDPVVK	99.7%	40.1	25	36.8	1	0	0	1297.75	41	51
39S ribosomal protein L33, mitochondrial	MRPL33	RM33_HUMAN	7.6	99.8%	2	3	3	0.00%	38.5%	MVSEAGTGFCFNTK	99.4%	36.7	25	36.7	2	0	0	1548.68	20	33
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	4	4	9	0.01%	12.5%	ESLLLQVR	99.7%	57.6	25	43.8	2	0	0	957.57	216	223
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	4	4	9	0.01%	12.5%	ETYCPVIVDNLIQLCK	99.7%	51.8	25	51.8	1	0	0	1964.98	174	189
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	4	4	9	0.01%	12.5%	MILFAFGSALAQAR	99.7%	106	25	101	3	0	0	1495.81	313	326
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	4	4	9	0.01%	12.5%	VYEIPGLEPITFAGK	99.7%	54.8	25	52.1	3	0	0	1633.88	49	63
39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	6	6	10	0.01%	16.3%	DLFHGATFVPR	99.7%	46.9	25	38.1	2	0	0	1259.65	160	170
39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	6	6	10	0.01%	16.3%	KQAIQELR	97.9%	31.1	25	14.7	1	0	0	985.58	107	114
39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	6	6	10	0.01%	16.3%	LAEYYGLYR	99.7%	55.7	25	44.8	2	0	0	1147.58	151	159
39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	6	6	10	0.01%	16.3%	LAFLLFK	99.2%	35.5	25	30.4	2	0	0	851.54	268	274
39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	6	6	10	0.01%	16.3%	TASVPLDAVR	94.6%	27.4	25	22.5	1	0	0	1028.57	127	136
39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	6	6	10	0.01%	16.3%	VAEGQVTCPYLPPFPAR	99.1%	34.6	25	28.2	2	0	0	1901.96	245	261
39S ribosomal protein L39, mitochondrial	MRPL39	RM39_HUMAN	38.7	100.0%	3	3	5	0.01%	11.5%	DLPFETLEVEAK	99.7%	57.5	25	47.1	2	0	0	1390.71	213	224
39S ribosomal protein L39, mitochondrial	MRPL39	RM39_HUMAN	38.7	100.0%	3	3	5	0.01%	11.5%	IGDFIDVSEGPLIPR	99.7%	41	25	31.9	2	0	0	1627.87	257	271
39S ribosomal protein L39, mitochondrial	MRPL39	RM39_HUMAN	38.7	100.0%	3	3	5	0.01%	11.5%	SCAMMMGCVIER	99.7%	40.7	25	40.7	1	0	0	1444.59	145	156
39S ribosomal protein L4, mitochondrial	MRPL4	RM04_HUMAN	34.9	99.8%	2	2	2	0.00%	11.3%	ATENPEQVASEGLPEPVLR	99.7%	55.4	25	50	1	0	0	2036.03	31	49
39S ribosomal protein L4, mitochondrial	MRPL4	RM04_HUMAN	34.9	99.8%	2	2	2	0.00%	11.3%	VGLADLHPDVFATAPR	99.2%	29.3	25	29.3	0	1	0	1678.89	77	92
39S ribosomal protein L40, mitochondrial	MRPL40	RM40_HUMAN	24.5	100.0%	2	2	3	0.00%	12.1%	ATQELIPIEDFITPLK	95.4%	28	25	28	1	0	0	1828.01	78	93
39S ribosomal protein L40, mitochondrial	MRPL40	RM40_HUMAN	24.5	100.0%	2	2	3	0.00%	12.1%	VYTQVEFKR	99.7%	63.7	25	59.3	2	0	0	1169.63	198	206
39S ribosomal protein L41, mitochondrial	MRPL41	RM41_HUMAN	15.4	100.0%	4	4	8	0.01%	29.9%	DFKDGTFDPDNLEK	95.2%	27.8	25	27.8	1	0	0	1640.74	103	116
39S ribosomal protein L41, mitochondrial	MRPL41	RM41_HUMAN	15.4	100.0%	4	4	8	0.01%	29.9%	GIGFLTSGWR	99.7%	63.6	25	53.9	3	0	0	1093.58	40	49
39S ribosomal protein L41, mitochondrial	MRPL41	RM41_HUMAN	15.4	100.0%	4	4	8	0.01%	29.9%	LFQLYPR	99.7%	53.2	25	43.6	2	0	0	936.53	127	133
39S ribosomal protein L41, mitochondrial	MRPL41	RM41_HUMAN	15.4	100.0%	4	4	8	0.01%	29.9%	YGFEPTQEGK	99.2%	35.2	25	23.9	2	0	0	1155.53	117	126
39S ribosomal protein L43, mitochondrial	MRPL43	RM43_HUMAN	23.4	100.0%	3	3	4	0.00%	15.8%	FLASVLHNGLGR	99.7%	58.4	25	51	1	0	0	1283.72	10	21
39S ribosomal protein L43, mitochondrial	MRPL43	RM43_HUMAN	23.4	100.0%	3	3	4	0.00%	15.8%	LADQSGLDVIR	99.7%	76.9	25	66.6	1	0	0	1186.64	104	114
39S ribosomal protein L43, mitochondrial	MRPL43	RM43_HUMAN	23.4	100.0%	3	3	4	0.00%	15.8%	SVEEISTLVQK	99.7%	64.1	25	45.2	2	0	0	1232.67	93	103
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	4	4	5	0.01%	14.5%	LIAEGPGETVLVAEEEAAR	99.7%	74.3	25	74.3	1	0	0	1954.01	280	298
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	4	4	5	0.01%	14.5%	LQENFSLDLLK	99.7%	51	25	37	2	0	0	1319.72	79	89
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	4	4	5	0.01%	14.5%	LYGFTENR	96.2%	28.7	25	28.7	1	0	0	999.49	304	311
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	4	4	5	0.01%	14.5%	TAFVNSCYIK	95.3%	27.9	25	27	1	0	0	1202.59	90	99
39S ribosomal protein L46, mitochondrial	MRPL46	RM46_HUMAN	31.7	100.0%	4	4	7	0.01%	15.4%	ALLLTGDFSQAGNK	99.7%	70.4	25	64.9	2	0	0	1434.76	236	249
39S ribosomal protein L46, mitochondrial	MRPL46	RM46_HUMAN	31.7	100.0%	4	4	7	0.01%	15.4%	NLVLLVR	98.2%	31.6	25	8.58	1	0	0	826.55	156	162
39S ribosomal protein L46, mitochondrial	MRPL46	RM46_HUMAN	31.7	100.0%	4	4	7	0.01%	15.4%	SLYSDHELR	99.7%	43.1	25	29.7	2	0	0	1119.54	82	90
39S ribosomal protein L46, mitochondrial	MRPL46	RM46_HUMAN	31.7	100.0%	4	4	7	0.01%	15.4%	TLATLSENNMEAK	99.7%	49.2	25	43.3	2	0	0	1437.69	191	203
39S ribosomal protein L47, mitochondrial	MRPL47	RM47_HUMAN	29.5	100.0%	4	5	7	0.01%	13.2%	NMLLTLEQEAK	99.7%	58	25	34.8	2	0	0	1289.68	110	120
39S ribosomal protein L47, mitochondrial	MRPL47	RM47_HUMAN	29.5	100.0%	4	5	7	0.01%	13.2%	NMLLTLEQEAKR	99.7%	56.5	25	45.7	2	0	0	1445.78	110	121
39S ribosomal protein L47, mitochondrial	MRPL47	RM47_HUMAN	29.5	100.0%	4	5	7	0.01%	13.2%	SGAAWTCQQLR	99.7%	45.4	25	36.2	2	0	0	1277.61	81	91
39S ribosomal protein L47, mitochondrial	MRPL47	RM47_HUMAN	29.5	100.0%	4	5	7	0.01%	13.2%	VVQEREDALR	98.2%	31.8	25	8.44	1	0	0	1214.65	145	154
39S ribosomal protein L48, mitochondrial	MRPL48	RM48_HUMAN	23.9	100.0%	3	4	7	0.01%	17.0%	ARPELEELLAK	99.7%	55.1	25	35.9	2	0	0	1268.72	200	210
39S ribosomal protein L48, mitochondrial	MRPL48	RM48_HUMAN	23.9	100.0%	3	4	7	0.01%	17.0%	MLLDSVLTTHER	99.7%	69.1	25	59.1	3	0	0	1414.74	144	155
39S ribosomal protein L48, mitochondrial	MRPL48	RM48_HUMAN	23.9	100.0%	3	4	7	0.01%	17.0%	TIEVLQLQDQGSK	99.7%	101	25	100	2	0	0	1458.78	131	143
39S ribosomal protein L53, mitochondrial	MRPL53	RM53_HUMAN	12.1	100.0%	3	3	5	0.01%	27.7%	STNLNCSVIADVR	99.7%	77.4	25	71.4	2	0	0	1448.72	44	56
39S ribosomal protein L53, mitochondrial	MRPL53	RM53_HUMAN	12.1	100.0%	3	3	5	0.01%	27.7%	TFLQTVSSEK	99.7%	47.9	25	40.4	2	0	0	1139.59	32	41
39S ribosomal protein L53, mitochondrial	MRPL53	RM53_HUMAN	12.1	100.0%	3	3	5	0.01%	27.7%	VQFCPFEK	96.8%	29.4	25	25.8	1	0	0	1054.50	18	25
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	4	5	8	0.01%	19.5%	ENLELILTQSVENVGVR	99.7%	42.2	25	42.2	2	0	0	1913.03	92	108

39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	4	5	8	0.01%	19.5%	LLPQGLAVYASPENK	99.7%	48	25	41.2	2	0	0	1599.87	123	137
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	4	5	8	0.01%	19.5%	LPEEPITR	98.8%	33.3	25	27.6	1	0	0	954.53	208	215
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	4	5	8	0.01%	19.5%	VPMSVVNFEKPK	99.6%	38.9	25	38.9	3	0	0	1374.75	233	244
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	5	7	11	0.01%	34.1%	GGIVGMTLPIAR	99.7%	65.5	25	56.6	2	0	0	1200.68	173	184
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	5	7	11	0.01%	34.1%	GLVAVITGGASGLGLATAER	99.7%	128	25	128	2	1	0	1813.02	10	29
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	5	7	11	0.01%	34.1%	GVIINTASVAAFEGQVGQAAYSASK	99.7%	39	25	39	0	1	0	2439.25	148	172
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	5	7	11	0.01%	34.1%	LVAGEMGQNEPDQGGQR	99.7%	98.7	25	98.7	3	0	0	1785.82	131	147
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	5	7	11	0.01%	34.1%	VDVAVNCAGIAVASK	99.7%	95.1	25	95.1	2	0	0	1473.77	85	99
3-ketoacyl-CoA thiolase, mitochondrial	ACAA2	THIM_HUMAN	41.9	100.0%	3	3	5	0.01%	8.3%	DFTATDLSEFAAK	99.7%	99.5	25	96.1	2	0	0	1415.67	26	38
3-ketoacyl-CoA thiolase, mitochondrial	ACAA2	THIM_HUMAN	41.9	100.0%	3	3	5	0.01%	8.3%	ETPALTINR	99.7%	46.3	25	46.3	2	0	0	1014.56	82	90
3-ketoacyl-CoA thiolase, mitochondrial	ACAA2	THIM_HUMAN	41.9	100.0%	3	3	5	0.01%	8.3%	TPFGAYGGLLK	99.7%	55.6	25	53.2	1	0	0	1123.61	15	25
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	5	7	26	0.03%	29.7%	AEAGAGSATEFQFR	99.7%	114	25	111	6	0	0	1441.67	140	153
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	5	7	26	0.03%	29.7%	DYLHLPPEIVPATLR	99.7%	43.9	25	33.4	2	1	0	1733.96	81	95
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	5	7	26	0.03%	29.7%	GYVKEQFAWR	99.7%	44.3	25	38.9	3	0	0	1283.65	56	65
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	5	7	26	0.03%	29.7%	IAIYELLFK	99.7%	63.9	25	63.9	6	0	0	1109.66	9	17
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	5	7	26	0.03%	29.7%	KAEAGAGSATEFQFR	99.7%	111	25	109	4	4	0	1569.77	139	153
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	11	14	42	0.04%	53.2%	CPFTGNVSIR	99.7%	67.7	25	47.7	7	0	0	1150.57	60	69
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	11	14	42	0.04%	53.2%	DVQIGDIVTVGECRPLSK	99.7%	78.6	25	69.3	5	4	0	1986.03	119	136
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	11	14	42	0.04%	53.2%	DYLHYIR	96.1%	28.6	25	18.1	3	0	0	979.50	91	97
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	11	14	42	0.04%	53.2%	EAIEGTYIDK	99.7%	64.2	25	55	2	0	0	1138.56	49	58
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	11	14	42	0.04%	53.2%	EAIEGTYIDKK	99.7%	58.1	25	47.4	5	0	0	1266.66	49	59
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	11	14	42	0.04%	53.2%	ILSGVVTK	99.7%	50.6	25	27.5	3	0	0	816.52	72	79
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	11	14	42	0.04%	53.2%	KCPFTGNVSIR	99.6%	38.2	25	35.8	2	0	0	1278.66	59	69
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	11	14	42	0.04%	53.2%	NMSVHLSPCFR	99.7%	39.9	25	38.4	4	2	0	1347.63	108	118
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	11	14	42	0.04%	53.2%	QPTIFQNK	98.2%	31.9	25	20.9	1	0	0	975.53	13	20
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	11	14	42	0.04%	53.2%	RDYLHYIR	99.7%	43.5	25	22.2	2	0	0	1135.60	90	97
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	11	14	42	0.04%	53.2%	VLLGETGKEK	99.7%	50.5	25	31	2	0	0	1073.62	23	32
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	9	28	0.03%	57.6%	DVIEEYFK	98.6%	32.7	25	32.7	1	0	0	1042.51	122	129
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	9	28	0.03%	57.6%	ESQAKDVIEEYFK	99.7%	40.7	25	33.1	1	0	0	1585.77	117	129
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	9	28	0.03%	57.6%	KVVGCSCVVVK	99.7%	46.8	25	42.2	3	0	0	1234.66	102	112
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	9	28	0.03%	57.6%	LGEWVGLCK	99.7%	61.8	25	55.4	8	0	0	1061.55	85	93
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	9	28	0.03%	57.6%	LVEALCAEHQINLIK	99.7%	55.7	25	54.3	4	2	0	1750.95	64	78
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	9	28	0.03%	57.6%	QAHLCVLASNCDEPMYVK	98.0%	25.7	25	25.7	0	2	0	2150.97	46	63
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	9	28	0.03%	57.6%	TALIHDGLAR	99.7%	50.4	25	34.4	5	0	0	1066.60	24	33
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	9	28	0.03%	57.6%	VVGCSCVVVK	99.7%	54.8	25	44.9	2	0	0	1106.57	103	112
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	10	12	32	0.03%	51.7%	FRLILIESR	99.7%	43.6	25	43.6	2	0	0	1146.70	113	121
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	10	12	32	0.03%	51.7%	FVTGNKILR	99.6%	38.3	25	32.2	1	0	0	1047.63	65	73
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	10	12	32	0.03%	51.7%	GLAPDLPEDLYHLIK	99.6%	38.5	25	38.5	2	0	0	1693.92	79	93
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	10	12	32	0.03%	51.7%	GLTPSQIGVILR	99.7%	73.4	25	57.9	4	0	0	1253.76	44	55
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	10	12	32	0.03%	51.7%	KGLTPSQIGVILR	99.7%	63.1	25	63.1	3	2	0	1381.85	43	55
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	10	12	32	0.03%	51.7%	LILIESR	99.7%	46.2	25	20.9	4	0	0	843.53	115	121
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	10	12	32	0.03%	51.7%	LTSDDVKEQIYK	99.7%	73.9	25	73.2	8	2	0	1438.74	28	39
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	10	12	32	0.03%	51.7%	SKGLAPDLPEDLYHLIK	97.1%	24.3	25	24.3	0	1	0	1909.04	77	93
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	10	12	32	0.03%	51.7%	VLPPNWKYESSTASALVA	97.0%	29.6	25	29.6	1	0	0	1933.01	134	151
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	10	12	32	0.03%	51.7%	YESSTASALVA	99.7%	39.3	25	39.3	2	0	0	1098.53	141	151
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	45	0.05%	41.7%	ADRDESSPYAAMLAAQDVAQR	99.7%	55.7	25	55.7	0	4	0	2281.05	64	84
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	45	0.05%	41.7%	CKELGITALHIK	99.7%	61.7	25	55.6	2	2	0	1382.78	85	96
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	45	0.05%	41.7%	DESSPYAAMLAAQDVAQR	99.7%	87.8	25	77.3	3	0	0	1938.89	67	84
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	45	0.05%	41.7%	ELGITALHIK	99.7%	51.5	25	39.2	2	0	0	1094.66	87	96
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	45	0.05%	41.7%	IEDVTPIPSDSTR	99.7%	69.9	25	59.7	4	0	0	1429.72	129	141
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	45	0.05%	41.7%	IEDVTPIPSDSTRR	99.7%	46.2	25	42.2	3	4	0	1585.82	129	142

40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	45	0.05%	41.7%	IGRIEDVTPIPSDSTR	99.7%	70.3	25	69.1	2	2	0	1755.92	126	141
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	45	0.05%	41.7%	TKTPGPGAQSALR	99.7%	42.8	25	32.4	2	2	0	1283.71	105	117
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	45	0.05%	41.7%	TPGPGAQSALR	99.7%	76.2	25	73.9	13	0	0	1054.56	107	117
40S ribosomal protein S15	RPS15	RS15_HUMAN	17.0	100.0%	3	7	17	0.02%	22.1%	DMIILPEMVGSMVGVYNGK	99.7%	82.2	25	51.6	9	0	0	2085.01	82	100
40S ribosomal protein S15	RPS15	RS15_HUMAN	17.0	100.0%	3	7	17	0.02%	22.1%	EAPPMEKPEVVK	99.7%	55.8	25	45.8	3	0	0	1353.71	66	77
40S ribosomal protein S15	RPS15	RS15_HUMAN	17.0	100.0%	3	7	17	0.02%	22.1%	KEAPPMEKPEVVK	99.7%	39.3	25	39.3	1	4	0	1497.80	65	77
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	9	11	26	0.03%	52.3%	DLEKWQNNLLPSR	97.6%	30.6	25	21.1	1	0	0	1612.84	85	97
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	9	11	26	0.03%	52.3%	FDVQLKDLEK	99.7%	62.5	25	17.1	5	1	0	1234.67	79	88
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	9	11	26	0.03%	52.3%	FLTVMMK	99.7%	42.1	25	0	5	0	0	885.46	37	43
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	9	11	26	0.03%	52.3%	HGYIGEFEIIDDHR	99.3%	29.8	25	29.8	0	2	0	1700.80	44	57
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	9	11	26	0.03%	52.3%	IVVNLTGR	99.7%	51.2	25	40.5	2	0	0	871.54	61	68
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	9	11	26	0.03%	52.3%	MNVLADALK	99.7%	52.1	25	45.7	5	0	0	974.53	4	12
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	9	11	26	0.03%	52.3%	QVLIRPCSK	98.5%	32.6	25	18.1	1	0	0	1100.62	24	32
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	9	11	26	0.03%	52.3%	VRMNVLADALK	99.1%	28.6	25	17.8	0	2	0	1245.70	2	12
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	9	11	26	0.03%	52.3%	WQNNLLPSR	99.3%	35.7	25	35	2	0	0	1127.60	89	97
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	13	20	88	0.09%	61.6%	ALVAYYQK	99.7%	50.8	25	38.9	6	0	0	955.52	91	98
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	13	20	88	0.09%	61.6%	EIKDILIQYDR	99.7%	68.8	25	60.8	11	10	0	1405.77	107	117
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	13	20	88	0.09%	61.6%	FAGVDIRVR	98.3%	32.1	25	19	2	0	0	1032.59	63	71
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	13	20	88	0.09%	61.6%	GGGHVAQIYAIR	99.7%	44.1	25	43.1	8	0	0	1241.68	74	85
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	13	20	88	0.09%	61.6%	GPLQSVQVFGR	99.7%	82.5	25	66.5	6	0	0	1187.65	5	15
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	13	20	88	0.09%	61.6%	GPLQSVQVFGRK	99.7%	40.8	25	40.8	1	1	0	1315.75	5	16
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	13	20	88	0.09%	61.6%	LLEPVLLLGK	99.7%	52.3	25	52.3	7	0	0	1094.72	51	60
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	13	20	88	0.09%	61.6%	LLEPVLLLGKER	99.7%	81.4	25	81.4	4	0	0	1379.86	51	62
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	13	20	88	0.09%	61.6%	PSKGPLQSVQVFGR	99.7%	66.1	25	66.1	3	4	0	1499.83	2	15
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	13	20	88	0.09%	61.6%	TLLVADPR	99.7%	45.2	25	22.2	6	0	0	884.52	118	125
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	13	20	88	0.09%	61.6%	TLLVADPRR	99.7%	49.7	25	30.2	4	0	0	1040.62	118	126
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	13	20	88	0.09%	61.6%	VKGGGHVAQIYAIR	99.7%	65.5	25	64.9	2	2	0	1468.84	72	85
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	13	20	88	0.09%	61.6%	VNGRPLEMIEPR	99.7%	40.9	25	35.9	3	8	0	1410.75	34	45
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	8	12	29	0.03%	47.4%	IAGYVTHLMK	99.7%	59.7	25	50.3	8	0	0	1132.62	50	59
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	8	12	29	0.03%	47.4%	IAGYVTHLMKR	97.7%	25.2	25	20.7	0	1	0	1304.71	50	60
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	8	12	29	0.03%	47.4%	LGNDFHTNK	99.1%	34.8	25	25.2	2	0	0	1045.51	24	32
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	8	12	29	0.03%	47.4%	LGNDFHTNKR	99.7%	54.1	25	37.6	2	2	0	1201.61	24	33
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	8	12	29	0.03%	47.4%	LLDFGSLSNLQVTQPTVGMNFK	99.7%	76.2	25	75.8	4	2	0	2409.25	108	129
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	8	12	29	0.03%	47.4%	VCEEIAIIPSK	99.7%	69.8	25	39.9	3	0	0	1258.67	34	44
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	8	12	29	0.03%	47.4%	VCEEIAIIPSKK	99.7%	59.2	25	45	3	0	0	1386.77	34	45
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	8	12	29	0.03%	47.4%	VIIEKYYTR	99.7%	60.9	25	54.3	2	0	0	1184.67	15	23
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	19	54	0.06%	59.2%	ADIDLTKR	99.7%	56	25	34.9	2	0	0	931.52	48	55
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	19	54	0.06%	59.2%	AGELTEDEVER	99.7%	56.3	25	56.3	3	0	0	1247.58	56	66
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	19	54	0.06%	59.2%	AGELTEDEVERVITIMQNPR	99.7%	38.8	25	38.8	0	3	0	2316.15	56	75
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	19	54	0.06%	59.2%	HFWGLR	97.3%	30	25	21.1	1	0	0	815.43	125	130
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	19	54	0.06%	59.2%	IAFAITAIK	99.7%	66.8	25	58.5	3	0	0	947.59	26	34
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	19	54	0.06%	59.2%	IAFAITAIKGVGR	99.7%	40.3	25	40.3	1	0	0	1316.81	26	38
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	19	54	0.06%	59.2%	IPDWFLNR	99.7%	47.7	25	36.5	7	0	0	1060.56	79	86
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	19	54	0.06%	59.2%	KIAFAITAIK	99.7%	54.8	25	50.7	2	0	0	1075.69	25	34
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	19	54	0.06%	59.2%	QYKIPDWFLNR	98.5%	26.8	25	15.1	0	1	0	1479.77	76	86
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	19	54	0.06%	59.2%	RAGELTEDEVER	99.7%	66.7	25	51.3	6	2	0	1403.68	55	66
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	19	54	0.06%	59.2%	VITIMQNPR	99.7%	56.3	25	49.8	10	0	0	1087.59	67	75
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	19	54	0.06%	59.2%	VLNTNIDGR	99.7%	57.2	25	48.8	7	0	0	1001.54	15	23
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	19	54	0.06%	59.2%	YAHVVLRK	97.7%	30.6	25	23.6	1	0	0	985.59	40	47
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	19	54	0.06%	59.2%	YSQVLANGLDNK	99.7%	74.2	25	67.8	2	0	0	1321.67	95	106
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	19	54	0.06%	59.2%	YSQVLANGLDNKLR	99.7%	42.9	25	42.1	2	1	0	1590.86	95	108

40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	5	5	7	0.01%	36.6%	ALAAFLKK	98.8%	33.3	25	24.4	1	0	0	861.56	17	24
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	5	5	7	0.01%	36.6%	DLDRIAGQVAAANK	99.4%	36.8	25	36.8	1	0	0	1441.78	130	143
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	5	5	7	0.01%	36.6%	DVNQQEFVR	99.7%	60.8	25	46.8	2	0	0	1134.55	8	16
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	5	5	7	0.01%	36.6%	ELAPYDENWFYTR	99.7%	44.2	25	42.5	1	0	0	1703.77	44	56
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	5	5	7	0.01%	36.6%	VLQALEGLK	99.7%	44.1	25	37.5	2	0	0	970.59	103	111
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	12	18	82	0.08%	42.3%	AEDKEWMPVTK	99.7%	60.3	25	43.3	8	2	0	1333.65	55	65
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	12	18	82	0.08%	42.3%	AFVAIGDYNGHVGLGVK	99.7%	88.1	25	88.1	2	0	0	1716.91	126	142
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	12	18	82	0.08%	42.3%	ATFDAISK	99.7%	51.8	25	29	4	0	0	852.45	239	246
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	12	18	82	0.08%	42.3%	GCTATLGNFAK	99.7%	65.5	25	57.4	6	0	0	1139.55	228	238
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	12	18	82	0.08%	42.3%	GTGIVSAPVPK	99.7%	49.4	25	49.4	7	0	0	1025.60	201	211
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	12	18	82	0.08%	42.3%	KLLMMAGIDDCYTSAR	99.7%	55.1	25	9.29	2	11	0	1860.87	212	227
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	12	18	82	0.08%	42.3%	LLMMAGIDDCYTSAR	99.7%	82.6	25	82.6	11	0	0	1716.78	213	227
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	12	18	82	0.08%	42.3%	LSIVPVRR	99.7%	46.6	25	26.3	6	0	0	939.61	160	167
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	12	18	82	0.08%	42.3%	SLEEIYLFSLPIK	99.7%	67.6	25	62.3	4	0	0	1551.87	77	89
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	12	18	82	0.08%	42.3%	SPYQEFTDHLVK	99.7%	63.3	25	63.3	8	4	0	1463.72	264	275
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	12	18	82	0.08%	42.3%	TYSYLTPDLWK	99.7%	71.2	25	65.7	6	0	0	1386.69	247	257
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	12	18	82	0.08%	42.3%	TYSYLTPDLWKETVFTK	98.8%	33.3	25	33.3	1	0	0	2092.06	247	263
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	4	7	15	0.02%	28.6%	DTGKTPVEPEVAIHR	99.7%	72.1	25	72.1	2	2	0	1648.87	5	19
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	4	7	15	0.02%	28.6%	LIDLHSPSEIVK	99.7%	52.8	25	43.5	4	1	0	1350.76	88	99
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	4	7	15	0.02%	28.6%	TPVEPEVAIHR	99.7%	56	25	56	2	2	0	1247.67	9	19
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	4	7	15	0.02%	28.6%	VCADLIR	99.7%	44.7	25	33.7	2	0	0	846.45	35	41
40S ribosomal protein S21	RPS21	RS21_HUMAN	9.1	99.8%	2	2	3	0.00%	22.9%	MGESDDSILR	99.7%	46	25	40.5	2	0	0	1138.50	62	71
40S ribosomal protein S21	RPS21	RS21_HUMAN	9.1	99.8%	2	2	3	0.00%	22.9%	TYAICGAIR	99.7%	41.1	25	32.6	1	0	0	1024.52	52	60
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	5	6	14	0.01%	29.4%	AHLGTALK	95.5%	28.1	25	9.72	1	0	0	810.48	30	37
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	5	6	14	0.01%	29.4%	ANPFGGASHAK	99.7%	43.4	25	43.4	5	0	0	1056.52	38	48
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	5	6	14	0.01%	29.4%	GHAVGDIPGVR	98.9%	33.7	25	30.7	1	0	0	1077.58	109	119
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	5	6	14	0.01%	29.4%	KGHAVGDIPGVR	99.7%	47.7	25	42.3	2	2	0	1205.68	108	119
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	5	6	14	0.01%	29.4%	VANVSLLALYK	99.7%	91.7	25	91.7	3	0	0	1190.71	125	135
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	8	42	0.04%	30.1%	KQMVIDVLHPGK	99.7%	48.5	25	46.8	2	3	0	1380.77	21	32
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	8	42	0.04%	30.1%	QMVIDVLHPGK	99.7%	50.1	25	37.3	2	0	0	1236.68	22	32
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	8	42	0.04%	30.1%	TTGFGMIYDSLDYAK	99.7%	77.1	25	77.1	17	0	0	1697.77	69	83
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	8	42	0.04%	30.1%	TTGFGMIYDSLDYAKK	99.7%	60.6	25	60.6	2	0	0	1809.87	69	84
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	8	42	0.04%	30.1%	TTPDVIFVFGFR	99.7%	75.2	25	67.5	16	0	0	1398.74	50	61
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	5	5	26	0.03%	36.0%	AALQELLSK	99.7%	78.8	25	62.5	11	0	0	972.57	86	94
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	5	5	26	0.03%	36.0%	AQVIYTR	98.8%	33.3	25	23.3	2	0	0	850.48	105	111
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	5	5	26	0.03%	36.0%	ATYDKLCK	99.7%	39.6	25	33.7	2	0	0	998.50	53	60
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	5	5	26	0.03%	36.0%	DKLNNLVLFDK	99.7%	69.3	25	63.7	2	0	0	1318.74	42	52
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	5	5	26	0.03%	36.0%	LITPAVVSER	99.7%	73.8	25	61.3	9	0	0	1084.64	67	76
40S ribosomal protein S26	RPS26	RS26_HUMAN	13.0	100.0%	3	4	20	0.02%	31.3%	DISEASVFDAYVLPK	99.7%	87.7	25	75.5	7	0	0	1653.84	52	66
40S ribosomal protein S26	RPS26	RS26_HUMAN	13.0	100.0%	3	4	20	0.02%	31.3%	LHYCVSCAIHSK	99.7%	65.2	25	58.2	2	2	0	1474.69	71	82
40S ribosomal protein S26	RPS26	RS26_HUMAN	13.0	100.0%	3	4	20	0.02%	31.3%	NIVEAAAVR	99.7%	62.1	25	46.8	9	0	0	942.54	43	51
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	4	7	22	0.02%	39.3%	DLLHPSPEEEK	99.3%	36.2	25	33.8	1	1	0	1293.63	6	16
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	4	7	22	0.02%	39.3%	DLLHPSPEEEKR	99.7%	34.2	25	28	1	2	0	1449.73	6	17
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	4	7	22	0.02%	39.3%	LTEGCSFR	99.7%	47.4	25	38.2	3	0	0	969.45	73	80
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	4	7	22	0.02%	39.3%	LVQSPNSYFMDVK	99.7%	59.2	25	57.4	14	0	0	1527.75	24	36
40S ribosomal protein S28	RPS28	RS28_HUMAN	7.8	99.8%	2	2	4	0.00%	30.4%	EGDVLTLLESER	99.7%	66	25	58.9	2	0	0	1360.70	52	63
40S ribosomal protein S28	RPS28	RS28_HUMAN	7.8	99.8%	2	2	4	0.00%	30.4%	VEFMDDTSR	99.7%	45.8	25	45.8	2	0	0	1115.47	32	40
40S ribosomal protein S29	RPS29	RS29_HUMAN	6.7	100.0%	3	4	6	0.01%	33.9%	GHQQLYWSHPR	99.1%	28.8	25	27.2	1	2	0	1408.69	2	12
40S ribosomal protein S29	RPS29	RS29_HUMAN	6.7	100.0%	3	4	6	0.01%	33.9%	KYGLNMCR	98.6%	32.8	25	28.7	1	0	0	1057.49	33	40
40S ribosomal protein S29	RPS29	RS29_HUMAN	6.7	100.0%	3	4	6	0.01%	33.9%	YGLNMCR	99.7%	41.8	25	34.8	2	0	0	913.40	34	40
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	18	24	108	0.11%	68.3%	ACYGVLR	99.5%	37.8	25	27.4	2	0	0	838.42	118	124

40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	18	24	108	0.11%	68.3%	AELNEFLTR	99.7%	67.9	25	48	14	0	0	1092.57	19	27
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	18	24	108	0.11%	68.3%	DEILPTTPISEQK	99.7%	84.4	25	67.4	6	0	0	1470.77	215	227
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	18	24	108	0.11%	68.3%	ELAEDGYSGVEVR	99.7%	93.2	25	81.9	13	0	0	1423.67	28	40
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	18	24	108	0.11%	68.3%	ELTAVVQK	99.7%	46.1	25	27.1	2	0	0	887.52	68	75
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	18	24	108	0.11%	68.3%	ELTAVVQKR	99.7%	55.8	25	45.7	2	0	0	1043.62	68	76
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	18	24	108	0.11%	68.3%	FGFPEGSVELYAEK	99.7%	103	25	98.6	11	0	0	1572.76	77	90
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	18	24	108	0.11%	68.3%	FIMESGAK	99.4%	36.4	25	14.2	1	0	0	882.44	125	132
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	18	24	108	0.11%	68.3%	FVADGIFK	98.2%	31.7	25	28	2	0	0	896.49	11	18
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	18	24	108	0.11%	68.3%	FVDGLMIHSGDPVNYYVDTAVR	99.7%	60.1	25	60.1	1	5	0	2484.19	152	173
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	18	24	108	0.11%	68.3%	GGKPEPPAMPQPVPTA	99.7%	64	25	59	6	0	0	1573.80	228	243
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	18	24	108	0.11%	68.3%	GLCAIAQAESLR	99.7%	87.2	25	77.2	9	0	0	1288.67	95	106
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	18	24	108	0.11%	68.3%	IMLPWDPTGK	99.7%	48.8	25	47.5	5	0	0	1173.60	188	197
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	18	24	108	0.11%	68.3%	IRELTAVVQK	99.7%	53.4	25	43.8	2	0	0	1156.70	66	75
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	18	24	108	0.11%	68.3%	KFVADGIFK	99.7%	53.2	25	43.7	4	0	0	1024.58	10	18
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	18	24	108	0.11%	68.3%	KPLPDHVSIVEPK	99.7%	47.3	25	37.5	2	1	0	1458.83	202	214
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	18	24	108	0.11%	68.3%	RFGFPEGSVELYAEK	99.7%	77.6	25	69.9	1	1	0	1728.86	76	90
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	18	24	108	0.11%	68.3%	TEIIILATR	99.7%	65.9	25	65.1	18	0	0	1029.63	46	54
40S ribosomal protein S30	FAU	RS30_HUMAN	6.6	99.8%	2	2	6	0.01%	18.6%	FVNVVPTFGK	99.2%	35.1	25	29.8	4	0	0	1107.62	42	51
40S ribosomal protein S30	FAU	RS30_HUMAN	6.6	99.8%	2	2	6	0.01%	18.6%	FVNVVPTFGKK	99.7%	39.2	25	39.2	2	0	0	1235.71	42	52
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	97	0.10%	63.3%	ACQSIYPLHDVFVR	99.7%	72.6	25	62.1	4	4	0	1704.85	200	213
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	97	0.10%	63.3%	ADGYEPPVQESV	99.7%	49.5	25	49.5	4	0	0	1290.58	253	264
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	97	0.10%	63.3%	APAMFNIR	99.7%	63.8	25	49	6	0	0	935.48	35	42
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	97	0.10%	63.3%	ATGDETGAKVER	99.7%	56	25	47.7	2	2	0	1233.61	241	252
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	97	0.10%	63.3%	DWYDVK	98.2%	31.7	25	16.1	2	0	0	825.38	29	34
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	97	0.10%	63.3%	EVQTNDLKEVVNK	99.7%	72.6	25	60.3	4	1	0	1515.80	175	187
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	97	0.10%	63.3%	FKLITEDVQGK	99.7%	60.7	25	37.1	4	0	0	1277.71	84	94
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	97	0.10%	63.3%	KDWYDVK	97.1%	29.8	25	16.9	1	0	0	953.47	28	34
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	97	0.10%	63.3%	KTSYAQHQQVR	99.0%	28.5	25	23.6	0	1	0	1345.70	152	162
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	97	0.10%	63.3%	LFCVGFTK	99.7%	49.5	25	36.1	7	0	0	971.50	137	144
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	97	0.10%	63.3%	LIPDSIGKDIEK	99.7%	53.5	25	50.1	4	0	0	1327.75	188	199
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	97	0.10%	63.3%	LITEDVQGK	99.7%	58	25	45.3	4	0	0	1002.55	86	94
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	97	0.10%	63.3%	LMELHGEGSSSGK	99.7%	71.7	25	69.4	6	4	0	1331.63	228	240
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	97	0.10%	63.3%	MMEIMTR	99.7%	42.4	25	32.6	4	0	0	911.41	168	174
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	97	0.10%	63.3%	NCLTNFHGMDLTR	99.7%	91.3	25	82.4	8	7	0	1578.72	95	107
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	97	0.10%	63.3%	TSYAQHQQVR	99.7%	80.1	25	59	2	1	0	1217.60	153	162
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	97	0.10%	63.3%	TTDGYLLR	99.7%	64.3	25	44.3	6	0	0	938.49	129	136
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	97	0.10%	63.3%	VERADGYEPPVQESV	99.7%	67.9	25	67.3	1	0	0	1674.80	250	264
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	97	0.10%	63.3%	VFEVSLADLQNDEVAFR	99.7%	75.4	25	75.4	2	0	0	1951.98	66	82
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	97	0.10%	63.3%	VFEVSLADLQNDEVAFRK	99.7%	43.6	25	43.6	2	4	0	2080.07	66	83
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	17	24	85	0.09%	57.0%	ECLPLIIFLR	99.7%	51.6	25	42.8	7	0	0	1273.73	40	49
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	17	24	85	0.09%	57.0%	ERHPGSFDVVHVK	99.7%	48.8	25	45.4	1	2	0	1506.78	199	211
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	17	24	85	0.09%	57.0%	FDTGNLCMVTGGANLGR	99.7%	109	25	108	10	1	0	1782.83	175	191
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	17	24	85	0.09%	57.0%	GIPHLVTHDAR	99.7%	56.4	25	48.9	2	2	0	1215.66	135	145
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	17	24	85	0.09%	57.0%	GNKPWISLPR	99.7%	41.8	25	36.1	2	0	0	1167.66	231	240
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	17	24	85	0.09%	57.0%	HPGSFDVVHVK	99.7%	74.5	25	74.5	2	2	0	1221.64	201	211
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	17	24	85	0.09%	57.0%	LRECLPLIIFLR	99.7%	49.6	25	47.5	2	2	0	1542.92	38	49
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	17	24	85	0.09%	57.0%	LSNIFVIGK	99.7%	79.2	25	73.5	12	0	0	990.60	222	230
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	17	24	85	0.09%	57.0%	LTGVFAPRPSTGPHK	99.7%	48.2	25	43.5	2	0	0	1564.86	23	37
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	17	24	85	0.09%	57.0%	LTIAEER	99.7%	43	25	14.9	8	0	0	831.46	246	252
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	17	24	85	0.09%	57.0%	TDITYPAGFMDVISIDK	99.7%	89.1	25	87.3	9	0	0	1885.93	78	94
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	17	24	85	0.09%	57.0%	TIRYPDPLIK	99.7%	35.3	25	20.2	0	2	0	1215.71	146	155

40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	17	24	85	0.09%	57.0%	VNDTIQIDLETGK	99.7%	102	25	102	7	0	0	1445.75	156	168
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	17	24	85	0.09%	57.0%	VNDTIQIDLETGKITDFIK	99.5%	31.3	25	31.3	0	1	0	2163.15	156	174
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	17	24	85	0.09%	57.0%	YALTGDEVK	99.7%	53.9	25	46.7	2	0	0	995.50	54	62
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	17	24	85	0.09%	57.0%	YALTGDEVKK	99.7%	54.3	25	46.5	6	0	0	1123.60	54	63
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	17	24	85	0.09%	57.0%	YPDPLIK	97.6%	30.6	25	7.19	1	0	0	845.48	149	155
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	7	8	16	0.02%	27.9%	AQCPIVER	98.2%	31.7	25	23.1	1	0	0	972.49	64	71
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	7	8	16	0.02%	27.9%	KAQCPIVER	99.7%	42.9	25	39.7	2	0	0	1100.59	63	71
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	7	8	16	0.02%	27.9%	LTNSMMMHGR	99.7%	67.4	25	61.1	3	0	0	1177.53	72	81
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	7	8	16	0.02%	27.9%	QAVDVSPLR	99.7%	69.2	25	59.2	3	0	0	984.55	137	145
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	7	8	16	0.02%	27.9%	QAVDVSPLRR	98.6%	32.8	25	28.5	1	0	0	1140.65	137	146
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	7	8	16	0.02%	27.9%	TIAECLADELINAAK	99.7%	114	25	108	4	0	0	1631.83	168	182
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	7	8	16	0.02%	27.9%	VNQAIWLLCTGAR	99.7%	90.5	25	85	2	0	0	1501.79	147	159
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	12	15	49	0.05%	42.2%	DIPGLTDTTVPR	99.7%	74.1	25	62.5	10	0	0	1284.68	120	131
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	12	15	49	0.05%	42.2%	DIPGLTDTTVPRR	95.3%	27.9	25	25.6	1	0	0	1440.78	120	132
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	12	15	49	0.05%	42.2%	EDDVRQYVVR	95.7%	28.3	25	16	1	0	0	1278.64	150	159
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	12	15	49	0.05%	42.2%	GCIVDANLSVLNLVIVK	99.7%	76.7	25	74.3	5	0	0	1827.04	99	115
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	12	15	49	0.05%	42.2%	GEKDIPGLTDTTVPR	99.7%	42.9	25	39.1	0	2	0	1598.84	117	131
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	12	15	49	0.05%	42.2%	ISGGNDKQGFPMK	99.7%	43.9	25	42.3	4	0	0	1378.68	52	64
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	12	15	49	0.05%	42.2%	LFNLSKEDDVR	99.7%	60	25	45.2	4	0	0	1335.69	144	154
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	12	15	49	0.05%	42.2%	LIEVDDER	99.7%	52.3	25	50.7	4	0	0	988.49	15	22
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	12	15	49	0.05%	42.2%	LIEVDDERK	99.7%	46.5	25	33	2	0	0	1116.59	15	23
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	12	15	49	0.05%	42.2%	MATEVAADALGEEWK	99.7%	116	25	116	7	0	0	1636.75	32	46
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	12	15	49	0.05%	42.2%	MATEVAADALGEEWKGYVVR	99.7%	76.2	25	76.2	3	1	0	2211.08	32	51
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	12	15	49	0.05%	42.2%	MKLNISFPATGCQK	99.7%	73.9	25	63.5	4	1	0	1610.80	1	14
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	9	10	28	0.03%	43.3%	AIIIFVPVPQLK	99.7%	80.7	25	80.7	7	0	0	1337.86	59	70
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	9	10	28	0.03%	43.3%	AQQNNVEHKVETFSGVYK	99.7%	79.9	25	79.9	2	2	0	2078.03	161	178
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	9	10	28	0.03%	43.3%	DVNFEFPEFQL	99.7%	71.3	25	69.4	2	0	0	1384.64	184	194
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	9	10	28	0.03%	43.3%	ELNITAAK	99.7%	40.4	25	30.9	1	0	0	859.49	42	49
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	9	10	28	0.03%	43.3%	HVVFIAQR	97.8%	31	25	31	4	0	0	969.56	91	98
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	9	10	28	0.03%	43.3%	KAIIIFVPVPQLK	99.7%	55	25	55	5	0	0	1465.95	58	70
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	9	10	28	0.03%	43.3%	LTGKDVNFEFPEFQL	99.7%	63.7	25	63.7	2	0	0	1783.89	180	194
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	9	10	28	0.03%	43.3%	TLTAVHDAILEDLVFPSEIVGK	95.5%	22.7	25	22.3	0	1	0	2367.28	121	142
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	9	10	28	0.03%	43.3%	VETFSGVYK	99.7%	41.9	25	15.4	2	0	0	1029.53	170	178
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	9	11	57	0.06%	51.4%	ADGYVLEGK	99.7%	59.4	25	52.2	2	0	0	951.48	185	193
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	9	11	57	0.06%	51.4%	ELEFYLR	99.7%	42.5	25	30.5	2	0	0	969.50	194	200
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	9	11	57	0.06%	51.4%	IIDVVYNASNNELVR	99.7%	116	25	110	12	2	0	1718.91	78	92
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	9	11	57	0.06%	51.4%	ISSLLEEQFQQGK	99.7%	85.5	25	65.1	15	0	0	1506.78	158	170
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	9	11	57	0.06%	51.4%	LDVGNFSWGSECCTR	99.7%	93.7	25	93.7	2	0	0	1787.75	60	74
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	9	11	57	0.06%	51.4%	LLACIASRPGQCGR	99.7%	40.5	25	33.7	2	2	0	1558.79	171	184
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	9	11	57	0.06%	51.4%	LTPEEEEILNK	99.7%	74.8	25	69.4	7	0	0	1314.68	129	139
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	9	11	57	0.06%	51.4%	NCIVLIDSTPYR	99.7%	85.4	25	75	9	0	0	1450.74	99	110
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	9	11	57	0.06%	51.4%	YELGRPAANTK	99.7%	42.9	25	36.2	2	0	0	1219.64	27	37
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	17	20	67	0.07%	51.0%	ELLTLDEKDPR	99.7%	43.8	25	36.4	1	0	0	1328.71	59	69
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	17	20	67	0.07%	51.0%	HIDFSLR	99.7%	43.3	25	23	2	0	0	887.47	156	162
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	17	20	67	0.07%	51.0%	IEDFLER	99.7%	54.7	25	45.9	2	0	0	921.47	102	108
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	17	20	67	0.07%	51.0%	IEDFLERR	99.0%	34.4	25	20.1	2	0	0	1077.57	102	109
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	17	20	67	0.07%	51.0%	IGVLDEGK	99.7%	53.6	25	30	7	0	0	830.46	84	91
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	17	20	67	0.07%	51.0%	IGVLDEGKMK	99.7%	41.8	25	33.2	4	0	0	1105.59	84	93
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	17	20	67	0.07%	51.0%	KQVVNIPSFIVR	99.7%	58.2	25	58.2	2	2	0	1399.84	139	150
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	17	20	67	0.07%	51.0%	LDYILGLK	99.7%	49.6	25	41.9	2	0	0	934.56	94	101
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	17	20	67	0.07%	51.0%	LFEGNALLR	99.7%	66	25	49	19	0	0	1032.58	71	79

40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	17	20	67	0.07%	51.0%	LIGEYGLR	99.7%	61	25	39.8	2	0	0	920.52	31	38
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	17	20	67	0.07%	51.0%	LQTQVFK	99.6%	38.7	25	19.1	2	0	0	863.50	110	116
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	17	20	67	0.07%	51.0%	MKLDYILGLK	99.7%	55.8	25	38.2	4	0	0	1193.70	92	101
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	17	20	67	0.07%	51.0%	QVVNIPSFIVR	99.7%	59	25	50	8	0	0	1271.75	140	150
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	17	20	67	0.07%	51.0%	RLFEGNALLR	99.7%	58.4	25	34.7	2	0	0	1188.68	70	79
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	17	20	67	0.07%	51.0%	RLQTQVFK	98.9%	34	25	24.6	2	0	0	1019.60	109	116
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	17	20	67	0.07%	51.0%	SPYGGGRPGR	98.9%	34	25	27.5	2	0	0	1003.51	163	172
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	17	20	67	0.07%	51.0%	SRLDQELK	97.6%	30.5	25	12	2	0	0	988.54	23	30
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	7	7	22	0.02%	25.4%	AIVAIENPADVSVISSR	99.7%	115	25	115	4	0	0	1740.95	64	80
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	7	7	22	0.02%	25.4%	FAAATGATPIAGR	99.7%	102	25	86.7	7	0	0	1203.65	90	102
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	7	7	22	0.02%	25.4%	FTPGTFTNQIQAAFR	99.7%	78	25	73.5	2	0	0	1698.86	103	117
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	7	7	22	0.02%	25.4%	KSDGIYIINLK	99.7%	63.2	25	33.3	2	0	0	1263.73	42	52
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	7	7	22	0.02%	25.4%	LLVVTDPR	99.7%	52.5	25	43.9	2	0	0	912.55	121	128
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	7	7	22	0.02%	25.4%	SDGIYIINLK	99.7%	53.9	25	37.1	3	0	0	1135.64	43	52
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	7	7	22	0.02%	25.4%	YVDIAIPCNNK	99.7%	39.6	25	37.8	2	0	0	1306.65	156	166
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	18	0.02%	16.7%	ADLLLSTQPGREEGSPLELER	99.7%	63.7	25	63.7	0	1	0	2310.19	593	613
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	18	0.02%	16.7%	GENSWFSTQVDTVATK	99.7%	92.1	25	92.1	1	0	0	1769.83	314	329
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	18	0.02%	16.7%	GLVLGPIHK	99.7%	44.5	25	37.3	1	0	0	933.59	258	266
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	18	0.02%	16.7%	GQSEDPGSLLSLFR	99.7%	70.5	25	63.6	6	0	0	1505.76	511	524
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	18	0.02%	16.7%	GRLDYLSSLK	99.7%	39.8	25	16.3	1	0	0	1151.64	246	255
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	18	0.02%	16.7%	LLTSFLPAQLLR	99.7%	61.3	25	60.7	3	0	0	1371.84	440	451
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	18	0.02%	16.7%	VAEDEAEAAAAAK	99.7%	86.5	25	86.5	1	0	0	1245.60	148	160
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	18	0.02%	16.7%	VILDLTPNYR	99.7%	78.2	25	68.4	4	0	0	1203.67	304	313
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	6	6	11	0.01%	8.3%	AALEEVYPDLTPEETRR	99.1%	28.8	25	28.8	0	1	0	1988.99	660	676
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	6	6	11	0.01%	8.3%	ELTMASLPFTFDVER	99.7%	55.8	25	52.5	2	0	0	1755.86	316	330
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	6	6	11	0.01%	8.3%	LFSIVRPR	99.7%	39.2	25	30.7	1	0	0	987.61	88	95
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	6	6	11	0.01%	8.3%	NSLGGDVLFVGK	99.7%	65.1	25	59.6	2	0	0	1205.65	677	688
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	6	6	11	0.01%	8.3%	NSPGSQVASNPR	99.7%	71.3	25	69.6	4	0	0	1213.59	447	458
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	6	6	11	0.01%	8.3%	YAWQGVALLPFVDER	99.7%	44.9	25	44.9	1	0	0	1763.91	642	656
5'-AMP-activated protein kinase catalytic subunit alpha-1	PRKAA1	AAPK1_HUMAN	64.0	100.0%	3	3	5	0.01%	11.6%	IADFGLSNMMSDGEFLR	99.7%	39.4	25	39.4	1	0	0	1934.86	166	182
5'-AMP-activated protein kinase catalytic subunit alpha-1	PRKAA1	AAPK1_HUMAN	64.0	100.0%	3	3	5	0.01%	11.6%	MSLQLYQVDSR	99.7%	63.7	25	50	2	0	0	1339.67	458	468
5'-AMP-activated protein kinase catalytic subunit alpha-1	PRKAA1	AAPK1_HUMAN	64.0	100.0%	3	3	5	0.01%	11.6%	SIDDEITEAK	97.5%	30.5	25	21.5	1	0	0	1120.54	476	485
5'-AMP-activated protein kinase catalytic subunit alpha-1	PRKAA1	AAPK1_HUMAN	64.0	100.0%	3	3	5	0.01%	11.6%	TSCGSPNYAAPEVISGR	99.7%	53.9	25	53.9	1	0	0	1765.82	183	199
5'-AMP-activated protein kinase catalytic subunit alpha-1	PRKAA1	AAPK1_HUMAN	64.0	100.0%	3	3	5	0.01%	11.6%	VPFLVAETPR	99.7%	61.2	25	57	2	0	0	1128.64	375	384
5'-AMP-activated protein kinase catalytic subunit alpha-2	PRKAA2	AAPK2_HUMAN	62.3	100.0%	4	4	5	0.01%	9.4%	IADFGLSNMMSDGEFLR	99.7%	39.4	25	39.4	1	0	0	1934.86	155	171
5'-AMP-activated protein kinase catalytic subunit alpha-2	PRKAA2	AAPK2_HUMAN	62.3	100.0%	4	4	5	0.01%	9.4%	MPPLIADSPK	99.7%	40.8	25	25.5	1	0	0	1084.57	370	379
5'-AMP-activated protein kinase catalytic subunit alpha-2	PRKAA2	AAPK2_HUMAN	62.3	100.0%	4	4	5	0.01%	9.4%	TSCGSPNYAAPEVISGR	99.7%	53.9	25	53.9	1	0	0	1765.82	172	188
5'-AMP-activated protein kinase catalytic subunit alpha-2	PRKAA2	AAPK2_HUMAN	62.3	100.0%	4	4	5	0.01%	9.4%	VVNAYHLR	99.7%	46.7	25	39.7	2	0	0	971.54	432	439
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	6	6	9	0.01%	21.5%	AFFALVTNGVR	99.7%	51.5	25	46.7	1	0	0	1194.66	60	70
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	6	6	9	0.01%	21.5%	FDVINLAAEK	99.7%	64.3	25	53	2	0	0	1119.60	244	253
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	6	6	9	0.01%	21.5%	LPVIDPESGNTLYILTHK	99.7%	39.4	25	39.4	0	1	0	2010.09	153	170
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	6	6	9	0.01%	21.5%	LVVFDTSLQVK	99.7%	50.4	25	50.2	1	0	0	1248.72	48	58
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	6	6	9	0.01%	21.5%	TYNNLDVSVTK	99.7%	51	25	45.9	2	0	0	1253.64	254	264
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	6	6	9	0.01%	21.5%	VSALPVVDEK	99.7%	51.4	25	37.3	2	0	0	1056.59	225	234
5-methylcytosine rRNA methyltransferase NSUN4	NSUN4	NSUN4_HUMAN	43.1	100.0%	3	3	5	0.01%	8.6%	NLAANDLSPSR	99.7%	72	25	59.8	2	0	0	1157.59	199	209
5-methylcytosine rRNA methyltransferase NSUN4	NSUN4	NSUN4_HUMAN	43.1	100.0%	3	3	5	0.01%	8.6%	TLALLQTGCCR	99.7%	58.5	25	44	2	0	0	1292.65	188	198
5-methylcytosine rRNA methyltransferase NSUN4	NSUN4	NSUN4_HUMAN	43.1	100.0%	3	3	5	0.01%	8.6%	VLVDVPCTTDR	99.3%	35.7	25	30.6	1	0	0	1274.64	252	262
5'-nucleotidase domain-containing protein 2	NT5DC2	NT5D2_HUMAN	60.7	99.8%	2	2	3	0.00%	4.6%	QGNLFDFLR	99.7%	46.7	25	34.8	2	0	0	1109.57	336	344
5'-nucleotidase domain-containing protein 2	NT5DC2	NT5D2_HUMAN	60.7	99.8%	2	2	3	0.00%	4.6%	QLFLITNSPFSFVDK	99.7%	73.3	25	73.3	1	0	0	1755.93	263	277
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	26	51	0.05%	40.3%	AAVEEGIVLGGGCALLR	99.7%	99.9	25	95.2	2	2	0	1684.91	430	446
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	26	51	0.05%	40.3%	ALMLQGVDLLADAVAVTMGPK	94.6%	22.1	25	22.1	0	1	0	2129.13	38	58

60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	26	51	0.05%	40.3%	CEFQDAYVLLSEK	99.7%	92.2	25	76	2	0	0	1601.75	237	249
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	26	51	0.05%	40.3%	CIPALDSLTPANEDQK	99.7%	100	25	99.2	2	0	0	1771.85	447	462
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	26	51	0.05%	40.3%	GANPVEIR	99.7%	43.7	25	11.6	2	0	0	855.47	134	141
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	26	51	0.05%	40.3%	GANPVEIRR	99.7%	51.6	25	42.8	2	0	0	1011.57	134	142
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	26	51	0.05%	40.3%	GYISPYFINTSK	99.7%	79.4	25	77.6	2	0	0	1389.70	222	233
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	26	51	0.05%	40.3%	IGIEIIKR	99.7%	63.9	25	31.8	2	0	0	941.61	463	470
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	26	51	0.05%	40.3%	ISSIQSIVPALEIANAHR	99.7%	34.2	25	34.2	0	1	0	1919.07	251	268
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	26	51	0.05%	40.3%	LSDGVAVLK	99.7%	81.2	25	64.3	2	0	0	901.54	397	405
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	26	51	0.05%	40.3%	LVQDVANNTNEEAGDGTTTATVLAR	99.7%	170	25	170	2	1	0	2560.25	97	121
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	26	51	0.05%	40.3%	NAGVEGSLIVEK	99.7%	79.2	25	64.9	2	0	0	1215.66	482	493
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	26	51	0.05%	40.3%	TLNDELEIIEGMK	99.7%	90.3	25	86.4	2	0	0	1504.76	206	218
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	26	51	0.05%	40.3%	TVIIEQSWGSPK	99.7%	86.9	25	77.7	2	0	0	1344.72	61	72
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	26	51	0.05%	40.3%	VGEVIVTK	99.7%	59.8	25	43.7	2	0	0	844.51	345	352
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	26	51	0.05%	40.3%	VGEVIVTKDDAMLLK	99.7%	70.3	25	70.2	4	4	0	1630.91	345	359
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	26	51	0.05%	40.3%	VGGTSDVEVNEK	99.7%	92.6	25	90.3	4	0	0	1233.60	406	417
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	26	51	0.05%	40.3%	VGGTSDVEVNEKK	99.7%	83.6	25	70.8	2	2	0	1361.69	406	418
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	26	51	0.05%	40.3%	VGLQVVAVK	99.7%	80.8	25	77.5	2	0	0	912.59	293	301
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	26	51	0.05%	40.3%	VTDALNATR	99.7%	75.9	25	59.7	2	0	0	960.51	421	429
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	7	10	20	0.02%	16.0%	AIADWYNEK	99.7%	45.6	25	43.1	2	0	0	1109.53	151	159
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	7	10	20	0.02%	16.0%	ALDAAFYK	99.7%	40.5	25	34.8	1	0	0	898.47	352	359
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	7	10	20	0.02%	16.0%	ALLQEMPLTALLR	99.7%	79.1	25	76.7	6	0	0	1468.86	271	283
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	7	10	20	0.02%	16.0%	FLCFGSEGGTYYIK	99.7%	79.5	25	76.4	2	0	0	1641.76	36	49
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	7	10	20	0.02%	16.0%	GGMALALAVTK	99.7%	65.6	25	49.1	4	0	0	1047.59	160	170
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	7	10	20	0.02%	16.0%	LGLENAEALIR	99.7%	81.3	25	75.5	3	0	0	1198.68	53	63
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	7	10	20	0.02%	16.0%	MTANSVLEPGNSEVSLVCEK	99.7%	58.5	25	58.5	2	0	0	2180.02	288	307
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	11	14	62	0.06%	51.7%	AFLADPSAFVAAAPVAAATTAAPAAAAAPAK	99.7%	87.4	25	87.4	4	5	0	2752.47	267	297
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	11	14	62	0.06%	51.7%	AGAIAPCEVTVPAQNTGLGPEK	99.7%	78.5	25	78.5	4	4	0	2180.10	113	134
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	11	14	62	0.06%	51.7%	CFIVGADNVGSK	99.7%	57.1	25	46.9	4	0	0	1266.61	27	38
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	11	14	62	0.06%	51.7%	EDLTEIR	97.3%	30.1	25	10	1	0	0	875.45	93	99
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	11	14	62	0.06%	51.7%	GHLENNPALEK	99.7%	60.6	25	43	2	2	0	1221.62	67	77
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	11	14	62	0.06%	51.7%	GNVGFVFTK	99.7%	54	25	44.3	8	0	0	968.52	84	92
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	11	14	62	0.06%	51.7%	GTIEILSDVQLIK	99.7%	73.3	25	61.5	5	0	0	1428.83	150	162
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	11	14	62	0.06%	51.7%	IIQLLDDYPK	99.7%	75.3	25	62.3	4	0	0	1217.68	17	26
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	11	14	62	0.06%	51.7%	TSFFQALGITTK	99.7%	99.5	25	99.5	14	0	0	1313.71	135	146
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	11	14	62	0.06%	51.7%	VEAKEESEESDEDMGFGLFD	99.7%	54.1	25	54.1	1	0	0	2262.92	298	317
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	11	14	62	0.06%	51.7%	VLALSVETDYTFPLAEK	99.7%	74.3	25	74.3	4	0	0	1896.00	248	264
60S acidic ribosomal protein P2	RPLP2	RLA2_HUMAN	11.7	100.0%	3	3	6	0.01%	53.0%	ILDSVGIEADDDRLNK	99.7%	45	25	38.6	2	0	0	1772.90	26	41
60S acidic ribosomal protein P2	RPLP2	RLA2_HUMAN	11.7	100.0%	3	3	6	0.01%	53.0%	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	99.7%	34	25	34	0	2	0	2774.43	62	94
60S acidic ribosomal protein P2	RPLP2	RLA2_HUMAN	11.7	100.0%	3	3	6	0.01%	53.0%	NIEDVIAQGIGK	99.7%	80.9	25	70.1	2	0	0	1256.68	50	61
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	12	19	39	0.04%	48.1%	AKVDEFPLCGHMVSDEYEQLSSEALEAAR	99.7%	125	25	125	0	2	0	3281.51	41	69
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	12	19	39	0.04%	48.1%	EHVIEALR	95.3%	27.9	25	20.4	1	0	0	966.54	146	153
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	12	19	39	0.04%	48.1%	EHVIEALRR	99.4%	36.9	25	10.3	2	0	0	1122.64	146	154
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	12	19	39	0.04%	48.1%	FNADEFEDMVAEK	99.7%	100	25	96.5	5	0	0	1560.65	176	188
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	12	19	39	0.04%	48.1%	FNADEFEDMVAEKR	99.7%	104	25	95.7	2	3	0	1700.76	176	189
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	12	19	39	0.04%	48.1%	GAFGKPQGTVAR	99.7%	59.9	25	45.9	4	0	0	1188.65	117	128
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	12	19	39	0.04%	48.1%	LQNKEHVIEALR	99.7%	37.8	25	37.8	0	2	0	1449.82	142	153
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	12	19	39	0.04%	48.1%	MLSCAGADR	98.9%	34	25	24.9	1	0	0	980.43	102	110
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	12	19	39	0.04%	48.1%	MLSCAGADRLQTGMR	97.1%	24.3	25	19.6	0	1	0	1682.78	102	116
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	12	19	39	0.04%	48.1%	RLIPDGCGVK	99.4%	36.8	25	25.5	2	0	0	1114.60	189	198
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	12	19	39	0.04%	48.1%	VDEFPLCGHMVSDEYEQLSSEALEAAR	99.7%	68.1	25	68.1	0	4	0	3082.38	43	69
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	12	19	39	0.04%	48.1%	VHIGQVIMSIR	99.7%	54.9	25	54.9	6	4	0	1252.72	129	139

60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	21	41	0.04%	39.2%	AVDIPHMDIEALK	99.7%	56.7	25	53.2	3	3	0	1451.76	79	91
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	21	41	0.04%	39.2%	AVDIPHMDIEALKK	99.7%	41.2	25	31.9	3	2	0	1595.85	79	92
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	21	41	0.04%	39.2%	DTLYEAVR	99.7%	50.7	25	30.7	5	0	0	966.49	8	15
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	21	41	0.04%	39.2%	FPSLLTHNENMVAK	99.7%	56.6	25	54.1	4	4	0	1600.82	134	147
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	21	41	0.04%	39.2%	FSVCVLGDQQHCDEAK	99.7%	78.2	25	78.2	2	2	0	1892.83	63	78
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	21	41	0.04%	39.2%	ILGPGLNK	99.6%	37.9	25	26.5	1	0	0	811.50	123	130
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	21	41	0.04%	39.2%	KYDAFLASESLIK	99.7%	75.8	25	75.8	3	2	0	1484.80	106	118
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	21	41	0.04%	39.2%	VLCLAVAVGHVK	99.7%	84.7	25	84.7	4	2	0	1265.74	162	173
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	21	41	0.04%	39.2%	YDAFLASESLIK	99.7%	40.9	25	34.7	1	0	0	1356.70	107	118
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	8	10	35	0.04%	33.7%	AEEILEK	99.7%	43.1	25	17.6	2	0	0	831.45	79	85
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	8	10	35	0.04%	33.7%	AEEILEKGLK	98.7%	33.2	25	27.3	1	0	0	1129.65	79	88
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	8	10	35	0.04%	33.7%	IAVHCTVR	99.7%	56.9	25	44.5	2	0	0	955.51	68	75
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	8	10	35	0.04%	33.7%	KLCLNICVGESGDR	99.7%	37.6	25	34.8	1	2	0	1620.78	19	32
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	8	10	35	0.04%	33.7%	LCLNICVGESGDR	99.7%	77.3	25	77.3	3	0	0	1492.69	20	32
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	8	10	35	0.04%	33.7%	VLEQLTGQTPVFSK	99.7%	100	25	95.2	14	0	0	1546.85	39	52
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	8	10	35	0.04%	33.7%	WFQQKYDGIILPGK	99.6%	39	25	35.1	1	2	0	1692.91	165	178
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	8	10	35	0.04%	33.7%	YDGIILPGK	99.7%	68.9	25	64.1	7	0	0	975.55	170	178
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	6	8	28	0.03%	48.5%	ATGDWKGLR	95.8%	28.3	25	13.8	1	0	0	1003.53	49	57
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	6	8	28	0.03%	48.5%	CTGGEVGATSALAPK	99.7%	103	25	83.1	4	0	0	1418.69	17	31
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	6	8	28	0.03%	48.5%	EILGTAQSVGCNVDGR	99.7%	95.1	25	95.1	2	0	0	1675.81	131	146
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	6	8	28	0.03%	48.5%	HSGNITFDEIVNIAR	99.7%	101	25	100	4	4	0	1685.86	100	114
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	6	8	28	0.03%	48.5%	IGPLGLSPK	99.7%	52	25	35.5	8	0	0	881.55	32	40
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	6	8	28	0.03%	48.5%	QAQIEVVPSASALIIK	99.7%	97.4	25	97.4	4	1	0	1666.97	68	83
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	12	86	0.09%	34.6%	GFSLEELR	99.7%	51.8	25	33.7	15	0	0	950.49	75	82
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	12	86	0.09%	34.6%	LATQLTGPVMPVR	99.7%	75.3	25	75.3	8	0	0	1382.78	146	158
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	12	86	0.09%	34.6%	NKSTESLQANVQR	99.7%	61.4	25	56.4	2	0	0	1474.76	104	116
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	12	86	0.09%	34.6%	RVATWFNQPAR	99.7%	39.8	25	39.5	2	2	0	1345.71	21	31
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	12	86	0.09%	34.6%	SKLILFPR	99.7%	39.3	25	39.3	4	0	0	973.62	122	129
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	12	86	0.09%	34.6%	STESLQANVQR	99.7%	80.9	25	68.8	21	0	0	1232.62	106	116
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	12	86	0.09%	34.6%	TIGISVDPR	99.7%	66.8	25	50.2	14	0	0	957.54	93	101
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	12	86	0.09%	34.6%	VATWFNQPAR	99.7%	84.5	25	69.8	8	0	0	1189.61	22	31
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	12	86	0.09%	34.6%	VATWFNQPARK	98.3%	32.1	25	30	1	0	0	1317.71	22	32
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	12	86	0.09%	34.6%	VITEEEKNFK	99.7%	50.2	25	39.2	9	0	0	1236.65	168	177
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	6	7	14	0.01%	25.1%	CEGINISGNFYR	99.7%	62.2	25	57.9	1	0	0	1429.65	38	49
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	6	7	14	0.01%	25.1%	IDKYTEVLK	99.7%	48.4	25	33.5	1	0	0	1108.63	189	197
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	6	7	14	0.01%	25.1%	KFAYLGR	99.7%	39.3	25	28.1	2	0	0	854.49	134	140
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	6	7	14	0.01%	25.1%	VFDGIPPPYDK	98.6%	32.7	25	25.1	2	0	0	1247.63	104	114
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	6	7	14	0.01%	25.1%	VFDGIPPPYDKK	99.5%	31.2	25	24.9	1	1	0	1375.73	104	115
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	6	7	14	0.01%	25.1%	YQAVTATLEEK	99.7%	82.1	25	67.4	6	0	0	1252.64	149	159
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	5	8	76	0.08%	24.7%	ALVDGPCTQVR	99.7%	73.6	25	68.8	5	0	0	1215.62	36	46
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	5	8	76	0.08%	24.7%	CMQLTDFILK	99.7%	54.2	25	38.5	13	0	0	1284.63	54	63
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	5	8	76	0.08%	24.7%	LVAIVDVIDQNR	99.7%	96.5	25	96.5	38	0	0	1354.77	24	35
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	5	8	76	0.08%	24.7%	MTDFDRFK	99.7%	42.3	25	42.3	4	0	0	1059.49	104	111
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	5	8	76	0.08%	24.7%	VAYVSFGPHAGK	99.7%	65.4	25	47.2	14	2	0	1232.64	12	23
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	6	7	12	0.01%	31.9%	FFEVILIDPFHK	99.7%	48.8	25	48.8	1	0	0	1504.82	129	140
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	6	7	12	0.01%	31.9%	GATYGKPVHHGVNQLK	99.7%	71.9	25	63.4	2	1	0	1705.91	78	93
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	6	7	12	0.01%	31.9%	NPDTQWITKPVHK	99.7%	35.8	25	35.1	0	1	0	1563.83	145	157
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	6	7	12	0.01%	31.9%	RNPDTQWITKPVHK	98.3%	26.2	25	23.8	0	2	0	1719.93	144	157
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	6	7	12	0.01%	31.9%	SLQSVAEER	99.7%	43.8	25	29.8	4	0	0	1018.52	97	105
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	6	7	12	0.01%	31.9%	VLNSYWVGEDSTYK	98.9%	33.6	25	33.6	1	0	0	1660.79	115	128
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	9	14	44	0.05%	38.6%	EQIVPKPEEEVAQK	99.7%	71	25	62.3	4	0	0	1623.86	154	167

60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	9	14	44	0.05%	38.6%	EQIVPKPEEEVAQKK	96.7%	23.8	25	23.1	1	1	0	1751.95	154	168
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	9	14	44	0.05%	38.6%	GLDVDSLVIEHIQVNK	99.7%	99.2	25	86.8	6	0	0	1778.96	106	121
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	9	14	44	0.05%	38.6%	KSAEFLLHMLK	99.7%	50.5	25	46.7	2	1	0	1332.73	86	96
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	9	14	44	0.05%	38.6%	QWGWTQGR	99.5%	37.4	25	20.2	4	0	0	1018.49	75	82
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	9	14	44	0.05%	38.6%	SAEFLLHMLK	99.7%	67.6	25	61.8	5	1	0	1188.64	87	96
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	9	14	44	0.05%	38.6%	VRYSLDPENPTK	99.7%	42.5	25	38.9	2	0	0	1418.73	2	13
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	9	14	44	0.05%	38.6%	YLKDVTLQK	99.7%	54.2	25	38.5	8	0	0	1107.64	47	55
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	9	14	44	0.05%	38.6%	YSLDPENPTK	99.7%	66.3	25	59.9	9	0	0	1163.56	4	13
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	9	11	53	0.05%	38.8%	GCGTVLLSGPR	99.7%	87	25	77.5	9	0	0	1116.58	133	143
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	9	11	53	0.05%	38.8%	ILTFDQLALDSPK	99.7%	105	25	93.5	19	0	0	1460.80	120	132
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	9	11	53	0.05%	38.8%	LKVCALR	98.9%	33.6	25	28.2	1	0	0	859.52	98	104
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	9	11	53	0.05%	38.8%	RTNSTFNQVVLK	99.1%	34.6	25	2.88	1	1	0	1406.78	38	49
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	9	11	53	0.05%	38.8%	TAVVVGTITDDVR	99.7%	114	25	105	10	0	0	1345.73	79	91
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	9	11	53	0.05%	38.8%	TAVVVGTITDDVRVQEVPK	99.7%	78.7	25	76.8	2	2	0	2026.12	79	97
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	9	11	53	0.05%	38.8%	TNRPPLSLSR	98.9%	34	25	30.1	3	0	0	1140.65	56	65
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	9	11	53	0.05%	38.8%	TNSTFNQVVLK	99.7%	75.4	25	56.2	3	0	0	1250.67	39	49
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	9	11	53	0.05%	38.8%	TNSTFNQVVLKR	99.7%	42.4	25	42.4	2	0	0	1406.78	39	50
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	9	12	48	0.05%	38.6%	AHSIQIMK	99.4%	36.7	25	24.9	4	0	0	943.50	121	128
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	9	12	48	0.05%	38.6%	DLTTAGAVTQCYR	99.7%	73.2	25	72.7	6	0	0	1455.69	99	111
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	9	12	48	0.05%	38.6%	EYRDLTTAGAVTQCYR	99.7%	78	25	72	4	4	0	1903.90	96	111
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	9	12	48	0.05%	38.6%	FWYFVSQLKK	99.7%	40.9	25	36.4	3	1	0	1345.73	44	53
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	9	12	48	0.05%	38.6%	IFAPNHVVAK	99.7%	46.6	25	37.2	4	0	0	1095.63	32	41
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	9	12	48	0.05%	38.6%	KSSGEIVYCGQVFEK	99.7%	70.3	25	70.3	2	2	0	1730.84	56	70
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	9	12	48	0.05%	38.6%	NFGIWLR	99.7%	40.8	25	27	4	0	0	905.50	77	83
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	9	12	48	0.05%	38.6%	SSGEIVYCGQVFEK	99.7%	93.1	25	90.8	11	0	0	1602.75	57	70
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	9	12	48	0.05%	38.6%	VKNFGIWLR	99.7%	47.6	25	41.2	3	0	0	1132.66	75	83
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	6	6	17	0.02%	23.0%	HMYHSLYLK	95.2%	27.8	25	21.3	1	0	0	1191.60	118	126
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	6	6	17	0.02%	23.0%	ILMEHIHK	97.6%	30.6	25	15.6	1	0	0	1020.57	137	144
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	6	6	17	0.02%	23.0%	KLLADQAEAR	98.2%	31.8	25	20.7	2	0	0	1114.62	153	162
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	6	6	17	0.02%	23.0%	KVWLDPNETNEIANANSR	99.7%	47.4	25	47.4	0	2	0	2071.02	21	38
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	6	6	17	0.02%	23.0%	LLADQAEAR	99.7%	68.6	25	55.9	8	0	0	986.53	154	162
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	6	6	17	0.02%	23.0%	VWLDPNETNEIANANSR	99.7%	125	25	125	3	0	0	1942.93	22	38
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	7	10	36	0.04%	42.5%	EKGTWVQLK	99.7%	40.1	25	24.9	2	0	0	1088.61	121	129
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	7	10	36	0.04%	42.5%	GDIVDIKGMGTVQK	99.5%	37.3	25	29.3	2	0	0	1476.77	37	50
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	7	10	36	0.04%	42.5%	GTWVQLK	96.5%	29.1	25	16.5	2	0	0	831.47	123	129
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	7	10	36	0.04%	42.5%	GTWVQLKR	99.7%	43.5	25	28	4	0	0	987.57	123	130
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	7	10	36	0.04%	42.5%	HGVVPLATYMR	99.7%	55.9	25	52.2	2	1	0	1243.66	22	32
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	7	10	36	0.04%	42.5%	TNGKEPELLEPIPYEFMA	99.7%	53.2	25	53.2	7	0	0	2094.01	143	160
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	7	10	36	0.04%	42.5%	VYNVTQHAVGIVVNK	99.7%	108	25	100	9	7	0	1640.91	64	78
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	32	0.03%	36.7%	AGNLGGGVVTIER	99.7%	95.6	25	84.2	7	0	0	1242.68	53	65
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	32	0.03%	36.7%	ITVTSEVPFSK	99.7%	74.8	25	69.9	6	0	0	1207.66	70	80
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	32	0.03%	36.7%	ITVTSEVPFSKR	99.7%	61.3	25	61.2	4	2	0	1363.76	70	81
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	32	0.03%	36.7%	NNLRDWLR	98.3%	31.9	25	17.1	3	0	0	1086.58	94	101
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	32	0.03%	36.7%	SKITVTSEVPFSK	99.7%	88.1	25	85.4	4	0	0	1422.78	68	80
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	32	0.03%	36.7%	VVANSKESYELR	99.7%	62.4	25	52.8	4	2	0	1394.73	102	113
60S ribosomal protein L22-like 1	RPL22L1	RL22L_HUMAN	14.6	99.8%	2	3	6	0.01%	26.2%	NNLRDWLR	98.3%	31.9	25	17.1	3	0	0	1086.58	88	95
60S ribosomal protein L22-like 1	RPL22L1	RL22L_HUMAN	14.6	99.8%	2	3	6	0.01%	26.2%	TGNLGNVVHIER	99.7%	48	25	39.4	2	0	0	1308.70	48	59
60S ribosomal protein L22-like 1	RPL22L1	RL22L_HUMAN	14.6	99.8%	2	3	6	0.01%	26.2%	VVASDKETYELR	99.7%	81.1	25	81.1	2	2	0	1409.73	96	107
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	7	9	47	0.05%	46.4%	ECADLWPR	99.7%	48.5	25	25.6	2	0	0	1046.47	124	131
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	7	9	47	0.05%	46.4%	GSAITGPVAK	99.7%	57.4	25	45.5	6	0	0	900.52	114	123
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	7	9	47	0.05%	46.4%	ISLGLPVGAVINCADNTGAK	99.7%	119	25	106	8	0	0	1970.04	16	35

60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	7	9	47	0.05%	46.4%	LNRLPAAGVGDMVMATVK	99.7%	52.2	25	6.61	0	8	0	1858.99	49	66
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	7	9	47	0.05%	46.4%	LPAAGVGDMVMATVK	99.7%	89.7	25	17.2	18	0	0	1475.76	52	66
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	7	9	47	0.05%	46.4%	LPAAGVGDMVMATVKK	99.7%	52.1	25	49.2	2	0	0	1619.85	52	67
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	7	9	47	0.05%	46.4%	NLYIISVK	99.7%	40	25	40	3	0	0	949.57	36	43
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	12	14	50	0.05%	51.3%	EAPAPPKAEAK	99.1%	34.7	25	29.8	3	0	0	1108.60	8	18
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	12	14	50	0.05%	51.3%	FPLTTESAMK	99.7%	57.3	25	49.4	7	0	0	1140.56	79	88
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	12	14	50	0.05%	51.3%	FPLTTESAMKK	99.0%	34.3	25	25.1	2	0	0	1268.66	79	89
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	12	14	50	0.05%	51.3%	IEDNNTLVFIVDVK	99.7%	74.8	25	67.1	2	0	0	1618.87	90	103
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	12	14	50	0.05%	51.3%	KIEDNNTLVFIVDVK	98.8%	27.6	25	27.6	0	1	0	1746.96	89	103
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	12	14	50	0.05%	51.3%	KLYDIDVAK	99.7%	51	25	44.9	2	0	0	1064.60	115	123
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	12	14	50	0.05%	51.3%	LAPDYDALDVANK	99.7%	81	25	81	10	0	0	1404.70	140	152
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	12	14	50	0.05%	51.3%	LDHYAIIK	99.7%	52.8	25	17.5	4	0	0	972.55	71	78
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	12	14	50	0.05%	51.3%	LYDIDVAK	99.7%	46.5	25	39	4	0	0	936.50	116	123
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	12	14	50	0.05%	51.3%	NKLDHYAIIK	99.7%	39.6	25	8.07	2	2	0	1214.69	69	78
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	12	14	50	0.05%	51.3%	VNTLIRPDGEK	99.7%	54.8	25	47.6	10	0	0	1241.69	124	134
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	12	14	50	0.05%	51.3%	VNTLIRPDGEKK	95.6%	22.8	25	22.8	0	1	0	1369.78	124	135
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	8	11	77	0.08%	35.0%	AITGASLADIMAK	99.7%	106	25	98.5	34	0	0	1277.68	81	93
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	8	11	77	0.08%	35.0%	AITGASLADIMAKR	99.7%	43.8	25	43.8	2	0	0	1417.78	81	94
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	8	11	77	0.08%	35.0%	CESAFLSK	99.7%	53.7	25	48.8	5	0	0	941.44	36	43
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	8	11	77	0.08%	35.0%	MKVELCSFSGYK	99.7%	74.2	25	63.5	8	3	0	1448.69	1	12
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	8	11	77	0.08%	35.0%	QINWTVLYR	99.7%	61.2	25	44.3	6	0	0	1192.65	48	56
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	8	11	77	0.08%	35.0%	TDGKVFQFLNAK	99.7%	33.2	25	33.2	0	2	0	1367.73	24	35
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	8	11	77	0.08%	35.0%	VELCSFSGYK	99.7%	57.8	25	47.3	2	0	0	1189.56	3	12
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	8	11	77	0.08%	35.0%	VFQFLNAK	99.7%	52.1	25	36.4	15	0	0	966.54	28	35
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	14	44	0.05%	46.9%	ANGTTVHVGIHPSK	99.7%	84.5	25	77.6	3	0	0	1417.75	90	103
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	14	44	0.05%	46.9%	DDEVQVVR	99.7%	60	25	40.8	3	0	0	959.48	52	59
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	14	44	0.05%	46.9%	FNPFVTSDR	99.7%	55.9	25	44.1	7	0	0	1082.53	3	11
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	14	44	0.05%	46.9%	HFNAPSHIR	94.9%	27.6	25	22	1	0	0	1078.55	18	26
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	14	44	0.05%	46.9%	IMSSPLSK	95.0%	27.7	25	18.5	1	0	0	878.47	29	36
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	14	44	0.05%	46.9%	KDDEVQVVR	99.7%	61.1	25	36.2	8	0	0	1087.57	51	59
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	14	44	0.05%	46.9%	KIMSSPLSK	97.7%	30.7	25	22.3	2	0	0	990.57	28	36
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	14	44	0.05%	46.9%	KYVIYIER	99.7%	49.8	25	46	3	0	0	1083.62	77	84
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	14	44	0.05%	46.9%	MKFNPFVTSDR	99.7%	64.7	25	57.6	8	1	0	1357.66	1	11
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	14	44	0.05%	46.9%	YKEETIEK	99.5%	37.4	25	31.4	2	0	0	1039.53	135	142
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	14	44	0.05%	46.9%	YVIYIER	99.7%	39.8	25	37.1	5	0	0	955.52	78	84
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	7	11	40	0.04%	47.8%	NIDDGTSDRPYSHALVAGIDR	99.7%	34.2	25	34.2	0	2	0	2272.10	28	48
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	7	11	40	0.04%	47.8%	NKWFFQK	98.9%	33.8	25	10.1	2	0	0	997.53	127	133
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	7	11	40	0.04%	47.8%	TVVNKDVFR	99.7%	49.1	25	42.5	1	0	0	1077.61	94	102
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	7	11	40	0.04%	47.8%	VVLVLAGR	99.7%	48.5	25	46.7	8	0	0	826.55	10	17
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	7	11	40	0.04%	47.8%	VYNYNHLMPTR	99.7%	53.3	25	48.9	8	5	0	1407.68	74	84
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	7	11	40	0.04%	47.8%	YSVDIPLDK	99.7%	49.4	25	44	11	0	0	1049.55	85	93
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	7	11	40	0.04%	47.8%	YSVDIPLDKTVVNK	99.7%	57.1	25	54.7	2	1	0	1590.87	85	98
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	7	9	36	0.04%	46.6%	IKSVGGACVLVA	99.7%	43.7	25	43.7	2	0	0	1173.67	137	148
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	7	9	36	0.04%	46.6%	INFDKYHPGYFGK	99.7%	59.4	25	51.4	2	3	0	1585.78	43	55
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	7	9	36	0.04%	46.6%	LWTLVSEQTR	99.7%	56.3	25	48.1	4	0	0	1232.66	78	87
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	7	9	36	0.04%	46.6%	NKTGAAPIIDVVR	99.7%	56.8	25	53.6	2	2	0	1353.79	93	105
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	7	9	36	0.04%	46.6%	NQSFCPTVNLDK	99.4%	36.9	25	29.5	3	0	0	1422.67	66	77
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	7	9	36	0.04%	46.6%	SGYYKVLGK	99.5%	37.8	25	33.9	2	0	0	1014.56	106	114
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	7	9	36	0.04%	46.6%	TGAAPIIDVVR	99.7%	75.1	25	75.1	16	0	0	1111.65	95	105
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	40	0.04%	38.7%	GVVVVIKR	99.7%	44.8	25	39.2	2	0	0	869.59	59	66
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	40	0.04%	38.7%	KTVGVEPAADGK	99.7%	78.5	25	69	2	0	0	1171.63	47	58

60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	40	0.04%	38.7%	NCSSFLIK	99.7%	42.2	25	25.9	3	0	0	968.49	12	19
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	40	0.04%	38.7%	NCSSFLIKR	99.7%	41.5	25	36.5	2	0	0	1124.59	12	20
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	40	0.04%	38.7%	NKQTYSTEPNNLK	99.7%	64.8	25	62.2	5	2	0	1536.77	21	33
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	40	0.04%	38.7%	NSFRYNGLIHR	95.0%	22.4	25	11.9	0	1	0	1376.72	36	46
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	40	0.04%	38.7%	QTYSTEPNNLK	99.7%	51.5	25	43.1	6	0	0	1294.63	23	33
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	40	0.04%	38.7%	TVGVEPAADGK	99.7%	49.3	25	45	4	0	0	1043.54	48	58
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	40	0.04%	38.7%	TVGVEPAADGKGVVVVIK	99.7%	64.9	25	62.1	4	4	0	1738.01	48	65
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	40	0.04%	38.7%	YNGLIHR	99.7%	40.8	25	24.8	4	0	0	872.47	40	46
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	40	0.04%	38.7%	YNGLIHRK	98.6%	32.8	25	27.1	1	0	0	1000.57	40	47
60S ribosomal protein L29	RPL29	RL29_HUMAN	17.8	100.0%	2	2	22	0.02%	14.5%	AQAAAPASVPAQAPK	99.7%	69.3	25	69.3	20	0	0	1377.75	135	149
60S ribosomal protein L29	RPL29	RL29_HUMAN	17.8	100.0%	2	2	22	0.02%	14.5%	LAYIAHPK	97.9%	31	25	24.4	2	0	0	912.53	96	103
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	25	64	0.07%	41.7%	AFMGPLKK	98.7%	33	25	22.3	2	0	0	907.51	387	394
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	25	64	0.07%	41.7%	AGMTHIVR	99.7%	56.2	25	47.8	4	0	0	884.48	51	58
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	25	64	0.07%	41.7%	AHLMEIQVNGGTVAEK	99.7%	35.8	25	35.8	0	2	0	1712.86	178	193
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	25	64	0.07%	41.7%	DDPSKPVHLTAFLGYK	99.7%	58.4	25	58.4	2	1	0	1787.93	35	50
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	25	64	0.07%	41.7%	ERLEQQVPVNQVFGQDEMIDVIGVTK	99.6%	32.3	25	32.3	0	1	0	2971.52	199	224
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	25	64	0.07%	41.7%	FQTMEEK	94.6%	27.4	25	22.8	1	0	0	912.41	379	385
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	25	64	0.07%	41.7%	HGSLGFLPR	99.7%	64.8	25	57.9	7	0	0	983.54	11	19
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	25	64	0.07%	41.7%	IGQGYLIK	99.7%	60.6	25	40.8	4	0	0	891.53	287	294
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	25	64	0.07%	41.7%	IGQGYLIKDGK	99.7%	68.9	25	62.1	2	0	0	1191.67	287	297
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	25	64	0.07%	41.7%	KVACIGAWHPAR	99.7%	54.7	25	49.3	0	2	0	1365.72	250	261
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	25	64	0.07%	41.7%	LEQQVPVNQVFGQDEMIDVIGVTK	99.7%	38.4	25	36.2	0	3	0	2686.38	201	224
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	25	64	0.07%	41.7%	NNASTDYDLSDK	99.7%	73.4	25	72.9	8	0	0	1342.58	301	312
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	25	64	0.07%	41.7%	SINPLGGFVHYGEVTNDFVMLK	99.7%	49.3	25	49.3	0	4	0	2437.22	313	334
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	25	64	0.07%	41.7%	TVFAEHISDECK	99.7%	71.8	25	71.8	7	1	0	1435.65	104	115
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	25	64	0.07%	41.7%	TVFAEHISDECKR	99.7%	59.7	25	56.2	2	4	0	1591.75	104	116
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	25	64	0.07%	41.7%	VACIGAWHPAR	99.7%	92.7	25	87.2	4	1	0	1237.63	251	261
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	25	64	0.07%	41.7%	VIAHTQMR	99.7%	43.9	25	36.1	2	0	0	955.51	162	169
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	7	8	22	0.02%	59.1%	KSEIEYYAMLAK	99.7%	40	25	39.6	1	0	0	1461.73	57	68
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	7	8	22	0.02%	59.1%	KSLESINSR	99.7%	64.1	25	47.3	2	0	0	1033.56	9	17
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	7	8	22	0.02%	59.1%	LVILANNCPALR	99.7%	72.7	25	54.7	6	0	0	1353.77	45	56
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	7	8	22	0.02%	59.1%	SEIEYYAMLAK	99.7%	72.9	25	62.1	5	0	0	1333.63	58	68
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	7	8	22	0.02%	59.1%	SLESINSR	99.6%	38	25	28.6	2	0	0	905.47	10	17
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	7	8	22	0.02%	59.1%	TGVHHYSGNNIELGTACGK	99.4%	30.4	25	30.4	0	2	0	2014.94	69	87
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	7	8	22	0.02%	59.1%	VCTLAIIDPGDSDIIR	99.7%	59.2	25	51.9	4	0	0	1757.91	91	106
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	9	42	0.04%	56.8%	EYTINIHK	99.1%	34.6	25	17.5	3	0	0	1017.54	24	31
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	9	42	0.04%	56.8%	EYTINIHKR	99.7%	55.5	25	32.7	4	0	0	1173.64	24	32
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	9	42	0.04%	56.8%	FAMKEMGTPDVR	99.7%	54.3	25	29.8	6	1	0	1397.66	52	63
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	9	42	0.04%	56.8%	IHGVGFKK	96.6%	29.2	25	25.4	1	0	0	885.53	33	40
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	9	42	0.04%	56.8%	LYTLVTYVPVTTFK	99.7%	78	25	78	7	0	0	1644.92	102	115
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	9	42	0.04%	56.8%	NEDEDSPNKLYTLVTYVPVTTFK	99.7%	43.7	25	39.8	0	2	0	2673.33	93	115
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	9	42	0.04%	56.8%	NLQTVNVDEN	99.7%	64.5	25	58	4	0	0	1145.54	116	125
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	9	42	0.04%	56.8%	SAINEVVTR	99.7%	73	25	59.5	14	0	0	988.54	15	23
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	5	11	33	0.03%	29.6%	ELEVLLMCNK	99.7%	64.7	25	52.4	9	0	0	1264.63	84	93
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	5	11	33	0.03%	29.6%	FKGQILMPNIGYGSNK	99.7%	50.7	25	50.7	4	1	0	1766.93	49	64
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	5	11	33	0.03%	29.6%	GQILMPNIGYGSNK	99.7%	48.2	25	48.2	5	0	0	1491.76	51	64
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	5	11	33	0.03%	29.6%	GQILMPNIGYGSNKK	99.7%	56.3	25	51	3	0	0	1619.86	51	65
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	5	11	33	0.03%	29.6%	SYCAEIAHNVSSK	99.7%	87.4	25	83.7	10	1	0	1465.67	94	106
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	8	9	30	0.03%	34.2%	AFLIEEQK	99.7%	47.2	25	30.3	8	0	0	977.53	94	101
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	8	9	30	0.03%	34.2%	AFLIEEQKIVVK	99.7%	54.9	25	54.8	2	1	0	1416.85	94	105
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	8	9	30	0.03%	34.2%	AYGGSMCAK	99.7%	47.4	25	47.4	2	0	0	944.40	77	85

60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	8	9	30	0.03%	34.2%	IVYLYTK	99.2%	35.4	25	23.6	2	0	0	899.52	30	36
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	8	9	30	0.03%	34.2%	IVYLYTKK	99.7%	44.1	25	35.8	4	0	0	1027.62	30	37
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	8	9	30	0.03%	34.2%	LSYNTASNK	99.7%	46.2	25	34.5	5	0	0	997.49	11	19
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	8	9	30	0.03%	34.2%	RAFLIEEQK	99.3%	35.8	25	25.6	2	0	0	1133.63	93	101
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	8	9	30	0.03%	34.2%	RLSYNTASNK	99.7%	41	25	35.7	4	0	0	1153.60	10	19
60S ribosomal protein L35	RPL35	RL35_HUMAN	14.6	100.0%	4	5	19	0.02%	29.3%	QLDDLKVELSQLR	99.7%	86.2	25	70.5	3	2	0	1556.86	20	32
60S ribosomal protein L35	RPL35	RL35_HUMAN	14.6	100.0%	4	5	19	0.02%	29.3%	VLTVINQTQK	99.7%	66.3	25	62.8	11	0	0	1143.67	57	66
60S ribosomal protein L35	RPL35	RL35_HUMAN	14.6	100.0%	4	5	19	0.02%	29.3%	VLTVINQTQKENLR	99.7%	94.3	25	94.3	2	0	0	1655.94	57	70
60S ribosomal protein L35	RPL35	RL35_HUMAN	14.6	100.0%	4	5	19	0.02%	29.3%	YKPLDLRPK	98.7%	33	25	33	1	0	0	1129.67	78	86
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	5	6	18	0.02%	23.6%	AIFAGYKR	99.7%	43.3	25	36.5	2	0	0	925.53	9	16
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	5	6	18	0.02%	23.6%	DETEFYLGK	99.7%	45.2	25	38.1	4	0	0	1101.51	37	45
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	5	6	18	0.02%	23.6%	DETEFYLGKR	99.7%	44.4	25	40.9	3	0	0	1257.61	37	46
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	5	6	18	0.02%	23.6%	VMLYPSR	96.5%	29	25	20.1	3	0	0	881.46	103	109
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	5	6	18	0.02%	23.6%	VMLYPSRI	99.7%	47.2	25	46.7	6	0	0	994.54	103	110
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	4	7	20	0.02%	31.4%	ALRYPMAVGLNK	99.7%	44.5	25	39.5	2	3	0	1348.74	2	13
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	4	7	20	0.02%	31.4%	EELSNVLAAMR	99.7%	68.4	25	61.8	7	0	0	1232.63	88	98
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	4	7	20	0.02%	31.4%	EVCGFAPYER	99.7%	44.7	25	44.7	5	0	0	1227.55	46	55
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	4	7	20	0.02%	31.4%	YPMAVGLNK	99.7%	42.2	25	28.8	3	0	0	1008.52	5	13
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	5	5	11	0.01%	28.3%	DSLYAQGR	95.8%	28.4	25	23.8	1	0	0	909.44	31	38
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	5	5	11	0.01%	28.3%	GKDSLYAQGR	99.7%	58.1	25	54.4	3	0	0	1094.56	29	38
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	5	5	11	0.01%	28.3%	IVLRLECVEPNCR	99.7%	39.1	25	39.1	0	2	0	1657.85	66	78
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	5	5	11	0.01%	28.3%	KGQVIQF	96.4%	29	25	29	1	0	0	819.47	100	106
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	5	5	11	0.01%	28.3%	LECVEPNCR	99.7%	47.8	25	47.8	4	0	0	1176.51	70	78
60S ribosomal protein L37a	RPL37A	RL37A_HUMAN	10.3	100.0%	3	5	24	0.02%	42.4%	AVGIWHCGSCMK	99.7%	50.1	25	50.1	7	1	0	1405.62	51	62
60S ribosomal protein L37a	RPL37A	RL37A_HUMAN	10.3	100.0%	3	5	24	0.02%	42.4%	KIEISQHAK	99.7%	43	25	36.8	2	0	0	1053.61	28	36
60S ribosomal protein L37a	RPL37A	RL37A_HUMAN	10.3	100.0%	3	5	24	0.02%	42.4%	TVAGGAWTYNTTSAVTVK	99.7%	79.6	25	77.6	14	0	0	1826.93	63	80
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	5	7	22	0.02%	51.4%	IEEIKDFLLTAR	99.7%	54.2	25	46.4	2	2	0	1447.82	5	16
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	5	7	22	0.02%	51.4%	LKQSLPPGLAVK	99.7%	43.5	25	43.5	4	0	0	1250.78	56	67
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	5	7	22	0.02%	51.4%	QSLPPGLAVK	99.7%	70.4	25	68	6	0	0	1009.60	58	67
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	5	7	22	0.02%	51.4%	YLYTLVITDK	99.7%	51.1	25	45	2	0	0	1228.68	41	50
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	5	7	22	0.02%	51.4%	YLYTLVITDKEK	99.7%	58.7	25	58.7	4	2	0	1485.82	41	52
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	120	0.12%	44.3%	AAAAAAALQAK	99.7%	82.1	25	80.5	16	0	0	956.55	354	364
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	120	0.12%	44.3%	APIRPDIVNFVHTNLR	99.7%	57.7	25	54.8	2	2	0	1862.04	30	45
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	120	0.12%	44.3%	EAVLLLKK	99.7%	45.5	25	25.7	2	0	0	913.61	166	173
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	120	0.12%	44.3%	FCIWTESAFR	99.7%	59.3	25	51.2	12	0	0	1316.61	249	258
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	120	0.12%	44.3%	GPCIIYNEDNGIIK	99.7%	63.8	25	63.8	2	0	0	1605.79	206	219
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	120	0.12%	44.3%	IEEVPELPLVVEDK	99.7%	51.6	25	51.6	2	0	0	1608.87	144	157
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	120	0.12%	44.3%	IEEVPELPLVVEDKVEGYK	99.7%	81	25	81	2	0	0	2185.16	144	162
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	120	0.12%	44.3%	KLDELYGTWR	99.7%	74.4	25	73.3	4	2	0	1280.66	259	268
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	120	0.12%	44.3%	LDELYGTWR	99.7%	63	25	55.4	1	0	0	1152.57	260	268
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	120	0.12%	44.3%	MINTDLSR	99.7%	59.8	25	49.6	10	0	0	949.48	284	291
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	120	0.12%	44.3%	NIPGITLLNVSK	99.7%	86.5	25	81.9	13	0	0	1268.76	223	234
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	120	0.12%	44.3%	NIPGITLLNVSKLNILK	99.7%	62.3	25	61.2	2	0	0	1850.15	223	239
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	120	0.12%	44.3%	NVTLPAVFK	99.6%	38.8	25	26	3	0	0	988.58	21	29
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	120	0.12%	44.3%	QPYAVSELAGHQTSAESWGTGR	99.7%	43.6	25	43.5	0	2	0	2332.10	50	71
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	120	0.12%	44.3%	RGPCIIYNEDNGIIK	99.7%	69.4	25	54.8	1	2	0	1761.90	205	219
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	120	0.12%	44.3%	SGQGAFGNMCR	99.7%	55.8	25	55.8	6	0	0	1184.49	87	97
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	120	0.12%	44.3%	SNYNLPMHK	99.6%	38.7	25	38.7	11	0	0	1119.53	275	283
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	120	0.12%	44.3%	TKEAVLLLK	99.7%	47.5	25	42.4	4	0	0	1014.66	164	172
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	120	0.12%	44.3%	VDKAAAAAAALQAK	99.7%	73.3	25	57.1	3	0	0	1298.74	351	364
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	120	0.12%	44.3%	YAICSALAASALPALVMSK	99.7%	110	25	110	10	6	0	1937.02	122	140

60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	24	61	0.06%	42.8%	DIICQIAYAR	99.7%	57.7	25	27.4	2	0	0	1222.63	59	68
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	24	61	0.06%	42.8%	EFNAEVHR	99.7%	45.3	25	25.9	2	0	0	1001.48	189	196
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	24	61	0.06%	42.8%	EFNAEVHRK	96.1%	28.6	25	21.7	1	0	0	1129.57	189	197
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	24	61	0.06%	42.8%	FPGYDSESK	99.7%	44.8	25	44.8	2	0	0	1029.45	180	188
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	24	61	0.06%	42.8%	GAVDGGLSIPHSTK	99.7%	73.9	25	61.6	4	2	0	1338.70	165	178
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	24	61	0.06%	42.8%	GAVDGGLSIPHSTKR	99.7%	43.4	25	37.8	0	2	0	1494.80	165	179
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	24	61	0.06%	42.8%	HIMGQNVADYMR	99.7%	64.5	25	51.5	8	2	0	1434.66	198	209
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	24	61	0.06%	42.8%	IEGDMIVCAAYAHELPK	99.7%	56.5	25	52.6	1	6	0	1916.92	69	85
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	24	61	0.06%	42.8%	NSVTPDMMEEMYK	99.7%	48.8	25	48.8	1	0	0	1574.65	229	241
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	24	61	0.06%	42.8%	NSVTPDMMEEMYKK	99.7%	62.7	25	62.7	3	0	0	1702.75	229	242
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	24	61	0.06%	42.8%	RFPGYDSESK	99.7%	39.2	25	29.9	2	0	0	1185.55	179	188
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	24	61	0.06%	42.8%	RLVIQDK	98.9%	33.7	25	19.4	1	0	0	871.54	35	41
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	24	61	0.06%	42.8%	VGLTNYAAAYCTGLLLAR	99.7%	93.7	25	93.7	4	0	0	1927.01	90	107
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	24	61	0.06%	42.8%	VTNRDIICQIAYAR	99.7%	57.9	25	48.5	4	4	0	1692.89	55	68
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	24	61	0.06%	42.8%	YLMEEDEDAYKK	99.7%	71.3	25	57.5	6	4	0	1533.68	210	221
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	9	11	48	0.05%	33.0%	AIPQLQGYLR	99.7%	51.1	25	41.8	5	0	0	1158.66	263	272
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	9	11	48	0.05%	33.0%	ASITPGTILIILTGR	99.7%	112	25	112	13	0	0	1525.93	142	156
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	9	11	48	0.05%	33.0%	AVDSQILPK	99.7%	63.9	25	41.6	2	0	0	970.56	252	260
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	9	11	48	0.05%	33.0%	HLTDAYFK	99.3%	35.5	25	21.3	1	0	0	994.50	211	218
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	9	11	48	0.05%	33.0%	QLASGLLLVTGPLVLNR	99.7%	80.7	25	80.7	6	3	0	1764.07	167	183
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	9	11	48	0.05%	33.0%	SVFALTNGIYPHK	99.7%	60.8	25	59.7	5	0	0	1446.77	273	285
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	9	11	48	0.05%	33.0%	VLATVTKPVGGDK	99.7%	69.9	25	65	8	1	0	1284.75	88	100
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	9	11	48	0.05%	33.0%	YYPTEDVPR	99.7%	57.9	25	55.8	2	0	0	1139.54	115	123
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	9	11	48	0.05%	33.0%	YYPTEDVPRK	98.4%	32.2	25	32	2	0	0	1267.63	115	124
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	15	20	41	0.04%	49.6%	AGNFYVPAEPK	99.7%	51.9	25	41.6	2	0	0	1192.60	78	88
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	15	20	41	0.04%	49.6%	ASINMLR	99.7%	61.4	25	46.3	6	0	0	804.44	128	134
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	15	20	41	0.04%	49.6%	EANNFLWPFK	99.7%	47.9	25	41	3	0	0	1265.63	203	212
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	15	20	41	0.04%	49.6%	EVPAVPETLKK	98.3%	31.9	25	23.7	1	1	0	1210.70	10	20
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	15	20	41	0.04%	49.6%	FKEANNFLWPFK	99.7%	66.8	25	60.1	2	2	0	1540.79	201	212
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	15	20	41	0.04%	49.6%	IALTDNALIAR	99.7%	84.9	25	70.3	4	0	0	1170.68	167	177
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	15	20	41	0.04%	49.6%	IVEPYIAWGYPNLK	99.7%	76.3	25	50.4	5	0	0	1662.89	135	148
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	15	20	41	0.04%	49.6%	KAGNFYVPAEPK	99.7%	51.4	25	51.4	2	1	0	1320.69	77	88
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	15	20	41	0.04%	49.6%	QIFNGTFVK	99.5%	37.4	25	28.9	1	0	0	1053.57	116	124
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	15	20	41	0.04%	49.6%	RIALTDNALIAR	99.7%	82.3	25	67.8	2	0	0	1326.79	166	177
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	15	20	41	0.04%	49.6%	SVNELIYK	99.7%	57.8	25	43.8	2	0	0	965.53	149	156
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	15	20	41	0.04%	49.6%	SVNELIYKR	99.7%	46.5	25	38	2	0	0	1121.63	149	157
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	15	20	41	0.04%	49.6%	TTHFVEGGDAGNR	99.1%	34.8	25	34.4	1	0	0	1360.62	224	236
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	15	20	41	0.04%	49.6%	TTHFVEGGDAGNREDQINR	99.7%	64.5	25	64.5	2	1	0	2115.98	224	242
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	15	20	41	0.04%	49.6%	YGIICMEDLIHEIYTVGK	99.6%	32.3	25	28.5	0	1	0	2154.06	182	199
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	23	61	0.06%	41.4%	AGVNTVTTLVENK	99.7%	97.2	25	93.2	9	0	0	1345.73	138	150
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	23	61	0.06%	41.4%	AGVNTVTTLVENKK	99.7%	82.8	25	82.8	6	3	0	1473.83	138	151
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	23	61	0.06%	41.4%	HWGGNVLGPK	99.7%	45.2	25	44.8	2	0	0	1064.56	236	245
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	23	61	0.06%	41.4%	KMGVPYCIIK	99.7%	43.9	25	34.2	2	4	0	1224.65	176	185
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	23	61	0.06%	41.4%	KTCTTVAFTQVNSEDK	99.7%	72.8	25	72.8	1	0	0	1828.87	197	212
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	23	61	0.06%	41.4%	KVVNPLFEK	99.7%	41.5	25	25.9	2	0	0	1073.64	26	34
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	23	61	0.06%	41.4%	LKVPPAINQFTQALDR	99.7%	63.4	25	60.7	2	2	0	1811.02	74	89
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	23	61	0.06%	41.4%	MGVPYCIIK	99.7%	40.8	25	33.3	3	0	0	1096.55	177	185
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	23	61	0.06%	41.4%	NFGIGQDIQPK	99.7%	77.4	25	64.7	4	0	0	1216.63	38	48
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	23	61	0.06%	41.4%	QTATQLLK	99.7%	55.1	25	35.2	3	0	0	902.53	90	97
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	23	61	0.06%	41.4%	TCTTVAFTQVNSEDK	99.7%	104	25	96.4	2	0	0	1700.78	198	212
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	23	61	0.06%	41.4%	TCTTVAFTQVNSEDKGALAK	99.7%	113	25	113	3	3	0	2141.05	198	217

60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	23	61	0.06%	41.4%	TNYNDRYDEIR	99.6%	38.3	25	31.4	2	1	0	1458.66	224	234
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	23	61	0.06%	41.4%	VPPAINQFTQALDR	99.7%	91.3	25	86.7	5	1	0	1569.84	76	89
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	23	61	0.06%	41.4%	VVNPLFEK	96.2%	28.7	25	28	1	0	0	945.54	27	34
60S ribosomal protein L7-like 1	RPL7L1	RL7L_HUMAN	28.7	100.0%	2	2	4	0.00%	9.8%	IDGVSLLVQR	99.7%	73.9	25	55	2	0	0	1099.65	96	105
60S ribosomal protein L7-like 1	RPL7L1	RL7L_HUMAN	28.7	100.0%	2	2	4	0.00%	9.8%	IVEPYVTWGFPNLK	99.7%	44.7	25	27.5	2	0	0	1662.89	133	146
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	7	9	28	0.03%	21.4%	ASGNYATVISHNPETK	99.7%	79.5	25	79.5	7	2	0	1688.82	129	144
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	7	9	28	0.03%	21.4%	ASGNYATVISHNPETKK	99.7%	40.9	25	40.9	2	1	0	1816.92	129	145
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	7	9	28	0.03%	21.4%	AVDFAER	99.7%	49.4	25	38.7	2	0	0	807.40	31	37
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	7	9	28	0.03%	21.4%	AVVGVVAGGGR	99.7%	89.2	25	74.2	9	0	0	941.55	164	174
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	7	9	28	0.03%	21.4%	DIIHDPGR	99.2%	35.1	25	27.4	2	0	0	922.47	47	54
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	7	9	28	0.03%	21.4%	GIVKDIIHDPGR	99.0%	28.3	25	28.3	0	2	0	1319.74	43	54
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	7	9	28	0.03%	21.4%	KVGLIAAR	94.6%	27.4	25	16.9	1	0	0	827.55	234	241
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	8	16	38	0.04%	35.4%	DFNHINVELSLLGK	99.7%	84.5	25	73.7	5	2	0	1598.85	37	50
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	8	16	38	0.04%	35.4%	DFNHINVELSLLGKK	99.7%	50.1	25	47	2	2	0	1726.95	37	51
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	8	16	38	0.04%	35.4%	FLDGIYVSEK	99.7%	62.6	25	49	9	0	0	1170.60	175	184
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	8	16	38	0.04%	35.4%	KFLDGIYVSEK	99.7%	87.5	25	79.8	2	1	0	1298.70	174	184
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	8	16	38	0.04%	35.4%	MRPGVACSVSQAQK	99.7%	62.8	25	58.8	2	4	0	1534.75	128	141
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	8	16	38	0.04%	35.4%	NFLGEKYIR	99.7%	42.7	25	22.9	2	0	0	1139.62	116	124
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	8	16	38	0.04%	35.4%	TICSHVQNMIK	99.7%	74.7	25	65.2	4	2	0	1330.66	72	82
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	8	16	38	0.04%	35.4%	VDKWWGNR	97.5%	30.5	25	23.4	1	0	0	1060.53	57	64
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	PFKFB3	F263_HUMAN	59.6	100.0%	3	3	6	0.01%	6.7%	CLLAYFLDK	99.7%	45.2	25	44.2	2	0	0	1142.59	394	402
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	PFKFB3	F263_HUMAN	59.6	100.0%	3	3	6	0.01%	6.7%	LEPVIMELER	99.7%	53	25	45	2	0	0	1228.66	370	379
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	PFKFB3	F263_HUMAN	59.6	100.0%	3	3	6	0.01%	6.7%	LTNSPTVIVMVGLPAR	99.7%	81.6	25	81.6	2	0	0	1667.95	31	46
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	9	10	15	0.02%	16.6%	AIGVLTSGGDAQGMNAAVR	99.7%	144	25	144	4	1	0	1787.91	26	44
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	9	10	15	0.02%	16.6%	EIGWTDVGGWTGQGGSILGTK	99.7%	41.8	25	41.8	1	0	0	2119.05	460	480
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	9	10	15	0.02%	16.6%	EWSGLLEELAR	99.7%	68.8	25	43.8	2	0	0	1302.67	140	150
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	9	10	15	0.02%	16.6%	IIEVVDAIMTTAQSHQR	99.7%	58.6	25	58.6	1	1	0	1912.00	194	210
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	9	10	15	0.02%	16.6%	NGQIDKEAVQK	99.7%	41.9	25	30.5	2	0	0	1229.65	151	161
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	9	10	15	0.02%	16.6%	NVIFQPVAELKK	99.6%	38.1	25	38.1	2	0	0	1385.82	726	737
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	9	10	15	0.02%	16.6%	SFAGNLNTYK	99.7%	47.1	25	45.6	2	0	0	1114.55	386	395
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	9	10	15	0.02%	16.6%	SFAGNLNTYKR	98.8%	33.4	25	33.4	1	0	0	1270.65	386	396
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	9	10	15	0.02%	16.6%	TFVLEVMGR	99.7%	62.8	25	52.8	2	0	0	1051.56	211	219
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	9	10	15	0.02%	16.6%	VTILGHVQR	98.2%	31.7	25	26.2	1	0	0	1022.61	302	310
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	9	10	15	0.02%	16.6%	YLEEIATQMR	99.7%	66.7	25	59.2	2	0	0	1253.62	487	496
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	35	0.04%	26.9%	AIGVLTSGGDAQGMNAAVR	99.7%	144	25	144	4	1	0	1787.91	17	35
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	35	0.04%	26.9%	AMLWLSEK	99.7%	44.2	25	35.5	2	0	0	977.51	682	689
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	35	0.04%	26.9%	AVAFSPVTELKK	98.3%	31.9	25	31.9	2	0	0	1289.75	716	727
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	35	0.04%	26.9%	EQWWLSLR	99.7%	41.5	25	23.6	2	0	0	1117.58	738	745
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	35	0.04%	26.9%	GQLESIVENIR	99.7%	64	25	52.5	2	0	0	1257.68	475	485
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	35	0.04%	26.9%	GQVQEVGWHDVAGWLGR	99.7%	46.8	25	44.6	0	2	0	1893.94	445	461
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	35	0.04%	26.9%	IMEVIDAITTTAQSHQR	99.7%	47.1	25	6.59	0	3	0	1929.97	185	201
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	35	0.04%	26.9%	LPLMECVQMTK	99.7%	48.3	25	44.6	1	0	0	1349.66	346	356
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	35	0.04%	26.9%	SEWGSLLEELVAEGK	99.7%	65.6	25	60	1	0	0	1646.83	130	144
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	35	0.04%	26.9%	SNFSLAILNVGAPAAGMNAAVR	99.7%	88.5	25	85.2	3	2	0	2144.13	398	419
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	35	0.04%	26.9%	TFVLEVMGR	99.7%	62.8	25	52.8	2	0	0	1051.56	202	210
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	35	0.04%	26.9%	TNVLGHLQQGGAPTPFDR	99.7%	58.3	25	56.5	0	3	0	1907.97	655	672
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	35	0.04%	26.9%	VFANAPDSACVIGLK	99.7%	78.5	25	72.4	2	0	0	1561.80	699	713
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	35	0.04%	26.9%	VFLIYEGYEGLVEGGENIK	99.7%	96	25	84.5	1	0	0	2129.08	48	66
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	35	0.04%	26.9%	VTVLGHVQR	99.7%	70.3	25	69.1	2	0	0	1008.59	293	301
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	14	0.01%	19.2%	AIAVLTSGGDAQGMNAAVR	99.7%	103	25	97.4	1	0	0	1801.92	17	35
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	14	0.01%	19.2%	ALVFQPVAELK	99.7%	62.3	25	57.4	1	0	0	1214.71	717	727

6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	14	0.01%	19.2%	DLQANVEHLVQK	99.7%	65.4	25	50.1	2	0	0	1393.74	604	615
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	14	0.01%	19.2%	GITNLCVIGGDGSLTGADTFR	99.7%	114	25	114	1	0	0	2124.04	109	129
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	14	0.01%	19.2%	IGLIQGNR	99.7%	56.7	25	50.7	1	0	0	870.52	425	432
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	14	0.01%	19.2%	IMEIVDAITTTAQSHQR	99.7%	40.2	25	1.2	0	1	0	1929.97	185	201
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	14	0.01%	19.2%	SEWSDLLSDLQK	99.7%	83	25	75.9	2	0	0	1420.70	130	141
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	14	0.01%	19.2%	SFEQISANITK	99.7%	58.6	25	51.7	1	0	0	1237.64	477	487
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	14	0.01%	19.2%	TFVLEVMGR	99.7%	62.8	25	52.8	2	0	0	1051.56	202	210
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	14	0.01%	19.2%	VGIFTGAR	99.7%	52.9	25	40.3	2	0	0	820.47	40	47
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	14	0.01%	19.2%	VLVVHDGFEGLAK	99.7%	63	25	54.1	2	0	0	1383.76	433	445
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	14	0.01%	19.2%	VTVLGHVQR	99.7%	70.3	25	69.1	2	0	0	1008.59	293	301
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	7	7	12	0.01%	19.5%	AGQAVDDFIEK	99.7%	47.7	25	31.8	2	0	0	1192.58	77	87
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	7	7	12	0.01%	19.5%	GILFVGSGVSGGEEGAR	99.7%	110	25	103	2	0	0	1591.81	120	136
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	7	7	12	0.01%	19.5%	IISYAQGFMLLR	99.7%	91.3	25	80.5	2	0	0	1411.78	332	343
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	7	7	12	0.01%	19.5%	LVPLLDTGDIIIDGGNSEYR	99.7%	96.9	25	96.9	2	0	0	2160.12	88	107
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	7	7	12	0.01%	19.5%	TIFQGIAAK	96.1%	28.7	25	19.9	1	0	0	948.55	155	163
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	7	7	12	0.01%	19.5%	TVSKVDDFLANEAK	99.7%	65.3	25	65.3	1	0	0	1536.79	35	48
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	7	7	12	0.01%	19.5%	YGPSLMPGGNK	99.7%	46.8	25	41.4	2	0	0	1136.54	137	147
6-phosphogluconolactonase	PGLS	6PGL_HUMAN	27.5	100.0%	3	3	5	0.01%	15.1%	ELPAAVAPAGPASLAR	99.7%	41.6	25	40.2	2	0	0	1490.83	57	72
6-phosphogluconolactonase	PGLS	6PGL_HUMAN	27.5	100.0%	3	3	5	0.01%	15.1%	TVIFVATGEGK	99.7%	65.1	25	58.3	2	0	0	1121.62	198	208
6-phosphogluconolactonase	PGLS	6PGL_HUMAN	27.5	100.0%	3	3	5	0.01%	15.1%	VTLTLPVLNAAR	95.8%	28.3	25	28.3	1	0	0	1267.77	186	197
6-pyruvoyl tetrahydrobiopterin synthase	PTS	PTPS_HUMAN	16.4	99.9%	2	2	4	0.00%	15.9%	FLSDEENLK	99.1%	34.6	25	7.59	2	0	0	1094.54	30	38
6-pyruvoyl tetrahydrobiopterin synthase	PTS	PTPS_HUMAN	16.4	99.9%	2	2	4	0.00%	15.9%	VYETDNNIVVYKGE	99.7%	47.7	25	45	2	0	0	1642.80	132	145
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	36	0.04%	38.8%	DAGTIAGLNVMR	99.7%	90.7	25	79.6	4	0	0	1217.63	186	197
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	36	0.04%	38.8%	DNHLLGTFDLTGIPPAPR	99.3%	29.6	25	29.6	0	1	0	1934.01	475	492
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	36	0.04%	38.8%	ELEEIVQPIISK	99.7%	53.8	25	47.8	2	0	0	1397.79	622	633
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	36	0.04%	38.8%	IINEPTAAAIAYGLDK	99.7%	130	25	129	2	0	0	1659.90	198	213
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	36	0.04%	38.8%	IINEPTAAAIAYGLDKR	99.7%	81.6	25	80.9	2	2	0	1816.00	198	214
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	36	0.04%	38.8%	ITPSYVAFTPEGER	99.7%	47.4	25	45	1	0	0	1566.78	61	74
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	36	0.04%	38.8%	LTPEEIER	98.4%	32.3	25	0	2	0	0	986.52	533	540
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	36	0.04%	38.8%	LYGSAGPPPTGEEDTAEKDEL	99.7%	59.8	25	59.8	1	0	0	2175.99	634	654
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	36	0.04%	38.8%	MKETAEAYLGK	99.7%	66.3	25	49.1	2	0	0	1256.62	153	163
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	36	0.04%	38.8%	NQLTSNPENTVFDAK	99.7%	114	25	103	2	0	0	1677.81	82	96
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	36	0.04%	38.8%	SDIDEIVLVGGSTR	99.7%	45.7	25	45.7	1	0	0	1460.76	354	367
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	36	0.04%	38.8%	SQIFSTASDNQPTVTIK	99.7%	119	25	110	2	0	0	1836.93	448	464
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	36	0.04%	38.8%	TFAPEEISAMVLTK	99.7%	96.8	25	88.3	2	0	0	1536.80	139	152
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	36	0.04%	38.8%	TKPYIQVDIGGGQTK	99.7%	70.3	25	67.6	2	0	0	1604.86	124	138
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	36	0.04%	38.8%	TWNDPSVQQDIK	99.7%	69.9	25	59.7	2	0	0	1430.69	102	113
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	36	0.04%	38.8%	VEIIANDQGNR	99.7%	58.8	25	0	2	0	0	1228.63	50	60
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	36	0.04%	38.8%	VLEDSDLKK	99.7%	49.2	25	29.2	2	0	0	1046.57	345	353
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	36	0.04%	38.8%	VMEHFIK	99.7%	40	25	22.1	2	0	0	903.48	262	268
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	36	0.04%	38.8%	VTHAVVTVPAYFNDAQR	99.7%	42.9	25	42.5	0	2	0	1887.97	165	181
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	36	0.04%	38.8%	VYEGERPLTK	99.7%	57.7	25	42.6	2	0	0	1191.64	465	474
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	5	6	23	0.02%	13.3%	FLPGYVGGIQEGAVTPAGVVNK	99.7%	97.6	25	97.5	6	1	0	2173.17	121	142
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	5	6	23	0.02%	13.3%	LLVSGFWGVAR	99.7%	84.5	25	84.1	6	0	0	1204.68	394	404
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	5	6	23	0.02%	13.3%	SLDGVTNDR	99.7%	43.7	25	31.7	2	0	0	976.47	14	22
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	5	6	23	0.02%	13.3%	VIECSYTSADGQR	99.7%	98.6	25	98.6	6	0	0	1485.66	377	389
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	5	6	23	0.02%	13.3%	YTAAVPYR	99.6%	38.4	25	26.1	2	0	0	940.49	462	469
Acetolactate synthase-like protein	ILVBL	ILVBL_HUMAN	67.9	100.0%	3	3	3	0.00%	8.5%	AAVETLGVPCFLGGMAR	94.7%	27.5	25	23.8	1	0	0	1748.88	306	322
Acetolactate synthase-like protein	ILVBL	ILVBL_HUMAN	67.9	100.0%	3	3	3	0.00%	8.5%	ADVIVLAGTVCDFR	99.7%	49.7	25	49.7	1	0	0	1535.79	344	357
Acetolactate synthase-like protein	ILVBL	ILVBL_HUMAN	67.9	100.0%	3	3	3	0.00%	8.5%	NAQMAQSPILLLGGAASTLLQNR	99.6%	31.9	25	31.9	0	1	0	2383.28	135	157
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	20	39	0.04%	39.6%	AGIPKEEVK	99.6%	38	25	27.1	2	0	0	970.56	79	87

Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	20	39	0.04%	39.6%	DGLTDVYNK	99.7%	48.1	25	39.2	2	0	0	1024.49	182	190
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	20	39	0.04%	39.6%	EAYMGNVLQGGEGQAPTR	99.7%	113	25	113	4	0	0	1893.88	88	105
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	20	39	0.04%	39.6%	EEVKEAYMGNVLQGGEGQAPTR	99.7%	43.5	25	43.5	0	3	0	2379.12	84	105
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	20	39	0.04%	39.6%	EVVIVSATR	99.7%	76.4	25	76.4	2	0	0	973.57	41	49
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	20	39	0.04%	39.6%	GSTPYGGVKLEDLIVK	99.7%	70.2	25	64.4	2	0	0	1675.93	166	181
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	20	39	0.04%	39.6%	IHMGSCAENTAK	99.7%	45.1	25	45.1	2	0	0	1318.59	191	202
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	20	39	0.04%	39.6%	IVGHLTHALK	99.7%	53.8	25	40.9	1	0	0	1088.66	394	403
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	20	39	0.04%	39.6%	LEDLIVKDGLTDVYNK	99.7%	51.8	25	51.1	1	0	0	1834.98	175	190
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	20	39	0.04%	39.6%	LNVTPLAR	99.7%	41.2	25	29.8	2	0	0	883.54	304	311
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	20	39	0.04%	39.6%	MLEIDPQK	94.6%	27.4	25	14.6	1	0	0	973.50	366	373
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	20	39	0.04%	39.6%	NEQDAYAINSYTR	99.7%	90.6	25	90.6	2	0	0	1544.70	209	221
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	20	39	0.04%	39.6%	QAVLGAGLPISTPCTTINK	99.7%	94.9	25	92	2	0	0	1941.05	106	124
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	20	39	0.04%	39.6%	RLNVTPLAR	99.7%	41.1	25	39.1	2	0	0	1039.64	303	311
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	20	39	0.04%	39.6%	TPIGSFLGSLSLLPATK	99.7%	105	25	102	6	0	0	1701.98	50	66
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	20	39	0.04%	39.6%	VNINGGAVSLGHPIGMSGAR	99.7%	51.4	25	51.4	1	4	0	1922.99	374	393
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	10	10	14	0.01%	4.9%	AIGIGAYLVR	99.7%	53.1	25	41.4	2	0	0	1032.62	1824	1833
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	10	10	14	0.01%	4.9%	ATLVDHGIR	99.5%	37.7	25	31.4	2	0	0	981.55	1317	1325
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	10	10	14	0.01%	4.9%	DFTVASPAEFVTR	99.1%	34.6	25	24.7	1	0	0	1439.72	99	111
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	10	10	14	0.01%	4.9%	DIIVIGNDITYR	99.7%	56.5	25	40.4	2	0	0	1391.75	1676	1687
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	10	10	14	0.01%	4.9%	GSVLEPEGTVEIK	98.6%	32.7	25	22.2	1	0	0	1357.72	2115	2127
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	10	10	14	0.01%	4.9%	IGSFGPQEDLLFLR	99.7%	74.9	25	66.1	2	0	0	1591.85	1688	1701
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	10	10	14	0.01%	4.9%	ILNVPQELYEK	98.4%	32.2	25	32.2	1	0	0	1345.74	278	288
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	10	10	14	0.01%	4.9%	SPEYPEGR	97.0%	29.6	25	19.9	1	0	0	934.43	1668	1675
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	10	10	14	0.01%	4.9%	VEVGTEVTDYR	99.7%	46.7	25	46.3	1	0	0	1267.62	1410	1420
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	10	10	14	0.01%	4.9%	VQQAELHTGSLPR	99.7%	76.4	25	71.2	1	0	0	1435.77	826	838
Acidic fibroblast growth factor intracellular-binding protein	FIBP	FIBP_HUMAN	41.9	100.0%	3	3	5	0.01%	9.6%	DYAAIVFFANNR	98.3%	32.1	25	32.1	1	0	0	1400.70	172	183
Acidic fibroblast growth factor intracellular-binding protein	FIBP	FIBP_HUMAN	41.9	100.0%	3	3	5	0.01%	9.6%	VLVADKDLLDLHK	97.7%	25.2	25	25.2	0	2	0	1478.86	246	258
Acidic fibroblast growth factor intracellular-binding protein	FIBP	FIBP_HUMAN	41.9	100.0%	3	3	5	0.01%	9.6%	YYAFDEAFVR	99.7%	60.6	25	56.7	2	0	0	1280.59	96	105
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	22	42	255	0.26%	68.0%	AGFAGDDAPR	99.7%	78.5	25	65.8	21	0	0	976.45	19	28
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	22	42	255	0.26%	68.0%	AVFPSIVGRPR	99.7%	59.2	25	59.2	6	0	0	1198.71	29	39
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	22	42	255	0.26%	68.0%	CPEALFQPSFLGMESCGIHETTFNSIMK	98.4%	26.6	25	26.6	0	3	0	3231.46	257	284
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	22	42	255	0.26%	68.0%	DLTDYLMK	99.7%	54.3	25	42	7	0	0	1014.48	184	191
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	22	42	255	0.26%	68.0%	DLYANTVLSGGTTMYPGIADR	99.7%	134	25	134	23	5	0	2215.07	292	312
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	22	42	255	0.26%	68.0%	DSYVGDEAQSK	99.7%	66.2	25	62	9	0	0	1198.52	51	61
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	22	42	255	0.26%	68.0%	DSYVGDEAQSKR	99.7%	68.4	25	67.3	14	3	0	1354.62	51	62
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	22	42	255	0.26%	68.0%	EITALAPSTMK	99.7%	68.5	25	64.4	35	0	0	1177.61	316	326
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	22	42	255	0.26%	68.0%	GYSFTTTAER	99.7%	76.3	25	70.2	22	0	0	1132.53	197	206
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	22	42	255	0.26%	68.0%	GYSFTTTAEREIVR	99.7%	40.8	25	33	2	1	0	1629.82	197	210
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	22	42	255	0.26%	68.0%	HQGVMVGMGQK	99.7%	70.1	25	36.6	10	2	0	1187.57	40	50
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	22	42	255	0.26%	68.0%	IIAPPERK	99.7%	42.3	25	33.5	2	0	0	923.57	329	336
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	22	42	255	0.26%	68.0%	IKIIAPPER	99.4%	36.5	25	36.5	1	0	0	1036.65	327	335
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	22	42	255	0.26%	68.0%	IWHHTFYNELR	99.7%	51.8	25	51.8	2	4	0	1515.75	85	95
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	22	42	255	0.26%	68.0%	KDLYANTVLSGGTTMYPGIADR	99.7%	68.2	25	68.2	0	2	0	2359.16	291	312
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	22	42	255	0.26%	68.0%	LCYVALDFEQEMATAASSSSLEK	99.7%	163	25	163	11	13	0	2566.17	216	238
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	22	42	255	0.26%	68.0%	LDLAGRDLTDYLMK	99.7%	39.6	25	37.5	4	2	0	1639.84	178	191
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	22	42	255	0.26%	68.0%	QEYDESGPSIVHR	99.7%	55.6	25	55.6	4	7	0	1516.70	360	372
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	22	42	255	0.26%	68.0%	QEYDESGPSIVHRK	99.7%	47.8	25	45.3	2	2	0	1644.80	360	373
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	22	42	255	0.26%	68.0%	SYELPDGQVITIGNER	99.7%	121	25	106	15	0	0	1790.89	239	254
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	22	42	255	0.26%	68.0%	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	99.7%	74.5	25	74.5	0	4	0	3183.61	148	177
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	22	42	255	0.26%	68.0%	VAPEEHPVLLTEAPLNPK	99.7%	81.4	25	49.2	10	7	0	1954.06	96	113
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	6	8	15	0.02%	19.3%	GYAFNHSADFETVR	99.7%	69.8	25	54.9	2	2	0	1613.73	201	214

Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	6	8	15	0.02%	19.3%	HIVLSGGSTMYPGLPSR	99.0%	28.5	25	27.8	0	2	0	1787.91	300	316
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	6	8	15	0.02%	19.3%	ILLTEPPMNPTK	99.7%	45	25	40.9	4	0	0	1353.74	107	118
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	6	8	15	0.02%	19.3%	KVVVCDNGTGFVK	99.0%	34.4	25	32.9	1	0	0	1422.74	7	19
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	6	8	15	0.02%	19.3%	LCYVGYNIEQEQK	99.7%	83.1	25	83.1	2	0	0	1643.77	220	232
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	6	8	15	0.02%	19.3%	RLDIAGR	99.2%	35.2	25	14.4	2	0	0	800.47	181	187
Actin-related protein 2/3 complex subunit 2	ARPC2	ARPC2_HUMAN	34.3	100.0%	3	3	3	0.00%	9.7%	DNTINLIHTFR	99.7%	41.2	25	36.4	1	0	0	1343.71	238	248
Actin-related protein 2/3 complex subunit 2	ARPC2	ARPC2_HUMAN	34.3	100.0%	3	3	3	0.00%	9.7%	MILLEVNNR	99.2%	35.4	25	26.1	1	0	0	1101.61	1	9
Actin-related protein 2/3 complex subunit 2	ARPC2	ARPC2_HUMAN	34.3	100.0%	3	3	3	0.00%	9.7%	NCFASVFEK	98.5%	32.6	25	25.7	1	0	0	1101.50	119	127
Actin-related protein 2/3 complex subunit 3	ARPC3	ARPC3_HUMAN	20.5	100.0%	2	2	5	0.01%	13.5%	DTDIVDEAIYYFK	99.7%	54	25	51.2	3	0	0	1591.75	38	50
Actin-related protein 2/3 complex subunit 3	ARPC3	ARPC3_HUMAN	20.5	100.0%	2	2	5	0.01%	13.5%	LIGNMALLPIR	99.7%	50.8	25	41.7	2	0	0	1210.73	15	25
Actin-related protein 2/3 complex subunit 4	ARPC4	ARPC4_HUMAN	19.7	100.0%	4	4	7	0.01%	19.0%	AENFFILR	99.7%	42.1	25	29.5	2	0	0	1009.55	98	105
Actin-related protein 2/3 complex subunit 4	ARPC4	ARPC4_HUMAN	19.7	100.0%	4	4	7	0.01%	19.0%	ELLLQPVTISR	99.7%	58.7	25	58.4	2	0	0	1268.76	45	55
Actin-related protein 2/3 complex subunit 4	ARPC4	ARPC4_HUMAN	19.7	100.0%	4	4	7	0.01%	19.0%	IVAEEFLKNF	96.7%	29.3	25	29.3	1	0	0	1209.65	159	168
Actin-related protein 2/3 complex subunit 4	ARPC4	ARPC4_HUMAN	19.7	100.0%	4	4	7	0.01%	19.0%	SSKELLLQPVTISR	99.7%	48.4	25	48.4	2	0	0	1570.92	42	55
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	8	9	14	0.01%	24.6%	DITYFIQQLLR	99.7%	73.6	25	58.4	2	0	0	1409.78	199	209
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	8	9	14	0.01%	24.6%	EFSIDVGYER	96.8%	29.4	25	25.6	1	0	0	1214.57	266	275
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	8	9	14	0.01%	24.6%	FMEQVIFK	98.2%	31.7	25	29.1	2	0	0	1041.54	92	99
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	8	9	14	0.01%	24.6%	GVDDLDFFIGDEAIEKPTYATK	99.7%	43.4	25	41.5	0	1	0	2444.19	54	75
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	8	9	14	0.01%	24.6%	LGYAGNTEPQFIIPSCIAIK	99.7%	77.1	25	77.1	2	0	0	2192.14	19	38
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	8	9	14	0.01%	24.6%	NIVLSGGSTMFR	99.7%	68.5	25	67.2	4	0	0	1281.66	318	329
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	8	9	14	0.01%	24.6%	QYTGINAISK	96.3%	28.9	25	27.9	1	0	0	1094.58	255	264
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	8	9	14	0.01%	24.6%	YSYVCPDLVK	98.1%	31.5	25	28.5	1	0	0	1243.60	231	240
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	4	4	7	0.01%	1.8%	DLADWLNIK	99.4%	36.7	25	31.7	2	0	0	1087.58	1498	1506
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	4	4	7	0.01%	1.8%	RLEPLGIIVK	99.7%	43.4	25	39	1	0	0	1137.74	553	562
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	4	4	7	0.01%	1.8%	TGYFSSTDLGR	99.7%	54.9	25	50.1	2	0	0	1203.56	973	983
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	4	4	7	0.01%	1.8%	TVAAELAIFR	99.7%	74.3	25	72.8	2	0	0	1090.63	1356	1365
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	8	9	13	0.01%	25.4%	DASNWSTDKLK	99.7%	44.8	25	33.9	2	0	0	1264.62	31	41
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	8	9	13	0.01%	25.4%	DEPDTNLVALMK	99.1%	34.5	25	26.1	1	0	0	1345.67	126	137
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	8	9	13	0.01%	25.4%	EAMGIYISTLK	99.7%	59.4	25	59.4	3	0	0	1225.65	146	156
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	8	9	13	0.01%	25.4%	ETFLTSPEELYR	99.7%	45.4	25	39.8	2	0	0	1484.73	213	224
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	8	9	13	0.01%	25.4%	GIPAPEEERTR	98.5%	32.6	25	29.5	1	0	0	1254.64	306	316
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	8	9	13	0.01%	25.4%	LDGEASINNR	99.7%	69.9	25	47.5	1	0	0	1088.53	64	73
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	8	9	13	0.01%	25.4%	NGETELCMEGR	99.7%	43.8	25	43.8	2	0	0	1295.54	295	305
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	8	9	13	0.01%	25.4%	QTFGYGAR	99.5%	37.8	25	28.5	1	0	0	899.44	329	336
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	23	43	0.04%	30.3%	FFTEEVDSR	99.7%	59.4	25	45.8	2	0	0	1129.52	77	85
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	23	43	0.04%	30.3%	FSMGSVVAGLLK	99.7%	71.8	25	63.6	4	0	0	1224.67	305	316
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	23	43	0.04%	30.3%	GIILAGTEEQK	99.7%	48.1	25	37	2	0	0	1158.64	152	162
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	23	43	0.04%	30.3%	GSNTCEVHFENTK	99.7%	74.7	25	73.9	2	0	0	1522.66	267	279
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	23	43	0.04%	30.3%	ILLIFEGTNEILR	99.7%	71.1	25	68.7	2	0	0	1530.89	421	433
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	23	43	0.04%	30.3%	IPVENILGEVGDGFK	99.7%	84.5	25	84.5	2	0	0	1586.84	280	294
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	23	43	0.04%	30.3%	ITAFIVER	99.7%	54.6	25	45.6	2	0	0	948.55	242	249
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	23	43	0.04%	30.3%	LIEMTAEYACTR	99.7%	88.1	25	88.1	4	0	0	1457.68	318	329
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	23	43	0.04%	30.3%	LSEFGLIQEK	99.7%	67.2	25	51.2	2	0	0	1163.63	336	345
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	23	43	0.04%	30.3%	MYIALTGLQHAGR	99.7%	58.1	25	53.3	1	1	0	1430.76	434	446
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	23	43	0.04%	30.3%	TEVVDSDGSVK	98.2%	31.8	25	27.7	2	0	0	1135.55	229	239
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	23	43	0.04%	30.3%	TEVVDSDGSVKDK	99.7%	60.1	25	52.5	2	0	0	1378.67	229	241
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	23	43	0.04%	30.3%	TIMEEQLVLK	99.7%	46	25	29.4	2	0	0	1203.67	522	531
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	23	43	0.04%	30.3%	TIMEEQLVLKR	99.2%	35.3	25	28.6	1	0	0	1359.77	522	532
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	23	43	0.04%	30.3%	TVETLLLR	99.7%	62.1	25	35	2	0	0	944.58	511	518
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	23	43	0.04%	30.3%	VAMNILNSGR	99.7%	82.3	25	72.5	2	0	0	1090.57	295	304
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	23	43	0.04%	30.3%	VSQQILEK	99.7%	52.4	25	32.6	2	0	0	944.54	601	608

Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	23	43	0.04%	30.3%	VSTVMDTVGR	99.7%	76.7	25	67.7	4	0	0	1064.54	460	469
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	23	43	0.04%	30.3%	YAPENLDEQIKK	99.7%	48	25	37.3	2	0	0	1447.74	589	600
Acyl-coenzyme A thioesterase 1	ACOT1	ACOT1_HUMAN	46.3	100.0%	3	3	6	0.01%	7.4%	AATLILEPAGR	99.7%	66	25	64.9	2	0	0	1111.65	2	12
Acyl-coenzyme A thioesterase 1	ACOT1	ACOT1_HUMAN	46.3	100.0%	3	3	6	0.01%	7.4%	GALFQAHAR	99.7%	42.7	25	28	2	0	0	970.52	43	51
Acyl-coenzyme A thioesterase 1	ACOT1	ACOT1_HUMAN	46.3	100.0%	3	3	6	0.01%	7.4%	GLAPEQPVTLR	99.7%	49.2	25	45.9	2	0	0	1180.67	25	35
Acyl-coenzyme A thioesterase 13	ACOT13	ACO13_HUMAN	15.0	99.8%	2	2	8	0.01%	15.7%	ITLVSAAPGK	99.7%	52.8	25	45.6	4	0	0	956.58	28	37
Acyl-coenzyme A thioesterase 13	ACOT13	ACO13_HUMAN	15.0	99.8%	2	2	8	0.01%	15.7%	TLAFTSVDLTNK	99.7%	92.8	25	85.9	4	0	0	1309.70	112	123
Acyl-coenzyme A thioesterase 8	ACOT8	ACOT8_HUMAN	35.9	99.8%	2	2	4	0.00%	7.8%	LFGGQIVGQALVAAAK	99.7%	40.4	25	35.6	2	0	0	1542.90	54	69
Acyl-coenzyme A thioesterase 8	ACOT8	ACOT8_HUMAN	35.9	99.8%	2	2	4	0.00%	7.8%	LPVLYQVER	99.7%	44.3	25	32.6	2	0	0	1116.64	92	100
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	ACOT9_HUMAN	49.9	100.0%	5	6	9	0.01%	11.8%	IAFSSTSLLK	98.4%	32.2	25	32.2	1	0	0	1066.61	241	250
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	ACOT9_HUMAN	49.9	100.0%	5	6	9	0.01%	11.8%	IFGGFLMR	99.7%	51.8	25	45.5	3	0	0	940.51	310	317
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	ACOT9_HUMAN	49.9	100.0%	5	6	9	0.01%	11.8%	SLEICHPQER	99.7%	45.8	25	45.8	2	0	0	1268.61	295	304
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	ACOT9_HUMAN	49.9	100.0%	5	6	9	0.01%	11.8%	TYGESMLYLDGQR	99.7%	79.3	25	79.3	1	0	0	1532.71	408	420
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	ACOT9_HUMAN	49.9	100.0%	5	6	9	0.01%	11.8%	VHSEVASLQEK	98.8%	33.4	25	27.9	2	0	0	1226.64	373	383
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	5	6	12	0.01%	13.3%	ATVFLNPAACK	99.7%	75	25	67.8	2	0	0	1191.62	63	73
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	5	6	12	0.01%	13.3%	EQPVFAMTGLR	99.7%	42.9	25	33	4	0	0	1264.64	200	210
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	5	6	12	0.01%	13.3%	GDFITIGSR	99.7%	65.4	25	55.5	2	0	0	965.51	343	351
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	5	6	12	0.01%	13.3%	GETVPLDVLQIK	99.7%	51.1	25	44.9	2	0	0	1311.75	185	196
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	5	6	12	0.01%	13.3%	VQHITDATLAIVK	99.7%	60.4	25	60.4	2	0	0	1408.82	172	184
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	6	8	22	0.02%	35.6%	AELEIQK	95.2%	27.8	25	12.9	1	0	0	830.46	108	114
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	6	8	22	0.02%	35.6%	AELEIQKDALEPGQR	99.7%	71.1	25	71.1	4	3	0	1696.89	108	122
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	6	8	22	0.02%	35.6%	DISPVLKDPASFR	99.7%	61.1	25	55.8	4	1	0	1444.78	28	40
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	6	8	22	0.02%	35.6%	IDYIAGLDSR	99.7%	64.6	25	59.1	4	0	0	1122.58	58	67
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	6	8	22	0.02%	35.6%	LAPVPFFSLLQYE	99.7%	63.1	25	63.1	2	0	0	1523.81	168	180
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	6	8	22	0.02%	35.6%	SFPDFPTPGVVFR	98.7%	33	25	30.4	3	0	0	1465.75	15	27
Adenosine 3'-phospho 5'-phosphosulfate transporter 1	SLC35B2	S35B2_HUMAN	47.5	99.8%	2	2	2	0.00%	5.3%	FVSFPTQVLAK	98.3%	32	25	26.5	1	0	0	1236.70	206	216
Adenosine 3'-phospho 5'-phosphosulfate transporter 1	SLC35B2	S35B2_HUMAN	47.5	99.8%	2	2	2	0.00%	5.3%	SYGATATSPGER	99.7%	41.2	25	33.6	1	0	0	1196.55	137	148
Adenosylhomocysteinase	AHCY	SAHH_HUMAN	47.7	100.0%	6	6	9	0.01%	15.3%	GISEETTTGVHNLYK	99.7%	54.5	25	53.1	1	0	0	1648.82	152	166
Adenosylhomocysteinase	AHCY	SAHH_HUMAN	47.7	100.0%	6	6	9	0.01%	15.3%	IILLAEGR	99.7%	42.9	25	36.4	2	0	0	884.56	336	343
Adenosylhomocysteinase	AHCY	SAHH_HUMAN	47.7	100.0%	6	6	9	0.01%	15.3%	SKFDNLYGCR	99.7%	42.8	25	39.3	1	0	0	1259.58	187	196
Adenosylhomocysteinase	AHCY	SAHH_HUMAN	47.7	100.0%	6	6	9	0.01%	15.3%	VAVVAGYGDVGK	99.7%	56.9	25	47.4	2	0	0	1134.62	215	226
Adenosylhomocysteinase	AHCY	SAHH_HUMAN	47.7	100.0%	6	6	9	0.01%	15.3%	VPAINVNDSVTK	99.7%	59.9	25	59.9	2	0	0	1256.68	175	186
Adenosylhomocysteinase	AHCY	SAHH_HUMAN	47.7	100.0%	6	6	9	0.01%	15.3%	YPQLLPGIR	98.8%	33.4	25	33.4	1	0	0	1056.62	143	151
Adenylate kinase 2, mitochondrial	AK2	KAD2_HUMAN	26.5	99.8%	2	2	4	0.00%	8.8%	AVLLGPPGAGK	98.9%	33.9	25	33.9	2	0	0	979.59	18	28
Adenylate kinase 2, mitochondrial	AK2	KAD2_HUMAN	26.5	99.8%	2	2	4	0.00%	8.8%	NGFLLDGFPR	98.4%	32.3	25	32.3	2	0	0	1135.59	94	103
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	5	7	13	0.01%	24.7%	AVILGPPGSGK	99.7%	45.2	25	39	2	0	0	995.59	8	18
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	5	7	13	0.01%	24.7%	DVAKPVIELYK	99.7%	43.9	25	35.4	2	1	0	1274.74	176	186
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	5	7	13	0.01%	24.7%	GVLHQFSGTETNK	99.7%	61.9	25	61.9	2	0	0	1417.71	189	201
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	5	7	13	0.01%	24.7%	LMMSELENR	99.7%	60.5	25	55.5	4	0	0	1122.53	72	80
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	5	7	13	0.01%	24.7%	SLLVPDHVITR	99.7%	45.9	25	38.2	2	0	0	1249.73	61	71
Adenylate kinase isoenzyme 6	AK6	KAD6_HUMAN	20.1	100.0%	3	3	3	0.00%	19.8%	MLLPNILLTGTPGVGK	98.1%	31.5	25	31.5	1	0	0	1623.95	1	16
Adenylate kinase isoenzyme 6	AK6	KAD6_HUMAN	20.1	100.0%	3	3	3	0.00%	19.8%	TDTNVLYER	99.7%	44.8	25	43.9	1	0	0	1110.54	97	105
Adenylate kinase isoenzyme 6	AK6	KAD6_HUMAN	20.1	100.0%	3	3	3	0.00%	19.8%	YINVGDLAR	99.6%	38.4	25	30.6	1	0	0	1020.55	31	39
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	7	7	11	0.01%	21.3%	FLEEEVYPLLKPYESVMK	99.7%	45.5	25	43.3	0	2	0	2214.14	460	477
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	7	7	11	0.01%	21.3%	IQVDAYFSPIHSQLDHLLDPSSFTGR	99.4%	30.2	25	30.2	0	1	0	2943.46	427	452
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	7	7	11	0.01%	21.3%	NALDLLLPK	99.7%	48	25	30.7	2	0	0	996.61	126	134
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	7	7	11	0.01%	21.3%	QELPFMATENIIMAMVK	99.7%	50.2	25	42.6	1	0	0	1965.98	375	391
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	7	7	11	0.01%	21.3%	SNLENIDFK	99.7%	57.9	25	51.1	2	0	0	1079.54	67	75
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	7	7	11	0.01%	21.3%	VLSQQAASVVK	99.7%	81.6	25	67	2	0	0	1129.66	405	415
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	7	7	11	0.01%	21.3%	YASPEMCFVFSDR	99.7%	40	25	31.7	1	0	0	1608.68	21	33
Adenylosuccinate synthetase isozyme 2	ADSS	PURA2_HUMAN	50.1	99.8%	2	2	4	0.00%	5.5%	FIEDELQIPVK	99.7%	48	25	36.8	2	0	0	1330.73	431	441

Adenylosuccinate synthetase isozyme 2	ADSS	PURA2_HUMAN	50.1	99.8%	2	2	4	0.00%	5.5%	VVDLLAQDADIVCR	99.7%	78.4	25	75.2	2	0	0	1586.82	46	59
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	14	0.01%	44.3%	AAYFGVYDTAK	99.7%	79.2	25	79.2	10	0	0	1205.58	189	199
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	14	0.01%	44.3%	DFLAGGVAAAVSK	99.7%	94.2	25	90.4	4	0	0	1205.65	11	23
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	14	0.01%	44.3%	EFHGLGDCIIK	99.7%	42	25	38.2	3	0	0	1288.64	153	163
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	14	0.01%	44.3%	EQGFLSFWR	99.7%	53.9	25	48.4	4	0	0	1169.57	64	72
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	14	0.01%	44.3%	GADIMYTGTVDCWR	99.7%	78.8	25	70.1	8	0	0	1644.71	246	259
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	14	0.01%	44.3%	GAWSNVLR	99.7%	58.8	25	41.2	4	0	0	902.48	273	280
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	14	0.01%	44.3%	GIIDCVVR	99.7%	39.2	25	21.8	2	0	0	931.50	53	60
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	14	0.01%	44.3%	GMGGAFVLVLYDEIK	99.7%	78.4	25	0	4	0	0	1627.84	281	295
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	14	0.01%	44.3%	GMGGAFVLVLYDEIKK	99.7%	44.5	25	0	3	0	0	1739.94	281	296
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	14	0.01%	44.3%	KGADIMYTGTVDCWR	99.7%	55.2	25	50.8	1	3	0	1788.80	245	259
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	14	0.01%	44.3%	LLLQVQHASK	99.7%	53.8	25	43.1	30	0	0	1136.68	34	43
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	14	0.01%	44.3%	QLFLGGVDR	99.7%	47.8	25	30	3	0	0	1004.55	97	105
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	14	0.01%	44.3%	TAVAPIER	99.4%	36.9	25	27.2	5	0	0	856.49	24	31
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	14	0.01%	44.3%	YFPTQALNFAFK	99.7%	83.8	25	71.1	32	0	0	1446.74	81	92
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	14	0.01%	44.3%	YFPTQALNFAFKDK	99.7%	91.1	25	84.2	5	1	0	1689.86	81	94
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	22	150	0.16%	44.0%	AAYFGIYDTAK	99.7%	72	25	57	6	0	0	1219.60	189	199
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	22	150	0.16%	44.0%	DFLAGGVAAAISK	99.7%	104	25	94.4	8	0	0	1219.67	11	23
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	22	150	0.16%	44.0%	EQGVLSFWR	99.7%	73.2	25	69.5	20	0	0	1121.57	64	72
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	22	150	0.16%	44.0%	GAWSNVLR	99.7%	58.8	25	41.2	4	0	0	902.48	273	280
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	22	150	0.16%	44.0%	GIIDCVVR	99.7%	39.2	25	21.8	2	0	0	931.50	53	60
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	22	150	0.16%	44.0%	GLGDCLVK	98.6%	32.8	25	8.26	1	0	0	861.45	156	163
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	22	150	0.16%	44.0%	GMGGAFVLVLYDEIK	99.7%	78.4	25	0	4	0	0	1627.84	281	295
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	22	150	0.16%	44.0%	GMGGAFVLVLYDEIKK	99.7%	44.5	25	0	3	0	0	1739.94	281	296
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	22	150	0.16%	44.0%	GTDIMYTGTLDCWR	99.7%	93.8	25	92.2	8	0	0	1704.74	246	259
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	22	150	0.16%	44.0%	GTDIMYTGTLDCWRK	99.7%	40.1	25	40.1	2	0	0	1816.84	246	260
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	22	150	0.16%	44.0%	KGTDIMYTGTLDCWR	99.7%	66.2	25	65	2	4	0	1832.83	245	259
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	22	150	0.16%	44.0%	LLLQVQHASK	99.7%	53.8	25	43.1	30	0	0	1136.68	34	43
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	22	150	0.16%	44.0%	QIFLGGVDK	99.7%	46.1	25	31.4	6	0	0	976.55	97	105
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	22	150	0.16%	44.0%	QIFLGGVDKR	99.7%	61.9	25	48	7	0	0	1132.65	97	106
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	22	150	0.16%	44.0%	TAVAPIER	99.4%	36.9	25	27.2	5	0	0	856.49	24	31
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	22	150	0.16%	44.0%	YFPTQALNFAFK	99.7%	83.8	25	71.1	32	0	0	1446.74	81	92
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	22	150	0.16%	44.0%	YFPTQALNFAFKDK	99.7%	91.1	25	84.2	5	1	0	1689.86	81	94
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	7	43	0.04%	40.6%	AAYFGVYDTAK	99.7%	79.2	25	79.2	10	0	0	1205.58	189	199
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	7	43	0.04%	40.6%	DFLAGGIAAAISK	99.7%	110	25	104	21	0	0	1233.68	11	23
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	7	43	0.04%	40.6%	EQGVLSFWR	99.7%	73.2	25	69.5	20	0	0	1121.57	64	72
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	7	43	0.04%	40.6%	GADIMYTGTVDCWR	99.7%	78.8	25	70.1	8	0	0	1644.71	246	259
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	7	43	0.04%	40.6%	GAWSNVLR	99.7%	58.8	25	41.2	4	0	0	902.48	273	280
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	7	43	0.04%	40.6%	GLGDCLVK	98.6%	32.8	25	8.26	1	0	0	861.45	156	163
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	7	43	0.04%	40.6%	GMGGAFVLVLYDELK	99.7%	78.4	25	0	4	0	0	1627.84	281	295
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	7	43	0.04%	40.6%	GMGGAFVLVLYDELKK	99.7%	44.5	25	0	3	0	0	1739.94	281	296
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	7	43	0.04%	40.6%	KGADIMYTGTVDCWR	99.7%	55.2	25	50.8	1	3	0	1788.80	245	259
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	7	43	0.04%	40.6%	LLLQVQHASK	99.7%	53.8	25	43.1	30	0	0	1136.68	34	43
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	7	43	0.04%	40.6%	QIFLGGVDK	99.7%	46.1	25	31.4	6	0	0	976.55	97	105
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	7	43	0.04%	40.6%	TAVAPIER	99.4%	36.9	25	27.2	5	0	0	856.49	24	31
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	7	43	0.04%	40.6%	YFPTQALNFAFK	99.7%	83.8	25	71.1	32	0	0	1446.74	81	92
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	7	43	0.04%	40.6%	YFPTQALNFAFKDK	99.7%	91.1	25	84.2	5	1	0	1689.86	81	94
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN	20.7	99.8%	2	3	7	0.01%	36.5%	DAVLLVFANK	99.7%	67.5	25	59.2	4	0	0	1089.63	118	127
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN	20.7	99.8%	2	3	7	0.01%	36.5%	ILMVGLDAAGK	99.7%	80.9	25	65.2	9	0	0	1103.61	20	30
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN	20.7	99.8%	2	3	7	0.01%	36.5%	LGEIVTTIPTIGFNVETVEYK	99.7%	43.6	25	43.6	2	0	0	2323.24	39	59
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN	20.7	99.8%	2	3	7	0.01%	36.5%	NISFTVWDVGGQDK	99.7%	114	25	103	4	0	0	1565.76	60	73

ADP-ribosylation factor 1	ARF1	ARF1_HUMAN	20.7	99.8%	2	3	7	0.01%	36.5%	VNEAREELMR	99.3%	35.7	25	27.8	2	1	0	1246.62	100	109
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	6	8	20	0.02%	43.9%	ILMVGLDAAGK	99.7%	80.9	25	65.2	9	0	0	1103.61	20	30
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	6	8	20	0.02%	43.9%	IQEVADELQK	99.7%	59.5	25	44.2	3	0	0	1172.62	100	109
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	6	8	20	0.02%	43.9%	LGEIVTTIPTIGFNVETVEYK	99.7%	43.6	25	43.6	2	0	0	2323.24	39	59
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	6	8	20	0.02%	43.9%	MLLVDELR	99.7%	40.8	25	13.2	2	0	0	988.55	110	117
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	6	8	20	0.02%	43.9%	NICFTVWDVGGQDR	99.7%	118	25	118	2	0	0	1666.76	60	73
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	6	8	20	0.02%	43.9%	QDLPNAMAISEMTDK	99.7%	49.9	25	48.8	2	0	0	1663.77	128	142
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	100.0%	3	3	8	0.01%	36.7%	DAVLLVFANK	99.7%	67.5	25	59.2	4	0	0	1089.63	118	127
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	100.0%	3	3	8	0.01%	36.7%	ILMVGLDAAGK	99.7%	80.9	25	65.2	9	0	0	1103.61	20	30
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	100.0%	3	3	8	0.01%	36.7%	LGEIVTTIPTIGFNVETVEYK	99.7%	43.6	25	43.6	2	0	0	2323.24	39	59
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	100.0%	3	3	8	0.01%	36.7%	NICFTVWDVGGQDK	99.7%	89.2	25	89.2	2	0	0	1638.76	60	73
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	100.0%	3	3	8	0.01%	36.7%	VQESADELQK	99.6%	38.3	25	35.1	2	0	0	1146.56	100	109
ADP-ribosylation factor 6	ARF6	ARF6_HUMAN	20.1	100.0%	3	5	10	0.01%	24.0%	DAIILIFANK	99.7%	58	25	0	2	0	0	1117.66	114	123
ADP-ribosylation factor 6	ARF6	ARF6_HUMAN	20.1	100.0%	3	5	10	0.01%	24.0%	ILMLGLDAAGK	99.7%	82.1	25	58.5	4	0	0	1117.63	16	26
ADP-ribosylation factor 6	ARF6	ARF6_HUMAN	20.1	100.0%	3	5	10	0.01%	24.0%	LGQSVTTIPTVGFNVETVTYK	99.7%	54.5	25	54.5	2	2	0	2254.20	35	55
ADP-ribosylation factor-like protein 1	ARL1	ARL1_HUMAN	20.4	100.0%	3	4	8	0.01%	16.0%	AILVVFANK	99.7%	68.4	25	68.4	2	0	0	974.60	119	127
ADP-ribosylation factor-like protein 1	ARL1	ARL1_HUMAN	20.4	100.0%	3	4	8	0.01%	16.0%	KWQIFK	99.7%	43.6	25	18.7	2	0	0	849.50	152	157
ADP-ribosylation factor-like protein 1	ARL1	ARL1_HUMAN	20.4	100.0%	3	4	8	0.01%	16.0%	SELVAMLEEEELRK	99.7%	54	25	53.7	4	0	0	1691.85	105	118
ADP-ribosylation factor-like protein 2	ARL2	ARL2_HUMAN	20.9	100.0%	6	7	12	0.01%	40.2%	ELQSLLVEER	99.7%	68.9	25	53.8	1	0	0	1215.66	105	114
ADP-ribosylation factor-like protein 2	ARL2	ARL2_HUMAN	20.9	100.0%	6	7	12	0.01%	40.2%	FNGEDIDTISPTLGFNIK	99.7%	51.2	25	51.2	1	0	0	1980.99	36	53
ADP-ribosylation factor-like protein 2	ARL2	ARL2_HUMAN	20.9	100.0%	6	7	12	0.01%	40.2%	LAGATLLIFANK	99.7%	77	25	71	2	0	0	1231.74	115	126
ADP-ribosylation factor-like protein 2	ARL2	ARL2_HUMAN	20.9	100.0%	6	7	12	0.01%	40.2%	LLMLGLDNAGK	99.7%	66.4	25	51.6	4	0	0	1160.63	19	29
ADP-ribosylation factor-like protein 2	ARL2	ARL2_HUMAN	20.9	100.0%	6	7	12	0.01%	40.2%	LNIWDVGGQK	99.7%	60.5	25	53.7	2	0	0	1129.60	62	71
ADP-ribosylation factor-like protein 2	ARL2	ARL2_HUMAN	20.9	100.0%	6	7	12	0.01%	40.2%	QDLPGALSSNAIR	99.7%	70.8	25	63.6	2	0	0	1341.71	127	139
ADP-ribosylation factor-like protein 3	ARL3	ARL3_HUMAN	20.5	99.8%	2	2	3	0.00%	11.5%	ILLLGLDNAGK	99.7%	55.2	25	53.2	2	0	0	1126.68	20	30
ADP-ribosylation factor-like protein 3	ARL3	ARL3_HUMAN	20.5	99.8%	2	2	3	0.00%	11.5%	LNVWDIGGQR	99.3%	35.6	25	28.3	1	0	0	1157.61	63	72
ADP-ribosylation factor-like protein 6	ARL6	ARL6_HUMAN	21.1	100.0%	5	6	8	0.01%	31.2%	EVHVLCLGLDNSGK	97.9%	25.5	25	25.5	0	1	0	1540.78	17	30
ADP-ribosylation factor-like protein 6	ARL6	ARL6_HUMAN	21.1	100.0%	5	6	8	0.01%	31.2%	IPILFFANK	99.7%	49	25	32.8	2	0	0	1062.63	123	131
ADP-ribosylation factor-like protein 6	ARL6	ARL6_HUMAN	21.1	100.0%	5	6	8	0.01%	31.2%	LSVLLGLK	99.6%	38.9	25	37.4	2	0	0	842.57	7	14
ADP-ribosylation factor-like protein 6	ARL6	ARL6_HUMAN	21.1	100.0%	5	6	8	0.01%	31.2%	SSSLSFTVFDMSGQGR	99.7%	57.5	25	57.5	2	0	0	1721.78	60	75
ADP-ribosylation factor-like protein 6	ARL6	ARL6_HUMAN	21.1	100.0%	5	6	8	0.01%	31.2%	VSQLLCLENIK	99.7%	39.7	25	31.9	1	0	0	1316.72	143	153
ADP-ribosylation factor-like protein 8B	ARL8B	ARL8B_HUMAN	21.5	99.9%	2	2	3	0.00%	12.4%	DLPNALDEKQLIEK	99.7%	59	25	59	2	0	0	1625.87	133	146
ADP-ribosylation factor-like protein 8B	ARL8B	ARL8B_HUMAN	21.5	99.9%	2	2	3	0.00%	12.4%	MNLSAIQDR	99.3%	35.5	25	26.9	1	0	0	1047.53	147	155
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	11	11	15	0.02%	14.9%	GAILTGPPGTGK	99.7%	43.5	25	42.6	1	0	0	1068.61	343	354
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	11	11	15	0.02%	14.9%	GLGYAQYLPK	98.5%	32.4	25	22.2	2	0	0	1109.60	602	611
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	11	11	15	0.02%	14.9%	GMGGLFSVGETTAK	99.7%	41.5	25	39.1	1	0	0	1370.66	284	297
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	11	11	15	0.02%	14.9%	ILINDAYKR	99.6%	39	25	27.5	1	0	0	1105.64	703	711
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	11	11	15	0.02%	14.9%	ITTGAQDDLRK	95.6%	22.8	25	20.7	0	1	0	1217.65	642	652
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	11	11	15	0.02%	14.9%	KTQVLQPEEK	97.6%	30.6	25	16.1	1	0	0	1199.66	559	568
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	11	11	15	0.02%	14.9%	NLETLQQELGIEGENR	99.7%	74.6	25	72.4	1	0	0	1842.92	225	240
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	11	11	15	0.02%	14.9%	QIFIGPPDIK	98.7%	33.1	25	17.9	1	0	0	1127.65	472	481
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	11	11	15	0.02%	14.9%	VALLLLEK	99.7%	47.4	25	47.4	2	0	0	898.60	726	733
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	11	11	15	0.02%	14.9%	VGQISFDLPR	99.7%	76.9	25	55.1	2	0	0	1131.62	670	679
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	11	11	15	0.02%	14.9%	VSEEIFFGR	99.7%	77.2	25	55.8	2	0	0	1083.55	633	641
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	5	5	8	0.01%	11.0%	FAVALLDDSVR	99.7%	78.3	25	55.8	2	0	0	1205.65	166	176
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	5	5	8	0.01%	11.0%	GALLSVGWSTGR	99.7%	74.4	25	67.4	1	0	0	1203.65	467	478
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	5	5	8	0.01%	11.0%	GQWINLPVLQLTK	99.7%	65.5	25	45.4	2	0	0	1509.88	40	52
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	5	5	8	0.01%	11.0%	ILATTPSAVFR	99.7%	59.1	25	51.4	2	0	0	1175.68	302	312
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	5	5	8	0.01%	11.0%	VYNASSTIVPSLK	99.7%	44.4	25	37.1	1	0	0	1378.76	177	189
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	20	0.02%	16.5%	AAFLNFFR	99.7%	54.8	25	43.3	2	0	0	985.53	44	51
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	20	0.02%	16.5%	AGLDPDLETR	99.7%	50.8	25	42.3	2	0	0	1086.54	178	187

Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	20	0.02%	16.5%	AGQEDVLFPVAR	99.7%	44	25	41.4	1	0	0	1301.68	581	592
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	20	0.02%	16.5%	DIWLSLGVPASR	99.7%	40.4	25	38.2	2	0	0	1313.72	188	199
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	20	0.02%	16.5%	EADGSLQPLPQR	99.6%	38.3	25	31.5	1	0	0	1310.67	251	262
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	20	0.02%	16.5%	ELGQSLAQEVK	99.7%	56.9	25	49.2	2	0	0	1201.64	791	801
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	20	0.02%	16.5%	GPLIVDTVSAESLSVLVK	99.7%	56	25	52.3	1	0	0	1827.05	881	898
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	20	0.02%	16.5%	GVQLDSAGLER	99.7%	65.8	25	50.8	1	0	0	1144.60	461	471
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	20	0.02%	16.5%	HVDTGMGLER	99.7%	41.6	25	37.1	1	0	0	1114.53	263	272
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	20	0.02%	16.5%	LLAVTGEQAQQAR	99.7%	81.6	25	68.8	2	0	0	1384.75	778	790
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	20	0.02%	16.5%	LVPSASVRPR	98.8%	33.3	25	28.1	1	0	0	1081.65	58	67
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	20	0.02%	16.5%	LWISYFDGDPK	99.7%	50.2	25	37.3	2	0	0	1340.65	167	177
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	20	0.02%	16.5%	SLDEVYPDPVR	99.7%	47.6	25	46.3	1	0	0	1289.64	712	722
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	20	0.02%	16.5%	TNFYAEQGGQASDR	99.7%	92.3	25	82.4	1	0	0	1543.68	562	575
Alcohol dehydrogenase class-3	ADH5	ADHX_HUMAN	39.7	100.0%	3	3	5	0.01%	9.6%	AFELMHSGK	95.0%	27.7	25	24.5	1	0	0	1019.50	358	366
Alcohol dehydrogenase class-3	ADH5	ADHX_HUMAN	39.7	100.0%	3	3	5	0.01%	9.6%	AGDTVIPLYIPQCGECK	99.7%	52.8	25	52.8	2	0	0	1920.92	85	101
Alcohol dehydrogenase class-3	ADH5	ADHX_HUMAN	39.7	100.0%	3	3	5	0.01%	9.6%	IIGVDINKDK	99.7%	52.9	25	23.8	2	0	0	1114.65	219	228
Aldehyde dehydrogenase family 16 member A1	ALDH16A1	A16A1_HUMAN	85.1	100.0%	2	2	3	0.00%	2.9%	GLDGAVDMGAR	99.7%	46.9	25	30.3	1	0	0	1061.50	335	345
Aldehyde dehydrogenase family 16 member A1	ALDH16A1	A16A1_HUMAN	85.1	100.0%	2	2	3	0.00%	2.9%	LLWTLESLVTGR	99.7%	64	25	59.7	2	0	0	1387.79	118	129
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	10	11	19	0.02%	23.4%	IAKEEIFGPVQPLFK	95.3%	22.5	25	22.5	0	1	0	1715.97	412	426
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	10	11	19	0.02%	23.4%	IEEVVER	99.1%	34.8	25	20.2	1	0	0	873.47	430	436
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	10	11	19	0.02%	23.4%	KIEEVVER	99.7%	57.3	25	42.8	2	0	0	1001.56	429	436
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	10	11	19	0.02%	23.4%	LAPALATGNTVVMK	99.7%	93.3	25	87	4	0	0	1385.78	196	209
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	10	11	19	0.02%	23.4%	LLNLLADLVER	99.7%	75.7	25	68.2	2	0	0	1268.76	104	114
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	10	11	19	0.02%	23.4%	TFVEESIYNEFLER	99.7%	87	25	76.4	2	0	0	1775.85	325	338
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	10	11	19	0.02%	23.4%	VAEQTPLSALYLASLIK	99.7%	92.3	25	92.3	2	0	0	1817.04	210	226
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	10	11	19	0.02%	23.4%	VGNPFELDTQQGPQVDKEQFER	99.7%	49.9	25	49.9	0	2	0	2561.23	348	369
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	10	11	19	0.02%	23.4%	VLGYIQLGQK	99.7%	57.3	25	45.2	2	0	0	1118.66	370	379
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	10	11	19	0.02%	23.4%	YGLAAAVFTR	99.7%	80.1	25	78.9	1	0	0	1068.58	442	451
Aldehyde dehydrogenase, mitochondrial	ALDH2	ALDH2_HUMAN	56.4	100.0%	4	4	4	0.00%	10.6%	ELGEYGLQAYTEVK	99.7%	44.6	25	44.6	1	0	0	1599.79	493	506
Aldehyde dehydrogenase, mitochondrial	ALDH2	ALDH2_HUMAN	56.4	100.0%	4	4	4	0.00%	10.6%	LLCGGGIAADR	99.7%	45.6	25	27.2	1	0	0	1102.57	384	394
Aldehyde dehydrogenase, mitochondrial	ALDH2	ALDH2_HUMAN	56.4	100.0%	4	4	4	0.00%	10.6%	VAEQTPLTALYVANLIK	99.7%	65.8	25	65.8	1	0	0	1844.05	210	226
Aldehyde dehydrogenase, mitochondrial	ALDH2	ALDH2_HUMAN	56.4	100.0%	4	4	4	0.00%	10.6%	VIQVAAGSSNLKR	99.2%	35.3	25	35.3	1	0	0	1342.78	269	281
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	7	7	10	0.01%	15.7%	AASAATAAPTATPAAQESGTIPK	99.7%	70.5	25	70.5	1	0	0	2083.07	63	85
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	7	7	10	0.01%	15.7%	ESISDVGFGMLK	99.7%	46.3	25	46.3	1	0	0	1282.63	629	640
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	7	7	10	0.01%	15.7%	GISDPLTVFEQTEAAAR	99.7%	93.5	25	90.5	2	0	0	1804.91	587	603
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	7	7	10	0.01%	15.7%	GVQFAPFSTCR	98.8%	33.4	25	29	1	0	0	1269.60	556	566
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	7	7	10	0.01%	15.7%	IRPVPEYQK	98.4%	32.2	25	24.1	1	0	0	1129.64	381	389
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	7	7	10	0.01%	15.7%	NIYGNIEDLVVHIK	99.7%	58.8	25	58.8	2	0	0	1626.89	324	337
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	7	7	10	0.01%	15.7%	YGSVAFPNFEQGVACLR	99.7%	49.3	25	49.3	2	0	0	1914.92	390	406
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	3	3	5	0.01%	7.4%	IWADIPAPK	97.9%	31.2	25	24.6	1	0	0	1010.57	101	109
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	3	3	5	0.01%	7.4%	VGNPWDPNVLYGPLHTK	99.7%	38.2	25	38.2	0	2	0	1906.98	359	375
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	3	3	5	0.01%	7.4%	VNLLSFTGSTQVGK	99.7%	116	25	116	2	0	0	1450.79	267	280
Alpha-aminoadipic semialdehyde synthase, mitochondrial	AASS	AASS_HUMAN	102.1	100.0%	3	3	4	0.00%	3.9%	EIYGPILER	99.2%	35.5	25	20.9	1	0	0	1089.59	902	910
Alpha-aminoadipic semialdehyde synthase, mitochondrial	AASS	AASS_HUMAN	102.1	100.0%	3	3	4	0.00%	3.9%	NSSQAVQAVR	99.7%	68.1	25	57.1	2	0	0	1059.55	190	199
Alpha-aminoadipic semialdehyde synthase, mitochondrial	AASS	AASS_HUMAN	102.1	100.0%	3	3	4	0.00%	3.9%	SIGPLTFVFTGTGNVSK	99.2%	35.2	25	35.2	1	0	0	1724.92	213	229
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	13	26	0.03%	40.2%	ACYLSINPQKDETLETEK	99.7%	80.9	25	80.2	2	2	0	2139.03	221	238
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	13	26	0.03%	40.2%	AGFAGDQIPK	99.7%	63.9	25	48.6	2	0	0	1003.52	23	32
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	13	26	0.03%	40.2%	AQYYLPDGSTIEIGPSR	99.7%	111	25	111	2	0	0	1866.92	239	255
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	13	26	0.03%	40.2%	DQLQTFSEEHPVLLTEAPLNPR	99.7%	62.4	25	59.9	0	2	0	2534.29	97	118
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	13	26	0.03%	40.2%	EGYDFHSSSEFEIVK	99.7%	54.9	25	45.3	2	0	0	1773.80	201	215
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	13	26	0.03%	40.2%	IWQYVYSK	99.7%	50	25	38.5	2	0	0	1086.56	89	96
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	13	26	0.03%	40.2%	LYSTWIGGSILASLDTFKK	99.7%	53.1	25	53.1	1	0	0	2100.14	337	355

Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	13	26	0.03%	40.2%	TLFSNIVLSGGSTLFK	99.7%	125	25	122	4	1	0	1683.93	293	308
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	13	26	0.03%	40.2%	VMAGALEGDIFIGPK	99.7%	100	25	0	4	0	0	1517.80	47	61
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	13	26	0.03%	40.2%	YCFPNYVGRPK	99.7%	58.9	25	54.1	2	0	0	1400.68	33	43
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	9	11	27	0.03%	30.6%	AAVPSGASTGIYEALELR	99.7%	101	25	98.8	2	0	0	1804.94	33	50
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	9	11	27	0.03%	30.6%	DATNVGDEGGFAPNILENKEGLELLK	99.7%	60	25	60	0	2	0	2743.38	203	228
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	9	11	27	0.03%	30.6%	GNPTVEVDLFTSK	99.7%	75.1	25	19.9	2	0	0	1406.72	16	28
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	9	11	27	0.03%	30.6%	IGAEVYHNLK	99.7%	64.1	25	56.4	2	0	0	1143.62	184	193
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	9	11	27	0.03%	30.6%	LAMQEFMILPVGAANFR	99.7%	89.1	25	89.1	6	1	0	1939.98	163	179
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	9	11	27	0.03%	30.6%	SCNCLLLK	97.1%	29.8	25	16.9	2	0	0	1007.50	336	343
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	9	11	27	0.03%	30.6%	VNQIGSVTESLQACK	99.7%	124	25	0	5	0	0	1633.82	344	358
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	9	11	27	0.03%	30.6%	VVIGMDVAASEFFR	99.7%	98.1	25	93.6	2	0	0	1556.78	240	253
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	9	11	27	0.03%	30.6%	YISPDQLADLYK	99.7%	74.3	25	71.9	3	0	0	1425.73	270	281
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	17	18	31	0.03%	32.1%	ALEAELAALR	99.7%	75.9	25	65.3	2	0	0	1056.60	121	130
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	17	18	31	0.03%	32.1%	AQLEEASSAR	99.7%	59.6	25	57.2	2	0	0	1061.52	152	161
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	17	18	31	0.03%	32.1%	AQYESLAAK	99.6%	39	25	0	2	0	0	980.50	270	278
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	17	18	31	0.03%	32.1%	DGLAEEVQR	99.1%	34.8	25	21.9	1	0	0	1016.50	169	177
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	17	18	31	0.03%	32.1%	DVDGATLAR	99.7%	44.8	25	35.3	2	0	0	917.47	202	210
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	17	18	31	0.03%	32.1%	EYQDLLNVK	99.7%	52.6	25	46.8	7	0	0	1121.58	378	386
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	17	18	31	0.03%	32.1%	FANLNEQAAR	99.7%	78.8	25	36	2	0	0	1133.57	291	300
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	17	18	31	0.03%	32.1%	LLEGEETR	98.9%	33.7	25	17.7	2	0	0	946.48	399	406
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	17	18	31	0.03%	32.1%	LSGAGGAGGFR	99.7%	71.4	25	57.6	2	0	0	949.49	29	39
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	17	18	31	0.03%	32.1%	NLQSAEEWYK	99.7%	42.6	25	30	1	0	0	1267.60	279	288
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	17	18	31	0.03%	32.1%	QILELEER	99.7%	56.4	25	19.6	2	0	0	1029.56	339	346
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	17	18	31	0.03%	32.1%	SNIEETTISSQK	99.7%	60.6	25	54.6	2	0	0	1336.66	487	498
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	17	18	31	0.03%	32.1%	SNIEETTISSQKI	99.7%	66	25	66	2	0	0	1449.74	487	499
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	17	18	31	0.03%	32.1%	SQALLER	99.2%	35.3	25	21.1	1	0	0	816.46	162	168
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	17	18	31	0.03%	32.1%	TIEIEGLR	99.6%	37.9	25	25	2	0	0	930.53	323	330
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	17	18	31	0.03%	32.1%	TNEKEQLQGLNDR	99.7%	58.4	25	54.2	2	1	0	1544.77	92	104
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	17	18	31	0.03%	32.1%	VGELFQR	99.7%	67.4	25	42.7	2	0	0	848.46	139	145
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	17	18	31	0.03%	32.1%	VHQLETQNR	95.4%	28	25	24.8	1	0	0	1124.58	112	120
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	7	8	16	0.02%	25.6%	GAEADQIIEYLK	99.7%	77	25	71.3	6	0	0	1349.69	15	26
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	7	8	16	0.02%	25.6%	IGCIITAR	99.7%	70.9	25	55.3	2	0	0	903.51	159	166
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	7	8	16	0.02%	25.6%	ITFDAFPGEPDKELNPK	99.3%	29.9	25	29.9	1	2	0	1917.96	251	267
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	7	8	16	0.02%	25.6%	KQQSIAGSADSKPIDVSR	98.1%	26	25	19	0	1	0	1886.99	137	154
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	7	8	16	0.02%	25.6%	QQSIAGSADSKPIDVSR	99.7%	33.8	25	28.2	0	1	0	1758.90	138	154
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	7	8	16	0.02%	25.6%	QQVSLLK	97.6%	30.6	25	10.8	1	0	0	815.50	27	33
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	7	8	16	0.02%	25.6%	TVVSGLVNHVPLEQMQNR	99.7%	47.1	25	47.1	0	2	0	2037.05	188	205
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	6	7	20	0.02%	25.9%	FLFSLFGQK	99.7%	43.8	25	34.7	3	0	0	1086.60	216	224
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	6	7	20	0.02%	25.9%	FSIQTMCPIEGEGNIAR	99.7%	77.2	25	77.2	8	0	0	1922.91	199	215
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	6	7	20	0.02%	25.9%	LLCEHFR	99.7%	42.3	25	29.1	2	0	0	974.49	141	147
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	6	7	20	0.02%	25.9%	SCENLAPFNTALK	99.7%	71.1	25	71	2	0	0	1464.72	305	317
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	6	7	20	0.02%	25.9%	SYGPAPGAGHVQEESNLSLQALESR	99.7%	51.4	25	51.4	0	2	0	2597.26	34	58
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	6	7	20	0.02%	25.9%	VLSTVHTHSSVK	99.7%	51.2	25	45.2	3	0	0	1294.71	148	159
Anaphase-promoting complex subunit 1	ANAPC1	APC1_HUMAN	216.5	100.0%	4	4	5	0.01%	2.8%	DLETLPFGIALPIR	97.5%	30.3	25	28.4	1	0	0	1554.89	943	956
Anaphase-promoting complex subunit 1	ANAPC1	APC1_HUMAN	216.5	100.0%	4	4	5	0.01%	2.8%	FSEQGGTPQNVATSSSLTAHLR	99.7%	36.8	25	36.8	0	1	0	2288.13	285	306
Anaphase-promoting complex subunit 1	ANAPC1	APC1_HUMAN	216.5	100.0%	4	4	5	0.01%	2.8%	HLYVLAAEPR	99.7%	41.1	25	29.1	1	0	0	1168.65	1608	1617
Anaphase-promoting complex subunit 1	ANAPC1	APC1_HUMAN	216.5	100.0%	4	4	5	0.01%	2.8%	LVLEFFSSR	99.7%	56.9	25	48.1	2	0	0	1097.60	1816	1824
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	15	19	29	0.03%	26.7%	AGQERPSVTSYK	99.7%	45.2	25	39.3	2	0	0	1322.67	182	193
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	15	19	29	0.03%	26.7%	AIQLNSNSVQALLLK	99.7%	91.3	25	81	2	0	0	1611.94	365	379
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	15	19	29	0.03%	26.7%	AISTICSLEK	99.7%	55.9	25	47.6	2	0	0	1121.59	254	263
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	15	19	29	0.03%	26.7%	ALTQRPDYIK	97.6%	30.5	25	13.6	1	0	0	1204.67	468	477

Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	15	19	29	0.03%	26.7%	AYAFVHTGDNSR	99.7%	63.9	25	59.9	1	0	0	1337.62	242	253
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	15	19	29	0.03%	26.7%	DMAAAGLHSNVR	99.7%	67.9	25	65.8	4	0	0	1241.61	43	54
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	15	19	29	0.03%	26.7%	DNVDLLGSLADLYFR	99.7%	61.4	25	56.8	1	0	0	1710.87	269	283
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	15	19	29	0.03%	26.7%	EAMVMANNVYK	99.7%	41	25	41	1	0	0	1269.60	425	435
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	15	19	29	0.03%	26.7%	EQKYEDGIALLR	98.3%	26.3	25	9.41	1	2	0	1434.76	489	500
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	15	19	29	0.03%	26.7%	FEQAQMLDPYLIK	99.7%	73.1	25	64.8	2	0	0	1595.81	294	306
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	15	19	29	0.03%	26.7%	GMDVYGYLLAR	99.7%	59	25	55.2	3	0	0	1273.62	307	317
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	15	19	29	0.03%	26.7%	LEDVENLGCR	99.7%	74.2	25	68.2	2	0	0	1204.56	321	330
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	15	19	29	0.03%	26.7%	MAECYTMLK	99.4%	36.7	25	35.8	1	0	0	1146.50	142	150
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	15	19	29	0.03%	26.7%	YEDGIALLR	99.7%	64.2	25	58.6	2	0	0	1049.56	492	500
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	15	19	29	0.03%	26.7%	YTMALQQK	99.7%	41	25	29.4	2	0	0	982.50	100	107
Ancient ubiquitous protein 1	AUP1	AUP1_HUMAN	53.0	100.0%	3	3	5	0.01%	8.2%	KQALYEYAR	98.9%	33.8	25	25.5	2	0	0	1141.60	456	464
Ancient ubiquitous protein 1	AUP1	AUP1_HUMAN	53.0	100.0%	3	3	5	0.01%	8.2%	LPPTPLLLFPEEEATNGR	99.3%	36.1	25	36.1	1	0	0	1994.06	217	234
Ancient ubiquitous protein 1	AUP1	AUP1_HUMAN	53.0	100.0%	3	3	5	0.01%	8.2%	QLGEANEEFALR	99.7%	57.6	25	50.9	2	0	0	1376.68	298	309
Angio-associated migratory cell protein	AAMP	AAMP_HUMAN	46.7	99.8%	2	2	3	0.00%	5.5%	AVVGYEDGTIR	99.7%	53.7	25	46.6	1	0	0	1179.60	230	240
Angio-associated migratory cell protein	AAMP	AAMP_HUMAN	46.7	99.8%	2	2	3	0.00%	5.5%	DASLVVTTSGDHK	99.7%	52.5	25	37.9	2	0	0	1329.66	411	423
Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	ANFY1_HUMAN	128.4	100.0%	8	8	13	0.01%	8.4%	ESSSESFISR	99.7%	61.9	25	51.2	2	0	0	1128.52	44	53
Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	ANFY1_HUMAN	128.4	100.0%	8	8	13	0.01%	8.4%	FQLQLLR	99.7%	44.6	25	14	2	0	0	917.56	145	151
Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	ANFY1_HUMAN	128.4	100.0%	8	8	13	0.01%	8.4%	GDLFAATFLIK	99.7%	68.2	25	55.3	2	0	0	1195.67	300	310
Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	ANFY1_HUMAN	128.4	100.0%	8	8	13	0.01%	8.4%	GVMSLVNVR	99.5%	37.5	25	19.4	1	0	0	990.54	157	165
Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	ANFY1_HUMAN	128.4	100.0%	8	8	13	0.01%	8.4%	LGVNNNQGVNIFNYQVATK	99.7%	86.2	25	86.2	2	0	0	2093.08	1070	1088
Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	ANFY1_HUMAN	128.4	100.0%	8	8	13	0.01%	8.4%	RLESIATTLVSHK	99.6%	32.2	25	30.2	0	1	0	1454.83	267	279
Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	ANFY1_HUMAN	128.4	100.0%	8	8	13	0.01%	8.4%	TQDGETALQLAIR	99.7%	68.7	25	58.9	2	0	0	1415.75	652	664
Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	ANFY1_HUMAN	128.4	100.0%	8	8	13	0.01%	8.4%	VLLTECTVDAEAFNLR	99.7%	49.6	25	49.6	1	0	0	1850.93	990	1005
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	14	15	26	0.03%	16.2%	AAMIWIVGEYAER	99.7%	92	25	90.7	2	0	0	1508.76	446	458
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	14	15	26	0.03%	16.2%	CVSTLLDLIQTK	99.7%	86.2	25	69.4	2	0	0	1390.76	391	402
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	14	15	26	0.03%	16.2%	DCEDPNPLIR	99.7%	43.8	25	34.1	2	0	0	1228.56	94	103
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	14	15	26	0.03%	16.2%	DCPLNAEAASSK	99.7%	63.2	25	49.3	2	0	0	1262.57	865	876
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	14	15	26	0.03%	16.2%	DLDYYGTLLK	99.7%	60.8	25	48.2	1	0	0	1200.61	273	282
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	14	15	26	0.03%	16.2%	GLEISGTFTR	99.7%	62.5	25	57.3	2	0	0	1080.57	731	740
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	14	15	26	0.03%	16.2%	KGEIFELK	98.6%	32.7	25	8.73	2	0	0	963.55	12	19
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	14	15	26	0.03%	16.2%	LASQANIAQVLAELK	99.7%	75.6	25	69.5	2	0	0	1568.90	345	359
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	14	15	26	0.03%	16.2%	LLSTDPVAAK	99.7%	40.9	25	23.7	1	0	0	1014.58	529	538
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	14	15	26	0.03%	16.2%	LQSSNIFTVAK	99.7%	60.3	25	52.5	2	0	0	1207.67	877	887
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	14	15	26	0.03%	16.2%	LSHANSAVVLSAVK	99.7%	68.4	25	68.4	1	2	0	1395.80	248	261
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	14	15	26	0.03%	16.2%	NINLIVQK	99.5%	37.3	25	26.1	2	0	0	941.58	305	312
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	14	15	26	0.03%	16.2%	VNYVVQEAIVVIK	99.7%	43.7	25	38.6	1	0	0	1473.87	403	415
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	14	15	26	0.03%	16.2%	YNDPIYVK	99.7%	41.8	25	26.1	2	0	0	1011.51	328	335
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	11	12	19	0.02%	13.6%	AALCAVHVIR	99.7%	75.8	25	70.9	2	0	0	1109.62	157	166
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	11	12	19	0.02%	13.6%	ADCASGIFLAAEK	99.7%	67.5	25	61.3	2	0	0	1352.65	398	410
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	11	12	19	0.02%	13.6%	AVEYNALFK	97.7%	30.8	25	27.6	1	0	0	1054.56	563	571
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	11	12	19	0.02%	13.6%	ELLYFLDSCEPEFK	99.7%	72.8	25	72.1	2	0	0	1789.84	384	397
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	11	12	19	0.02%	13.6%	FTCTVNR	99.7%	39.7	25	31.2	2	0	0	897.42	537	543
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	11	12	19	0.02%	13.6%	IEFTFER	99.4%	36.8	25	32.1	1	0	0	941.47	717	723
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	11	12	19	0.02%	13.6%	IGYLGAMLLLDER	99.7%	61.8	25	58.3	1	0	0	1463.79	84	96
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	11	12	19	0.02%	13.6%	SSFREEDNTYR	99.6%	31.9	25	24.8	1	1	0	1403.62	36	46
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	11	12	19	0.02%	13.6%	VLAINILGR	99.7%	74.3	25	60	2	0	0	968.63	307	315
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	11	12	19	0.02%	13.6%	VLTTAGSYVR	99.7%	75.1	25	68.8	2	0	0	1066.59	425	434
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	11	12	19	0.02%	13.6%	YVALTSLLK	99.7%	41.2	25	41.2	2	0	0	1007.61	326	334
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	13	23	0.02%	35.0%	FEIPYFTTSGIQVR	99.7%	111	25	108	2	0	0	1657.86	380	393
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	13	23	0.02%	35.0%	HNNLYLVATSK	99.7%	65.3	25	56.4	2	0	0	1259.67	62	72

AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	13	23	0.02%	35.0%	ILQEYITQEGHK	99.7%	71.5	25	51.1	2	0	0	1458.76	130	141
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	13	23	0.02%	35.0%	LETGAPRPPATVTNAVSWR	99.7%	39	25	39	0	2	0	2023.07	142	160
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	13	23	0.02%	35.0%	LGLNDKVLFDNTGR	99.7%	41.2	25	35.1	1	1	0	1561.83	212	225
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	13	23	0.02%	35.0%	SGYQALPWVR	99.3%	35.9	25	29.7	2	0	0	1176.62	401	410
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	13	23	0.02%	35.0%	STANNVEIHIPVPNDADSPK	99.7%	40	25	40	0	2	0	2118.05	305	324
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	13	23	0.02%	35.0%	SVELEDVKFHQCVR	99.7%	36	25	31.6	0	2	0	1745.86	230	243
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	13	23	0.02%	35.0%	VFLSGMPELR	99.7%	53.7	25	38.7	4	0	0	1164.61	202	211
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	13	23	0.02%	35.0%	WVPENSEIVWSIK	98.7%	33	25	30.4	1	0	0	1586.82	334	346
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	13	23	0.02%	35.0%	YITQNGDYQLR	99.7%	41	25	38	2	0	0	1370.67	411	421
AP-1 complex subunit sigma-1A	AP1S1	AP1S1_HUMAN	18.7	100.0%	5	5	11	0.01%	31.6%	AIEQADLLQEEDESPR	99.7%	101	25	101	2	0	0	1842.87	134	149
AP-1 complex subunit sigma-1A	AP1S1	AP1S1_HUMAN	18.7	100.0%	5	5	11	0.01%	31.6%	ELMQVVLAR	99.7%	64.2	25	51.3	4	0	0	1058.60	34	42
AP-1 complex subunit sigma-1A	AP1S1	AP1S1_HUMAN	18.7	100.0%	5	5	11	0.01%	31.6%	FMLLFSR	97.7%	30.7	25	22.9	2	0	0	913.50	4	10
AP-1 complex subunit sigma-1A	AP1S1	AP1S1_HUMAN	18.7	100.0%	5	5	11	0.01%	31.6%	MCSFLEWR	98.6%	32.7	25	32.5	2	0	0	1128.50	46	53
AP-1 complex subunit sigma-1A	AP1S1	AP1S1_HUMAN	18.7	100.0%	5	5	11	0.01%	31.6%	WYLATSDKER	97.6%	30.5	25	19.9	1	0	0	1268.63	19	28
AP-1 complex subunit sigma-2	AP1S2	AP1S2_HUMAN	18.6	100.0%	3	3	11	0.01%	26.8%	AIEQADLLQEEAETPR	99.7%	65.3	25	57.9	4	0	0	1812.90	133	148
AP-1 complex subunit sigma-2	AP1S2	AP1S2_HUMAN	18.6	100.0%	3	3	11	0.01%	26.8%	ELVQTVLAR	99.7%	69.3	25	42	6	0	0	1028.61	33	41
AP-1 complex subunit sigma-2	AP1S2	AP1S2_HUMAN	18.6	100.0%	3	3	11	0.01%	26.8%	MCSFLEWR	98.6%	32.7	25	32.5	2	0	0	1128.50	45	52
AP-1 complex subunit sigma-2	AP1S2	AP1S2_HUMAN	18.6	100.0%	3	3	11	0.01%	26.8%	MQFMLLFSR	97.8%	30.9	25	22.2	1	0	0	1172.60	1	9
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	12	12	19	0.02%	14.0%	ACNQLGQFLQHR	99.7%	33.5	25	27.2	0	2	0	1471.72	330	341
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	12	12	19	0.02%	14.0%	ALLLSTYIK	99.7%	55.8	25	55.8	2	0	0	1021.63	539	547
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	12	12	19	0.02%	14.0%	DFLTPPLLSVR	98.1%	31.5	25	30.8	1	0	0	1257.72	833	843
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	12	12	19	0.02%	14.0%	EMGEAFAADIPR	99.7%	43.9	25	43	1	0	0	1322.60	142	153
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	12	12	19	0.02%	14.0%	FFQPTEMAAQDFFQR	99.7%	92.3	25	92.3	2	0	0	1862.85	864	878
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	12	12	19	0.02%	14.0%	FINLFPETK	99.7%	41.2	25	29.9	2	0	0	1108.60	548	556
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	12	12	19	0.02%	14.0%	GLAVFISDIR	99.7%	80.9	25	68	2	0	0	1090.63	12	21
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	12	12	19	0.02%	14.0%	IAGDYVSEEVWYR	99.7%	77.7	25	77.7	2	0	0	1586.75	452	464
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	12	12	19	0.02%	14.0%	QIVSEMLR	99.7%	43.9	25	0	1	0	0	991.52	404	411
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	12	12	19	0.02%	14.0%	TCVSLAVSR	99.7%	52.7	25	29.4	1	0	0	992.52	224	232
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	12	12	19	0.02%	14.0%	THIDTVINALK	99.7%	40.3	25	39.7	1	0	0	1224.69	368	378
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	12	12	19	0.02%	14.0%	VGGYILGEFGNLIAGDPR	99.7%	88.7	25	85.3	2	0	0	1847.97	499	516
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	9	13	0.01%	20.0%	ACNQLGQFLQHR	99.7%	33.5	25	27.2	0	2	0	1471.72	329	340
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	9	13	0.01%	20.0%	ALLLSTYIK	99.7%	55.8	25	55.8	2	0	0	1021.63	538	546
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	9	13	0.01%	20.0%	FFQPTEMASQDFFQR	99.7%	98.6	25	29	2	0	0	1878.85	826	840
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	9	13	0.01%	20.0%	FVNLFPEVKPTIQDVLR	95.3%	22.5	25	22.5	0	1	0	2015.13	547	563
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	9	13	0.01%	20.0%	GLAVFISDIR	99.7%	80.9	25	68	2	0	0	1090.63	12	21
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	9	13	0.01%	20.0%	IAGDYVSEEVWYR	99.7%	77.7	25	77.7	2	0	0	1586.75	451	463
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	9	13	0.01%	20.0%	LTECLETILNK	99.7%	79.1	25	64	1	0	0	1333.70	279	289
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	9	13	0.01%	20.0%	NNGVLFENQLLQIGLK	97.5%	30.4	25	30.4	1	0	0	1800.00	713	728
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	9	13	0.01%	20.0%	THIETVINALK	99.7%	52.2	25	49.1	1	0	0	1238.71	367	377
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	9	13	0.01%	20.0%	TTQIGCLLR	99.7%	44.8	25	35.4	2	0	0	1061.58	898	906
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	9	13	0.01%	20.0%	TVFEALQAPACHENLVK	99.7%	57	25	57	1	0	0	1926.97	481	497
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	9	13	0.01%	20.0%	VGGYILGEFGNLIAGDPR	99.7%	88.7	25	85.3	2	0	0	1847.97	498	515
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	9	13	0.01%	20.0%	VLVAGDTMDSVK	99.7%	59.5	25	39.9	2	0	0	1250.63	154	165
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	9	13	0.01%	20.0%	YGGTFQNVSVQLPITLNK	99.7%	99.5	25	99.5	2	0	0	1979.06	808	825
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	7	7	12	0.01%	18.6%	ASENAIVWK	99.7%	49.7	25	39.1	1	0	0	1017.54	346	354
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	7	7	12	0.01%	18.6%	IPTPLNTSGVQVICMK	99.7%	57	25	56	2	0	0	1757.93	324	339
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	7	7	12	0.01%	18.6%	LNYSDHDVIK	99.7%	58	25	51	2	0	0	1203.60	411	420
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	7	7	12	0.01%	18.6%	MCDVMAAYFGK	99.7%	63.4	25	63.4	2	0	0	1292.55	85	95
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	7	7	12	0.01%	18.6%	SISFIPPDGEFELMR	99.5%	37.5	25	31.1	1	0	0	1737.85	262	276
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	7	7	12	0.01%	18.6%	SNFKPSLLAQK	99.7%	47.7	25	38.3	2	0	0	1232.70	309	319
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	7	7	12	0.01%	18.6%	TFITQQGIK	99.2%	35.4	25	30	2	0	0	1035.58	131	139

AP-2 complex subunit sigma	AP2S1	AP2S1_HUMAN	17.0	100.0%	2	2	2	0.00%	10.6%	FILIQNR	99.7%	39.2	25	19.3	1	0	0	903.54	4	10
AP-2 complex subunit sigma	AP2S1	AP2S1_HUMAN	17.0	100.0%	2	2	2	0.00%	10.6%	HTNFVEFR	99.1%	34.9	25	27.7	1	0	0	1049.52	46	53
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	22	0.02%	12.6%	ASILWLIGENCER	99.7%	81.8	25	81.8	2	0	0	1560.78	497	509
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	22	0.02%	12.6%	EGSTAQLIINTEK	99.7%	54	25	44.8	1	0	0	1403.74	1064	1076
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	22	0.02%	12.6%	KIENIHIGEK	99.7%	48.8	25	45.9	2	0	0	1180.67	913	922
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	22	0.02%	12.6%	LLDSITVPVAR	99.7%	51.4	25	44.1	2	0	0	1183.70	486	496
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	22	0.02%	12.6%	LLTQYILNLGK	99.7%	87.5	25	74.7	4	0	0	1275.77	553	563
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	22	0.02%	12.6%	LQILNLGAK	99.7%	50	25	34.2	2	0	0	969.61	534	542
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	22	0.02%	12.6%	LYSLDPEQK	99.0%	34.3	25	20.2	2	0	0	1092.56	177	185
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	22	0.02%	12.6%	NASELFPAVVK	99.7%	55.7	25	40.3	2	0	0	1174.65	75	85
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	22	0.02%	12.6%	QFAAATIQTIGR	99.7%	88.7	25	79.3	1	0	0	1276.70	419	430
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	22	0.02%	12.6%	VPIIVPIMMLAIK	95.1%	27.8	25	27.8	1	0	0	1469.88	144	156
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	22	0.02%	12.6%	YAEEQQDLALLSISTFQR	99.7%	41.9	25	40.7	1	0	0	2112.06	105	122
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	22	0.02%	12.6%	YDQNYDIR	99.7%	59.3	25	47.5	2	0	0	1086.49	564	571
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	5	5	7	0.01%	4.6%	ALDLLYGMVSK	99.7%	71.2	25	66.7	1	0	0	1209.65	360	370
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	5	5	7	0.01%	4.6%	AVFHEEEQR	99.7%	43.9	25	38.2	1	0	0	1144.54	643	651
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	5	5	7	0.01%	4.6%	ILIEDSDQNLK	99.6%	38.2	25	38.2	1	0	0	1287.68	310	320
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	5	5	7	0.01%	4.6%	LFGALTPLEPR	99.7%	48.2	25	38.7	2	0	0	1213.69	244	254
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	5	5	7	0.01%	4.6%	NYLSLAPLFFK	99.7%	56.5	25	54.5	2	0	0	1312.73	217	227
AP-3 complex subunit mu-1	AP3M1	AP3M1_HUMAN	46.9	99.9%	2	2	3	0.00%	9.6%	GLVNLQSGAPKPEENPSLNIQFK	99.7%	51.5	25	50.5	0	2	0	2480.31	356	378
AP-3 complex subunit mu-1	AP3M1	AP3M1_HUMAN	46.9	99.9%	2	2	3	0.00%	9.6%	SVVSQSVCDYFFEAQEK	99.7%	66	25	66	1	0	0	2022.91	22	38
AP-3 complex subunit sigma-1	AP3S1	AP3S1_HUMAN	21.7	100.0%	4	5	10	0.01%	23.3%	FYQPYSEDTQQQIIR	99.7%	79.2	25	72.2	2	0	0	1915.92	19	33
AP-3 complex subunit sigma-1	AP3S1	AP3S1_HUMAN	21.7	100.0%	4	5	10	0.01%	23.3%	NINIGDISIK	99.7%	49.5	25	42.6	2	0	0	1086.62	176	185
AP-3 complex subunit sigma-1	AP3S1	AP3S1_HUMAN	21.7	100.0%	4	5	10	0.01%	23.3%	NMNLPEIPR	99.7%	40.3	25	30	4	0	0	1099.56	167	175
AP-3 complex subunit sigma-1	AP3S1	AP3S1_HUMAN	21.7	100.0%	4	5	10	0.01%	23.3%	SEAGLAGAPAR	99.7%	64.1	25	55.1	2	0	0	999.52	150	160
AP-3 complex subunit sigma-2	AP3S2	AP3S2_HUMAN	22.0	100.0%	3	3	5	0.01%	16.1%	FPEEIQQQIVR	99.4%	36.9	25	34.2	2	0	0	1386.74	23	33
AP-3 complex subunit sigma-2	AP3S2	AP3S2_HUMAN	22.0	100.0%	3	3	5	0.01%	16.1%	NINLPEIPR	96.3%	28.8	25	28.8	1	0	0	1065.61	167	175
AP-3 complex subunit sigma-2	AP3S2	AP3S2_HUMAN	22.0	100.0%	3	3	5	0.01%	16.1%	SEGGLSAAPAR	98.4%	32.1	25	26.2	2	0	0	1015.52	150	160
Apolipoprotein O-like	APOOL	APOOL_HUMAN	29.2	100.0%	3	3	5	0.01%	16.0%	HSVPLPTELSSEAK	99.7%	43.6	25	35.8	2	0	0	1494.78	219	232
Apolipoprotein O-like	APOOL	APOOL_HUMAN	29.2	100.0%	3	3	5	0.01%	16.0%	MGVITVSGLAGLVSAR	99.7%	80.9	25	73.4	2	0	0	1530.87	115	130
Apolipoprotein O-like	APOOL	APOOL_HUMAN	29.2	100.0%	3	3	5	0.01%	16.0%	VYATSQQIFGAVK	99.7%	50.1	25	39.4	1	0	0	1411.76	168	180
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	45	0.05%	37.4%	AALSASEGEEVPQDK	99.7%	83.2	25	74.6	2	0	0	1530.73	113	127
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	45	0.05%	37.4%	ALGTEVIQLFPEK	99.7%	91.4	25	84.4	4	0	0	1444.80	325	337
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	45	0.05%	37.4%	CLIATGGTPR	99.7%	61.1	25	43.5	2	0	0	1045.55	256	265
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	45	0.05%	37.4%	DGEQHEDLNEVAK	99.7%	64	25	63.5	2	0	0	1483.67	594	606
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	45	0.05%	37.4%	ELWFSDDPNVTK	99.7%	44.8	25	42.1	2	0	0	1450.69	178	189
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	45	0.05%	37.4%	ILPEYLSNWTMEK	99.7%	70.9	25	63.2	4	0	0	1623.81	343	355
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	45	0.05%	37.4%	ISGLGLTPEQK	99.7%	50.2	25	39.2	4	0	0	1142.64	99	109
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	45	0.05%	37.4%	KVVQLDVR	99.7%	40	25	23.6	2	0	0	956.59	232	239
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	45	0.05%	37.4%	LFNIHED	98.4%	32.2	25	32.2	2	0	0	887.43	607	613
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	45	0.05%	37.4%	LNDGSQITYEK	99.7%	78.4	25	70.1	2	0	0	1267.62	245	255
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	45	0.05%	37.4%	SATEQSGTGIR	99.7%	77.2	25	49.8	2	0	0	1106.54	519	529
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	45	0.05%	37.4%	SITIIGGGFLGSELACALGR	99.7%	81.3	25	81.3	1	0	0	1992.06	302	321
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	45	0.05%	37.4%	SNIWVAGDAACFYDIK	99.7%	110	25	110	4	0	0	1829.85	431	446
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	45	0.05%	37.4%	TGGLEIDSDFGGFR	99.7%	79.2	25	79.2	2	0	0	1470.69	409	422
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	45	0.05%	37.4%	VETDHIVAAVGLEPNVELAK	99.7%	46.5	25	46.5	0	2	0	2104.13	389	408
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	45	0.05%	37.4%	VLIVSEDPELPYMRPPLSK	99.7%	54	25	54	0	2	0	2183.18	159	177
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	45	0.05%	37.4%	VMPNAIVQSVGVSSGK	99.7%	99.1	25	97.6	4	0	0	1588.84	363	378
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	45	0.05%	37.4%	VVQLDVR	99.7%	51.2	25	39.8	2	0	0	828.49	233	239
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	3	3	4	0.00%	2.8%	GVPAGNSDTEGGQPGR	99.7%	42.3	25	41	1	0	0	1498.69	832	847
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	3	3	4	0.00%	2.8%	SGVSITIDDPVR	99.7%	48.6	25	26.9	2	0	0	1258.66	987	998

Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	3	3	4	0.00%	2.8%	SQEQEVLER	99.7%	42.6	25	17.8	1	0	0	1117.55	328	336
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	64	0.07%	40.0%	AAYPDLENPPLLVTPSQQAK	99.7%	76.7	25	76.7	2	0	0	2152.13	90	109
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	64	0.07%	40.0%	AYQCVVLLQGK	99.7%	85.9	25	57.9	2	0	0	1278.69	290	300
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	64	0.07%	40.0%	EIAENITK	99.0%	34.3	25	17.9	2	0	0	917.49	136	143
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	64	0.07%	40.0%	FPEILQK	99.7%	40.1	25	7.91	2	0	0	874.50	581	587
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	64	0.07%	40.0%	GESFYQDR	98.9%	33.7	25	32	1	0	0	1001.43	334	341
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	64	0.07%	40.0%	GFDILGIKPVQR	99.7%	53.8	25	47.6	2	2	0	1342.78	648	659
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	64	0.07%	40.0%	GFVQVDDGRK	99.6%	38.7	25	25	1	0	0	1120.57	353	362
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	64	0.07%	40.0%	GNTAAYLLYAFTR	99.7%	77	25	65.6	2	0	0	1460.75	528	540
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	64	0.07%	40.0%	IVFVPGCSIPLTIVK	99.7%	82.2	25	75.7	4	0	0	1642.96	363	377
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	64	0.07%	40.0%	LANIDEEMLQK	99.7%	68.6	25	54.5	4	0	0	1303.66	547	557
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	64	0.07%	40.0%	LFEFAGYDVLR	99.7%	69.1	25	61.3	3	0	0	1329.68	224	234
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	64	0.07%	40.0%	LLQQEEEIK	99.7%	54.8	25	32.9	2	0	0	1129.61	12	20
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	64	0.07%	40.0%	LMDLLGEGLKR	99.7%	53	25	45.7	2	1	0	1244.70	462	472
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	64	0.07%	40.0%	LNDYIFSFDK	99.7%	86.8	25	85.3	4	0	0	1261.61	513	522
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	64	0.07%	40.0%	MLLCEAVAAVMAK	99.7%	77.2	25	72.6	6	0	0	1406.72	635	647
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	64	0.07%	40.0%	MNDIVKEFEDR	96.7%	29.3	25	29.3	1	0	0	1395.66	342	352
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	64	0.07%	40.0%	NMINIISR	99.7%	49.3	25	25.6	3	0	0	960.53	72	79
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	64	0.07%	40.0%	SDGGYTYDTSDLAAIK	99.7%	113	25	106	3	0	0	1676.77	378	393
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	64	0.07%	40.0%	SLTAEIDR	99.7%	47.3	25	34.1	2	0	0	904.47	21	28
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	64	0.07%	40.0%	STIIGESISR	99.7%	65	25	52.5	5	0	0	1062.58	214	223
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	64	0.07%	40.0%	VEIAGPGFINVHLR	99.7%	74.9	25	74.9	1	2	0	1521.85	154	167
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	64	0.07%	40.0%	VLTAEELNAAQTSVAYGCIK	99.7%	93.2	25	93.2	1	0	0	2138.08	485	504
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	64	0.07%	40.0%	YADLSHNR	99.7%	56.9	25	50.2	4	0	0	975.46	505	512
Argininosuccinate synthase	ASS1	ASSY_HUMAN	46.5	100.0%	2	2	4	0.00%	5.1%	FELSCYSLAPQIK	99.7%	68.3	25	56.1	2	0	0	1555.78	128	140
Argininosuccinate synthase	ASS1	ASSY_HUMAN	46.5	100.0%	2	2	4	0.00%	5.1%	GQVYILGR	99.7%	39.5	25	26.4	2	0	0	905.52	356	363
Armadillo repeat-containing protein 6	ARMC6	ARMC6_HUMAN	54.1	99.9%	2	2	4	0.00%	5.4%	GAYPIIFTAWK	99.7%	71.2	25	64.5	2	0	0	1266.69	135	145
Armadillo repeat-containing protein 6	ARMC6	ARMC6_HUMAN	54.1	99.9%	2	2	4	0.00%	5.4%	IIVEGGGAVAALQAMK	99.7%	73.8	25	72.5	2	0	0	1527.86	407	422
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	21	39	0.04%	34.0%	AMTEDGFLAVCSEAK	99.7%	102	25	102	4	0	0	1644.72	148	162
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	21	39	0.04%	34.0%	APSPEKAEEESER	99.7%	47.1	25	47.1	2	1	0	1458.67	380	392
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	21	39	0.04%	34.0%	ASVGMYLISK	99.7%	47.9	25	36.6	2	0	0	1084.57	341	350
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	21	39	0.04%	34.0%	DVPLHALYDNVEK	99.7%	63.2	25	61.8	2	0	0	1512.77	209	221
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	21	39	0.04%	34.0%	EAFSDGITSVK	99.7%	71.7	25	64.3	4	0	0	1153.57	468	478
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	21	39	0.04%	34.0%	ELYLFDVLR	99.7%	46.1	25	39.3	2	0	0	1167.64	396	404
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	21	39	0.04%	34.0%	ETFEDSNLIPK	99.0%	34.1	25	25.4	2	0	0	1292.64	450	460
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	21	39	0.04%	34.0%	FSSYYLSLPPEMR	99.7%	52.8	25	52.8	2	0	0	1589.77	425	437
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	21	39	0.04%	34.0%	HSATPFLK	98.6%	32.9	25	22.2	1	0	0	900.49	169	176
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	21	39	0.04%	34.0%	IGCLLSGGLDSSLVAATLLK	99.7%	87.4	25	87.4	2	0	0	1988.11	253	272
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	21	39	0.04%	34.0%	ILFNNAVK	97.7%	30.7	25	5.03	2	0	0	918.54	237	244
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	21	39	0.04%	34.0%	LAVVDPLFGMQPIR	99.7%	62.9	25	58.7	4	0	0	1571.86	50	63
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	21	39	0.04%	34.0%	LFPGFEIETVK	99.7%	42.2	25	24.9	1	0	0	1279.69	222	232
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	21	39	0.04%	34.0%	TTAAHGLELR	99.7%	45	25	31.6	1	0	0	1068.58	408	417
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	21	39	0.04%	34.0%	VASVEMVK	97.3%	30.1	25	13.7	3	0	0	878.47	196	203
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	21	39	0.04%	34.0%	VPFLDHR	99.7%	39.8	25	33.6	2	0	0	883.48	418	424
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	21	39	0.04%	34.0%	WINATDPSAR	97.9%	31.1	25	25.9	2	0	0	1130.56	541	550
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	7	7	12	0.01%	17.7%	ASAELALGENSEVLK	99.7%	96.2	25	93.7	2	0	0	1530.80	108	122
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	7	7	12	0.01%	17.7%	DAGMQLQGYR	99.7%	53.4	25	45.5	1	0	0	1154.53	171	180
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	7	7	12	0.01%	17.7%	FVTVQTISGTGALR	99.7%	95.8	25	91.8	2	0	0	1449.81	126	139
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	7	7	12	0.01%	17.7%	IAAAILNTPDLR	99.7%	72.2	25	58.5	2	0	0	1267.74	326	337
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	7	7	12	0.01%	17.7%	IAAAILNTPDLRK	99.7%	49	25	49	2	0	0	1395.83	326	338
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	7	7	12	0.01%	17.7%	TCGFDFTGAVEDISK	99.7%	50.5	25	46.6	1	0	0	1646.74	186	200

Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	7	7	12	0.01%	17.7%	VGAFTMVCK	99.7%	46.2	25	42.2	2	0	0	1012.50	288	296
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	22	28	49	0.05%	49.9%	ADEVVWVR	99.7%	51.6	25	42.9	2	0	0	973.51	56	63
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	22	28	49	0.05%	49.9%	ALHHGIDLEK	99.0%	34	25	23.3	2	0	0	1132.61	442	451
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	22	28	49	0.05%	49.9%	EIMDAAEDYAK	99.7%	51.4	25	51.4	2	0	0	1271.55	16	26
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	22	28	49	0.05%	49.9%	ESIVDVEGVVR	99.7%	73.8	25	66.8	2	0	0	1201.64	111	121
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	22	28	49	0.05%	49.9%	FGAPPHAGGGIGLER	99.7%	43	25	33	1	2	0	1435.74	461	475
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	22	28	49	0.05%	49.9%	FLEPTLR	98.8%	33.5	25	19.9	2	0	0	875.50	339	345
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	22	28	49	0.05%	49.9%	GFVEIQTPK	99.7%	52.5	25	33	3	0	0	1018.56	214	222
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	22	28	49	0.05%	49.9%	IGSCTQQDVELHVQK	99.7%	61	25	61	1	1	0	1741.85	127	141
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	22	28	49	0.05%	49.9%	IHDPQLLTER	99.1%	28.7	25	13.2	0	2	0	1221.66	432	441
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	22	28	49	0.05%	49.9%	IYVISLAEPR	99.7%	55.3	25	47.8	2	0	0	1160.67	142	151
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	22	28	49	0.05%	49.9%	LEYCEALAMLR	99.7%	68.2	25	61.4	2	0	0	1368.67	346	356
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	22	28	49	0.05%	49.9%	LPLQLDDAVRPEAEGEEEGR	99.7%	45	25	45	0	2	0	2223.09	152	171
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	22	28	49	0.05%	49.9%	LQSGICHLFR	99.7%	50.6	25	41.2	2	0	0	1230.64	198	207
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	22	28	49	0.05%	49.9%	NNAYLAQSPQLYK	99.7%	92.6	25	85.3	2	0	0	1509.77	242	254
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	22	28	49	0.05%	49.9%	QCFLVLR	99.7%	40.9	25	10.1	2	0	0	935.51	75	81
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	22	28	49	0.05%	49.9%	QMCICADFEK	95.2%	27.9	25	25.5	1	0	0	1301.53	255	264
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	22	28	49	0.05%	49.9%	QQQFNVQALVAVGDHASK	99.7%	34.4	25	34.4	0	2	0	1940.00	82	99
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	22	28	49	0.05%	49.9%	QSNSYDMFMR	99.7%	49.5	25	49.5	2	0	0	1278.52	412	421
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	22	28	49	0.05%	49.9%	TSTSQAVFR	99.7%	73.2	25	58.4	2	0	0	996.51	189	197
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	22	28	49	0.05%	49.9%	VFSIGPVFR	99.7%	54.3	25	48.8	3	0	0	1021.58	265	273
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	22	28	49	0.05%	49.9%	VTMLFLGLHNVR	99.7%	73.6	25	68	3	2	0	1399.79	476	487
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	22	28	49	0.05%	49.9%	YGISSMIQSQEKPDR	99.7%	61.1	25	58.8	1	1	0	1754.84	29	43
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	11	12	20	0.02%	30.5%	CGLQFLGNIASR	99.7%	49.7	25	43.3	2	0	0	1335.68	134	145
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	11	12	20	0.02%	30.5%	ETTNIFSNCGCVR	99.7%	51.7	25	51.7	2	0	0	1557.68	346	358
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	11	12	20	0.02%	30.5%	ITSDEPLTKDDIPVFLR	99.7%	51.8	25	42.3	0	2	0	1959.04	254	270
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	11	12	20	0.02%	30.5%	LASEEPPDDEEALATIR	99.7%	86.8	25	82.5	1	0	0	1855.89	289	305
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	11	12	20	0.02%	30.5%	LIGNLCYK	99.7%	40.8	25	35	2	0	0	980.52	377	384
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	11	12	20	0.02%	30.5%	LSGVMVPAPIQDLEALR	99.2%	35.2	25	35.2	1	0	0	1824.99	11	27
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	11	12	20	0.02%	30.5%	NACIECSVNQNSIR	99.7%	78.9	25	74	2	0	0	1664.75	90	103
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	11	12	20	0.02%	30.5%	NLTEDNSQNQDLIAK	99.7%	99.5	25	96.8	1	0	0	1702.82	424	438
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	11	12	20	0.02%	30.5%	SPELVQAMFPK	99.7%	58.4	25	50.8	2	0	0	1262.65	227	237
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	11	12	20	0.02%	30.5%	VEQESLLTAFR	99.7%	66.3	25	58	1	0	0	1292.68	123	133
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	11	12	20	0.02%	30.5%	VTLLDLMIAK	99.7%	76.5	25	64.4	4	0	0	1116.67	244	253
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	6	7	11	0.01%	35.5%	HVVQSISTQQEKETIAK	99.7%	43.6	25	42.8	0	1	0	1926.03	222	238
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	6	7	11	0.01%	35.5%	HYLFDVQR	99.6%	38	25	30.9	2	0	0	1077.55	164	171
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	6	7	11	0.01%	35.5%	QASIQHIQNAIDTEK	99.7%	80.7	25	71.1	1	0	0	1695.87	140	154
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	6	7	11	0.01%	35.5%	TGVTGPYVLGTGLILYALSK	99.7%	89.4	25	89.4	2	1	0	2023.15	71	90
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	6	7	11	0.01%	35.5%	YGLIPEEFFQFLYPK	99.7%	59.6	25	59.6	3	0	0	1890.97	56	70
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	6	7	11	0.01%	35.5%	YGPFVADFADKLNEQK	99.7%	41.8	25	40.7	0	1	0	1841.91	116	131
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	AVDSLVPIGR	99.7%	82.2	25	81.1	11	0	0	1026.59	195	204
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	EAYPGDVFYLHSR	99.7%	95.7	25	93.7	10	3	0	1553.74	335	347
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	EIVTNFLAGFEA	99.7%	74.7	25	74.7	4	0	0	1310.66	542	553
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	ELIIGDR	98.6%	32.9	25	24.3	4	0	0	815.46	208	214
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	EPMQTGIK	99.7%	49	25	37.8	2	0	0	903.46	187	194
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	EVAAFAQFGSDLDAATQQLLSR	99.7%	124	25	124	5	4	0	2338.17	442	463
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	FENAFLSHVVSQHQALLGTIR	99.7%	65.5	25	65.5	0	2	0	2367.26	507	527
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	GIRPAINVGLSVSR	99.7%	67.9	25	67.9	3	5	0	1438.85	403	416
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	GMSLNLEPDNVGVVVFGNDK	99.7%	102	25	97.9	7	0	0	2104.04	104	123
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	GYLDKLEPSK	99.7%	52.5	25	41.5	10	0	0	1149.62	494	503
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	HALIIYDDLSK	99.7%	75.7	25	72.4	5	0	0	1287.69	306	316

ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	ILGADTSVDLEETGR	99.7%	129	25	129	8	0	0	1575.79	59	73
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	ISVREPMQTGIK	99.7%	58.2	25	44.8	2	0	0	1358.75	183	194
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	LELAQYR	99.2%	35.1	25	19.2	2	0	0	892.49	435	441
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	LKEIVTNFLAGFEA	99.7%	87.9	25	87.9	9	0	0	1551.84	540	553
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	LYCIYVAIGQK	99.7%	72.7	25	67.6	6	0	0	1327.71	242	252
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	NVQAEEMVEFSSGLK	99.7%	108	25	102	5	0	0	1667.79	89	103
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	QGQYSPMAIEEQVAVIYAGVR	99.7%	123	25	111	5	4	0	2309.16	473	493
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	QMSLLLR	99.7%	44.7	25	24.1	4	0	0	860.50	323	329
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	STVAQLVK	99.7%	64.9	25	38.3	6	0	0	845.51	254	261
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	TGAIVDVPVGEELLGR	99.7%	74.6	25	68.8	15	0	0	1624.89	134	149
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	TGTAEMSSILEER	99.7%	105	25	95	6	0	0	1423.67	46	58
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	TSIAIDTIINQK	99.7%	102	25	85.2	8	0	0	1316.74	219	230
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	TSIAIDTIINQKR	99.7%	45.3	25	42.8	4	0	0	1472.84	219	231
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	VLSIGDGIAR	99.7%	68.4	25	55.4	14	0	0	1000.58	74	83
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	VVDALGNAIDGK	99.7%	90	25	81.8	6	0	0	1171.63	150	161
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	27	38	193	0.20%	55.7%	VVDALGNAIDGKGPIGSK	99.7%	79.5	25	79.5	8	6	0	1710.94	150	167
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	24	45	206	0.21%	66.4%	AHGGYSVFAGVGER	99.7%	94.1	25	92.2	6	8	0	1406.68	226	239
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	24	45	206	0.21%	66.4%	AIAELGIYPAVDPLDSTSR	99.7%	90	25	85.7	8	0	0	1988.03	388	406
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	24	45	206	0.21%	66.4%	DQEGQDVLLFIDNIFR	99.7%	84.6	25	84.6	2	1	0	1921.97	295	310
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	24	45	206	0.21%	66.4%	EGNDLYHEMIESGVINLK	99.7%	89.5	25	83.8	2	2	0	2061.00	242	259
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	24	45	206	0.21%	66.4%	FLSQPFQVAEVFTGHMGK	99.7%	79.2	25	79.2	2	6	0	2023.01	463	480
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	24	45	206	0.21%	66.4%	FTQAGSEVSALLGR	99.7%	103	25	91.3	12	0	0	1435.75	311	324
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	24	45	206	0.21%	66.4%	GFQQILAGEYDHLPEQAFYMVGPIEEAVAK	99.7%	63.4	25	63.4	0	4	0	3366.64	490	519
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	24	45	206	0.21%	66.4%	GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	99.7%	91.7	25	91.7	0	2	0	3714.89	352	387
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	24	45	206	0.21%	66.4%	IGLFGGAGVGK	99.7%	50.6	25	44.6	8	0	0	975.56	202	212
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	24	45	206	0.21%	66.4%	IMDPNIVGSEHYDVAR	99.7%	86.7	25	86.7	6	8	0	1815.87	407	422
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	24	45	206	0.21%	66.4%	IMNVIGEPIDER	99.7%	70.4	25	58.8	10	0	0	1385.71	144	155
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	24	45	206	0.21%	66.4%	IMNVIGEPIDERGPIK	99.7%	62.8	25	62.8	4	2	0	1796.96	144	159
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	24	45	206	0.21%	66.4%	IPSAVGYQPTLATDMGTMQER	99.7%	107	25	107	6	6	0	2266.08	325	345
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	24	45	206	0.21%	66.4%	IPVGPETLGR	99.7%	54.4	25	48.8	2	0	0	1038.59	134	143
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	24	45	206	0.21%	66.4%	KGSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	99.7%	73	25	73	0	1	0	3842.98	351	387
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	24	45	206	0.21%	66.4%	LVLEVAQHLGESTVR	99.7%	106	25	106	6	6	0	1650.92	95	109
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	24	45	206	0.21%	66.4%	SLQDIIAILGMDELSEEDKLTVSR	99.7%	76.4	25	74.5	0	4	0	2691.38	433	456
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	24	45	206	0.21%	66.4%	TIAMDGTEGLVR	99.7%	75.6	25	63	16	0	0	1262.64	110	121
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	24	45	206	0.21%	66.4%	TVLIMELINNVAK	99.7%	97.9	25	97.9	18	0	0	1473.83	213	225
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	24	45	206	0.21%	66.4%	VALTGLTVAEYFR	99.7%	108	25	90.6	6	0	0	1439.79	282	294
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	24	45	206	0.21%	66.4%	VALVYGQMNEPPGAR	99.7%	97.2	25	80.3	17	0	0	1601.81	265	279
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	24	45	206	0.21%	66.4%	VLDSGAPIK	99.7%	57.7	25	47	5	0	0	899.52	125	133
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	24	45	206	0.21%	66.4%	VLDSGAPIKIPVGPETLGR	99.7%	74.9	25	74.9	5	8	0	1919.10	125	143
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	24	45	206	0.21%	66.4%	VVDLLAPYAK	99.7%	60	25	60	7	0	0	1088.64	189	198
ATP synthase subunit d, mitochondrial	ATP5H	ATP5H_HUMAN	18.5	100.0%	2	2	2	0.00%	11.8%	SCAEWVSLSK	99.7%	61.8	25	56.4	1	0	0	1166.55	100	109
ATP synthase subunit d, mitochondrial	ATP5H	ATP5H_HUMAN	18.5	100.0%	2	2	2	0.00%	11.8%	SWNETLTSR	99.4%	36.4	25	28.6	1	0	0	1093.53	33	41
ATP synthase subunit e, mitochondrial	ATP5I	ATP5I_HUMAN	7.9	99.9%	2	2	4	0.00%	24.6%	ELAEDDSILK	99.4%	36.2	25	31.7	2	0	0	1132.57	60	69
ATP synthase subunit e, mitochondrial	ATP5I	ATP5I_HUMAN	7.9	99.9%	2	2	4	0.00%	24.6%	YNYLKPR	99.7%	40.9	25	30.9	2	0	0	953.52	30	36
ATP synthase subunit f, mitochondrial	ATP5J2	ATPK_HUMAN	10.9	99.8%	2	3	11	0.01%	25.5%	DFSPSGIFGAFQR	99.7%	61.1	25	53.1	4	0	0	1428.69	34	46
ATP synthase subunit f, mitochondrial	ATP5J2	ATPK_HUMAN	10.9	99.8%	2	3	11	0.01%	25.5%	LGELPSWILMR	99.7%	61.3	25	42.6	7	0	0	1314.72	23	33
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	27	0.03%	47.6%	IVNSAQTGSFK	99.7%	75.3	25	56.6	5	0	0	1151.61	56	66
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	27	0.03%	47.6%	KIVNSAQTGSFK	99.7%	49.9	25	45.8	4	0	0	1279.70	55	66
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	27	0.03%	47.6%	LATFWYYAK	99.7%	48.6	25	43.8	4	0	0	1162.59	27	35
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	27	0.03%	47.6%	TPALVNAAVTYSKPR	99.7%	78.6	25	78.6	6	5	0	1587.89	12	26
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	27	0.03%	47.6%	VELVPPTPAEIPR	99.7%	47.3	25	37.7	3	0	0	1417.81	36	48

ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	14	38	0.04%	32.2%	ELIEIISGAAALD	99.7%	84.2	25	83.2	3	0	0	1314.72	286	298
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	14	38	0.04%	32.2%	EVMLVGIGDK	99.7%	42.8	25	35.3	4	0	0	1076.57	127	136
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	14	38	0.04%	32.2%	EVMLVGIGDKIR	99.7%	79.3	25	61	4	0	0	1329.76	127	138
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	14	38	0.04%	32.2%	GLCGAIHSSIAK	99.7%	67.8	25	63.3	4	0	0	1213.64	101	112
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	14	38	0.04%	32.2%	HLLIGVSSDR	99.7%	65.3	25	47.8	4	0	0	1096.61	91	100
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	14	38	0.04%	32.2%	IYGLGSLALYEK	99.7%	91.4	25	88.1	4	0	0	1326.73	68	79
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	14	38	0.04%	32.2%	NASEMIDKLTLTFNR	99.7%	79.1	25	79.1	4	3	0	1752.90	263	277
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	14	38	0.04%	32.2%	SEVATLTAAGK	99.7%	74.2	25	53.8	4	0	0	1047.57	116	126
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	14	38	0.04%	32.2%	THSDQFLVAFK	99.7%	72.4	25	64.2	4	0	0	1292.66	144	154
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	8	11	19	0.02%	50.7%	GEVPCTVTSASPLEEATLSELK	99.7%	63.9	25	63.9	1	0	0	2318.14	137	158
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	8	11	19	0.02%	50.7%	LSNTQGVVSAFSTMMSVHR	99.7%	45.6	25	45.6	1	1	0	2083.99	118	136
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	8	11	19	0.02%	50.7%	LVRPPVQVYGIEGR	99.7%	45.4	25	45.4	2	1	0	1582.91	27	40
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	8	11	19	0.02%	50.7%	SFLSQGQVLK	99.7%	60.4	25	51.2	2	0	0	1106.62	163	172
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	8	11	19	0.02%	50.7%	TDPSILGGMIVR	99.7%	60.4	25	54.3	4	0	0	1258.68	177	188
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	8	11	19	0.02%	50.7%	VAASVLNPYVK	99.7%	87.5	25	82.4	2	0	0	1160.67	74	84
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	8	11	19	0.02%	50.7%	VAQILKEPK	99.7%	47.9	25	37.8	2	0	0	1025.64	65	73
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	8	11	19	0.02%	50.7%	YATALYSAASK	99.7%	92.6	25	82.4	3	0	0	1145.58	41	51
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	AEGPGRGDEPSPS	99.7%	39.2	25	39.2	3	0	0	1255.56	622	634
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	AERENADIIR	99.0%	34.2	25	16.4	2	0	0	1186.62	247	256
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	ATLNAFLYR	99.7%	71.9	25	58	2	0	0	1068.58	479	487
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	DALNLAQMQEQTLQLEQQSK	99.7%	113	25	109	3	2	0	2316.15	73	92
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	DKWSNFDPTGLER	99.6%	32	25	32	0	2	0	1564.74	45	57
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	GEGAGPPPPLPPAQPGAEGGGDR	99.7%	94.5	25	94.5	1	0	0	2081.01	13	35
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	GLGDRPAPK	99.7%	47.9	25	41.1	3	0	0	910.51	36	44
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	GLLLFVDEADAFLR	99.7%	91.6	25	86.3	2	0	0	1578.85	453	466
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	INEMVHFDLPGQEER	99.7%	40.6	25	40.6	0	1	0	1813.85	515	529
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	INEMVHFDLPGQEERER	99.7%	37.6	25	37.6	0	2	0	2099.00	515	531
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	ITVLEALR	99.7%	57.7	25	36.2	4	0	0	914.57	339	346
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	LALHSGMDYAIMTGGDVAPMGR	98.5%	26.8	25	26.8	0	1	0	2311.05	413	434
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	LAQFDYGR	99.7%	49.8	25	25.5	4	0	0	969.48	554	561
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	LAQFDYGRK	99.7%	49.3	25	37.8	3	0	0	1097.57	554	562
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	LFDWANTSR	99.7%	59.6	25	49.6	4	0	0	1109.54	443	451
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	LGKPSLVR	99.7%	39.8	25	28.1	3	0	0	869.56	327	334
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	LLSRPQDALEGVVLSPSLEAR	99.7%	56.9	25	56.9	0	2	0	2250.25	355	375
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	LTEGMSGR	99.7%	49.6	25	44	2	0	0	850.41	569	576
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	MYFDKYVLKPATEGK	99.7%	33.5	25	33.5	0	2	0	1789.92	535	549
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	NATLVAGR	97.1%	29.8	25	16.4	1	0	0	801.46	314	321
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	NILMYGPPGTGK	99.7%	71.2	25	61.2	8	0	0	1263.64	395	406
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	QQQLLNEENLR	99.7%	87.4	25	78.4	4	0	0	1384.72	195	205
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	QRYEDQLK	99.2%	35.2	25	22.6	1	0	0	1079.55	187	194
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	QTVLESIR	99.7%	46.4	25	17.9	4	0	0	945.54	268	275
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	TAGTLFGEGFR	99.7%	74.8	25	69.9	4	0	0	1155.58	276	286
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	VRDIAIATR	99.7%	42.2	25	37	4	0	0	1014.61	376	384
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	27	31	76	0.08%	46.5%	YVLKPATEGK	99.6%	38.9	25	32.8	2	0	0	1105.63	540	549
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	8	16	0.02%	39.5%	AERENADIIR	99.0%	34.2	25	16.4	2	0	0	1186.62	199	208
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	8	16	0.02%	39.5%	DKWSNFDPTGLER	99.6%	32	25	32	0	2	0	1564.74	45	57
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	8	16	0.02%	39.5%	EALNLAQMQEQTLQLEQQSK	99.7%	109	25	109	2	0	0	2330.17	73	92
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	8	16	0.02%	39.5%	GEGAGPPPPLPPAQPGAEGGGDR	99.7%	94.5	25	94.5	1	0	0	2081.01	13	35
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	8	16	0.02%	39.5%	GLGDRPAPK	99.7%	47.9	25	41.1	3	0	0	910.51	36	44
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	8	16	0.02%	39.5%	GLLLFMDEADAFLR	99.7%	61.7	25	55.6	2	0	0	1610.82	405	418
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	8	16	0.02%	39.5%	HILLYGPPGTGK	99.7%	47.1	25	39.5	2	0	0	1252.71	347	358

ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	8	16	0.02%	39.5%	ICSWMGTGLCPGPLSPR	99.7%	67.1	25	61.9	1	0	0	1888.89	615	631
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	8	16	0.02%	39.5%	ITVLEALR	99.7%	57.7	25	36.2	4	0	0	914.57	291	298
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	8	16	0.02%	39.5%	LALHSGMDYAIMTGGDVAPMGR	98.5%	26.8	25	26.8	0	1	0	2311.05	365	386
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	8	16	0.02%	39.5%	LAQFDYGR	99.7%	49.8	25	25.5	4	0	0	969.48	506	513
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	8	16	0.02%	39.5%	LAQFDYGRK	99.7%	49.3	25	37.8	3	0	0	1097.57	506	514
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	8	16	0.02%	39.5%	LFDWANTSR	99.7%	59.6	25	49.6	4	0	0	1109.54	395	403
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	8	16	0.02%	39.5%	LGKPSLVR	99.7%	39.8	25	28.1	3	0	0	869.56	279	286
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	8	16	0.02%	39.5%	LHFDNCVLKPATEGK	98.9%	28	25	23.2	0	2	0	1728.87	487	501
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	8	16	0.02%	39.5%	LKEYEAAVEQLK	99.7%	75.6	25	72.3	4	3	0	1420.77	93	104
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	8	16	0.02%	39.5%	LTEGMSGR	99.7%	49.6	25	44	2	0	0	850.41	521	528
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	8	16	0.02%	39.5%	QQQLLNEENLR	99.7%	87.4	25	78.4	4	0	0	1384.72	147	157
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	8	16	0.02%	39.5%	QRYEDQLK	99.2%	35.2	25	22.6	1	0	0	1079.55	139	146
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	8	16	0.02%	39.5%	QTVLESIR	99.7%	46.4	25	17.9	4	0	0	945.54	220	227
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	8	16	0.02%	39.5%	TAGTLFGEGFR	99.7%	74.8	25	69.9	4	0	0	1155.58	228	238
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	8	16	0.02%	39.5%	VRDIAIATR	99.7%	42.2	25	37	4	0	0	1014.61	328	336
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	7	7	13	0.01%	9.9%	LSSDTALLGR	99.7%	53.7	25	43.3	2	0	0	1032.57	275	284
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	7	7	13	0.01%	9.9%	SFQGALEFK	99.7%	41.2	25	29.9	2	0	0	1026.53	487	495
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	7	7	13	0.01%	9.9%	STVLSLLLR	99.7%	57.8	25	24.3	2	0	0	1001.64	534	542
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	7	7	13	0.01%	9.9%	TSLFSSILR	99.7%	44.6	25	27.7	2	0	0	1023.58	249	257
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	7	7	13	0.01%	9.9%	TVLVIAHR	99.7%	56	25	51.5	2	0	0	908.57	684	691
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	7	7	13	0.01%	9.9%	VAEVANAVAFIR	99.7%	75.3	25	67.4	2	0	0	1259.71	606	617
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	7	7	13	0.01%	9.9%	VTQDSLAQATQLAEER	99.7%	94	25	80.7	1	0	0	1759.88	342	357
ATP-binding cassette sub-family B member 7, mitochondrial	ABCB7	ABCB7_HUMAN	82.6	100.0%	3	3	8	0.01%	4.4%	AGAAFFNEVR	99.7%	61	25	54.2	3	0	0	1081.54	201	210
ATP-binding cassette sub-family B member 7, mitochondrial	ABCB7	ABCB7_HUMAN	82.6	100.0%	3	3	8	0.01%	4.4%	AMNIVVPFMFK	99.7%	39.9	25	36	1	0	0	1296.68	152	162
ATP-binding cassette sub-family B member 7, mitochondrial	ABCB7	ABCB7_HUMAN	82.6	100.0%	3	3	8	0.01%	4.4%	VAISLGFLGGAK	99.7%	71.6	25	65.6	4	0	0	1132.67	140	151
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	6	7	11	0.01%	10.6%	AVVDKVFFSR	99.7%	45	25	42	1	0	0	1167.65	57	66
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	6	7	11	0.01%	10.6%	DQVIYPDGREDQK	99.7%	54.7	25	37	1	0	0	1562.74	521	533
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	6	7	11	0.01%	10.6%	FSMGFIDSIIAK	99.7%	60.4	25	56.1	3	0	0	1328.69	311	322
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	6	7	11	0.01%	10.6%	IANPDQLLTQDVEK	99.7%	98.7	25	98.7	2	0	0	1583.83	182	195
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	6	7	11	0.01%	10.6%	ITELMQVLK	99.7%	42.2	25	27.1	1	0	0	1090.62	391	399
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	6	7	11	0.01%	10.6%	VLGELWPLFGGR	99.7%	70	25	57.8	3	0	0	1343.75	485	496
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	6	13	0.01%	12.0%	ADIFMFDEPSSYLDVK	99.7%	64.9	25	64.9	2	0	0	1876.87	235	250
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	6	13	0.01%	12.0%	AIIKPQYVDQIPK	97.1%	24.3	25	23.6	0	1	0	1512.88	166	178
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	6	13	0.01%	12.0%	GSELQNYFTK	99.7%	44	25	36.7	2	0	0	1186.57	149	158
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	6	13	0.01%	12.0%	GTVGSILDR	99.7%	63.8	25	39.7	2	0	0	917.51	182	190
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	6	13	0.01%	12.0%	NVEDLSGGELQR	99.7%	72.2	25	62.6	2	0	0	1316.64	213	224
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	6	13	0.01%	12.0%	VAETANEEEVKK	99.7%	70.2	25	64.6	4	0	0	1346.68	333	344
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	5	5	11	0.01%	6.5%	AVSEEQQPALK	99.7%	52.7	25	43	3	0	0	1199.63	164	174
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	5	5	11	0.01%	6.5%	GAVIVVSHDAR	99.7%	60.9	25	48.9	3	0	0	1123.62	790	800
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	5	5	11	0.01%	6.5%	GFNLPYQDAR	99.7%	41	25	28.2	1	0	0	1180.57	714	723
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	5	5	11	0.01%	6.5%	IGFFNQQYAEQLR	99.7%	70.1	25	56.2	2	0	0	1613.81	690	702
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	5	5	11	0.01%	6.5%	STLLLLLTGK	99.7%	58.9	25	58.9	2	0	0	1058.68	665	674
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	15	24	0.02%	18.9%	FHWEQDQIAHMK	98.0%	25.6	25	25.6	0	1	0	1569.73	328	339
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	15	24	0.02%	18.9%	ILHGLGFTPAMQR	99.7%	53.2	25	46.5	3	0	0	1440.78	211	223
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	15	24	0.02%	18.9%	IPPPVIMVQNVSFK	99.7%	87.3	25	84.5	2	2	0	1568.89	391	404
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	15	24	0.02%	18.9%	LEELDADKAEMR	99.7%	64.1	25	56.2	2	0	0	1419.68	196	207
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	15	24	0.02%	18.9%	LIQQVAQEIWVCEK	99.7%	65.7	25	53.9	2	0	0	1743.91	575	588
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	15	24	0.02%	18.9%	LLTGELLPTDGMIR	99.7%	73.3	25	69.8	4	0	0	1528.84	442	455
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	15	24	0.02%	18.9%	LVDEEPQLTK	99.7%	43.5	25	25.7	2	0	0	1171.62	609	618
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	15	24	0.02%	18.9%	MMASGLTER	99.6%	38	25	30.9	2	0	0	995.46	366	374
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	15	24	0.02%	18.9%	SMLLSAIGK	98.3%	31.9	25	9.51	2	0	0	935.52	125	133

ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	15	24	0.02%	18.9%	YYTGNYDQYVK	99.7%	73	25	65.3	2	0	0	1413.63	305	315
ATP-binding cassette sub-family F member 3	ABCF3	ABCF3_HUMAN	79.7	99.8%	2	2	4	0.00%	3.2%	ASVILAGLGFTPK	99.6%	38.2	25	38	2	0	0	1273.75	307	319
ATP-binding cassette sub-family F member 3	ABCF3	ABCF3_HUMAN	79.7	99.8%	2	2	4	0.00%	3.2%	LLLGDLAPVR	99.7%	53.3	25	43.4	2	0	0	1066.66	537	546
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	AFDSGIIPMEFVNK	99.7%	97.1	25	89.6	10	0	0	1583.78	949	962
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	AIVWGMQTR	99.7%	53.6	25	37.5	8	0	0	1061.56	499	507
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	AKPAMPQDSVPSPR	99.4%	36.5	25	27	2	0	0	1480.76	470	483
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	AVQGMLDFDYVCSR	99.7%	108	25	108	6	0	0	1676.74	508	521
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	DEPSVAAMVYPFTGDHK	99.7%	69.1	25	69.1	6	0	0	1879.85	522	538
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	DGVYVLDLAAK	99.7%	80.4	25	71.9	5	0	0	1163.63	210	220
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	DLVSSLTSGLLTIGDR	99.7%	117	25	114	5	0	0	1646.90	919	934
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	DYQGPLKEHEVTIFVR	99.7%	41.9	25	41.9	0	4	0	1931.00	363	378
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	EAGVFVPR	99.6%	38	25	28.9	1	0	0	874.48	781	788
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	EAYPEEAYIADLDAK	99.7%	91.3	25	91.3	4	0	0	1697.79	245	259
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	EGDYVLFHHEGGVDVGDVDAK	99.7%	67.6	25	67.6	0	4	0	2258.04	128	148
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	EILIPVFK	95.0%	27.7	25	18.2	1	0	0	958.60	547	554
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	FGGALDAAAK	99.7%	76.3	25	56.1	2	0	0	920.48	935	944
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	FICTTSAIQNR	99.7%	75.1	25	69.5	5	0	0	1310.65	18	28
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	GQELIYAGMPITEVFK	99.7%	63.2	25	63.2	2	0	0	1795.93	849	864
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	GVTIIGPATVGGIKPGCFK	99.7%	77.8	25	77.8	4	2	0	1872.04	617	635
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	HPWDDISYVLPEHMSM	94.7%	22.1	25	22.1	0	1	0	1988.85	1086	1101
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	IGNTGGMLDNILASK	99.7%	99.4	25	87.2	8	0	0	1503.78	636	650
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	KPASFMTSICDER	99.7%	59.6	25	46.7	5	4	0	1541.71	836	848
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	LGLVGVNLTLDGVK	99.7%	83.8	25	81.4	6	0	0	1397.84	69	82
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	LGQEATVGK	99.7%	72.1	25	56.2	4	0	0	902.49	89	97
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	LIMGIGHR	99.7%	41.5	25	29	4	0	0	912.51	969	976
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	LLVGVDEK	99.7%	46.3	25	26	2	0	0	872.51	152	159
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	LNPEDIKK	98.0%	31.3	25	15.9	2	0	0	956.54	160	167
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	LYRPGSVAYVSR	99.7%	39.3	25	32.5	4	6	0	1367.74	651	662
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	MIVVLGEIGGTEEYK	99.7%	131	25	131	6	0	0	1637.85	712	726
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	RGGPNYQEGLR	99.7%	42.7	25	33.4	3	0	0	1246.63	379	389
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	SAYDSTMETMNYAQIR	99.7%	98.2	25	98.2	8	0	0	1880.82	577	592
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	SGGMSNELNNIISR	99.7%	83.2	25	75.6	8	0	0	1491.72	663	676
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	SINNPDMR	97.8%	30.9	25	11	1	0	0	946.44	979	986
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	SMGFIGHYLDQK	99.7%	47.1	25	44.3	6	0	0	1395.67	1066	1077
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	SMGFIGHYLDQKR	99.7%	46.8	25	44.1	0	1	0	1551.77	1066	1078
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	STTLFSR	99.2%	35.5	25	14.4	1	0	0	811.43	489	495
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	TASFSESR	96.3%	28.8	25	18.2	1	0	0	884.41	453	460
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	TIAIIAEGIPEALTR	99.7%	135	25	128	11	1	0	1567.91	593	607
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	TILSLMTR	99.7%	59.3	25	47.2	8	0	0	934.54	322	329
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	TTDGVYEGVAIGGDR	99.7%	110	25	98.9	4	0	0	1509.72	677	691
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	VDATADYICK	99.7%	68.1	25	66.6	4	0	0	1155.54	221	230
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	VTPDTDWAR	99.6%	38.7	25	34.8	3	0	0	1060.51	34	42
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	WGDIEFPPPFGR	99.7%	39.8	25	37.8	3	0	0	1417.69	233	244
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	41	56	188	0.20%	44.6%	YQDTPGVK	96.3%	28.9	25	22.2	2	0	0	907.45	704	711
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	11	11	20	0.02%	21.5%	AAAAADLANR	99.7%	69.2	25	63.9	2	0	0	943.50	453	462
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	11	11	20	0.02%	21.5%	DLIEFGMIPEFVGR	99.7%	42.9	25	42.6	2	0	0	1638.82	486	499
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	11	11	20	0.02%	21.5%	DVGGEGVQQGLLK	99.7%	87.3	25	76.6	2	0	0	1299.69	374	386
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	11	11	20	0.02%	21.5%	LLEGTIVNVPEK	99.7%	55.8	25	55.8	2	0	0	1311.75	387	398
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	11	11	20	0.02%	21.5%	LLQDANYNVEK	99.7%	67.3	25	55.1	2	0	0	1306.66	339	349
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	11	11	20	0.02%	21.5%	LPVVVPLHSLDEK	99.4%	36.5	25	36.5	1	0	0	1445.84	500	512
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	11	11	20	0.02%	21.5%	SGESNTHQDIEEKDR	99.7%	47	25	47	0	2	0	1744.77	463	477

ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	11	11	20	0.02%	21.5%	SIIKEPESAAEAVK	99.7%	67.9	25	51.1	1	0	0	1471.80	145	158
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	11	11	20	0.02%	21.5%	SNILLLGPTGSGK	99.7%	87.6	25	85.4	2	0	0	1256.72	287	299
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	11	11	20	0.02%	21.5%	TLLAQTLAK	99.7%	51.7	25	48.2	2	0	0	958.59	300	308
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	11	11	20	0.02%	21.5%	YLGFGTPSNLGK	99.7%	58	25	56.8	2	0	0	1253.65	438	449
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	AAECNIVVTQPR	99.7%	76.8	25	76.3	4	0	0	1357.69	435	446
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	AAMEALVVEVTK	99.7%	81.6	25	66	6	0	0	1276.68	1105	1116
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	AENNSEVGASGYGVPGPTWDR	99.7%	103	25	103	2	0	0	2162.97	121	141
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	AIEPPPLDAVIEAEHTLR	99.7%	65.7	25	65.7	2	0	0	1971.05	820	837
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	DFVNYLVR	99.7%	53.1	25	41.1	6	0	0	1025.54	64	71
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	DINTDFLLVVLR	99.7%	86.7	25	78.2	5	0	0	1417.81	517	528
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	DVVQAYPEVR	99.7%	67.4	25	57.2	5	0	0	1175.61	529	538
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	ELDALDANDELTPLGR	99.7%	100	25	90.8	6	0	0	1741.86	838	853
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	ETPFELIEALLK	99.7%	45.2	25	39.7	2	0	0	1402.78	631	642
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	FESEILEAISQNSVVIIR	98.8%	33.4	25	33.4	1	0	0	2047.11	393	410
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	GANLKDYYSR	99.7%	58.9	25	53	3	0	0	1186.59	142	151
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	GISHVIVDEIHER	99.7%	67.3	25	67.3	2	2	0	1503.79	504	516
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	GMTLVTPLQLLLFASK	99.7%	77.2	25	77.2	9	0	0	1748.00	1058	1073
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	ISAVSVAER	99.7%	66.4	25	52.8	6	0	0	931.52	448	456
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	KILTTEGR	94.7%	27.5	25	10.6	1	0	0	917.54	1011	1018
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	KMTPSYEIR	99.5%	37.5	25	22.7	1	0	0	1124.58	16	24
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	KVFDPVPVGVTK	99.7%	62.5	25	60	2	0	0	1285.75	697	708
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	LAAQSCALSLVR	99.7%	82	25	74.5	4	0	0	1288.70	237	248
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	LAQFEPSQR	99.7%	54.9	25	45.2	2	0	0	1075.55	315	323
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	LETHMTPEMFR	95.5%	28.1	25	8.65	1	0	0	1407.64	785	795
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	LFTAHNNMTNYATVWASK	99.7%	42.2	25	36.1	0	4	0	2084.99	738	755
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	LGGIGQFLAK	99.7%	73	25	59.8	9	0	0	1003.59	810	819
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	LNMATLR	99.7%	56.3	25	37	2	0	0	818.46	945	951
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	LNQYFQK	99.7%	51.5	25	37.9	4	0	0	940.49	185	191
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	LQISHEAAACITGLR	99.7%	80.3	25	80.3	1	2	0	1639.86	1090	1104
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	LSMSQLNEK	99.7%	62.3	25	49.9	4	0	0	1065.52	622	630
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	MGGEEAEIR	99.7%	79.4	25	63.7	6	0	0	991.45	930	938
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	NFLYAWCGK	99.7%	42	25	13.9	2	0	0	1158.54	6	14
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	QISRPSAAGINLMIGSTR	99.3%	29.7	25	27.2	0	1	0	1888.01	1137	1154
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	QLYHLGVVEAYSGLTK	99.7%	40.6	25	35.7	1	0	0	1777.95	249	264
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	QPAIISQLDPVNER	99.7%	88.3	25	88.3	3	0	0	1579.84	1117	1130
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	RISAVSVAER	99.7%	48.2	25	37.2	2	0	0	1087.62	447	456
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	RLNMATLR	99.1%	34.6	25	15.5	1	0	0	974.56	944	951
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	SFIAEMTIYIK	99.7%	77.5	25	69.4	2	0	0	1331.69	210	220
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	SSVNCPFSSQDMK	99.7%	51.8	25	51.8	4	0	0	1502.63	1025	1037
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	TPLHEIALSIK	99.7%	40.1	25	40.1	0	4	0	1221.72	796	806
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	TTQVPQFILDDFIQNDR	99.7%	71	25	58.3	6	0	0	2050.02	418	434
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	VFDPVPVGVTK	99.7%	53.1	25	53.1	4	0	0	1157.66	698	708
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	VRPGFCFHLCSR	99.7%	50.3	25	50.3	0	2	0	1535.74	768	779
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	YGDGPRPPK	99.6%	38	25	31.6	5	0	0	986.51	1155	1163
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	YPSPFFVFGEK	99.7%	55	25	52	7	0	0	1317.65	1038	1048
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	YQILPLHSQIPR	99.7%	54.9	25	52.8	2	3	0	1464.83	681	692
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	43	52	156	0.16%	38.4%	YTQVGPDHNR	99.7%	62.1	25	50.5	3	0	0	1186.56	200	209
ATP-dependent RNA helicase DDX1	DDX1	DDX1_HUMAN	82.4	100.0%	3	3	4	0.00%	3.8%	ELLIIGGVAAR	99.7%	63.3	25	53.9	2	0	0	1111.68	320	330
ATP-dependent RNA helicase DDX1	DDX1	DDX1_HUMAN	82.4	100.0%	3	3	4	0.00%	3.8%	FLICTDVAAR	99.7%	56.6	25	50.1	1	0	0	1165.60	568	577
ATP-dependent RNA helicase DDX1	DDX1	DDX1_HUMAN	82.4	100.0%	3	3	4	0.00%	3.8%	LNLSQVR	99.7%	40.6	25	10.4	1	0	0	829.49	359	365
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	6	7	12	0.01%	9.6%	ELAMQTFGVLK	99.7%	55.5	25	54.2	2	0	0	1236.67	262	272

ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	6	7	12	0.01%	9.6%	FLLLFTFLK	99.7%	46.6	25	23.3	2	0	0	1141.70	413	421
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	6	7	12	0.01%	9.6%	ISDIQSQLEK	99.7%	59.3	25	10.9	2	0	0	1160.62	558	567
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	6	7	12	0.01%	9.6%	QTMLFSATQTR	99.7%	69.6	25	43.6	3	0	0	1283.64	359	369
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	6	7	12	0.01%	9.6%	SIRPLLEGR	97.3%	30.1	25	23	1	0	0	1040.62	209	217
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	6	7	12	0.01%	9.6%	TLAFLIPAVELIVK	99.7%	60.4	25	60.4	2	0	0	1526.96	230	243
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	13	26	0.03%	31.8%	DPNSPLYSVK	99.7%	43.8	25	33.3	3	0	0	1119.57	82	91
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	13	26	0.03%	31.8%	GLAVNMVDSK	99.7%	54.7	25	45.8	3	0	0	1033.53	436	445
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	13	26	0.03%	31.8%	HSMNILNR	99.7%	40.6	25	31.8	2	0	0	984.50	446	453
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	13	26	0.03%	31.8%	ISEQIVIGTPGTVLDWCSK	99.7%	75.7	25	75.7	2	0	0	2103.08	208	226
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	13	26	0.03%	31.8%	LDTDDLDEIEK	99.7%	66.4	25	54.8	2	0	0	1305.61	465	475
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	13	26	0.03%	31.8%	SMTNLQIKEEK	99.7%	40.7	25	39.3	2	0	0	1320.68	19	29
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	13	26	0.03%	31.8%	SNLVDNTNQVEVLQR	99.7%	108	25	98.4	3	0	0	1728.89	67	81
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	13	26	0.03%	31.8%	TAAFVLAMLSR	99.7%	81.6	25	71.7	3	0	0	1179.66	144	154
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	13	26	0.03%	31.8%	VEPSDRYPQCLCLSPTYELALQTGK	99.7%	53.4	25	53.4	0	2	0	2925.41	155	179
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	13	26	0.03%	31.8%	VFVLDEADVMIATQGHQDQSIR	99.7%	37.3	25	36.8	0	1	0	2472.22	237	258
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	13	26	0.03%	31.8%	VLVTTNVCAR	99.7%	53.8	25	48.6	3	0	0	1132.61	385	394
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	22	0.02%	28.3%	CMALAQLLVEQNFPAIAIHR	99.7%	60.1	25	60.1	0	3	0	2311.21	299	318
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	22	0.02%	28.3%	DFLLKPELLR	98.0%	31.3	25	23.8	1	0	0	1243.74	48	57
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	22	0.02%	28.3%	DVQEIFR	99.5%	37.7	25	24.2	2	0	0	906.47	209	215
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	22	0.02%	28.3%	ELAFQISK	99.7%	40.6	25	32.1	2	0	0	935.52	123	130
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	22	0.02%	28.3%	GLAITFVSDENDAK	99.7%	66.6	25	58.8	2	0	0	1479.73	384	397
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	22	0.02%	28.3%	GSYVSIHSSGFR	99.7%	63	25	61.1	2	0	0	1296.63	36	47
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	22	0.02%	28.3%	ILNDVQDR	98.6%	32.7	25	20.7	1	0	0	972.51	398	405
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	22	0.02%	28.3%	ILVATNLFGR	99.7%	65.8	25	54.4	1	0	0	1103.66	339	348
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	22	0.02%	28.3%	NCPHVVVGTPGR	99.7%	61.7	25	51.5	2	2	0	1292.65	163	174
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	22	0.02%	28.3%	VSVFFGGLSIK	99.7%	57.1	25	53.3	3	0	0	1153.66	144	154
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	22	0.02%	28.3%	YQQFKDFQR	99.7%	40.3	25	40.3	1	0	0	1259.62	329	337
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	41	0.04%	32.2%	DKDAYSSFGSR	99.7%	61	25	61	2	0	0	1232.55	65	75
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	41	0.04%	32.2%	DLLDLLVEAK	99.7%	67.6	25	63.6	2	0	0	1128.65	555	564
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	41	0.04%	32.2%	DLMACAQTGSGK	99.7%	64.7	25	50.4	4	0	0	1254.55	219	230
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	41	0.04%	32.2%	DREEALHQFR	99.7%	45	25	37.7	1	1	0	1300.64	479	488
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	41	0.04%	32.2%	EIQMLAR	99.2%	35.2	25	18.4	1	0	0	876.46	388	394
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	41	0.04%	32.2%	ELAVQIYEEAR	99.7%	60.4	25	46.2	2	0	0	1320.68	277	287
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	41	0.04%	32.2%	ELAVQIYEEARK	99.7%	58.7	25	53.4	1	0	0	1448.77	277	288
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	41	0.04%	32.2%	IGLDFCK	99.7%	39.8	25	36.3	2	0	0	852.43	336	342
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	41	0.04%	32.2%	IVEQDTMPPK	99.7%	48.7	25	48.2	2	0	0	1173.58	364	373
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	41	0.04%	32.2%	LEQELFSGGNTGINFEK	99.7%	91.6	25	91.6	1	0	0	1882.92	146	162
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	41	0.04%	32.2%	MLDMGFEPQIR	99.7%	72.6	25	66.5	6	0	0	1336.64	352	362
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	41	0.04%	32.2%	QSSGASSSSFSSSR	99.7%	113	25	102	2	0	0	1361.59	604	617
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	41	0.04%	32.2%	QYPISLVLAPTR	99.7%	40.9	25	38.3	2	0	0	1357.78	265	276
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	41	0.04%	32.2%	SDYDGIGSR	99.7%	45.5	25	45.5	2	0	0	969.43	102	110
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	41	0.04%	32.2%	SFLLDLLNATGK	99.7%	106	25	91.1	4	0	0	1291.73	429	440
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	41	0.04%	32.2%	SPILVATAVAAR	99.7%	119	25	110	4	0	0	1168.70	492	503
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	41	0.04%	32.2%	VGSTSENITQK	99.7%	81	25	67.5	2	0	0	1163.59	408	418
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	41	0.04%	32.2%	VRPCVVYGGADIGQQIR	99.7%	76.2	25	67.6	0	2	0	1887.99	295	311
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	41	0.04%	32.2%	VVWVEESDKR	98.2%	26	25	23.2	0	2	0	1246.64	419	428
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	41	0.04%	32.2%	YLVLDEADR	99.7%	52	25	34.2	2	0	0	1093.55	343	351
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	4	4	8	0.01%	9.5%	EGAFSNFPISEETIK	99.7%	62.2	25	62.2	8	0	0	1668.81	136	150
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	4	4	8	0.01%	9.5%	GVTYLFPIQVK	99.7%	75.4	25	59.8	2	0	0	1264.73	156	166
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	4	4	8	0.01%	9.5%	NGIDILVGTPGR	99.7%	103	25	92.8	3	0	0	1211.67	258	269
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	4	4	8	0.01%	9.5%	SRYEQVDLVGK	99.2%	35	25	3.96	1	0	0	1293.68	343	353

ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	4	4	8	0.01%	9.5%	TFSFAIPLIER	99.7%	45.3	25	44.2	3	0	0	1293.72	188	198
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	4	4	8	0.01%	9.5%	VLVATNVAAR	99.7%	75.7	25	69.9	2	0	0	1013.61	441	450
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L1_HUMAN	86.5	100.0%	6	7	12	0.01%	9.2%	EIQIVLEGK	97.4%	30.3	25	19.3	2	0	0	1028.60	760	768
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L1_HUMAN	86.5	100.0%	6	7	12	0.01%	9.2%	LAETQNIAPSFVK	99.7%	73.5	25	68.5	2	0	0	1417.77	225	237
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L1_HUMAN	86.5	100.0%	6	7	12	0.01%	9.2%	LGVMTYSDTGK	99.7%	41.2	25	41.2	2	0	0	1171.57	698	708
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L1_HUMAN	86.5	100.0%	6	7	12	0.01%	9.2%	LSPETQSAIEQEIR	99.7%	68.8	25	59.1	2	0	0	1600.82	709	722
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L1_HUMAN	86.5	100.0%	6	7	12	0.01%	9.2%	TGFAEGFLK	99.7%	60.6	25	56.8	2	0	0	969.50	270	278
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L1_HUMAN	86.5	100.0%	6	7	12	0.01%	9.2%	TTTGLDSAVDPVQMK	99.7%	88.4	25	78.8	2	0	0	1562.77	320	334
Basic leucine zipper and W2 domain-containing protein 1	BZW1	BZW1_HUMAN	48.0	99.8%	2	2	3	0.00%	4.8%	AEVLSEEPILK	99.7%	69	25	57.5	2	0	0	1227.68	369	379
Basic leucine zipper and W2 domain-containing protein 1	BZW1	BZW1_HUMAN	48.0	99.8%	2	2	3	0.00%	4.8%	LMELFPANK	99.7%	41.6	25	29.5	1	0	0	1062.57	215	223
Basic leucine zipper and W2 domain-containing protein 2	BZW2	BZW2_HUMAN	48.2	99.8%	2	2	4	0.00%	4.5%	EGIAASFAVK	99.7%	40.2	25	29.2	2	0	0	992.54	180	189
Basic leucine zipper and W2 domain-containing protein 2	BZW2	BZW2_HUMAN	48.2	99.8%	2	2	4	0.00%	4.5%	LLELFPVNR	99.2%	35.4	25	21.4	2	0	0	1100.65	216	224
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	4	4	9	0.01%	4.8%	LLASTLVHSVK	99.7%	49.2	25	44.6	3	0	0	1167.71	570	580
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	4	4	9	0.01%	4.8%	NTEEEGLKYK	98.7%	33	25	27.1	2	0	0	1210.60	430	439
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	4	4	9	0.01%	4.8%	SSFYPDGGDQETAK	94.8%	27.5	25	14.6	1	0	0	1501.64	319	332
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	4	4	9	0.01%	4.8%	TIAPQNAPR	99.2%	35	25	26.2	3	0	0	967.53	304	312
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	11	21	0.02%	16.4%	AGATLDLLVENMGR	99.7%	81.1	25	73.4	4	0	0	1459.76	469	482
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	11	21	0.02%	16.4%	AYVAVDGIPQGVLER	99.7%	87.3	25	87.3	2	0	0	1586.85	443	457
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	11	21	0.02%	16.4%	MFEIDYSR	99.7%	44.8	25	44.8	3	0	0	1060.48	31	38
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	11	21	0.02%	16.4%	SLYPLTFIQVK	99.7%	53.8	25	53.8	2	0	0	1308.76	400	410
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	11	21	0.02%	16.4%	SSDPDYLAAVDK	99.7%	70.1	25	40.6	2	0	0	1280.60	149	160
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	11	21	0.02%	16.4%	TEAVASSLYDILAR	99.7%	79.5	25	67.7	2	0	0	1508.80	286	299
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	11	21	0.02%	16.4%	TVGAALDILCPSGPIK	99.7%	88.5	25	87.5	2	0	0	1611.88	384	399
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	11	21	0.02%	16.4%	VNYGAYINDFK	99.7%	68.5	25	60.7	2	0	0	1303.63	483	493
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	11	21	0.02%	16.4%	YISGSIHYSR	99.7%	70.3	25	67.6	2	0	0	1182.59	50	59
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	7	7	13	0.01%	17.9%	ASYISSAR	98.0%	31.2	25	24.5	1	0	0	854.44	544	551
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	7	7	13	0.01%	17.9%	AVAQAGTVGTLLIVK	99.7%	101	25	94.3	2	0	0	1440.88	95	109
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	7	7	13	0.01%	17.9%	EGPPPASPAQLLSK	99.7%	56.6	25	53.2	2	0	0	1391.75	421	434
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	7	7	13	0.01%	17.9%	LEQPDPGAVAAAAILR	99.7%	62.2	25	59	2	0	0	1591.88	552	567
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	7	7	13	0.01%	17.9%	SPGADLLQVLTK	99.7%	92.8	25	83.5	2	0	0	1241.71	511	522
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	7	7	13	0.01%	17.9%	VAGALAEAGVGLEEIAK	99.7%	118	25	109	2	0	0	1597.88	163	179
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	7	7	13	0.01%	17.9%	VAPAEPQEAPDSTAAGGSASK	99.7%	86.6	25	86	2	0	0	1940.92	352	372
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	AALLNQHYQVNFK	99.7%	69.3	25	62.8	2	0	0	1545.82	217	229
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	AIQGGTSHHLGQNFSK	95.1%	27.7	25	22	1	0	0	1681.84	1235	1250
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	AYVDDTPAEQMK	99.7%	54.9	25	52.7	3	0	0	1367.61	289	300
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	DQDLEPGAPSMGAK	99.7%	64.8	25	38.5	4	0	0	1431.64	1464	1477
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	DQVDIAVQELLQLK	99.7%	51.7	25	40.9	1	0	0	1611.90	926	939
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	EYIPGQPPLSQSSDSSPTR	99.7%	73.1	25	72.6	3	0	0	2045.98	871	889
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	FVELPGAEMGK	99.7%	44.3	25	36	2	0	0	1177.59	187	197
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	GNAAWQEQLK	99.7%	41.6	25	29.6	2	0	0	1144.57	130	139
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	GSQFGQSCCLR	99.7%	45.4	25	45.4	2	0	0	1299.56	329	339
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	INEAVECLLSLK	99.7%	93.9	25	84.1	6	0	0	1388.75	850	861
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	KPYIWEYSR	99.6%	38.8	25	27.4	1	0	0	1241.63	417	425
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	KVIDPVAPR	99.7%	40.5	25	40.5	2	0	0	994.60	498	506
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	LGVENCYFPMFVSQSALEK	99.7%	41.1	25	41.1	1	0	0	2219.05	1071	1089
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	LNLNNTVLSK	99.7%	58.6	25	39.9	4	0	0	1115.64	426	435
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	LNQWCNVVR	99.7%	42.1	25	30.7	2	0	0	1188.59	1144	1152
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	LQAILEDIQVTLFTR	99.6%	38.4	25	38.4	2	0	0	1760.00	1401	1415
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	LTVAENEAETK	99.7%	74	25	73.4	8	0	0	1204.61	1390	1400
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	NPEVGLKPVWYSPK	98.6%	32.8	25	32.8	1	0	0	1613.87	536	549
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	NQGGGLSSSGAGEGQGPK	99.7%	79.9	25	79.9	6	0	0	1587.74	992	1009

Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	NSEPAGLETPEAK	99.7%	64.8	25	53.7	4	0	0	1342.65	890	902
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	SCQFVAVR	99.7%	55	25	40.2	5	0	0	966.48	1376	1383
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	SLCIPFKPLCELQPGAK	99.5%	30.8	25	28.4	0	2	0	1958.02	1478	1494
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	SLYDEVAAQGEVVR	99.7%	97.6	25	95.5	3	0	0	1535.77	825	838
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	SLYDEVAAQGEVVRK	99.7%	58	25	58	1	0	0	1663.87	825	839
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	TELAEPIAIRPTSETVMYPAYAK	99.7%	43.4	25	43.4	0	1	0	2551.31	1110	1132
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	TGQEYKPGNPPAEIGQNISSNSSASILESK	99.7%	53.8	25	53.8	0	1	0	3103.52	795	824
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	VASQGEVVR	99.7%	58.6	25	49.1	4	0	0	944.52	908	916
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	VAVQGDVVR	99.7%	59.3	25	32.8	4	0	0	942.54	757	765
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	VIDPVAPR	99.7%	41.5	25	41.5	4	0	0	866.51	499	506
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	84	0.09%	25.6%	WFGFLEAQQAFQSVGTK	99.7%	61.7	25	61.7	2	0	0	1943.97	150	166
Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	MTHFD2	MTDC_HUMAN	37.9	100.0%	2	2	4	0.00%	6.6%	EGAAVIDVGINR	99.7%	99.6	25	83.4	2	0	0	1213.65	267	278
Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	MTHFD2	MTDC_HUMAN	37.9	100.0%	2	2	4	0.00%	6.6%	LVGDVDFEGVR	99.7%	55.4	25	40.6	2	0	0	1205.62	289	299
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	14	14	23	0.02%	16.5%	ANSSVVSVNCK	99.7%	64.1	25	59.9	2	0	0	1164.57	587	597
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	14	14	23	0.02%	16.5%	EIPVESIEEVSK	99.7%	74	25	61.9	2	0	0	1358.71	258	269
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	14	14	23	0.02%	16.5%	ESQATLEER	99.6%	38.4	25	25.7	2	0	0	1062.51	5	13
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	14	14	23	0.02%	16.5%	GAFCEVRPDDKR	94.9%	22.2	25	17.3	0	1	0	1449.69	875	886
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	14	14	23	0.02%	16.5%	GGLAGEFQR	99.4%	36.5	25	30	1	0	0	934.47	683	691
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	14	14	23	0.02%	16.5%	ILEFYSK	94.8%	27.5	25	17.6	1	0	0	899.49	887	893
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	14	14	23	0.02%	16.5%	LGCFEIAK	99.7%	43.4	25	38.8	2	0	0	937.48	894	901
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	14	14	23	0.02%	16.5%	LLPGIEVLWTGPK	99.7%	59.5	25	59.5	2	0	0	1422.84	241	253
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	14	14	23	0.02%	16.5%	LLPIDGANDLFFQPPPLTPTSK	99.7%	57.4	25	57.4	2	0	0	2381.28	692	713
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	14	14	23	0.02%	16.5%	SFVQWLGCR	99.7%	55.9	25	40	2	0	0	1152.56	656	664
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	14	14	23	0.02%	16.5%	SMMACLLSSLK	99.7%	52.3	25	41.5	2	0	0	1240.61	859	869
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	14	14	23	0.02%	16.5%	STELIPR	99.3%	36	25	23.2	1	0	0	815.46	300	306
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	14	14	23	0.02%	16.5%	VYTIRPYFPK	97.3%	30.1	25	25.6	1	0	0	1283.71	714	723
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	14	14	23	0.02%	16.5%	WELNTYLYAPK	99.7%	89.9	25	87	2	0	0	1397.71	88	98
Bifunctional purine biosynthesis protein PURH	ATIC	PUR9_HUMAN	64.6	100.0%	6	6	11	0.01%	12.5%	DVSELTGFPEMLGGR	99.7%	68.2	25	68.2	2	0	0	1607.77	50	64
Bifunctional purine biosynthesis protein PURH	ATIC	PUR9_HUMAN	64.6	100.0%	6	6	11	0.01%	12.5%	NLTALGLNLVASGGTAK	99.7%	91.5	25	91.5	2	0	0	1599.91	23	39
Bifunctional purine biosynthesis protein PURH	ATIC	PUR9_HUMAN	64.6	100.0%	6	6	11	0.01%	12.5%	SLFSNVVTK	99.7%	46.8	25	42.7	2	0	0	994.56	398	406
Bifunctional purine biosynthesis protein PURH	ATIC	PUR9_HUMAN	64.6	100.0%	6	6	11	0.01%	12.5%	TLTPISAAYAR	96.3%	28.8	25	27.2	2	0	0	1163.64	295	305
Bifunctional purine biosynthesis protein PURH	ATIC	PUR9_HUMAN	64.6	100.0%	6	6	11	0.01%	12.5%	VVACNLYPFVK	96.1%	28.7	25	24.4	1	0	0	1309.70	98	108
Bifunctional purine biosynthesis protein PURH	ATIC	PUR9_HUMAN	64.6	100.0%	6	6	11	0.01%	12.5%	YTQSNSVCYAK	99.7%	45	25	45	2	0	0	1320.59	427	437
Biliverdin reductase A	BLVRA	BIEA_HUMAN	33.4	99.8%	2	2	4	0.00%	8.1%	FGVVVVGVGR	99.7%	46.8	25	46.8	2	0	0	988.59	9	18
Biliverdin reductase A	BLVRA	BIEA_HUMAN	33.4	99.8%	2	2	4	0.00%	8.1%	SGSLENVPNVGVNK	99.7%	52	25	52	2	0	0	1413.73	235	248
BolA-like protein 2	BOLA2	BOLA2_HUMAN	10.1	100.0%	2	3	6	0.01%	29.1%	DLEAEHVEVEDTTLNR	99.7%	76.2	25	76.2	2	2	0	1869.88	15	30
BolA-like protein 2	BOLA2	BOLA2_HUMAN	10.1	100.0%	2	3	6	0.01%	29.1%	FEGKPLLQR	99.7%	49.6	25	48.4	2	0	0	1087.63	44	52
BRCA1-A complex subunit BRE	BRE	BRE_HUMAN	43.6	99.8%	2	2	2	0.00%	7.3%	ISPMLSPFISSVVR	99.2%	35.5	25	35.5	1	0	0	1532.85	10	23
BRCA1-A complex subunit BRE	BRE	BRE_HUMAN	43.6	99.8%	2	2	2	0.00%	7.3%	LPVDFSNIPTYLLK	99.7%	45.8	25	45.8	1	0	0	1619.90	177	190
Bromodomain adjacent to zinc finger domain protein 1A	BAZ1A	BAZ1A_HUMAN	178.7	100.0%	4	4	7	0.01%	3.2%	APLDASDSGR	99.2%	35.3	25	19.6	1	0	0	988.47	1098	1107
Bromodomain adjacent to zinc finger domain protein 1A	BAZ1A	BAZ1A_HUMAN	178.7	100.0%	4	4	7	0.01%	3.2%	DFIEDYVDILR	99.7%	47.1	25	44.9	4	0	0	1397.69	632	642
Bromodomain adjacent to zinc finger domain protein 1A	BAZ1A	BAZ1A_HUMAN	178.7	100.0%	4	4	7	0.01%	3.2%	IQSAIACTNIFPLGR	99.7%	46.7	25	44.6	1	0	0	1660.88	793	807
Bromodomain adjacent to zinc finger domain protein 1A	BAZ1A	BAZ1A_HUMAN	178.7	100.0%	4	4	7	0.01%	3.2%	SLDLDSCTLSEILR	99.7%	48.2	25	46.1	1	0	0	1621.81	541	554
Bystin	BYSL	BYST_HUMAN	49.6	99.8%	2	2	3	0.00%	3.9%	EALLELLR	99.7%	41.4	25	31.2	2	0	0	956.58	399	406
Bystin	BYSL	BYST_HUMAN	49.6	99.8%	2	2	3	0.00%	3.9%	FYNLVLLPR	99.7%	42	25	28.1	1	0	0	1134.67	249	257
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	AAEEIGIK	99.7%	59	25	34	2	0	0	830.46	59	66
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	AAQAPSSFQLLYDLK	99.7%	102	25	102	2	0	0	1651.87	805	819
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	APAEILNGK	99.7%	45.8	25	43	2	0	0	912.52	2	10
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	DDSNLYINVK	99.3%	35.9	25	32.3	2	0	0	1180.58	47	56
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	DVDGLTSINAGR	99.7%	69.3	25	61.1	1	0	0	1217.61	123	134
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	EIGLLSEEVELYGETK	99.7%	113	25	113	2	0	0	1808.92	337	352

C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	EISAQIR	99.7%	46.8	25	8.05	1	0	0	816.46	11	17
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	EQVPGFTPR	96.4%	29	25	23.4	1	0	0	1030.53	29	37
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	ETGVPIAGR	99.7%	40.1	25	31	2	0	0	899.49	158	166
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	FSDIQIR	99.7%	46.5	25	10.1	4	0	0	878.47	489	495
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	GALALAQAVQR	99.7%	82.3	25	76.7	3	0	0	1097.64	794	804
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	GDLNDCFIPCTPK	99.7%	41.6	25	41.6	2	0	0	1536.68	138	150
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	GVPTGFILPIR	99.7%	80.2	25	72.5	4	0	0	1169.70	879	889
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	IFHELTQTDK	99.7%	52	25	35.3	2	2	0	1231.63	464	473
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	ITIGQAPTEK	99.5%	37.4	25	37.4	2	0	0	1057.59	544	553
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	IYGADDIELLPEAQHK	99.7%	81	25	75.1	2	2	0	1811.92	833	848
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	KITIGQAPTEK	99.7%	53.6	25	31.2	3	0	0	1185.68	543	553
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	KVVGDVAYDEAK	99.7%	67.5	25	60.2	2	0	0	1293.67	251	262
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	LAILQVGNR	99.7%	83.2	25	74.6	2	0	0	983.60	38	46
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	LDIDPETITWQR	99.7%	81.8	25	81.4	2	0	0	1486.75	521	532
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	LPVEDKIR	99.7%	39.9	25	31	1	0	0	969.57	820	827
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	LVGPEGFVVTEAGFGADIGMEK	99.7%	91.8	25	91.8	2	1	0	2239.10	658	679
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	MFGIPVVVAVNAFK	99.7%	76.6	25	73.4	7	0	0	1507.83	747	760
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	MHGGGPTVTAGLPLPK	99.7%	34.9	25	34.9	0	4	0	1548.82	706	721
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	QGFGNLPICMAK	99.7%	48.6	25	46.8	2	0	0	1335.66	855	866
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	QPSQGPTFGIK	97.4%	30.2	25	25.3	2	0	0	1159.61	411	421
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	RFSDIQIR	97.1%	29.9	25	9.49	2	0	0	1034.57	488	495
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	TDPTTLTDEEINR	99.7%	80.4	25	62.5	5	0	0	1504.71	505	517
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	TDTESELDLISR	99.7%	83.3	25	78	2	0	0	1378.67	761	772
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	THLSLSHNPEQK	99.7%	64.5	25	64.5	1	0	0	1390.71	867	878
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	TPVPSDIDISR	99.7%	42.5	25	42.5	2	0	0	1199.63	314	324
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	VLLSALER	99.7%	51.8	25	37.4	5	0	0	900.55	355	362
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	VVGDVAYDEAK	99.7%	68.1	25	66	2	0	0	1165.57	252	262
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	VVGDVAYDEAKER	99.7%	84.8	25	70.4	2	0	0	1450.72	252	264
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	WMIQYNNLNLK	99.7%	54	25	34.3	4	0	0	1436.74	303	313
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	YSGLCPHVVVLVATVR	99.7%	58.8	25	55	0	2	0	1769.97	687	702
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	43	95	0.10%	41.9%	YVVVTGITPTPLGEGK	99.7%	105	25	102	2	0	0	1630.91	371	386
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	AAFALGGLGSGFASNR	99.7%	98.3	25	98.3	2	0	0	1495.77	556	571
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	ATGYPLAYVAAK	99.7%	58.4	25	52.9	2	0	0	1224.66	697	708
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	EATAGNPGGQTVR	99.7%	67.4	25	63.2	2	0	0	1257.62	359	371
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	ELSDLESAR	99.7%	50.9	25	44.4	2	0	0	1019.50	1067	1075
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	FLSSAAAVSK	99.7%	55.5	25	39.7	2	0	0	980.54	1110	1119
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	GHNQPCLLVGSGR	99.2%	35.2	25	35.2	1	0	0	1394.70	275	287
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	IIAHAQLLEQHR	99.7%	41.5	25	40.6	0	2	0	1428.81	843	854
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	ILALDCGLK	99.7%	47.4	25	26.9	2	0	0	1002.57	178	186
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	KEEILLIK	94.8%	27.5	25	12.9	1	0	0	985.63	1618	1625
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	LALGIPLPELR	99.7%	55.4	25	53.3	2	0	0	1191.75	709	719
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	LFVEALGQIGPAPPLK	99.7%	77.5	25	77.5	2	0	0	1649.96	1435	1450
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	LGGAVLSFSEATSSVQK	99.7%	105	25	103	2	0	0	1680.88	1987	2003
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	LGYPVLVR	99.7%	43.1	25	35.2	2	0	0	916.56	548	555
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	LLDTIGISQPQWR	99.7%	55.5	25	55.5	2	0	0	1526.83	1054	1066
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	LYLNETFSELR	99.7%	42.8	25	39.5	1	0	0	1384.71	1557	1567
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	MALLATVLGR	99.7%	88.9	25	71.2	3	0	0	1044.62	2215	2224
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	MALLATVLGRF	99.7%	70.8	25	66	2	0	0	1207.69	2215	2225
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	NILLTIGSYK	99.7%	48.4	25	42.6	2	0	0	1121.66	1314	1323
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	NKSELLPTVR	99.6%	38.3	25	33	2	0	0	1156.67	1324	1333
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	NSVTGGTAAFEPSVDYCVVK	99.7%	102	25	102	2	0	0	2100.99	720	739

CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	SELLPTVR	96.8%	29.5	25	29.5	1	0	0	914.53	1326	1333
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	SFEEAFQK	99.7%	41.8	25	31	2	0	0	985.46	771	778
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	SILEQLAEK	99.7%	55.1	25	39.5	2	0	0	1030.58	1379	1387
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	SVGEVMGIGR	99.7%	55.5	25	47.1	4	0	0	1020.51	761	770
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	TLGVDLVALATR	99.7%	81	25	72.6	4	0	0	1228.73	1229	1240
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	TPHVLVLGSGVYR	99.7%	42.3	25	42.3	2	2	0	1397.79	932	944
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	TSSSFAAAMAR	99.7%	80.1	25	71.4	4	0	0	1115.51	1976	1986
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	VFNTGGAPR	99.7%	55.5	25	40.8	2	0	0	918.48	169	177
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	VIMGEEVEPVGLMTGSGVVGVK	99.7%	66.2	25	42	3	0	0	2203.14	1241	1262
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	VLGTSPEAIDSAENR	99.7%	97.1	25	97.1	2	0	0	1558.77	1034	1048
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	31	36	68	0.07%	15.6%	VPQFSFSR	99.7%	43.4	25	39.5	2	0	0	967.50	1263	1270
Calcium/calmodulin-dependent protein kinase type II subunit gamma	CAMK2G	KCC2G_HUMAN	62.6	99.9%	2	2	3	0.00%	4.7%	FTDDYQLFEELGK	99.7%	48.6	25	48.6	1	0	0	1604.75	10	22
Calcium/calmodulin-dependent protein kinase type II subunit gamma	CAMK2G	KCC2G_HUMAN	62.6	99.9%	2	2	3	0.00%	4.7%	NLINQMLTINPAK	99.7%	50.5	25	44.1	2	0	0	1469.81	247	259
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	11	0.01%	20.5%	AGQTTYSGVIDCFRK	99.7%	75.6	25	75.6	2	0	0	1702.82	552	566
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	11	0.01%	20.5%	DIPFSAIYFPVYAHCK	99.6%	38	25	23.9	2	0	0	1927.94	491	506
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	11	0.01%	20.5%	GLIPQLIGVAPEK	99.7%	56.6	25	0	3	0	0	1334.80	391	403
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	11	0.01%	20.5%	IVQLLAGVADQTK	99.7%	86.1	25	78.8	2	0	0	1355.79	56	68
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	11	0.01%	20.5%	KIYSTLAGTR	99.7%	58	25	45.7	2	0	0	1109.63	234	243
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	11	0.01%	20.5%	LATATFAGIENK	99.7%	70.4	25	52.5	2	0	0	1235.66	641	652
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	11	0.01%	20.5%	LQVAGEITTGPR	99.7%	68.4	25	42.7	2	0	0	1241.69	454	465
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	11	0.01%	20.5%	LTLADIER	96.9%	29.5	25	22.3	1	0	0	930.53	284	291
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	11	0.01%	20.5%	LTVNDFVR	99.7%	57.5	25	51.8	2	0	0	963.53	407	414
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	11	0.01%	20.5%	NIFLQYASTEVDGER	99.7%	88.3	25	88.3	2	0	0	1741.84	18	32
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	11	0.01%	20.5%	VSALNVLR	99.7%	50.2	25	23.4	2	0	0	871.54	466	473
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	11	0.01%	20.5%	YEGFFGLYR	99.7%	45.5	25	45.5	2	0	0	1151.55	382	390
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	45	0.05%	40.1%	AGQTTYSGVIDCFRK	99.7%	75.6	25	75.6	2	0	0	1702.82	554	568
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	45	0.05%	40.1%	ASGDSARPVLLQVAESAYR	99.7%	50.7	25	50.7	0	2	0	1990.04	313	331
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	45	0.05%	40.1%	DIPFSAIYFPCYAHVK	99.7%	46.2	25	16.3	2	0	0	1927.94	493	508
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	45	0.05%	40.1%	DLGFFGIYK	99.7%	48.2	25	47.5	2	0	0	1059.55	476	484
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	45	0.05%	40.1%	FGLGSVAGAVGATAVYPIDLVK	99.7%	91.2	25	91.2	2	1	0	2105.16	332	353
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	45	0.05%	40.1%	GLLPQLLGVAPEK	99.7%	56.6	25	0	3	0	0	1334.80	393	405
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	45	0.05%	40.1%	IAPLEEGTLPFNLAEAQR	99.7%	99	25	99	2	1	0	1969.04	293	310
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	45	0.05%	40.1%	ILREEGPK	99.7%	39.7	25	28.9	2	0	0	941.54	569	576
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	45	0.05%	40.1%	INLPAPNPDHVGGYK	99.7%	55	25	48.4	2	0	0	1591.82	627	641
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	45	0.05%	40.1%	KIYSTLAGTR	99.7%	58	25	45.7	2	0	0	1109.63	235	244
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	45	0.05%	40.1%	LAVATFAGIENK	99.7%	89.5	25	85.8	2	0	0	1233.68	642	653
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	45	0.05%	40.1%	LQVAGEITTGPR	99.7%	68.4	25	42.7	2	0	0	1241.69	456	467
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	45	0.05%	40.1%	LTVNDFVR	99.7%	57.5	25	51.8	2	0	0	963.53	409	416
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	45	0.05%	40.1%	MTLADIER	99.7%	50.6	25	38.6	2	0	0	948.48	285	292
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	45	0.05%	40.1%	NGEFFMSPNDFVTR	99.7%	72.4	25	71.2	2	0	0	1660.74	30	43
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	45	0.05%	40.1%	SSPQFGVTLLTYELLQR	99.7%	114	25	107	2	0	0	1952.05	589	605
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	45	0.05%	40.1%	STGSFVGELMYK	99.7%	61.9	25	54.8	2	0	0	1318.63	361	372
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	45	0.05%	40.1%	TVELLSGVVDQTK	99.7%	110	25	99.8	2	0	0	1388.76	57	69
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	45	0.05%	40.1%	VSALSVVR	99.7%	49.6	25	43.8	2	0	0	830.51	468	475
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	45	0.05%	40.1%	YEGFFGLYR	99.7%	45.5	25	45.5	2	0	0	1151.55	384	392
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	23	45	0.05%	40.1%	YLNIFGESQPNPK	99.7%	72.7	25	72.7	2	0	0	1506.76	44	56
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	7	8	15	0.02%	16.6%	EGIPGLYR	99.2%	35.2	25	24.1	2	0	0	904.49	438	445
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	7	8	15	0.02%	16.6%	HEGLGAFYK	99.7%	42.7	25	42.7	2	0	0	1021.51	337	345
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	7	8	15	0.02%	16.6%	MNIFGGFR	99.7%	50.7	25	41.9	2	0	0	941.47	232	239
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	7	8	15	0.02%	16.6%	NLGIPLGQDAEEK	99.7%	59.9	25	57.3	1	0	0	1383.71	50	62
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	7	8	15	0.02%	16.6%	QLLAGGIAGAVSR	99.7%	121	25	105	2	0	0	1212.71	197	209

Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	7	8	15	0.02%	16.6%	TGQYSGIYDCAK	99.7%	68.3	25	68.3	2	0	0	1362.60	321	332
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	7	8	15	0.02%	16.6%	VLPAVGISYVVYENMK	99.7%	111	25	111	4	0	0	1781.95	454	469
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	7	7	11	0.01%	7.9%	AAASLAWVLR	99.7%	72.5	25	58.4	1	0	0	1057.62	34	43
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	7	7	11	0.01%	7.9%	ALYTLSGETEELSR	99.7%	75.6	25	70.5	1	0	0	1568.78	1171	1184
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	7	7	11	0.01%	7.9%	APAEEEVGPR	99.7%	51.8	25	49.1	3	0	0	1054.52	964	973
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	7	7	11	0.01%	7.9%	ASPAAPADGAAPAQPSIR	99.7%	68.9	25	68.9	2	0	0	1647.85	192	209
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	7	7	11	0.01%	7.9%	AVASSPAATNSEVK	99.7%	52.1	25	46.5	2	0	0	1331.68	550	563
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	7	7	11	0.01%	7.9%	AVTFSPDLGPVPHEGLGEYNR	96.8%	23.9	25	23.9	0	1	0	2255.11	681	701
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	7	7	11	0.01%	7.9%	DLPDGHAASPR	99.7%	42	25	40.8	1	0	0	1135.55	326	336
Calpain-2 catalytic subunit	CAPN2	CAN2_HUMAN	80.0	100.0%	4	4	5	0.01%	7.1%	FADDQLIIDFDNFVR	99.7%	39.7	25	32.5	1	0	0	1827.89	650	664
Calpain-2 catalytic subunit	CAPN2	CAN2_HUMAN	80.0	100.0%	4	4	5	0.01%	7.1%	MPCQLHQVIVAR	99.7%	33.1	25	31.8	0	1	0	1451.76	638	649
Calpain-2 catalytic subunit	CAPN2	CAN2_HUMAN	80.0	100.0%	4	4	5	0.01%	7.1%	NYPNTFWMNPQYLIK	99.7%	65.2	25	63.6	2	0	0	1928.94	376	390
Calpain-2 catalytic subunit	CAPN2	CAN2_HUMAN	80.0	100.0%	4	4	5	0.01%	7.1%	SDTFINLR	99.7%	55.1	25	21.5	1	0	0	965.51	462	469
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	4	4	7	0.01%	11.1%	ILQAVNFPFLVR	99.7%	74.3	25	74.2	2	0	0	1416.84	95	106
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	4	4	7	0.01%	11.1%	KVEAPFIPK	98.3%	31.9	25	26.4	2	0	0	1028.61	310	318
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	4	4	7	0.01%	11.1%	NLLQVDLTK	97.9%	31.1	25	13.6	2	0	0	1043.61	272	280
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	4	4	7	0.01%	11.1%	TLGTGSFGR	96.1%	28.6	25	22.8	1	0	0	895.46	49	57
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	7	8	16	0.02%	42.6%	GKPLALVEEIR	99.7%	50.5	25	50	2	2	0	1224.73	149	159
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	7	8	16	0.02%	42.6%	IGFDVVTLSGTR	99.7%	88.3	25	83	2	0	0	1264.69	48	59
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	7	8	16	0.02%	42.6%	NHLLPDIVTCVQSSR	99.7%	48.8	25	48.8	2	0	0	1738.89	175	189
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	7	8	16	0.02%	42.6%	QTLSTPGTIILGTIPVPK	99.7%	65.3	25	65.3	2	0	0	1836.08	131	148
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	7	8	16	0.02%	42.6%	RIGFDVVTLSGTR	99.7%	49.1	25	49.1	2	0	0	1420.79	47	59
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	7	8	16	0.02%	42.6%	SSGVPVDGFYTEEVR	99.7%	77.8	25	67.3	2	0	0	1641.78	28	42
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	7	8	16	0.02%	42.6%	VCVIDEIGK	97.3%	30.1	25	21.8	2	0	0	1032.54	109	117
Carbamoyl-phosphate synthase [ammonia], mitochondrial	CPS1	CPSM_HUMAN	164.9	100.0%	3	3	5	0.01%	2.6%	AVNTLNEALEFAK	99.7%	42.9	25	39.4	1	0	0	1419.75	1108	1120
Carbamoyl-phosphate synthase [ammonia], mitochondrial	CPS1	CPSM_HUMAN	164.9	100.0%	3	3	5	0.01%	2.6%	IALGIPLPEIK	98.6%	32.9	25	23.8	2	0	0	1163.74	741	751
Carbamoyl-phosphate synthase [ammonia], mitochondrial	CPS1	CPSM_HUMAN	164.9	100.0%	3	3	5	0.01%	2.6%	IAPSFAVESIEDALK	99.7%	51.4	25	48.8	2	0	0	1589.84	561	575
Carbonic anhydrase 2	CA2	CAH2_HUMAN	29.2	99.9%	2	2	2	0.00%	10.0%	AVQQPDGLAVLGIFLK	99.3%	36.1	25	36.1	1	0	0	1668.97	133	148
Carbonic anhydrase 2	CA2	CAH2_HUMAN	29.2	99.9%	2	2	2	0.00%	10.0%	SADFTNFDPR	99.6%	38.4	25	34	1	0	0	1169.52	172	181
Carbonyl reductase [NADPH] 1	CBR1	CBR1_HUMAN	30.4	100.0%	3	3	11	0.01%	15.9%	EYGGLDVLVNNAGIAFK	99.7%	79	25	78.6	3	0	0	1779.93	80	96
Carbonyl reductase [NADPH] 1	CBR1	CBR1_HUMAN	30.4	100.0%	3	3	11	0.01%	15.9%	GQAAVQQLQAEGLSPR	99.7%	108	25	94.7	4	0	0	1652.87	43	58
Carbonyl reductase [NADPH] 1	CBR1	CBR1_HUMAN	30.4	100.0%	3	3	11	0.01%	15.9%	LFSGDVVLTAR	99.7%	80	25	65.5	4	0	0	1177.66	28	38
Carboxymethylenebutenolidase homolog	CMBL	CMBL_HUMAN	28.0	100.0%	2	2	4	0.00%	7.4%	AGVSVYGIVK	99.7%	60.7	25	53.7	2	0	0	992.58	150	159
Carboxymethylenebutenolidase homolog	CMBL	CMBL_HUMAN	28.0	100.0%	2	2	4	0.00%	7.4%	LEYGGLGR	97.3%	30.1	25	23.5	2	0	0	864.46	16	23
Cartilage-associated protein	CRTAP	CRTAP_HUMAN	46.6	100.0%	5	5	7	0.01%	14.7%	AFYECLAACEGSR	99.7%	87.8	25	87.8	2	0	0	1533.65	239	251
Cartilage-associated protein	CRTAP	CRTAP_HUMAN	46.6	100.0%	5	5	7	0.01%	14.7%	FLQFAYFK	97.2%	30	25	14.6	1	0	0	1063.56	150	157
Cartilage-associated protein	CRTAP	CRTAP_HUMAN	46.6	100.0%	5	5	7	0.01%	14.7%	SLPGAEDYIKDLETK	99.7%	65.2	25	62.5	2	0	0	1678.85	190	204
Cartilage-associated protein	CRTAP	CRTAP_HUMAN	46.6	100.0%	5	5	7	0.01%	14.7%	SYESLFIR	99.7%	39.4	25	34	1	0	0	1014.53	205	212
Cartilage-associated protein	CRTAP	CRTAP_HUMAN	46.6	100.0%	5	5	7	0.01%	14.7%	TSITDMELALPDFFK	99.7%	77.4	25	77.4	1	0	0	1727.86	224	238
Casein kinase II subunit alpha	CSNK2A1	CSK21_HUMAN	45.1	100.0%	2	2	2	0.00%	5.9%	FYMYEILK	95.3%	27.9	25	0	1	0	0	1106.56	135	142
Casein kinase II subunit alpha	CSNK2A1	CSK21_HUMAN	45.1	100.0%	2	2	2	0.00%	5.9%	TPALVFEHVNNTDFK	99.7%	48	25	48	1	0	0	1731.87	108	122
Casein kinase II subunit alpha'	CSNK2A2	CSK22_HUMAN	41.2	99.8%	2	2	3	0.00%	8.0%	FYMYELLK	95.3%	27.9	25	0	1	0	0	1106.56	136	143
Casein kinase II subunit alpha'	CSNK2A2	CSK22_HUMAN	41.2	99.8%	2	2	3	0.00%	8.0%	LIDTVKDPVSK	99.7%	42.9	25	40.6	1	0	0	1214.70	98	108
Casein kinase II subunit alpha'	CSNK2A2	CSK22_HUMAN	41.2	99.8%	2	2	3	0.00%	8.0%	VYAEVNSLR	99.7%	54.1	25	41.5	2	0	0	1050.56	12	20
Caspase-14	CASP14	CASPE_HUMAN	27.7	99.8%	2	2	5	0.01%	8.7%	MAEAELVQEGK	99.7%	73.1	25	59.6	4	0	0	1204.59	213	223
Caspase-14	CASP14	CASPE_HUMAN	27.7	99.8%	2	2	5	0.01%	8.7%	TNPEIQSTLR	97.7%	30.8	25	26.3	1	0	0	1158.61	227	236
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	12	24	0.02%	28.8%	ATHDGAPELGAGGTR	99.7%	65.3	25	57	2	2	0	1409.68	332	346
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	12	24	0.02%	28.8%	IEGVLLLGEPVR	99.7%	59.3	25	49.1	1	0	0	1294.77	189	200
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	12	24	0.02%	28.8%	LFSEYHEK	98.7%	33.2	25	23.3	1	0	0	1052.50	125	132
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	12	24	0.02%	28.8%	LVNSQGQLR	99.7%	60	25	50.1	2	0	0	1014.57	74	82
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	12	24	0.02%	28.8%	MAFPLLDMVDLER	99.7%	73.6	25	63.1	6	0	0	1549.78	162	174

Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	12	24	0.02%	28.8%	MLVSGQGPVMENAQGLGFR	99.7%	113	25	112	2	0	0	1990.98	134	152
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	12	24	0.02%	28.8%	NPQSTEPVLGGGEPPFHGHR	99.7%	41.7	25	41.7	0	2	0	2113.02	370	389
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	12	24	0.02%	28.8%	NVVTVDELR	99.7%	49.9	25	25.6	2	0	0	1044.57	153	161
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	12	24	0.02%	28.8%	VPVVFVTNAGNILQHSK	99.7%	72.7	25	72.7	2	2	0	1823.02	83	99
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	12	13	19	0.02%	15.3%	AAALVLQTIWGYK	99.7%	70.1	25	70.1	2	0	0	1433.82	821	833
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	12	13	19	0.02%	15.3%	ALSAIADLLTNEHER	99.7%	102	25	95.5	2	1	0	1652.86	711	725
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	12	13	19	0.02%	15.3%	FVGDADLER	99.7%	42.9	25	27.3	1	0	0	1021.50	69	77
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	12	13	19	0.02%	15.3%	GIPVLVGLLDHPK	99.7%	69.7	25	69.7	2	0	0	1357.82	409	421
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	12	13	19	0.02%	15.3%	GSLASLDSLRK	99.7%	41.1	25	17.7	1	0	0	1146.65	345	355
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	12	13	19	0.02%	15.3%	GYELLFQPEVVR	99.7%	67.1	25	49.7	3	0	0	1449.77	655	666
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	12	13	19	0.02%	15.3%	HAIPNLVK	95.3%	27.9	25	20.6	1	0	0	891.54	750	757
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	12	13	19	0.02%	15.3%	LVENCVCLLR	99.7%	54.1	25	33.4	1	0	0	1275.65	575	584
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	12	13	19	0.02%	15.3%	SDFQVNLNNASR	99.7%	61.2	25	55.5	1	0	0	1364.66	847	858
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	12	13	19	0.02%	15.3%	SLDNNYSTPNER	99.7%	40.5	25	36.8	1	0	0	1409.63	899	910
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	12	13	19	0.02%	15.3%	VGGSSVDLHR	99.7%	73.3	25	52.8	2	0	0	1026.53	265	274
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	12	13	19	0.02%	15.3%	YQEAAPNVANNTGPHAASCFGAK	99.7%	57.8	25	57.8	0	1	0	2375.08	600	622
CCAAT/enhancer-binding protein zeta	CEBPZ	CEBPZ_HUMAN	121.0	100.0%	3	3	5	0.01%	2.9%	ALLVQVVNK	99.7%	61.6	25	50	3	0	0	983.62	382	390
CCAAT/enhancer-binding protein zeta	CEBPZ	CEBPZ_HUMAN	121.0	100.0%	3	3	5	0.01%	2.9%	ELLITDLLPDNR	99.7%	39.3	25	37.6	1	0	0	1411.78	291	302
CCAAT/enhancer-binding protein zeta	CEBPZ	CEBPZ_HUMAN	121.0	100.0%	3	3	5	0.01%	2.9%	LYQHEINLFK	99.6%	38.7	25	25.8	1	0	0	1304.70	212	221
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	12	12	19	0.02%	5.7%	AVQELVHPVVDR	99.7%	48.9	25	45.9	1	0	0	1361.75	1400	1411
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	12	12	19	0.02%	5.7%	EPLLMSISTNLK	98.1%	31.4	25	31.4	1	0	0	1345.74	1459	1470
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	12	12	19	0.02%	5.7%	GAFGVGQEQIDAFLK	99.7%	66.7	25	57.9	2	0	0	1579.81	194	208
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	12	12	19	0.02%	5.7%	GQQELLYVVPFVAK	99.7%	89.5	25	89.5	2	0	0	1590.89	1228	1241
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	12	12	19	0.02%	5.7%	IVEPPENIQEK	95.7%	28.3	25	25.1	1	0	0	1295.68	1088	1098
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	12	12	19	0.02%	5.7%	MYYFGIAALDR	99.7%	55.5	25	47.7	1	0	0	1319.65	950	960
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	12	12	19	0.02%	5.7%	NIIVQFGVR	97.8%	30.9	25	27.7	1	0	0	1045.62	275	283
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	12	12	19	0.02%	5.7%	NLDEQLSAPK	99.7%	42	25	35.1	2	0	0	1114.57	1311	1320
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	12	12	19	0.02%	5.7%	NLILSAFPR	99.7%	47.4	25	29.8	2	0	0	1030.60	2130	2138
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	12	12	19	0.02%	5.7%	SLLEVVVLSR	99.7%	67.9	25	31.2	2	0	0	1114.68	1641	1650
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	12	12	19	0.02%	5.7%	SPVTFLSDLR	99.7%	69.5	25	54.2	2	0	0	1134.62	2188	2197
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	12	12	19	0.02%	5.7%	YLFLNAIANQLR	94.7%	27.5	25	25.1	2	0	0	1435.81	2264	2275
CCR4-NOT transcription complex subunit 2	CNOT2	CNOT2_HUMAN	59.7	99.8%	2	2	4	0.00%	5.6%	EGSGNPTPLINPLAGR	99.7%	60.4	25	60.4	2	0	0	1592.84	240	255
CCR4-NOT transcription complex subunit 2	CNOT2	CNOT2_HUMAN	59.7	99.8%	2	2	4	0.00%	5.6%	TNSMSSSGLGSPNR	99.7%	46	25	46	2	0	0	1410.63	155	168
CDK5 regulatory subunit-associated protein 1	CDK5RAP1	CK5P1_HUMAN	67.7	99.8%	2	2	3	0.00%	3.3%	IGILGCMAER	95.7%	28.2	25	18.2	1	0	0	1119.57	178	187
CDK5 regulatory subunit-associated protein 1	CDK5RAP1	CK5P1_HUMAN	67.7	99.8%	2	2	3	0.00%	3.3%	ITSASSQTLR	99.7%	54.7	25	41	2	0	0	1063.57	576	585
CDP-diacylglycerol--inositol 3-phosphatidyltransferase	CDIPT	CDIPT_HUMAN	23.5	100.0%	4	8	16	0.02%	21.1%	FGAMLDMLTDR	99.7%	61.7	25	45.7	3	0	0	1269.60	63	73
CDP-diacylglycerol--inositol 3-phosphatidyltransferase	CDIPT	CDIPT_HUMAN	23.5	100.0%	4	8	16	0.02%	21.1%	MGLWVTAPIALLK	99.7%	52	25	52	5	0	0	1428.83	174	186
CDP-diacylglycerol--inositol 3-phosphatidyltransferase	CDIPT	CDIPT_HUMAN	23.5	100.0%	4	8	16	0.02%	21.1%	MIDLSGNPVLR	99.7%	78	25	69.7	5	0	0	1214.66	122	132
CDP-diacylglycerol--inositol 3-phosphatidyltransferase	CDIPT	CDIPT_HUMAN	23.5	100.0%	4	8	16	0.02%	21.1%	NMAALDAADR	99.7%	52.8	25	46	3	0	0	1063.48	200	209
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	14	15	24	0.02%	18.5%	AAYNPGQAVPWNAVK	99.7%	57.9	25	57.9	1	0	0	1585.81	98	112
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	14	15	24	0.02%	18.5%	EAAPDAGAEPITADSDPAYSSK	99.7%	78.5	25	78.5	1	0	0	2162.97	288	309
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	14	15	24	0.02%	18.5%	FAEFQYLQPGPPR	99.7%	70.3	25	69.7	2	0	0	1549.78	405	417
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	14	15	24	0.02%	18.5%	FSATEVTNK	99.7%	43.3	25	37.8	2	0	0	996.50	847	855
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	14	15	24	0.02%	18.5%	GRLPQLGEK	98.1%	31.5	25	20.7	1	0	0	997.58	85	93
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	14	15	24	0.02%	18.5%	ILLTLGIR	99.7%	47.2	25	44.8	2	0	0	898.61	728	735
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	14	15	24	0.02%	18.5%	LAEAEETAR	99.7%	55.9	25	50.1	2	0	0	989.49	868	876
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	14	15	24	0.02%	18.5%	LTPLQLEIQR	99.5%	37.7	25	29.6	1	0	0	1210.72	896	905
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	14	15	24	0.02%	18.5%	QGILGAQPQLIFQPHR	99.7%	49	25	49	0	2	0	1803.00	139	154
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	14	15	24	0.02%	18.5%	SPAPPLLHVAALGQK	99.7%	60.8	25	60.5	1	2	0	1498.87	124	138
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	14	15	24	0.02%	18.5%	TLAAEMQELR	99.7%	43.6	25	36.3	1	0	0	1177.59	856	865
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	14	15	24	0.02%	18.5%	VLLLSSPGLEELYR	99.7%	62.1	25	62.1	3	0	0	1588.89	310	323

Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	14	15	24	0.02%	18.5%	VQTLSNQPLLK	99.7%	53.5	25	39.6	1	0	0	1240.73	113	123
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	14	15	24	0.02%	18.5%	VVTQNICQYR	99.7%	53.5	25	53.2	2	0	0	1280.64	748	757
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	5	5	9	0.01%	18.4%	ENALLELSK	98.6%	32.8	25	30.1	2	0	0	1016.56	36	44
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	5	5	9	0.01%	18.4%	IYQWINELSSPETR	99.7%	79	25	70.9	1	0	0	1735.87	22	35
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	5	5	9	0.01%	18.4%	LTSLGVIGALVK	99.7%	76.1	25	72.1	2	0	0	1170.75	137	148
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	5	5	9	0.01%	18.4%	NLQEGQVTDPR	99.7%	49.3	25	44.5	2	0	0	1256.62	282	292
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	5	5	9	0.01%	18.4%	TVATFILQK	99.7%	59.2	25	44.7	2	0	0	1020.61	180	188
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	4	5	9	0.01%	7.4%	EFYEVVQSQR	99.7%	58.4	25	51.1	2	0	0	1284.62	9	18
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	4	5	9	0.01%	7.4%	EMIEESANK	98.8%	33.3	25	33.3	2	0	0	1050.48	342	350
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	4	5	9	0.01%	7.4%	LQEFLADMGLPLK	99.7%	68	25	61.5	3	0	0	1474.80	311	323
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	4	5	9	0.01%	7.4%	YVTDVGVLQR	99.7%	62.5	25	45.7	2	0	0	1149.63	238	247
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	9	9	15	0.02%	14.8%	AAGIEIQK	94.8%	27.5	25	21.3	1	0	0	829.48	193	200
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	9	9	15	0.02%	14.8%	ESDLPSAILQTSGVSEFTK	99.7%	95.7	25	95.7	2	0	0	2009.01	272	290
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	9	9	15	0.02%	14.8%	GVDYNAEIPFEK	99.7%	46.7	25	46.7	2	0	0	1381.66	207	218
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	9	9	15	0.02%	14.8%	ILLGGYQSR	99.5%	37.2	25	23.7	2	0	0	1006.57	719	727
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	9	9	15	0.02%	14.8%	ILQEAQNLMALTNVDTPLK	99.7%	71.6	25	71.6	1	0	0	2112.14	362	380
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	9	9	15	0.02%	14.8%	LGLLGLPAPK	99.7%	73.6	25	73.6	2	0	0	978.63	478	487
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	9	9	15	0.02%	14.8%	LVLPAPQISDAELQEVVK	99.7%	79.4	25	78.5	2	0	0	1949.10	295	312
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	9	9	15	0.02%	14.8%	QVVQTPNTVLSTPFR	99.7%	58.6	25	49.2	1	0	0	1686.92	400	414
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	9	9	15	0.02%	14.8%	VGQASEIAR	99.7%	64.4	25	45.3	2	0	0	930.50	313	321
Cell division cycle protein 16 homolog	CDC16	CDC16_HUMAN	71.7	100.0%	3	3	3	0.00%	4.4%	IYDALDNR	99.5%	37.6	25	30	1	0	0	979.48	139	146
Cell division cycle protein 16 homolog	CDC16	CDC16_HUMAN	71.7	100.0%	3	3	3	0.00%	4.4%	LCNEEQELLR	99.7%	39.9	25	35.2	1	0	0	1303.63	193	202
Cell division cycle protein 16 homolog	CDC16	CDC16_HUMAN	71.7	100.0%	3	3	3	0.00%	4.4%	YAEALDYHR	99.5%	37.6	25	33.1	1	0	0	1137.53	461	469
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	8	9	15	0.02%	15.1%	AWYGLGQTYEILK	99.7%	83.5	25	79.8	1	0	0	1541.80	401	413
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	8	9	15	0.02%	15.1%	AYAVGDVEK	99.7%	42.4	25	32.2	2	0	0	951.48	459	467
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	8	9	15	0.02%	15.1%	IENMDTFSNLLYVR	99.7%	42.8	25	32.5	3	0	0	1714.85	297	310
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	8	9	15	0.02%	15.1%	MLVALGECYEK	99.7%	54.5	25	53.5	2	0	0	1312.63	435	445
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	8	9	15	0.02%	15.1%	QLLLIAGLTR	99.7%	73.7	25	64	2	0	0	1097.70	35	44
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	8	9	15	0.02%	15.1%	VETCCVIGNYYSLR	99.7%	41.3	25	41.3	1	0	0	1733.80	331	344
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	8	9	15	0.02%	15.1%	YLAQYYFK	99.7%	39.9	25	28.6	2	0	0	1095.55	515	522
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	8	9	15	0.02%	15.1%	YQNLIDVGFSK	99.7%	54.1	25	54.1	2	0	0	1283.66	251	261
Cell division cycle protein 27 homolog	CDC27	CDC27_HUMAN	91.9	99.8%	2	2	3	0.00%	3.0%	ESLVYFLIGK	99.7%	63	25	63	2	0	0	1168.66	736	745
Cell division cycle protein 27 homolog	CDC27	CDC27_HUMAN	91.9	99.8%	2	2	3	0.00%	3.0%	LAEGEQILSGGVFNK	99.7%	89.6	25	82.1	1	0	0	1561.82	85	99
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	7	7	10	0.01%	21.1%	ELLEQISAFDNVPR	99.7%	100	25	86.1	2	0	0	1630.84	96	109
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	7	7	10	0.01%	21.1%	EQDQRPLHPVANPHAEISTK	99.7%	32.8	25	32.8	0	1	0	2267.15	149	168
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	7	7	10	0.01%	21.1%	LPEHPEGGEPEDDEAPAK	96.3%	23.4	25	23.4	0	1	0	1916.85	289	306
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	7	7	10	0.01%	21.1%	VFFTCNACGESVK	99.7%	51.1	25	51.1	2	0	0	1518.67	2	14
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	7	7	10	0.01%	21.1%	VFFTCNACGESVKK	99.7%	61.5	25	61.5	1	0	0	1646.77	2	15
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	7	7	10	0.01%	21.1%	VKDAVEQQGEVK	99.7%	67.2	25	60.7	2	0	0	1329.70	174	185
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	7	7	10	0.01%	21.1%	VRELLEQISAFDNVPR	99.7%	42.4	25	42.4	0	1	0	1886.01	94	109
Cellular tumor antigen p53	TP53	P53_HUMAN	43.7	100.0%	3	3	11	0.01%	8.7%	ALPNNTSSSPQPK	99.7%	55.4	25	50.9	4	0	0	1340.68	307	319
Cellular tumor antigen p53	TP53	P53_HUMAN	43.7	100.0%	3	3	11	0.01%	8.7%	SVTCTYSPALNK	99.7%	47.5	25	45.8	4	0	0	1340.65	121	132
Cellular tumor antigen p53	TP53	P53_HUMAN	43.7	100.0%	3	3	11	0.01%	8.7%	TYQGSYGFR	99.3%	36	25	36	3	0	0	1078.50	102	110
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	5	5	7	0.01%	30.2%	LLLDTFEYQGLVK	99.7%	64.3	25	51.7	2	0	0	1538.85	135	147
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	5	5	7	0.01%	30.2%	SGASGASAAPAASAAAALAPSATR	99.7%	86.8	25	84.2	2	0	0	1985.00	18	41
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	5	5	7	0.01%	30.2%	SMVTEEFNGSDWEK	99.7%	41.2	25	41.2	1	0	0	1658.70	248	261
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	5	5	7	0.01%	30.2%	SNPGGFGIAPHCLDEGTVR	97.7%	25.2	25	23.6	0	1	0	1983.93	229	247
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	5	5	7	0.01%	30.2%	SQAVEKPPSEKPR	96.1%	23.2	25	23.2	0	1	0	1452.78	53	65
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	4	5	8	0.01%	6.7%	AMGTLLNTAISEVIGK	99.7%	58.4	25	58.4	2	0	0	1633.88	652	667
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	4	5	8	0.01%	6.7%	LEKEDLGTR	99.7%	39.3	25	27.4	1	0	0	1060.56	15	23
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	4	5	8	0.01%	6.7%	NLMTSEIHNTVK	99.7%	74.4	25	61.1	3	0	0	1402.70	413	424

Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	4	5	8	0.01%	6.7%	QLLDLPLDTDLENEK	99.7%	71.2	25	71.2	2	0	0	1755.90	306	320
Chaperone activity of bc1 complex-like, mitochondrial	ADCK3	ADCK3_HUMAN	72.0	100.0%	3	3	3	0.00%	7.4%	AVLGSSPFLSEANAER	99.7%	58.9	25	57.2	1	0	0	1647.83	247	262
Chaperone activity of bc1 complex-like, mitochondrial	ADCK3	ADCK3_HUMAN	72.0	100.0%	3	3	3	0.00%	7.4%	LANFGGLAVGLGFGALAEVAKK	99.7%	58.7	25	55.7	0	1	0	2103.20	214	235
Chaperone activity of bc1 complex-like, mitochondrial	ADCK3	ADCK3_HUMAN	72.0	100.0%	3	3	3	0.00%	7.4%	MGGSFLICSK	99.7%	49.6	25	44	1	0	0	1099.53	613	622
Chitobiosyldiphosphodolichol beta-mannosyltransferase	ALG1	ALG1_HUMAN	52.5	99.9%	2	3	4	0.00%	6.5%	AVTVYDKPASFFK	99.7%	47.6	25	47	1	0	0	1472.78	211	223
Chitobiosyldiphosphodolichol beta-mannosyltransferase	ALG1	ALG1_HUMAN	52.5	99.9%	2	3	4	0.00%	6.5%	IQIVGLTELQSLAVGPR	99.7%	76.8	25	76.8	2	1	0	1794.05	83	99
Chloride channel CLIC-like protein 1	CLCC1	CLCC1_HUMAN	62.0	100.0%	3	3	5	0.01%	6.4%	AFDVPDAEAR	99.7%	40	25	27.9	1	0	0	1090.52	444	453
Chloride channel CLIC-like protein 1	CLCC1	CLCC1_HUMAN	62.0	100.0%	3	3	5	0.01%	6.4%	GQMGPTEQGPYAK	99.7%	57	25	57	2	0	0	1379.63	402	414
Chloride channel CLIC-like protein 1	CLCC1	CLCC1_HUMAN	62.0	100.0%	3	3	5	0.01%	6.4%	LAFAQHQAEVAK	99.7%	64.4	25	58	2	0	0	1312.70	235	246
Chromatin target of PRMT1 protein	CHTOP	CHTOP_HUMAN	26.4	100.0%	3	6	16	0.02%	16.9%	ASMQQQQQLASAR	99.7%	68.8	25	60	9	0	0	1462.71	39	51
Chromatin target of PRMT1 protein	CHTOP	CHTOP_HUMAN	26.4	100.0%	3	6	16	0.02%	16.9%	EQLDNQLDAYMSK	99.7%	81.9	25	81.9	2	0	0	1570.71	214	226
Chromatin target of PRMT1 protein	CHTOP	CHTOP_HUMAN	26.4	100.0%	3	6	16	0.02%	16.9%	LAQQMENRPSVQAALK	99.7%	49.2	25	33.6	3	2	0	1783.95	55	70
Chromobox protein homolog 3	CBX3	CBX3_HUMAN	20.8	99.8%	2	3	5	0.01%	16.4%	IIGATDSSGELMFLMK	99.7%	74.5	25	72.2	4	0	0	1712.86	126	141
Chromobox protein homolog 3	CBX3	CBX3_HUMAN	20.8	99.8%	2	3	5	0.01%	16.4%	KVEEAEPEEFVVEK	99.7%	59.1	25	54.9	1	0	0	1661.83	21	34
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	4	4	5	0.01%	4.4%	GGQAPGFLLR	99.7%	45.8	25	26	1	0	0	1015.57	10	19
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	4	4	5	0.01%	4.4%	GIPTYIYYFPR	99.7%	60.2	25	59.8	2	0	0	1389.72	867	877
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	4	4	5	0.01%	4.4%	LLQPFLLR	99.7%	41.3	25	34.6	1	0	0	999.64	253	260
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	4	4	5	0.01%	4.4%	SFEQLVNLQK	99.7%	40.2	25	31.5	1	0	0	1205.65	591	600
Chromodomain-helicase-DNA-binding protein 4	CHD4	CHD4_HUMAN	218.0	100.0%	3	3	3	0.00%	1.9%	GAADVEKVEEK	99.7%	39.1	25	19.4	1	0	0	1174.60	1637	1647
Chromodomain-helicase-DNA-binding protein 4	CHD4	CHD4_HUMAN	218.0	100.0%	3	3	3	0.00%	1.9%	TVQTAVFLYSLYK	98.1%	31.5	25	26.8	1	0	0	1532.84	758	770
Chromodomain-helicase-DNA-binding protein 4	CHD4	CHD4_HUMAN	218.0	100.0%	3	3	3	0.00%	1.9%	VGGNIEVLGFNAR	99.7%	58.3	25	53.2	1	0	0	1345.72	1407	1419
Chromosome transmission fidelity protein 18 homolog	CHTF18	CTF18_HUMAN	107.4	100.0%	5	5	7	0.01%	6.5%	ACINTLQFLYSR	99.7%	49.5	25	48	1	0	0	1485.75	551	562
Chromosome transmission fidelity protein 18 homolog	CHTF18	CTF18_HUMAN	107.4	100.0%	5	5	7	0.01%	6.5%	GGGQLDLLGVSLASLK	99.7%	50.5	25	47.6	1	0	0	1527.87	212	227
Chromosome transmission fidelity protein 18 homolog	CHTF18	CTF18_HUMAN	107.4	100.0%	5	5	7	0.01%	6.5%	NLIQTLVSGIAPATR	99.7%	66.3	25	66.3	2	0	0	1553.90	735	749
Chromosome transmission fidelity protein 18 homolog	CHTF18	CTF18_HUMAN	107.4	100.0%	5	5	7	0.01%	6.5%	TTLAHVIAR	96.5%	29	25	25.4	1	0	0	981.58	381	389
Chromosome transmission fidelity protein 18 homolog	CHTF18	CTF18_HUMAN	107.4	100.0%	5	5	7	0.01%	6.5%	VVQGLFDNFLR	99.7%	55.9	25	47	2	0	0	1307.71	648	658
Citrate synthase, mitochondrial	CS	CISY_HUMAN	51.7	99.9%	2	2	4	0.00%	4.9%	ALGVLAQLIWSR	99.7%	60.1	25	55.1	2	0	0	1326.79	429	440
Citrate synthase, mitochondrial	CS	CISY_HUMAN	51.7	99.9%	2	2	4	0.00%	4.9%	IVPNVLLEQGK	99.3%	36	25	36	2	0	0	1209.72	383	393
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	ALEHFTDLYDIKR	99.7%	48.5	25	45.4	0	2	0	1620.84	626	638
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	ENPYYDSR	98.5%	32.4	25	23.8	1	0	0	1043.44	896	903
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	ESNCYDPER	99.7%	43.1	25	43.1	1	0	0	1169.45	750	758
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	ESYVETELIFALAK	99.7%	52.6	25	44.7	2	0	0	1612.85	1166	1179
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	EVCFACVDGK	99.7%	57.6	25	57.6	2	0	0	1184.51	1255	1264
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	GQCDLELINVCNENSLFK	99.7%	56.6	25	56.6	2	0	0	2153.00	924	941
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	GQFSTDELVAEVEK	99.7%	82.8	25	82.8	2	0	0	1551.75	838	851
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	GQFSTDELVAEVEKR	99.7%	93.1	25	93	1	0	0	1707.85	838	852
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	HSSLAGCQIINYR	99.7%	53.9	25	46.8	1	0	0	1518.75	145	157
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	IAAYLFK	97.7%	30.8	25	19.8	1	0	0	825.49	1510	1516
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	ISGETIFVTAPHEATAGIIGVNR	99.7%	59	25	59	0	2	0	2353.25	298	320
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	IVLDNSVFSEHR	99.7%	64.9	25	64.9	2	2	0	1415.73	1011	1022
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	IYIDSNNNPER	99.7%	65.4	25	53.1	2	0	0	1334.63	882	892
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	KFNALFAQGNYSEAAK	99.7%	48	25	44.9	0	2	0	1758.88	367	382
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	LASTLVHLGEYQAAVDGAR	98.2%	26	25	21.8	0	1	0	1971.03	1227	1245
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	LHIIEVGTPPTGNQPFPK	99.2%	29	25	28.3	0	2	0	1945.05	228	245
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	LLLPWLEAR	99.3%	35.7	25	23.7	2	0	0	1110.67	857	865
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	LLYNNVSNFGR	99.7%	49.4	25	49.4	2	0	0	1296.67	1216	1226
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	LPVVIGGLLDVDCSEDVIK	99.7%	73	25	68.3	2	0	0	2041.09	812	830
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	LTDQLPLIIVCDR	99.5%	37.8	25	37.4	1	0	0	1555.85	768	780
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	NLQNLLILTAIK	99.7%	89.5	25	89.5	7	0	0	1353.85	1023	1034
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	NNLAGAEELFAR	99.7%	85.5	25	82.5	2	0	0	1304.66	355	366
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	NNRPSEGPLQTR	95.4%	22.6	25	18.1	0	1	0	1368.70	572	583

Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	RPISADSAIMNPASK	97.3%	30.1	25	30	1	0	0	1573.80	64	78
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	SVDPTLALSVYLR	99.5%	37	25	37	1	0	0	1433.80	469	481
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	TLQIFNIEMK	99.7%	60.8	25	48	2	0	0	1252.66	87	96
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	VANVELYYR	99.7%	82.9	25	77.6	2	0	0	1126.59	1398	1406
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	VDKLDASESLR	95.8%	28.3	25	12.3	1	0	0	1232.65	1610	1620
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	VGYTPDWIFLLR	99.7%	57.9	25	52.3	3	0	0	1479.80	508	519
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	VIQCFAETGQVQK	99.7%	108	25	92.8	2	0	0	1507.76	488	500
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	VMEYINR	97.2%	29.9	25	16.5	1	0	0	940.46	1040	1046
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	VVGAMQLYSVDR	99.7%	58	25	55.9	2	0	0	1337.69	177	188
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	33	34	63	0.07%	24.4%	WLLLTGISAQQNR	99.7%	86.8	25	78.5	3	0	0	1499.83	164	176
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	6	6	11	0.01%	5.1%	EVLLVALGSR	99.7%	78.3	25	63.5	2	0	0	1056.64	848	857
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	6	6	11	0.01%	5.1%	NVLDGELLNR	99.7%	59.9	25	51.2	2	0	0	1142.62	1397	1406
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	6	6	11	0.01%	5.1%	SSFLPSYIIDVR	99.7%	66.7	25	54.7	2	0	0	1396.75	183	194
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	6	6	11	0.01%	5.1%	VLVDSSFGQPTTQGEAR	99.7%	85.3	25	85.3	2	0	0	1791.89	817	833
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	6	6	11	0.01%	5.1%	VYAVATSTNTPCAR	99.7%	84.3	25	75.2	1	0	0	1510.73	1033	1046
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	6	6	11	0.01%	5.1%	YIVQVSPLGIR	99.7%	40.6	25	35.2	2	0	0	1244.74	617	627
Cleavage and polyadenylation specificity factor subunit 3	CPSF3	CPSF3_HUMAN	77.5	99.8%	2	2	2	0.00%	2.8%	GLIPVFALGR	99.7%	42.4	25	34.3	1	0	0	1042.64	236	245
Cleavage and polyadenylation specificity factor subunit 3	CPSF3	CPSF3_HUMAN	77.5	99.8%	2	2	2	0.00%	2.8%	LYEALTPVH	96.3%	28.9	25	28.1	1	0	0	1042.56	676	684
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	3	3	6	0.01%	15.4%	LFLVQLQEK	99.7%	60	25	45.9	2	0	0	1117.66	174	182
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	3	3	6	0.01%	15.4%	LMTEILGR	99.7%	39.7	25	29.3	2	0	0	932.52	124	131
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	3	3	6	0.01%	15.4%	LPGGELNPGEDEVEGLKR	99.7%	76.4	25	75.7	0	2	0	1908.97	106	123
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	5	6	10	0.01%	10.5%	AISSSAISR	99.7%	39.8	25	22.7	1	0	0	891.49	423	431
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	5	6	10	0.01%	10.5%	GAAPNVVYTYTGK	99.7%	83.5	25	81.3	2	0	0	1340.68	67	79
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	5	6	10	0.01%	10.5%	GDYGPPGR	96.6%	29.2	25	19.4	1	0	0	818.38	393	400
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	5	6	10	0.01%	10.5%	GFALVGVGSEASSK	99.7%	101	25	94.2	2	0	0	1308.68	125	138
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	5	6	10	0.01%	10.5%	TPLSEAEFEEIMNR	99.7%	109	25	109	4	0	0	1665.78	407	420
CLIP-associating protein 2	CLASP2	CLAP2_HUMAN	141.1	99.9%	2	2	4	0.00%	2.6%	VLNTGSDVEEAVADALK	99.7%	88.6	25	88.4	2	0	0	1730.88	591	607
CLIP-associating protein 2	CLASP2	CLAP2_HUMAN	141.1	99.9%	2	2	4	0.00%	2.6%	VLTTTALSTVSSGVQR	99.7%	76.8	25	64.6	2	0	0	1619.90	467	482
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	ASNLENSTYDLYTIPK	99.7%	105	25	97.8	2	0	0	1828.90	383	398
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	CPLSGACYSPEFK	99.7%	49.9	25	44.4	2	0	0	1515.66	1185	1197
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	DADSQNPDAPEGKR	99.7%	50.5	25	45.9	2	0	0	1499.67	399	412
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	DVAVMQLR	99.7%	51.2	25	39.6	5	0	0	931.50	351	358
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	EYIVGLSVETER	99.7%	64.9	25	58.3	2	0	0	1394.72	1059	1070
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	GFFEGTIASK	99.7%	62.7	25	60.6	3	0	0	1056.54	816	825
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	GHYNNVSCAVFHPR	99.7%	48.4	25	48.4	0	1	0	1657.77	247	260
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	GITGVDLFGTTDAVVK	99.7%	87.5	25	87.5	4	0	0	1592.85	183	198
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	KLDALCNIHENIR	99.7%	42.3	25	41.6	0	2	0	1595.83	517	529
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	KYDEVLHMVR	99.7%	33.2	25	26.8	0	2	0	1305.66	607	616
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	LLELGPKPEVAQQTR	99.7%	47.3	25	43.2	0	2	0	1678.95	1128	1142
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	LNDLIQR	99.7%	55.9	25	41.6	3	0	0	871.50	1003	1009
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	LSFLYLITGNLEK	99.7%	71.1	25	71.1	2	0	0	1510.85	703	715
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	LVGQSIIAYLQK	99.7%	103	25	103	3	0	0	1332.79	620	631
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	MCTLIDKFDEHDGPVR	99.6%	32.4	25	32.4	0	1	0	1932.89	40	55
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	NLSPGAVESDVR	99.7%	56	25	44.8	2	0	0	1243.63	171	182
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	QELILSNSEDK	99.7%	42.8	25	37.3	1	0	0	1275.64	261	271
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	QLDFNSSK	96.5%	29	25	13	1	0	0	938.46	343	350
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	QLFLQTYAR	99.7%	49.5	25	44.8	2	0	0	1139.62	957	965
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	SILLSVPLLVVDNK	99.7%	66.6	25	66.6	5	0	0	1509.93	1031	1044
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	SSGLTAVWVAR	99.7%	76.3	25	44.6	2	0	0	1146.63	413	423
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	TALNLFFK	99.7%	55.5	25	44.9	3	0	0	953.55	1107	1114
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	TLDLPIYVTR	99.7%	59	25	54	3	0	0	1190.68	563	572

Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	VLTIDPTEFK	99.7%	42.6	25	36.1	4	0	0	1162.64	589	598
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	VTTVTEIGKDVIGLR	99.7%	77.6	25	77.6	2	0	0	1600.93	1203	1217
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	VWDISGLR	99.5%	37.7	25	17.9	1	0	0	945.52	161	168
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	27	29	66	0.07%	25.9%	YAVTTGDHGIIR	99.7%	68.2	25	59.5	3	1	0	1302.68	551	562
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	AAAQCYIDLIIK	99.7%	79.1	25	68.7	2	0	0	1378.74	280	291
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	CIYNLLQSSSPAVK	99.7%	90.3	25	90.3	2	0	0	1579.81	248	261
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	DLQHPNEFIR	99.7%	43.6	25	31.5	2	0	0	1268.64	108	117
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	EAELLEPLMPAIR	99.7%	54.2	25	43.8	2	0	0	1481.80	129	141
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	EAGELKPEEEITVGPVQK	99.7%	70.6	25	69.3	2	0	0	1953.02	496	513
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	GALWILGEYCSTK	99.7%	81.1	25	78.7	2	0	0	1497.74	457	469
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	KPITDDDVDR	99.7%	50.2	25	35	2	0	0	1173.57	603	612
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	LEEEKLSQK	99.7%	41.5	25	14.2	2	0	0	1103.59	647	655
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	LLLVFWEIVPK	99.7%	80.2	25	63	4	0	0	1356.83	77	87
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	LPGLLMTIIR	99.7%	59	25	58.4	4	0	0	1126.70	55	64
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	LVEKPSPLTLAPHDFANIK	99.7%	46.5	25	46.5	0	2	0	2090.16	768	786
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	LVTEMGTYATQSALSSSRPTK	99.7%	36.3	25	36.3	0	3	0	2228.12	514	534
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	MLEVFHAIK	99.7%	39.3	25	28.4	2	0	0	1087.60	442	450
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	NAVLAIYTIYR	99.7%	78.5	25	78.5	2	0	0	1296.73	154	164
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	NVEELVIVLK	99.0%	34.2	25	28.8	2	0	0	1155.70	352	361
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	NVEELVIVLKK	99.7%	49.2	25	49.2	2	0	0	1283.79	352	362
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	NVTVQPDDPISFMQLTAK	99.7%	98.7	25	95.4	3	0	0	2004.01	662	679
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	SLGEIPIVESEIKK	99.7%	69.7	25	69.7	2	0	0	1541.88	482	495
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	SQGMALSLGDK	99.7%	53.7	25	45.7	2	0	0	1106.55	933	943
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	TLQLALDLVSSR	99.7%	89.1	25	86.6	2	0	0	1315.76	340	351
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	TNNVSEHEDTDKYR	99.7%	48.4	25	48.4	0	2	0	1707.76	367	380
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	VASTENGIIFGNIVYDVSGAASDR	99.7%	87.4	25	87.4	1	1	0	2455.21	791	814
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	VIIMILNGEK	99.7%	48.1	25	35.5	2	0	0	1129.67	45	54
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	VLQDLVMDILR	99.7%	82.5	25	75	7	0	0	1314.75	317	327
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	VLSECSPLMNDIFNK	99.7%	78.1	25	78.1	2	0	0	1766.85	619	633
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	VLSTPDLEVR	99.7%	45.3	25	37.3	2	0	0	1128.63	328	337
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	27	32	65	0.07%	35.5%	YVALVQEK	99.6%	38.6	25	24.7	2	0	0	949.54	568	575
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	5	5	8	0.01%	6.3%	AAESLADPTEYENLFPGLK	99.7%	72.7	25	72.7	2	0	0	2065.01	784	802
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	5	5	8	0.01%	6.3%	HSEVQQANLK	99.7%	44.9	25	42	3	0	0	1153.60	319	328
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	5	5	8	0.01%	6.3%	TMYLLGYIPK	96.0%	28.5	25	22.3	1	0	0	1198.65	560	569
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	5	5	8	0.01%	6.3%	TYLPSQVSR	99.0%	34.4	25	34.4	1	0	0	1050.56	760	768
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	5	5	8	0.01%	6.3%	VFNYNTLER	99.7%	57.4	25	46.1	1	0	0	1155.58	83	91
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	18	33	0.03%	32.7%	ENVNLAQIR	99.7%	73.4	25	54.7	2	0	0	1056.58	123	131
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	18	33	0.03%	32.7%	GKEVDNFVDK	96.0%	28.5	25	19.5	1	0	0	1150.57	232	241
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	18	33	0.03%	32.7%	GVQLQTHPNVDKK	99.0%	28.5	25	22.3	1	2	0	1463.80	324	336
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	18	33	0.03%	32.7%	IEGLLAAFPK	99.7%	48.6	25	36	2	0	0	1058.62	29	38
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	18	33	0.03%	32.7%	KNYCNIQVTK	99.7%	66.9	25	58.7	2	0	0	1267.65	476	485
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	18	33	0.03%	32.7%	LFTAESLIGLK	99.7%	74.3	25	61.7	2	0	0	1191.70	337	347
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	18	33	0.03%	32.7%	LYMVLITTK	99.7%	66.1	25	66.1	2	0	0	1081.63	64	72
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	18	33	0.03%	32.7%	NSNILEDLETLR	99.7%	70.3	25	68.1	2	0	0	1416.73	73	84
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	18	33	0.03%	32.7%	NTLEWCLPVIDAK	99.7%	66.2	25	54.6	2	0	0	1558.79	436	448
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	18	33	0.03%	32.7%	NYCNIQVTK	99.7%	44	25	38.7	2	0	0	1139.55	477	485
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	18	33	0.03%	32.7%	SEGETIMSSSMGK	99.7%	59.3	25	50	4	0	0	1343.58	244	256
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	18	33	0.03%	32.7%	SFPVNSDVGVLK	99.7%	52.9	25	44.4	2	0	0	1261.68	352	363
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	18	33	0.03%	32.7%	TFTEMDSHEEK	99.7%	55	25	41.8	2	0	0	1353.56	132	142
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	18	33	0.03%	32.7%	VAPAPARPSGPSK	99.5%	37.8	25	23.6	1	0	0	1234.69	212	224
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	18	33	0.03%	32.7%	VLLAAAVCTK	99.7%	65.1	25	58.9	2	0	0	1045.61	2	11

Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	16	18	33	0.03%	32.7%	VTQVDGNSPVR	99.7%	60.6	25	48.4	2	0	0	1171.61	486	496
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	6	6	8	0.01%	31.8%	APPAPGPASGGSGEVDELFDVK	99.7%	69.9	25	69.9	2	0	0	2097.01	2	23
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	6	6	8	0.01%	31.8%	DVERDVFLYR	97.8%	30.9	25	23.9	1	0	0	1311.67	49	58
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	6	6	8	0.01%	31.8%	ENDFDRLVLQYAPSA	98.9%	33.8	25	25.6	1	0	0	1737.84	294	308
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	6	6	8	0.01%	31.8%	FGVVLDEIKPSSAPELQAVR	99.7%	40	25	40	0	1	0	2155.18	66	85
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	6	6	8	0.01%	31.8%	LQDAYYIFQEMADK	99.7%	67.7	25	62.4	2	0	0	1734.80	198	211
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	6	6	8	0.01%	31.8%	NAFYIGSYQQCINEAQR	99.7%	89.7	25	89.7	1	0	0	2061.94	24	40
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	17	20	43	0.04%	26.1%	ALQQYTLEPSEKPFDLK	99.7%	46.7	25	37.6	1	1	0	2007.04	561	577
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	17	20	43	0.04%	26.1%	ATFYLNVLEQK	99.7%	74.4	25	65.1	3	0	0	1325.71	528	538
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	17	20	43	0.04%	26.1%	ELAPAVSVLQLFCSSPK	99.7%	107	25	107	5	1	0	1845.98	284	300
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	17	20	43	0.04%	26.1%	FGAQNEEMLPSILVLLK	99.7%	53.3	25	53.3	1	0	0	1902.04	498	514
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	17	20	43	0.04%	26.1%	ILHLLGQEGPK	99.7%	65.6	25	65.6	2	2	0	1204.71	455	465
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	17	20	43	0.04%	26.1%	LLLLDTVTMQVTAR	99.7%	80.8	25	75.2	2	0	0	1589.89	846	859
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	17	20	43	0.04%	26.1%	QEIFQEQLAAVPEFR	99.7%	62.7	25	56.6	2	0	0	1804.92	610	624
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	17	20	43	0.04%	26.1%	SAVLQEAR	99.5%	37.6	25	13.7	2	0	0	873.48	25	32
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	17	20	43	0.04%	26.1%	SIATLAITTLLK	99.7%	84.4	25	84.4	7	0	0	1244.78	339	350
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	17	20	43	0.04%	26.1%	SLEELPVDIILASVG	97.4%	30.2	25	23.1	1	0	0	1554.86	860	874
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	17	20	43	0.04%	26.1%	SLPYNQPGTCYTLVALPK	99.7%	72.2	25	71.3	2	0	0	2022.04	697	714
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	17	20	43	0.04%	26.1%	SPFAYCMMIR	99.7%	54.6	25	43.1	1	0	0	1275.57	225	234
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	17	20	43	0.04%	26.1%	SSPEPVALTESETEYVIR	99.7%	121	25	115	2	0	0	2006.99	632	649
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	17	20	43	0.04%	26.1%	SVPLATAPMAEQR	97.2%	29.9	25	29.1	1	0	0	1386.70	578	590
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	17	20	43	0.04%	26.1%	VFNETPINPR	99.7%	40.2	25	29.9	2	0	0	1186.62	33	42
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	17	20	43	0.04%	26.1%	VVLEHEEVR	99.7%	54.7	25	48.2	3	0	0	1109.59	480	488
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	17	20	43	0.04%	26.1%	VVVVQAISALCQK	99.7%	69.6	25	69.6	2	0	0	1414.81	377	389
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	8	9	19	0.02%	14.6%	AEITLVATKPEK	99.7%	56.5	25	52	2	0	0	1299.75	591	602
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	8	9	19	0.02%	14.6%	AIVDCIISIVEENPESK	99.7%	69.9	25	69.9	1	0	0	1915.97	416	432
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	8	9	19	0.02%	14.6%	ATFYLNVLQQR	99.7%	63.5	25	63.5	4	0	0	1352.73	528	538
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	8	9	19	0.02%	14.6%	IFNETPINPR	99.7%	50.8	25	38.8	4	0	0	1200.64	33	42
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	8	9	19	0.02%	14.6%	ITDGTMLQAIER	99.7%	44.8	25	29	1	0	0	1347.69	131	142
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	8	9	19	0.02%	14.6%	LFQSNDQTLR	99.7%	42.2	25	34.7	1	0	0	1221.62	76	85
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	8	9	19	0.02%	14.6%	SAVLQEAR	99.5%	37.6	25	13.7	2	0	0	873.48	25	32
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	8	9	19	0.02%	14.6%	SIATLAITTLLK	99.7%	84.4	25	84.4	7	0	0	1244.78	339	350
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	8	9	19	0.02%	14.6%	SIPLAMAPVFEQK	99.7%	65.4	25	56.7	2	0	0	1430.77	578	590
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	8	9	19	0.02%	14.6%	VVLENEAVR	99.7%	58.9	25	51.9	4	0	0	1028.57	480	488
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	8	9	19	0.02%	14.6%	VVVVQAISALCQK	99.7%	69.6	25	69.6	2	0	0	1414.81	377	389
COBW domain-containing protein 1	CBWD1	CBWD1_HUMAN	44.1	99.8%	2	2	3	0.00%	6.3%	IPVTIITGYLGAGK	99.7%	71.8	25	71.8	2	0	0	1402.83	42	55
COBW domain-containing protein 1	CBWD1	CBWD1_HUMAN	44.1	99.8%	2	2	3	0.00%	6.3%	TDLVPEEDVKK	96.0%	28.5	25	20.9	1	0	0	1272.67	205	215
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	5	5	9	0.01%	38.6%	AVLFCLSEDKK	99.7%	53	25	53	2	0	0	1309.68	35	45
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	5	5	9	0.01%	38.6%	EILVGDVGQTVDDPYATFVK	99.7%	51.8	25	51.8	2	0	0	2166.10	54	73
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	5	5	9	0.01%	38.6%	LGGSAVISLEGKPL	99.7%	70.5	25	64.6	2	0	0	1340.78	153	166
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	5	5	9	0.01%	38.6%	VFNDMKVR	95.9%	28.4	25	23.4	1	0	0	1024.52	14	21
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	5	5	9	0.01%	38.6%	YALYDATYETK	99.7%	61.8	25	54.7	2	0	0	1337.63	82	92
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	7	7	12	0.01%	6.8%	EDVWLPLMSYR	98.4%	32.2	25	32.2	1	0	0	1408.69	1035	1045
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	7	7	12	0.01%	6.8%	FALTFGLDQLK	99.7%	60.7	25	0	3	0	0	1252.69	955	965
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	7	7	12	0.01%	6.8%	HTDTDVLEACSK	99.7%	45.4	25	44	2	0	0	1375.62	623	634
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	7	7	12	0.01%	6.8%	ITELFAVALPQLLAK	98.9%	33.9	25	33.9	1	0	0	1626.98	563	577
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	7	7	12	0.01%	6.8%	SQLIDELADKFNR	99.7%	56.7	25	56.7	1	0	0	1548.80	655	667
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	7	7	12	0.01%	6.8%	SSFCEFIGVLVR	99.7%	71.2	25	68.6	2	0	0	1413.72	173	184
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	7	7	12	0.01%	6.8%	YYNDYGDIIK	99.7%	49.1	25	43.8	2	0	0	1263.59	892	901
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	11	12	19	0.02%	24.4%	ARVEENFLK	99.7%	40.1	25	24.2	2	0	0	1105.60	411	419
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	11	12	19	0.02%	24.4%	ELLESNFTLVGDDGTNK	99.7%	105	25	102	2	0	0	1851.90	173	189

Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	11	12	19	0.02%	24.4%	ELLESNFTLVGDDGTNKEATSTGK	99.7%	44.1	25	44.1	0	2	0	2526.22	173	196
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	11	12	19	0.02%	24.4%	EMQDLSEFCSDKPK	99.7%	43.5	25	42.9	1	0	0	1713.75	275	288
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	11	12	19	0.02%	24.4%	IMNEEDPEKQR	99.7%	55.2	25	49.9	2	1	0	1388.65	444	454
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	11	12	19	0.02%	24.4%	IMQEEGQPLK	99.4%	36.9	25	22.9	1	0	0	1172.60	342	351
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	11	12	19	0.02%	24.4%	MMRPVSDQVQIK	99.7%	36.1	25	27.5	0	1	0	1463.73	237	248
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	11	12	19	0.02%	24.4%	RQDLLNVLAR	99.7%	46.3	25	35.6	2	0	0	1197.71	227	236
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	11	12	19	0.02%	24.4%	TLLFTFNVPGSGNTYPK	99.7%	42.2	25	42	2	0	0	1855.96	358	374
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	11	12	19	0.02%	24.4%	VCCEGMLIQLR	99.7%	69.1	25	62.6	2	0	0	1378.66	213	223
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	11	12	19	0.02%	24.4%	VEENFLK	98.0%	31.2	25	11	1	0	0	878.46	413	419
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	4	4	8	0.01%	15.4%	LSENVIDR	99.7%	54.2	25	47.2	2	0	0	945.50	28	35
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	4	4	8	0.01%	15.4%	VAEELALEQAK	99.7%	95.1	25	82.1	2	0	0	1200.65	66	76
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	4	4	8	0.01%	15.4%	YSGAYGASVSDEELK	99.7%	110	25	110	2	0	0	1575.72	49	63
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	4	4	8	0.01%	15.4%	YSGAYGASVSDEELKR	99.7%	89.4	25	89.4	2	0	0	1731.82	49	64
Coilin	COIL	COIL_HUMAN	62.6	99.8%	2	2	3	0.00%	3.1%	MAASETVR	95.2%	27.8	25	8.26	1	0	0	864.42	1	8
Coilin	COIL	COIL_HUMAN	62.6	99.8%	2	2	3	0.00%	3.1%	VVTDLISLIR	99.7%	65.8	25	58	2	0	0	1128.70	37	46
COMM domain-containing protein 3	COMMD3	COMD3_HUMAN	22.2	100.0%	3	4	6	0.01%	17.9%	NSLEILLGSIGR	99.7%	57.3	25	49.8	1	0	0	1271.73	109	120
COMM domain-containing protein 3	COMMD3	COMD3_HUMAN	22.2	100.0%	3	4	6	0.01%	17.9%	SFDSNAFTLLLR	99.7%	84.9	25	74.7	2	0	0	1383.73	19	30
COMM domain-containing protein 3	COMMD3	COMD3_HUMAN	22.2	100.0%	3	4	6	0.01%	17.9%	SLPHITDVSWR	99.7%	40.5	25	37.8	2	1	0	1310.69	121	131
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	C1QBP_HUMAN	31.4	100.0%	4	7	13	0.01%	22.0%	AFVDFLSDEIKEER	99.7%	79.9	25	76.4	2	2	0	1697.84	81	94
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	C1QBP_HUMAN	31.4	100.0%	4	7	13	0.01%	22.0%	EVSFQSTGESEWK	99.7%	91.5	25	82.2	2	0	0	1513.68	208	220
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	C1QBP_HUMAN	31.4	100.0%	4	7	13	0.01%	22.0%	MSGGWELELNGTEAK	99.7%	103	25	98.1	4	0	0	1621.75	105	119
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	C1QBP_HUMAN	31.4	100.0%	4	7	13	0.01%	22.0%	VEEQEPELTSTPNFVVEVIK	99.7%	84.3	25	84.3	2	1	0	2287.17	155	174
Complex I assembly factor TIMMDC1, mitochondrial	TIMMDC1	TIDC1_HUMAN	32.2	99.8%	2	2	3	0.00%	8.8%	FDAVQSAHR	99.7%	41.1	25	35.9	2	0	0	1030.51	117	125
Complex I assembly factor TIMMDC1, mitochondrial	TIMMDC1	TIDC1_HUMAN	32.2	99.8%	2	2	3	0.00%	8.8%	LPYVPEPYYPESGWDR	99.7%	52.7	25	52.7	1	0	0	1967.92	42	57
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	10	10	21	0.02%	8.8%	DLAYCVSQLPLTER	99.7%	58	25	58	2	0	0	1664.83	1225	1238
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	10	10	21	0.02%	8.8%	EAITHLLGVALTR	99.7%	62.1	25	62.1	2	0	0	1393.82	221	233
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	10	10	21	0.02%	8.8%	EAVLNAYR	99.7%	51.8	25	39.3	4	0	0	935.49	691	698
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	10	10	21	0.02%	8.8%	GNAIYNLLPDIISR	99.4%	36.4	25	32.7	2	0	0	1558.86	1160	1173
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	10	10	21	0.02%	8.8%	LSDADLAGPLQK	99.7%	46.5	25	35.3	2	0	0	1227.66	441	452
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	10	10	21	0.02%	8.8%	QTLAAFVPLLLK	99.7%	60	25	54.8	4	0	0	1313.82	1009	1020
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	10	10	21	0.02%	8.8%	SGGVNQYVVQEVLSIK	99.7%	66.1	25	64.4	2	0	0	1719.93	20	35
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	10	10	21	0.02%	8.8%	SIVGEIVR	99.0%	34.4	25	14.4	1	0	0	872.52	273	280
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	10	10	21	0.02%	8.8%	VLQLFTR	99.7%	40.2	25	13.6	1	0	0	876.53	384	390
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	10	10	21	0.02%	8.8%	YQPLASTASDNDFVTPEPR	99.7%	75.1	25	75.1	1	0	0	2107.99	1325	1343
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	5	5	9	0.01%	6.9%	APLQQCAEDR	99.7%	51.8	25	48.1	2	0	0	1187.55	304	313
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	5	5	9	0.01%	6.9%	LLASPSSR	99.5%	37.9	25	28.1	1	0	0	830.47	84	91
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	5	5	9	0.01%	6.9%	VAAGTLDASTK	99.7%	47.5	25	47.5	2	0	0	1033.55	153	163
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	5	5	9	0.01%	6.9%	VDAVHADVYR	99.7%	42.9	25	31.9	2	0	0	1144.57	169	178
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	5	5	9	0.01%	6.9%	VFDLQFSTDSPR	99.7%	94	25	92.6	2	0	0	1411.69	72	83
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	11	11	24	0.02%	11.5%	APIVTVGVNNDPADVR	99.7%	67	25	63.8	2	0	0	1636.87	471	486
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	11	11	24	0.02%	11.5%	ASELKEEIK	97.8%	30.9	25	12.9	2	0	0	1046.57	518	526
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	11	11	24	0.02%	11.5%	CLILCYELLK	99.7%	39.9	25	35.3	1	0	0	1324.70	560	569
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	11	11	24	0.02%	11.5%	EALENCITLQDFNR	99.7%	80.6	25	80.6	1	0	0	1722.81	504	517
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	11	11	24	0.02%	11.5%	GDFSYIGNLMTK	99.7%	56.6	25	56.6	2	0	0	1345.65	387	398
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	11	11	24	0.02%	11.5%	IQAVLALSR	99.7%	49.3	25	40	2	0	0	970.60	160	168
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	11	11	24	0.02%	11.5%	KLAYQVLAEK	99.3%	36.1	25	23.1	1	0	0	1162.68	226	235
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	11	11	24	0.02%	11.5%	LAYQVLAEK	98.1%	31.5	25	25	1	0	0	1034.59	227	235
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	11	11	24	0.02%	11.5%	LLSDFLDSEVSELR	99.7%	94.8	25	88.2	4	0	0	1622.83	695	708
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	11	11	24	0.02%	11.5%	LMFSGLLVSSR	99.7%	77.8	25	73.4	4	0	0	1209.67	718	728
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	11	11	24	0.02%	11.5%	TQIVTEIISEIR	99.7%	94.2	25	87.2	4	0	0	1401.79	459	470
Condensin-2 complex subunit D3	NCAPD3	CNDD3_HUMAN	168.9	100.0%	3	3	6	0.01%	2.3%	FLVQEIMFDR	99.7%	41.9	25	41.9	2	0	0	1297.66	443	452

Condensin-2 complex subunit D3	NCAPD3	CNDD3_HUMAN	168.9	100.0%	3	3	6	0.01%	2.3%	SALQVLVSILK	99.7%	52.4	25	49.8	2	0	0	1170.75	560	570
Condensin-2 complex subunit D3	NCAPD3	CNDD3_HUMAN	168.9	100.0%	3	3	6	0.01%	2.3%	TFAAQSLVQLLSK	99.7%	74.5	25	71.1	2	0	0	1405.81	372	384
Condensin-2 complex subunit G2	NCAPG2	CNDG2_HUMAN	131.0	100.0%	3	3	4	0.00%	2.9%	GFSEAAAPR	99.7%	43.2	25	32.7	2	0	0	905.45	812	820
Condensin-2 complex subunit G2	NCAPG2	CNDG2_HUMAN	131.0	100.0%	3	3	4	0.00%	2.9%	ILSFIQDQEEDYLK	99.6%	38.6	25	37.5	1	0	0	1740.87	858	871
Condensin-2 complex subunit G2	NCAPG2	CNDG2_HUMAN	131.0	100.0%	3	3	4	0.00%	2.9%	LETDSRPVSR	96.8%	29.4	25	22	1	0	0	1159.61	507	516
Conserved oligomeric Golgi complex subunit 1	COG1	COG1_HUMAN	109.0	100.0%	4	4	6	0.01%	4.6%	ALQLLYDLR	99.7%	65.5	25	58.6	2	0	0	1104.64	806	814
Conserved oligomeric Golgi complex subunit 1	COG1	COG1_HUMAN	109.0	100.0%	4	4	6	0.01%	4.6%	AQICSLVELLATTLK	97.4%	30.3	25	30.3	1	0	0	1659.94	253	267
Conserved oligomeric Golgi complex subunit 1	COG1	COG1_HUMAN	109.0	100.0%	4	4	6	0.01%	4.6%	AQQPQQPSQEK	94.6%	27.4	25	27.3	1	0	0	1268.62	103	113
Conserved oligomeric Golgi complex subunit 1	COG1	COG1_HUMAN	109.0	100.0%	4	4	6	0.01%	4.6%	QALTDFLLAR	99.7%	51.5	25	48.4	2	0	0	1147.65	225	234
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	9	9	15	0.02%	10.4%	AEGSSTASSGSQLAEGK	99.7%	73.8	25	73.8	2	0	0	1566.72	503	519
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	9	9	15	0.02%	10.4%	EAALEAAVLNKEE	96.8%	29.4	25	19.6	1	0	0	1386.71	1106	1118
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	9	9	15	0.02%	10.4%	GVISTPVIR	99.6%	38.5	25	28.1	2	0	0	941.58	987	995
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	9	9	15	0.02%	10.4%	GVQGFQDYIEK	99.7%	56.5	25	52.8	1	0	0	1283.63	2	12
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	9	9	15	0.02%	10.4%	LYEPDQLQELK	99.7%	44.1	25	35.3	2	0	0	1375.71	748	758
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	9	9	15	0.02%	10.4%	NIQDTSDLDAIAK	99.7%	71.2	25	64.7	2	0	0	1403.70	292	304
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	9	9	15	0.02%	10.4%	QYVYGVLFSLAESR	99.7%	68.3	25	63.6	2	0	0	1631.84	607	620
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	9	9	15	0.02%	10.4%	SPQTPELVEALAFR	99.7%	74.7	25	74.7	2	0	0	1557.83	652	665
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	9	9	15	0.02%	10.4%	SQGGVQPIPSQGGK	99.6%	38.3	25	38.3	1	0	0	1339.70	933	946
Coordinator of PRMT5 and differentiation stimulator	COPRS	COPRS_HUMAN	20.1	99.8%	2	2	3	0.00%	13.6%	GTQSIPNDSPAR	99.6%	37.9	25	37.4	1	0	0	1242.61	58	69
Coordinator of PRMT5 and differentiation stimulator	COPRS	COPRS_HUMAN	20.1	99.8%	2	2	3	0.00%	13.6%	MVFETGQFDDAED	99.6%	37.9	25	37.9	2	0	0	1503.59	172	184
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	5	6	8	0.01%	11.4%	AESTPEIAEQR	99.2%	35.1	25	29.6	1	0	0	1230.60	225	235
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	5	6	8	0.01%	11.4%	DSQTQAILTK	96.0%	28.5	25	11.8	1	0	0	1104.59	239	248
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	5	6	8	0.01%	11.4%	EGSQGELTPANSQSR	99.7%	57	25	52	3	0	0	1560.72	472	486
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	5	6	8	0.01%	11.4%	LQFIADHCPTLR	96.7%	23.8	25	17.1	0	1	0	1470.75	60	71
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	5	6	8	0.01%	11.4%	MALSFVQR	99.4%	36.8	25	32.1	2	0	0	967.50	77	84
COP9 signalosome complex subunit 4	COPS4	CSN4_HUMAN	46.3	100.0%	3	4	4	0.00%	8.4%	ATTADGSSILDR	99.7%	55.9	25	45	1	0	0	1206.60	291	302
COP9 signalosome complex subunit 4	COPS4	CSN4_HUMAN	46.3	100.0%	3	4	4	0.00%	8.4%	AVIEHNLLSASK	99.7%	49.9	25	48.8	1	0	0	1281.72	303	314
COP9 signalosome complex subunit 4	COPS4	CSN4_HUMAN	46.3	100.0%	3	4	4	0.00%	8.4%	IASQMITEGR	99.7%	69.9	25	60	2	0	0	1105.57	338	347
COP9 signalosome complex subunit 7a	COPS7A	CSN7A_HUMAN	30.3	99.8%	2	2	2	0.00%	8.4%	LEVDYSIGR	99.7%	49.8	25	36.8	1	0	0	1051.54	152	160
COP9 signalosome complex subunit 7a	COPS7A	CSN7A_HUMAN	30.3	99.8%	2	2	2	0.00%	8.4%	VTGQNQEQFLLLAK	99.7%	40	25	30.4	1	0	0	1588.87	7	20
COUP transcription factor 2	NR2F2	COT2_HUMAN	45.6	99.7%	2	2	2	0.00%	5.6%	SQYPNQPTR	94.9%	27.6	25	23	1	0	0	1090.53	351	359
COUP transcription factor 2	NR2F2	COT2_HUMAN	45.6	99.7%	2	2	2	0.00%	5.6%	TVSSSVIEQLFFVR	99.7%	57.3	25	53.6	1	0	0	1611.87	372	385
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	5	5	9	0.01%	16.8%	FCTGLTQIETLFK	99.7%	79.6	25	72.8	2	0	0	1557.80	253	265
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	5	5	9	0.01%	16.8%	FSEVLKR	99.7%	39.5	25	19.6	2	0	0	878.51	308	314
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	5	5	9	0.01%	16.8%	LAVEALSSLDGDLAGR	99.7%	100	25	100	2	0	0	1586.84	157	172
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	5	5	9	0.01%	16.8%	LGFSEVELVQMVVDGVK	99.7%	63.5	25	63.5	1	0	0	1864.97	342	358
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	5	5	9	0.01%	16.8%	VLTPELYAELR	99.7%	50.8	25	41.2	2	0	0	1303.73	33	43
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	99.8%	2	2	2	0.00%	3.0%	FAELETILGDIDR	99.7%	56.6	25	49.2	1	0	0	1491.77	646	658
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	99.8%	2	2	2	0.00%	3.0%	LVESDAEAEAVR	99.7%	66.7	25	61.9	1	0	0	1288.64	500	511
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	5	5	8	0.01%	18.0%	DVATVAFCDAQSTQEIHEK	99.7%	34.4	25	31.7	0	1	0	2148.99	47	65
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	5	5	8	0.01%	18.0%	GAALDVHESEPFSFSQGPLK	99.7%	38.2	25	38.2	0	1	0	2116.03	286	305
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	5	5	8	0.01%	18.0%	IGSGFDNIDIK	99.7%	70.6	25	50.9	2	0	0	1178.61	98	108
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	5	5	8	0.01%	18.0%	IRGETLGIIGLGR	99.7%	36.2	25	35.4	0	2	0	1354.82	172	184
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	5	5	8	0.01%	18.0%	VGQAVALR	99.7%	58.6	25	43	2	0	0	813.49	185	192
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	5	5	8	0.01%	18.0%	VQSVEQIR	99.7%	39.5	25	22.9	2	0	0	958.53	156	163
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	4	4	8	0.01%	11.7%	GAALDVHESEPFSFAQGPLK	99.7%	56	25	54.8	0	2	0	2100.04	292	311
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	4	4	8	0.01%	11.7%	IGSGYDNVDIK	99.7%	46.2	25	32.5	2	0	0	1180.58	104	114
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	4	4	8	0.01%	11.7%	IRGETLGLIGFGR	99.7%	60	25	60	2	0	0	1388.80	178	190
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	4	4	8	0.01%	11.7%	VQSVEQIR	99.7%	39.5	25	22.9	2	0	0	958.53	162	169
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	47	0.05%	39.8%	ALEHSALAINHK	99.7%	55	25	50.8	2	2	0	1303.71	320	331
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	47	0.05%	39.8%	CSNPLDTSVK	99.7%	40.1	25	35.9	2	0	0	1120.53	218	227

CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	47	0.05%	39.8%	ENFCNIHVSLVPQPSSTGEQK	98.7%	27.2	25	27.2	0	2	0	2371.13	173	193
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	47	0.05%	39.8%	FEVNPVWK	95.9%	28.5	25	10.5	1	0	0	1018.54	482	489
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	47	0.05%	39.8%	FSDSYASVIK	99.7%	70.9	25	45.4	2	0	0	1116.56	310	319
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	47	0.05%	39.8%	FVGQDVEGER	99.7%	71.1	25	55.6	2	0	0	1135.54	499	508
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	47	0.05%	39.8%	GIIASSVGTILK	99.7%	85	25	78.9	2	0	0	1158.71	17	28
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	47	0.05%	39.8%	GLGLSPDLVVCR	99.7%	50.2	25	46.4	2	0	0	1285.69	206	217
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	47	0.05%	39.8%	IQAIAWAR	99.7%	57.2	25	42	2	0	0	928.54	382	389
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	47	0.05%	39.8%	IYQYVINK	99.7%	43.4	25	32.4	2	0	0	1040.58	93	100
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	47	0.05%	39.8%	KLYGDADYLEER	99.7%	74.6	25	70.1	2	2	0	1471.71	466	477
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	47	0.05%	39.8%	LCSAHGVLVPGGFGVR	99.7%	65.6	25	61.5	1	2	0	1625.86	361	376
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	47	0.05%	39.8%	LLETCSIALVGK	99.7%	65.2	25	59.7	2	0	0	1303.73	295	306
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	47	0.05%	39.8%	LYGDADYLEER	99.7%	69.5	25	62	2	0	0	1343.61	467	477
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	47	0.05%	39.8%	RLDLPIER	99.7%	45.8	25	29.5	2	0	0	1011.59	269	276
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	47	0.05%	39.8%	SCGLHVTSIK	99.7%	46.1	25	37.6	2	0	0	1101.57	29	38
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	47	0.05%	39.8%	TVQVVPHITDAIQEWVMR	99.7%	62.1	25	62.1	0	4	0	2122.11	110	127
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	47	0.05%	39.8%	VPLLLEEQGVVDYFLR	99.7%	91	25	91	2	1	0	1890.04	253	268
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	47	0.05%	39.8%	YIDSADLEPITSQEEPVR	99.7%	92.4	25	82.3	2	0	0	2062.00	336	353
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	47	0.05%	39.8%	YILVTGGVISGIGK	99.7%	129	25	129	2	0	0	1376.82	3	16
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	4	4	8	0.01%	11.9%	ALEHSALAINHK	99.7%	55	25	50.8	2	2	0	1303.71	320	331
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	4	4	8	0.01%	11.9%	GIIASSIGTILK	99.7%	74.8	25	56.8	1	0	0	1172.73	17	28
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	4	4	8	0.01%	11.9%	GLGLSPDLIVCR	99.7%	55.8	25	50.1	3	0	0	1299.71	206	217
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	4	4	8	0.01%	11.9%	LQAISWAR	99.7%	54.7	25	37.8	2	0	0	944.53	382	389
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	4	4	8	0.01%	11.9%	VPVLLEEQSIVK	99.7%	63.8	25	63.8	2	0	0	1353.80	253	264
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	4	4	8	0.01%	11.9%	YILVTGGVISGIGK	99.7%	129	25	129	2	0	0	1376.82	3	16
Cullin-1	CUL1	CUL1_HUMAN	89.7	99.8%	2	2	3	0.00%	2.7%	LLIQAAIVR	99.7%	62.6	25	51.1	1	0	0	996.66	709	717
Cullin-1	CUL1	CUL1_HUMAN	89.7	99.8%	2	2	3	0.00%	2.7%	QIGLDQIWDDLR	99.7%	68	25	60.4	2	0	0	1471.75	14	25
Cullin-4B	CUL4B	CUL4B_HUMAN	104.0	100.0%	3	3	4	0.00%	3.4%	ETVEEQASTTER	99.7%	72.6	25	72.6	1	0	0	1379.63	830	841
Cullin-4B	CUL4B	CUL4B_HUMAN	104.0	100.0%	3	3	4	0.00%	3.4%	SIFLFLDR	99.0%	34.3	25	31.1	1	0	0	1010.57	305	312
Cullin-4B	CUL4B	CUL4B_HUMAN	104.0	100.0%	3	3	4	0.00%	3.4%	TIDGILLLIER	99.7%	66.9	25	60	2	0	0	1255.76	346	356
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	AADIDQEVK	99.7%	52.9	25	37.2	2	0	0	988.49	578	586
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	AADIDQEVKER	99.7%	67.8	25	54.5	4	2	0	1273.64	578	588
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	ADVFHAYLSLLK	99.7%	68.7	25	64.5	4	2	0	1376.76	392	403
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	ALTLIAGSPLK	99.7%	81.9	25	81.9	5	0	0	1083.68	631	641
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	AVAALLTIPEAEK	99.7%	73.1	25	53.6	2	0	0	1325.77	1179	1191
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	CLGPLVSK	99.3%	35.8	25.2	15.9	2	0	0	873.49	71	78
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	DISSIGLK	94.7%	27.4	25	15.2	1	0	0	832.48	104	111
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	DLLDTVLPHLYNETK	99.7%	49	25	49	3	0	0	1770.93	1043	1057
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	DSIKLDDDSER	98.4%	32.2	25	25.2	1	0	0	1292.60	37	47
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	DSSSTNLESMDTS	99.7%	44	25	44	1	0	0	1389.53	1218	1230
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	EGPAVVGQFIQDVK	99.7%	65.8	25	59.7	5	0	0	1486.79	813	826
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	EYCIQAFESFVR	99.7%	66.3	25	63.7	2	0	0	1548.72	273	284
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	FMATNDLMTELQK	99.7%	88.8	25	72.1	6	0	0	1557.73	24	36
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	FTISDHPQPIDPLLK	99.7%	61.8	25	50.6	2	4	0	1720.93	991	1005
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	GYLISGSSYAR	99.7%	61.4	25	48.9	4	0	0	1173.59	972	982
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	HTVDDGLDIR	99.7%	49.3	25	36	2	0	0	1140.56	1073	1082
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	HTVDDGLDIRK	99.7%	53.7	25	46.5	2	1	0	1268.66	1073	1083
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	IGEYLEK	99.7%	39.1	25	27.4	2	0	0	851.45	249	255
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	ISGSILNELIGLVR	99.7%	96.8	25	83.7	5	0	0	1483.88	730	743
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	ITSEALLVTQQLVK	99.7%	76.2	25	68.9	4	2	0	1542.91	535	548
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	LGTLSALDILIK	99.7%	84.6	25	73.2	4	0	0	1256.78	668	679
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	LSTLCPSAVLQR	99.7%	47.3	25	41.2	2	0	0	1344.73	1130	1141

Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	LTLIDPETLLPR	99.7%	69.5	25	69.5	8	0	0	1380.81	958	969
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	MLTFLMLVR	99.7%	76	25	65.6	11	0	0	1123.64	1121	1129
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	MLTGPVYSQSTALTHK	99.7%	100	25	94.7	4	4	0	1733.89	778	793
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	MTSSDKDFR	99.4%	36.5	25	21.2	2	0	0	1086.49	15	23
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	NCIGDFLK	98.8%	33.4	25	21	1	0	0	966.47	1006	1013
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	NVVAECLGK	99.6%	38.4	25	37.2	3	0	0	989.51	949	957
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	QSYYSIAK	96.3%	28.8	25	17.2	1	0	0	959.48	794	801
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	SVILEAFSSPSEEVK	99.7%	96.2	25	90.3	5	0	0	1621.83	859	873
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	TLEDPDLNVR	99.7%	75.6	25	61.7	2	0	0	1171.60	1014	1023
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	TVIGELPPASSGSALAANVCK	99.7%	122	25	115	2	1	0	2042.06	112	132
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	TVSPALISR	99.7%	42.9	25	22.3	2	0	0	943.56	374	382
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	TYIQCIAAISR	99.7%	98.1	25	89.4	3	0	0	1295.68	233	243
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	35	47	130	0.14%	31.9%	VIRPLDQPSSFDATPYIK	99.7%	51.4	25	51.4	2	3	0	2047.09	549	566
Cullin-associated NEDD8-dissociated protein 2	CAND2	CAND2_HUMAN	135.3	99.8%	2	2	3	0.00%	2.7%	AVLLEALGSPSEDVR	99.7%	57.8	25	57.8	2	0	0	1555.83	864	878
Cullin-associated NEDD8-dissociated protein 2	CAND2	CAND2_HUMAN	135.3	99.8%	2	2	3	0.00%	2.7%	MTSSDKDFR	99.4%	36.5	25	21.2	2	0	0	1086.49	15	23
Cullin-associated NEDD8-dissociated protein 2	CAND2	CAND2_HUMAN	135.3	99.8%	2	2	3	0.00%	2.7%	VPTSPTAIR	99.7%	51.8	25	31.8	1	0	0	941.54	227	235
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	55	0.06%	53.5%	ALGTPNNEVWPEVESLQDYK	99.7%	69.4	25	69.4	2	0	0	2289.10	219	238
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	55	0.06%	53.5%	DLKPQNLLIDDKGTIK	99.7%	72.5	25	72.5	2	2	0	1811.03	128	143
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	55	0.06%	53.5%	IGEGTYGVVYK	99.7%	95.8	25	56.2	4	0	0	1185.62	10	20
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	55	0.06%	53.5%	IRLESEEEGVPSTAIR	99.7%	97.1	25	96.9	3	0	0	1785.93	35	50
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	55	0.06%	53.5%	LADFGLAR	99.7%	50.6	25	0	6	0	0	862.48	144	151
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	55	0.06%	53.5%	LESEEEGVPSTAIR	99.7%	73.3	25	60.7	2	0	0	1516.75	37	50
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	55	0.06%	53.5%	MALNHPYFNDLDNQIK	99.7%	61.8	25	58.3	4	4	0	1948.92	280	295
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	55	0.06%	53.5%	MALNHPYFNDLDNQIKK	99.3%	30.1	25	30.1	0	1	0	2077.02	280	296
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	55	0.06%	53.5%	MLIYDPAK	98.7%	33.2	25	21.3	2	0	0	950.50	267	274
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	55	0.06%	53.5%	MLIYDPAKR	99.7%	46.5	25	41.5	4	0	0	1122.60	267	275
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	55	0.06%	53.5%	NLDENGLDLLSK	99.7%	82	25	62.2	3	0	0	1330.69	255	266
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	55	0.06%	53.5%	SPEVLLGSAR	99.7%	84.9	25	77.9	7	0	0	1028.57	171	180
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	55	0.06%	53.5%	VYTHEVVTLWYR	99.7%	71.7	25	70.3	2	2	0	1565.81	159	170
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	55	0.06%	53.5%	WKPGSLASHVK	99.7%	41.7	25	40.9	0	2	0	1209.67	244	254
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	15	22	55	0.06%	53.5%	YLDSIPPGQYMDSSLVK	99.1%	35	25	27.4	3	0	0	1912.94	90	106
Cyclin-dependent kinase 11B	CDK11B	CD11B_HUMAN	92.7	100.0%	3	3	5	0.01%	3.5%	APELLLGAK	99.6%	38.9	25	30.3	1	0	0	911.56	605	613
Cyclin-dependent kinase 11B	CDK11B	CD11B_HUMAN	92.7	100.0%	3	3	5	0.01%	3.5%	IEEGTYGVVYR	99.7%	48	25	44.7	2	0	0	1285.64	444	454
Cyclin-dependent kinase 11B	CDK11B	CD11B_HUMAN	92.7	100.0%	3	3	5	0.01%	3.5%	TLMIQLLR	99.7%	47	25	34.9	2	0	0	987.60	541	548
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	6	9	17	0.02%	33.6%	ALFPGDSEIDQLFR	99.7%	60	25	55.5	2	0	0	1607.81	201	214
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	6	9	17	0.02%	33.6%	APEILLGCK	99.7%	56.9	25	54.8	2	0	0	1000.55	170	178
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	6	9	17	0.02%	33.6%	DLKPQNLLINTEGAIK	99.7%	81.2	25	81.2	2	2	0	1767.00	127	142
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	6	9	17	0.02%	33.6%	FMDASALTGIPLPLIK	99.7%	76.7	25	76.7	4	0	0	1686.95	90	105
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	6	9	17	0.02%	33.6%	IGEGTYGVVYK	99.7%	95.8	25	56.2	4	0	0	1185.62	10	20
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	6	9	17	0.02%	33.6%	IRLDTETEGVPSTAIR	99.7%	70.2	25	63.6	2	1	0	1757.94	35	50
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	6	9	17	0.02%	33.6%	LADFGLAR	99.7%	50.6	25	0	6	0	0	862.48	143	150
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	6	9	17	0.02%	33.6%	LTGEVVALKK	99.7%	48.2	25	40.8	2	0	0	1057.66	25	34
Cyclin-dependent kinase 5	CDK5	CDK5_HUMAN	33.3	100.0%	4	4	6	0.01%	15.8%	DLKPQNLLINR	98.7%	33	25	33	1	0	0	1323.77	126	136
Cyclin-dependent kinase 5	CDK5	CDK5_HUMAN	33.3	100.0%	4	4	6	0.01%	15.8%	DLLQNLLK	98.7%	33.2	25	22.5	1	0	0	956.58	261	268
Cyclin-dependent kinase 5	CDK5	CDK5_HUMAN	33.3	100.0%	4	4	6	0.01%	15.8%	IGEGTYGTVFK	99.7%	60	25	53.3	2	0	0	1171.60	10	20
Cyclin-dependent kinase 5	CDK5	CDK5_HUMAN	33.3	100.0%	4	4	6	0.01%	15.8%	LADFGLAR	99.7%	50.6	25	0	6	0	0	862.48	142	149
Cyclin-dependent kinase 5	CDK5	CDK5_HUMAN	33.3	100.0%	4	4	6	0.01%	15.8%	SFLFQLLK	99.4%	36.5	25	14.6	2	0	0	995.59	105	112
Cyclin-dependent kinase 9	CDK9	CDK9_HUMAN	42.8	99.9%	2	2	4	0.00%	7.8%	LADFGLAR	99.7%	50.6	25	0	6	0	0	862.48	165	172
Cyclin-dependent kinase 9	CDK9	CDK9_HUMAN	42.8	99.9%	2	2	4	0.00%	7.8%	LLVLDPAQR	99.7%	42	25	33.4	2	0	0	1024.62	295	303
Cyclin-dependent kinase 9	CDK9	CDK9_HUMAN	42.8	99.9%	2	2	4	0.00%	7.8%	NPATTNQTEFER	99.7%	66.1	25	65.3	2	0	0	1407.65	359	370
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	7	7	12	0.01%	12.3%	AAQELQEGQR	99.7%	56.4	25	43.8	2	0	0	1129.56	360	369

Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	7	7	12	0.01%	12.3%	CVVILPDSVR	96.5%	29.1	25	22.5	1	0	0	1157.63	370	379
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	7	7	12	0.01%	12.3%	GFLKEEDLTEK	99.7%	63.2	25	51.5	2	0	0	1308.67	395	405
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	7	7	12	0.01%	12.3%	IGDTPMVR	97.5%	30.4	25	21.3	2	0	0	904.46	84	91
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	7	7	12	0.01%	12.3%	KIGDTPMVR	99.2%	35	25	21.1	1	0	0	1032.55	83	91
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	7	7	12	0.01%	12.3%	PSETPQAEVGPTGCPHR	99.7%	66.6	25	65.1	0	2	0	1819.84	2	18
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	7	7	12	0.01%	12.3%	SNDEEAFTFAR	99.7%	82.8	25	81.2	2	0	0	1286.56	326	336
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	6	6	8	0.01%	14.2%	AIGTDEDLAHSSIR	99.7%	87.8	25	82.8	2	0	0	1484.73	394	407
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	6	6	8	0.01%	14.2%	GVGAIYIR	98.5%	32.5	25	18.2	1	0	0	848.50	264	271
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	6	6	8	0.01%	14.2%	IPLDVNDMK	99.7%	43.9	25	40.9	2	0	0	1044.54	240	248
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	6	6	8	0.01%	14.2%	QPIAEIGR	99.7%	49.3	25	39.4	1	0	0	883.50	213	220
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	6	6	8	0.01%	14.2%	QQVASLIGADPR	99.7%	47.6	25	44.3	1	0	0	1254.68	108	119
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	6	6	8	0.01%	14.2%	VRVEALQSGGGQER	99.7%	44.8	25	38.4	1	0	0	1485.78	276	289
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	8	10	17	0.02%	20.4%	ADLTEYLSTHYK	99.7%	81.2	25	78.7	2	0	0	1440.70	214	225
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	8	10	17	0.02%	20.4%	FTGSEIR	99.3%	35.8	25	25.2	1	0	0	809.42	270	276
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	8	10	17	0.02%	20.4%	IAEVDASVVR	99.7%	80.1	25	50.6	2	0	0	1058.58	433	442
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	8	10	17	0.02%	20.4%	LCTSATESEVAR	99.7%	90.9	25	83.6	2	0	0	1323.62	379	390
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	8	10	17	0.02%	20.4%	MVLAAAGGVEHQQLLDLAQK	99.7%	64.2	25	64.2	0	4	0	2092.12	229	248
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	8	10	17	0.02%	20.4%	NALVSHLDGTTPVCEDIGR	99.7%	41.3	25	41.3	0	1	0	2054.00	397	415
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	8	10	17	0.02%	20.4%	RIPLAEWESR	98.2%	31.7	25	26.8	2	0	0	1256.67	423	432
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	8	10	17	0.02%	20.4%	SGMFWLRF	99.7%	49.5	25	49.5	3	0	0	1059.51	473	480
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	46	0.05%	43.5%	ATAAPAGAPPQPQDLEFTK	99.7%	65.3	25	65.3	2	0	0	1909.97	24	42
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	46	0.05%	43.5%	AVAFQNPQTHVIENLHAAAYR	99.7%	51	25	51	0	2	0	2350.21	163	183
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	46	0.05%	43.5%	ENMAYTVECLR	99.7%	65	25	54.5	5	0	0	1401.61	117	127
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	46	0.05%	43.5%	GSNTTSHLHQAVAK	99.7%	59.2	25	50.2	2	0	0	1450.74	302	315
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	46	0.05%	43.5%	LPNGLVIASLENYSPVSR	99.7%	104	25	104	2	2	0	1929.04	43	60
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	46	0.05%	43.5%	MALIGLGVSHPVLK	99.7%	81.7	25	81.7	2	4	0	1450.85	218	231
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	46	0.05%	43.5%	NALANPLYCPDYR	99.7%	64.5	25	52.5	2	0	0	1566.74	184	196
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	46	0.05%	43.5%	QVAEQFLNMR	99.7%	82.7	25	73.7	4	0	0	1235.62	232	241
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	46	0.05%	43.5%	RWEVADLQPQLK	99.7%	71.1	25	62.7	2	2	0	1482.81	148	159
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	46	0.05%	43.5%	SMAASGNLGHTPFVDEL	99.7%	95.6	25	95.6	4	0	0	1745.82	437	453
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	46	0.05%	43.5%	TIAQGNLSNTDVQAAK	99.7%	110	25	106	4	0	0	1630.84	360	375
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	46	0.05%	43.5%	VTSEELHYFVQNHFTSAR	99.7%	50.4	25	50.4	0	2	0	2165.04	200	217
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	46	0.05%	43.5%	WEVADLQPQLK	99.7%	42.6	25	30.3	2	0	0	1326.71	149	159
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	46	0.05%	43.5%	YEDFSNLGTTHLLR	99.7%	84.9	25	84.9	2	1	0	1665.82	71	84
Cytochrome b-c1 complex subunit 8	UQCRQ	QCR8_HUMAN	9.9	100.0%	5	5	11	0.01%	47.6%	GREFGNLTR	94.6%	27.4	25	9.02	1	0	0	1049.55	2	10
Cytochrome b-c1 complex subunit 8	UQCRQ	QCR8_HUMAN	9.9	100.0%	5	5	11	0.01%	47.6%	HVISYSLSPFEQR	99.7%	60.4	25	56.6	4	0	0	1562.80	13	25
Cytochrome b-c1 complex subunit 8	UQCRQ	QCR8_HUMAN	9.9	100.0%	5	5	11	0.01%	47.6%	IRESFFR	98.7%	33.2	25	24	3	0	0	954.52	42	48
Cytochrome b-c1 complex subunit 8	UQCRQ	QCR8_HUMAN	9.9	100.0%	5	5	11	0.01%	47.6%	KNPAAYENDK	98.6%	32.9	25	32.9	2	0	0	1149.55	73	82
Cytochrome b-c1 complex subunit 8	UQCRQ	QCR8_HUMAN	9.9	100.0%	5	5	11	0.01%	47.6%	NPAAYENDK	99.0%	34.2	25	32.4	1	0	0	1021.46	74	82
Cytochrome b-c1 complex subunit 9	UQCR10	QCR9_HUMAN	7.3	99.8%	2	3	5	0.01%	38.1%	AFDQGADAIYDHINEGK	99.7%	74.4	25	74.4	2	2	0	1863.85	35	51
Cytochrome b-c1 complex subunit 9	UQCR10	QCR9_HUMAN	7.3	99.8%	2	3	5	0.01%	38.1%	LYSLLFR	98.8%	33.5	25	23.7	1	0	0	911.53	10	16
Cytochrome b-c1 complex subunit Rieske, mitochondrial	UQCRFS1	UCRI_HUMAN	29.7	100.0%	3	3	6	0.01%	16.1%	EIEQEAAVELSQLR	99.7%	59.5	25	42.9	2	0	0	1614.83	183	196
Cytochrome b-c1 complex subunit Rieske, mitochondrial	UQCRFS1	UCRI_HUMAN	29.7	100.0%	3	3	6	0.01%	16.1%	NAVTQFVSSMSASADVLALAK	99.7%	86.3	25	84.9	2	0	0	2126.08	131	151
Cytochrome b-c1 complex subunit Rieske, mitochondrial	UQCRFS1	UCRI_HUMAN	29.7	100.0%	3	3	6	0.01%	16.1%	RLEVLDSTK	99.7%	46	25	33.1	2	0	0	1060.60	93	101
Cytochrome c	CYCS	CYC_HUMAN	11.7	100.0%	2	2	3	0.00%	23.8%	TGPNLHGLFGR	96.1%	28.6	25	16.8	1	0	0	1168.62	29	39
Cytochrome c	CYCS	CYC_HUMAN	11.7	100.0%	2	2	3	0.00%	23.8%	TGQAPGYSYTAANK	99.7%	41.3	25	41.3	2	0	0	1428.68	41	54
Cytochrome c oxidase assembly protein COX11, mitochondrial	COX11	COX11_HUMAN	31.4	100.0%	2	2	4	0.00%	8.7%	IQCFCFEEQR	99.7%	39.3	25	39.3	2	0	0	1416.60	215	224
Cytochrome c oxidase assembly protein COX11, mitochondrial	COX11	COX11_HUMAN	31.4	100.0%	2	2	4	0.00%	8.7%	VDLITLSYTFFEAK	99.7%	80.7	25	76.1	2	0	0	1646.87	252	265
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	5	7	23	0.02%	18.9%	IFEMGPVFTL	99.7%	45.3	25	37.9	4	0	0	1153.60	218	227
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	5	7	23	0.02%	18.9%	ILYMTDEVNDPSLTIK	99.7%	90	25	83.4	8	0	0	1851.94	83	98
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	5	7	23	0.02%	18.9%	LLDVDNR	99.7%	54.6	25	31.4	4	0	0	844.45	135	141

Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	5	7	23	0.02%	18.9%	LLDVDNRVVLPIEAPIR	99.7%	43.2	25	33.4	0	4	0	1932.13	135	151
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	5	7	23	0.02%	18.9%	VVLPIEAPIR	99.7%	48.8	25	48.8	3	0	0	1106.69	142	151
Cytochrome c oxidase subunit 7A2, mitochondrial	COX7A2	CX7A2_HUMAN	9.4	99.8%	2	2	4	0.00%	27.7%	GGVADALLYR	99.7%	75.6	25	53.1	2	0	0	1034.56	47	56
Cytochrome c oxidase subunit 7A2, mitochondrial	COX7A2	CX7A2_HUMAN	9.4	99.8%	2	2	4	0.00%	27.7%	LFQEDDEIPLYLK	99.7%	60.3	25	48	2	0	0	1622.83	34	46
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	7	7	11	0.01%	10.3%	FVEFFGPGVAQLSIADR	99.7%	83.4	25	75.8	2	0	0	1852.96	277	293
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	7	7	11	0.01%	10.3%	GPFLLGIK	99.7%	53	25	38.8	2	0	0	844.53	786	793
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	7	7	11	0.01%	10.3%	NIEVPFKPAR	98.3%	31.9	25	17.9	1	0	0	1170.66	73	82
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	7	7	11	0.01%	10.3%	SPPFFENLTLDLQPPK	97.9%	31	25	31	1	0	0	1842.96	645	660
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	7	7	11	0.01%	10.3%	VILQDFTGVPAVVDFAAMR	99.7%	78.2	25	78.2	1	0	0	2065.08	83	101
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	7	7	11	0.01%	10.3%	VLLEAAIR	99.7%	49.6	25	43.1	2	0	0	884.56	41	48
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	7	7	11	0.01%	10.3%	YQQAGLPLIVLAGK	99.7%	79.3	25	79.3	2	0	0	1470.87	759	772
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	AATSPALFNR	99.7%	63.6	25	50	2	0	0	1047.56	3079	3088
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	AERPDVDEKR	99.7%	33.9	25	27.3	0	2	0	1214.61	3719	3728
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	ALGEYLER	99.7%	52.2	25	47.1	2	0	0	950.49	1614	1621
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	ALGHQLGR	99.7%	39.8	25	28.4	2	0	0	851.48	1918	1925
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	ANEVEQMIR	99.7%	50	25	32.2	2	0	0	1089.54	3430	3438
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	ASLACGPMVK	98.9%	33.8	25	27.5	1	0	0	1033.52	3385	3394
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	ASVVTLPVYLNFTR	99.7%	45	25	43.8	4	0	0	1579.88	4602	4615
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	CYLTMTQALEAR	99.7%	66.5	25	65.3	2	0	0	1456.69	1888	1899
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	DAATIMQPYFTSNGLVTK	99.7%	54.5	25	54.5	1	0	0	1972.97	2418	2435
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	DLFQVAFNR	99.7%	54.3	25	49.8	5	0	0	1109.57	3862	3870
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	DLPPVSGSIIWAK	99.7%	53	25	53	2	0	0	1382.77	640	652
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	DSAIQQQVANLQMK	99.7%	82.5	25	74.7	2	0	0	1573.80	1229	1242
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	DYIPVDQEELRDYVK	99.7%	52.8	25	48.3	2	0	0	1881.92	2880	2894
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	EAIVNSCVFVHQTLHQANAR	99.4%	30.8	25	30.8	0	2	0	2294.15	3141	3160
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	EALELTDTGLLSGSEER	99.7%	114	25	113	2	0	0	1819.89	1302	1318
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	EFGPVVIDYGK	98.6%	32.7	25	27.4	1	0	0	1223.63	1101	1111
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	EGLMLDSHEELYK	99.7%	42	25	30.7	1	0	0	1563.74	3040	3052
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	EHINSVSAMK	99.7%	44.8	25	41.5	1	0	0	1131.55	1499	1508
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	ESPEVLLTLDILK	99.7%	43.1	25	36	2	0	0	1469.85	293	305
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	EWTDGLFTHVLR	99.7%	55.6	25	48.8	2	0	0	1473.75	2274	2285
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	EYQTQLIQR	99.7%	45.8	25	31.3	2	0	0	1178.62	603	611
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	FNYGFEYLGVQDK	99.7%	91.8	25	91.8	2	0	0	1579.74	1866	1878
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	FQSISTEFLALMK	99.7%	71.2	25	68.5	2	0	0	1530.79	1568	1580
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	FTQDTQPHYIYSPR	99.7%	71.8	25	71.8	2	0	0	1752.83	2784	2797
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	IAFIMDESNVLDSGFLER	99.7%	75.8	25	69	2	0	0	2072.00	2990	3007
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	IFTIESTR	99.7%	56	25	38.6	2	0	0	966.53	717	724
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	IFVFEPPPGVK	99.7%	47.1	25	36.2	2	0	0	1229.69	4144	4154
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	IMFEVQDLK	99.7%	47.1	25	25.4	2	0	0	1138.58	2341	2349
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	INEWLTLVEK	99.7%	58.8	25	49.1	2	0	0	1244.69	1698	1707
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	INMLVIELK	99.7%	63.6	25	48.1	2	0	0	1088.64	1396	1404
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	IQFVGACNPPTDPGR	99.7%	99.5	25	92	2	0	0	1628.79	2706	2720
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	IQGLTVEQAEAVVR	99.7%	87.1	25	79.3	3	0	0	1512.84	3924	3937
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	ITNQVIYLNPPIEECR	99.7%	41.6	25	41.6	1	0	0	1959.00	964	979
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	KYEFGESDLR	99.7%	51.3	25	42.8	2	0	0	1243.60	4204	4213
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	LFLTMEINPK	99.7%	47.6	25	36.5	2	0	0	1205.66	4124	4133
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	LGGSPFGPAGTGK	99.7%	78.5	25	74.2	2	0	0	1145.60	1900	1912
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	LKQDGDSFR	99.7%	48	25	45	2	0	0	1065.53	682	690
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	LLNTFLER	99.7%	50.8	25	42.9	2	0	0	1005.57	4264	4271
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	LNTQEIFDDWAR	99.7%	71.6	25	63.9	2	0	0	1507.72	693	704
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	LQGEFQLR	99.7%	53	25	41.5	2	0	0	990.54	3734	3741

Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	LRDQLGTAK	99.7%	55.1	25	43	2	0	0	1001.57	568	576
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	LSCLPAFK	99.5%	37.2	25	29.3	2	0	0	935.50	3938	3945
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	LSLSNAISTALPLTQLR	99.6%	38.1	25	38.1	2	0	0	1798.04	4575	4591
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	LVEDEERR	98.3%	31.9	25	26.1	2	0	0	1045.53	2837	2844
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	LVQTPLTDR	98.4%	32.3	25	27.9	2	0	0	1042.59	1879	1887
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	MVVLSLPR	99.7%	54.3	25	54.3	4	0	0	914.55	991	998
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	NANEMFR	94.9%	27.6	25	23.5	1	0	0	881.39	577	583
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	NTISLLVAGLK	99.7%	67.6	25	51.8	2	0	0	1128.70	799	809
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	NTISLLVAGLKK	99.7%	58.8	25	58.8	1	0	0	1256.79	799	810
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	NYMSNPSYNYEIVNR	99.7%	101	25	96.4	2	0	0	1879.83	3370	3384
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	QLQNISLAAASGGAK	99.4%	36.8	25	29.8	1	0	0	1428.78	4488	4502
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	QNLDALLNQLK	99.7%	69	25	53.4	2	0	0	1269.72	1361	1371
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	QTDVLQQLSIQMANAK	99.7%	76.7	25	76.7	1	0	0	1787.93	1850	1865
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	QYASYEFVQR	99.7%	48	25	41.3	2	0	0	1290.61	1379	1388
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	SIPLDEGEDEAQR	99.7%	69.3	25	62	2	0	0	1458.67	2384	2396
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	SIPLDEGEDEAQRR	99.7%	40.1	25	40.1	1	0	0	1614.77	2384	2397
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	SLETCMYDHK	99.7%	49.2	25	49.2	1	0	0	1283.54	863	872
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	SLLQALNEVK	99.7%	70.5	25	54.2	5	0	0	1114.65	3748	3757
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	SMANPPAAVK	98.1%	31.5	25	26.5	2	0	0	1001.51	3309	3318
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	SNSLAFIK	99.7%	47.2	25	34.2	2	0	0	879.49	113	120
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	SPLVMDVLNIQGVQR	99.7%	80.2	25	76.7	4	1	0	1684.91	1585	1599
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	SSLQSQCLNEVLK	99.7%	75.2	25	64.5	2	0	0	1505.76	3706	3718
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	SVLVSAGNVK	98.5%	32.4	25	22.9	1	0	0	973.57	2095	2104
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	SVLVSAGNVKR	99.7%	44.1	25	38.2	2	0	0	1129.67	2095	2105
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	TEYLSNADER	99.7%	56.8	25	52.8	3	0	0	1197.54	3550	3559
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	TFSEILNR	99.7%	47.6	25	36.7	2	0	0	979.52	873	880
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	TFSSIPVSR	98.6%	32.9	25	28.7	3	0	0	993.54	4160	4168
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	TLINELVK	99.0%	34.2	25	11.4	2	0	0	929.57	4450	4457
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	TMTLFSALR	99.7%	54.1	25	47.6	2	0	0	1055.56	2602	2610
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	TPNGVVLAPVQLGK	99.7%	52.3	25	52.3	2	0	0	1392.82	2644	2657
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	TPVIDADKPVSSQLR	99.7%	59.7	25	57.9	2	2	0	1625.89	122	136
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	TPVSITEHPK	99.7%	62.2	25	56	2	0	0	1108.60	1688	1697
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	TSAPITCELLNK	99.7%	70.1	25	56.1	2	0	0	1346.70	1993	2004
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	TSFLDDAFRK	99.7%	51.5	25	44.8	2	0	0	1199.61	3612	3621
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	VAAPDVVVPTLDTVR	99.7%	55.7	25	55.7	2	0	0	1551.87	2562	2576
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	VDNEFDQR	99.7%	52.8	25	43.8	2	0	0	1022.45	4256	4263
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	VEPLRNELQK	98.4%	32.2	25	20.4	2	0	0	1225.69	3409	3418
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	VLLTTQGVDMISK	99.7%	106	25	100	5	0	0	1404.78	4330	4342
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	VLRPQVTAVAQQNQGEVPEPQDMK	99.7%	44.6	25	44.5	0	4	0	2662.36	483	506
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	VMSQEIQEQLHK	99.7%	48.4	25	33.9	2	0	0	1469.74	3255	3266
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	VNFLPEIITLSK	99.7%	55	25	49.7	2	0	0	1373.80	737	748
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	VPLAIVNK	99.7%	45	25	45	1	0	0	853.55	760	767
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	VPQIEVETHK	99.7%	47	25	35.2	2	0	0	1179.64	2552	2561
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	VPVNLLR	98.4%	32.3	25	23.1	4	0	0	810.52	4134	4140
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	VQYPQSQACK	99.6%	38.2	25	17	2	0	0	1208.57	625	634
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	VTDFGDKVEDPTFLNQLQSGVNR	99.7%	34.5	25	34.5	0	1	0	2579.27	229	251
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	VTFVNFTVTR	99.7%	90.3	25	83.4	2	0	0	1183.65	3696	3705
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	WTDENIDTVALK	99.7%	66.1	25	66.1	2	0	0	1404.70	2845	2856
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	89	96	188	0.20%	21.5%	YATLATVSR	99.7%	55.5	25	45.4	2	0	0	981.54	2350	2358
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	7	7	10	0.01%	18.7%	AGATSEGVLANFFNSLLSK	99.7%	91.7	25	91.7	1	0	0	1926.00	436	454
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	7	7	10	0.01%	18.7%	IGILHENFQTLK	98.3%	26.2	25	23	0	1	0	1412.79	333	344

Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	7	7	10	0.01%	18.7%	IPAVVVEK	99.7%	39.8	25	27.5	2	0	0	854.53	311	318
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	7	7	10	0.01%	18.7%	NVLLLGEDGAGK	99.7%	61.6	25	56.8	1	0	0	1185.65	69	80
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	7	7	10	0.01%	18.7%	QPPTAAGRPVDASPR	99.7%	32.7	25	32.3	0	1	0	1519.80	386	400
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	7	7	10	0.01%	18.7%	SGQKPVLDVHAELDR	99.7%	47	25	46.4	0	2	0	1663.88	487	501
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	7	7	10	0.01%	18.7%	SVSSNVASVSPIPAGSK	99.7%	81.3	25	69.6	2	0	0	1586.84	412	428
Cytoplasmic dynein 2 heavy chain 1	DYNC2H1	DYHC2_HUMAN	492.6	100.0%	4	4	7	0.01%	1.1%	FYEFSLSDLR	99.7%	65.2	25	62.7	2	0	0	1276.62	3888	3897
Cytoplasmic dynein 2 heavy chain 1	DYNC2H1	DYHC2_HUMAN	492.6	100.0%	4	4	7	0.01%	1.1%	IAEALLSDLPGFR	96.5%	29	25	27.6	1	0	0	1401.77	502	514
Cytoplasmic dynein 2 heavy chain 1	DYNC2H1	DYHC2_HUMAN	492.6	100.0%	4	4	7	0.01%	1.1%	NSLLTILDQLQR	98.4%	32.3	25	24.7	2	0	0	1413.81	1399	1410
Cytoplasmic dynein 2 heavy chain 1	DYNC2H1	DYHC2_HUMAN	492.6	100.0%	4	4	7	0.01%	1.1%	VLSFPGGSLLLAGR	99.7%	45	25	45	2	0	0	1386.81	2643	2656
Cytoplasmic dynein 2 light intermediate chain 1	DYNC2LI1	DC2L1_HUMAN	39.6	99.8%	2	2	3	0.00%	6.3%	GVINQLAFGIDK	99.2%	35.5	25	35.5	2	0	0	1274.71	232	243
Cytoplasmic dynein 2 light intermediate chain 1	DYNC2LI1	DC2L1_HUMAN	39.6	99.8%	2	2	3	0.00%	6.3%	PSETLWEIAK	99.7%	49	25	32.2	1	0	0	1173.62	2	11
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	18	21	39	0.04%	16.8%	ALNLAYSSIYGSYR	99.7%	90.9	25	77.5	2	0	0	1577.80	893	906
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	18	21	39	0.04%	16.8%	AVGPSSTQLYMVR	99.7%	61.3	25	47.5	2	0	0	1424.72	551	563
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	18	21	39	0.04%	16.8%	DFVSEAYLITLGK	99.7%	78.4	25	0	4	0	0	1455.77	151	163
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	18	21	39	0.04%	16.8%	EANHNVSAPYGR	99.1%	34.8	25	30.1	1	1	0	1314.62	827	838
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	18	21	39	0.04%	16.8%	EFFLELTMGR	99.7%	66.8	25	66.8	2	0	0	1258.61	625	634
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	18	21	39	0.04%	16.8%	FINMFAVLDELK	99.7%	71.2	25	64.5	2	0	0	1439.76	164	175
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	18	21	39	0.04%	16.8%	LCCGLSMFEVILTR	99.7%	58.4	25	58.4	1	0	0	1698.84	1086	1099
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	18	21	39	0.04%	16.8%	LGTPQQIAIAR	99.7%	64.2	25	51.8	2	0	0	1167.68	1066	1076
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	18	21	39	0.04%	16.8%	NAFVTGIAR	99.7%	46.3	25	31.5	2	0	0	948.53	50	58
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	18	21	39	0.04%	16.8%	NVIQSVLQAIR	99.7%	88.3	25	62.8	2	0	0	1240.74	505	515
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	18	21	39	0.04%	16.8%	SFLDDPIWR	99.6%	38.7	25	28.5	2	0	0	1148.57	1102	1110
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	18	21	39	0.04%	16.8%	SLLQGTILQYVK	99.7%	49	25	49	2	0	0	1362.80	939	950
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	18	21	39	0.04%	16.8%	SSLEGPTILDIEK	99.7%	72.9	25	59.7	2	0	0	1401.75	582	594
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	18	21	39	0.04%	16.8%	TVEVLEPEVTK	99.7%	43.7	25	35.6	2	0	0	1243.68	111	121
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	18	21	39	0.04%	16.8%	TVLPFSQEFQR	99.7%	51.1	25	45.9	1	0	0	1351.70	867	877
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	18	21	39	0.04%	16.8%	YAPLHLVPLIER	99.7%	52.1	25	52.1	2	1	0	1420.83	1054	1065
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	18	21	39	0.04%	16.8%	YLTLDGFDAMFR	99.7%	67	25	65.6	4	0	0	1448.69	815	826
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	18	21	39	0.04%	16.8%	YSNSEVVTGSGR	99.7%	98.6	25	88.4	2	0	0	1255.59	366	377
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	100.0%	3	3	4	0.00%	12.4%	DFVSEAYLLTLGK	99.7%	78.4	25	0	4	0	0	1455.77	151	163
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	100.0%	3	3	4	0.00%	12.4%	EANHNVSAPYGR	99.1%	34.8	25	30.1	1	1	0	1314.62	851	862
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	100.0%	3	3	4	0.00%	12.4%	EFFLELTMGR	99.7%	66.8	25	66.8	2	0	0	1258.61	649	658
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	100.0%	3	3	4	0.00%	12.4%	FINMFAVLDELK	99.7%	71.2	25	64.5	2	0	0	1439.76	164	175
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	100.0%	3	3	4	0.00%	12.4%	LCCGLSMFEVILTR	99.7%	58.4	25	58.4	1	0	0	1698.84	1110	1123
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	100.0%	3	3	4	0.00%	12.4%	LGTPQQIAIAR	99.7%	64.2	25	51.8	2	0	0	1167.68	1090	1100
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	100.0%	3	3	4	0.00%	12.4%	NAFVTGIAR	99.7%	46.3	25	31.5	2	0	0	948.53	50	58
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	100.0%	3	3	4	0.00%	12.4%	SLLQGTILQYVK	99.7%	49	25	49	2	0	0	1362.80	963	974
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	100.0%	3	3	4	0.00%	12.4%	SVETDSSTVEHVR	99.7%	69.7	25	61.5	2	0	0	1445.69	1252	1264
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	100.0%	3	3	4	0.00%	12.4%	TVEVLEPEVTK	99.7%	43.7	25	35.6	2	0	0	1243.68	111	121
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	100.0%	3	3	4	0.00%	12.4%	YAPLHLVPLIER	99.7%	52.1	25	52.1	2	1	0	1420.83	1078	1089
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	100.0%	3	3	4	0.00%	12.4%	YQILNNEVFAILNK	99.4%	36.8	25	36.8	1	0	0	1678.92	1235	1248
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	100.0%	3	3	4	0.00%	12.4%	YSNSEVVTGSGLDSQK	99.7%	76.6	25	76.6	1	0	0	1670.79	366	381
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	7	7	7	0.01%	4.3%	EGLDEVAGIINDAK	99.7%	52.1	25	51.5	1	0	0	1443.73	879	892
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	7	7	7	0.01%	4.3%	HINDSAPEVR	95.5%	28.1	25	26	1	0	0	1137.56	447	456
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	7	7	7	0.01%	4.3%	NLGIPIITVLGDSK	98.3%	32.1	25	32.1	1	0	0	1439.85	941	954
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	7	7	7	0.01%	4.3%	TALAATNPAVR	99.7%	56.2	25	45	1	0	0	1084.61	762	772
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	7	7	7	0.01%	4.3%	TEISDKITSELVSK	99.7%	54.9	25	54.9	1	0	0	1549.83	855	868
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	7	7	7	0.01%	4.3%	TSAQVVLDGLVDK	99.7%	52.9	25	37.7	1	0	0	1344.74	677	689
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	7	7	7	0.01%	4.3%	TTGEVVSGVVSK	99.7%	46.7	25	37.5	1	0	0	1162.63	85	96
Cytosolic carboxypeptidase 1	AGTPBP1	CBPC1_HUMAN	138.5	100.0%	3	3	6	0.01%	2.6%	IVGLLAQLEK	99.7%	42.2	25	35.2	2	0	0	1083.68	18	27
Cytosolic carboxypeptidase 1	AGTPBP1	CBPC1_HUMAN	138.5	100.0%	3	3	6	0.01%	2.6%	TLQQQPGDQNR	99.7%	48.6	25	43.1	2	0	0	1284.63	508	518

Cytosolic carboxypeptidase 1	AGTPBP1	CBPC1_HUMAN	138.5	100.0%	3	3	6	0.01%	2.6%	VALDTLAALLK	99.7%	50.5	25	45.5	2	0	0	1127.70	222	232
Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	NUBP2_HUMAN	28.8	99.8%	2	2	4	0.00%	8.9%	GWAPVFLDR	95.0%	27.7	25	8.96	1	0	0	1060.56	75	83
Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	NUBP2_HUMAN	28.8	99.8%	2	2	4	0.00%	8.9%	VGILDVDLCGPSIPR	99.7%	69.2	25	65.6	3	0	0	1610.86	46	60
Cytosolic non-specific dipeptidase	CNDP2	CNDP2_HUMAN	52.9	100.0%	3	3	4	0.00%	5.9%	MMEVAAADVK	99.7%	49.7	25	40.4	1	0	0	1064.51	44	53
Cytosolic non-specific dipeptidase	CNDP2	CNDP2_HUMAN	52.9	100.0%	3	3	4	0.00%	5.9%	TGQEIPVNVR	99.3%	35.9	25	24.4	2	0	0	1112.61	150	159
Cytosolic non-specific dipeptidase	CNDP2	CNDP2_HUMAN	52.9	100.0%	3	3	4	0.00%	5.9%	YNYIEGTK	99.6%	39	25	32.5	1	0	0	987.48	454	461
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	26	99	0.10%	50.1%	AGTGVDNVDLEAATR	99.7%	105	25	92.9	8	0	0	1488.73	76	90
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	26	99	0.10%	50.1%	AGTGVDNVDLEAATRK	99.7%	115	25	110	2	0	0	1616.82	76	91
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	26	99	0.10%	50.1%	ALQSGQCAGAALDVFTEEPPRDR	99.7%	75.9	25	75.9	0	2	0	2488.19	248	270
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	26	99	0.10%	50.1%	ALVDHENVISCPHLGASTK	99.7%	63.6	25	63.6	2	3	0	2048.02	271	289
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	26	99	0.10%	50.1%	CGEEIAVQFVDMVK	99.7%	99.8	25	99.8	6	0	0	1624.77	295	308
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	26	99	0.10%	50.1%	DLPLLLFR	99.7%	55.8	25	48.5	11	0	0	986.60	462	469
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	26	99	0.10%	50.1%	EELIAELQDCEGLIVR	99.7%	53.5	25	53.5	2	0	0	1886.95	39	54
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	26	99	0.10%	50.1%	FMGTELNGK	99.7%	51.4	25	43.5	2	0	0	996.48	138	146
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	26	99	0.10%	50.1%	GGIVDEGALLR	99.7%	81.2	25	51.9	6	0	0	1099.61	237	247
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	26	99	0.10%	50.1%	GTIQVITQGTSLK	99.7%	95.6	25	84.4	9	0	0	1345.77	352	364
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	26	99	0.10%	50.1%	ILQDGGLQVVEK	99.7%	76.7	25	66.5	3	0	0	1298.73	22	33
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	26	99	0.10%	50.1%	LLSYQTSLVSDGETWHVMGISSLLPSLEAWK	99.7%	66.2	25	66.2	0	1	0	3463.75	492	522
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	26	99	0.10%	50.1%	NAGNCLSPAVIVGLLK	99.7%	59.6	25	56.2	6	1	0	1625.90	365	380
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	26	99	0.10%	50.1%	QADVNLVNAK	99.7%	60.6	25	53.1	2	0	0	1071.58	385	394
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	26	99	0.10%	50.1%	QIPQATASMK	94.9%	27.6	25	10.5	1	0	0	1090.56	120	129
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	26	99	0.10%	50.1%	QNLSKEELIAELQDCEGLIVR	99.7%	37.3	25	32.3	0	2	0	2457.27	34	54
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	26	99	0.10%	50.1%	TLGILGLGR	99.7%	70.1	25	58.4	10	0	0	899.57	147	155
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	26	99	0.10%	50.1%	TQTSDPAMLPTMIGLLAEAGVR	99.7%	112	25	109	7	3	0	2272.17	470	491
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	26	99	0.10%	50.1%	VLISDSLDPCCR	99.7%	97.6	25	97.6	2	0	0	1434.67	9	20
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	26	99	0.10%	50.1%	VTADVINAAEK	99.7%	100	25	80.4	8	0	0	1130.61	59	69
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	3	3	4	0.00%	6.5%	ESVLTATSILNNPIVK	99.7%	108	25	96.6	2	0	0	1698.96	444	459
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	3	3	4	0.00%	6.5%	NQGGSSWEAPYSR	98.2%	31.8	25	31.8	1	0	0	1438.63	126	138
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	3	3	4	0.00%	6.5%	NSLDSFGGR	96.6%	29.2	25	18.8	1	0	0	952.45	117	125
DDB1- and CUL4-associated factor 7	DCAF7	DCAF7_HUMAN	38.9	100.0%	3	3	4	0.00%	12.9%	GVYPDLLATSGDYLR	99.7%	97.9	25	95.5	2	0	0	1639.83	82	96
DDB1- and CUL4-associated factor 7	DCAF7	DCAF7_HUMAN	38.9	100.0%	3	3	4	0.00%	12.9%	LALGSFVEEYNNK	99.7%	73	25	73	1	0	0	1483.74	34	46
DDB1- and CUL4-associated factor 7	DCAF7	DCAF7_HUMAN	38.9	100.0%	3	3	4	0.00%	12.9%	VQLVGLDEESSEFICR	99.7%	93	25	93	1	0	0	1880.91	47	62
D-dopachrome decarboxylase	DDT	DOPD_HUMAN	12.7	100.0%	3	3	4	0.00%	27.1%	ELALGQDR	95.6%	28.2	25	21.8	1	0	0	901.47	88	95
D-dopachrome decarboxylase	DDT	DOPD_HUMAN	12.7	100.0%	3	3	4	0.00%	27.1%	FFPLESWQIGK	98.1%	31.5	25	29.7	1	0	0	1351.70	100	110
D-dopachrome decarboxylase	DDT	DOPD_HUMAN	12.7	100.0%	3	3	4	0.00%	27.1%	PFLELDTNLPANR	99.7%	52.5	25	52.5	2	0	0	1499.79	2	14
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	8	8	13	0.01%	5.1%	ESFCITSFLCSTK	99.7%	45.6	25	45.5	2	0	0	1579.71	565	577
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	8	8	13	0.01%	5.1%	ESGVSLIATVTR	99.7%	77.8	25	64.8	2	0	0	1232.68	1146	1157
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	8	8	13	0.01%	5.1%	EYSSVFSHGVSITR	98.9%	33.7	25	27.9	1	0	0	1568.77	374	387
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	8	8	13	0.01%	5.1%	IGCTVSLLNFYK	99.7%	60.5	25	60.5	2	0	0	1414.74	1179	1190
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	8	8	13	0.01%	5.1%	ILSNVFCLIK	95.5%	28.1	25	18.4	1	0	0	1206.69	854	863
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	8	8	13	0.01%	5.1%	NSAPASVSPDGTR	99.7%	46.8	25	43.7	2	0	0	1258.60	1613	1625
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	8	8	13	0.01%	5.1%	TSLYLVQSLPGISR	99.7%	46.3	25	46.2	2	0	0	1533.86	1441	1454
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	8	8	13	0.01%	5.1%	TVESQLYTNPDSR	99.7%	84.6	25	74.5	1	0	0	1509.72	815	827
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	5	9	23	0.02%	20.9%	GTIMDTTVDVDKR	97.2%	29.9	25	29.9	3	0	0	1450.72	149	161
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	5	9	23	0.02%	20.9%	NAVVVITGATSGLGK	99.7%	97.8	25	88.7	4	0	0	1386.80	52	66
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	5	9	23	0.02%	20.9%	TLAPGLFFSLMASR	99.7%	96.3	25	94.9	3	0	0	1510.81	302	315
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	5	9	23	0.02%	20.9%	VMETNYFGPVALTK	99.7%	114	25	84.2	8	0	0	1569.80	162	175
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	5	9	23	0.02%	20.9%	YGVMDTTTAQGR	99.7%	87.5	25	87.5	5	0	0	1299.60	256	267
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	6	6	11	0.01%	13.5%	NAAGNFYINDK	98.8%	33.3	25	33.3	1	0	0	1226.58	499	509
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	6	6	11	0.01%	13.5%	SADVESVVSGTLR	99.7%	91.1	25	84.6	2	0	0	1319.68	326	338
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	6	6	11	0.01%	13.5%	SAFEYGGQK	96.6%	29.2	25	29.2	2	0	0	986.46	339	347

Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	6	6	11	0.01%	13.5%	SSPSLTILAGGK	99.7%	53.5	25	43.3	2	0	0	1130.64	409	420
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	6	6	11	0.01%	13.5%	STGSIVGQQPFGGAR	99.7%	55.7	25	55.7	2	0	0	1461.74	510	524
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	6	6	11	0.01%	13.5%	VANEPVLAFTQGSPER	99.7%	100	25	100	2	0	0	1714.88	32	47
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	CEYPAACNALETLLIHR	99.7%	51.1	25	50.9	0	2	0	2030.98	606	622
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	DLEEAEGR	99.7%	44.7	25	35.5	2	0	0	918.42	410	417
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	EAVQLVNTR	99.7%	51.8	25	42.1	2	0	0	1029.57	531	539
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	EAVQLVNTREEVEDLCR	99.7%	46.5	25	46.2	1	2	0	2060.01	531	547
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	EMAIPVLEAR	99.7%	56.1	25	44.6	2	0	0	1144.60	150	159
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	EMMLVTSGAVAFGK	99.7%	70.6	25	14.6	5	0	0	1456.72	111	124
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	FASYLTFSPSEVK	99.7%	73.2	25	68.3	4	0	0	1475.74	650	662
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	FGLGAEVGISTSR	99.7%	91.9	25	86.3	2	0	0	1293.68	733	745
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	GKDHVVSDFSEHGSLK	99.7%	73.3	25	72.2	0	2	0	1741.85	766	781
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	GPVGLEGLLTTK	99.7%	71.7	25	71.7	2	0	0	1184.69	750	761
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	ILHLLTQEALSIHGVK	99.7%	63.4	25	63.4	0	2	0	1772.04	515	530
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	LAAPLLKR	99.7%	46.5	25	45.7	2	0	0	881.59	418	425
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	LASIVEQVSVLQNQGR	99.7%	92.9	25	82	4	0	0	1740.96	95	110
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	LGSAVVTR	99.7%	74.6	25	53.5	4	0	0	802.48	77	84
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	LIDIFYPGDQQSVTFGTK	99.7%	84.6	25	82.4	4	0	0	2029.03	283	300
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	LNSLAIGLR	99.7%	85	25	68.9	4	0	0	956.59	433	441
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	LRHEILLSQSVR	99.7%	47.5	25	47.5	1	2	0	1450.85	127	138
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	MIDLIIPR	99.7%	65	25	51.4	6	0	0	970.58	551	558
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	MLATLEPEQR	99.7%	63.5	25	47.1	6	0	0	1203.60	376	385
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	NLNGTLHELLR	99.7%	50.4	25	43.2	2	0	0	1279.71	202	212
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	QALHSGQNQLK	99.5%	37.7	25	32.9	2	0	0	1223.65	139	149
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	QIAASSQDSVGR	99.7%	80.3	25	77.3	2	0	0	1218.61	442	453
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	SWSNIPFITVPLSR	99.7%	88.3	25	78.3	2	0	0	1616.88	42	55
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	TPLFDQIIDMLR	99.7%	86.8	25	80.5	5	0	0	1477.77	627	638
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	VGMGGMEAK	99.7%	45.8	25	39.5	2	0	0	879.41	303	311
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	VGTFFSEVKPAGPTVEQQGEMAR	99.7%	88.7	25	88.7	0	4	0	2465.21	349	371
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	VSGHVITDIVEGK	99.7%	76.7	25	69.8	2	2	0	1353.74	335	347
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	VSGHVITDIVEGKK	99.7%	58.2	25	58.2	0	2	0	1481.83	335	348
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	29	38	89	0.09%	43.0%	YLHENLPIPQR	99.5%	31.6	25	31	1	2	0	1379.74	782	792
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	15	17	29	0.03%	27.6%	EQIVGPLESPVEDSLWPYK	99.7%	77	25	77	2	0	0	2186.10	270	288
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	15	17	29	0.03%	27.6%	FAEQLIR	99.6%	38.7	25	15.9	2	0	0	876.49	545	551
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	15	17	29	0.03%	27.6%	FENLGVSSLGER	99.7%	55.9	25	55.9	2	0	0	1307.66	86	97
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	15	17	29	0.03%	27.6%	FIPLARPEVK	98.9%	33.9	25	21.4	2	0	0	1169.70	221	230
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	15	17	29	0.03%	27.6%	GGFEEPVLLK	99.7%	53.2	25	34.2	2	0	0	1088.60	57	66
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	15	17	29	0.03%	27.6%	IIDTPQFQR	99.7%	56.3	25	46.4	2	0	0	1117.60	135	143
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	15	17	29	0.03%	27.6%	ISTAIDDMEAYTK	99.7%	91.2	25	80.6	2	0	0	1457.68	409	421
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	15	17	29	0.03%	27.6%	LLSYIQR	99.1%	34.8	25	19.5	1	0	0	892.53	100	106
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	15	17	29	0.03%	27.6%	LVQIHVDTMK	99.7%	53	25	46.3	1	0	0	1199.65	107	116
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	15	17	29	0.03%	27.6%	NQVSQLLPEK	99.2%	35.4	25	14.9	2	0	0	1155.64	535	544
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	15	17	29	0.03%	27.6%	QLGGGYYVFPGASHNR	99.7%	39.8	25	39.8	0	2	0	1722.83	149	164
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	15	17	29	0.03%	27.6%	SFLYEIVSNKR	99.7%	65.8	25	65.8	2	0	0	1355.73	295	305
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	15	17	29	0.03%	27.6%	TWGPEQVCSFLR	99.7%	43	25	32.6	2	0	0	1479.71	44	55
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	15	17	29	0.03%	27.6%	VGNIIDTMITDAFLK	99.7%	103	25	103	3	0	0	1650.88	378	392
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	15	17	29	0.03%	27.6%	YVGETQPTGQIK	99.7%	57.8	25	51.6	2	0	0	1320.68	456	467
Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial	DUT	DUT_HUMAN	26.6	100.0%	2	2	4	0.00%	7.1%	IAQLICER	99.7%	40.7	25	32.5	2	0	0	1002.54	217	224
Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial	DUT	DUT_HUMAN	26.6	100.0%	2	2	4	0.00%	7.1%	LSEHATAPTR	99.7%	51.1	25	46.2	2	0	0	1082.56	119	128
Dephospho-CoA kinase domain-containing protein	DCAKD	DCAKD_HUMAN	26.6	100.0%	5	5	7	0.01%	27.3%	HVLDNSGEWSVTK	98.3%	32	25	32	1	0	0	1471.72	174	186
Dephospho-CoA kinase domain-containing protein	DCAKD	DCAKD_HUMAN	26.6	100.0%	5	5	7	0.01%	27.3%	INAQLPLTDK	99.7%	54.6	25	38.5	2	0	0	1112.63	159	168

Dephospho-CoA kinase domain-containing protein	DCAKD	DCAKD_HUMAN	26.6	100.0%	5	5	7	0.01%	27.3%	MFLVGLTGGIASGK	99.7%	101	25	101	2	0	0	1350.75	1	14
Dephospho-CoA kinase domain-containing protein	DCAKD	DCAKD_HUMAN	26.6	100.0%	5	5	7	0.01%	27.3%	VLGDLIFNQPDRR	99.6%	32.2	25	28.5	0	1	0	1542.84	68	80
Dephospho-CoA kinase domain-containing protein	DCAKD	DCAKD_HUMAN	26.6	100.0%	5	5	7	0.01%	27.3%	YVILDIPLLFETK	99.7%	42.7	25	42.7	1	0	0	1563.90	109	121
Dermcidin	DCD	DCD_HUMAN	11.3	100.0%	3	4	44	0.05%	22.7%	DAVEDLESVGK	99.7%	74.7	25	71	9	0	0	1161.56	86	96
Dermcidin	DCD	DCD_HUMAN	11.3	100.0%	3	4	44	0.05%	22.7%	ENAGEDPGLAR	99.7%	86.8	25	81.7	27	0	0	1128.53	43	53
Dermcidin	DCD	DCD_HUMAN	11.3	100.0%	3	4	44	0.05%	22.7%	LGKDAVEDLESVGK	99.7%	91.4	25	85.4	5	3	0	1459.76	83	96
Desmoglein-1	DSG1	DSG1_HUMAN	113.7	100.0%	3	3	6	0.01%	3.5%	ESSNVVVTER	99.7%	54.2	25	38.1	1	0	0	1119.56	916	925
Desmoglein-1	DSG1	DSG1_HUMAN	113.7	100.0%	3	3	6	0.01%	3.5%	MTGFELTEGVK	96.5%	29	25	24.3	1	0	0	1211.60	651	661
Desmoglein-1	DSG1	DSG1_HUMAN	113.7	100.0%	3	3	6	0.01%	3.5%	YVMGNNPADLLAVDSR	99.7%	71.1	25	69.8	4	0	0	1750.84	423	438
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	16	16	31	0.03%	6.4%	AELIVQPELK	99.7%	47.7	25	33.1	7	0	0	1139.67	85	94
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	16	16	31	0.03%	6.4%	AITGFDDPFSGK	99.5%	37.2	25	37.2	1	0	0	1254.60	2092	2103
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	16	16	31	0.03%	6.4%	ALLQAILQTEDMLK	99.7%	96	25	90.9	1	0	0	1586.88	772	785
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	16	16	31	0.03%	6.4%	GFFDPNTEENLTYLQLK	99.7%	87.7	25	78.3	3	0	0	2028.99	2414	2430
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	16	16	31	0.03%	6.4%	GLVGIEFKEK	97.7%	30.8	25	25.2	1	0	0	1119.64	2319	2328
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	16	16	31	0.03%	6.4%	IEVLEEELR	99.7%	46.8	25	40.6	3	0	0	1129.61	1034	1042
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	16	16	31	0.03%	6.4%	IQSQFTDAQK	99.7%	55.9	25	45.8	2	0	0	1165.58	608	617
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	16	16	31	0.03%	6.4%	LNDSILQATEQR	99.7%	64.2	25	57	1	0	0	1387.72	1256	1267
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	16	16	31	0.03%	6.4%	NQCTQVVQER	99.5%	37.6	25	24.5	1	0	0	1261.60	1803	1812
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	16	16	31	0.03%	6.4%	QLLQEQESVK	99.7%	44.7	25	39.7	1	0	0	1201.64	1667	1676
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	16	16	31	0.03%	6.4%	QLQNIIQATSR	99.7%	75.3	25	75.1	2	0	0	1271.71	271	281
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	16	16	31	0.03%	6.4%	RVEEDIQQQK	99.7%	46.5	25	35.5	2	0	0	1272.65	1425	1434
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	16	16	31	0.03%	6.4%	SVEEVASEIQPFLR	98.2%	31.8	25	18.8	1	0	0	1603.83	2000	2013
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	16	16	31	0.03%	6.4%	TLELQGLINDLQR	99.7%	82.8	25	82.8	2	0	0	1512.84	1763	1775
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	16	16	31	0.03%	6.4%	YEVTSGGGGTSR	99.7%	53.6	25	46.4	1	0	0	1170.54	28	39
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	16	16	31	0.03%	6.4%	YGDGIQLTR	99.7%	52.3	25	42.6	2	0	0	1022.53	95	103
Developmentally-regulated GTP-binding protein 2	DRG2	DRG2_HUMAN	40.7	99.8%	2	2	3	0.00%	6.6%	TADVIIMMLDATK	99.7%	57	25	50.1	1	0	0	1421.74	139	151
Developmentally-regulated GTP-binding protein 2	DRG2	DRG2_HUMAN	40.7	99.8%	2	2	3	0.00%	6.6%	VALIGFPSVGK	99.7%	46.8	25	42.3	2	0	0	1087.65	65	75
Diablo homolog, mitochondrial	DIABLO	DBLOH_HUMAN	27.1	99.8%	2	2	2	0.00%	8.8%	LAEAQIEELR	99.6%	38	25	28.3	1	0	0	1171.63	208	217
Diablo homolog, mitochondrial	DIABLO	DBLOH_HUMAN	27.1	99.8%	2	2	2	0.00%	8.8%	LQVEEVHQLSR	99.7%	55.2	25	50.7	1	0	0	1337.72	192	202
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	7	8	12	0.01%	49.2%	IMQDFESDTFFPEIDLEK	99.7%	56.8	25	56.8	1	0	0	2220.01	139	156
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	7	8	12	0.01%	49.2%	INLVLSR	99.7%	53.3	25	35.6	2	0	0	814.51	72	78
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	7	8	12	0.01%	49.2%	KTWFSIPEK	99.5%	37	25	28.6	1	0	0	1135.61	56	64
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	7	8	12	0.01%	49.2%	LLPEYPGVLSDVQEEK	99.7%	73.7	25	71.3	2	0	0	1815.94	159	174
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	7	8	12	0.01%	49.2%	LTEQPELANK	97.1%	29.8	25	21.4	1	0	0	1142.61	100	109
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	7	8	12	0.01%	49.2%	VDMVWIVGGSSVYK	99.7%	59.3	25	54.7	2	0	0	1539.79	110	123
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	7	8	12	0.01%	49.2%	VGSLNCIVAVSQNMGIGK	99.7%	73	25	60.3	2	1	0	1862.95	2	19
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	17	22	39	0.04%	50.3%	ADGGTQVIDTK	99.7%	46.6	25	39.3	2	0	0	1104.55	167	177
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	17	22	39	0.04%	50.3%	AEVITCDVLLVCIGR	99.7%	40.7	25	40.7	2	0	0	1717.90	301	315
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	17	22	39	0.04%	50.3%	ALLNNSHYYHMAHGK	98.2%	26	25	26	0	2	0	1755.84	90	104
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	17	22	39	0.04%	50.3%	ALTGGIAHLFK	99.7%	62.7	25	53.7	2	0	0	1127.66	133	143
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	17	22	39	0.04%	50.3%	EANLAASFGK	99.7%	70.4	25	63.6	2	0	0	1007.52	496	505
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	17	22	39	0.04%	50.3%	FPFAANSR	99.5%	37.5	25	24.9	2	0	0	909.46	421	428
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	17	22	39	0.04%	50.3%	GRIPVNTR	96.8%	29.4	25	17.3	2	0	0	912.54	335	342
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	17	22	39	0.04%	50.3%	IPNIYAIGDVVAGPMLAHK	99.7%	102	25	102	2	4	0	1979.08	347	365
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	17	22	39	0.04%	50.3%	LGADVTAVEFLGHVGGVGIDMEISK	99.7%	61.2	25	61.2	0	1	0	2514.29	235	259
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	17	22	39	0.04%	50.3%	MVVIGAGVIGVELGSVWQR	99.7%	34.5	25	34.5	0	1	0	1986.08	216	234
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	17	22	39	0.04%	50.3%	NETLGGTCLNVGCIPSK	99.7%	104	25	104	2	0	0	1819.87	73	89
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	17	22	39	0.04%	50.3%	NLGLEELGIELDPR	99.7%	96.5	25	87.8	2	0	0	1567.83	321	334
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	17	22	39	0.04%	50.3%	SDGKIDVSIEAASGGK	99.7%	70.1	25	68.5	1	1	0	1533.78	285	300
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	17	22	39	0.04%	50.3%	SEEQLKEEGIEYK	99.7%	68.3	25	68.3	2	2	0	1581.76	405	417
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	17	22	39	0.04%	50.3%	VCHAHPTLSEAFR	99.7%	45.3	25	41.1	0	2	0	1524.74	483	495

Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	17	22	39	0.04%	50.3%	VLGAHILGPGAGEMVNEAALALEYGASCEDIAR	99.7%	79.6	25	70.2	0	4	0	3354.65	450	482
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	17	22	39	0.04%	50.3%	VVHVNGYGK	96.6%	29.2	25	29	1	0	0	972.53	147	155
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	7	8	11	0.01%	13.8%	DVPLGTPLCIIVEK	99.7%	83.7	25	83.7	2	0	0	1553.86	283	296
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	7	8	11	0.01%	13.8%	GVETIANDVVSLATK	99.7%	88.4	25	83.5	2	0	0	1516.82	533	547
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	7	8	11	0.01%	13.8%	ILVAEGTR	95.2%	27.8	25	13.7	1	0	0	858.50	148	155
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	7	8	11	0.01%	13.8%	ISVNDFIIK	99.7%	39.8	25	36.3	1	0	0	1048.60	474	482
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	7	8	11	0.01%	13.8%	VPLPSLSPTMQAGTIAR	99.7%	96.1	25	96.1	3	0	0	1738.95	94	110
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	7	8	11	0.01%	13.8%	VVDGAVGAQWLAEFRK	98.8%	27.6	25	19.6	0	1	0	1745.93	622	637
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	7	8	11	0.01%	13.8%	YLEKPITMLL	99.4%	36.5	25	35.8	1	0	0	1236.69	638	647
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	6	6	11	0.01%	11.9%	GMYDGPVYEVPATPK	99.7%	64.8	25	64.8	2	0	0	1623.77	497	511
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	6	6	11	0.01%	11.9%	INCPVYITK	99.7%	41.3	25	36.7	1	0	0	1107.59	246	254
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	6	6	11	0.01%	11.9%	IVFEDGNINVNK	99.7%	63.3	25	58	2	0	0	1361.71	452	463
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	6	6	11	0.01%	11.9%	QIGENLIVPGGVK	99.7%	49.8	25	49.8	2	0	0	1323.76	44	56
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	6	6	11	0.01%	11.9%	SAADIIALAR	99.7%	93.2	25	73.7	2	0	0	1000.58	259	268
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	6	6	11	0.01%	11.9%	VFGLQGVSR	99.7%	49.3	25	40.5	2	0	0	962.54	488	496
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	6	6	10	0.01%	11.4%	GAPAVVISQGR	99.7%	73.8	25	67.4	2	0	0	1054.60	441	451
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	6	6	10	0.01%	11.4%	IFNFYPR	99.4%	36.5	25	12.9	2	0	0	956.50	391	397
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	6	6	10	0.01%	11.4%	LAEIHGVPR	99.7%	67.8	25	59	2	0	0	991.57	488	496
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	6	6	10	0.01%	11.4%	MDENEFVAVTSTNAAK	99.7%	61.5	25	61.5	1	0	0	1726.80	375	390
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	6	6	10	0.01%	11.4%	MFVTPGAGR	99.5%	37	25	35.7	1	0	0	935.48	459	467
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	6	6	10	0.01%	11.4%	QIGENLIVPGGIK	99.7%	48	25	48	2	0	0	1337.78	44	56
Dihydropyrimidinase-related protein 5	DPYSL5	DPYL5_HUMAN	61.4	100.0%	5	5	7	0.01%	11.2%	EMGTPLADTPTRPVTR	95.8%	22.9	25	20.7	0	1	0	1757.89	506	521
Dihydropyrimidinase-related protein 5	DPYSL5	DPYL5_HUMAN	61.4	100.0%	5	5	7	0.01%	11.2%	FVAVTSSNAAK	99.7%	59.5	25	53.7	2	0	0	1094.58	373	383
Dihydropyrimidinase-related protein 5	DPYSL5	DPYL5_HUMAN	61.4	100.0%	5	5	7	0.01%	11.2%	GVNSFQMFMTYK	99.7%	43.8	25	43.8	1	0	0	1452.67	153	164
Dihydropyrimidinase-related protein 5	DPYSL5	DPYL5_HUMAN	61.4	100.0%	5	5	7	0.01%	11.2%	VHAENGELVAEGAK	99.7%	83.9	25	83.9	2	0	0	1423.72	190	203
Dihydropyrimidinase-related protein 5	DPYSL5	DPYL5_HUMAN	61.4	100.0%	5	5	7	0.01%	11.2%	VKAEMETLVR	99.7%	39.6	25	33.9	1	0	0	1175.65	141	150
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	6	7	13	0.01%	20.2%	FIPGLQMLSDAAPGK	99.2%	35.1	25	34.2	2	0	0	1544.81	90	104
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	6	7	13	0.01%	20.2%	LLELADIDPTLRPR	99.7%	39.3	25	35.9	2	2	0	1621.93	280	293
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	6	7	13	0.01%	20.2%	LSVMAQYLCNVR	99.7%	76.5	25	76.4	2	0	0	1453.73	196	207
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	6	7	13	0.01%	20.2%	QLSQNFLLDLR	99.7%	59	25	47.8	2	0	0	1346.74	32	42
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	6	7	13	0.01%	20.2%	TQMTLTFQK	99.7%	41.2	25	41.2	1	0	0	1097.57	170	178
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	6	7	13	0.01%	20.2%	VVQNVFQFR	99.7%	53.2	25	46.6	2	0	0	1136.62	248	256
Dimethyladenosine transferase 2, mitochondrial	TFB2M	TFB2M_HUMAN	45.4	99.8%	2	2	4	0.00%	6.3%	LYLIQMIPR	99.7%	69.8	25	43.9	2	0	0	1146.67	296	304
Dimethyladenosine transferase 2, mitochondrial	TFB2M	TFB2M_HUMAN	45.4	99.8%	2	2	4	0.00%	6.3%	NLGIEAVPWTADIPLK	99.7%	58.6	25	58.6	2	0	0	1736.96	175	190
Dimethylaniline monooxygenase [N-oxide-forming] 1	FMO1	FMO1_HUMAN	60.3	99.8%	2	2	2	0.00%	4.0%	EFVLNDELPGR	96.5%	23.6	25	19	0	1	0	1288.65	281	291
Dimethylaniline monooxygenase [N-oxide-forming] 1	FMO1	FMO1_HUMAN	60.3	99.8%	2	2	2	0.00%	4.0%	MYANHFDLLK	98.2%	31.7	25	14.7	1	0	0	1251.62	93	102
Diphosphoinositol polyphosphate phosphohydrolase 3-beta	NUDT11	NUD11_HUMAN	18.6	100.0%	2	2	3	0.00%	12.2%	EVYEEAGVK	96.2%	28.7	25	22.1	1	0	0	1023.50	65	73
Diphosphoinositol polyphosphate phosphohydrolase 3-beta	NUDT11	NUD11_HUMAN	18.6	100.0%	2	2	3	0.00%	12.2%	LLGVFEQNQDR	99.0%	34.4	25	34.4	2	0	0	1318.68	79	89
DNA damage-binding protein 1	DDB1	DDB1_HUMAN	127.0	100.0%	4	4	5	0.01%	5.2%	EMLGGEIIPR	95.7%	28.2	25	0.98	1	0	0	1114.59	580	589
DNA damage-binding protein 1	DDB1	DDB1_HUMAN	127.0	100.0%	4	4	5	0.01%	5.2%	IEVQDTSGGTTALRPSASTQALSSSVSSSK	99.7%	65.1	25	65.1	0	1	0	2952.48	740	769
DNA damage-binding protein 1	DDB1	DDB1_HUMAN	127.0	100.0%	4	4	5	0.01%	5.2%	IVVFQYSDGK	99.7%	68.1	25	65.3	2	0	0	1155.60	848	857
DNA damage-binding protein 1	DDB1	DDB1_HUMAN	127.0	100.0%	4	4	5	0.01%	5.2%	LPSFELLHK	99.7%	41.5	25	37.8	1	0	0	1083.62	571	579
DNA ligase 3	LIG3	DNLI3_HUMAN	112.9	100.0%	3	3	4	0.00%	3.3%	GASFVTSTNPR	95.8%	28.3	25	28.3	1	0	0	1136.57	214	224
DNA ligase 3	LIG3	DNLI3_HUMAN	112.9	100.0%	3	3	4	0.00%	3.3%	VIQEGLEGLVLK	99.7%	102	25	92	1	0	0	1297.77	649	660
DNA ligase 3	LIG3	DNLI3_HUMAN	112.9	100.0%	3	3	4	0.00%	3.3%	VLLDIFTGVR	99.7%	75.7	25	75.7	2	0	0	1132.67	933	942
DNA methyltransferase 1-associated protein 1	DMAP1	DMAP1_HUMAN	53.0	100.0%	2	2	3	0.00%	4.9%	AETDHLFDLSR	99.5%	37.5	25	29.7	1	0	0	1303.63	155	165
DNA methyltransferase 1-associated protein 1	DMAP1	DMAP1_HUMAN	53.0	100.0%	2	2	3	0.00%	4.9%	LITAADTTAEQR	99.7%	83.7	25	51.4	2	0	0	1289.67	271	282
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	15.3%	ALNLFQGSVEDTTGSQSLAALLNK	99.7%	112	25	112	2	0	0	2477.29	309	332
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	15.3%	DSLIIIDELGR	99.7%	67.1	25	55.9	2	0	0	1243.69	742	752
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	15.3%	LDSSAQFGYYFR	99.7%	83.6	25	79.4	2	0	0	1453.67	513	524
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	15.3%	LLLAVFVTPLTDLR	99.7%	76.9	25	76.9	2	0	0	1570.96	431	444

DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	15.3%	LNLVEAFVEDAELR	99.7%	103	25	102	1	0	0	1617.85	360	373
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	15.3%	LTSLNEEYTK	99.7%	48.9	25	44.5	2	0	0	1197.60	556	565
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	15.3%	LYQGINQLPNVIQALEK	99.7%	79.5	25	79.5	2	0	0	1941.08	407	423
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	15.3%	NLQSVVLSK	99.7%	48.9	25	23.8	2	0	0	987.58	74	82
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	15.3%	NNSFVNEIISR	99.7%	61.6	25	49.2	2	0	0	1292.66	919	929
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	15.3%	QTLQEDLLR	99.7%	40.4	25	37.2	2	0	0	1115.61	374	382
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	15.3%	QVGVGYVDSIQR	99.7%	55.4	25	48.9	1	0	0	1320.69	160	171
DNA mismatch repair protein Msh3	MSH3	MSH3_HUMAN	127.4	100.0%	3	3	5	0.01%	4.1%	DTTLFDLSQFGSSNTSHENLQK	98.3%	26.3	25	26.3	0	1	0	2469.15	194	215
DNA mismatch repair protein Msh3	MSH3	MSH3_HUMAN	127.4	100.0%	3	3	5	0.01%	4.1%	FFGEDAEIAAR	99.7%	56	25	44.2	2	0	0	1225.58	258	268
DNA mismatch repair protein Msh3	MSH3	MSH3_HUMAN	127.4	100.0%	3	3	5	0.01%	4.1%	STLIGEDVNPLIK	99.7%	57.5	25	48.2	2	0	0	1398.78	337	349
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	15	17	31	0.03%	13.1%	AIMYEETTYSK	99.7%	49.3	25	49.3	2	0	0	1335.61	842	852
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	15	17	31	0.03%	13.1%	AYGVCFVDTSLGK	99.7%	63.8	25	63.8	2	0	0	1416.68	555	567
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	15	17	31	0.03%	13.1%	EVCLASER	97.9%	31.1	25	27.3	1	0	0	963.46	1335	1342
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	15	17	31	0.03%	13.1%	GTATFDGTAIANAVVK	99.7%	106	25	88.8	1	0	0	1535.81	1218	1233
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	15	17	31	0.03%	13.1%	GTQTYSVLEGDPSENYSK	99.7%	88.1	25	88.1	2	0	0	1974.89	520	537
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	15	17	31	0.03%	13.1%	IHNVGSPLK	94.7%	27.5	25	20.2	1	0	0	964.56	825	833
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	15	17	31	0.03%	13.1%	IIDFLSALEGFK	99.7%	76	25	67.2	4	0	0	1352.75	855	866
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	15	17	31	0.03%	13.1%	IIGIMEEVADGFK	99.7%	65.8	25	62.2	2	0	0	1421.73	871	883
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	15	17	31	0.03%	13.1%	LANLPEEVIQK	99.7%	45.5	25	29.6	2	0	0	1253.71	1305	1315
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	15	17	31	0.03%	13.1%	LSDGIGVMLPQVLK	99.7%	52.7	25	47.7	4	0	0	1485.83	647	660
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	15	17	31	0.03%	13.1%	STVDAEAVHK	99.7%	45.1	25	36.7	2	0	0	1056.53	1343	1352
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	15	17	31	0.03%	13.1%	TLLEEEYFR	99.6%	38.8	25	32.2	2	0	0	1199.59	636	644
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	15	17	31	0.03%	13.1%	VDTCHTPFGK	96.7%	29.3	25	24.5	1	0	0	1161.54	762	771
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	15	17	31	0.03%	13.1%	VHVQFFDDSPTR	99.7%	47.7	25	47.7	2	1	0	1447.70	129	140
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	15	17	31	0.03%	13.1%	YQLEIPENFTTR	99.7%	39.2	25	29	2	0	0	1510.75	977	988
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	22	24	46	0.05%	25.1%	DLEDQEQLLR	99.7%	60	25	41.1	2	0	0	1258.63	1088	1097
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	22	24	46	0.05%	25.1%	DNCPLVANLVTASLR	99.7%	63.6	25	62.2	2	0	0	1642.86	835	849
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	22	24	46	0.05%	25.1%	ELNLAISR	99.7%	44.6	25	27.4	2	0	0	915.53	167	174
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	22	24	46	0.05%	25.1%	ELTGPAVLAVELCSR	99.7%	109	25	109	2	0	0	1614.85	181	195
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	22	24	46	0.05%	25.1%	EVSHLNALEER	99.7%	49.8	25	38.2	2	0	0	1296.65	1040	1050
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	22	24	46	0.05%	25.1%	FGVSSVAEAMALGR	99.7%	90.3	25	90.3	3	0	0	1394.71	763	776
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	22	24	46	0.05%	25.1%	IDISQLVITK	99.7%	85.3	25	56.1	2	0	0	1129.68	876	885
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	22	24	46	0.05%	25.1%	IFEPILGEGR	99.7%	62.6	25	55.9	2	0	0	1130.62	969	978
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	22	24	46	0.05%	25.1%	LALTLRPCAPILGAK	99.7%	53.7	25	53.7	2	0	0	1593.95	353	367
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	22	24	46	0.05%	25.1%	LGLTEDQFIR	99.7%	72.3	25	61.7	2	0	0	1191.64	630	639
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	22	24	46	0.05%	25.1%	LLEQGIR	99.7%	41.7	25	0	1	0	0	828.49	226	232
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	22	24	46	0.05%	25.1%	LMVLVNAVEMAR	99.1%	34.8	25	34.8	1	0	0	1345.73	526	537
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	22	24	46	0.05%	25.1%	LPCLEISQSVTGFGR	99.7%	77.4	25	77.4	2	0	0	1663.85	711	725
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	22	24	46	0.05%	25.1%	SEGGEDYTGATVIEPLK	99.7%	83.8	25	79.2	2	0	0	1765.85	575	591
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	22	24	46	0.05%	25.1%	TPTGDEFVK	99.7%	42.3	25	25.9	2	0	0	993.49	640	648
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	22	24	46	0.05%	25.1%	TVLSHQGAVCEFCQPR	99.7%	57.7	25	57.7	0	2	0	1888.88	1017	1032
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	22	24	46	0.05%	25.1%	VLSFDIECAGR	99.7%	65.9	25	65.1	2	0	0	1266.61	312	322
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	22	24	46	0.05%	25.1%	VQMDMLQVLLR	99.7%	66.3	25	43.6	4	0	0	1345.73	455	465
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	22	24	46	0.05%	25.1%	VQTFPFLGR	99.7%	40.8	25	28.7	2	0	0	1064.59	415	423
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	22	24	46	0.05%	25.1%	VSANSVYGFTGAQVGK	99.7%	84.9	25	79.4	2	0	0	1584.80	695	710
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	22	24	46	0.05%	25.1%	VTGVPLSYLLSR	99.7%	54.4	25	44.3	2	0	0	1304.76	538	549
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	22	24	46	0.05%	25.1%	VYFPYLLISK	99.0%	34.3	25	34.3	2	0	0	1242.71	797	806
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	22	24	46	0.05%	25.1%	YAGLLFSSRPDAHDR	99.7%	48.1	25	47.6	0	2	0	1704.85	809	823
DNA polymerase delta subunit 2	POLD2	DPOD2_HUMAN	51.3	99.8%	2	2	3	0.00%	6.0%	FLGTSGQNVSDIFR	99.7%	78.7	25	69.6	1	0	0	1540.78	341	354
DNA polymerase delta subunit 2	POLD2	DPOD2_HUMAN	51.3	99.8%	2	2	3	0.00%	6.0%	LVTGTVLAVFGSVR	99.7%	83.8	25	73.1	2	0	0	1418.84	153	166
DNA polymerase delta subunit 3	POLD3	DPOD3_HUMAN	51.4	100.0%	4	4	6	0.01%	11.6%	DSGPLFNTDYDILK	99.7%	60.9	25	40.3	2	0	0	1597.77	110	123

DNA polymerase delta subunit 3	POLD3	DPOD3_HUMAN	51.4	100.0%	4	4	6	0.01%	11.6%	EVTNASAAGNKAPGK	99.7%	40	25	35.5	1	0	0	1414.73	217	231
DNA polymerase delta subunit 3	POLD3	DPOD3_HUMAN	51.4	100.0%	4	4	6	0.01%	11.6%	FSAIQCAAAVPR	99.7%	51.2	25	37.1	1	0	0	1290.66	132	143
DNA polymerase delta subunit 3	POLD3	DPOD3_HUMAN	51.4	100.0%	4	4	6	0.01%	11.6%	IVEQPTVSVTEPK	99.7%	78.7	25	69.9	2	0	0	1426.78	262	274
DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	4	4	6	0.01%	2.3%	AIPLAIFQAEPTVR	99.7%	41.8	25	41.8	2	0	0	1525.87	1093	1106
DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	4	4	6	0.01%	2.3%	GSTLEEVYGSVAK	99.7%	40.6	25	36	1	0	0	1339.67	996	1008
DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	4	4	6	0.01%	2.3%	IFQSSVFEAFLK	99.7%	54.4	25	48.5	2	0	0	1415.76	984	995
DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	4	4	6	0.01%	2.3%	VLSLDTNITNQVNK	99.7%	45.7	25	45.7	1	0	0	1558.84	2111	2124
DNA primase large subunit	PRIM2	PRI2_HUMAN	58.8	100.0%	4	4	6	0.01%	9.2%	IPFADALDLFR	99.7%	70.1	25	61.6	1	0	0	1277.69	186	196
DNA primase large subunit	PRIM2	PRI2_HUMAN	58.8	100.0%	4	4	6	0.01%	9.2%	ISLDQIDLLSTK	99.7%	76.3	25	69	1	0	0	1345.76	271	282
DNA primase large subunit	PRIM2	PRI2_HUMAN	58.8	100.0%	4	4	6	0.01%	9.2%	ISPGGISQILDLVK	99.7%	52.1	25	49.2	2	0	0	1439.85	403	416
DNA primase large subunit	PRIM2	PRI2_HUMAN	58.8	100.0%	4	4	6	0.01%	9.2%	SLPAVQSDER	97.7%	30.7	25	27.9	2	0	0	1101.55	236	245
DNA primase small subunit	PRIM1	PRI1_HUMAN	49.9	100.0%	3	3	4	0.00%	8.8%	LGAFQAQEK	99.7%	40.6	25	29.8	1	0	0	991.52	96	104
DNA primase small subunit	PRIM1	PRI1_HUMAN	49.9	100.0%	3	3	4	0.00%	8.8%	SGIVEYLSLVK	99.7%	43.9	25	37.8	2	0	0	1207.69	183	193
DNA primase small subunit	PRIM1	PRI1_HUMAN	49.9	100.0%	3	3	4	0.00%	8.8%	VDQFDPFTVPTISFICR	98.6%	32.8	25	32.8	1	0	0	2042.01	339	355
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	26	27	45	0.05%	18.4%	DVNGELIAVQR	99.7%	75.7	25	68.6	2	0	0	1213.65	88	98
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	26	27	45	0.05%	18.4%	EQVSPLETTLEK	99.7%	52.1	25	45.5	2	0	0	1373.72	910	921
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	26	27	45	0.05%	18.4%	FDEIFSATR	99.7%	56.9	25	38.6	1	0	0	1085.53	176	184
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	26	27	45	0.05%	18.4%	GQDIEYIEIR	99.7%	81.5	25	66.8	2	0	0	1235.63	1157	1166
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	26	27	45	0.05%	18.4%	ILELDQELIK	99.7%	61.2	25	27	2	0	0	1213.70	474	483
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	26	27	45	0.05%	18.4%	KEEQLSSYEDK	99.7%	47.8	25	46	1	0	0	1355.63	618	628
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	26	27	45	0.05%	18.4%	KLIQDQQEQIQHLK	95.4%	22.6	25	22.6	0	1	0	1748.97	851	864
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	26	27	45	0.05%	18.4%	LEENIDNIKR	99.7%	65.5	25	49.4	2	0	0	1243.66	1060	1069
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	26	27	45	0.05%	18.4%	LIQDQQEQIQHLK	99.7%	41.2	25	37.8	1	0	0	1620.87	852	864
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	26	27	45	0.05%	18.4%	LKEIEHNLSK	99.7%	46.1	25	29.8	2	0	0	1210.68	255	264
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	26	27	45	0.05%	18.4%	LQGIDLDR	99.7%	59.7	25	48.1	2	0	0	929.51	816	823
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	26	27	45	0.05%	18.4%	MEVISLQNEK	99.7%	42.1	25	23	2	0	0	1190.61	502	511
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	26	27	45	0.05%	18.4%	NIDQCSEIVK	99.7%	60.8	25	45.7	2	0	0	1205.58	1292	1301
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	26	27	45	0.05%	18.4%	QKFDEIFSATR	99.7%	58.6	25	55.2	2	0	0	1341.68	174	184
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	26	27	45	0.05%	18.4%	QLEDWLHSK	98.2%	31.6	25	19.7	1	0	0	1155.58	575	583
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	26	27	45	0.05%	18.4%	QSIIDLK	95.5%	28.1	25	10.2	1	0	0	816.48	737	743
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	26	27	45	0.05%	18.4%	SDADENVSASDK	99.7%	69.9	25	69.9	2	0	0	1237.52	1167	1178
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	26	27	45	0.05%	18.4%	SELLVEQGR	99.7%	62.7	25	46.9	2	0	0	1030.55	344	352
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	26	27	45	0.05%	18.4%	SYENELDPLK	97.7%	30.7	25	26.5	1	0	0	1207.58	243	252
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	26	27	45	0.05%	18.4%	TLDQAIMK	98.8%	33.3	25	21.9	2	0	0	935.49	1127	1134
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	26	27	45	0.05%	18.4%	VCLTDVTIMER	99.7%	72.3	25	66.5	3	0	0	1336.66	787	797
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	26	27	45	0.05%	18.4%	VIAQLSECEK	99.7%	51.1	25	47.4	2	0	0	1176.59	983	992
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	26	27	45	0.05%	18.4%	VKEYQMELK	97.7%	30.7	25	18.9	1	0	0	1167.61	203	211
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	26	27	45	0.05%	18.4%	VLASLIIR	99.7%	64.5	25	46.7	2	0	0	884.59	1207	1214
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	26	27	45	0.05%	18.4%	WLQDNLTLR	99.7%	51.9	25	37.3	2	0	0	1158.63	1017	1025
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	26	27	45	0.05%	18.4%	YELQQLEGSSDR	99.7%	84.9	25	76.9	2	0	0	1424.67	462	473
DNA repair protein RAD51 homolog 3	RAD51C	RA51C_HUMAN	42.2	99.8%	2	2	3	0.00%	6.1%	AEALETLQIIR	99.7%	62.6	25	39.5	1	0	0	1256.72	55	65
DNA repair protein RAD51 homolog 3	RAD51C	RA51C_HUMAN	42.2	99.8%	2	2	3	0.00%	6.1%	DLVSFPLSPAVR	99.7%	53.5	25	47.6	2	0	0	1300.73	13	24
DNA replication licensing factor MCM2	MCM2	MCM2_HUMAN	101.9	100.0%	3	3	5	0.01%	3.8%	AGIVTSLQAR	99.7%	46.2	25	36.6	2	0	0	1015.59	614	623
DNA replication licensing factor MCM2	MCM2	MCM2_HUMAN	101.9	100.0%	3	3	5	0.01%	3.8%	GLALALFGGEPK	99.7%	66.8	25	58.9	2	0	0	1172.67	494	505
DNA replication licensing factor MCM2	MCM2	MCM2_HUMAN	101.9	100.0%	3	3	5	0.01%	3.8%	VAVGELTDEDVK	99.7%	79.4	25	79.4	1	0	0	1274.65	451	462
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	23	51	0.05%	29.5%	AILCLLLGGVER	99.7%	79.3	25	68.2	9	0	0	1313.76	316	327
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	23	51	0.05%	29.5%	ALKDFVASIDATYAK	99.7%	88.7	25	82.2	1	0	0	1612.86	79	93
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	23	51	0.05%	29.5%	APAGQLPR	99.7%	54.1	25	35.5	2	0	0	809.46	208	215
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	23	51	0.05%	29.5%	DAQPSFSAEDIAK	99.7%	67.6	25	65.4	2	0	0	1378.65	271	283
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	23	51	0.05%	29.5%	EAHAQSIGMNR	99.7%	77.4	25	74.9	2	0	0	1213.57	757	767
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	23	51	0.05%	29.5%	ELISDNQYR	99.7%	66.5	25	63.3	3	0	0	1137.55	38	46

DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	23	51	0.05%	29.5%	GDINILLIGDPSVAK	99.7%	83.2	25	83.2	2	0	0	1524.86	337	351
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	23	51	0.05%	29.5%	GGYTSGTFR	99.7%	46.5	25	40.8	2	0	0	945.44	249	257
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	23	51	0.05%	29.5%	GSSGVGLTAAVTTDQETGER	99.7%	123	25	123	2	0	0	1935.93	372	391
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	23	51	0.05%	29.5%	LIVNVNDLR	99.7%	54.6	25	44.2	2	0	0	1055.62	47	55
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	23	51	0.05%	29.5%	LLNNAFEELVAFQR	99.7%	70.7	25	68.8	3	0	0	1663.88	65	78
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	23	51	0.05%	29.5%	SKDIFDQLAK	99.7%	55.7	25	48.3	1	0	0	1164.63	292	301
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	23	51	0.05%	29.5%	SLAPSIHGHDYVK	99.6%	38.5	25	36.4	1	0	0	1423.73	302	314
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	23	51	0.05%	29.5%	SVDVILDDDLVDK	99.7%	51.3	25	44.9	2	0	0	1445.74	216	228
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	23	51	0.05%	29.5%	SVHYCPATK	97.6%	30.6	25	21.2	1	0	0	1062.50	144	152
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	23	51	0.05%	29.5%	TAIHEVMEQGR	99.7%	57.9	25	57.7	2	1	0	1270.62	420	430
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	23	51	0.05%	29.5%	TLETLIR	99.4%	36.2	25	9.23	2	0	0	845.51	617	623
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	23	51	0.05%	29.5%	TPMENIGLQDSLLSR	99.7%	86.4	25	85.7	4	0	0	1689.85	464	478
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	23	51	0.05%	29.5%	TVLIACNVK	99.6%	38.3	25	18	2	0	0	1017.58	258	266
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	23	51	0.05%	29.5%	VALLDVFR	99.7%	48.6	25	39.4	2	0	0	932.56	749	756
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	23	51	0.05%	29.5%	YVLCTAPR	99.7%	46.7	25	39.4	3	0	0	979.50	357	364
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	13	13	25	0.03%	18.8%	ALADDDFLTVTGK	99.7%	97	25	97	2	0	0	1365.69	846	858
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	13	13	25	0.03%	18.8%	DMFEEALR	97.5%	30.4	25	17.6	1	0	0	1010.46	838	845
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	13	13	25	0.03%	18.8%	GILLQLFGGTR	99.7%	87.1	25	84.5	5	0	0	1174.69	479	489
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	13	13	25	0.03%	18.8%	GMVSAYPR	99.3%	36.2	25	26.2	1	0	0	880.43	725	732
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	13	13	25	0.03%	18.8%	IAEPSVCGR	99.7%	55.5	25	35.1	2	0	0	988.49	322	330
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	13	13	25	0.03%	18.8%	LASALAPSIYEHEDIKK	98.1%	25.8	25	24.7	0	2	0	1885.01	462	478
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	13	13	25	0.03%	18.8%	LVIWGTDVNVAACK	99.7%	80.9	25	80.9	2	0	0	1545.81	150	163
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	13	13	25	0.03%	18.8%	QRPDLGSAQK	99.4%	36.6	25	21.2	2	0	0	1099.59	114	123
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	13	13	25	0.03%	18.8%	SQLLQYVYNLVPR	99.7%	92.4	25	86.8	1	0	0	1592.88	517	529
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	13	13	25	0.03%	18.8%	TGIVDISILTTGMSATSR	99.7%	81.7	25	81.7	2	0	0	1822.96	778	795
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	13	13	25	0.03%	18.8%	TSVLAAANPIESQWNPK	99.7%	77.4	25	71.8	2	0	0	1825.94	611	627
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	13	13	25	0.03%	18.8%	TTIENIQLPHTLLSR	99.7%	58.1	25	45.9	1	0	0	1735.97	629	643
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	13	13	25	0.03%	18.8%	YQQLFEDIR	99.7%	61.4	25	39.5	2	0	0	1211.61	820	828
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	18	31	0.03%	26.6%	AGITTTLNSR	99.7%	66.4	25	49	1	0	0	1033.56	472	481
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	18	31	0.03%	26.6%	AIACLLFGGSR	99.7%	79.8	25	76.7	3	0	0	1164.62	352	362
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	18	31	0.03%	26.6%	CSVLAAANSVFGR	99.7%	86.2	25	82.6	2	0	0	1351.68	482	494
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	18	31	0.03%	26.6%	FAIGSQVSEHSIIK	99.7%	63.7	25	57.1	1	0	0	1515.82	683	696
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	18	31	0.03%	26.6%	HMQLYCDR	99.7%	41.8	25	27	2	0	0	1138.48	244	251
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	18	31	0.03%	26.6%	IPGIIIAASAVR	99.7%	89	25	89	2	0	0	1180.74	151	162
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	18	31	0.03%	26.6%	LAALPNVYEVISK	99.7%	83.3	25	83.3	3	0	0	1416.81	325	337
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	18	31	0.03%	26.6%	LQELPDAVPHGEMPR	99.7%	44.9	25	44.9	1	0	0	1704.84	229	243
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	18	31	0.03%	26.6%	LQPFATEADVEEALR	99.7%	97.1	25	94.2	2	0	0	1688.85	628	642
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	18	31	0.03%	26.6%	NTLTNIAMRPGLEGYALPR	99.7%	52.6	25	44.3	0	2	0	2087.11	177	195
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	18	31	0.03%	26.6%	QLEAIVR	98.4%	32.4	25	12.5	2	0	0	828.49	612	618
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	18	31	0.03%	26.6%	QPAEHLQLLEEAAK	99.0%	28.2	25	23.4	0	2	0	1576.83	91	104
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	18	31	0.03%	26.6%	SIAPSIFGGTDMKK	99.7%	55.1	25	50.4	2	0	0	1451.76	338	351
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	18	31	0.03%	26.6%	VLGIQVDTDGSGR	99.7%	90.8	25	90.8	2	0	0	1316.68	296	308
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	18	31	0.03%	26.6%	VLQLMLR	99.7%	46.6	25	29.2	2	0	0	872.54	711	717
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	18	31	0.03%	26.6%	VTIMGIYSIK	99.7%	58.7	25	44.6	2	0	0	1124.64	263	272
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	30	0.03%	24.0%	DFYVAFQDLPTR	99.7%	74.3	25	62.2	2	0	0	1471.72	109	120
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	30	0.03%	24.0%	EIESEIDSEEELINK	99.7%	90.2	25	82.1	1	0	0	1776.84	755	769
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	30	0.03%	24.0%	ELRDEEQTAESIK	99.7%	63.7	25	53.6	1	0	0	1547.75	314	326
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	30	0.03%	24.0%	ESEDFIVEQYK	99.7%	45	25	45	1	0	0	1386.64	589	599
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	30	0.03%	24.0%	GDINVCIVGDPSTAK	99.7%	49.4	25	48.6	1	0	0	1545.76	388	402
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	30	0.03%	24.0%	GVLLMLFGGVPK	99.7%	69.1	25	49.5	2	0	0	1230.73	367	378
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	30	0.03%	24.0%	HVEEFSPR	99.0%	34.3	25	34.3	2	0	0	1000.48	408	415

DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	30	0.03%	24.0%	IQETQAELPR	99.7%	75.1	25	59.4	2	0	0	1184.63	208	217
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	30	0.03%	24.0%	ISNLIVLHLR	99.7%	41.2	25	33.9	2	0	0	1177.74	723	732
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	30	0.03%	24.0%	LGFSEYCR	99.7%	41	25	41	2	0	0	1031.46	715	722
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	30	0.03%	24.0%	LVFLACCVAPTNPR	99.7%	91.1	25	90.3	2	0	0	1617.82	296	309
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	30	0.03%	24.0%	QNINLSAPIMSR	99.3%	36.1	25	27	2	0	0	1343.71	518	529
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	30	0.03%	24.0%	SLEVILR	99.7%	46.2	25	35.7	2	0	0	829.51	223	229
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	30	0.03%	24.0%	TSILAAANPISGHYDR	99.7%	56.5	25	55.3	1	1	0	1685.86	497	512
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	30	0.03%	24.0%	VSGVDGYETEGIR	99.7%	79	25	50.3	2	0	0	1381.66	270	282
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	30	0.03%	24.0%	YLQLAEELIRPER	99.7%	43.7	25	43.7	2	0	0	1629.90	46	58
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	30	0.03%	24.0%	YTQPNICR	99.7%	39.4	25	36	2	0	0	1051.50	174	181
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	19	22	46	0.05%	33.9%	AGILTTLNAR	99.7%	73.3	25	57.5	2	0	0	1029.61	472	481
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	19	22	46	0.05%	33.9%	ALLLLLVGGVDQSPR	99.7%	94.3	25	94.3	5	0	0	1550.93	353	367
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	19	22	46	0.05%	33.9%	CSILAAANPAYGR	99.7%	73.7	25	69.4	2	0	0	1363.68	482	494
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	19	22	46	0.05%	33.9%	DSLLGDKGQTAR	99.7%	56.9	25	54.6	2	0	0	1260.65	642	653
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	19	22	46	0.05%	33.9%	GNINICLMGDPGVAK	99.7%	44.8	25	44.8	1	0	0	1558.77	373	387
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	19	22	46	0.05%	33.9%	GSSGVGLTAAVLR	99.7%	91.3	25	76.2	2	0	0	1187.67	408	420
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	19	22	46	0.05%	33.9%	IAQPGDHVSVTGIFLPILR	99.7%	57.1	25	48.5	2	2	0	2033.15	264	282
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	19	22	46	0.05%	33.9%	LAASIAPEIYGHEDVKK	98.1%	25.9	25	24.1	0	1	0	1840.98	336	352
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	19	22	46	0.05%	33.9%	LFADAVQELLPQYK	99.7%	80.7	25	65.7	4	0	0	1634.88	76	89
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	19	22	46	0.05%	33.9%	MQEHSDQVPVGNIPR	98.1%	25.8	25	18.3	0	1	0	1722.82	237	251
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	19	22	46	0.05%	33.9%	QIAEEDFYEK	99.7%	44.7	25	42.3	2	0	0	1271.58	326	335
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	19	22	46	0.05%	33.9%	QVVQGLLSETYLEAHR	99.7%	74.3	25	74.3	0	2	0	1842.97	287	302
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	19	22	46	0.05%	33.9%	SITVLVEGENTR	99.7%	92.9	25	76.6	2	0	0	1317.70	252	263
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	19	22	46	0.05%	33.9%	SLEQNIQLPAALLSR	99.7%	89.1	25	89.1	2	0	0	1652.93	500	514
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	19	22	46	0.05%	33.9%	SPQNQYPAELMR	99.7%	41.7	25	41.7	4	0	0	1433.68	121	132
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	19	22	46	0.05%	33.9%	SQLLSYIDR	99.7%	54.2	25	33.9	2	0	0	1094.58	388	396
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	19	22	46	0.05%	33.9%	TLLAILR	99.7%	46.4	25	13.5	2	0	0	799.54	605	611
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	19	22	46	0.05%	33.9%	TQRPADVIFATVR	99.7%	35.1	25	30.3	2	2	0	1473.82	654	666
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	19	22	46	0.05%	33.9%	YGNQLVR	99.7%	49.7	25	29.2	2	0	0	849.46	33	39
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	11	26	0.03%	15.7%	AEEVATFFAK	99.7%	60.4	25	46.3	4	0	0	1112.56	253	262
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	11	26	0.03%	15.7%	AVAILCNHQR	99.7%	70.8	25	61.3	2	0	0	1181.62	625	634
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	11	26	0.03%	15.7%	AVALYFIDK	99.7%	53.1	25	31.1	2	0	0	1039.58	476	484
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	11	26	0.03%	15.7%	ELTAPDENIPAK	99.7%	41.4	25	38.2	1	0	0	1297.66	604	615
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	11	26	0.03%	15.7%	GPVFAPPYEPLPENVK	99.7%	57.5	25	55.3	4	0	0	1753.92	224	239
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	11	26	0.03%	15.7%	HLQDLMEGLTAK	99.7%	53.6	25	28.6	2	0	0	1355.70	576	587
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	11	26	0.03%	15.7%	LEVQATDREENK	99.7%	55.1	25	55.1	3	0	0	1431.71	701	712
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	11	26	0.03%	15.7%	LNTGILNK	97.8%	30.9	25	17	1	0	0	872.52	568	575
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	11	26	0.03%	15.7%	MLDHEYTTK	99.7%	42.5	25	36.8	2	0	0	1137.52	263	271
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	11	26	0.03%	15.7%	TYNASITLQQQLK	99.7%	80.5	25	73.4	4	0	0	1507.81	591	603
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	11	26	0.03%	15.7%	YIMLNPSSR	98.8%	33.5	25	31.2	1	0	0	1080.55	426	434
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	17	18	35	0.04%	13.2%	DKYGVFPLR	98.8%	33.4	25	31.1	2	0	0	1094.60	479	487
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	17	18	35	0.04%	13.2%	DPALNSGVSQKPDPAK	99.7%	41.5	25	38.9	1	0	0	1623.83	1444	1459
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	17	18	35	0.04%	13.2%	ELILFSNSDNER	99.7%	67.3	25	63.5	2	0	0	1436.70	702	713
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	17	18	35	0.04%	13.2%	EWLLGMLGAESAK	99.5%	37.7	25	35.3	1	0	0	1404.72	1035	1047
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	17	18	35	0.04%	13.2%	FLEEFITPIVK	99.7%	50.6	25	44.6	4	0	0	1335.76	569	579
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	17	18	35	0.04%	13.2%	FTVETASR	99.7%	56.3	25	47.6	2	0	0	910.46	177	184
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	17	18	35	0.04%	13.2%	GFQQISFVNSIATSK	99.7%	95.7	25	95.7	2	0	0	1626.85	307	321
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	17	18	35	0.04%	13.2%	HVDYVADQIVTK	99.7%	82.2	25	81.1	2	0	0	1387.72	325	336
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	17	18	35	0.04%	13.2%	IFDEILVNAADNK	99.7%	97.4	25	92	4	0	0	1461.76	84	96
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	17	18	35	0.04%	13.2%	IIIENKPK	98.0%	31.4	25	22.5	1	0	0	954.60	1063	1070
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	17	18	35	0.04%	13.2%	LCNIFSTK	96.0%	28.5	25	19.7	1	0	0	982.50	169	176

DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	17	18	35	0.04%	13.2%	NSTECTLILTEGDSAK	99.7%	89.6	25	80.6	1	0	0	1738.82	451	466
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	17	18	35	0.04%	13.2%	SFGSTCQLSEK	99.7%	49	25	41.4	2	0	0	1243.56	387	397
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	17	18	35	0.04%	13.2%	TLAVSGLGVVGR	99.7%	64.4	25	59.1	2	0	0	1128.67	467	478
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	17	18	35	0.04%	13.2%	TQMAEVLPSPR	99.3%	35.6	25	30.5	1	0	0	1228.64	1205	1215
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	17	18	35	0.04%	13.2%	YIFTMLSSLAR	99.7%	53.1	25	52.6	5	0	0	1301.69	805	815
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	17	18	35	0.04%	13.2%	YSGPEDDAAISLAFSK	99.7%	66.8	25	57.7	2	0	0	1670.79	640	655
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	8	8	19	0.02%	7.7%	DLIQMLVQR	99.7%	57	25	48.8	4	0	0	1115.62	1093	1101
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	8	8	19	0.02%	7.7%	ELILFSNSDNER	99.7%	67.3	25	63.5	2	0	0	1436.70	723	734
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	8	8	19	0.02%	7.7%	GFQQISFVNSIATTK	99.7%	84.9	25	70.4	2	0	0	1640.86	328	342
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	8	8	19	0.02%	7.7%	IFDEILVNAADNK	99.7%	97.4	25	92	4	0	0	1461.76	105	117
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	8	8	19	0.02%	7.7%	LAQAEAAGLHK	99.7%	53.7	25	42.1	3	0	0	1108.61	998	1008
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	8	8	19	0.02%	7.7%	LCNIFSTK	96.0%	28.5	25	19.7	1	0	0	982.50	190	197
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	8	8	19	0.02%	7.7%	LLFPAVDDNLLK	99.7%	74.5	25	65.9	4	0	0	1357.77	837	848
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	8	8	19	0.02%	7.7%	LPNYDAR	97.0%	29.7	25	22.2	1	0	0	848.43	885	891
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	8	8	19	0.02%	7.7%	NTVEITELPVR	99.7%	51.5	25	48.2	2	0	0	1270.70	940	950
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	8	8	19	0.02%	7.7%	SQDFGNLFSFPSYSQK	99.5%	37.6	25	37.6	1	0	0	1851.85	1441	1456
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	8	8	19	0.02%	7.7%	YIFTMLSTLAR	99.7%	52.1	25	46.8	2	0	0	1315.71	826	836
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	AALSALESFLK	99.7%	84.2	25	59.1	9	0	0	1149.65	311	321
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	AAYLSDPR	99.0%	34.3	25	19.7	2	0	0	892.45	3826	3833
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	AIRPQIDLKR	96.5%	29.1	25	12.3	2	0	0	1209.74	255	264
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	AQEPESGLSEETQVK	99.7%	73.1	25	63.3	2	0	0	1631.78	4091	4105
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	ATQMPEGGQGAPPMYQLYK	99.7%	51.3	25	49.1	1	0	0	2082.96	945	963
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	ATQQQHDFTLTQTADGR	99.7%	66.5	25	60.7	1	2	0	1917.91	2637	2653
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	AYVPALQMAFK	98.7%	33.3	25	33.3	4	0	0	1238.66	747	757
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	CFFLSK	99.1%	34.5	25	23.9	2	0	0	801.40	3187	3192
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	CGAALAGHQLIR	99.7%	69.7	25	65.1	2	0	0	1266.67	25	36
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	DCLSIPYR	96.4%	28.9	25	22.5	1	0	0	1023.49	2247	2254
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	DFGLLVFVR	99.7%	69	25	56.3	4	0	0	1065.61	62	70
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	DFSAFINLVEFCR	99.7%	44.1	25	38.8	2	0	0	1617.77	619	631
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	DILETHLR	99.7%	43.2	25	28	2	0	0	996.55	1413	1420
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	DILPCLDGYLK	99.7%	45.9	25	29.8	2	0	0	1306.67	791	801
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	DLCNTHLMR	98.9%	33.7	25	33.4	1	0	0	1175.53	1362	1370
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	DLLLNTMSQEEK	98.8%	33.4	25	27.3	1	0	0	1436.69	3814	3825
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	DQNILLGTTYR	99.7%	90.9	25	78.5	4	0	0	1293.68	3325	3335
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	DVDFMYVELIQR	99.7%	89.1	25	79.1	4	0	0	1543.75	380	391
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	EFDKHFGK	94.5%	27.3	25	21	1	0	0	1007.49	3639	3646
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	EIFNFVLK	99.4%	36.9	25	19.1	2	0	0	1009.57	247	254
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	ELLNPVVEFVSHPSTTCR	99.7%	84.5	25	77.5	2	2	0	2085.04	2453	2470
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	EQQHVMEELFQSSFR	99.7%	47.6	25	39.2	0	3	0	1910.87	1769	1783
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	ETGLMYSIMVHALR	99.7%	50	25	46.3	1	0	0	1620.82	3976	3989
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	FMNAVFFLLPK	99.7%	72.1	25	60.9	4	0	0	1326.73	2378	2388
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	FNNYVDCMK	99.6%	38	25	31.6	1	0	0	1190.50	1736	1744
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	FNNYVDCMKK	98.1%	31.5	25	20.1	2	0	0	1318.59	1736	1745
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	FYGELALK	99.2%	35.1	25	29.2	1	0	0	940.51	156	163
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	FYQGFLFSEKPEK	99.7%	49.5	25	44.4	2	0	0	1619.81	1961	1973
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	GGSWIQEINVAEK	99.7%	55.2	25	47.1	1	0	0	1430.73	4024	4036
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	GIFTSEIGTK	99.7%	70.2	25	63.1	3	0	0	1052.56	2941	2950
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	GLSSLLCNFTK	99.7%	58.6	25	44.2	2	0	0	1239.64	226	236
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	GPESESEDHRASGEVR	95.5%	22.7	25	22.7	0	1	0	1741.77	500	515
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	GYGLFAGPCK	99.5%	37	25	26.3	1	0	0	1069.51	365	374
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	HGDLPDIQIK	99.7%	51.7	25	43.6	2	0	0	1135.61	2777	2786

DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	HNLEIIK	99.7%	50.3	25	19.9	2	0	0	866.51	2233	2239
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	HSSLITPLQAVAQR	99.7%	67.5	25	64.4	2	2	0	1520.85	2787	2800
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	IAGFDER	96.6%	29.1	25	25.7	1	0	0	807.40	3719	3725
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	IAPYSVEIK	99.3%	35.6	25	20.7	2	0	0	1019.58	100	108
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	ICSKPVVLPK	98.7%	33.2	25	12.6	2	0	0	1140.68	490	499
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	IKYFEGVSPK	98.2%	31.8	25	23.2	1	0	0	1167.64	680	689
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	ILDVMYSR	99.7%	52.3	25	50.7	4	0	0	1012.51	1876	1883
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	ILELSGSSSEDSEK	99.7%	106	25	98.8	3	0	0	1480.70	3359	3372
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	IMEFTTTLLNTSPEGWK	99.7%	85.8	25	72.4	4	0	0	1983.97	1341	1357
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	INQVFHGSCITEGNELTK	99.7%	54.4	25	54.4	0	2	0	2046.99	1896	1913
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	IPALDLLIK	99.3%	35.9	25	35.9	1	0	0	995.65	125	133
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	KNILEESLCELVAK	99.7%	69.4	25	69.4	2	0	0	1645.88	2334	2347
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	KQNNFSLAMK	99.7%	59.7	25	51.6	4	0	0	1180.61	3248	3257
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LAAVVSACK	99.7%	68.2	25	54.1	2	0	0	918.51	1448	1456
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LACDVDQVTR	99.7%	67	25	48.7	2	0	0	1176.57	972	981
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LAGANPAVITCDELLLGHEK	99.7%	49.4	25	44.7	0	1	0	2121.10	4051	4070
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LATTILQHWK	99.7%	44.9	25	44.9	2	0	0	1210.69	1618	1627
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LCYDAFTENMAGENQLLER	99.7%	97.7	25	90.8	3	0	0	2274.02	1918	1936
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LGASLAFNNIYR	99.7%	69.8	25	41.9	4	0	0	1338.72	1076	1087
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LGLPGDEVDNK	96.3%	28.8	25	28.5	1	0	0	1156.58	2705	2715
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LGLPGDEVDNKVK	99.7%	46.9	25	36.7	2	0	0	1383.75	2705	2717
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LGNPIVPLNIR	99.7%	54.3	25	54.3	2	0	0	1205.74	2133	2143
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LLEEALLR	99.7%	66.6	25	61.3	4	0	0	956.58	2892	2899
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LLLQGEADQSLLTFIDK	99.7%	82.2	25	82.2	4	0	0	1904.04	3051	3067
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LLNFLMK	99.7%	39.1	25	28.4	3	0	0	878.52	2215	2221
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LLNTWTNR	99.7%	42	25	38.1	3	0	0	1017.55	3160	3167
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LLPAELPAKR	98.5%	32.5	25	32.5	1	0	0	1107.69	2900	2909
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LLQDFNR	99.4%	36.3	25	19.3	2	0	0	905.48	2836	2842
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LLQIIER	99.7%	45.2	25	24.9	4	0	0	884.56	3468	3474
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LLSITVR	99.7%	39.8	25	15.6	2	0	0	801.52	669	675
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LNESTFDTQITK	99.7%	84.6	25	79.2	2	0	0	1396.70	1858	1869
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LNESTFDTQITKK	99.7%	60.5	25	56.5	2	0	0	1524.79	1858	1870
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LPKDDVHAK	99.7%	43	25	24.8	2	0	0	1022.56	1884	1892
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LPSNTLDR	99.5%	37.7	25	26.5	2	0	0	915.49	2531	2538
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LPVLAGCLK	99.7%	47.4	25	40.1	2	0	0	970.58	217	225
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LQETLSAADR	99.7%	77.4	25	60.1	3	0	0	1103.57	15	24
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LQYFMEQFYGIIR	99.7%	61.8	25	53.7	1	0	0	1707.86	338	350
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LSDFNDITNMLLLK	99.7%	74.8	25	67.8	4	0	0	1652.86	3656	3669
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LSFAVPFR	99.7%	52.2	25	44.8	4	0	0	936.53	892	899
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LSLMYAR	99.7%	51.3	25	25.8	4	0	0	869.46	2739	2745
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LVINTEEVFRPYAK	99.7%	54.5	25	50.8	2	1	0	1678.92	2149	2162
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	LYSLALHPNAFK	99.7%	39.7	25	39.7	2	2	0	1373.76	1063	1074
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	MAVLALLAK	99.7%	62.1	25	48	4	0	0	929.59	1643	1651
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	MDPMNIWDDIITNR	99.7%	67.9	25	67.9	2	0	0	1765.79	3173	3186
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	MEVQEQEEDISSLIR	99.7%	115	25	103	1	0	0	1805.86	3218	3232
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	MKQDAQVVLYR	99.7%	71.2	25	61.8	2	1	0	1350.72	2763	2773
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	MSPYKDILETHLR	99.7%	47.4	25	44.1	0	2	0	1618.83	1408	1420
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	MSTSPEAFLALR	99.7%	71.2	25	60	9	0	0	1322.68	3890	3901
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	MYAALGDPK	99.7%	44.8	25	43.3	4	0	0	965.48	3613	3621
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	NCISTVVHQGLIR	99.7%	68.3	25	59.4	2	2	0	1496.80	477	489
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	NILEESLCELVAK	99.7%	78	25	77.4	2	0	0	1517.79	2335	2347

DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	NLDLAVLELMQSSVDNTK	99.7%	116	25	116	3	0	0	2006.01	1574	1591
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	NLLIFENLIDLK	99.7%	94.3	25	81.4	2	0	0	1444.84	1974	1985
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	NLLIFENLIDLKR	99.7%	43	25	37.6	1	0	0	1600.94	1974	1986
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	NLLTVTSSDEMMK	99.7%	103	25	99.2	6	0	0	1500.69	869	881
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	NLSSNEAISLEEIR	99.7%	114	25	78	3	0	0	1574.80	839	852
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	NNWEVSALSR	99.7%	66.2	25	58.4	4	0	0	1175.58	811	820
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	NVDSNNKELSIAIR	99.7%	75.4	25	69.2	2	0	0	1572.83	351	364
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	QCLPSLDLSCK	99.7%	62.9	25	50.2	2	0	0	1320.63	1498	1508
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	QDAQVVLYR	99.5%	37.5	25	11.8	1	0	0	1091.58	2765	2773
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	QFINLMLPMK	99.7%	40.7	25	37.2	3	0	0	1266.66	3966	3975
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	QGNLSSQVPLKR	99.7%	45	25	36.6	1	0	0	1326.75	3148	3159
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	QITPQQQEK	98.3%	32	25	24.3	1	0	0	1099.57	1043	1051
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	QITQSALLAEAR	99.7%	81.5	25	58.4	4	0	0	1300.72	2951	2962
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	QLFSSLFSGILK	99.7%	87.1	25	72.1	3	0	0	1339.76	2807	2818
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	QMFLTQTDTGDDR	99.7%	60.3	25	60.3	1	0	0	1527.67	394	406
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	RLSFAVPFR	99.7%	41.1	25	40.5	2	0	0	1092.63	891	899
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	SDPGLLTNTMDVFVK	99.7%	83.9	25	78.6	6	0	0	1636.83	3993	4007
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	SIELFYK	98.0%	31.4	25	17.3	2	0	0	899.49	1187	1193
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	SIGEYDVLR	99.7%	48.8	25	45.5	3	0	0	1051.54	2932	2940
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	SKDFVQVMR	99.7%	50.8	25	39.4	2	0	0	1109.58	2417	2425
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	SLEYCSTASIDSENPPDLNK	99.7%	92.4	25	92.4	2	0	0	2240.00	3010	3029
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	SLGPPQGEEDSVPR	99.7%	73.8	25	73.4	2	0	0	1467.71	2107	2120
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	SLGTIQQCCDAIDHLCR	99.7%	39.7	25	39.7	0	2	0	2046.92	1120	1136
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	SLNSIEFR	99.6%	38.3	25	25.3	2	0	0	965.51	72	79
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	SMEEDPQTSR	98.7%	33.2	25	25.8	2	0	0	1179.49	237	246
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	SQGCSEQVLTVLK	99.7%	83.6	25	77.5	4	0	0	1448.74	3290	3302
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	STVLTPMFVETQASQGTLQTR	99.7%	112	25	112	4	1	0	2295.17	2599	2619
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	TETVTSFR	99.7%	49.5	25	42	5	0	0	940.47	3865	3872
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	TFPVLLR	98.3%	32.1	25	23.2	1	0	0	845.52	965	971
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	TSALSDETKNNWEVSALSR	99.7%	46.8	25	46.8	0	2	0	2108.03	802	820
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	TVGALQVLGTEAQSSLLK	99.7%	108	25	105	4	0	0	1815.02	1275	1292
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	TVSLLDENNVSSYLSK	99.7%	121	25	114	4	0	0	1768.90	3303	3318
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	TYSVVPMTSR	98.8%	33.5	25	27.4	2	0	0	1140.57	3790	3799
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	VCLDIIYK	98.9%	33.7	25	14.2	2	0	0	1023.55	2434	2441
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	VFLALAAK	99.4%	36.5	25	22	2	0	0	832.53	464	471
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	VLEQLIVAHFPMQSR	99.7%	41.3	25	41.3	3	1	0	1767.96	1713	1727
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	VPADLLKR	99.7%	51.8	25	39.3	2	0	0	911.57	3878	3885
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	VTELALTASDR	99.7%	103	25	91.2	4	0	0	1175.63	914	924
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	VTVMASLR	99.7%	43.6	25	32.7	2	0	0	876.50	3726	3733
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	VVQMLGSLGGQINK	99.7%	84.4	25	55.1	5	0	0	1459.79	855	868
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	YAVPSAGLR	98.2%	31.8	25	25.7	3	0	0	933.52	265	273
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	YNFPVEVEVPMER	99.7%	64.9	25	61.2	3	0	0	1608.77	1988	2000
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	YPEETLSLMTK	99.7%	42.3	25	36.5	1	0	0	1311.65	3475	3485
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	129	160	336	0.35%	33.7%	YSCFALFVK	99.7%	39.1	25	33.3	2	0	0	1134.57	701	709
DNA-directed RNA polymerase I subunit RPA2	POLR1B	RPA2_HUMAN	128.2	100.0%	3	3	3	0.00%	3.3%	ELFFLPLGFALK	99.1%	34.8	25	34.8	1	0	0	1394.81	243	254
DNA-directed RNA polymerase I subunit RPA2	POLR1B	RPA2_HUMAN	128.2	100.0%	3	3	3	0.00%	3.3%	HLTDPSYGIPR	96.4%	28.9	25	27.9	1	0	0	1255.64	18	28
DNA-directed RNA polymerase I subunit RPA2	POLR1B	RPA2_HUMAN	128.2	100.0%	3	3	3	0.00%	3.3%	SDTIDTVSVPYVFR	99.7%	40.5	25	36	1	0	0	1598.81	1104	1117
DNA-directed RNA polymerase I subunit RPA49	POLR1E	RPA49_HUMAN	54.0	100.0%	4	4	5	0.01%	9.8%	AAETIIDTK	98.9%	33.8	25	26.7	1	0	0	961.52	233	241
DNA-directed RNA polymerase I subunit RPA49	POLR1E	RPA49_HUMAN	54.0	100.0%	4	4	5	0.01%	9.8%	CIWFLDTLIK	99.7%	44.6	25	37.3	1	0	0	1308.70	338	347
DNA-directed RNA polymerase I subunit RPA49	POLR1E	RPA49_HUMAN	54.0	100.0%	4	4	5	0.01%	9.8%	LSYVGNNFGTGALK	97.3%	30.1	25	30.1	1	0	0	1440.75	129	142
DNA-directed RNA polymerase I subunit RPA49	POLR1E	RPA49_HUMAN	54.0	100.0%	4	4	5	0.01%	9.8%	SALGPGVPHIINTK	99.7%	47.3	25	43.4	2	0	0	1403.80	358	371

DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	6	6	12	0.01%	5.3%	EGEEQLQTQHQK	99.7%	44.3	25	35.8	2	0	0	1454.69	135	146
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	6	6	12	0.01%	5.3%	GPIQILNR	99.7%	53	25	44.5	2	0	0	910.55	1065	1072
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	6	6	12	0.01%	5.3%	LLLAALGR	99.5%	37.5	25	15.1	2	0	0	826.55	372	379
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	6	6	12	0.01%	5.3%	NLTYSAPLYVDITK	99.7%	61.7	25	56.1	2	0	0	1597.85	117	130
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	6	6	12	0.01%	5.3%	QEVPIIIVFR	99.7%	55.2	25	42.7	2	0	0	1213.73	265	274
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	6	6	12	0.01%	5.3%	VSGDDVIIGK	99.6%	38.8	25	27	2	0	0	1002.55	860	869
DNA-directed RNA polymerase II subunit RPB7	POLR2G	RPB7_HUMAN	19.3	100.0%	3	3	4	0.00%	22.7%	LFTEVEGTCTGK	99.7%	46.5	25	39.4	1	0	0	1341.64	30	41
DNA-directed RNA polymerase II subunit RPB7	POLR2G	RPB7_HUMAN	19.3	100.0%	3	3	4	0.00%	22.7%	VGLFTEIGPMSCFISR	98.3%	31.9	25	31.9	1	0	0	1829.89	95	110
DNA-directed RNA polymerase II subunit RPB7	POLR2G	RPB7_HUMAN	19.3	100.0%	3	3	4	0.00%	22.7%	YFGPNLLNTVK	99.7%	50.9	25	41.7	2	0	0	1265.69	17	27
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	9	9	14	0.01%	7.2%	AEALVLMGTK	98.3%	31.9	25	28.9	1	0	0	1048.57	517	526
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	9	9	14	0.01%	7.2%	AQENLNPLVVLNLFK	99.7%	74.5	25	74.5	2	0	0	1711.97	214	228
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	9	9	14	0.01%	7.2%	GFSIGIGDVTPGQGLLK	99.7%	54.3	25	54.3	2	0	0	1658.91	695	711
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	9	9	14	0.01%	7.2%	IDEVAVPVHVAK	99.7%	52.4	25	38.6	1	0	0	1276.73	377	388
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	9	9	14	0.01%	7.2%	LAPVYLSNR	99.6%	38.3	25	34.5	1	0	0	1032.58	686	694
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	9	9	14	0.01%	7.2%	LLVEGDNLR	99.7%	39.1	25	22.1	1	0	0	1028.57	1225	1233
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	9	9	14	0.01%	7.2%	LTEIIFLNDVIK	99.7%	58.3	25	52	2	0	0	1417.83	283	294
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	9	9	14	0.01%	7.2%	NNIFYILLR	99.7%	51.2	25	35.6	3	0	0	1165.67	661	669
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	9	9	14	0.01%	7.2%	YGDIVER	99.5%	37.5	25	31.1	1	0	0	851.43	446	452
DNA-directed RNA polymerase III subunit RPC2	POLR3B	RPC2_HUMAN	127.8	100.0%	3	3	3	0.00%	3.4%	GAVGASVTSSTHEK	99.7%	69.2	25	68.8	1	0	0	1330.66	197	210
DNA-directed RNA polymerase III subunit RPC2	POLR3B	RPC2_HUMAN	127.8	100.0%	3	3	3	0.00%	3.4%	LNECPLDPGGYFIVK	99.7%	39.8	25	39.7	1	0	0	1721.86	158	172
DNA-directed RNA polymerase III subunit RPC2	POLR3B	RPC2_HUMAN	127.8	100.0%	3	3	3	0.00%	3.4%	VILIQEQLSK	99.7%	85	25	59.1	1	0	0	1170.71	177	186
DNA-directed RNA polymerase III subunit RPC3	POLR3C	RPC3_HUMAN	60.6	99.8%	2	2	3	0.00%	3.2%	LADTHFVQR	97.4%	30.2	25	15.9	1	0	0	1086.57	151	159
DNA-directed RNA polymerase III subunit RPC3	POLR3C	RPC3_HUMAN	60.6	99.8%	2	2	3	0.00%	3.2%	SIANLIER	99.7%	44.3	25	37.2	2	0	0	915.53	442	449
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	14	15	23	0.02%	13.9%	ILEASQLK	99.0%	34.2	25	12.9	1	0	0	901.54	1198	1205
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	14	15	23	0.02%	13.9%	LLQEAPGK	98.7%	33	25	15.3	1	0	0	855.49	194	201
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	14	15	23	0.02%	13.9%	LQALFTAVLLSEEDR	96.3%	28.8	25	28.8	1	0	0	1704.92	330	344
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	14	15	23	0.02%	13.9%	LQMPFQSGEFK	99.7%	45.2	25	32.1	2	0	0	1327.64	144	154
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	14	15	23	0.02%	13.9%	LSLAQHLR	99.7%	44	25	36.8	2	0	0	937.56	783	790
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	14	15	23	0.02%	13.9%	LSLDVEQAPSGQHSQAQLSGQQQR	99.7%	62.4	25	62.4	0	2	0	2592.28	202	225
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	14	15	23	0.02%	13.9%	QDQDAGTIER	99.7%	49.5	25	42.5	2	0	0	1132.52	309	318
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	14	15	23	0.02%	13.9%	QLQAESVSEVVVNR	99.7%	91.6	25	90.7	2	0	0	1557.82	72	85
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	14	15	23	0.02%	13.9%	QYWEELGAPEALR	99.7%	52.5	25	42.1	1	0	0	1561.76	551	563
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	14	15	23	0.02%	13.9%	SLQEMFSGTR	99.7%	52.2	25	46.6	1	0	0	1155.55	1039	1048
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	14	15	23	0.02%	13.9%	VAQVLEGFITR	99.7%	74.2	25	65.3	2	0	0	1232.70	977	987
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	14	15	23	0.02%	13.9%	VCVVSVEKPTLPSK	99.7%	41.9	25	40.3	1	1	0	1542.86	412	425
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	14	15	23	0.02%	13.9%	VLDLVLQLFQAK	99.7%	77.2	25	62.3	2	0	0	1386.84	713	724
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	14	15	23	0.02%	13.9%	VSGQVQALQNHYR	99.7%	57.5	25	51.8	2	0	0	1499.77	519	531
DNA-directed RNA polymerases I and III subunit RPAC1	POLR1C	RPAC1_HUMAN	39.2	100.0%	3	4	6	0.01%	11.3%	FSPVATASYR	99.7%	56.8	25	50.3	2	0	0	1098.56	225	234
DNA-directed RNA polymerases I and III subunit RPAC1	POLR1C	RPAC1_HUMAN	39.2	100.0%	3	4	6	0.01%	11.3%	ILLAEVPTMAVEK	99.7%	63.7	25	63.7	3	0	0	1413.80	79	91
DNA-directed RNA polymerases I and III subunit RPAC1	POLR1C	RPAC1_HUMAN	39.2	100.0%	3	4	6	0.01%	11.3%	NQGDEEGTEIDTLQFR	99.7%	89.6	25	89.6	1	0	0	1851.84	126	141
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	4	5	10	0.01%	26.7%	ADQFEYVMYGK	99.7%	66.7	25	64.5	2	0	0	1350.60	85	95
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	4	5	10	0.01%	26.7%	IEGDETSTEAATR	99.7%	71.4	25	71.4	2	0	0	1379.63	99	111
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	4	5	10	0.01%	26.7%	LSAYVSYGGLLMR	99.7%	80.6	25	72.4	4	0	0	1445.75	112	124
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	4	5	10	0.01%	26.7%	VYRIEGDETSTEAATR	99.7%	53.9	25	53.9	2	0	0	1797.86	96	111
DNA-directed RNA polymerases I, II, and III subunit RPABC5	POLR2L	RPAB5_HUMAN	7.6	99.8%	2	3	5	0.01%	29.9%	LLNYAPLEK	99.1%	34.7	25	24.6	1	0	0	1060.60	59	67
DNA-directed RNA polymerases I, II, and III subunit RPABC5	POLR2L	RPAB5_HUMAN	7.6	99.8%	2	3	5	0.01%	29.9%	MLLAHVDLIEK	99.7%	57.8	25	53.2	4	0	0	1297.72	48	58
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	4	4	7	0.01%	13.1%	ELYDKGGEQAIK	99.7%	49.3	25	33.6	2	0	0	1350.69	62	73
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	4	4	7	0.01%	13.1%	ILEVHIDK	99.3%	35.9	25	12.5	2	0	0	966.56	207	214
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	4	4	7	0.01%	13.1%	TIVITSHPGQIVK	99.7%	67	25	64.9	2	0	0	1392.82	284	296
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	4	4	7	0.01%	13.1%	VNFPENGFLSPDKLSLLEK	97.8%	25.3	25	20.7	0	1	0	2147.14	326	344
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	10	10	16	0.02%	27.2%	DGNDLHMTYK	99.7%	46	25	43.2	2	0	0	1193.53	263	272

DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	10	10	16	0.02%	27.2%	EISFAYEVLSNPEK	99.7%	60.6	25	53.1	1	0	0	1625.81	49	62
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	10	10	16	0.02%	27.2%	EISFAYEVLSNPEKR	99.7%	72.7	25	59.1	2	0	0	1781.91	49	63
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	10	10	16	0.02%	27.2%	FDVQFPENNWINPDK	99.6%	38.9	25	38.9	1	0	0	1862.87	333	347
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	10	10	16	0.02%	27.2%	IGLVEALCGFQFTFK	99.7%	76	25	69.1	2	0	0	1729.90	273	287
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	10	10	16	0.02%	27.2%	ILEVHVDK	99.5%	37.2	25	20.9	1	0	0	952.55	216	223
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	10	10	16	0.02%	27.2%	LYDILGVPPGASENELKK	99.7%	36.1	25	35.8	0	1	0	1943.05	9	26
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	10	10	16	0.02%	27.2%	NVLCSACSGQGGK	99.7%	85	25	85	2	0	0	1337.59	140	152
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	10	10	16	0.02%	27.2%	VIEPGCVR	99.6%	38.8	25	30.5	2	0	0	929.49	303	310
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	10	10	16	0.02%	27.2%	VSLEDLYNGK	99.7%	68	25	59	2	0	0	1137.58	122	131
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	6	9	17	0.02%	16.7%	EAGEDEEGFLSK	98.7%	33	25	33	2	0	0	1310.57	462	473
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	6	9	17	0.02%	16.7%	EFTVNIMDTCER	99.7%	66.7	25	66.7	2	0	0	1530.66	227	238
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	6	9	17	0.02%	16.7%	FSQLAEAYEVLSDEVK	99.7%	72.8	25	72.8	2	0	0	1827.90	135	150
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	6	9	17	0.02%	16.7%	GGPTVDPEELFR	99.7%	49.4	25	42	2	0	0	1316.65	176	187
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	6	9	17	0.02%	16.7%	GSIIISPCVVCR	99.7%	59	25	46.3	3	0	0	1360.71	282	293
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	6	9	17	0.02%	16.7%	VMIPVPAGVEDGQTVR	99.7%	67.5	25	63.4	5	1	0	1683.87	304	319
DnaJ homolog subfamily B member 11	DNAJB11	DJB11_HUMAN	40.5	100.0%	3	3	5	0.01%	7.8%	FQDLGAAYEVLSDSEK	99.7%	114	25	107	2	0	0	1771.84	67	82
DnaJ homolog subfamily B member 11	DNAJB11	DJB11_HUMAN	40.5	100.0%	3	3	5	0.01%	7.8%	FQDLGAAYEVLSDSEKR	94.6%	22.1	25	15.6	0	1	0	1927.94	67	83
DnaJ homolog subfamily B member 11	DNAJB11	DJB11_HUMAN	40.5	100.0%	3	3	5	0.01%	7.8%	TLEVEIEPGVR	99.7%	66.1	25	54.9	2	0	0	1241.67	207	217
DnaJ homolog subfamily B member 12	DNAJB12	DJB12_HUMAN	41.8	100.0%	3	3	5	0.01%	9.9%	AIGTAYAVLSNPEK	99.7%	66.7	25	60.8	2	0	0	1433.76	153	166
DnaJ homolog subfamily B member 12	DNAJB12	DJB12_HUMAN	41.8	100.0%	3	3	5	0.01%	9.9%	GYTAEQVAAVKR	99.7%	46.4	25	36.2	1	0	0	1292.70	93	104
DnaJ homolog subfamily B member 12	DNAJB12	DJB12_HUMAN	41.8	100.0%	3	3	5	0.01%	9.9%	NVEDDYIANLR	99.7%	59	25	59	2	0	0	1321.64	316	326
DnaJ homolog subfamily B member 6	DNAJB6	DNJB6_HUMAN	36.1	100.0%	3	3	6	0.01%	11.0%	APGPWDPLASAAGLK	99.7%	56.1	25	54.2	2	0	0	1450.77	288	302
DnaJ homolog subfamily B member 6	DNAJB6	DNJB6_HUMAN	36.1	100.0%	3	3	6	0.01%	11.0%	VDYYEVLGVQR	99.7%	70.8	25	53.2	3	0	0	1340.68	2	12
DnaJ homolog subfamily B member 6	DNAJB6	DNJB6_HUMAN	36.1	100.0%	3	3	6	0.01%	11.0%	VEVEEDGQLK	99.6%	38.5	25	38	1	0	0	1145.57	216	225
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	11	11	30	0.03%	16.0%	AIAALISEK	99.7%	58.8	25	50.8	2	0	0	915.55	770	778
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	11	11	30	0.03%	16.0%	ASNLLYGQLK	99.7%	58.8	25	49.7	4	0	0	1106.62	493	502
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	11	11	30	0.03%	16.0%	GLEDNQGGQYESWNYYR	99.7%	82.9	25	82.9	1	0	0	2078.88	103	119
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	11	11	30	0.03%	16.0%	GVNSYPSLFIFR	99.7%	47.2	25	46.8	2	0	0	1399.74	197	208
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	11	11	30	0.03%	16.0%	IGAVNCGDDR	99.7%	44.6	25	44.3	1	0	0	1076.48	181	190
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	11	11	30	0.03%	16.0%	ILYDILAFAK	99.7%	62.5	25	60.7	6	0	0	1166.68	439	448
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	11	11	30	0.03%	16.0%	NDHIQVGR	98.5%	32.4	25	25.3	2	0	0	938.48	393	400
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	11	11	30	0.03%	16.0%	NFQEEQINTR	99.7%	68.2	25	45.5	3	0	0	1278.61	757	766
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	11	11	30	0.03%	16.0%	NSILFLNSLDAK	99.7%	82.7	25	77.3	4	0	0	1334.73	326	337
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	11	11	30	0.03%	16.0%	VDCQAYAQTCQK	99.7%	50.3	25	50.3	2	0	0	1471.63	726	737
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	11	11	30	0.03%	16.0%	YDFGIYDDDPEIITLER	99.7%	73.8	25	73.8	3	0	0	2073.97	120	136
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	6	6	13	0.01%	12.3%	AGFFGTVVEYGAER	99.7%	104	25	95.7	4	0	0	1502.73	328	341
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	6	6	13	0.01%	12.3%	ESAATDVLQK	99.3%	36.2	25	29.1	2	0	0	1061.55	425	434
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	6	6	13	0.01%	12.3%	GIRPGLTTVLAR	99.7%	44.5	25	23.1	2	0	0	1253.77	249	260
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	6	6	13	0.01%	12.3%	GLEMEGWEVVER	99.7%	64.9	25	53.6	1	0	0	1433.67	85	96
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	6	6	13	0.01%	12.3%	IIEAEESR	99.7%	47	25	32.3	2	0	0	946.48	452	459
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	6	6	13	0.01%	12.3%	VIDVTVPLQCLVK	99.7%	60.6	25	60.6	2	0	0	1483.86	485	497
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	7	7	11	0.01%	4.1%	DQDNAIIRPLPK	99.4%	36.4	25	30.5	1	0	0	1379.76	1062	1073
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	7	7	11	0.01%	4.1%	DSLLASLLDGVR	99.7%	44.7	25	35.7	2	0	0	1258.70	312	323
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	7	7	11	0.01%	4.1%	ELIVGEIFVR	99.7%	71.2	25	71.2	2	0	0	1174.68	1685	1694
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	7	7	11	0.01%	4.1%	IFIAQPAWVLR	99.7%	45.4	25	37.2	1	0	0	1313.77	1987	1997
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	7	7	11	0.01%	4.1%	IVDGPDPENIILILK	99.7%	51.8	25	46.9	2	0	0	1648.95	1360	1374
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	7	7	11	0.01%	4.1%	VYNEVPTFQLEVPK	97.5%	30.4	25	30	1	0	0	1662.87	1695	1708
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	7	7	11	0.01%	4.1%	YSTDESITSLAEFVVQK	99.7%	44.1	25	42.3	2	0	0	1916.95	226	242
DnaJ homolog subfamily C member 7	DNAJC7	DNJC7_HUMAN	56.4	100.0%	3	3	5	0.01%	6.9%	AVQFFVQALR	99.7%	59.9	25	45.5	2	0	0	1178.67	229	238
DnaJ homolog subfamily C member 7	DNAJC7	DNJC7_HUMAN	56.4	100.0%	3	3	5	0.01%	6.9%	EALGDAQQSVR	99.7%	74.1	25	67.6	2	0	0	1173.59	80	90
DnaJ homolog subfamily C member 7	DNAJC7	DNJC7_HUMAN	56.4	100.0%	3	3	5	0.01%	6.9%	YPEAQSVASDILR	99.7%	44.2	25	42.3	1	0	0	1448.74	192	204

DnaJ homolog subfamily C member 9	DNAJC9	DNJC9_HUMAN	29.9	99.7%	2	2	2	0.00%	8.9%	ELGLDEGVDSLK	94.8%	27.5	25	27.5	1	0	0	1274.65	206	217
DnaJ homolog subfamily C member 9	DNAJC9	DNJC9_HUMAN	29.9	99.7%	2	2	2	0.00%	8.9%	ISLEDIQAFEK	99.5%	37.6	25	37.6	1	0	0	1292.67	108	118
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	8	19	0.02%	33.1%	EGNFDIVSGTR	99.7%	66.3	25	65.2	2	0	0	1194.58	137	147
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	8	19	0.02%	33.1%	ENLPLIVWLLVK	99.7%	51.6	25	51.6	1	0	0	1436.89	38	49
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	8	19	0.02%	33.1%	GYVFQMEMIVR	99.7%	44.1	25	44.1	2	0	0	1404.67	206	216
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	8	19	0.02%	33.1%	LGGNEIVSFLK	99.7%	76.6	25	76.6	2	0	0	1176.66	241	251
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	8	19	0.02%	33.1%	LGLGTAYIHGMK	99.7%	48.4	25	47.1	2	0	0	1260.68	96	107
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	8	19	0.02%	33.1%	QKEGNFDIVSGTR	99.7%	47.5	25	39.4	0	2	0	1450.73	135	147
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	8	19	0.02%	33.1%	QLNYTIGEVPISFVDR	99.7%	68.7	25	68.7	4	0	0	1850.96	219	234
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	8	19	0.02%	33.1%	YSVLLPTYNER	99.4%	36.5	25	33.9	4	0	0	1354.70	27	37
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	6	6	14	0.01%	14.9%	LPDVYGVFQFK	99.7%	62.2	25	53.9	2	0	0	1312.69	381	391
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	6	6	14	0.01%	14.9%	NTLLIAGLQAR	99.7%	96.2	25	73.7	5	0	0	1169.70	240	250
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	6	6	14	0.01%	14.9%	SSLNPILFR	99.7%	53.9	25	37.6	2	0	0	1046.60	190	198
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	6	6	14	0.01%	14.9%	TADDPSLSLIK	94.7%	27.5	25	15	1	0	0	1159.62	78	88
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	6	6	14	0.01%	14.9%	TLVLLDNLNVR	99.7%	77.1	25	57.2	2	0	0	1269.75	47	57
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	6	6	14	0.01%	14.9%	YSQTGNYELAVALSR	99.7%	113	25	102	2	0	0	1671.83	283	297
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	22	43	0.04%	36.6%	ALTSEIALLQSR	99.7%	85	25	78.1	2	0	0	1301.74	525	536
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	22	43	0.04%	36.6%	ATSFLLALEPELEAR	99.7%	78.8	25	78.8	4	0	0	1659.90	66	80
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	22	43	0.04%	36.6%	DVPAYSQDTFK	99.7%	51.1	25	42	2	0	0	1270.60	205	215
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	22	43	0.04%	36.6%	FPLFGGWK	99.5%	37	25	20.1	2	0	0	951.51	320	327
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	22	43	0.04%	36.6%	FVDHVFDEQVIDSLTVK	99.7%	79.3	25	75.4	2	2	0	1991.01	355	371
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	22	43	0.04%	36.6%	GEDEEENNLEVR	99.7%	62.6	25	56.7	2	0	0	1432.62	90	101
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	22	43	0.04%	36.6%	HFDETVNR	96.4%	29	25	15.1	2	0	0	1017.47	495	502
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	22	43	0.04%	36.6%	LKTEGSDLCDR	99.7%	47	25	31.9	2	2	0	1293.61	537	547
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	22	43	0.04%	36.6%	LPVALDPGAK	99.6%	38.8	25	38.8	2	0	0	980.58	117	126
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	22	43	0.04%	36.6%	NIEIDSPYEISR	99.7%	71.5	25	58.8	2	0	0	1435.71	380	391
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	22	43	0.04%	36.6%	NLVEQHIQDIVVHYTFNK	99.7%	33.5	25	33.5	0	1	0	2197.14	415	432
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	22	43	0.04%	36.6%	QFVVFEGNHYFYSPYPTK	99.7%	51.6	25	47.6	0	1	0	2223.05	152	169
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	22	43	0.04%	36.6%	QPDSGISSIR	99.7%	44.3	25	30.5	1	0	0	1059.54	269	278
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	22	43	0.04%	36.6%	SEDLLDYGPFR	99.7%	71.2	25	67	2	0	0	1311.62	194	204
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	22	43	0.04%	36.6%	VACITEQVLTLVNKR	99.7%	77.9	25	68.3	2	2	0	1743.98	475	489
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	22	43	0.04%	36.6%	VHYENNSPFLTITSMTR	99.7%	39.6	25	38.3	0	4	0	2009.97	216	232
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	17	22	43	0.04%	36.6%	VTAEVVLAHLGGGSTSR	99.7%	98.8	25	98.8	2	2	0	1653.89	49	65
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	9	10	21	0.02%	18.1%	FELDTSER	99.4%	36.9	25	23.6	2	0	0	996.46	461	468
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	9	10	21	0.02%	18.1%	ISTEVGITNVDLSTVDKDQSIAPK	99.7%	47.3	25	47.3	0	3	0	2530.33	369	392
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	9	10	21	0.02%	18.1%	LQVTNVLSQPLTQATVK	99.7%	137	25	122	4	0	0	1840.05	290	306
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	9	10	21	0.02%	18.1%	MLAQQAVK	98.7%	33	25	22.1	2	0	0	904.49	620	627
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	9	10	21	0.02%	18.1%	SIVEEIEDLVAR	99.7%	65.1	25	42.9	1	0	0	1372.73	179	190
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	9	10	21	0.02%	18.1%	TGQEVVFVAEPDNK	99.7%	81.7	25	69.9	3	0	0	1532.76	443	456
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	9	10	21	0.02%	18.1%	TGQEVVFVAEPDNKNVYK	99.7%	42.8	25	42.8	1	0	0	2037.03	443	460
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	9	10	21	0.02%	18.1%	TSFTPVGDVFELNFMNVK	99.7%	74.1	25	73.2	4	0	0	2045.00	323	340
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	9	10	21	0.02%	18.1%	YIANTVELR	99.4%	36.3	25	28.4	1	0	0	1078.59	358	366
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	DAD1	DAD1_HUMAN	12.5	100.0%	3	3	10	0.01%	28.3%	ADFQGISPER	99.7%	51.8	25	33.4	4	0	0	1119.54	83	92
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	DAD1	DAD1_HUMAN	12.5	100.0%	3	3	10	0.01%	28.3%	FLEEYLSSTPQR	99.7%	72.6	25	63.3	4	0	0	1469.73	12	23
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	DAD1	DAD1_HUMAN	12.5	100.0%	3	3	10	0.01%	28.3%	SASVVSVISR	99.7%	62	25	52.6	2	0	0	1004.57	2	11
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	5	5	8	0.01%	7.4%	ENDYYTPTGEFR	99.3%	35.7	25	35.6	1	0	0	1491.64	614	625
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	5	5	8	0.01%	7.4%	FGQVYTEAK	99.7%	46.5	25	39	2	0	0	1042.52	647	655
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	5	5	8	0.01%	7.4%	FLAEEGFYK	99.7%	48	25	31.8	2	0	0	1103.54	59	67
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	5	5	8	0.01%	7.4%	FYSLLDPSYAK	99.7%	42.9	25	32.7	2	0	0	1303.66	330	340
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	5	5	8	0.01%	7.4%	VGQAMASTEEK	98.3%	32	25	30.7	1	0	0	1150.54	555	565
Dolichyl-phosphate beta-glucosyltransferase	ALG5	ALG5_HUMAN	36.9	99.8%	2	2	4	0.00%	7.7%	ETLPSIWDSPTK	99.7%	46	25	37.5	2	0	0	1373.69	54	65

Dolichyl-phosphate beta-glucosyltransferase	ALG5	ALG5_HUMAN	36.9	99.8%	2	2	4	0.00%	7.7%	QLSVVVPSYNEEK	99.7%	56.4	25	38.7	2	0	0	1491.77	66	78
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	3	3	3	0.00%	5.7%	LAQIQQAK	99.5%	37.1	25	27.8	1	0	0	899.53	291	298
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	3	3	3	0.00%	5.7%	VPQAQPTKPALK	99.5%	37.3	25	34	1	0	0	1277.76	356	367
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	3	3	3	0.00%	5.7%	VSVGEFVGEGEGK	99.7%	60.6	25	60.6	1	0	0	1293.63	220	232
Double-stranded RNA-specific adenosine deaminase	ADAR	DSRAD_HUMAN	136.1	100.0%	4	4	8	0.01%	3.8%	AMTILLEEAK	99.7%	50.7	25	41.9	2	0	0	1134.61	565	574
Double-stranded RNA-specific adenosine deaminase	ADAR	DSRAD_HUMAN	136.1	100.0%	4	4	8	0.01%	3.8%	LVDQSGPPHEPK	99.7%	51.5	25	51.5	2	0	0	1303.66	746	757
Double-stranded RNA-specific adenosine deaminase	ADAR	DSRAD_HUMAN	136.1	100.0%	4	4	8	0.01%	3.8%	SHGFAAEFK	96.8%	29.4	25	27.3	1	0	0	993.48	737	745
Double-stranded RNA-specific adenosine deaminase	ADAR	DSRAD_HUMAN	136.1	100.0%	4	4	8	0.01%	3.8%	YLNTNPVGGLLEYAR	99.7%	84	25	84	3	0	0	1679.88	722	736
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	6	6	11	0.01%	17.2%	DVKPSNILVNSR	99.7%	61.7	25	60.9	2	0	0	1341.75	194	205
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	6	6	11	0.01%	17.2%	ISELGAGNGGVVTK	99.7%	81.7	25	81	2	0	0	1301.71	75	88
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	6	6	11	0.01%	17.2%	RIPEEILGK	99.7%	40.7	25	38	2	0	0	1054.63	164	172
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	6	6	11	0.01%	17.2%	RLEAFLTQK	99.7%	42.3	25	28.7	2	0	0	1105.64	53	61
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	6	6	11	0.01%	17.2%	SEVEEVDFAGWLCK	99.7%	50.5	25	50.5	1	0	0	1668.76	372	385
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	6	6	11	0.01%	17.2%	VGELKDDDFER	99.7%	53.3	25	47.2	2	0	0	1322.62	64	74
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	8	10	17	0.02%	30.3%	DVKPSNVLINK	99.1%	34.9	25	29.4	2	0	0	1226.71	190	200
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	8	10	17	0.02%	30.3%	FPYESWGTPFQQLK	99.7%	45.4	25	40	2	0	0	1727.84	266	279
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	8	10	17	0.02%	30.3%	FSPEFVDFTAQCLR	99.7%	94.1	25	94.1	2	0	0	1716.81	294	307
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	8	10	17	0.02%	30.3%	HAQSGTIMAVK	96.1%	28.6	25	22.6	1	0	0	1142.60	83	93
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	8	10	17	0.02%	30.3%	ISCMSKPPAPNPTPPR	99.7%	39.3	25	36.3	0	3	0	1749.88	27	42
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	8	10	17	0.02%	30.3%	KTDIAAFVK	99.7%	40.8	25	25.1	1	0	0	992.58	332	340
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	8	10	17	0.02%	30.3%	MCDFGISGYLVDSVAK	99.7%	77.2	25	77.2	4	0	0	1777.81	206	221
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	8	10	17	0.02%	30.3%	QVVEEPSPQLPADR	99.7%	58.6	25	55.9	2	0	0	1564.80	280	293
Dual specificity protein phosphatase 3	DUSP3	DUS3_HUMAN	20.5	99.8%	2	2	4	0.00%	14.1%	AADFIDQALAQK	99.7%	60.7	25	60.7	2	0	0	1290.67	105	116
Dual specificity protein phosphatase 3	DUSP3	DUS3_HUMAN	20.5	99.8%	2	2	4	0.00%	14.1%	IYVGNASVAQDIPK	99.7%	53.1	25	50.1	2	0	0	1474.79	37	50
Dual specificity protein phosphatase 9	DUSP9	DUS9_HUMAN	41.9	100.0%	3	3	6	0.01%	12.2%	ASFPVQILPNLYLGSAR	99.7%	52	25	52	2	0	0	1846.02	201	217
Dual specificity protein phosphatase 9	DUSP9	DUS9_HUMAN	41.9	100.0%	3	3	6	0.01%	12.2%	IGGALSVALPALLLR	99.7%	66.6	25	66.6	2	0	0	1463.93	38	52
Dual specificity protein phosphatase 9	DUSP9	DUS9_HUMAN	41.9	100.0%	3	3	6	0.01%	12.2%	YILNVTPNLPNFFEK	99.7%	45.7	25	45.6	2	0	0	1808.96	232	246
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	AEITDAEGLGLK	99.7%	80.6	25	69.2	2	0	0	1216.64	933	944
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	AESLQQEVEALK	99.7%	64.5	25	51.8	2	0	0	1344.70	318	329
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	AESLQQEVEALKER	99.3%	30	25	28	0	2	0	1629.84	318	331
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	AFLQGGQEATDIALLLR	99.7%	78.9	25	67.3	2	0	0	1816.00	769	785
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	AIEMELR	94.9%	27.6	25	17.1	1	0	0	877.44	568	574
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	ASEQIYGTPSSSPYECLR	99.7%	59.7	25	52	1	0	0	2044.93	873	890
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	ASLASLPPLHVAK	99.7%	39.1	25	35.2	1	0	0	1303.77	1121	1133
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	DLEEKLETLR	99.7%	55.9	25	31.8	2	0	0	1245.67	226	235
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	DLETSCSDIR	99.7%	71.2	25	60.3	2	0	0	1195.53	786	795
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	DSPLLLQQISAMR	99.7%	84.7	25	81.2	3	0	0	1487.79	1089	1101
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	ELTNQQEASVER	99.7%	72.6	25	64.7	2	0	0	1403.68	533	544
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	EQLDMAGAR	99.7%	47.7	25	40.3	3	0	0	990.47	487	495
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	FTQSALDCMSVEVGR	99.7%	69.8	25	65.7	3	0	0	1715.77	752	766
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	GSDGAASSYQLK	99.7%	78.4	25	67.7	2	0	0	1183.56	350	361
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	GTVAYVGATLFATGK	99.7%	96.8	25	96.8	2	0	0	1455.78	42	56
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	IKGEELSEANVR	99.7%	65.5	25	62.2	2	2	0	1344.71	961	972
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	IQLEQVQEWK	99.7%	70.8	25	59	2	0	0	1300.69	253	262
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	KNQELEVVR	99.7%	46.1	25	24.5	1	0	0	1114.62	398	406
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	LEDRETVIK	98.1%	31.4	25	16.1	1	0	0	1102.61	945	953
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	LEETQALLR	99.7%	57.5	25	37.6	1	0	0	1072.60	998	1006
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	LHISQLQHENSILK	96.6%	23.7	25	18.9	0	1	0	1659.92	1102	1115
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	LSHEGPGSELPAGALYR	99.7%	49.4	25	49.4	1	2	0	1753.89	1134	1150
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	MQEQQADLQR	99.7%	68.7	25	58.4	5	0	0	1246.58	265	274
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	NQELEVVR	99.7%	45.6	25	28.4	2	0	0	986.53	399	406

Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	QLTAHLQDVNR	99.7%	47.9	25	39.3	2	2	0	1294.69	522	532
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	QSCNILISTMNK	99.7%	41.4	25	39.2	1	0	0	1408.69	891	902
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	SPSAQLMEQVAQLK	99.7%	93.6	25	88.8	4	0	0	1529.80	1180	1193
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	VDELTTDLEILK	99.7%	95.7	25	72.2	2	0	0	1388.75	332	343
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	VEAAQETVADYQQTIK	99.7%	79.8	25	77.4	1	0	0	1793.89	503	518
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	VTFSCAAGFGQR	99.7%	98.7	25	93.5	2	0	0	1300.61	1248	1259
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	31	39	66	0.07%	27.7%	WVGVILDEAK	99.7%	44.8	25	32.9	2	0	0	1129.63	57	66
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	9	10	16	0.02%	15.1%	ALQGASQIIAEIR	99.7%	51.1	25	44.5	1	0	0	1369.78	719	731
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	9	10	16	0.02%	15.1%	FATEYCNTIEGTAK	99.7%	79.5	25	70.7	2	0	0	1604.73	340	353
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	9	10	16	0.02%	15.1%	GVSPEPIHLK	98.3%	32	25	21.3	1	0	0	1076.61	124	133
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	9	10	16	0.02%	15.1%	IFSPNVVNLTLVDLPGMTK	99.7%	115	25	109	3	0	0	2058.13	134	152
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	9	10	16	0.02%	15.1%	LGIIGVVNR	99.7%	82.7	25	64.9	2	0	0	940.59	239	247
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	9	10	16	0.02%	15.1%	RLEEPSLR	99.7%	44.8	25	33.2	2	0	0	999.56	423	430
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	9	10	16	0.02%	15.1%	SQLDINNKK	98.6%	32.9	25	16.1	1	0	0	1059.58	248	256
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	9	10	16	0.02%	15.1%	SSLLDDLLTESEDMAQR	99.7%	63.1	25	63.1	2	0	0	1938.90	693	709
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	9	10	16	0.02%	15.1%	YIETSELCGGAR	99.7%	63	25	47.1	2	0	0	1355.63	354	365
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	13	23	0.02%	17.5%	ALLQMVQQFGVDFEK	99.7%	53.8	25	53.8	1	0	0	1768.89	328	342
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	13	23	0.02%	17.5%	DMILQFISR	99.7%	48.7	25	22	2	0	0	1122.60	158	166
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	13	23	0.02%	17.5%	ESSLILAVTPANMDLANSDALK	99.7%	45.1	25	45.1	1	0	0	2273.17	167	188
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	13	23	0.02%	17.5%	EVDPQGLR	99.4%	36.5	25	24.6	2	0	0	913.47	192	199
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	13	23	0.02%	17.5%	FPFELVK	99.7%	49.1	25	0	2	0	0	879.50	370	376
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	13	23	0.02%	17.5%	GISPVPINLR	99.1%	34.6	25	34.6	2	0	0	1065.64	114	123
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	13	23	0.02%	17.5%	GMEELIPLVNK	99.7%	62.6	25	52	2	0	0	1242.68	5	15
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	13	23	0.02%	17.5%	GYIGVVNR	99.6%	39.1	25	27.2	3	0	0	877.49	230	237
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	13	23	0.02%	17.5%	LQSQLLSLEK	99.7%	62.9	25	0	2	0	0	1158.67	300	309
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	13	23	0.02%	17.5%	NLVDSYVAIINK	99.7%	81.5	25	64.2	2	0	0	1348.75	658	669
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	13	23	0.02%	17.5%	SSVLENFVGR	99.7%	68.8	25	50.5	2	0	0	1107.58	45	54
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	13	23	0.02%	17.5%	TGLFTPDLAFEAIVK	99.7%	72.1	25	70	1	0	0	1621.88	400	414
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	13	23	0.02%	17.5%	VPVGDQPPDIEYQIK	99.7%	64.9	25	55.9	1	0	0	1697.87	143	157
Dynamin-like 120 kDa protein, mitochondrial	OPA1	OPA1_HUMAN	111.6	99.8%	2	2	2	0.00%	2.0%	QQLTNTEVR	97.1%	29.8	25	16.1	1	0	0	1088.57	896	904
Dynamin-like 120 kDa protein, mitochondrial	OPA1	OPA1_HUMAN	111.6	99.8%	2	2	2	0.00%	2.0%	VIQHNALEDR	99.7%	51.3	25	43.6	1	0	0	1194.62	724	733
Dynein light chain 1, cytoplasmic	DYNLL1	DYL1_HUMAN	10.4	100.0%	3	3	9	0.01%	49.4%	NADMSEEMQQDSVECATQALEK	98.7%	27.5	25	27.5	0	1	0	2546.03	10	31
Dynein light chain 1, cytoplasmic	DYNLL1	DYL1_HUMAN	10.4	100.0%	3	3	9	0.01%	49.4%	NFGSYVTHETK	99.7%	49.3	25	37.5	4	0	0	1282.61	61	71
Dynein light chain 1, cytoplasmic	DYNLL1	DYL1_HUMAN	10.4	100.0%	3	3	9	0.01%	49.4%	YNPTWHCIVGR	99.7%	50.5	25	49	4	0	0	1402.67	50	60
Dynein light chain Tctex-type 1	DYNLT1	DYLT1_HUMAN	12.5	99.8%	2	3	6	0.01%	23.0%	EAIESAIGGNAYQHSK	99.7%	68	25	61.6	2	0	0	1674.81	23	38
Dynein light chain Tctex-type 1	DYNLT1	DYLT1_HUMAN	12.5	99.8%	2	3	6	0.01%	23.0%	YIVTCVIMQK	99.7%	49.1	25	43.7	4	0	0	1254.66	63	72
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	14	14	23	0.02%	5.5%	EGQWDCSVCLVR	99.7%	50.8	25	50.8	1	0	0	1508.66	1607	1618
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	14	14	23	0.02%	5.5%	EIVETFANK	98.8%	33.6	25	22.9	2	0	0	1050.55	371	379
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	14	14	23	0.02%	5.5%	ELLQSFDSALQSVK	99.7%	84.2	25	77.7	4	0	0	1564.82	257	270
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	14	14	23	0.02%	5.5%	ELVGPPLAETVFTPK	99.7%	74.3	25	73.6	2	0	0	1597.88	1384	1398
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	14	14	23	0.02%	5.5%	FGESTTGFNFSFK	99.7%	45.9	25	44.5	1	0	0	1468.67	2260	2272
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	14	14	23	0.02%	5.5%	FGISEPGNQEK	99.7%	42.9	25	33.7	2	0	0	1205.58	1900	1910
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	14	14	23	0.02%	5.5%	GVIFGQTSSTFTFADLAK	99.7%	79.1	25	79.1	2	0	0	1889.96	1935	1952
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	14	14	23	0.02%	5.5%	IAVAVLEETTR	99.7%	91.7	25	84.1	2	0	0	1201.68	2467	2477
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	14	14	23	0.02%	5.5%	IIDDSDSNLSVVK	99.7%	78.2	25	0	1	0	0	1404.72	721	733
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	14	14	23	0.02%	5.5%	SGFEGMFTK	99.7%	46.3	25	37	1	0	0	1003.46	1597	1605
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	14	14	23	0.02%	5.5%	SGSSFVHQASFK	99.7%	50.5	25	39.5	1	0	0	1281.62	1447	1458
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	14	14	23	0.02%	5.5%	SNNSETSSVAQSGSESK	99.7%	60.8	25	60.8	1	0	0	1698.74	2555	2571
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	14	14	23	0.02%	5.5%	STSGEGFQFGK	99.7%	46	25	44.5	1	0	0	1144.53	1953	1963
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	14	14	23	0.02%	5.5%	YIASVQGSTPSPR	99.7%	83.1	25	81.7	2	0	0	1362.70	11	23
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	24	24	37	0.04%	6.7%	AALPLTTSDTK	99.7%	40.7	25	37.6	2	0	0	1117.61	1498	1508

E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	24	24	37	0.04%	6.7%	ADGTATAPPPR	99.4%	36.2	25	36.2	1	0	0	1053.53	707	717
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	24	24	37	0.04%	6.7%	AIQDPAFSDGIR	99.7%	50	25	50	1	0	0	1289.65	518	529
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	24	24	37	0.04%	6.7%	ALAELFGLLVK	99.7%	91.5	25	74.5	3	0	0	1173.72	1062	1072
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	24	24	37	0.04%	6.7%	DSAVAISGADSR	99.7%	68.4	25	61.2	1	0	0	1148.55	2930	2941
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	24	24	37	0.04%	6.7%	EMFNPMYALFR	99.7%	39.5	25	37.1	2	0	0	1418.66	4072	4082
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	24	24	37	0.04%	6.7%	FLGDEQDQITFVTR	99.7%	63.1	25	58.5	1	0	0	1668.82	418	431
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	24	24	37	0.04%	6.7%	FLQFVTGTSK	99.7%	72.8	25	67.4	2	0	0	1127.61	4296	4305
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	24	24	37	0.04%	6.7%	GLQSFVQCQPFER	99.7%	59.1	25	50	2	0	0	1595.76	617	629
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	24	24	37	0.04%	6.7%	GNDTPLALESTNTEKETSLEETK	99.4%	30.7	25	30.7	0	1	0	2507.20	1719	1741
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	24	24	37	0.04%	6.7%	HADHSSLTLGSGSSTTR	96.7%	23.8	25	23.8	0	1	0	1713.82	2522	2538
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	24	24	37	0.04%	6.7%	IVNQPSSLFGSK	99.4%	36.2	25	15.7	1	0	0	1276.69	2256	2267
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	24	24	37	0.04%	6.7%	LGSSGLGSASSIQAAVR	99.7%	100	25	96.1	2	0	0	1560.83	3750	3766
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	24	24	37	0.04%	6.7%	LLECYFTR	99.7%	44.8	25	27.7	2	0	0	1101.54	4123	4130
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	24	24	37	0.04%	6.7%	LLSLISIALPENK	99.6%	38.8	25	38.8	2	0	0	1410.86	3456	3468
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	24	24	37	0.04%	6.7%	LPGGVQNFPQFSALR	99.7%	51.5	25	51.5	2	0	0	1630.87	1226	1240
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	24	24	37	0.04%	6.7%	NLCYHAQTR	98.2%	31.8	25	26.2	1	0	0	1162.54	3211	3219
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	24	24	37	0.04%	6.7%	NPDIFTEVANCCIR	99.7%	67.4	25	66	2	0	0	1708.78	1881	1894
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	24	24	37	0.04%	6.7%	QIGTLLAELR	98.9%	33.8	25	30.3	2	0	0	1113.66	3637	3646
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	24	24	37	0.04%	6.7%	SILTLSHEPK	95.7%	28.3	25	25.9	1	0	0	1124.63	830	839
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	24	24	37	0.04%	6.7%	SLLSILQR	99.7%	41.2	25	20.4	1	0	0	929.58	3225	3232
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	24	24	37	0.04%	6.7%	TLTSIVHLER	99.7%	59.5	25	53	1	0	0	1168.67	330	339
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	24	24	37	0.04%	6.7%	TPTEAPADCR	99.3%	35.8	25	35.8	1	0	0	1117.49	11	20
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	24	24	37	0.04%	6.7%	VLLSPDYLPAMR	98.6%	32.8	25	32.8	2	0	0	1374.75	633	644
E3 ubiquitin-protein ligase MYCBP2	MYCBP2	MYCB2_HUMAN	510.1	100.0%	2	2	5	0.01%	0.5%	MLVIVVLPVR	97.8%	30.9	25	30.9	1	0	0	1138.74	1627	1636
E3 ubiquitin-protein ligase MYCBP2	MYCBP2	MYCB2_HUMAN	510.1	100.0%	2	2	5	0.01%	0.5%	NAIAETIIALTK	99.7%	56	25	56	4	0	0	1257.74	4159	4170
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	16	17	29	0.03%	32.2%	ALCWVCAQSR	99.7%	52	25	45.1	2	0	0	1250.58	109	118
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	16	17	29	0.03%	32.2%	DHAMVPLEEAAQEYQEK	99.7%	79.2	25	78	1	0	0	1987.91	122	138
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	16	17	29	0.03%	32.2%	DLDITSPELR	99.7%	55.3	25	46.3	2	0	0	1158.60	261	270
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	16	17	29	0.03%	32.2%	EAWDLGVCR	99.7%	66.5	25	66.5	2	0	0	1105.51	352	360
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	16	17	29	0.03%	32.2%	HYWEVDVTGK	99.7%	47.4	25	47.4	2	0	0	1233.59	342	351
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	16	17	29	0.03%	32.2%	IHAEFVQQK	95.5%	28	25	13.5	1	0	0	1099.59	178	186
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	16	17	29	0.03%	32.2%	LAQQSQALQELISELDR	99.7%	53	25	52.1	1	0	0	1942.02	218	234
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	16	17	29	0.03%	32.2%	LAQQSQALQELISELDRR	99.7%	35.8	25	35.8	0	2	0	2098.13	218	235
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	16	17	29	0.03%	32.2%	LGDTQQSIPGNEER	99.7%	67.9	25	65.7	2	0	0	1543.73	311	324
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	16	17	29	0.03%	32.2%	LQVALGELR	99.7%	69.2	25	33.2	2	0	0	998.60	139	147
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	16	17	29	0.03%	32.2%	LQVALGELRR	97.9%	31	25	25.7	1	0	0	1154.70	139	148
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	16	17	29	0.03%	32.2%	NFLVEEEQR	99.7%	50.9	25	25	2	0	0	1163.57	187	195
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	16	17	29	0.03%	32.2%	QLANMVNNLK	99.7%	43.8	25	41.5	2	0	0	1160.61	68	77
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	16	17	29	0.03%	32.2%	SESWNLKDLDITSPELR	99.7%	63.8	25	58	2	2	0	2003.01	254	270
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	16	17	29	0.03%	32.2%	SGFWTIWLWNK	99.7%	67.5	25	56.9	2	0	0	1437.73	375	385
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	16	17	29	0.03%	32.2%	SVCHVPGLK	98.0%	31.4	25	27	1	0	0	996.53	271	279
E3 ubiquitin-protein ligase UBR4	UBR4	UBR4_HUMAN	573.8	100.0%	3	3	4	0.00%	0.7%	GVLPYVGNLITK	98.4%	32.3	25	25.2	2	0	0	1273.75	4204	4215
E3 ubiquitin-protein ligase UBR4	UBR4	UBR4_HUMAN	573.8	100.0%	3	3	4	0.00%	0.7%	IISLDLPVAEVYK	95.8%	28.3	25	28.3	1	0	0	1459.84	4414	4426
E3 ubiquitin-protein ligase UBR4	UBR4	UBR4_HUMAN	573.8	100.0%	3	3	4	0.00%	0.7%	VCLNLPYFLR	97.3%	30.1	25	18.8	1	0	0	1294.70	259	268
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	12	12	20	0.02%	16.6%	AQFAEATQR	99.7%	50.6	25	42.4	2	0	0	1021.51	18	26
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	12	12	20	0.02%	16.6%	AVFVPDIYSR	99.3%	35.9	25	32.5	1	0	0	1166.62	242	251
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	12	12	20	0.02%	16.6%	CVPQIIAFLNSK	99.7%	39.6	25	37.6	1	0	0	1389.76	708	719
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	12	12	20	0.02%	16.6%	FFADDTQAALTK	99.7%	85.7	25	84.6	2	0	0	1327.65	560	571
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	12	12	20	0.02%	16.6%	FINDCTELFR	99.7%	45.8	25	44.4	1	0	0	1314.61	368	377
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	12	12	20	0.02%	16.6%	GVIFTEAFVAR	99.7%	80.5	25	73.1	2	0	0	1209.66	175	185
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	12	12	20	0.02%	16.6%	IISGHIDLDNR	99.7%	45.9	25	36.3	2	0	0	1252.66	164	174

E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	12	12	20	0.02%	16.6%	LAADFQR	99.7%	40.1	25	30.9	2	0	0	820.43	11	17
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	12	12	20	0.02%	16.6%	LGIPDAVSYIK	99.7%	41	25	25.4	2	0	0	1175.67	275	285
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	12	12	20	0.02%	16.6%	QISTLESVSTSK	99.7%	47	25	44.9	1	0	0	1279.67	403	414
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	12	12	20	0.02%	16.6%	TQSTWVDSFFR	99.7%	53	25	47.3	2	0	0	1373.65	252	262
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	12	12	20	0.02%	16.6%	TYDLPGNFLTQALTQR	99.7%	104	25	85.8	2	0	0	1837.94	145	160
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	12	18	0.02%	19.1%	ADQIETQQLMR	99.7%	56.1	25	42.3	4	0	0	1332.66	221	231
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	12	18	0.02%	19.1%	EHQISPGDFPSLR	99.7%	34.3	25	28.8	1	2	0	1482.73	345	357
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	12	18	0.02%	19.1%	ELVNNLGEIYQK	99.7%	65.9	25	64.7	2	0	0	1419.75	330	341
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	12	18	0.02%	19.1%	KLNDLIK	99.7%	39.3	25	7.6	1	0	0	843.53	293	299
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	12	18	0.02%	19.1%	LLDTVDDMLANDIAR	99.7%	64.8	25	64.8	1	0	0	1674.84	378	392
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	12	18	0.02%	19.1%	LNAFGNAFLNR	99.7%	58.6	25	48.2	2	0	0	1236.65	125	135
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	12	18	0.02%	19.1%	QEESLMPSQVVK	99.0%	34.2	25	25.5	2	0	0	1374.69	399	410
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	12	18	0.02%	19.1%	SKLPNTVLGK	99.7%	40.3	25	40.3	2	0	0	1056.64	474	483
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	12	18	0.02%	19.1%	VYGALMWSLGK	98.8%	33.3	25	33.3	1	0	0	1240.64	232	242
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	5	5	7	0.01%	14.6%	ADQVDTQQLMR	99.7%	41.9	25	33	1	0	0	1304.63	224	234
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	5	5	7	0.01%	14.6%	AGGADAVQTVTGGLR	99.7%	63	25	58.2	2	0	0	1372.72	15	29
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	5	5	7	0.01%	14.6%	EGADEEEWVVAK	99.7%	45.3	25	45.3	1	0	0	1361.62	435	446
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	5	5	7	0.01%	14.6%	EYQISAGDFPEVK	99.7%	65.1	25	63.9	2	0	0	1482.71	348	360
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	5	5	7	0.01%	14.6%	KLNDLIK	99.7%	39.3	25	7.6	1	0	0	843.53	296	302
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	5	5	7	0.01%	14.6%	LPEIYIQLQR	99.7%	46.9	25	34	1	0	0	1272.73	338	347
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	5	5	7	0.01%	14.6%	VYGALMWSLGK	98.8%	33.3	25	33.3	1	0	0	1240.64	235	245
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	7	8	19	0.02%	24.8%	AINTLNGLR	99.7%	39.8	25	28.5	2	0	0	971.56	77	85
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	7	8	19	0.02%	24.8%	FAANPNQNK	99.7%	40.3	25	28.1	1	0	0	1003.50	183	191
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	7	8	19	0.02%	24.8%	SLFSSIGEVESAK	99.7%	78.8	25	72.3	4	0	0	1353.69	38	50
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	7	8	19	0.02%	24.8%	TNLIVNYLPQNMTQDELR	99.7%	59.7	25	59.7	6	0	0	2162.09	20	37
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	7	8	19	0.02%	24.8%	VIRDFNTNK	98.8%	33.3	25	24.1	1	0	0	1106.60	275	283
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	7	8	19	0.02%	24.8%	VLVDQTTGLSR	99.7%	89.5	25	67	4	0	0	1188.66	137	147
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	7	8	19	0.02%	24.8%	VSYARPSSEVIK	97.4%	30.2	25	17	1	0	0	1335.73	93	104
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	12	16	35	0.04%	50.2%	AAVDAGFVPNDMQVGQTGK	99.7%	95.4	25	95.4	4	0	0	1920.91	250	268
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	12	16	35	0.04%	50.2%	ASSTSPVEISEWLDQK	99.7%	84.2	25	81.9	2	0	0	1776.87	188	203
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	12	16	35	0.04%	50.2%	GLLPEELTPLILATQK	99.7%	87.3	25	85.9	2	1	0	1736.02	86	101
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	12	16	35	0.04%	50.2%	GTSFDAAATSGGSASSEK	99.7%	139	25	135	2	0	0	1630.72	170	187
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	12	16	35	0.04%	50.2%	LEVAPISDIIAIK	99.7%	86.8	25	73.8	4	0	0	1381.83	127	139
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	12	16	35	0.04%	50.2%	LGGEVSCLVAGTK	99.7%	89.1	25	86.5	4	0	0	1290.67	47	59
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	12	16	35	0.04%	50.2%	LLYDLADQLHAAVGASR	99.7%	101	25	87.8	2	2	0	1812.96	233	249
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	12	16	35	0.04%	50.2%	QFNYTHICAGASAFGK	99.7%	68.9	25	64.8	2	0	0	1771.82	102	117
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	12	16	35	0.04%	50.2%	SPDTFVR	99.7%	46.7	25	30.8	2	0	0	821.42	140	146
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	12	16	35	0.04%	50.2%	TIYAGNALCTVK	99.7%	86	25	76.4	2	0	0	1310.68	147	158
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	12	16	35	0.04%	50.2%	VLVAQHDVYK	99.7%	60.1	25	50.1	2	0	0	1171.65	76	85
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	12	16	35	0.04%	50.2%	VVPEMTEILK	99.7%	52.1	25	47.3	4	0	0	1158.64	322	331
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	21	0.02%	45.9%	EIDGGLETLR	99.7%	85.1	25	77.4	2	0	0	1102.57	165	174
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	21	0.02%	45.9%	EKVDLVLLGK	98.0%	31.2	25	24.9	2	0	0	1113.69	115	124
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	21	0.02%	45.9%	EVIAVSCGPAQCQETIR	99.7%	110	25	109	2	0	0	1917.92	60	76
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	21	0.02%	45.9%	GIHVEVPPAEAER	97.4%	24.7	25	20.9	0	1	0	1403.73	86	98
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	21	0.02%	45.9%	IEVIKPGDLGVDLTSK	99.7%	53.2	25	53.2	2	0	0	1683.95	206	221
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	21	0.02%	45.9%	LGPLQVAR	99.7%	67.7	25	59	2	0	0	853.53	99	106
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	21	0.02%	45.9%	LKLPAVVTADLR	99.4%	36.6	25	30.8	2	0	0	1295.80	175	186
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	21	0.02%	45.9%	LPAVVTADLR	99.7%	48.4	25	31.8	2	0	0	1054.63	177	186
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	21	0.02%	45.9%	LSVISVEDPPQR	99.7%	55.9	25	54.8	2	0	0	1339.72	222	233
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	21	0.02%	45.9%	TALAMGADR	99.7%	40.1	25	20.6	2	0	0	905.45	77	85
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	21	0.02%	45.9%	VETTEDLVAK	99.7%	48.9	25	35.2	2	0	0	1104.58	239	248

ELMO domain-containing protein 2	ELMOD2	ELMD2_HUMAN	35.0	100.0%	4	5	10	0.01%	13.0%	IENSLTYSK	99.7%	40.2	25	38.7	2	0	0	1054.54	47	55
ELMO domain-containing protein 2	ELMOD2	ELMD2_HUMAN	35.0	100.0%	4	5	10	0.01%	13.0%	IFDTYVGAQR	99.7%	86.9	25	75.2	2	0	0	1169.60	34	43
ELMO domain-containing protein 2	ELMOD2	ELMD2_HUMAN	35.0	100.0%	4	5	10	0.01%	13.0%	LWNLLMPTK	99.7%	45.4	25	37.7	2	0	0	1115.63	134	142
ELMO domain-containing protein 2	ELMOD2	ELMD2_HUMAN	35.0	100.0%	4	5	10	0.01%	13.0%	MCLLQITGYK	99.6%	38.3	25	28.4	4	0	0	1242.62	97	106
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	27	244	0.25%	54.1%	DGNASGTTLLEALDCILPPTRPTDKPLR	99.2%	29.5	25	29.5	0	1	0	3021.57	220	247
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	27	244	0.25%	54.1%	EHALLAYTLGVK	99.7%	73.7	25	63.1	24	9	0	1314.74	135	146
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	27	244	0.25%	54.1%	EVSTYIK	97.8%	30.9	25	10.6	2	0	0	839.45	173	179
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	27	244	0.25%	54.1%	EVSTYIKK	98.8%	33.3	25	26.9	3	0	0	967.55	173	180
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	27	244	0.25%	54.1%	FEKEAAEMGK	99.7%	53.6	25	43.3	2	0	0	1139.54	42	51
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	27	244	0.25%	54.1%	IGGIGTVPVGR	99.7%	89.5	25	88.8	34	0	0	1025.61	256	266
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	27	244	0.25%	54.1%	LPLQDVYK	99.7%	60	25	50.9	17	0	0	975.55	248	255
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	27	244	0.25%	54.1%	MDSTEPPYSQK	99.7%	53.1	25	53.1	2	0	0	1282.56	155	165
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	27	244	0.25%	54.1%	NMITGTSQADCAVLIVAAGVGEFEAGISK	99.7%	94.1	25	94.1	0	3	0	2925.43	101	129
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	27	244	0.25%	54.1%	QLIVGVNK	99.7%	46.8	25	31.8	18	0	0	870.54	147	154
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	27	244	0.25%	54.1%	QTVAVGVIK	99.7%	66.1	25	45.2	11	0	0	914.57	431	439
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	27	244	0.25%	54.1%	SGDAAIVDMVPGKPMCVESFSDYPPLGR	99.7%	71.5	25	70.7	0	6	0	3027.39	396	423
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	27	244	0.25%	54.1%	STTTGHLIYK	99.7%	50	25	38.1	25	0	0	1120.60	21	30
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	27	244	0.25%	54.1%	SVEMHHEALSEALPGDNVGFNVK	99.7%	86	25	78.2	0	2	0	2480.19	291	313
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	27	244	0.25%	54.1%	THINIVVIGHVDSGK	99.7%	109	25	109	10	26	0	1588.88	6	20
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	27	244	0.25%	54.1%	VETGVLKPGMVVTFAPVNVTTEVK	99.7%	69.2	25	69.2	4	14	0	2515.38	267	290
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	27	244	0.25%	54.1%	YYVTIIDAPGHR	99.7%	65.6	25	64	17	10	0	1404.73	85	96
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	27	244	0.25%	54.1%	YYVTIIDAPGHRDFIK	99.7%	67.6	25	67.6	2	2	0	1908.00	85	100
Elongation factor 1-beta	EEF1B2	EF1B_HUMAN	24.8	99.8%	2	2	4	0.00%	12.4%	SIQADGLVWGSSK	99.7%	81.6	25	75.7	2	0	0	1347.69	164	176
Elongation factor 1-beta	EEF1B2	EF1B_HUMAN	24.8	99.8%	2	2	4	0.00%	12.4%	SPAGLQVLNDYLADK	99.7%	105	25	105	2	0	0	1603.83	8	22
Elongation factor 1-delta	EEF1D	EF1D_HUMAN	31.1	100.0%	3	3	4	0.00%	13.9%	ATAPQTQHVSPMR	99.7%	39.3	25	38.2	1	0	0	1439.71	124	136
Elongation factor 1-delta	EEF1D	EF1D_HUMAN	31.1	100.0%	3	3	4	0.00%	13.9%	FYEQMNGPVAGASR	99.7%	49.7	25	44.2	1	0	0	1526.71	25	38
Elongation factor 1-delta	EEF1D	EF1D_HUMAN	31.1	100.0%	3	3	4	0.00%	13.9%	IASLEVENQSLR	99.7%	79.1	25	61.5	2	0	0	1358.73	84	95
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	9	12	26	0.03%	23.6%	ALIAAQYSGAQVR	99.7%	104	25	101	4	0	0	1347.74	18	30
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	9	12	26	0.03%	23.6%	EYFSWEGAFQHVGK	99.7%	75.8	25	73.8	2	2	0	1684.78	415	428
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	9	12	26	0.03%	23.6%	ILGLLDAYLK	99.7%	58.4	25	51.1	4	0	0	1118.68	138	147
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	9	12	26	0.03%	23.6%	KLDPGSEETQTLVR	99.7%	71.7	25	66.9	2	2	0	1572.82	401	414
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	9	12	26	0.03%	23.6%	QAFPNTNR	99.0%	34.3	25	28	1	0	0	947.47	182	189
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	9	12	26	0.03%	23.6%	STFVLDEFKR	99.7%	52.6	25	52.1	2	1	0	1241.65	286	295
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	9	12	26	0.03%	23.6%	TFLVGER	99.7%	41.9	25	30.6	2	0	0	821.45	150	156
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	9	12	26	0.03%	23.6%	VLSAPPHFHFGQTNR	99.7%	32.8	25	29.2	0	2	0	1707.87	31	45
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	9	12	26	0.03%	23.6%	WFLTCINQPQFR	99.7%	56.6	25	38.4	2	0	0	1609.79	190	201
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	25	51	0.05%	31.1%	ALLELQLEPEELYQTFQR	99.7%	42.4	25	42.4	1	0	0	2220.15	163	180
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	25	51	0.05%	31.1%	AYLPVNESFGFTADLR	99.7%	92.4	25	92.2	2	0	0	1799.90	786	801
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	25	51	0.05%	31.1%	CLYASVLTAQPR	99.7%	75.3	25	73	2	0	0	1378.71	728	739
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	25	51	0.05%	31.1%	EGALCEENMR	99.7%	77.2	25	60.2	3	0	0	1208.50	689	698
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	25	51	0.05%	31.1%	EGIPALDNFLDKL	99.7%	63.3	25	58.4	3	0	0	1444.77	846	858
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	25	51	0.05%	31.1%	ETVSEESNVLCLSK	99.7%	89	25	79.4	2	0	0	1594.76	581	594
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	25	51	0.05%	31.1%	FSVSPVVR	96.1%	28.6	25	21	1	0	0	890.51	499	506
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	25	51	0.05%	31.1%	GEGQLGPAER	99.7%	53.5	25	42.9	2	0	0	1013.50	240	249
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	25	51	0.05%	31.1%	GGGQIIPTAR	98.6%	32.8	25	23.9	5	0	0	969.55	717	726
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	25	51	0.05%	31.1%	GHVFEESQVAGTPMFVVK	96.2%	23.3	25	23.3	0	1	0	1961.98	768	785
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	25	51	0.05%	31.1%	GPLMMYISK	99.7%	40.3	25	40.3	2	0	0	1039.53	392	400
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	25	51	0.05%	31.1%	IMGPNYTPGK	99.7%	53.4	25	43.5	2	0	0	1077.54	429	438
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	25	51	0.05%	31.1%	IMGPNYTPGKK	99.4%	36.8	25	29.7	2	0	0	1205.63	429	439
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	25	51	0.05%	31.1%	KEDLYLKPIQR	99.7%	39.5	25	32.7	0	3	0	1402.81	439	449
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	25	51	0.05%	31.1%	NMSVIAHVDHGK	99.7%	45.2	25	29.3	1	0	0	1323.65	21	32

Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	25	51	0.05%	31.1%	QFAEMYVAK	99.7%	53.5	25	45.9	2	0	0	1086.53	227	235
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	25	51	0.05%	31.1%	SDPVVSYR	99.7%	43.7	25	34.8	2	0	0	922.46	573	580
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	25	51	0.05%	31.1%	STLTDSLVCK	99.7%	63.3	25	52.5	2	0	0	1123.57	33	42
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	25	51	0.05%	31.1%	TFCQLILDPIFK	99.7%	55.2	25	52.4	2	0	0	1494.80	288	299
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	25	51	0.05%	31.1%	TGTITTFEHAHNMR	99.7%	36	25	36	0	2	0	1615.76	482	495
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	25	51	0.05%	31.1%	VFDAIMNFK	99.7%	52.2	25	48.9	2	0	0	1084.55	300	308
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	25	51	0.05%	31.1%	VFSGLVSTGLK	99.7%	87.3	25	75.2	4	0	0	1107.64	416	426
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	25	51	0.05%	31.1%	VNFTVDQIR	99.7%	76.6	25	59.9	4	0	0	1091.58	2	10
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	25	51	0.05%	31.1%	YEWDVAEAR	99.7%	59.6	25	53	2	0	0	1138.52	639	647
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	25	51	0.05%	31.1%	YLAEKYEWDVAEAR	99.7%	33.3	25	33.3	0	2	0	1742.84	634	647
Elongation factor Ts, mitochondrial	TSFM	EFTS_HUMAN	35.4	99.8%	2	2	4	0.00%	9.2%	GFLNSSELSGLPAGPDR	99.7%	69.8	25	68.3	2	0	0	1716.86	162	178
Elongation factor Ts, mitochondrial	TSFM	EFTS_HUMAN	35.4	99.8%	2	2	4	0.00%	9.2%	YGALVICETSEQK	99.7%	58.4	25	52.4	2	0	0	1497.73	234	246
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	40	122	0.13%	59.1%	ADAVQDSEMVELVELEIR	99.7%	99.5	25	99.5	3	2	0	2062.00	183	200
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	40	122	0.13%	59.1%	AEAGDNLGALVR	99.7%	105	25	86.3	7	0	0	1185.62	316	327
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	40	122	0.13%	59.1%	DKPHVNVGTIGHVDHGK	98.7%	27.2	25	27.2	0	2	0	1809.94	54	70
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	40	122	0.13%	59.1%	DLEKPFLLPVEAVYSVPGR	99.7%	70.9	25	70.9	3	1	0	2129.16	253	271
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	40	122	0.13%	59.1%	EHLLLAR	99.7%	48.2	25	40.2	5	0	0	851.51	163	169
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	40	122	0.13%	59.1%	ELAMPGEDLK	99.7%	42.6	25	33.7	3	0	0	1102.55	396	405
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	40	122	0.13%	59.1%	ELAMPGEDLKFNLILR	99.7%	50.4	25	41.4	3	2	0	1875.00	396	411
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	40	122	0.13%	59.1%	ELLTEFGYK	99.1%	34.8	25	34.8	1	0	0	1099.57	201	209
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	40	122	0.13%	59.1%	GDECELLGHSK	99.7%	52.3	25	50.7	2	0	0	1244.56	287	297
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	40	122	0.13%	59.1%	GITINAAHVEYSTAAR	99.7%	93	25	84.2	6	5	0	1673.86	105	120
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	40	122	0.13%	59.1%	GLVMVKPGSIKPHQK	95.8%	23	25	23	0	1	0	1618.95	337	351
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	40	122	0.13%	59.1%	GTVVTGTLER	99.7%	64	25	40.4	9	0	0	1032.57	272	281
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	40	122	0.13%	59.1%	HYAHTDCPGHADYVK	99.7%	46.7	25	46.7	2	2	0	1770.77	121	135
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	40	122	0.13%	59.1%	IILPPEKELAMPGEDLK	99.6%	32.5	25	31.1	0	4	0	1909.04	389	405
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	40	122	0.13%	59.1%	KGDECELLGHSK	99.7%	65.9	25	60.1	2	2	0	1372.65	286	297
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	40	122	0.13%	59.1%	LLDAVDTYIPVPAR	99.7%	87.8	25	84.5	10	0	0	1542.85	239	252
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	40	122	0.13%	59.1%	QIGVEHVVVYVNK	99.7%	78	25	64.2	2	1	0	1483.83	170	182
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	40	122	0.13%	59.1%	TIGTGLVTNTLAMTEEEK	99.7%	117	25	115	8	0	0	1923.96	430	447
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	40	122	0.13%	59.1%	TIGTGLVTNTLAMTEEEKNIK	99.7%	106	25	106	1	1	0	2263.19	430	450
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	40	122	0.13%	59.1%	TTLTAAITK	99.7%	61.3	25	48	2	0	0	919.55	71	79
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	40	122	0.13%	59.1%	TVVTGIEMFHK	99.7%	62.3	25	38	14	2	0	1261.66	301	311
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	40	122	0.13%	59.1%	VEAQVYILSK	99.7%	80.2	25	71.5	8	0	0	1149.65	352	361
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	40	122	0.13%	59.1%	VEAQVYILSKEEGGR	99.7%	87.7	25	85.2	2	2	0	1677.88	352	366
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	40	122	0.13%	59.1%	YEEIDNAPEER	99.7%	83.3	25	77.4	2	0	0	1364.60	92	102
Elongator complex protein 1	IKBKAP	ELP1_HUMAN	150.3	100.0%	7	7	12	0.01%	5.9%	ALVLAQIR	99.7%	45.7	25	39.3	2	0	0	883.57	723	730
Elongator complex protein 1	IKBKAP	ELP1_HUMAN	150.3	100.0%	7	7	12	0.01%	5.9%	DIQGPGNPQCFSLR	99.7%	54.3	25	54.3	1	0	0	1588.75	14	27
Elongator complex protein 1	IKBKAP	ELP1_HUMAN	150.3	100.0%	7	7	12	0.01%	5.9%	EYLPFLNTLK	95.5%	28.1	25	26.8	1	0	0	1237.68	916	925
Elongator complex protein 1	IKBKAP	ELP1_HUMAN	150.3	100.0%	7	7	12	0.01%	5.9%	IVSLMWDPVTPYR	99.7%	46.8	25	42.1	2	0	0	1576.82	346	358
Elongator complex protein 1	IKBKAP	ELP1_HUMAN	150.3	100.0%	7	7	12	0.01%	5.9%	IVTVVPQDTK	99.3%	36.2	25	30	2	0	0	1099.64	697	706
Elongator complex protein 1	IKBKAP	ELP1_HUMAN	150.3	100.0%	7	7	12	0.01%	5.9%	SVVLQLADGQIFK	99.7%	82.8	25	73.5	2	0	0	1417.81	568	580
Elongator complex protein 1	IKBKAP	ELP1_HUMAN	150.3	100.0%	7	7	12	0.01%	5.9%	VFLGNVETFIK	99.7%	47.9	25	43.4	2	0	0	1266.71	762	772
Elongator complex protein 3	ELP3	ELP3_HUMAN	62.3	100.0%	3	3	3	0.00%	6.8%	AVCESFHLAK	99.2%	35.2	25	23	1	0	0	1161.57	266	275
Elongator complex protein 3	ELP3	ELP3_HUMAN	62.3	100.0%	3	3	3	0.00%	6.8%	LEIGVQSVYEDVAR	99.7%	70.3	25	70	1	0	0	1577.82	243	256
Elongator complex protein 3	ELP3	ELP3_HUMAN	62.3	100.0%	3	3	3	0.00%	6.8%	SYSPSDLVELVAR	99.7%	54.2	25	53.2	1	0	0	1435.74	339	351
Emerin	EMD	EMD_HUMAN	29.0	100.0%	6	6	10	0.01%	28.0%	APGAGLGQDR	99.7%	44.6	25	39.2	2	0	0	941.48	212	221
Emerin	EMD	EMD_HUMAN	29.0	100.0%	6	6	10	0.01%	28.0%	DSAYQSITHYRPVSASR	99.7%	35.9	25	35.9	0	2	0	1937.95	158	174
Emerin	EMD	EMD_HUMAN	29.0	100.0%	6	6	10	0.01%	28.0%	GDADMYDLPK	99.6%	38.4	25	37.9	2	0	0	1124.49	69	78
Emerin	EMD	EMD_HUMAN	29.0	100.0%	6	6	10	0.01%	28.0%	GYNDDYYEESYFTTR	99.7%	93.5	25	93.5	2	0	0	1922.77	89	103
Emerin	EMD	EMD_HUMAN	29.0	100.0%	6	6	10	0.01%	28.0%	KEDALLYQSK	99.7%	46.9	25	34.7	1	0	0	1194.64	79	88

Emerin	EMD	EMD_HUMAN	29.0	100.0%	6	6	10	0.01%	28.0%	KIFEYETQR	99.7%	44	25	43.2	1	0	0	1213.62	37	45
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	6	6	7	0.01%	9.7%	ELISNASDALDK	99.7%	71.1	25	53.4	7	0	0	1275.64	103	114
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	6	6	7	0.01%	9.7%	ELISNASDALDKIR	99.7%	92.6	25	73.4	10	2	0	1544.83	103	116
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	6	6	7	0.01%	9.7%	FAFQAEVNR	99.6%	38.5	25	24.8	1	0	0	1081.54	76	84
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	6	6	7	0.01%	9.7%	GVVDSDDLPLNVSR	99.7%	59.1	25	49.4	2	0	0	1485.75	435	448
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	6	6	7	0.01%	9.7%	LIINSLYK	97.6%	30.6	25	16.3	1	0	0	963.59	88	95
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	6	6	7	0.01%	9.7%	SGTSEFLNK	99.5%	37	25	33.3	1	0	0	982.48	169	177
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	6	6	7	0.01%	9.7%	SGYLLPDTK	99.4%	36.2	25	27	1	0	0	993.53	725	733
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	6	6	7	0.01%	9.7%	YSQFINFPIYVWSSK	99.7%	62.2	25	62.2	1	0	0	1878.94	271	285
Enhancer of mRNA-decapping protein 3	EDC3	EDC3_HUMAN	56.1	100.0%	5	5	8	0.01%	11.6%	AGDITELK	99.7%	50.7	25	15.1	2	0	0	846.46	56	63
Enhancer of mRNA-decapping protein 3	EDC3	EDC3_HUMAN	56.1	100.0%	5	5	8	0.01%	11.6%	FVIPLHSA	97.5%	30.4	25	30.4	1	0	0	883.50	501	508
Enhancer of mRNA-decapping protein 3	EDC3	EDC3_HUMAN	56.1	100.0%	5	5	8	0.01%	11.6%	KPASSSSAPQNIPK	99.7%	64.9	25	58.2	2	0	0	1411.75	106	119
Enhancer of mRNA-decapping protein 3	EDC3	EDC3_HUMAN	56.1	100.0%	5	5	8	0.01%	11.6%	MLESITNELSLFSK	99.7%	46.2	25	46.2	2	0	0	1627.82	374	387
Enhancer of mRNA-decapping protein 3	EDC3	EDC3_HUMAN	56.1	100.0%	5	5	8	0.01%	11.6%	SQDVAVSPQQQQCSK	99.7%	72.7	25	72.7	1	0	0	1689.79	125	139
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	5	6	11	0.01%	45.2%	ADTQTYQPYNK	99.7%	45.3	25	43.3	2	0	0	1328.61	74	84
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	5	6	11	0.01%	45.2%	ADTQTYQPYNKDWIK	99.7%	46.2	25	46.2	1	0	0	1870.90	74	88
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	5	6	11	0.01%	45.2%	IYVLLRR	97.6%	30.5	25	12.4	2	0	0	932.60	91	97
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	5	6	11	0.01%	45.2%	MYEEHLKR	99.7%	39.5	25	33.5	2	0	0	1105.55	35	42
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	5	6	11	0.01%	45.2%	TYADYESVNECMEGVCK	99.7%	82.8	25	82.8	4	0	0	2054.81	18	34
Enoyl-CoA delta isomerase 1, mitochondrial	ECI1	ECI1_HUMAN	32.8	100.0%	3	4	6	0.01%	11.9%	AVQELWLR	97.2%	29.9	25	14.2	1	0	0	1014.57	127	134
Enoyl-CoA delta isomerase 1, mitochondrial	ECI1	ECI1_HUMAN	32.8	100.0%	3	4	6	0.01%	11.9%	DADVQNFVSFISK	99.7%	80.4	25	74.3	2	0	0	1469.73	271	283
Enoyl-CoA delta isomerase 1, mitochondrial	ECI1	ECI1_HUMAN	32.8	100.0%	3	4	6	0.01%	11.9%	VLVEPDAGAGVAVMK	99.7%	67.4	25	63.5	3	0	0	1471.78	47	61
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	7	10	23	0.02%	31.0%	AFAAGADIK	99.6%	38.3	25	20.1	2	0	0	863.46	93	101
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	7	10	23	0.02%	31.0%	AQFAQPEILIGTIPGAGGTQR	99.7%	83.8	25	81.3	2	1	0	2125.14	158	178
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	7	10	23	0.02%	31.0%	EGMTAFVEK	99.7%	46.4	25	33.3	2	0	0	1011.48	274	282
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	7	10	23	0.02%	31.0%	EMQNLSFQDCYSSK	99.7%	58.1	25	58.1	4	0	0	1736.73	102	115
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	7	10	23	0.02%	31.0%	LFYSTFATDDRK	99.7%	61.8	25	58.1	2	0	0	1463.72	262	273
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	7	10	23	0.02%	31.0%	NNTVGLIQLNRPK	99.7%	78.5	25	76.4	2	0	0	1466.84	44	56
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	7	10	23	0.02%	31.0%	SLAMEMVLTGDR	99.7%	86.3	25	32	8	0	0	1338.64	186	197
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	8	8	14	0.01%	9.2%	ADGLLGMFLK	99.7%	46.8	25	34.7	1	0	0	1064.58	477	486
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	8	8	14	0.01%	9.2%	FASLEFSPGSK	99.7%	60.2	25	50.6	1	0	0	1169.58	42	52
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	8	8	14	0.01%	9.2%	FNVEDGEIVQQVR	99.7%	87.9	25	77.2	1	0	0	1532.77	202	214
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	8	8	14	0.01%	9.2%	LFGIESSSGTILWK	99.7%	71.9	25	67.2	2	0	0	1537.83	545	558
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	8	8	14	0.01%	9.2%	NVIAALNSR	99.7%	51.1	25	36.6	3	0	0	957.55	61	69
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	8	8	14	0.01%	9.2%	RPEIPTEQSR	99.7%	47.8	25	41.6	1	0	0	1212.63	882	891
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	8	8	14	0.01%	9.2%	TFIGIFLIDGVTGR	99.7%	80.4	25	70.6	4	0	0	1508.85	755	768
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	8	8	14	0.01%	9.2%	WSQVAPPVLK	99.0%	34.2	25	34.2	1	0	0	1124.65	611	620
ER membrane protein complex subunit 2	EMC2	EMC2_HUMAN	34.8	99.8%	2	2	2	0.00%	8.4%	AVEDMLETLQITQS	99.2%	35.5	25	35.5	1	0	0	1577.77	284	297
ER membrane protein complex subunit 2	EMC2	EMC2_HUMAN	34.8	99.8%	2	2	2	0.00%	8.4%	YASWAASQINR	99.4%	36.2	25	32.5	1	0	0	1266.62	256	266
ER membrane protein complex subunit 3	EMC3	EMC3_HUMAN	30.0	100.0%	5	5	8	0.01%	19.9%	AGPELLLDSNIR	99.7%	62.6	25	51.6	2	0	0	1297.71	2	13
ER membrane protein complex subunit 3	EMC3	EMC3_HUMAN	30.0	100.0%	5	5	8	0.01%	19.9%	KLTQEQVSDSQVLIR	99.0%	28.5	25	25.8	0	1	0	1743.96	43	57
ER membrane protein complex subunit 3	EMC3	EMC3_HUMAN	30.0	100.0%	5	5	8	0.01%	19.9%	LTQEQVSDSQVLIR	99.7%	99.6	25	79.1	2	0	0	1615.87	44	57
ER membrane protein complex subunit 3	EMC3	EMC3_HUMAN	30.0	100.0%	5	5	8	0.01%	19.9%	SIYSLILGQDNAADQSR	99.7%	117	25	116	2	0	0	1850.92	181	197
ER membrane protein complex subunit 3	EMC3	EMC3_HUMAN	30.0	100.0%	5	5	8	0.01%	19.9%	VPFPLTLR	98.5%	32.4	25	21.4	1	0	0	942.58	140	147
ER membrane protein complex subunit 4	EMC4	EMC4_HUMAN	20.1	100.0%	2	2	7	0.01%	15.8%	GSGQGDSLYPVGYLDK	99.7%	60.5	25	60.5	4	0	0	1655.79	35	50
ER membrane protein complex subunit 4	EMC4	EMC4_HUMAN	20.1	100.0%	2	2	7	0.01%	15.8%	WAIELSGPGGGSR	99.7%	43.7	25	38.2	3	0	0	1286.65	17	29
ER membrane protein complex subunit 6	EMC6	EMC6_HUMAN	12.0	99.8%	2	2	4	0.00%	20.0%	EGPPFISEAAVR	99.7%	39.5	25	35.3	2	0	0	1272.66	9	20
ER membrane protein complex subunit 6	EMC6	EMC6_HUMAN	12.0	99.8%	2	2	4	0.00%	20.0%	GNAAVLDYCR	99.7%	58.3	25	52.2	2	0	0	1138.53	21	30
ER membrane protein complex subunit 7	EMC7	EMC7_HUMAN	26.5	100.0%	2	2	2	0.00%	9.5%	SSGPPSYFIK	99.7%	41.7	25	34.8	1	0	0	1082.55	142	151
ER membrane protein complex subunit 7	EMC7	EMC7_HUMAN	26.5	100.0%	2	2	2	0.00%	9.5%	VLVDGEEHVGFLK	99.7%	55.8	25	55.8	1	0	0	1441.77	67	79
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	5	7	14	0.01%	25.7%	ADAEYYAAHK	99.7%	52.6	25	48.2	2	0	0	1138.52	258	267

Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	5	7	14	0.01%	25.7%	DLNLMAPGLTIQAVR	99.7%	106	25	95	4	0	0	1611.89	155	169
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	5	7	14	0.01%	25.7%	EALEPSGENVIQNK	99.7%	76.7	25	75.5	2	0	0	1527.77	329	342
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	5	7	14	0.01%	25.7%	ESSLPSKEALEPSGENVIQNK	99.5%	30.9	25	13.1	0	2	0	2256.14	322	342
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	5	7	14	0.01%	25.7%	ISEIEDAAFLAR	99.7%	110	25	94.2	4	0	0	1334.70	242	253
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	5	7	14	0.01%	25.7%	IYFGSNIPNMFVDSSCALK	99.7%	83.3	25	83.3	4	0	0	2163.03	295	313
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	5	7	14	0.01%	25.7%	SVQTTLQTDEVK	99.7%	80	25	63.9	4	0	0	1348.70	61	72
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	12	29	0.03%	33.9%	ADAECYTAMK	99.6%	39	25	39	2	0	0	1159.48	258	267
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	12	29	0.03%	33.9%	AKADAECYTAMK	99.4%	36.3	25	33.3	1	0	0	1358.61	256	267
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	12	29	0.03%	33.9%	DIPNMFMDSAGSVSK	99.7%	77.1	25	66.4	4	0	0	1598.72	300	314
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	12	29	0.03%	33.9%	ISEIEDAAFLAR	99.7%	110	25	94.2	4	0	0	1334.70	242	253
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	12	29	0.03%	33.9%	KISEIEDAAFLAR	99.7%	79.7	25	68.5	3	0	0	1462.79	241	253
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	12	29	0.03%	33.9%	LALQQDLTSMAPGLVIQAVR	99.7%	74.7	25	72.9	1	0	0	2124.18	150	169
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	12	29	0.03%	33.9%	LTPEYLQLMK	99.7%	40.3	25	34.2	3	0	0	1251.67	276	285
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	12	29	0.03%	33.9%	NYELMESEK	98.7%	33	25	29	1	0	0	1142.50	182	190
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	12	29	0.03%	33.9%	SVQTTLQTDEVK	99.7%	80	25	63.9	4	0	0	1348.70	61	72
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	12	29	0.03%	33.9%	VAQVAEITYGQK	99.7%	79.4	25	79.4	2	0	0	1306.70	221	232
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	12	29	0.03%	33.9%	VTKPNIPEAIR	99.5%	37.7	25	37.7	3	0	0	1237.73	170	180
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	12	29	0.03%	33.9%	VTKPNIPEAIRR	95.3%	22.5	25	20.4	0	1	0	1393.83	170	181
ERO1-like protein alpha	ERO1L	ERO1A_HUMAN	54.4	100.0%	3	3	3	0.00%	8.1%	FDGILTEGEGPR	99.1%	34.8	25	32.4	1	0	0	1290.63	288	299
ERO1-like protein alpha	ERO1L	ERO1A_HUMAN	54.4	100.0%	3	3	3	0.00%	8.1%	LGAVDESLSEETQK	99.7%	63.8	25	59.3	1	0	0	1505.73	137	150
ERO1-like protein alpha	ERO1L	ERO1A_HUMAN	54.4	100.0%	3	3	3	0.00%	8.1%	QEIVSLFNAFGR	99.5%	37.8	25	33	1	0	0	1380.73	438	449
Erythrocyte band 7 integral membrane protein	STOM	STOM_HUMAN	31.7	99.9%	2	2	3	0.00%	6.9%	LLAQTTLR	99.7%	51	25	39.1	2	0	0	915.56	145	152
Erythrocyte band 7 integral membrane protein	STOM	STOM_HUMAN	31.7	99.9%	2	2	3	0.00%	6.9%	VIAAEGEMNASR	99.7%	48.8	25	42	1	0	0	1263.60	221	232
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	8	11	28	0.03%	33.3%	GVFVQSVLPYFVATK	99.7%	60.4	25	60.4	3	0	0	1654.92	224	238
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	8	11	28	0.03%	33.3%	ISYSLFTALR	99.7%	106	25	96.5	4	0	0	1170.65	26	35
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	8	11	28	0.03%	33.3%	KPTLDKPSPETFVK	98.8%	27.6	25	27.6	0	2	0	1586.88	244	257
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	8	11	28	0.03%	33.3%	LDQVSSEIKEK	99.7%	52.6	25	39.6	2	0	0	1275.68	87	97
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	8	11	28	0.03%	33.3%	MININILSVCK	99.7%	77.8	25	74.8	5	0	0	1320.70	157	167
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	8	11	28	0.03%	33.3%	MTQLVLPGMVER	99.7%	63	25	50.2	6	0	0	1389.72	168	179
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	8	11	28	0.03%	33.3%	TFVDFFSQCLHEEYR	99.7%	65.6	25	65.6	2	2	0	1977.88	207	221
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	8	11	28	0.03%	33.3%	TIAVDFASEDIYDKIK	99.7%	91.5	25	87.4	2	0	0	1827.94	104	119
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	8	8	19	0.02%	33.2%	DLLGTVWGGPANLEAIAK	99.7%	62.3	25	62.3	2	0	0	1824.99	284	301
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	8	8	19	0.02%	33.2%	ELYLEEALQNER	99.7%	76.6	25	71.8	2	0	0	1506.74	272	283
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	8	8	19	0.02%	33.2%	LVEIIGSR	99.7%	51.7	25	48.9	1	0	0	886.54	199	206
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	8	8	19	0.02%	33.2%	NALNIGMVEEVLQSSDETK	99.7%	74.7	25	72.8	1	0	0	2077.01	222	240
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	8	8	19	0.02%	33.2%	NTFSSGSDLNAVK	99.7%	66.8	25	60.3	2	0	0	1339.65	109	121
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	8	8	19	0.02%	33.2%	QFIQGPPEVIR	99.7%	60.9	25	36	4	0	0	1283.71	251	261
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	8	8	19	0.02%	33.2%	SLEEAQEWLK	99.7%	62.9	25	51.4	4	0	0	1232.62	241	250
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	8	8	19	0.02%	33.2%	VIELENWTEGK	99.7%	73.2	25	73.2	3	0	0	1317.67	90	100
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	23	47	0.05%	47.5%	ATQALVLAPTR	99.7%	58.2	25	36.2	2	0	0	1140.67	100	110
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	23	47	0.05%	47.5%	DFTVSAMHGDMDQKER	99.7%	45.1	25	45.1	0	5	0	1866.81	296	311
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	23	47	0.05%	47.5%	ELAQQIQK	99.2%	35.4	25	22.3	2	0	0	957.54	111	118
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	23	47	0.05%	47.5%	GFKDQIYDIFQK	99.7%	63.9	25	54.9	2	1	0	1501.77	191	202
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	23	47	0.05%	47.5%	GIYAYGFEKPSAIQQR	99.7%	78	25	73.5	2	0	0	1827.94	46	61
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	23	47	0.05%	47.5%	GVAINMVTEEDKR	99.7%	75.9	25	69	2	0	0	1461.74	370	382
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	23	47	0.05%	47.5%	GYDVIAQAQSGTGK	99.7%	128	25	115	1	0	0	1394.69	69	82
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	23	47	0.05%	47.5%	KEELTLEGIR	99.7%	50.2	25	38.1	2	0	0	1187.66	238	247
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	23	47	0.05%	47.5%	KVDWLTEK	99.7%	39.5	25	23.5	2	0	0	1018.56	284	291
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	23	47	0.05%	47.5%	LNSNTQVVLLSATMPSDVLEVTK	99.7%	67.2	25	67.2	4	1	0	2459.31	203	225
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	23	47	0.05%	47.5%	LNSNTQVVLLSATMPSDVLEVTKK	97.3%	24.6	25	24.6	0	1	0	2603.40	203	226
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	23	47	0.05%	47.5%	LQMEAPHIIVGTPGR	99.7%	63.6	25	63.6	4	4	0	1634.87	147	161

Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	23	47	0.05%	47.5%	MFVLDEADEMLSR	99.7%	119	25	112	7	0	0	1555.71	178	190
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	23	47	0.05%	47.5%	VLITTDLLAR	99.7%	69.8	25	66.5	3	0	0	1114.68	325	334
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	23	47	0.05%	47.5%	VVMALGDYMGASCHACIGGTNVR	99.7%	55.6	25	55.6	0	2	0	2471.09	119	141
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	13	21	0.02%	32.4%	ELAVQIQK	99.7%	45.5	25	36.3	2	0	0	928.55	117	124
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	13	21	0.02%	32.4%	ETQALILAPTR	99.7%	70.5	25	66.3	2	0	0	1212.69	106	116
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	13	21	0.02%	32.4%	GFKEQIYDVYR	99.7%	54.8	25	51	1	0	0	1417.71	196	206
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	13	21	0.02%	32.4%	GIYAYGFEKPSAIQQR	99.7%	78	25	73.5	2	0	0	1827.94	52	67
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	13	21	0.02%	32.4%	GRDVIAQSQSGTGK	99.7%	59	25	59	2	1	0	1403.72	75	88
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	13	21	0.02%	32.4%	KGVAINFVK	99.5%	37.4	25	26.8	2	0	0	975.60	374	382
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	13	21	0.02%	32.4%	KLDYGQHVVAGTPGR	99.7%	41.3	25	31.9	0	2	0	1597.84	152	166
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	13	21	0.02%	32.4%	KVDWLTEK	99.7%	39.5	25	23.5	2	0	0	1018.56	289	296
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	13	21	0.02%	32.4%	LDYGQHVVAGTPGR	99.7%	47.1	25	43.5	1	2	0	1469.75	153	166
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	13	21	0.02%	32.4%	MLVLDEADEMLNK	99.7%	73.2	25	73.2	1	0	0	1536.73	183	195
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	13	21	0.02%	32.4%	QFFVAVER	99.7%	52.1	25	37.1	2	0	0	995.53	253	260
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	13	21	0.02%	32.4%	RDELTLEGIK	99.1%	34.5	25	21.2	1	0	0	1173.65	243	252
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	13	21	0.02%	32.4%	VLISTDVWAR	99.7%	57.9	25	52.8	2	0	0	1159.65	330	339
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	5	6	12	0.01%	25.9%	AIVQQWLEYR	99.7%	59.1	25	46.8	2	0	0	1305.70	69	78
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	5	6	12	0.01%	25.9%	EYLLGSTAEEK	99.7%	42.9	25	42.9	2	0	0	1239.61	58	68
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	5	6	12	0.01%	25.9%	FIVDLTVQEKEK	99.7%	63.7	25	57.8	2	0	0	1448.80	127	138
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	5	6	12	0.01%	25.9%	NDIHTLLK	99.4%	36.8	25	29.3	2	0	0	953.54	89	96
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	5	6	12	0.01%	25.9%	QANKEYLLGSTAEEK	99.7%	55.8	25	53.4	2	2	0	1680.84	54	68
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	8	10	20	0.02%	27.9%	AGLNCSTENMPIK	99.7%	62.6	25	54	4	0	0	1434.67	214	226
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	8	10	20	0.02%	27.9%	GVFNVQMEPK	99.7%	43.6	25	33.9	3	0	0	1148.58	267	276
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	8	10	20	0.02%	27.9%	RPGYGAYDAFK	97.1%	29.9	25	20.8	1	0	0	1244.61	144	154
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	8	10	20	0.02%	27.9%	TAWVFDDKYK	99.7%	40.4	25	40.4	1	0	0	1272.63	134	143
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	8	10	20	0.02%	27.9%	TEGLSVLSQAMAVIK	99.7%	99.9	25	94.3	4	0	0	1546.85	245	259
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	8	10	20	0.02%	27.9%	TVYSILR	99.1%	34.8	25	22.5	1	0	0	851.50	107	113
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	8	10	20	0.02%	27.9%	VVTDTDETELAR	99.7%	102	25	95.6	4	0	0	1348.66	277	288
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	8	10	20	0.02%	27.9%	YVMTTTTLER	99.7%	44.5	25	36.8	2	0	0	1230.60	235	244
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	IF2G_HUMAN	51.1	100.0%	4	4	5	0.01%	9.8%	GVTIKPTVDDD	99.7%	51.9	25	51.9	1	0	0	1159.58	462	472
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	IF2G_HUMAN	51.1	100.0%	4	4	5	0.01%	9.8%	IVLTNPVCTEVGEK	99.7%	65.6	25	61.9	1	0	0	1558.81	427	440
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	IF2G_HUMAN	51.1	100.0%	4	4	5	0.01%	9.8%	LTPLSHEVISR	99.7%	43	25	42.7	2	0	0	1251.71	28	38
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	IF2G_HUMAN	51.1	100.0%	4	4	5	0.01%	9.8%	QDLTTLDVTK	99.1%	34.7	25	23.8	1	0	0	1133.61	18	27
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	ANEFLEVGK	99.7%	47	25	36.1	3	0	0	1006.52	15	23
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	ANEFLEVGKK	99.5%	37.2	25	25.3	2	0	0	1134.62	15	24
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	AVEDIHGLFSLSK	99.7%	93	25	93	4	0	0	1415.75	252	264
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	EDAPIGPHLQSMPSEQIR	99.7%	49.8	25	42.7	0	8	0	2020.98	503	520
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	EEELREYQER	99.6%	39	25	32.6	2	0	0	1380.64	838	847
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	EGLYQYK	99.5%	37	25	23.2	1	0	0	900.45	69	75
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	ELEIEERER	99.7%	43.4	25	1.31	2	0	0	1202.60	862	870
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	ERLEQIK	95.1%	27.8	25	6.61	1	0	0	915.53	638	644
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	FCLQYTR	99.7%	39.8	25	31.7	4	0	0	987.47	184	190
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	FLWESYR	97.0%	29.6	25	21.8	1	0	0	1000.49	152	158
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	FNVLQYVVPEVK	99.7%	85.8	25	76.3	8	0	0	1434.80	377	388
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	GLDEDRGSWR	95.1%	27.8	25	14.3	1	0	0	1190.56	1021	1030
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	IGLINDMVR	99.7%	58.1	25	50.2	10	0	0	1046.57	368	376
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	IHEPIMLK	95.0%	27.7	25	15	1	0	0	980.56	46	53
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	ILQEHEQIK	99.7%	43.9	25	38.6	6	0	0	1137.63	624	632
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	ITTMQLER	99.7%	60.5	25	41.9	4	0	0	991.52	733	740
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	KIDYFER	99.7%	40	25	27	4	0	0	970.50	694	700
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	LATLLGLQAPPTR	99.7%	49	25	47.7	4	0	0	1350.81	355	367

Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	LEEIPLIK	97.0%	29.7	25	16.1	4	0	0	954.59	704	711
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	LESLNIQR	99.7%	53.9	25	18.9	4	0	0	972.55	582	589
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	LKQFEER	94.6%	27.4	25	0.99	1	0	0	949.51	776	782
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	LLDMDGIIVEK	99.7%	78.4	25	74.2	7	0	0	1245.68	341	351
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	LLLTPWVK	99.7%	43.4	25	21.8	4	0	0	969.61	144	151
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	LLQQVSQIYQSIEFSR	99.7%	92.7	25	92.7	5	0	0	1939.03	439	454
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	LTSLVPFVDAFQLER	99.7%	85	25	85	7	0	0	1734.94	455	469
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	LYHDIAQQAFK	99.7%	55.7	25	40.5	4	0	0	1333.69	173	183
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	MHLSQIQR	99.7%	39.9	25	28.3	4	0	0	1028.53	203	210
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	MLEDRDLFVMR	99.7%	34.2	25	30.8	1	2	0	1440.70	753	763
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	NICQQVNIK	99.7%	45	25	26.6	4	0	0	1116.58	76	84
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	NLTQDEMQR	99.7%	45	25	42.3	7	0	0	1134.52	309	317
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	NMDDDRLSR	98.8%	33.3	25	20.9	2	0	0	1121.50	1142	1150
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	NQLTAMSSVLAK	99.7%	93.3	25	80.2	11	0	0	1262.68	521	532
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	PAYFQRPENALK	98.8%	33.6	25	23	1	0	0	1433.75	2	13
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	PAYFQRPENALKR	98.6%	26.9	25	22.2	0	1	0	1589.85	2	14
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	QCLDLLR	99.4%	36.5	25	1.71	2	0	0	917.49	159	165
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	QPALDVLYDVMK	99.7%	41.5	25	39.3	3	0	0	1391.72	25	36
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	RGPAEESSSWR	99.2%	35.1	25	35.1	1	0	0	1261.59	1250	1260
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	RLEEIPLIK	95.6%	28.1	25	27.1	1	0	0	1110.69	703	711
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	RLGDSSLSR	99.7%	47.6	25	29	2	0	0	990.53	877	885
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	RVPPPALSR	98.0%	31.2	25	27	2	0	0	992.60	1329	1337
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	SGNALFHASTLHR	99.7%	55.3	25	53.5	1	6	0	1410.72	286	298
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	SLEDVVR	99.4%	36.8	25	16.6	3	0	0	817.44	85	91
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	TLSFGSDLNYATR	99.7%	96.3	25	89.5	5	0	0	1444.71	490	502
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	VLLATLSIPITPER	99.7%	63.6	25	63.6	8	0	0	1522.92	322	335
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	45	55	170	0.18%	30.8%	YLELCVDLRK	98.2%	31.8	25	21.1	1	0	0	1308.70	54	63
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	AQAVSEDAGGNEGR	99.7%	100	25	100	7	0	0	1360.61	121	134
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	DQYSVIFESGDR	99.7%	62.5	25	62.5	1	0	0	1415.64	304	315
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	ETIIAFAWEPNGSK	99.7%	73.2	25	72.6	2	0	0	1562.79	563	576
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	FAVLHGEAPR	99.7%	54.8	25	50.3	3	0	0	1096.59	577	586
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	FSHQGVQLIDFSPCER	99.7%	43.2	25	43.2	0	2	0	1919.91	371	386
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	GIALWGGEK	99.7%	41.4	25	35.4	3	0	0	930.50	356	364
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	GTQGVVTNFEIFR	99.7%	72.4	25	72.4	7	0	0	1467.76	536	548
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	GTYLATFHQR	99.7%	70.3	25	63.2	6	0	0	1193.61	346	355
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	GYIFLEYASPAHAVDAVK	99.7%	90.7	25	90.7	4	2	0	1951.00	231	248
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	ISVSFYHVK	99.6%	37.9	25	27.4	2	0	0	1079.59	587	595
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	ITNDFYPEEDGK	99.7%	71.8	25	71.8	2	0	0	1427.63	217	228
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	ITNDFYPEEDGKTK	99.7%	69	25	69	2	3	0	1656.78	217	230
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	MAQELYMEQK	99.7%	87.5	25	70	8	0	0	1270.58	763	772
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	MTLDTLSIYETPSMGLLDK	99.7%	65.9	25	61.7	2	0	0	2128.06	441	459
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	MTLDTLSIYETPSMGLLDKK	99.7%	39	25	39	0	2	0	2256.15	441	460
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	NADGYKLDK	99.7%	46	25	34.5	2	0	0	1023.51	249	257
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	NGDYLCVK	99.7%	59.6	25	46.3	2	0	0	968.45	522	529
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	NLFNVVDCK	99.7%	59.4	25	50	4	0	0	1108.55	508	516
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	QVPVDVVEMK	99.7%	59.2	25	55.2	2	0	0	1143.61	553	562
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	TMMEDFRK	97.3%	30	25	23	1	0	0	1057.48	752	759
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	TSIFWNDVKDPVSIEER	99.7%	75.7	25	75.3	2	2	0	2035.01	316	332
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	VDNAYWLWTFQGR	99.7%	76.6	25	75.8	2	0	0	1655.80	677	689
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	VNLFTDFDK	99.7%	51.2	25	44.4	1	0	0	1098.55	263	271
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	VTLMQLPTR	99.7%	62.6	25	44	6	0	0	1058.60	493	501

Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	WTETYVR	96.3%	28.8	25	18.7	1	0	0	954.47	335	341
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	YVVTSVSWWSHK	99.7%	42	25	34.4	2	0	0	1478.74	665	676
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	27	32	86	0.09%	35.5%	YWLEEAECR	99.4%	36.8	25	36.8	1	0	0	1255.54	295	303
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	12	12	21	0.02%	12.4%	AKELLGQGLLLR	99.7%	48.2	25	44.7	1	0	0	1310.82	642	653
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	12	12	21	0.02%	12.4%	DFESHITSYK	96.6%	29.2	25	23.5	2	0	0	1226.57	151	160
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	12	12	21	0.02%	12.4%	ELLGQGLLLR	99.7%	61.9	25	45.7	2	0	0	1111.68	644	653
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	12	12	21	0.02%	12.4%	FEELTNLIR	99.7%	63.3	25	39	2	0	0	1134.62	57	65
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	12	12	21	0.02%	12.4%	GCILTLVER	99.7%	63.3	25	49.3	2	0	0	1060.58	442	450
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	12	12	21	0.02%	12.4%	GTEITHAVVIK	99.7%	54.5	25	41.1	2	0	0	1167.67	321	331
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	12	12	21	0.02%	12.4%	KIQEESLR	99.7%	40.6	25	28	2	0	0	1002.56	782	789
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	12	12	21	0.02%	12.4%	KLNEILQAR	99.7%	45	25	23.8	1	0	0	1084.65	332	340
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	12	12	21	0.02%	12.4%	LGSLVENNER	99.7%	74.2	25	57.2	2	0	0	1130.58	863	872
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	12	12	21	0.02%	12.4%	QGTYGGYFR	99.1%	34.9	25	32	1	0	0	1048.48	878	886
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	12	12	21	0.02%	12.4%	SIVDKEGVPR	99.7%	44.6	25	33.2	2	0	0	1099.61	95	104
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	12	12	21	0.02%	12.4%	TEPTAQQNLALQLAEK	99.7%	93.6	25	91.5	2	0	0	1754.93	847	862
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	12	14	32	0.03%	21.5%	GAVIATELK	99.7%	40.1	25	11.9	2	0	0	901.54	418	426
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	12	14	32	0.03%	21.5%	GAVIATELKNNSYK	99.7%	66.9	25	54.5	1	0	0	1507.81	418	431
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	12	14	32	0.03%	21.5%	IFHTVTTTDDPVIR	99.7%	64.1	25	56	3	2	0	1614.85	223	236
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	12	14	32	0.03%	21.5%	IFHTVTTTDDPVIRK	98.1%	25.9	25	23.6	0	1	0	1742.94	223	237
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	12	14	32	0.03%	21.5%	LGDDIDLIVR	99.7%	93.4	25	77.6	4	0	0	1128.63	365	374
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	12	14	32	0.03%	21.5%	NMLQFNLQILPK	99.7%	80.5	25	74.3	3	0	0	1458.81	113	124
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	12	14	32	0.03%	21.5%	SVYSWDIVVQR	99.7%	63.4	25	60.5	4	0	0	1351.70	261	271
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	12	14	32	0.03%	21.5%	TQGNVFATDAILATLMSCTR	99.7%	56.5	25	56.5	1	0	0	2170.06	241	260
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	12	14	32	0.03%	21.5%	VADWTGATYQDK	99.7%	56.5	25	55.2	1	0	0	1354.63	42	53
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	12	14	32	0.03%	21.5%	VADWTGATYQDKR	99.7%	69.2	25	69.2	4	2	0	1510.73	42	54
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	12	14	32	0.03%	21.5%	WTCCALLAGSEYLK	99.7%	53.4	25	53.4	3	0	0	1671.79	435	448
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	12	14	32	0.03%	21.5%	YLILKDPNK	98.7%	33	25	29.9	1	0	0	1103.65	506	514
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	32	65	0.07%	56.6%	EIYNEKELLQGK	99.7%	59	25	35.5	2	0	0	1463.77	30	41
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	32	65	0.07%	56.6%	ETIDNNSVSSPLQSLQQR	99.7%	86.6	25	82	1	0	0	2016.00	194	211
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	32	65	0.07%	56.6%	FQYECGNYSGAAEYLYFFR	99.7%	71	25	71	2	0	0	2385.03	137	155
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	32	65	0.07%	56.6%	IAHFLDR	98.8%	33.6	25	24.1	2	0	0	871.48	10	16
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	32	65	0.07%	56.6%	LASEILMQNWDAAMEDLTR	99.7%	107	25	107	2	0	0	2207.05	173	191
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	32	65	0.07%	56.6%	LDLLSDTNMVDFAMDVYK	99.7%	64.7	25	46	1	0	0	2105.98	42	59
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	32	65	0.07%	56.6%	LFIFETFCR	99.7%	68.3	25	57.5	5	0	0	1232.61	338	346
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	32	65	0.07%	56.6%	LGHVVMGNNAVSPYQQVIEK	99.7%	102	25	102	1	4	0	2183.13	388	407
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	32	65	0.07%	56.6%	LKETIDNNSVSSPLQSLQQR	99.7%	90.1	25	90.1	1	2	0	2257.18	192	211
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	32	65	0.07%	56.6%	MFEDPETTR	99.7%	49.1	25	32.5	4	0	0	1141.48	94	102
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	32	65	0.07%	56.6%	MLFDYLADK	99.7%	53.9	25	39.3	3	0	0	1115.54	112	120
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	32	65	0.07%	56.6%	NALSSLWGK	99.7%	57.8	25	53.3	2	0	0	975.53	164	172
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	32	65	0.07%	56.6%	NLYSDDIPHALR	99.7%	66.8	25	59.4	3	2	0	1413.71	60	71
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	32	65	0.07%	56.6%	QEYLDTLYR	99.7%	51.3	25	42.7	2	0	0	1200.59	125	133
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	32	65	0.07%	56.6%	QLQAETEPIVK	99.7%	74.7	25	56	4	0	0	1255.69	83	93
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	32	65	0.07%	56.6%	QVLKDLVK	96.0%	28.5	25	19	1	0	0	942.60	272	279
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	32	65	0.07%	56.6%	RTTVVAQLK	95.4%	28	25	16.2	1	0	0	1015.63	74	82
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	32	65	0.07%	56.6%	SEAPNWATQDSGFY	99.7%	77.3	25	77.3	2	0	0	1572.66	432	445
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	32	65	0.07%	56.6%	SQMLAMNIEK	99.7%	63.2	25	52.6	5	0	0	1164.58	415	424
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	32	65	0.07%	56.6%	TTVVAQLK	98.2%	31.8	25	15.6	2	0	0	859.52	75	82
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	32	65	0.07%	56.6%	VLVPATDR	99.5%	37.1	25	36.3	2	0	0	870.50	156	163
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	32	65	0.07%	56.6%	WIVNLIR	99.7%	39.5	25	12.8	2	0	0	913.56	370	376
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	32	65	0.07%	56.6%	YLTTAVITNK	99.7%	70.8	25	59.7	5	0	0	1123.64	256	265
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	32	65	0.07%	56.6%	YLTTAVITNKDVR	99.7%	73.7	25	70.4	2	0	0	1493.83	256	268

Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	9	15	0.02%	22.1%	AYVSTLMGVPGR	99.7%	55.3	25	54.9	4	0	0	1266.65	215	226
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	9	15	0.02%	22.1%	FLMSLVNQVPK	99.7%	77	25	60.9	3	0	0	1275.71	307	317
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	9	15	0.02%	22.1%	IGVDLIMK	98.4%	32.3	25	23.1	1	0	0	904.52	247	254
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	9	15	0.02%	22.1%	TMGVMFTPLTVK	99.7%	60.5	25	60.1	1	0	0	1324.70	227	238
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	9	15	0.02%	22.1%	VIGLSSDLQQVGGASAR	99.7%	129	25	129	2	0	0	1657.89	262	278
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	9	15	0.02%	22.1%	VIGTLLGTVDK	99.7%	61	25	55.6	2	0	0	1115.67	116	126
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	9	15	0.02%	22.1%	YAYYDTER	98.6%	32.8	25	32.8	2	0	0	1080.46	239	246
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	7	8	15	0.02%	23.4%	CPYKDTLGPMQK	98.9%	33.8	25	24.1	1	1	0	1453.68	169	180
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	7	8	15	0.02%	23.4%	EKLPGELEPVQATQNK	99.7%	36.4	25	35.2	0	2	0	1780.94	194	209
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	7	8	15	0.02%	23.4%	ELAEQLGLSTGEK	99.7%	64.3	25	58.1	2	0	0	1374.71	181	193
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	7	8	15	0.02%	23.4%	ETDLQELFRPFGSISR	99.7%	48.3	25	46.6	0	2	0	1894.97	252	267
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	7	8	15	0.02%	23.4%	GFAFISFHR	99.7%	42.9	25	29.6	3	0	0	1081.56	281	289
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	7	8	15	0.02%	23.4%	LPGELEPVQATQNK	99.7%	62.3	25	61.1	2	0	0	1523.81	196	209
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	7	8	15	0.02%	23.4%	VTNLSEDTR	99.7%	44.9	25	23.8	2	0	0	1034.51	243	251
Eukaryotic translation initiation factor 3 subunit H	EIF3H	EIF3H_HUMAN	39.9	99.8%	2	2	4	0.00%	6.5%	LFMAQALQEYNN	99.7%	52.8	25	52.8	2	0	0	1441.68	341	352
Eukaryotic translation initiation factor 3 subunit H	EIF3H	EIF3H_HUMAN	39.9	99.8%	2	2	4	0.00%	6.5%	QVQIDGLVVLK	99.7%	48.4	25	33.3	2	0	0	1211.74	38	48
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	15	47	0.05%	46.5%	DMTMFVTASK	99.7%	72	25	64.2	8	0	0	1130.52	199	208
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	15	47	0.05%	46.5%	DPIVNVWYSVNGER	99.7%	50	25	50	2	0	0	1647.81	31	44
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	15	47	0.05%	46.5%	EGDLLFTVAK	99.7%	58.1	25	52.7	4	0	0	1092.59	21	30
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	15	47	0.05%	46.5%	GHFGPINSVAFHPDGK	99.7%	48.2	25	48.2	0	4	0	1679.83	283	298
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	15	47	0.05%	46.5%	HVLTGSADNSCR	99.7%	46.9	25	39.8	2	0	0	1316.60	66	77
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	15	47	0.05%	46.5%	IGKFEAR	99.5%	37.2	25	22.2	1	0	0	820.47	262	268
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	15	47	0.05%	46.5%	LFDSTTLEHQK	99.7%	68.9	25	52.3	4	0	0	1318.66	214	224
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	15	47	0.05%	46.5%	MKPILLQGHER	99.7%	35.2	25	29.9	0	2	0	1321.74	1	11
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	15	47	0.05%	46.5%	QINDIQLSR	99.7%	76.3	25	20.6	6	0	0	1086.59	190	198
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	15	47	0.05%	46.5%	SGEVLVNVK	99.7%	81.7	25	71.6	4	0	0	944.54	177	185
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	15	47	0.05%	46.5%	SGEVLVNVKEHSR	99.7%	46.9	25	44.5	0	2	0	1453.78	177	189
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	15	47	0.05%	46.5%	SITQIKYNR	99.5%	37	25	31.1	2	0	0	1122.63	12	20
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	15	47	0.05%	46.5%	SYSSGGEDGYVR	99.7%	77.2	25	76.4	4	0	0	1276.54	299	310
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	14	15	47	0.05%	46.5%	TCGFDFGGNIIMFSTDK	99.7%	53.5	25	53.5	2	0	0	1909.85	98	114
Eukaryotic translation initiation factor 3 subunit K	EIF3K	EIF3K_HUMAN	25.1	100.0%	4	5	10	0.01%	19.7%	ALTNLPHTDFTLCK	99.7%	77.7	25	71.1	2	0	0	1630.83	73	86
Eukaryotic translation initiation factor 3 subunit K	EIF3K	EIF3K_HUMAN	25.1	100.0%	4	5	10	0.01%	19.7%	ENAYDLEANLAVLK	99.7%	96.3	25	84.1	2	0	0	1562.81	39	52
Eukaryotic translation initiation factor 3 subunit K	EIF3K	EIF3K_HUMAN	25.1	100.0%	4	5	10	0.01%	19.7%	GIDRYNPENLATLER	99.7%	61	25	61	2	2	0	1760.89	17	31
Eukaryotic translation initiation factor 3 subunit K	EIF3K	EIF3K_HUMAN	25.1	100.0%	4	5	10	0.01%	19.7%	YNPENLATLER	99.7%	68.3	25	49.1	2	0	0	1319.66	21	31
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	64	0.07%	38.8%	EPFLQQLK	99.7%	39.9	25	14.5	2	0	0	1002.56	438	445
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	64	0.07%	38.8%	IDESIHLQLR	99.7%	50.3	25	41.3	2	2	0	1223.67	382	391
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	64	0.07%	38.8%	KSEEEIDFLR	99.7%	61.8	25	54.2	2	0	0	1265.64	207	216
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	64	0.07%	38.8%	LAGFLDLTEQEFR	99.7%	93.9	25	90.4	5	0	0	1538.79	475	487
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	64	0.07%	38.8%	LHSLLGDYYQAIK	99.7%	80.8	25	76.4	2	2	0	1520.81	280	292
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	64	0.07%	38.8%	LYTTMPVAK	99.7%	44.3	25	29.6	2	0	0	1039.55	466	474
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	64	0.07%	38.8%	MLGYFSLVGLLR	99.7%	71.7	25	67	4	0	0	1384.77	268	279
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	64	0.07%	38.8%	NFIQYFHK	98.8%	33.5	25	16.4	1	0	0	1096.56	54	61
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	64	0.07%	38.8%	QDLAYER	97.7%	30.6	25	16.1	2	0	0	894.43	32	38
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	64	0.07%	38.8%	QLEVYTSGGDPESVAGEYGR	99.7%	113	25	113	3	0	0	2113.97	243	262
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	64	0.07%	38.8%	QYEQQTYQVIPEVIK	99.7%	78.5	25	76.7	2	0	0	1865.96	39	53
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	64	0.07%	38.8%	RYGDFFIR	96.2%	28.7	25	20.1	1	0	0	1073.55	538	545
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	64	0.07%	38.8%	SEEEIDFLR	99.7%	58.7	25	45.2	2	0	0	1137.54	208	216
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	64	0.07%	38.8%	TTYKYEMINK	99.1%	34.9	25	29.3	1	0	0	1290.64	353	362
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	64	0.07%	38.8%	TVSDLIDQK	98.9%	33.9	25	28.1	3	0	0	1018.54	62	70
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	64	0.07%	38.8%	VFSDEVQQQAQLSTIR	99.7%	97.6	25	97.6	6	0	0	1848.95	446	461
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	64	0.07%	38.8%	VLENIELNKK	99.7%	52.3	25	41.8	2	2	0	1199.70	293	302

Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	64	0.07%	38.8%	VSGGPSLEQR	99.7%	80.5	25	69.2	4	0	0	1029.53	144	153
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	64	0.07%	38.8%	VSSDVIDQK	99.7%	64.4	25	46.5	4	0	0	990.51	79	87
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	64	0.07%	38.8%	VYEIQDIYENSWTK	99.7%	87.3	25	84.4	2	0	0	1787.85	88	101
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	64	0.07%	38.8%	VYELQASR	99.7%	57.4	25	45.7	4	0	0	965.51	71	78
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	64	0.07%	38.8%	YGDFFIR	99.7%	52	25	34.9	2	0	0	917.45	539	545
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	7	7	11	0.01%	7.7%	GLSFLFPLLK	99.7%	64.3	25	63.5	2	0	0	1134.69	723	732
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	7	7	11	0.01%	7.7%	GVILLIVDK	99.7%	46	25	32.8	2	0	0	969.63	113	121
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	7	7	11	0.01%	7.7%	LEVDIPLVK	99.6%	37.9	25	33.5	1	0	0	1025.62	632	640
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	7	7	11	0.01%	7.7%	SDFFLEGPFMPPR	99.7%	47.9	25	37.4	2	0	0	1539.73	348	360
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	7	7	11	0.01%	7.7%	SYLAQFAAR	99.7%	51.5	25	44.4	2	0	0	1026.54	641	649
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	7	7	11	0.01%	7.7%	TNPPLIQEKPAK	99.4%	36.5	25	36.5	1	0	0	1335.76	521	532
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	7	7	11	0.01%	7.7%	VIILSLDR	99.3%	35.9	25	26.8	1	0	0	928.58	585	592
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	13	15	61	0.06%	22.7%	AASIFGGAKPVDTAAR	99.7%	64.3	25	63	8	5	0	1531.82	357	372
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	13	15	61	0.06%	22.7%	DENKVDGMNAPK	99.7%	42.2	25	42.2	1	0	0	1333.61	526	537
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	13	15	61	0.06%	22.7%	DSDKTDTDWR	97.8%	30.9	25	28.9	1	0	0	1238.53	191	200
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	13	15	61	0.06%	22.7%	GDDSFGDKYR	99.2%	35	25	34.9	1	0	0	1159.50	216	225
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	13	15	61	0.06%	22.7%	GLNISAVR	99.7%	60.5	25	34	4	0	0	829.49	118	125
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	13	15	61	0.06%	22.7%	QLDEPKLER	97.4%	30.2	25	11.8	1	0	0	1127.61	390	398
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	13	15	61	0.06%	22.7%	SILPTAPR	99.7%	44.3	25	31.2	4	0	0	854.51	71	78
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	13	15	61	0.06%	22.7%	SQSSDTEQQSPTSGGGK	99.7%	111	25	111	4	0	0	1680.73	495	511
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	13	15	61	0.06%	22.7%	SRTGSESSQTGTSTTSSR	98.8%	27.7	25	27.7	0	2	0	1816.83	418	435
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	13	15	61	0.06%	22.7%	STPKEDDSSASTSQSTR	99.7%	57.7	25	57.7	4	4	0	1783.79	340	356
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	13	15	61	0.06%	22.7%	TGSESSQTGTSTTSSR	99.7%	80.6	25	80.6	4	0	0	1573.69	420	435
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	13	15	61	0.06%	22.7%	VAPAQPSEEGPGR	99.7%	64.9	25	61	14	0	0	1294.64	512	524
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	13	15	61	0.06%	22.7%	VAPAQPSEEGPGRK	99.7%	60.1	25	57.7	4	0	0	1422.73	512	525
Eukaryotic translation initiation factor 4E type 2	EIF4E2	IF4E2_HUMAN	28.4	99.8%	2	2	4	0.00%	9.8%	FQEDIISIWNK	99.7%	60.8	25	48.5	2	0	0	1392.72	175	185
Eukaryotic translation initiation factor 4E type 2	EIF4E2	IF4E2_HUMAN	28.4	99.8%	2	2	4	0.00%	9.8%	QIGTFASVEQFWR	99.7%	46.2	25	43.8	2	0	0	1568.79	84	96
Eukaryotic translation initiation factor 6	EIF6	IF6_HUMAN	26.6	99.8%	2	2	4	0.00%	9.8%	LNEAQPSTIATSMR	99.7%	64	25	59.3	2	0	0	1534.75	224	237
Eukaryotic translation initiation factor 6	EIF6	IF6_HUMAN	26.6	99.8%	2	2	4	0.00%	9.8%	NSLPDTVQIR	99.3%	35.8	25	29.8	2	0	0	1142.62	86	95
Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	ECSIT	ECSIT_HUMAN	49.1	100.0%	4	4	5	0.01%	16.9%	ALVPFEDLFGQAPGGER	99.7%	73.4	25	72.2	1	0	0	1802.91	68	84
Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	ECSIT	ECSIT_HUMAN	49.1	100.0%	4	4	5	0.01%	16.9%	DLAVYNQLLNIFPK	99.7%	77.5	25	77.5	2	0	0	1647.91	125	138
Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	ECSIT	ECSIT_HUMAN	49.1	100.0%	4	4	5	0.01%	16.9%	DLPQDPVELAMFGLR	99.7%	71	25	61.4	1	0	0	1700.87	218	232
Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	ECSIT	ECSIT_HUMAN	49.1	100.0%	4	4	5	0.01%	16.9%	DSTGAADPPQPHIVGIQSPDQQAALAR	99.7%	37.4	25	37.4	0	1	0	2740.37	252	278
Exocyst complex component 2	EXOC2	EXOC2_HUMAN	104.1	100.0%	4	4	6	0.01%	5.0%	ASNTADTLFQEVLGR	99.7%	95.1	25	82.8	2	0	0	1621.82	249	263
Exocyst complex component 2	EXOC2	EXOC2_HUMAN	104.1	100.0%	4	4	6	0.01%	5.0%	GALLPLSIR	99.7%	47.3	25	45.6	1	0	0	939.60	519	527
Exocyst complex component 2	EXOC2	EXOC2_HUMAN	104.1	100.0%	4	4	6	0.01%	5.0%	LVLSQLPNFWK	99.7%	59.9	25	59.9	2	0	0	1344.77	458	468
Exocyst complex component 2	EXOC2	EXOC2_HUMAN	104.1	100.0%	4	4	6	0.01%	5.0%	VIEAVSEELSR	98.3%	31.9	25	6.69	1	0	0	1231.65	828	838
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	6	6	10	0.01%	8.6%	DASVPLIDVTNLPTPR	99.7%	83.4	25	76.4	2	0	0	1707.93	224	239
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	6	6	10	0.01%	8.6%	ESEVLIGNLGDK	99.7%	74.6	25	69.6	2	0	0	1273.66	682	693
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	6	6	10	0.01%	8.6%	NITVIFHPLLR	99.7%	42.4	25	42.4	2	0	0	1322.79	495	505
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	6	6	10	0.01%	8.6%	SGELQGGPDDNLIEGGGTK	99.7%	75.7	25	75.7	1	0	0	1843.87	468	486
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	6	6	10	0.01%	8.6%	SQTGVGELTTQNTR	99.7%	75.7	25	69.5	1	0	0	1491.74	935	948
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	6	6	10	0.01%	8.6%	STTQVADSGYQR	99.7%	57.5	25	52	2	0	0	1312.61	314	325
Exocyst complex component 5	EXOC5	EXOC5_HUMAN	81.9	99.8%	2	2	3	0.00%	3.0%	LIQNVFEIK	99.0%	34.2	25	21.9	1	0	0	1103.65	275	283
Exocyst complex component 5	EXOC5	EXOC5_HUMAN	81.9	99.8%	2	2	3	0.00%	3.0%	NVDTVLMELGVR	99.7%	51	25	48.9	2	0	0	1345.71	598	609
Exocyst complex component 8	EXOC8	EXOC8_HUMAN	81.8	99.8%	2	2	2	0.00%	3.5%	IQALAEETAQNLKR	98.8%	27.8	25	26.2	0	1	0	1584.87	48	61
Exocyst complex component 8	EXOC8	EXOC8_HUMAN	81.8	99.8%	2	2	2	0.00%	3.5%	RFEEGVGKPAK	99.6%	32.2	25	27.9	0	1	0	1217.66	692	702
Exosome complex component CSL4	EXOSC1	EXOS1_HUMAN	21.5	100.0%	4	4	6	0.01%	29.7%	ETESQLLPDVGAIVTCK	99.7%	52.5	25	52.2	1	0	0	1859.94	58	74
Exosome complex component CSL4	EXOSC1	EXOS1_HUMAN	21.5	100.0%	4	4	6	0.01%	29.7%	LCNLEEGSPGSGTYTR	99.7%	91.3	25	91.3	1	0	0	1740.79	14	29
Exosome complex component CSL4	EXOSC1	EXOS1_HUMAN	21.5	100.0%	4	4	6	0.01%	29.7%	SFRPGDIVLAK	99.7%	43.5	25	26.6	2	0	0	1202.69	121	131
Exosome complex component CSL4	EXOSC1	EXOS1_HUMAN	21.5	100.0%	4	4	6	0.01%	29.7%	SSENGALPVVSVVR	99.7%	59.5	25	57.2	2	0	0	1413.77	44	57

Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	5	5	11	0.01%	22.8%	ELALALQEALEPAVR	99.7%	63.4	25	57.3	2	0	0	1622.91	121	135
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	5	5	11	0.01%	22.8%	GGGPAGAGGEAPAALR	99.7%	71.1	25	71.1	3	0	0	1308.67	78	93
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	5	5	11	0.01%	22.8%	GSAYLEAGGTK	99.7%	42.3	25	41.3	2	0	0	1053.52	51	61
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	5	5	11	0.01%	22.8%	LYPVLQQSLVR	99.7%	55.5	25	46.3	2	0	0	1315.77	251	261
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	5	5	11	0.01%	22.8%	VLCAVSGPR	99.7%	58.7	25	47.8	2	0	0	958.51	62	70
Exosome complex component RRP4	EXOSC2	EXOS2_HUMAN	32.8	99.8%	2	2	3	0.00%	8.5%	LGQGVLVQVSPSLVK	99.5%	37.5	25	35.3	1	0	0	1523.92	166	180
Exosome complex component RRP4	EXOSC2	EXOS2_HUMAN	32.8	99.8%	2	2	3	0.00%	8.5%	NCIISLVTQR	99.7%	57.6	25	54.1	2	0	0	1203.65	239	248
Exosome complex component RRP41	EXOSC4	EXOS4_HUMAN	26.4	100.0%	3	4	7	0.01%	12.7%	ALAVVYGPHEIR	99.4%	36.5	25	36.5	2	0	0	1324.74	48	59
Exosome complex component RRP41	EXOSC4	EXOS4_HUMAN	26.4	100.0%	3	4	7	0.01%	12.7%	SCEMGLQLR	99.7%	50.8	25	50.2	3	0	0	1109.51	96	104
Exosome complex component RRP41	EXOSC4	EXOS4_HUMAN	26.4	100.0%	3	4	7	0.01%	12.7%	VLEAAAQAAR	99.7%	92.7	25	72.8	2	0	0	999.56	213	222
Exosome complex component RRP43	EXOSC8	EXOS8_HUMAN	30.0	99.8%	2	2	4	0.00%	10.9%	LGNTTVICGVK	99.7%	50.8	25	42.2	2	0	0	1161.63	53	63
Exosome complex component RRP43	EXOSC8	EXOS8_HUMAN	30.0	99.8%	2	2	4	0.00%	10.9%	TTTVNIGSISTADGSALVK	99.7%	88.5	25	87.7	2	0	0	1834.98	34	52
Exosome complex component RRP45	EXOSC9	EXOS9_HUMAN	49.0	100.0%	2	2	4	0.00%	4.8%	FGFAESIANQR	99.7%	64.7	25	56.9	2	0	0	1239.61	282	292
Exosome complex component RRP45	EXOSC9	EXOS9_HUMAN	49.0	100.0%	2	2	4	0.00%	4.8%	VAEITELILK	99.7%	75.1	25	68.9	2	0	0	1128.69	258	267
Exosome complex component RRP46	EXOSC5	EXOS5_HUMAN	25.2	100.0%	3	3	6	0.01%	14.9%	AVLTFALDSVER	99.7%	80.3	25	58.9	2	0	0	1320.72	179	190
Exosome complex component RRP46	EXOSC5	EXOS5_HUMAN	25.2	100.0%	3	3	6	0.01%	14.9%	IGLPGVAEK	98.4%	32.3	25	16.7	2	0	0	883.52	84	92
Exosome complex component RRP46	EXOSC5	EXOS5_HUMAN	25.2	100.0%	3	3	6	0.01%	14.9%	NTCEAVVLGTLHPR	99.7%	67.2	25	67.1	2	0	0	1566.81	100	113
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	8	8	16	0.02%	9.6%	ASLTYAEAQLR	99.5%	37.7	25	26.7	2	0	0	1222.64	586	596
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	8	8	16	0.02%	9.6%	AVHEDIVAVELLPK	99.7%	40.8	25	38.4	2	0	0	1532.87	286	299
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	8	8	16	0.02%	9.6%	IIVAIDGWPR	99.7%	61.5	25	58.5	2	0	0	1139.66	398	407
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	8	8	16	0.02%	9.6%	LACLSEEGNEIESGK	99.7%	79.7	25	79.7	1	0	0	1635.75	211	225
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	8	8	16	0.02%	9.6%	NVIVLQTVLQEVR	99.7%	92	25	91.9	4	0	0	1510.90	87	99
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	8	8	16	0.02%	9.6%	RGTTVYLCEK	94.7%	27.4	25	21.3	1	0	0	1226.62	526	535
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	8	8	16	0.02%	9.6%	SLTANPELIDR	99.7%	40.5	25	27.8	3	0	0	1228.65	200	210
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	8	8	16	0.02%	9.6%	YADVIVHR	99.6%	37.9	25	32.2	1	0	0	972.53	782	789
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	5	5	8	0.01%	5.7%	AAAEQAISVR	99.7%	82.8	25	57.6	2	0	0	1015.55	759	768
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	5	5	8	0.01%	5.7%	FALGSVVAVTK	99.7%	77	25	72.2	1	0	0	1091.65	38	48
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	5	5	8	0.01%	5.7%	LAQVQVQK	99.7%	43	25	27.2	2	0	0	913.55	726	733
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	5	5	8	0.01%	5.7%	LYCNVDSNK	98.5%	32.5	25	27.1	1	0	0	1112.50	409	417
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	5	5	8	0.01%	5.7%	TEDFIIDTLELR	99.7%	81.4	25	72.1	2	0	0	1464.76	335	346
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	AIIASNIMYIVGQYPR	99.7%	98.6	25	91	5	2	0	1824.97	538	553
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	AVGHPFVIQLGR	99.7%	51.5	25	51	2	2	0	1293.74	701	712
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	DFEEYPEHR	99.1%	34.8	25	34.8	1	0	0	1221.52	837	845
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	EFAGEDTSDLFLEER	99.7%	117	25	102	2	0	0	1757.79	1024	1038
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	EFMKDTDSINLYK	99.7%	50.5	25	41.4	1	0	0	1619.76	443	455
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	EPEVLSTMAIIVNK	99.7%	85.5	25	85.5	4	0	0	1543.84	797	810
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	ETLVYLTHLDYVDTER	99.7%	82.8	25	77.4	2	2	0	1966.98	459	474
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	FLNVPMFR	97.5%	30.4	25	18.2	3	0	0	1023.54	254	261
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	FLNWIPLGYIFETK	99.7%	41.4	25	34.7	2	0	0	1740.94	232	245
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	FLVTVIK	99.7%	47.6	25	15.9	2	0	0	819.53	516	522
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	HWPTFISDIVGASR	97.9%	31.1	25	31.1	1	0	0	1585.81	145	158
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	IYLDMLNVYK	99.7%	69.6	25	66.9	3	0	0	1271.67	713	722
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	LDINLLDNVVNCLYHGEGAQQR	99.7%	46.6	25	44.6	0	1	0	2541.25	23	44
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	LFVTGLFSLNQDIPAFK	99.7%	46.2	25	46.2	1	0	0	1910.04	996	1012
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	LISGWVSR	99.7%	55.5	25	35.2	2	0	0	917.52	758	765
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	LISTLIYK	99.7%	53.3	25	48.4	2	0	0	950.59	246	253
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	LLSEEVFDFSSGQITQVK	99.7%	101	25	101	5	2	0	2027.03	173	190
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	LNMILVQILK	99.7%	75.2	25	60.4	4	0	0	1184.74	130	139
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	LVLDSIIWAFK	99.7%	83.1	25	83.1	7	0	0	1304.76	873	883
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	MAKPEEVLVVENDQGEVVR	99.7%	62.3	25	61	0	4	0	2157.09	424	442
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	MAQEVLTHLK	99.7%	63.2	25	53.8	4	0	0	1185.63	45	54

Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	NVDILKDPETVK	99.7%	45.5	25	41	2	1	0	1370.75	675	686
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	PAIMTMLADHAAR	99.7%	54.7	25	54.7	0	2	0	1397.70	2	14
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	QLLDFSQK	97.7%	30.7	25	21.6	1	0	0	978.53	15	22
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	QMLPLNTNIR	99.7%	69.6	25	56.7	4	0	0	1199.66	296	305
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	SAFPHLQDAQVK	99.7%	55.9	25	49.3	2	1	0	1340.70	984	995
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	TSESLCQNNMVILK	99.7%	101	25	90.5	4	0	0	1636.80	159	172
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	TSSDPTCVEK	99.7%	47.4	25	30.3	2	0	0	1123.49	113	122
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	TSSDPTCVEKEK	99.7%	57.2	25	43.6	2	0	0	1380.63	113	124
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	VDTILEFSQNMNTK	99.7%	105	25	98.5	4	0	0	1639.80	63	76
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	YMLLPNQVWDSIIQQATK	99.7%	52	25	49	2	0	0	2164.11	657	674
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	YVVGLIIK	99.7%	46.9	25	34.2	2	0	0	904.59	105	112
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	33	50	100	0.10%	37.7%	YYGLQILENVIK	99.7%	82.1	25	82.1	5	0	0	1452.81	77	88
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	AACDLVR	99.7%	44.5	25	23	2	0	0	804.40	385	391
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	AADEEAFEDNSEEYIR	99.7%	107	25	107	2	0	0	1887.79	356	371
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	AADEEAFEDNSEEYIRR	99.7%	49.7	25	49.7	2	2	0	2043.89	356	372
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	ALTLPGSSENEYIMK	99.7%	94.4	25	84.2	4	0	0	1668.82	560	574
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	ANIVHLMLSSPEQIQK	99.7%	86.3	25	83.7	2	3	0	1807.97	94	109
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	ATIELCSTHANDASALR	99.7%	105	25	101	2	2	0	1829.88	190	206
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	DAAIYLVTSLASK	99.7%	105	25	95	2	0	0	1351.75	428	440
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	DLEGSDIDTR	99.7%	40.7	25	31.4	2	0	0	1120.51	373	382
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	DLEGSDIDTRR	99.7%	45.8	25	26.5	2	0	0	1276.61	373	383
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	EHDPVGQMVNNPK	99.7%	69.6	25	69	2	2	0	1480.69	913	925
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	FQSGDFHVINGVLR	99.7%	54.5	25	49.1	1	1	0	1588.82	138	151
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	GSNTIASAAADK	99.7%	45.6	25	36.5	2	0	0	1105.55	715	726
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	GSNTIASAAADKIPGLLGVFQK	99.7%	57.4	25	55.4	0	2	0	2158.19	715	736
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	ICAVGITK	96.8%	29.4	25	15.2	1	0	0	861.49	841	848
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	IHLAQSLHK	99.6%	39	25	37.4	2	0	0	1046.61	926	934
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	IIIPEIQK	97.7%	30.6	25	0	2	0	0	953.60	825	832
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	ILFSSLILISK	99.7%	88	25	88	2	0	0	1233.78	207	217
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	IVEDEPNKICEADR	99.7%	99.8	25	99.8	2	2	0	1687.80	76	89
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	KICAVGITK	99.7%	43.1	25	30.9	3	0	0	989.58	840	848
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	LLQAFLER	99.7%	62.1	25	48.3	8	0	0	989.58	707	714
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	LLQTDDEEEAGLLELLK	99.7%	110	25	102	4	0	0	1929.01	252	268
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	LLTECPPMMDTEYTK	99.7%	75	25	75	4	0	0	1828.82	849	863
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	LSTACPGR	98.1%	31.6	25	22.4	2	0	0	861.42	935	942
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	LVLDAFALPLTNLFK	99.7%	74.7	25	74.7	2	0	0	1674.98	175	189
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	MFGMVLEK	95.9%	28.4	25	23.1	2	0	0	970.47	817	824
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	NLFEDQNTLTSICEK	99.7%	96.5	25	96.5	2	0	0	1811.85	332	346
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	NPSVNWK	98.1%	31.5	25	17.3	2	0	0	844.43	419	425
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	QIFILLFQR	99.7%	59.3	25	58.6	6	0	0	1177.71	769	777
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	QLSDAISIIGR	99.7%	88	25	65.2	2	0	0	1172.66	110	120
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	SANVNEFPVLK	99.7%	58.3	25	47.9	2	0	0	1217.65	471	481
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	SNELWTEIK	99.7%	54.3	25	42	2	0	0	1119.57	166	174
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	SQICDNAALYAQK	99.7%	86.8	25	67.9	2	0	0	1481.71	269	281
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	TGNIPALVR	99.7%	61.2	25	58.7	4	0	0	940.56	698	706
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	VCASVTFK	99.3%	36	25	31.6	2	0	0	911.47	60	67
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	YDEEFQR	99.7%	46.1	25	46.1	2	0	0	986.42	282	288
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	YGALALQEIFDGIQPK	99.7%	101	25	99.3	3	0	0	1762.94	801	816
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	37	48	103	0.11%	40.0%	YIMIFR	98.5%	32.5	25	20.5	1	0	0	842.46	487	492
Exportin-4	XPO4	XPO4_HUMAN	130.1	100.0%	4	4	6	0.01%	4.6%	AQETDSPLFLATR	99.7%	52.2	25	45.5	2	0	0	1448.74	1039	1051
Exportin-4	XPO4	XPO4_HUMAN	130.1	100.0%	4	4	6	0.01%	4.6%	HQQQLLASPGSSTVDNK	98.1%	25.9	25	25.5	0	1	0	1809.91	514	530

Exportin-4	XPO4	XPO4_HUMAN	130.1	100.0%	4	4	6	0.01%	4.6%	LVFDMLVLQK	99.7%	45.9	25	32.4	2	0	0	1205.70	1056	1065
Exportin-4	XPO4	XPO4_HUMAN	130.1	100.0%	4	4	6	0.01%	4.6%	SPPLNFLSSPVQR	99.7%	77.7	25	77.7	1	0	0	1441.78	737	749
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	25	26	48	0.05%	25.4%	AGGFVVGYTSSGNPIFR	99.7%	110	25	110	2	0	0	1728.87	746	762
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	25	26	48	0.05%	25.4%	ALDMLDAEK	99.7%	45.6	25	39.1	2	0	0	1021.49	802	810
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	25	26	48	0.05%	25.4%	ASMTNLVK	95.7%	28.3	25	10.1	1	0	0	863.47	400	407
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	25	26	48	0.05%	25.4%	AVMEQIPEIQK	99.7%	52	25	45.2	2	0	0	1285.68	1113	1123
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	25	26	48	0.05%	25.4%	AVTVMMDPNSTQR	99.7%	74.6	25	74.6	2	0	0	1481.67	16	28
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	25	26	48	0.05%	25.4%	DIQQTLTQNMER	99.7%	63.4	25	56.7	3	0	0	1476.71	177	188
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	25	26	48	0.05%	25.4%	DPLLLAIIPK	99.7%	49	25	49	6	0	0	1092.70	387	396
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	25	26	48	0.05%	25.4%	EVMDLITVCCVSK	99.7%	56.2	25	49.7	2	0	0	1553.74	968	980
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	25	26	48	0.05%	25.4%	FCEEFKEK	95.5%	28	25	12.4	1	0	0	1116.50	36	43
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	25	26	48	0.05%	25.4%	IFSFLLNTLQENVNK	99.7%	103	25	92.3	2	0	0	1779.96	189	203
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	25	26	48	0.05%	25.4%	IVVEMIKR	96.8%	29.4	25	15.4	1	0	0	987.60	119	126
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	25	26	48	0.05%	25.4%	LFSSVTFETVEESK	99.7%	97.4	25	97.4	2	0	0	1602.79	577	590
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	25	26	48	0.05%	25.4%	LIAGCIGKPLGEQFR	99.7%	32.9	25	31.5	0	2	0	1658.91	1153	1167
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	25	26	48	0.05%	25.4%	LLDNLLALIR	99.7%	78.9	25	60.1	3	0	0	1153.73	772	781
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	25	26	48	0.05%	25.4%	LLNPSLQK	97.3%	30.1	25	4.57	1	0	0	912.55	1133	1140
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	25	26	48	0.05%	25.4%	NPCTEQILK	99.3%	36	25	28.2	1	0	0	1102.56	763	771
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	25	26	48	0.05%	25.4%	QGETQTELVMFILLR	99.7%	60.7	25	58.7	1	0	0	1793.95	145	159
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	25	26	48	0.05%	25.4%	QLLSNELLLTQMEK	99.7%	78.1	25	66.8	2	0	0	1659.90	632	645
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	25	26	48	0.05%	25.4%	SAILGLPQPLLELNDSPVFK	99.7%	55.4	25	55.4	1	0	0	2151.21	811	830
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	25	26	48	0.05%	25.4%	TCWPTDLEEAK	99.7%	50.3	25	49.8	2	0	0	1349.60	735	745
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	25	26	48	0.05%	25.4%	TDSPSCEYSR	99.7%	58.7	25	58.2	2	0	0	1201.48	414	423
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	25	26	48	0.05%	25.4%	TSFQMAGEWLK	99.7%	78.5	25	72.8	2	0	0	1297.62	457	467
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	25	26	48	0.05%	25.4%	TTSQLCWPLLK	99.7%	58.6	25	49.4	2	0	0	1346.71	1047	1057
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	25	26	48	0.05%	25.4%	VLSDVDAFIAYVGTDQK	99.7%	104	25	104	2	0	0	1840.93	688	704
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	25	26	48	0.05%	25.4%	YLESFLAFTTHPSQFLR	99.0%	34.4	25	34.4	1	0	0	2057.05	352	368
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	6	6	9	0.01%	5.5%	AELFELLFR	99.7%	66.2	25	48.3	2	0	0	1137.63	936	944
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	6	6	9	0.01%	5.5%	FCLYFLSSTR	99.7%	44.9	25	44.9	2	0	0	1293.63	47	56
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	6	6	9	0.01%	5.5%	FNDALTVVER	99.7%	71.9	25	64.4	1	0	0	1163.61	580	589
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	6	6	9	0.01%	5.5%	LAEYFIGDVFAAR	99.7%	62.6	25	57.5	2	0	0	1471.76	567	579
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	6	6	9	0.01%	5.5%	MFQQTFYLLQK	99.6%	38.3	25	34.5	1	0	0	1446.75	336	346
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	6	6	9	0.01%	5.5%	STVLASVQR	99.7%	46.5	25	28.1	1	0	0	960.55	956	964
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	28	0.03%	19.0%	AALSGSYVNFGVFR	99.7%	92	25	92	2	0	0	1487.76	841	854
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	28	0.03%	19.0%	ALVEFTNSPDCLSK	99.7%	69.9	25	64.6	2	0	0	1580.76	33	46
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	28	0.03%	19.0%	DSSLFDIFTLSCNLLK	99.7%	69.5	25	69.5	1	0	0	1872.94	183	198
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	28	0.03%	19.0%	GIAFAFNAK	99.7%	51.4	25	38	2	0	0	938.51	728	736
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	28	0.03%	19.0%	GSSSYSQLLAATCLTK	99.7%	64.8	25	61.4	1	0	0	1686.84	54	69
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	28	0.03%	19.0%	IYIGDQVQK	99.7%	44.4	25	25.6	2	0	0	1063.58	560	568
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	28	0.03%	19.0%	LESVHIILR	99.7%	67.9	25	67.9	2	0	0	1079.66	418	426
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	28	0.03%	19.0%	LLLSIPHSDLLDYPK	98.1%	31.5	25	29	1	0	0	1723.96	871	885
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	28	0.03%	19.0%	LMAELVHNR	99.7%	59.4	25	53.7	1	0	0	1082.58	774	782
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	28	0.03%	19.0%	LQFDVSSPNGILLFR	99.7%	80.8	25	80.4	2	0	0	1705.93	786	800
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	28	0.03%	19.0%	LYGDDALDNALQTFIK	99.7%	113	25	113	1	0	0	1796.91	855	870
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	28	0.03%	19.0%	NSIVNSQPPEK	99.7%	46	25	37.9	2	0	0	1212.62	1021	1031
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	28	0.03%	19.0%	NYVLNYLATRPK	99.7%	74.1	25	74.1	2	0	0	1451.80	88	99
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	28	0.03%	19.0%	QLYETTDTTTR	99.7%	58.9	25	49.2	2	0	0	1328.63	17	27
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	28	0.03%	19.0%	SNYQLGELVK	99.7%	41.5	25	34.5	1	0	0	1150.61	339	348
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	28	0.03%	19.0%	TNNPLPLEQR	99.7%	48.8	25	39	2	0	0	1181.63	74	83
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	17	17	28	0.03%	19.0%	VLQLMNLTDSR	99.7%	75	25	62.8	2	0	0	1289.69	527	537
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	20	41	0.04%	22.1%	ALAYFEQLK	99.7%	64.3	25	59.5	3	0	0	1082.59	21	29

Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	20	41	0.04%	22.1%	ANVEAIMLAVMK	99.7%	108	25	94.5	2	0	0	1289.70	370	381
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	20	41	0.04%	22.1%	DGPVGFADFVYK	99.7%	72.2	25	72.2	2	0	0	1314.64	860	871
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	20	41	0.04%	22.1%	DLQEFIPLINQITAK	99.7%	85.8	25	83.7	2	0	0	1742.97	738	752
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	20	41	0.04%	22.1%	DVVHTSEEAR	96.8%	29.4	25	24.7	2	0	0	1142.54	157	166
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	20	41	0.04%	22.1%	FFCFQVLEHQVK	99.7%	63.4	25	63.4	2	2	0	1581.79	54	65
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	20	41	0.04%	22.1%	ISPDAWQVCAEALAQR	99.7%	87	25	87	1	0	0	1814.89	30	45
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	20	41	0.04%	22.1%	LAQVSPELLLASVR	99.7%	85.3	25	78.9	6	0	0	1495.88	415	428
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	20	41	0.04%	22.1%	LMLAQDEER	99.4%	36.5	25	23.6	2	0	0	1104.54	635	643
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	20	41	0.04%	22.1%	NAQEALQAIETK	99.7%	61.9	25	22.8	1	0	0	1315.69	317	328
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	20	41	0.04%	22.1%	QASLADCLNHAVGFASR	99.7%	35.2	25	35.2	0	1	0	1816.88	644	660
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	20	41	0.04%	22.1%	QLTVLSDQQK	98.9%	33.9	25	17.3	2	0	0	1159.63	360	369
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	20	41	0.04%	22.1%	QMNPFIEDILNR	99.7%	68.6	25	63.4	3	0	0	1489.75	558	569
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	20	41	0.04%	22.1%	TCFIILSK	99.7%	48.2	25	40.7	2	0	0	981.54	844	851
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	20	41	0.04%	22.1%	VFSSTLQNWQTTR	99.7%	83.8	25	79.1	2	0	0	1567.79	430	442
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	20	41	0.04%	22.1%	VLVTVIQGAVEYPDPIAQK	99.7%	98.5	25	98.5	2	2	0	2040.14	825	843
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	17	20	41	0.04%	22.1%	YSELTTVQQQLIR	99.7%	75.1	25	67.4	2	0	0	1578.85	68	80
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	6	6	8	0.01%	7.7%	ALALLEDEER	99.7%	52.7	25	41.4	1	0	0	1158.60	163	172
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	6	6	8	0.01%	7.7%	ITVPLVSEVQIAQLR	99.7%	98.9	25	98.9	2	0	0	1665.99	365	379
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	6	6	8	0.01%	7.7%	LLDEWFTLDEVPK	99.7%	64.1	25	57	2	0	0	1604.82	484	496
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	6	6	8	0.01%	7.7%	SSSSLLASPGHISVK	98.4%	32.2	25	20.9	1	0	0	1469.80	736	750
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	6	6	8	0.01%	7.7%	VDVGQQPLR	99.7%	46.5	25	34.7	1	0	0	1011.56	240	248
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	6	6	8	0.01%	7.7%	VGNQIFQSR	99.7%	42.9	25	38.6	1	0	0	1048.55	420	428
FACT complex subunit SPT16	SUPT16H	SP16H_HUMAN	119.9	100.0%	2	2	3	0.00%	3.1%	APGEQTVPALNLQNAFR	98.6%	32.9	25	32.9	1	0	0	1825.96	607	623
FACT complex subunit SPT16	SUPT16H	SP16H_HUMAN	119.9	100.0%	2	2	3	0.00%	3.1%	NEGNIFPNPEATFVK	99.7%	46.4	25	36.9	2	0	0	1676.83	582	596
F-actin-capping protein subunit alpha-1	CAPZA1	CAZA1_HUMAN	32.9	100.0%	3	3	4	0.00%	14.0%	EASDPQPEEADGGLK	96.8%	29.4	25	28.1	1	0	0	1542.69	104	118
F-actin-capping protein subunit alpha-1	CAPZA1	CAZA1_HUMAN	32.9	100.0%	3	3	4	0.00%	14.0%	FTITPPTAQVVGVLK	99.3%	35.9	25	35.9	1	0	0	1570.92	179	193
F-actin-capping protein subunit alpha-1	CAPZA1	CAZA1_HUMAN	32.9	100.0%	3	3	4	0.00%	14.0%	LLLNNDNLLR	99.7%	56.7	25	41.2	2	0	0	1197.70	38	47
Fanconi anemia group D2 protein	FANCD2	FACD2_HUMAN	166.5	99.9%	2	2	4	0.00%	1.7%	DGGPVTSQESGQK	97.4%	30.2	25	30.2	1	0	0	1289.60	711	723
Fanconi anemia group D2 protein	FANCD2	FACD2_HUMAN	166.5	99.9%	2	2	4	0.00%	1.7%	LVSPLCLAPYFR	99.7%	53.1	25	53.1	3	0	0	1435.78	724	735
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	22	22	35	0.04%	20.0%	DCLILVLR	99.4%	36.9	25	23.9	1	0	0	1001.58	515	522
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	22	22	35	0.04%	20.0%	DLQLLQGSK	99.5%	37.6	25	25.6	2	0	0	1001.56	340	348
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	22	22	35	0.04%	20.0%	DSIQSHQESLSVLR	99.3%	35.7	25	35.7	1	0	0	1598.81	820	833
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	22	22	35	0.04%	20.0%	DVPLTAEEVEFVVEK	99.7%	76.6	25	64.4	2	0	0	1703.87	183	197
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	22	22	35	0.04%	20.0%	EALLLVTVLTSLSK	97.7%	30.8	25	30.8	1	0	0	1486.91	981	994
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	22	22	35	0.04%	20.0%	EGDLTNLLQNQAVK	99.7%	74.3	25	62.7	2	0	0	1542.81	26	39
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	22	22	35	0.04%	20.0%	ETGHVSGPDGQNPEK	99.7%	58.4	25	51.7	2	0	0	1551.70	855	869
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	22	22	35	0.04%	20.0%	FVSSLLTALFR	99.7%	80.9	25	80.9	2	0	0	1253.73	809	819
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	22	22	35	0.04%	20.0%	GSPCSEEAGTLR	99.7%	65	25	64.9	1	0	0	1263.56	53	64
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	22	22	35	0.04%	20.0%	IFQNLCDITR	99.7%	50.3	25	28.5	2	0	0	1279.65	870	879
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	22	22	35	0.04%	20.0%	IFSAVQQFYQPK	99.7%	68.5	25	50.5	1	0	0	1455.76	915	926
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	22	22	35	0.04%	20.0%	LMLYEGFYDVLR	99.7%	54.3	25	50.1	2	0	0	1534.76	603	614
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	22	22	35	0.04%	20.0%	QLINTLCSGR	99.7%	40.3	25	29.9	1	0	0	1161.60	159	168
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	22	22	35	0.04%	20.0%	SADFSQSTSIGIK	99.7%	54.9	25	49.6	2	0	0	1340.67	726	738
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	22	22	35	0.04%	20.0%	SAVAGFLLLLK	99.7%	54.5	25	54.5	1	0	0	1131.71	535	545
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	22	22	35	0.04%	20.0%	SISLLCLEGLQK	99.7%	60.2	25	20.2	2	0	0	1360.75	903	914
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	22	22	35	0.04%	20.0%	SLLNLLSSQEEDFNSK	99.7%	104	25	102	2	0	0	1823.90	965	980
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	22	22	35	0.04%	20.0%	SYVSTMILEVVK	99.7%	40.9	25	34.8	1	0	0	1384.74	358	369
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	22	22	35	0.04%	20.0%	TAAPTVCLLVLSQAEK	99.7%	65.3	25	65.3	2	0	0	1700.93	1079	1094
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	22	22	35	0.04%	20.0%	TIETSPSLSR	99.5%	37.4	25	29.8	2	0	0	1090.57	403	412
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	22	22	35	0.04%	20.0%	VLEEVDWLITK	99.7%	40.2	25	19.8	1	0	0	1344.74	1095	1105
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	22	22	35	0.04%	20.0%	YAVNVALQK	99.6%	38.9	25	35.2	2	0	0	1005.57	841	849

Far upstream element-binding protein 2	KHSRP	FUBP2_HUMAN	73.1	100.0%	5	5	8	0.01%	8.4%	AINQQTGAFVEISR	99.7%	88.3	25	80.4	1	0	0	1533.80	449	462
Far upstream element-binding protein 2	KHSRP	FUBP2_HUMAN	73.1	100.0%	5	5	8	0.01%	8.4%	DAFADAVQR	99.7%	47	25	37	1	0	0	992.48	72	80
Far upstream element-binding protein 2	KHSRP	FUBP2_HUMAN	73.1	100.0%	5	5	8	0.01%	8.4%	IGGGIDVPVPR	99.7%	69	25	49.3	2	0	0	1079.62	321	331
Far upstream element-binding protein 2	KHSRP	FUBP2_HUMAN	73.1	100.0%	5	5	8	0.01%	8.4%	SVSLTGAPESVQK	99.7%	47.2	25	37.4	2	0	0	1302.69	191	203
Far upstream element-binding protein 2	KHSRP	FUBP2_HUMAN	73.1	100.0%	5	5	8	0.01%	8.4%	VQISPDSGGLPER	99.7%	52.7	25	49.7	2	0	0	1354.70	178	190
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	6	6	10	0.01%	11.0%	AEGFVDALHR	99.7%	41.5	25	32.8	2	0	0	1114.56	16	25
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	6	6	10	0.01%	11.0%	EMVLEIIR	99.7%	42.4	25	0	1	0	0	1002.57	226	233
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	6	6	10	0.01%	11.0%	GVPQQIEVAR	99.7%	41.2	25	28.1	2	0	0	1096.61	409	418
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	6	6	10	0.01%	11.0%	IQFKPDDGISPER	99.6%	31.7	25	31.6	0	1	0	1501.76	287	299
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	6	6	10	0.01%	11.0%	LLGQIVDR	99.7%	40.7	25	27.9	2	0	0	913.55	140	147
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	6	6	10	0.01%	11.0%	SINQQSGAHVELQR	99.7%	56.7	25	51.2	2	0	0	1566.80	379	392
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	7	11	21	0.02%	19.6%	ATPEQYQILK	99.6%	38.8	25	32.6	1	0	0	1190.64	344	353
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	7	11	21	0.02%	19.6%	CSWLVVQCLQR	99.7%	70.3	25	60.1	2	0	0	1448.71	333	343
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	7	11	21	0.02%	19.6%	GLTVVVAFR	99.7%	68.8	25	59.2	2	0	0	961.58	127	135
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	7	11	21	0.02%	19.6%	IGTDIQDNK	99.2%	35.4	25	28.4	2	0	0	1003.51	324	332
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	7	11	21	0.02%	19.6%	LKEVLEYNAIGGK	99.7%	79.1	25	68	2	2	0	1433.80	111	123
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	7	11	21	0.02%	19.6%	QDFVQHFSQIVR	99.7%	41.9	25	36.3	2	2	0	1503.77	81	92
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	7	11	21	0.02%	19.6%	VLTEDEMGHPEIGDAIAR	99.7%	67.6	25	67.6	2	4	0	1952.94	93	110
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	6	8	14	0.01%	18.2%	ENTYPFLAMIMLK	99.7%	55.1	25	54	2	0	0	1570.80	227	239
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	6	8	14	0.01%	18.2%	FTYYTILDIFR	99.7%	76.4	25	69.8	3	0	0	1451.76	105	115
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	6	8	14	0.01%	18.2%	HTLEQHNWNIEAAVQDR	99.7%	52.5	25	52.5	0	1	0	2060.99	34	50
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	6	8	14	0.01%	18.2%	IIFKLPNDSR	98.2%	26.1	25	18.7	0	1	0	1202.69	364	373
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	6	8	14	0.01%	18.2%	IYSYVVSRPQPR	98.1%	26	25	25.2	1	2	0	1464.80	78	89
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	6	8	14	0.01%	18.2%	VTDPVGDIVSFMHSFEEK	99.7%	96.7	25	96.2	2	2	0	2036.96	129	146
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	13	14	26	0.03%	22.1%	DAPIALKR	99.7%	48.3	25	16.6	2	0	0	883.54	320	327
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	13	14	26	0.03%	22.1%	DIISELLTSDDMK	99.7%	56.5	25	42.6	4	0	0	1479.73	523	535
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	13	14	26	0.03%	22.1%	ILVDQQVWK	99.6%	38.2	25	34.1	2	0	0	1128.64	295	303
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	13	14	26	0.03%	22.1%	IVEDPESLNMK	97.3%	30.1	25	26	1	0	0	1274.63	444	454
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	13	14	26	0.03%	22.1%	IYSVEALPVAAVNVQSTQ	98.2%	31.8	25	31.8	2	0	0	1889.00	693	710
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	13	14	26	0.03%	22.1%	LDDTVYLR	99.7%	60.9	25	46	2	0	0	994.52	549	556
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	13	14	26	0.03%	22.1%	LGIPQNTILVQTLLR	99.7%	49.5	25	49.5	2	0	0	1679.02	242	256
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	13	14	26	0.03%	22.1%	NQVLPLSDVDTTSATDIQR	99.7%	137	25	137	2	0	0	2073.05	615	633
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	13	14	26	0.03%	22.1%	SAYCLGSSHPR	99.7%	53.4	25	48	2	0	0	1234.56	642	652
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	13	14	26	0.03%	22.1%	SLILLDECSK	99.7%	44.1	25	37.4	1	0	0	1177.61	359	368
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	13	14	26	0.03%	22.1%	VAVLCVSR	99.7%	47.5	25	35.7	2	0	0	903.51	634	641
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	13	14	26	0.03%	22.1%	VNLNHEVSNEDVLTK	99.7%	45.9	25	45.3	0	2	0	1710.87	133	147
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	13	14	26	0.03%	22.1%	VVLDNIHGCPLR	99.7%	49	25	26.5	2	0	0	1392.74	369	380
FAST kinase domain-containing protein 3	FASTKD3	FAKD3_HUMAN	75.7	99.8%	2	2	2	0.00%	2.7%	ELVEYLQR	98.5%	32.4	25	30	1	0	0	1049.56	642	649
FAST kinase domain-containing protein 3	FASTKD3	FAKD3_HUMAN	75.7	99.8%	2	2	2	0.00%	2.7%	IGLTNLLGAR	99.7%	50	25	32.3	1	0	0	1027.63	542	551
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	22	22	42	0.04%	10.1%	AALQEELQLCK	99.7%	48	25	26.5	2	0	0	1302.67	1132	1142
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	22	22	42	0.04%	10.1%	ADEASELACPTPK	99.7%	60.9	25	60.9	1	0	0	1388.64	2194	2206
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	22	22	42	0.04%	10.1%	AGLYGLPR	99.2%	35.5	25	30	1	0	0	846.48	42	49
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	22	22	42	0.04%	10.1%	AINCATSGVVGLVNCLR	99.7%	103	25	102	1	0	0	1803.92	1445	1461
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	22	22	42	0.04%	10.1%	AQVADVVVSR	99.7%	67.9	25	49	1	0	0	1043.58	1073	1082
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	22	22	42	0.04%	10.1%	DNLEFFLAGIGR	99.7%	72.7	25	50.4	4	0	0	1351.70	791	802
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	22	22	42	0.04%	10.1%	EDGLAQQQTQLNLR	99.7%	79.1	25	74.6	2	0	0	1613.82	2207	2220
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	22	22	42	0.04%	10.1%	FDASFFGVHPK	99.7%	62.1	25	51	2	0	0	1251.62	60	70
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	22	22	42	0.04%	10.1%	FPQLDSTSFANSR	99.7%	70.5	25	60.7	2	0	0	1469.70	1712	1724
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	22	22	42	0.04%	10.1%	GLVQALQTK	99.7%	50.6	25	31.3	2	0	0	957.57	1143	1151
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	22	22	42	0.04%	10.1%	GVDLVLNSLAEEK	99.7%	67.5	25	53.9	2	0	0	1386.75	1740	1752
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	22	22	42	0.04%	10.1%	HGLYLPTR	97.4%	30.2	25	28.7	2	0	0	956.53	1044	1051

Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	22	22	42	0.04%	10.1%	LLEQGLR	99.7%	41.7	25	0	1	0	0	828.49	437	443
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	22	22	42	0.04%	10.1%	LPEDPLLSGLLDSPALK	99.7%	84	25	84	2	0	0	1778.00	1209	1225
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	22	22	42	0.04%	10.1%	LQVVDQPLPVR	99.7%	59.1	25	59.1	3	0	0	1263.74	374	384
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	22	22	42	0.04%	10.1%	SDEAVKPFGLK	99.7%	44.3	25	37.7	1	0	0	1190.64	523	533
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	22	22	42	0.04%	10.1%	SEGVVAVLLTK	99.7%	61.7	25	54.8	2	0	0	1115.67	225	235
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	22	22	42	0.04%	10.1%	SFYGSTLFLCR	99.7%	58.9	25	47.9	3	0	0	1350.65	1394	1404
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	22	22	42	0.04%	10.1%	TGTVSLEVR	99.7%	70.9	25	55.8	2	0	0	961.53	928	936
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	22	22	42	0.04%	10.1%	VLEALLPLK	99.7%	41.8	25	41.8	1	0	0	995.65	2383	2391
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	22	22	42	0.04%	10.1%	VVEVLAGHGHLYSR	97.7%	25.1	25	20.8	0	1	0	1536.83	1242	1255
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	22	22	42	0.04%	10.1%	VVVQVLAEEPEAVLK	99.7%	98.9	25	80.9	4	0	0	1622.94	1852	1866
Fermitin family homolog 2	FERMT2	FERM2_HUMAN	77.9	100.0%	3	3	3	0.00%	4.6%	GCEVTPDVNISGQK	99.7%	48.4	25	40.1	1	0	0	1503.71	425	438
Fermitin family homolog 2	FERMT2	FERM2_HUMAN	77.9	100.0%	3	3	3	0.00%	4.6%	INQLYEQAK	99.7%	40.3	25	20.3	1	0	0	1106.58	291	299
Fermitin family homolog 2	FERMT2	FERM2_HUMAN	77.9	100.0%	3	3	3	0.00%	4.6%	LQFTPQHK	98.4%	32.2	25	15.6	1	0	0	998.54	90	97
FH1/FH2 domain-containing protein 1	FHOD1	FHOD1_HUMAN	126.6	99.8%	2	2	3	0.00%	2.2%	AALLNFDEFAVSK	99.7%	56.1	25	56.1	2	0	0	1424.74	718	730
FH1/FH2 domain-containing protein 1	FHOD1	FHOD1_HUMAN	126.6	99.8%	2	2	3	0.00%	2.2%	FLENVAAAETEK	99.7%	52.7	25	47.4	1	0	0	1321.66	443	454
Filaggrin-2	FLG2	FILA2_HUMAN	248.1	100.0%	3	3	14	0.01%	2.0%	FSNSSSSNEFSK	99.7%	65.4	25	65.4	5	0	0	1320.57	404	415
Filaggrin-2	FLG2	FILA2_HUMAN	248.1	100.0%	3	3	14	0.01%	2.0%	SGQSSYGQHSSGSSQSSGYGQHGSR	95.5%	22.7	25	22.7	0	1	0	2500.05	613	637
Filaggrin-2	FLG2	FILA2_HUMAN	248.1	100.0%	3	3	14	0.01%	2.0%	SVVTVIDVFYK	99.7%	76.5	25	76.5	8	0	0	1269.71	7	17
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	23	23	35	0.04%	11.4%	AFGPGLQGGSAGSPAR	99.7%	74.9	25	69	2	0	0	1429.72	1072	1087
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	23	23	35	0.04%	11.4%	AGVAPLQVK	99.3%	35.9	25	34	2	0	0	882.54	1478	1486
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	23	23	35	0.04%	11.4%	ALTQTGGPHVK	99.7%	39.2	25	30.2	2	0	0	1108.61	1284	1294
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	23	23	35	0.04%	11.4%	ANLPQSFQVDTSK	99.7%	61.5	25	59.5	2	0	0	1434.72	1465	1477
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	23	23	35	0.04%	11.4%	DAPQDFHPDR	97.8%	30.9	25	22.1	1	0	0	1197.53	665	674
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	23	23	35	0.04%	11.4%	DKGEYTLVVK	96.4%	28.9	25	16.9	1	0	0	1151.63	2622	2631
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	23	23	35	0.04%	11.4%	EATTEFSVDAR	99.7%	62.1	25	61.1	2	0	0	1225.57	1273	1283
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	23	23	35	0.04%	11.4%	EGPYSISVLYGDEEVPR	99.7%	81.2	25	81.2	2	0	0	1909.92	1516	1532
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	23	23	35	0.04%	11.4%	IANLQTDLSDGLR	99.7%	70.8	25	67.5	1	0	0	1415.75	64	76
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	23	23	35	0.04%	11.4%	IVGPSGAAVPCK	94.9%	27.6	25	25.3	1	0	0	1155.62	1008	1019
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	23	23	35	0.04%	11.4%	LYSVSYLLK	97.6%	30.5	25	18.8	1	0	0	1085.62	2613	2621
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	23	23	35	0.04%	11.4%	SPFSVAVSPSLDLSK	99.7%	70.7	25	59.2	2	0	0	1533.82	959	973
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	23	23	35	0.04%	11.4%	TGVAVNKPAEFTVDAK	99.5%	31.3	25	31	0	1	0	1646.87	685	700
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	23	23	35	0.04%	11.4%	TGVELGKPTHFTVNAK	98.1%	25.9	25	25.9	0	2	0	1698.92	885	900
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	23	23	35	0.04%	11.4%	TPCEEILVK	99.6%	38	25	28.6	2	0	0	1088.57	2599	2607
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	23	23	35	0.04%	11.4%	VANPSGNLTETYVQDR	99.7%	101	25	99.2	1	0	0	1763.86	1297	1312
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	23	23	35	0.04%	11.4%	VEPGLGADNSVVR	98.8%	33.3	25	22.6	1	0	0	1312.69	1020	1032
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	23	23	35	0.04%	11.4%	VNVGAGSHPNK	99.7%	48.7	25	48.7	2	0	0	1079.56	761	771
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	23	23	35	0.04%	11.4%	VPVHDVTDASK	99.7%	56.3	25	47.5	2	0	0	1167.60	1440	1450
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	23	23	35	0.04%	11.4%	VTAQGPGLEPSGNIANK	99.7%	88.4	25	83.9	2	0	0	1652.86	384	400
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	23	23	35	0.04%	11.4%	VTVLFAGQHIAK	99.7%	49.5	25	49.5	1	0	0	1283.75	356	367
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	23	23	35	0.04%	11.4%	YGGDEIPFSPYR	99.7%	46.6	25	25.3	1	0	0	1400.65	1622	1633
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	23	23	35	0.04%	11.4%	YTPVQQGPVGVNVTYGGDPIPK	99.7%	73.3	25	73.3	1	0	0	2286.18	937	958
Flap endonuclease 1	FEN1	FEN1_HUMAN	42.6	100.0%	4	4	7	0.01%	11.3%	KLPIQEFHLSR	99.6%	31.8	25	29.4	0	2	0	1367.78	201	211
Flap endonuclease 1	FEN1	FEN1_HUMAN	42.6	100.0%	4	4	7	0.01%	11.3%	LIADVAPSAIR	99.7%	74.5	25	62.1	2	0	0	1125.66	9	19
Flap endonuclease 1	FEN1	FEN1_HUMAN	42.6	100.0%	4	4	7	0.01%	11.3%	LIADVAPSAIRENDIK	99.7%	41.5	25	36.5	1	0	0	1724.95	9	24
Flap endonuclease 1	FEN1	FEN1_HUMAN	42.6	100.0%	4	4	7	0.01%	11.3%	QLQQAQAAGAEQEVEK	99.7%	108	25	98.2	2	0	0	1727.86	110	125
Formin-like protein 2	FMNL2	FMNL2_HUMAN	123.3	100.0%	3	3	4	0.00%	3.5%	AAAVSLENVLLDVK	99.7%	65	25	58.6	2	0	0	1441.83	891	904
Formin-like protein 2	FMNL2	FMNL2_HUMAN	123.3	100.0%	3	3	4	0.00%	3.5%	LQSLDLLLDTK	99.7%	41	25	41	1	0	0	1258.73	845	855
Formin-like protein 2	FMNL2	FMNL2_HUMAN	123.3	100.0%	3	3	4	0.00%	3.5%	TTPPSVFFPVFVR	97.7%	30.7	25	30.7	1	0	0	1493.82	964	976
Fragile X mental retardation protein 1	FMR1	FMR1_HUMAN	71.2	99.8%	2	2	3	0.00%	4.0%	LIQEIVDK	99.0%	34.5	25	17	1	0	0	957.56	303	310
Fragile X mental retardation protein 1	FMR1	FMR1_HUMAN	71.2	99.8%	2	2	3	0.00%	4.0%	LQIDEQLR	99.7%	51.5	25	37.9	3	0	0	1014.56	435	442
Fragile X mental retardation protein 1	FMR1	FMR1_HUMAN	71.2	99.8%	2	2	3	0.00%	4.0%	VRIEAENEK	99.4%	36.6	25	25.4	2	0	0	1087.57	316	324

Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	3	3	7	0.01%	5.2%	AGYSTDESSSSSLHATR	97.6%	25	25	25	0	2	0	1755.78	407	423
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	3	3	7	0.01%	5.2%	IYGETPEACR	99.7%	51.8	25	46.1	2	0	0	1195.54	274	283
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	3	3	7	0.01%	5.2%	LQIDEQLR	99.7%	51.5	25	37.9	3	0	0	1014.56	379	386
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	8	8	13	0.01%	28.3%	ADDGRPFPQVIK	99.2%	35	25	24.5	2	0	0	1342.71	88	99
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	8	8	13	0.01%	28.3%	ALANSLACQGK	99.7%	52.1	25	38.8	2	0	0	1132.58	332	342
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	8	8	13	0.01%	28.3%	ELSDIAHR	97.3%	30.1	25	21	2	0	0	940.48	15	22
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	8	8	13	0.01%	28.3%	GGVVGIKVDK	94.9%	27.6	25	20	1	0	0	971.59	102	111
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	8	8	13	0.01%	28.3%	GILAADESTGSIAK	99.7%	89.8	25	86	2	0	0	1332.70	29	42
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	8	8	13	0.01%	28.3%	LQSIGTENTEENRR	98.7%	27.3	25	11.1	0	1	0	1646.81	44	57
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	8	8	13	0.01%	28.3%	PYQYPALTPEQK	99.7%	59.4	25	50.6	1	0	0	1434.73	2	13
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	8	8	13	0.01%	28.3%	YTPSGQAGAAASESLFVSNHAY	99.7%	99.4	25	99.4	2	0	0	2228.03	343	364
Fumarylacetoacetate hydrolase domain-containing protein 2A	FAHD2A	FAH2A_HUMAN	34.6	99.8%	2	2	5	0.01%	8.3%	ALAAQLPVLPR	99.7%	41.2	25	30.7	1	0	0	1148.72	83	93
Fumarylacetoacetate hydrolase domain-containing protein 2A	FAHD2A	FAH2A_HUMAN	34.6	99.8%	2	2	5	0.01%	8.3%	TFDTFCPLGPALVTK	99.7%	69.7	25	68.2	4	0	0	1666.85	210	224
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	7	7	14	0.01%	21.9%	EVQLEELEAAR	99.7%	77.3	25	66.6	2	0	0	1286.66	257	267
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	7	7	14	0.01%	21.9%	GHALLIDCR	99.7%	63.6	25	61.1	2	0	0	1054.55	196	204
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	7	7	14	0.01%	21.9%	HSLASSEYPVR	99.7%	52.1	25	42.3	2	0	0	1245.62	229	239
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	7	7	14	0.01%	21.9%	KDGLVSLLTTSEGADEPQR	99.7%	42	25	35.1	0	2	0	2016.02	69	87
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	7	7	14	0.01%	21.9%	LAVLITNSNVR	99.7%	46	25	4.26	2	0	0	1199.71	218	228
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	7	7	14	0.01%	21.9%	QPQVAELLAEAR	99.7%	83.1	25	80.6	2	0	0	1324.72	6	17
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	7	7	14	0.01%	21.9%	SLETSLVPLSDPK	99.7%	49.8	25	49.8	2	0	0	1385.75	205	217
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	4	4	7	0.01%	5.3%	LWFYIQPAMR	99.7%	47.5	25	42.5	1	0	0	1324.69	324	333
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	4	4	7	0.01%	5.3%	NLDPLVYLLSK	99.7%	74.9	25	73	2	0	0	1274.74	77	87
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	4	4	7	0.01%	5.3%	TFLVDPNLDLSIR	99.7%	65.7	25	55.7	2	0	0	1502.82	245	257
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	4	4	7	0.01%	5.3%	YTIVQQQIPSFLQK	99.7%	69	25	69	2	0	0	1692.93	432	445
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	9	9	13	0.01%	28.8%	EMVHADVELMR	99.7%	56.9	25	53.6	1	0	0	1329.63	357	367
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	9	9	13	0.01%	28.8%	FYQASTSELYGK	99.7%	67.4	25	56.6	2	0	0	1393.66	150	161
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	9	9	13	0.01%	28.8%	GYEVHGIVR	99.7%	43	25	40.3	2	0	0	1029.55	47	55
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	9	9	13	0.01%	28.8%	IINEVKPTEIYNLGAQSHVK	99.7%	38.2	25	38.2	0	1	0	2253.22	96	115
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	9	9	13	0.01%	28.8%	IYLGQLECFSLGNLDAK	99.7%	52.1	25	45.5	1	0	0	1940.98	230	246
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	9	9	13	0.01%	28.8%	LHYGDLTDSTCLVK	99.7%	70.8	25	65.3	2	0	0	1621.79	82	95
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	9	9	13	0.01%	28.8%	SFLHIGK	98.4%	32.6	25.3	21.7	1	0	0	801.46	288	294
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	9	9	13	0.01%	28.8%	TCGLINSVK	99.5%	37.4	25	15.4	2	0	0	991.52	141	149
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	9	9	13	0.01%	28.8%	VAFDELVR	99.4%	36.4	25	22.5	1	0	0	948.51	349	356
Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	7	7	9	0.01%	8.0%	EWGEELQAVLR	99.7%	44.4	25	37.1	1	0	0	1329.68	326	336
Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	7	7	9	0.01%	8.0%	IFIQTLEANACR	99.7%	66.4	25	66.4	2	0	0	1435.74	673	684
Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	7	7	9	0.01%	8.0%	QVVSELAECVR	99.7%	46.6	25	33.2	1	0	0	1289.65	374	384
Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	7	7	9	0.01%	8.0%	SDPDACPTMPLLAMLLR	97.1%	29.8	25	29.8	1	0	0	1900.93	205	221
Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	7	7	9	0.01%	8.0%	SFFEGHFK	96.5%	29	25	23.6	1	0	0	998.47	776	783
Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	7	7	9	0.01%	8.0%	SIAEGIGPEER	99.7%	51.7	25	45.2	2	0	0	1157.58	1037	1047
Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	7	7	9	0.01%	8.0%	VLQPHPVTPSDTETR	99.7%	44.7	25	44.7	0	1	0	1676.86	77	91
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	9	9	13	0.01%	6.4%	GVLQTAAER	99.7%	48.5	25	21.9	2	0	0	944.52	934	942
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	9	9	13	0.01%	6.4%	LSGEAFDINK	99.7%	51.5	25	38	1	0	0	1093.55	515	524
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	9	9	13	0.01%	6.4%	SLEAFFLYGR	99.7%	81	25	73	2	0	0	1202.62	1275	1284
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	9	9	13	0.01%	6.4%	TSVFLVR	97.6%	30.5	25	11.1	1	0	0	821.49	34	40
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	9	9	13	0.01%	6.4%	TVAEVQETLAEMIR	99.7%	59.7	25	59.7	1	0	0	1589.82	1373	1386
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	9	9	13	0.01%	6.4%	VGPGAGESPGTPPFR	99.7%	53.6	25	53.6	1	0	0	1425.71	41	55
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	9	9	13	0.01%	6.4%	VIGELVGHTER	99.7%	88.1	25	87.3	2	0	0	1209.66	56	66
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	9	9	13	0.01%	6.4%	VYEAVELLK	99.7%	39.4	25	32.5	2	0	0	1063.60	991	999
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	9	9	13	0.01%	6.4%	YPSATNNTPAK	96.0%	28.5	25	20.4	1	0	0	1163.57	1188	1198
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	6	6	7	0.01%	3.1%	DMLTQTYDLIER	99.7%	57.6	25	41.3	1	0	0	1497.73	367	378
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	6	6	7	0.01%	3.1%	IASNVLNTK	95.0%	27.7	25	23.4	1	0	0	959.55	1278	1286

General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	6	6	7	0.01%	3.1%	LCYMGLLQFGPTEK	97.7%	30.7	25	25	2	0	0	1656.81	972	985
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	6	6	7	0.01%	3.1%	NLIIEAVTNLR	99.7%	64.7	25	60.4	1	0	0	1255.74	619	629
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	6	6	7	0.01%	3.1%	NLSEEGLLR	98.5%	32.4	25	19.4	1	0	0	1030.55	665	673
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	6	6	7	0.01%	3.1%	VCLAEVYQDK	97.7%	30.8	25	30.8	1	0	0	1224.59	1335	1344
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	5	5	7	0.01%	5.4%	AIFAVLTSVLTK	99.7%	104	25	104	2	0	0	1262.77	611	622
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	5	5	7	0.01%	5.4%	DDWWNLLLK	99.6%	38.6	25	30	1	0	0	1202.62	623	631
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	5	5	7	0.01%	5.4%	GLMGEANIR	99.5%	37	25	18.2	1	0	0	976.49	151	159
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	5	5	7	0.01%	5.4%	STLLFSQGK	99.7%	43.6	25	33	1	0	0	980.54	540	548
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	5	5	7	0.01%	5.4%	YNLAVVWLR	99.7%	70.3	25	52.8	2	0	0	1133.65	453	461
General transcription factor 3C polypeptide 4	GTF3C4	TF3C4_HUMAN	92.0	100.0%	3	3	4	0.00%	3.8%	LSDVFGSVR	99.7%	42.4	25	24.4	1	0	0	979.52	468	476
General transcription factor 3C polypeptide 4	GTF3C4	TF3C4_HUMAN	92.0	100.0%	3	3	4	0.00%	3.8%	NYQVQFVTLK	99.7%	53.6	25	47.2	2	0	0	1239.67	507	516
General transcription factor 3C polypeptide 4	GTF3C4	TF3C4_HUMAN	92.0	100.0%	3	3	4	0.00%	3.8%	QLIPIFTDVALK	97.0%	29.6	25	20.3	1	0	0	1357.81	449	460
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	11	12	21	0.02%	23.5%	DPYCHPVCANR	99.4%	36.8	25	33.7	2	0	0	1388.58	68	78
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	11	12	21	0.02%	23.5%	EGYNNPPISGENLIGLSR	99.7%	73.2	25	73.2	2	0	0	1929.97	192	209
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	11	12	21	0.02%	23.5%	FSTSSLLLR	99.7%	54.3	25	43.4	2	0	0	1023.58	79	87
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	11	12	21	0.02%	23.5%	HGYAPSDLPVK	99.7%	45.6	25	40.1	2	0	0	1183.61	329	339
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	11	12	21	0.02%	23.5%	IYQVLDFR	99.7%	54.4	25	43.7	2	0	0	1053.57	315	322
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	11	12	21	0.02%	23.5%	LKDSVYIFR	99.7%	43.1	25	39.2	2	0	0	1140.64	388	396
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	11	12	21	0.02%	23.5%	MLPTLGGEEGVSR	99.7%	62	25	57.5	3	0	0	1345.68	39	51
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	11	12	21	0.02%	23.5%	MVCVEYPGVVR	99.6%	38.9	25	37.5	1	0	0	1308.64	24	34
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	11	12	21	0.02%	23.5%	QGLGPSGTSGAR	99.7%	63.2	25	50.8	2	0	0	1087.55	368	379
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	11	12	21	0.02%	23.5%	STYNYSLPITVK	99.7%	72.2	25	69	2	0	0	1385.73	343	354
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	11	12	21	0.02%	23.5%	VLMLRPEK	94.7%	27.4	25	15.1	1	0	0	985.59	149	156
General transcription factor II-I	GTF2I	GTF2I_HUMAN	112.4	100.0%	9	9	11	0.01%	9.6%	ANELPQPPVPEPANAGK	99.7%	42.3	25	36.6	1	0	0	1728.89	327	343
General transcription factor II-I	GTF2I	GTF2I_HUMAN	112.4	100.0%	9	9	11	0.01%	9.6%	APSYLEISSMR	99.7%	51.4	25	42.5	1	0	0	1253.62	917	927
General transcription factor II-I	GTF2I	GTF2I_HUMAN	112.4	100.0%	9	9	11	0.01%	9.6%	EQVNDLFSR	99.7%	43.4	25	32.7	2	0	0	1107.54	870	878
General transcription factor II-I	GTF2I	GTF2I_HUMAN	112.4	100.0%	9	9	11	0.01%	9.6%	FAEALGSTEAK	99.7%	90.4	25	78.4	1	0	0	1123.56	478	488
General transcription factor II-I	GTF2I	GTF2I_HUMAN	112.4	100.0%	9	9	11	0.01%	9.6%	FAQALGLTEAVK	99.7%	70.4	25	50.8	2	0	0	1247.70	583	594
General transcription factor II-I	GTF2I	GTF2I_HUMAN	112.4	100.0%	9	9	11	0.01%	9.6%	QVEEIFNLK	96.9%	29.6	25	0	1	0	0	1119.60	574	582
General transcription factor II-I	GTF2I	GTF2I_HUMAN	112.4	100.0%	9	9	11	0.01%	9.6%	RPSTFGIPR	98.1%	31.6	25	18.7	1	0	0	1030.58	782	790
General transcription factor II-I	GTF2I	GTF2I_HUMAN	112.4	100.0%	9	9	11	0.01%	9.6%	RPSTYGIPR	94.7%	27.4	25	19.1	1	0	0	1046.57	410	418
General transcription factor II-I	GTF2I	GTF2I_HUMAN	112.4	100.0%	9	9	11	0.01%	9.6%	SPTWFGIPR	99.7%	40	25	28.9	1	0	0	1060.56	620	628
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	12	13	25	0.03%	16.2%	EQDDLLVLLADQDQK	99.7%	73.9	25	59.3	2	0	0	1742.88	905	919
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	12	13	25	0.03%	16.2%	EQDLQLEELR	99.7%	41.7	25	10.5	1	0	0	1272.64	661	670
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	12	13	25	0.03%	16.2%	GVMGGQSAGPQHTEAETIQK	99.6%	32.5	25	32.5	0	2	0	2041.96	6	25
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	12	13	25	0.03%	16.2%	IVAFENAFER	99.7%	70.5	25	66.3	2	0	0	1195.61	203	212
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	12	13	25	0.03%	16.2%	LMDLLADSR	99.7%	70.6	25	58.2	4	0	0	1049.53	171	179
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	12	13	25	0.03%	16.2%	LSALLQETK	99.7%	49.5	25	37.9	2	0	0	1002.58	850	858
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	12	13	25	0.03%	16.2%	NDGVLLLQALTR	99.7%	105	25	95.2	2	0	0	1312.76	184	195
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	12	13	25	0.03%	16.2%	QSEDLGSQFTEIFIK	99.7%	114	25	111	2	0	0	1741.86	105	119
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	12	13	25	0.03%	16.2%	SQLNSQSVEITK	99.7%	89.6	25	83.7	2	0	0	1333.70	799	810
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	12	13	25	0.03%	16.2%	SSQTSGTNEQSSAIVSAR	99.7%	136	25	122	2	0	0	1809.86	765	782
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	12	13	25	0.03%	16.2%	SVEVQGETETIIATK	99.7%	113	25	97.1	2	0	0	1604.84	828	842
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	12	13	25	0.03%	16.2%	VASSTLLDDRR	96.0%	28.5	25	15.7	2	0	0	1232.66	30	40
Glomulin	GLMN	GLMN_HUMAN	68.2	100.0%	3	3	4	0.00%	5.7%	GLELLENSLLR	99.7%	61.4	25	52	1	0	0	1256.72	335	345
Glomulin	GLMN	GLMN_HUMAN	68.2	100.0%	3	3	4	0.00%	5.7%	IEDNSLLYQYLEIK	99.7%	52.1	25	52.1	1	0	0	1740.91	346	359
Glomulin	GLMN	GLMN_HUMAN	68.2	100.0%	3	3	4	0.00%	5.7%	IMASLNLLR	99.7%	52.2	25	40	2	0	0	1030.61	471	479
Glucose-6-phosphate isomerase	GPI	G6PI_HUMAN	63.1	99.9%	2	2	3	0.00%	5.7%	ILLANFLAQTEALMR	99.7%	96.9	25	96.9	1	0	0	1703.95	424	438
Glucose-6-phosphate isomerase	GPI	G6PI_HUMAN	63.1	99.9%	2	2	3	0.00%	5.7%	TLAQLNPESSLFIIASK	99.7%	67.2	25	67.2	2	0	0	1832.02	195	211
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	6	6	11	0.01%	17.7%	AQTGAPCLSFDIVR	99.7%	57.5	25	56.2	2	0	0	1534.77	60	73
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	6	6	11	0.01%	17.7%	GQVEVFALR	99.7%	50.8	25	35	2	0	0	1018.57	173	181

Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	6	6	11	0.01%	17.7%	LLQVVEEPQALAAFLR	99.7%	134	25	134	2	0	0	1797.03	183	198
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	6	6	11	0.01%	17.7%	REPFLLSGGDDGALK	99.7%	34.7	25	34.7	0	2	0	1574.82	319	333
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	6	6	11	0.01%	17.7%	SGSPVATFK	95.3%	27.9	25	19	1	0	0	893.47	342	350
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	6	6	11	0.01%	17.7%	VSWLGEEPVAGVWSEK	99.7%	67.1	25	67.1	2	0	0	1772.89	157	172
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	10	10	15	0.02%	16.7%	AVQTLQMELQQIMK	99.7%	59.6	25	59.6	2	0	0	1660.88	323	336
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	10	10	15	0.02%	16.7%	EIFEQPESVVNTMR	99.7%	63.7	25	42.1	1	0	0	1678.81	346	359
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	10	10	15	0.02%	16.7%	EILETLIK	99.7%	41.3	25	24.6	1	0	0	958.58	18	25
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	10	10	15	0.02%	16.7%	ESQDTSFTTLVER	99.7%	67.3	25	67.3	1	0	0	1512.72	164	176
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	10	10	15	0.02%	16.7%	EVLSMDDEIQK	99.6%	39	25	36.1	1	0	0	1322.61	537	547
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	10	10	15	0.02%	16.7%	GSPLLIGVR	99.7%	51.9	25	34.8	2	0	0	911.57	204	212
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	10	10	15	0.02%	16.7%	GYDFESETDTETIAK	99.7%	103	25	103	2	0	0	1705.74	140	154
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	10	10	15	0.02%	16.7%	GYDVDFPR	99.5%	37	25	32.6	1	0	0	968.45	683	690
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	10	10	15	0.02%	16.7%	LATELYHQK	99.7%	45.1	25	19.6	2	0	0	1102.59	548	556
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	10	10	15	0.02%	16.7%	VIFLEDDDVAAVVDGR	99.7%	77.7	25	76.4	2	0	0	1732.88	291	306
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	12	12	22	0.02%	16.1%	AINFNFGYAK	99.7%	50.5	25	34.9	2	0	0	1144.58	283	292
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	12	12	22	0.02%	16.1%	FDDTNPEKEEAK	99.7%	58.1	25	48.8	2	0	0	1422.64	302	313
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	12	12	22	0.02%	16.1%	FHKPGENYK	96.9%	29.5	25	25.5	1	0	0	1119.56	231	239
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	12	12	22	0.02%	16.1%	FSEGEATLR	99.7%	56.6	25	45.3	2	0	0	1009.49	395	403
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	12	12	22	0.02%	16.1%	GLAYVCHQR	99.7%	55.8	25	47	2	0	0	1103.54	353	361
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	12	12	22	0.02%	16.1%	HTGYVIELQHVVK	99.7%	50.7	25	49.7	0	2	0	1522.84	640	652
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	12	12	22	0.02%	16.1%	ILQLVATGAVR	99.7%	96.4	25	91.1	2	0	0	1140.71	499	509
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	12	12	22	0.02%	16.1%	LAWGQPVGLR	99.7%	59.3	25	48.2	2	0	0	1096.63	630	639
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	12	12	22	0.02%	16.1%	LFTLTALR	99.7%	70.2	25	51.2	2	0	0	934.57	516	523
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	12	12	22	0.02%	16.1%	LGYFSVDPDSHQGK	99.7%	44.6	25	44.6	1	0	0	1549.73	746	759
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	12	12	22	0.02%	16.1%	LSFLVSYIASK	99.7%	76	25	71.4	2	0	0	1227.70	69	79
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	12	12	22	0.02%	16.1%	NSALSAQLR	99.7%	83.8	25	73.8	2	0	0	959.53	26	34
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	10	13	27	0.03%	23.0%	ELRVPLIGSLPEAR	99.7%	40.2	25	40.2	2	2	0	1549.91	67	80
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	10	13	27	0.03%	23.0%	FLEATLR	99.7%	46.8	25	33.3	2	0	0	849.48	118	124
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	10	13	27	0.03%	23.0%	GLMEPLLPPK	99.7%	44.8	25	25.7	4	0	0	1110.62	17	26
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	10	13	27	0.03%	23.0%	HLAQLMESIPHSPGPTR	99.7%	39.8	25	39.8	0	4	0	1886.95	242	258
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	10	13	27	0.03%	23.0%	HLTLACHYDSK	99.7%	61.1	25	60.9	2	0	0	1344.64	162	172
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	10	13	27	0.03%	23.0%	KFLEATLR	99.7%	40.3	25	18	2	0	0	977.58	117	124
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	10	13	27	0.03%	23.0%	TEELPLGR	97.2%	29.9	25	15.2	2	0	0	914.49	59	66
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	10	13	27	0.03%	23.0%	TPGSPGNLQVR	99.7%	72.1	25	57	3	0	0	1125.60	106	116
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	10	13	27	0.03%	23.0%	VPLIGSLPEAR	99.7%	57.2	25	53	2	0	0	1151.68	70	80
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	10	13	27	0.03%	23.0%	VVGQLDPQR	99.7%	46.6	25	46.6	2	0	0	1011.56	84	92
Glutaryl-CoA dehydrogenase, mitochondrial	GCDH	GCDH_HUMAN	48.1	99.8%	2	2	2	0.00%	6.6%	AITGIQAFTASK	99.7%	74.2	25	67.9	1	0	0	1207.67	427	438
Glutaryl-CoA dehydrogenase, mitochondrial	GCDH	GCDH_HUMAN	48.1	99.8%	2	2	2	0.00%	6.6%	EIISEMGELGVLGPTIK	98.6%	32.7	25	32.7	1	0	0	1785.97	95	111
Glutathione S-transferase kappa 1	GSTK1	GSTK1_HUMAN	25.5	100.0%	3	3	4	0.00%	17.3%	AGMSAEQAQGLLEK	99.7%	85	25	76.2	2	0	0	1432.71	145	158
Glutathione S-transferase kappa 1	GSTK1	GSTK1_HUMAN	25.5	100.0%	3	3	4	0.00%	17.3%	DFLSVMLEK	99.5%	37.9	25	19.4	1	0	0	1097.55	86	94
Glutathione S-transferase kappa 1	GSTK1	GSTK1_HUMAN	25.5	100.0%	3	3	4	0.00%	17.3%	NEDITEPQSILAAAEK	99.7%	59.5	25	59.5	1	0	0	1728.87	129	144
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	8	10	34	0.04%	29.0%	GALQNIIPASTGAAK	99.7%	84.1	25	81.9	9	0	0	1411.79	201	215
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	8	10	34	0.04%	29.0%	IISNASCTTNCLAPLAK	99.7%	105	25	101	5	0	0	1833.92	146	162
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	8	10	34	0.04%	29.0%	LISWYDNEFGYSNR	99.7%	81.3	25	81.3	2	0	0	1763.80	310	323
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	8	10	34	0.04%	29.0%	LTGMAFR	99.7%	39.2	25	31.3	2	0	0	811.41	228	234
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	8	10	34	0.04%	29.0%	LVINGNPITIFQER	99.7%	54.1	25	49.8	1	0	0	1613.90	67	80
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	8	10	34	0.04%	29.0%	LVINGNPITIFQERDPSK	99.7%	33.8	25	30.7	0	1	0	2041.11	67	84
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	8	10	34	0.04%	29.0%	VPTANVSVVDLTCR	99.7%	94.1	25	94.1	6	2	0	1530.79	235	248
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	8	10	34	0.04%	29.0%	VVDLMAHMASKE	99.7%	82.7	25	73	6	0	0	1330.65	324	335
Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	GPD1L_HUMAN	38.4	100.0%	4	4	6	0.01%	14.8%	ITVVDDADTVELCGALK	99.7%	59.9	25	55.5	2	0	0	1818.92	190	206
Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	GPD1L_HUMAN	38.4	100.0%	4	4	6	0.01%	14.8%	LQGPQTSAEVYR	99.7%	48.9	25	45.1	2	0	0	1348.69	299	310

Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	GPD1L_HUMAN	38.4	100.0%	4	4	6	0.01%	14.8%	NIVAVGAGFCDGLR	99.7%	56.6	25	55.5	1	0	0	1448.73	207	220
Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	GPD1L_HUMAN	38.4	100.0%	4	4	6	0.01%	14.8%	VMENGLLFK	98.3%	32	25	26.3	1	0	0	1050.57	172	180
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	10	11	19	0.02%	18.0%	CSVLPLSQNQEFMPFVK	99.7%	47.9	25	47.9	1	0	0	2024.00	616	632
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	10	11	19	0.02%	18.0%	IYLYLTK	98.8%	33.3	25	7.03	1	0	0	913.54	413	419
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	10	11	19	0.02%	18.0%	LPFAAAQIGNSFR	99.7%	72.5	25	64.7	2	0	0	1391.74	319	331
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	10	11	19	0.02%	18.0%	SCYDLSCHAR	99.7%	44.5	25	44.5	2	0	0	1268.51	465	474
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	10	11	19	0.02%	18.0%	SPITGNDLSPPVSFNLMFK	99.7%	63.8	25	63.8	4	0	0	2080.04	265	283
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	10	11	19	0.02%	18.0%	TFFSFPAVVAPFK	99.7%	49.7	25	45.2	2	0	0	1457.78	603	615
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	10	11	19	0.02%	18.0%	TLYVEEVVPNVIEPSFGLGR	99.7%	76.2	25	76.2	2	0	0	2218.18	564	583
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	10	11	19	0.02%	18.0%	TVNVVQFEPSK	99.7%	64.3	25	55.7	2	0	0	1247.66	491	501
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	10	11	19	0.02%	18.0%	VDDSSGSIGR	99.7%	43.2	25	35.6	2	0	0	992.46	647	656
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	10	11	19	0.02%	18.0%	VPLVAEKPLKEPK	99.7%	46.2	25	46.2	1	0	0	1447.89	478	490
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	16.1%	DYFFALAHTVR	99.7%	57.7	25	48.2	2	0	0	1339.68	51	61
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	16.1%	GLAGLGDVAEVR	99.7%	82.3	25	74.4	2	0	0	1156.63	18	29
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	16.1%	IGEEFLTDLSQLK	99.7%	63.4	25	53.5	1	0	0	1492.79	508	520
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	16.1%	IGEEFLTDLSQLKK	99.7%	37.8	25	37	0	2	0	1620.88	508	521
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	16.1%	LLPLVSDEVFIR	99.7%	41.9	25	41.5	2	0	0	1400.81	522	533
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	16.1%	LVTSIGDVVNHDPVVGDR	99.7%	43.7	25	43.7	0	2	0	1891.99	623	640
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	16.1%	NLAENISR	99.7%	51.7	25	30.4	2	0	0	916.48	271	278
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	16.1%	VEDVEALDR	99.7%	46.6	25	42.2	2	0	0	1045.52	716	724
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	16.1%	VIFLENYR	99.7%	53.7	25	43.2	3	0	0	1053.57	643	650
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	16.1%	VLYPNDNFFEGK	99.7%	68.2	25	67	2	0	0	1442.70	279	290
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	16.1%	WLLLCNPGLADTIVEK	99.7%	46.4	25	46.4	1	0	0	1841.98	492	507
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	16.1%	YEFGIFNQK	99.7%	42.6	25	35.9	2	0	0	1145.56	162	170
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	16.1%	YGNPWEK	95.1%	27.7	25	21	1	0	0	893.42	186	192
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	APNDFNLR	99.7%	60.2	25	45	2	0	0	946.47	249	256
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	AWNTMVLK	99.3%	36.1	25	22.6	1	0	0	962.51	797	804
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	DFNVGDYIQAVLDR	99.7%	75.1	25	63	2	0	0	1624.80	257	270
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	DFSELEPDKFQNK	99.7%	53.8	25	51.7	2	0	0	1596.75	471	483
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	DYYFALAHTVR	99.7%	57.7	25	45.2	2	0	0	1355.67	51	61
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	EYAQNIWNVEPSDLK	99.7%	47	25	41.5	2	0	0	1805.87	820	834
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	EYYEALPELK	99.7%	44.1	25	42.8	2	0	0	1254.63	731	740
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	FSQFLETEYK	99.7%	65.6	25	60.7	2	0	0	1291.62	546	555
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	GIVGVENVAELK	99.7%	45.3	25	33.6	1	0	0	1227.69	18	29
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	GIVGVENVAELKK	99.7%	60	25	59.3	2	0	0	1355.79	18	30
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	HLEIIYEINQK	99.7%	65	25	54.5	2	0	0	1399.76	400	410
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	IDDVAALDK	99.7%	58.8	25	49.9	1	0	0	959.50	716	724
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	IFVDIEKLPWSK	99.7%	38.3	25	36	0	2	0	1474.83	353	364
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	IGEDYVKDLSQLTK	99.7%	61.5	25	49.1	1	0	0	1608.85	508	521
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	INPSSMFDVQVK	99.7%	69.6	25	52.1	2	0	0	1364.69	558	569
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	LHSFLGDDVFLR	99.7%	66.6	25	54.4	2	2	0	1418.74	522	533
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	LITSVADVVNNDPMVGSK	99.7%	103	25	96.3	4	0	0	1874.95	623	640
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	LVIDQIDNGFFSPK	99.7%	89	25	89	4	0	0	1592.83	741	754
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	MSLIEEEGSKR	99.7%	44.6	25	36.1	2	0	0	1294.63	429	439
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	NLAENISR	99.7%	51.7	25	30.4	2	0	0	916.48	271	278
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	TFAYTNHTVLPEALER	99.7%	42.9	25	33.3	0	2	0	1861.94	372	387
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	VFADYEAYVK	99.7%	54.5	25	51.3	2	0	0	1204.59	774	783
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	VIFLENYR	99.7%	53.7	25	43.2	3	0	0	1053.57	643	650
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	VIPATDLSEQISTAGTEASGTGNMK	99.7%	40.4	25	40.4	0	3	0	2478.20	657	681
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	VLYPNDNFFEGK	99.7%	68.2	25	67	2	0	0	1442.70	279	290
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	VSQLYMNPK	99.7%	62.1	25	52.7	3	0	0	1079.56	788	796

Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	YEYGIFNQK	98.9%	33.7	25	33.7	1	0	0	1161.56	162	170
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	28	32	59	0.06%	37.7%	YGNPWEK	95.1%	27.7	25	21	1	0	0	893.42	186	192
GMP synthase [glutamine-hydrolyzing]	GMPS	GUAA_HUMAN	76.7	100.0%	3	3	5	0.01%	5.9%	EPPTDVTPTFLTTGVLSTLR	99.7%	68.3	25	68.3	2	0	0	2145.14	570	589
GMP synthase [glutamine-hydrolyzing]	GMPS	GUAA_HUMAN	76.7	100.0%	3	3	5	0.01%	5.9%	ESQSVEEALKK	99.7%	41.1	25	32	1	0	0	1247.65	279	289
GMP synthase [glutamine-hydrolyzing]	GMPS	GUAA_HUMAN	76.7	100.0%	3	3	5	0.01%	5.9%	VVYIFGPPVK	99.3%	35.7	25	35.7	2	0	0	1118.66	560	569
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	5	5	7	0.01%	2.9%	FSCLLPDPR	99.3%	35.9	25	34.4	2	0	0	1104.55	683	691
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	5	5	7	0.01%	2.9%	GATPEGIFLR	99.7%	39.4	25	15.8	2	0	0	1060.58	907	916
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	5	5	7	0.01%	2.9%	LLEAFTER	99.7%	40.7	25	22.1	1	0	0	978.53	801	808
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	5	5	7	0.01%	2.9%	SEDTTGPITGLALTSVNK	99.7%	116	25	112	1	0	0	1803.93	74	91
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	5	5	7	0.01%	2.9%	SLEETIIQK	99.7%	40	25	31	1	0	0	1060.59	945	953
GPI transamidase component PIG-T	PIGT	PIGT_HUMAN	65.7	100.0%	4	4	6	0.01%	5.9%	AGLSVLLK	98.6%	32.9	25	8.95	1	0	0	800.52	199	206
GPI transamidase component PIG-T	PIGT	PIGT_HUMAN	65.7	100.0%	4	4	6	0.01%	5.9%	LYVHTLTITSK	99.7%	48.9	25	48.7	2	0	0	1275.73	395	405
GPI transamidase component PIG-T	PIGT	PIGT_HUMAN	65.7	100.0%	4	4	6	0.01%	5.9%	TFHIEEPR	99.1%	34.9	25	23.6	2	0	0	1028.52	550	557
GPI transamidase component PIG-T	PIGT	PIGT_HUMAN	65.7	100.0%	4	4	6	0.01%	5.9%	VSIQFER	99.7%	48.5	25	16.7	1	0	0	878.47	442	448
GPI-anchor transamidase	PIGK	GPI8_HUMAN	45.3	100.0%	3	3	5	0.01%	7.6%	HVANTLSVYR	99.7%	45.9	25	45.9	1	0	0	1159.62	61	70
GPI-anchor transamidase	PIGK	GPI8_HUMAN	45.3	100.0%	3	3	5	0.01%	7.6%	KVEITTETIK	99.7%	43	25	33.2	2	0	0	1161.67	309	318
GPI-anchor transamidase	PIGK	GPI8_HUMAN	45.3	100.0%	3	3	5	0.01%	7.6%	SLCVSTPGHR	99.4%	36.6	25	36.6	2	0	0	1113.55	278	287
Growth arrest and DNA damage-inducible proteins-interacting protein 1	GADD45GIP1	G45IP_HUMAN	25.4	99.8%	2	2	4	0.00%	11.7%	FQELLQDLEK	99.7%	48.2	25	21.1	2	0	0	1262.66	175	184
Growth arrest and DNA damage-inducible proteins-interacting protein 1	GADD45GIP1	G45IP_HUMAN	25.4	99.8%	2	2	4	0.00%	11.7%	LQAEAQELLGYQVDPR	99.7%	68.5	25	68.5	2	0	0	1829.94	156	171
GrpE protein homolog 1, mitochondrial	GRPEL1	GRPE1_HUMAN	24.3	100.0%	4	4	8	0.01%	21.2%	ALADTENLR	98.0%	31.4	25	23.6	2	0	0	1002.52	81	89
GrpE protein homolog 1, mitochondrial	GRPEL1	GRPE1_HUMAN	24.3	100.0%	4	4	8	0.01%	21.2%	DLLEVADVLEK	99.7%	74.2	25	60.8	2	0	0	1243.68	110	120
GrpE protein homolog 1, mitochondrial	GRPEL1	GRPE1_HUMAN	24.3	100.0%	4	4	8	0.01%	21.2%	NLYEGLVMTEVQIQK	99.7%	52.1	25	49	2	0	0	1764.92	139	153
GrpE protein homolog 1, mitochondrial	GRPEL1	GRPE1_HUMAN	24.3	100.0%	4	4	8	0.01%	21.2%	TLRPALVGVVK	99.7%	47	25	47	2	0	0	1152.75	205	215
GTP:AMP phosphotransferase AK3, mitochondrial	AK3	KAD3_HUMAN	25.6	100.0%	4	4	6	0.01%	18.5%	HLSSGDLLR	99.0%	34.2	25	24.7	1	0	0	997.54	35	43
GTP:AMP phosphotransferase AK3, mitochondrial	AK3	KAD3_HUMAN	25.6	100.0%	4	4	6	0.01%	18.5%	ITTHFELK	97.2%	29.9	25	15.6	1	0	0	988.55	27	34
GTP:AMP phosphotransferase AK3, mitochondrial	AK3	KAD3_HUMAN	25.6	100.0%	4	4	6	0.01%	18.5%	TLPQAEALDR	95.2%	27.8	25	21.8	2	0	0	1113.59	95	104
GTP:AMP phosphotransferase AK3, mitochondrial	AK3	KAD3_HUMAN	25.6	100.0%	4	4	6	0.01%	18.5%	TVGIDDLTGEPLIQR	99.7%	54.7	25	45.5	2	0	0	1626.87	147	161
GTPase Era, mitochondrial	ERAL1	ERAL1_HUMAN	48.3	100.0%	6	6	11	0.01%	18.8%	DPNTQSVGNPQR	99.7%	50.4	25	50.4	2	0	0	1312.62	285	296
GTPase Era, mitochondrial	ERAL1	ERAL1_HUMAN	48.3	100.0%	6	6	11	0.01%	18.8%	EIFMLSALSQEDVK	99.7%	68.7	25	60.5	2	0	0	1609.81	304	317
GTPase Era, mitochondrial	ERAL1	ERAL1_HUMAN	48.3	100.0%	6	6	11	0.01%	18.8%	ETQVILLDTPGIISPGK	99.7%	73.6	25	70.8	2	0	0	1781.01	160	176
GTPase Era, mitochondrial	ERAL1	ERAL1_HUMAN	48.3	100.0%	6	6	11	0.01%	18.8%	STLSNQLLGR	99.7%	60	25	13.1	2	0	0	1088.61	127	136
GTPase Era, mitochondrial	ERAL1	ERAL1_HUMAN	48.3	100.0%	6	6	11	0.01%	18.8%	TAVWEEGPGGELVIQQK	99.7%	77.7	25	65.5	2	0	0	1840.94	372	388
GTPase Era, mitochondrial	ERAL1	ERAL1_HUMAN	48.3	100.0%	6	6	11	0.01%	18.8%	YSQIPSVLVMNK	98.8%	33.3	25	32.4	1	0	0	1378.74	226	237
GTPase NRas	NRAS	RASN_HUMAN	21.2	100.0%	2	2	2	0.00%	12.2%	LVVVGAGGVGK	95.4%	28	25	28	1	0	0	955.59	6	16
GTPase NRas	NRAS	RASN_HUMAN	21.2	100.0%	2	2	2	0.00%	12.2%	QGVEDAFYTLVR	96.4%	29	25	29	1	0	0	1397.71	150	161
GTPase-activating protein and VPS9 domain-containing protein 1	GAPVD1	GAPD1_HUMAN	165.0	100.0%	2	2	5	0.01%	2.0%	AVETPPLSSVNLLEGLSR	99.7%	60.2	25	60.2	3	0	0	1882.03	387	404
GTPase-activating protein and VPS9 domain-containing protein 1	GAPVD1	GAPD1_HUMAN	165.0	100.0%	2	2	5	0.01%	2.0%	LIASSLVAGEK	99.7%	63.1	25	50	2	0	0	1087.64	109	119
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	8	9	29	0.03%	38.0%	FNVWDTAGQEK	96.3%	28.8	25	18.7	1	0	0	1294.61	61	71
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	8	9	29	0.03%	38.0%	GPIKFNVWDTAGQEK	99.5%	30.9	25	30.9	0	2	0	1689.86	57	71
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	8	9	29	0.03%	38.0%	KYVATLGVEVHPLVFHTNR	99.7%	65.7	25	58.2	0	1	0	2180.20	38	56
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	8	9	29	0.03%	38.0%	LVLVGDGGTGK	99.7%	41.3	25	10.9	6	0	0	1015.58	13	23
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	8	9	29	0.03%	38.0%	NLQYYDISAK	99.7%	46	25	46	9	0	0	1214.61	143	152
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	8	9	29	0.03%	38.0%	SNYNFEKPFLWLAR	99.7%	52.4	25	51.8	2	4	0	1784.91	153	166
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	8	9	29	0.03%	38.0%	VCENIPIVLCGNK	99.7%	67.6	25	65	2	0	0	1515.77	111	123
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	8	9	29	0.03%	38.0%	YVATLGVEVHPLVFHTNR	99.7%	35.1	25	35.1	0	2	0	2052.10	39	56
GTP-binding protein 10	GTPBP10	GTPBA_HUMAN	42.9	99.9%	2	2	4	0.00%	5.2%	LLTNFLPLK	99.0%	34.2	25	23.9	2	0	0	1058.66	127	135
GTP-binding protein 10	GTPBP10	GTPBA_HUMAN	42.9	99.9%	2	2	4	0.00%	5.2%	TAFETIILLTK	99.7%	50.9	25	50.9	2	0	0	1249.74	249	259
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	6	9	17	0.02%	33.7%	ALAESWNAAFLESSAK	99.7%	80.4	25	80.4	2	0	0	1694.84	136	151
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	6	9	17	0.02%	33.7%	ENQTAVDVFR	99.7%	74.9	25	60.1	2	0	0	1178.58	152	161
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	6	9	17	0.02%	33.7%	IAILGYR	99.7%	40.6	25	37.7	2	0	0	805.49	9	15
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	6	9	17	0.02%	33.7%	IILEAEKMDGAASQGK	99.7%	78	25	78	4	2	0	1660.86	163	178

GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	6	9	17	0.02%	33.7%	KIAILGYR	99.7%	39.2	25	21.2	2	0	0	933.59	8	15
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	6	9	17	0.02%	33.7%	VQIPIMLVGNKK	98.9%	33.6	25	30.6	2	1	0	1355.81	110	121
GTP-binding protein SAR1a	SAR1A	SAR1A_HUMAN	22.4	99.8%	2	2	3	0.00%	9.6%	LVFLGLDNAGK	99.7%	60.3	25	59.2	2	0	0	1146.65	28	38
GTP-binding protein SAR1a	SAR1A	SAR1A_HUMAN	22.4	99.8%	2	2	3	0.00%	9.6%	QGYGEGFR	95.3%	27.9	25	19.9	1	0	0	913.42	184	191
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	GBB2_HUMAN	37.3	100.0%	3	3	5	0.01%	8.8%	LIIWDSYTTNK	99.7%	61.5	25	56	2	0	0	1353.71	79	89
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	GBB2_HUMAN	37.3	100.0%	3	3	5	0.01%	8.8%	TFVSGACDASIK	99.7%	65.6	25	62	2	0	0	1255.60	198	209
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	GBB2_HUMAN	37.3	100.0%	3	3	5	0.01%	8.8%	VHAIPLR	95.5%	28.1	25	28.1	1	0	0	805.50	90	96
Guanine nucleotide-binding protein G(k) subunit alpha	GNAI3	GNAI3_HUMAN	40.5	99.8%	2	2	3	0.00%	10.7%	ISQSNYIPTQQDVLR	99.5%	37.8	25	32.7	1	0	0	1761.91	162	176
Guanine nucleotide-binding protein G(k) subunit alpha	GNAI3	GNAI3_HUMAN	40.5	99.8%	2	2	3	0.00%	10.7%	LLLLGAGESGK	99.7%	65.9	25	0	6	0	0	1057.63	36	46
Guanine nucleotide-binding protein G(k) subunit alpha	GNAI3	GNAI3_HUMAN	40.5	99.8%	2	2	3	0.00%	10.7%	TTGIVETHFTFK	99.7%	51.1	25	34.8	2	0	0	1380.72	181	192
Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	GNAS	GNAS1_HUMAN	45.7	100.0%	3	3	5	0.01%	4.5%	LLLLGAGESGK	99.7%	65.9	25	0	6	0	0	1057.63	43	53
Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	GNAS	GNAS1_HUMAN	45.7	100.0%	3	3	5	0.01%	4.5%	TISVILFLNK	99.7%	62.1	25	57.7	2	0	0	1147.71	284	293
Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	GNAS	GNAS1_HUMAN	45.7	100.0%	3	3	5	0.01%	4.5%	VLTSGIFETK	99.7%	64.9	25	58.6	2	0	0	1094.61	202	211
Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	GNAS	GNAS1_HUMAN	45.7	100.0%	3	3	5	0.01%	4.5%	YTTPEDATPEPGEDPR	99.7%	50.2	25	50.2	1	0	0	1774.78	318	333
Guanine nucleotide-binding protein subunit alpha-11	GNA11	GNA11_HUMAN	42.1	99.8%	2	2	4	0.00%	7.2%	IATLGYLPTQQDVLR	99.7%	58.5	25	55.2	2	0	0	1687.94	167	181
Guanine nucleotide-binding protein subunit alpha-11	GNA11	GNA11_HUMAN	42.1	99.8%	2	2	4	0.00%	7.2%	LLLLGTGESGK	99.7%	59.3	25	33.1	2	0	0	1087.64	42	52
Guanine nucleotide-binding protein subunit alpha-13	GNA13	GNA13_HUMAN	44.1	100.0%	3	3	8	0.01%	8.0%	APMAAQGMVETR	99.7%	39.3	25	35.7	1	0	0	1293.59	129	140
Guanine nucleotide-binding protein subunit alpha-13	GNA13	GNA13_HUMAN	44.1	100.0%	3	3	8	0.01%	8.0%	FLVECFR	98.8%	33.4	25	26.6	1	0	0	970.48	325	331
Guanine nucleotide-binding protein subunit alpha-13	GNA13	GNA13_HUMAN	44.1	100.0%	3	3	8	0.01%	8.0%	ILLLGAGESGK	99.7%	65.9	25	0	6	0	0	1057.63	51	61
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	19	78	0.08%	47.6%	DETNYGIPQR	99.7%	69.3	25	59.4	5	0	0	1192.56	48	57
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	19	78	0.08%	47.6%	DGQAMLWDLNEGK	99.7%	97.8	25	90.1	8	0	0	1492.67	213	225
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	19	78	0.08%	47.6%	DKTIIMWK	99.7%	39.8	25	27.3	3	0	0	1034.57	37	44
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	19	78	0.08%	47.6%	DVLSVAFSSDNR	99.7%	92.8	25	85.5	10	0	0	1309.64	107	118
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	19	78	0.08%	47.6%	FSPNSSNPIIVSCGWDK	99.7%	94	25	82.5	4	0	0	1907.90	156	172
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	19	78	0.08%	47.6%	IIVDELKQEVISTSSK	99.7%	90.8	25	90.8	5	2	0	1789.00	265	280
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	19	78	0.08%	47.6%	IWDLEGK	99.2%	35.4	25	20	2	0	0	860.45	258	264
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	19	78	0.08%	47.6%	LTRDETNYGIPQR	99.7%	53.4	25	51.4	4	2	0	1562.79	45	57
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	19	78	0.08%	47.6%	LWDLTTGTTTR	99.7%	79.3	25	78	4	0	0	1264.65	89	99
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	19	78	0.08%	47.6%	LWNTLGVCK	99.7%	59.7	25	54.6	6	0	0	1090.57	131	139
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	19	78	0.08%	47.6%	VWNLANCK	99.7%	45.7	25	39.7	3	0	0	1004.50	176	183
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	19	78	0.08%	47.6%	VWQVTIGTR	99.7%	75.8	25	69.2	7	0	0	1059.59	309	317
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	19	78	0.08%	47.6%	YTVQDESHSEWVSCVR	99.7%	89	25	89	4	7	0	1981.87	140	155
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	19	78	0.08%	47.6%	YWLCAATGPSIK	99.7%	74	25	67.3	2	0	0	1366.68	246	257
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	7	7	11	0.01%	14.9%	CPQVEEAIVQSGQK	99.7%	68.8	25	67.3	1	0	0	1572.77	158	171
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	7	7	11	0.01%	14.9%	ELPTVVFR	99.2%	35.3	25	35.3	2	0	0	960.55	198	205
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	7	7	11	0.01%	14.9%	GGIPNVEGAAK	96.7%	29.3	25	24.5	1	0	0	1012.54	378	388
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	7	7	11	0.01%	14.9%	KDPGVPNSAPFK	99.7%	47.4	25	42.5	2	0	0	1256.66	46	57
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	7	7	11	0.01%	14.9%	LLGGFQETCSK	99.7%	47.7	25	47.7	2	0	0	1239.60	243	253
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	7	7	11	0.01%	14.9%	VGVIGFPNVGK	99.7%	55.3	25	42.5	2	0	0	1086.63	257	267
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	7	7	11	0.01%	14.9%	VIEASDVVLEVLDAR	99.7%	91.6	25	76.1	1	0	0	1627.89	137	151
H/ACA ribonucleoprotein complex subunit 1	GAR1	GAR1_HUMAN	22.3	100.0%	2	2	4	0.00%	7.4%	FYIDPYK	99.7%	48.4	25	44.7	2	0	0	945.47	144	150
H/ACA ribonucleoprotein complex subunit 1	GAR1	GAR1_HUMAN	22.3	100.0%	2	2	4	0.00%	7.4%	VDEIFGQLR	99.7%	60.9	25	47.8	2	0	0	1076.57	113	121
H/ACA ribonucleoprotein complex subunit 2	NHP2	NHP2_HUMAN	17.2	99.8%	2	3	6	0.01%	19.0%	NLPYVYIPSK	99.4%	36.9	25	29.3	2	0	0	1193.66	102	111
H/ACA ribonucleoprotein complex subunit 2	NHP2	NHP2_HUMAN	17.2	99.8%	2	3	6	0.01%	19.0%	TYQELLVNQNPIAQPLASR	99.7%	87.1	25	87.1	2	2	0	2155.15	23	41
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	7	7	11	0.01%	13.4%	APQVVAEAAK	99.7%	42.9	25	41.3	2	0	0	983.55	434	443
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	7	7	11	0.01%	13.4%	DSAVNAICYGAK	99.7%	53.4	25	47.2	2	0	0	1268.59	303	314
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	7	7	11	0.01%	13.4%	EIGDYIR	97.9%	31.1	25	22.2	1	0	0	865.44	82	88
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	7	7	11	0.01%	13.4%	EVVAEVVK	98.7%	33	25	23.1	2	0	0	872.51	426	433
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	7	7	11	0.01%	13.4%	IMLPGVLR	98.9%	33.7	25	19.4	1	0	0	914.55	315	322
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	7	7	11	0.01%	13.4%	LHNAIEGGTQLSR	99.7%	75	25	75	2	0	0	1395.73	159	171
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	7	7	11	0.01%	13.4%	QEYVDYSESAK	98.6%	32.9	25	32.9	1	0	0	1318.58	414	424

HCLS1-associated protein X-1	HAX1	HAX1_HUMAN	31.6	99.9%	2	2	4	0.00%	7.2%	GFFGFPGPR	97.6%	30.5	25	24.2	2	0	0	981.49	9	17
HCLS1-associated protein X-1	HAX1	HAX1_HUMAN	31.6	99.9%	2	2	4	0.00%	7.2%	IFGGVLESDAR	99.7%	78.3	25	59.2	2	0	0	1163.61	140	150
HEAT repeat-containing protein 1	HEATR1	HEAT1_HUMAN	242.4	100.0%	3	3	4	0.00%	1.7%	LDDTYSFQVINK	99.7%	44.1	25	43.3	1	0	0	1442.72	1337	1348
HEAT repeat-containing protein 1	HEATR1	HEAT1_HUMAN	242.4	100.0%	3	3	4	0.00%	1.7%	LVPDLLAIVQR	99.7%	46.6	25	44.6	2	0	0	1236.77	1644	1654
HEAT repeat-containing protein 1	HEATR1	HEAT1_HUMAN	242.4	100.0%	3	3	4	0.00%	1.7%	VSLLNEQFLPLIR	99.7%	54.2	25	54.2	1	0	0	1541.91	418	430
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	18	0.02%	17.7%	AIQDAILEVLK	99.7%	76.6	25	69.1	2	0	0	1212.72	804	814
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	18	0.02%	17.7%	ATDTINSQGQFPSYLETVTK	99.7%	71.3	25	71.3	1	0	0	2200.08	636	655
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	18	0.02%	17.7%	CSLLDPFAAVR	99.7%	42.9	25	36.2	2	0	0	1248.64	173	183
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	18	0.02%	17.7%	EGSGLFPDLLVR	99.7%	58.7	25	52.9	2	0	0	1302.71	815	826
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	18	0.02%	17.7%	LFDDVPQVR	99.7%	57.6	25	48.9	2	0	0	1088.57	254	262
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	18	0.02%	17.7%	LIPLLLSSLNDEVPEVR	99.7%	76.2	25	71.7	1	0	0	1907.09	286	302
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	18	0.02%	17.7%	LLPGLEADSKPGR	99.7%	39.2	25	35.4	1	0	0	1352.75	34	46
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	18	0.02%	17.7%	MAAASTLVTWLQCVK	99.7%	58.7	25	56.2	1	0	0	1678.87	761	775
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	18	0.02%	17.7%	SAELVGTFVSPEVFLK	99.7%	94.6	25	94.6	3	0	0	1722.93	423	438
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	18	0.02%	17.7%	SVDDVLSHFAQR	99.7%	70.5	25	62	1	0	0	1373.68	242	253
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	18	0.02%	17.7%	TPSASGLLVLASAMR	99.7%	91.4	25	91.4	2	0	0	1473.81	447	461
HEAT repeat-containing protein 6	HEATR6	HEAT6_HUMAN	128.8	100.0%	5	6	8	0.01%	5.6%	ALGVYVLFPCLR	99.0%	34.2	25	34.2	1	0	0	1407.78	837	848
HEAT repeat-containing protein 6	HEATR6	HEAT6_HUMAN	128.8	100.0%	5	6	8	0.01%	5.6%	IWNALVTALQK	99.7%	67.4	25	64.8	1	0	0	1256.74	1042	1052
HEAT repeat-containing protein 6	HEATR6	HEAT6_HUMAN	128.8	100.0%	5	6	8	0.01%	5.6%	LEALQVLTLLAR	99.7%	99.7	25	80.2	2	0	0	1339.83	689	700
HEAT repeat-containing protein 6	HEATR6	HEAT6_HUMAN	128.8	100.0%	5	6	8	0.01%	5.6%	SGAEGDDTGAPHSPQER	99.5%	31.3	25	28.5	0	1	0	1710.73	1112	1128
HEAT repeat-containing protein 6	HEATR6	HEAT6_HUMAN	128.8	100.0%	5	6	8	0.01%	5.6%	YLPELLGNTGLLMK	99.7%	59	25	58	3	0	0	1577.86	157	170
Heat shock 70 kDa protein 12A	HSPA12A	HS12A_HUMAN	75.0	100.0%	3	3	4	0.00%	5.8%	ETAPTSAYSSPAR	99.7%	63.4	25	59.8	1	0	0	1337.63	14	26
Heat shock 70 kDa protein 12A	HSPA12A	HS12A_HUMAN	75.0	100.0%	3	3	4	0.00%	5.8%	GAVLFGLDPAVIK	99.7%	74.7	25	70	2	0	0	1299.77	517	529
Heat shock 70 kDa protein 12A	HSPA12A	HS12A_HUMAN	75.0	100.0%	3	3	4	0.00%	5.8%	IIIPQDVGLTILK	95.0%	27.6	25	26.1	1	0	0	1422.89	504	516
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	AAAIGIDLGTTYSCVGVFQHGK	99.7%	75.5	25	75.5	0	2	0	2265.13	4	25
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	AFYPEEISSMVLTK	99.7%	99.8	25	93.9	6	0	0	1630.80	113	126
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	AQIHDLVLVGGSTR	99.7%	97.9	25	89.7	2	2	0	1465.81	329	342
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	ARFEELCSDLFR	99.7%	60.8	25	55.9	2	2	0	1542.74	300	311
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	ATAGDTHLGGEDFDNR	99.7%	71	25	71	2	2	0	1675.73	221	236
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	DAGVIAGLNVLR	99.7%	98.9	25	88.8	5	0	0	1197.70	160	171
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	DNNLLGR	99.7%	45	25	36.1	2	0	0	801.42	452	458
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	FEELCSDLFR	99.7%	47.9	25	47.9	2	0	0	1315.60	302	311
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	FGDPVVQSDMK	99.7%	46.8	25	46.8	2	0	0	1222.58	78	88
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	GGSGSGPTIEEVD	99.7%	43.2	25	43.2	2	0	0	1204.53	629	641
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	HWPFQVINDGDKPK	99.7%	51.4	25	51.4	0	2	0	1680.85	89	102
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	IINEPTAAAIAYGLDR	99.7%	98.4	25	84.9	4	2	0	1687.90	172	187
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	ITITNDKGR	99.7%	54.8	25	43	2	0	0	1017.57	501	509
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	KFGDPVVQSDMK	99.7%	41.3	25	41.3	2	0	0	1350.67	77	88
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	LLQDFFNGR	99.7%	58.2	25	41.1	2	0	0	1109.57	349	357
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	LSKEEIER	99.7%	47.6	25	24.6	2	0	0	1003.54	510	517
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	LVNHFVEEFK	97.9%	31	25	31	1	0	0	1261.66	237	246
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	LVNHFVEEFKR	99.7%	42.4	25	41.2	0	2	0	1417.76	237	247
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	MVQEAEKYK	98.7%	33.2	25	28	4	0	0	1125.56	518	526
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	NALESYAFNMK	99.7%	85.7	25	85.7	6	0	0	1303.60	540	550
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	NQVALNPQNTVFDAK	99.7%	106	25	102	3	0	0	1658.85	57	71
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	NQVALNPQNTVFDAKR	99.3%	29.7	25	29.5	0	1	0	1814.95	57	72
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	SAVEDEGLK	99.1%	34.9	25	31.6	1	0	0	947.47	551	559
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	TTPSYVAFTDTER	99.7%	78.1	25	72.8	7	0	0	1487.70	37	49
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	VEIIANDQGNR	99.7%	58.8	25	0	2	0	0	1228.63	26	36
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	VQVSYKGETK	99.7%	51.8	25	44.1	2	0	0	1138.61	103	112
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	23	29	67	0.07%	42.9%	YKAEDEVQR	99.7%	49.5	25	36.4	4	0	0	1137.55	525	533

Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	13	0.01%	13.6%	AFSDPFVEAEK	99.7%	43.7	25	35.7	2	0	0	1239.59	74	84
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	13	0.01%	13.6%	AGGIETIANEYSDR	99.7%	59.9	25	59.9	2	0	0	1495.70	20	33
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	13	0.01%	13.6%	EFSITDVVPYPISLR	99.7%	85.7	25	85.7	2	0	0	1735.93	391	405
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	13	0.01%	13.6%	FQESEERPK	99.7%	42.1	25	28.7	2	0	0	1149.55	689	697
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	13	0.01%	13.6%	GCALQCAILSPAFK	99.7%	95.1	25	82.4	2	0	0	1535.77	375	388
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	13	0.01%	13.6%	MIMQDKLEK	96.8%	29.4	25	21.3	1	0	0	1135.59	604	612
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	13	0.01%	13.6%	NAVEEYVYEMR	99.7%	51.7	25	51.7	1	0	0	1402.63	619	629
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	13	0.01%	13.6%	SNLAYDIVQLPTGLTGIK	99.7%	96.4	25	96.4	2	0	0	1903.05	85	102
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	13	0.01%	13.6%	VLATAFDTTLGGR	99.7%	110	25	97.6	2	0	0	1321.71	222	234
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	ARFEELNADLFR	99.7%	45.6	25	31.9	0	2	0	1480.75	300	311
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	DAGTIAGLNVLR	99.7%	90.4	25	78.4	4	0	0	1199.67	160	171
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	EIAEAYLGK	99.7%	43.2	25	35.6	2	0	0	993.53	129	137
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	FDDAVVQSDMK	99.7%	43.6	25	38.2	1	0	0	1254.57	78	88
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	FEELNADLFR	99.7%	62.1	25	54.7	2	0	0	1253.62	302	311
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	GPAVGIDLGTTYSCVGVFQHGK	99.7%	61.1	25	61.1	0	2	0	2263.12	4	25
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	HWPFMVVNDAGRPK	99.7%	46.7	25	46.7	0	2	0	1653.83	89	102
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	IINEPTAAAIAYGLDK	99.7%	130	25	129	2	0	0	1659.90	172	187
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	IINEPTAAAIAYGLDKK	99.7%	102	25	102	2	2	0	1787.99	172	188
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	ITITNDKGR	99.7%	54.8	25	43	2	0	0	1017.57	501	509
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	LDKSQIHDIVLVGGSTR	99.7%	51	25	51	0	2	0	1838.01	326	342
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	LLQDFFNGK	99.7%	40.5	25	24.8	2	0	0	1081.57	349	357
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	LSKEDIER	99.7%	61.9	25	13.1	2	0	0	989.53	510	517
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	MKEIAEAYLGK	99.7%	61.4	25	50.2	4	1	0	1268.66	127	137
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	MVNHFIAEFK	99.7%	59.5	25	44.7	4	2	0	1235.62	237	246
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	MVNHFIAEFKR	99.7%	35.4	25	33.8	0	2	0	1391.73	237	247
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	MVQEAEKYK	98.7%	33.2	25	28	4	0	0	1125.56	518	526
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	NQVAMNPTNTVFDAK	99.7%	97.1	25	97.1	4	0	0	1649.80	57	71
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	NSLESYAFNMK	99.7%	48.3	25	48.3	2	0	0	1319.59	540	550
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	RFDDAVVQSDMK	99.7%	66.6	25	63.6	2	0	0	1410.67	77	88
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	SFYPEEVSSMVLTK	99.7%	97.5	25	97.5	4	0	0	1616.79	113	126
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	SINPDEAVAYGAAVQAAILSGDK	99.7%	100	25	100	2	0	0	2260.15	362	384
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	SQIHDIVLVGGSTR	99.7%	93.3	25	88.3	2	2	0	1481.81	329	342
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	STAGDTHLGGEDFDNR	99.7%	77.4	25	76.7	2	2	0	1691.73	221	236
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	TTPSYVAFTDTER	99.7%	78.1	25	72.8	7	0	0	1487.70	37	49
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	TVTNAVVTVPAYFNDSQR	99.7%	88.2	25	84.6	2	2	0	1982.00	138	155
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	VCNPIITK	99.4%	36.5	25	16.3	2	0	0	944.52	602	609
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	VEIIANDQGNR	99.7%	58.8	25	0	2	0	0	1228.63	26	36
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	29	40	87	0.09%	46.7%	VQVEYKGETK	99.7%	51.7	25	44.8	4	0	0	1180.62	103	112
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	14	14	29	0.03%	18.6%	DISTTLNADEAVAR	99.7%	84.1	25	76.1	2	0	0	1475.73	361	374
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	14	14	29	0.03%	18.6%	DLLNMYIETEGK	99.7%	49.1	25	43.9	1	0	0	1425.69	609	620
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	14	14	29	0.03%	18.6%	EKENLSYDLVPLK	99.7%	50.3	25	37.9	1	0	0	1547.83	83	95
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	14	14	29	0.03%	18.6%	FQEAEERPK	99.7%	49.5	25	34.7	2	0	0	1133.56	706	714
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	14	14	29	0.03%	18.6%	FVVQNVSAQK	99.7%	40.8	25	40.8	1	0	0	1119.62	462	471
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	14	14	29	0.03%	18.6%	GCALQCAILSPAFK	99.7%	95.1	25	82.4	2	0	0	1535.77	375	388
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	14	14	29	0.03%	18.6%	LKETAENSLK	99.7%	43.9	25	19.5	2	0	0	1132.62	125	134
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	14	14	29	0.03%	18.6%	MFEELGQR	97.7%	30.7	25	25.3	1	0	0	1009.48	715	722
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	14	14	29	0.03%	18.6%	MIMQDKLEK	96.8%	29.4	25	21.3	1	0	0	1135.59	621	629
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	14	14	29	0.03%	18.6%	NAVEEYVYEFR	99.7%	56.1	25	51.9	2	0	0	1418.66	636	646
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	14	14	29	0.03%	18.6%	SLDQDPVVR	99.7%	41	25	30.7	2	0	0	1028.54	773	781
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	14	14	29	0.03%	18.6%	SQFEELCAELLQK	99.7%	99.2	25	90.7	2	0	0	1594.78	304	316
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	14	14	29	0.03%	18.6%	SVLDAAQIVGLNCLR	99.7%	108	25	104	3	0	0	1628.88	155	169

Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	14	14	29	0.03%	18.6%	VLGTAFDPFLGGK	99.7%	70.9	25	59.4	7	0	0	1321.72	222	234
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	16	17	29	0.03%	28.8%	AFLDALQNQAEASSK	99.7%	126	25	125	2	0	0	1592.79	182	196
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	16	17	29	0.03%	28.8%	AQLLQPTLEINPR	99.7%	82.2	25	80.5	2	0	0	1492.85	635	647
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	16	17	29	0.03%	28.8%	ELGSSVALYSR	99.7%	66.2	25	65.4	2	0	0	1181.62	358	368
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	16	17	29	0.03%	28.8%	ELISNASDALEK	99.7%	92.3	25	80.4	2	0	0	1289.66	115	126
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	16	17	29	0.03%	28.8%	ELLQESALIR	99.7%	75.9	25	61.5	2	0	0	1171.67	403	412
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	16	17	29	0.03%	28.8%	FFEDYGLFMR	99.7%	64	25	61.7	4	0	0	1324.60	440	449
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	16	17	29	0.03%	28.8%	GVVDSEDIPLNLSR	99.7%	129	25	0	15	0	0	1513.79	389	402
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	16	17	29	0.03%	28.8%	LNELLVK	99.7%	45.3	25	21.9	2	0	0	828.52	693	699
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	16	17	29	0.03%	28.8%	LRDVLQQR	98.4%	32.2	25	19.9	1	0	0	1027.60	414	421
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	16	17	29	0.03%	28.8%	LVSDGQALPEMEIHLQTNAEK	99.7%	42	25	42	0	1	0	2339.16	131	151
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	16	17	29	0.03%	28.8%	MNTLQAIWMMDPK	99.7%	74.6	25	74.6	2	0	0	1578.75	292	304
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	16	17	29	0.03%	28.8%	NIYYLCAPNR	99.7%	42.7	25	37.1	2	0	0	1283.62	496	505
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	16	17	29	0.03%	28.8%	SDCKEFSSEAR	99.7%	42.4	25	42.4	1	0	0	1315.56	259	269
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	16	17	29	0.03%	28.8%	TDAPLNIR	99.7%	40.2	25	30.2	2	0	0	899.49	333	340
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	16	17	29	0.03%	28.8%	YESSALPSGQLTSLSEYASR	99.7%	111	25	107	2	0	0	2146.03	470	489
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	16	17	29	0.03%	28.8%	YSNFVSFPLYLNGR	99.5%	37.3	25	37.3	1	0	0	1676.84	277	290
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	16	17	29	0.03%	28.8%	YTLHYK	96.7%	29.2	25	21.8	1	0	0	824.43	327	332
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	ADLINNLGTIAK	99.7%	78.3	25	66.4	21	0	0	1242.71	101	112
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	ALLFVPR	99.5%	37	25	0	3	0	0	815.51	339	345
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	APFDLFENR	99.7%	54.1	25	50.3	2	0	0	1108.54	347	355
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	DNSTMGYMAAK	99.7%	60.5	25	54.1	4	0	0	1188.50	621	631
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	DQVANSAFVER	99.7%	73.5	25	65.4	6	0	0	1235.60	500	510
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	EDQTEYLEER	99.7%	62.6	25	57.5	4	0	0	1311.57	192	201
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	EDQTEYLEERR	94.6%	22.1	25	22.1	0	1	0	1467.67	192	202
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	EGLELPEDEEEK	96.8%	29.4	25	28.6	2	0	0	1416.64	547	558
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	EGLELPEDEEEKK	99.7%	51.8	25	49.4	2	0	0	1544.73	547	559
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	EKYIDQEELNK	99.7%	63.2	25	51	2	0	0	1408.70	282	292
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	ELHINLIPNK	99.1%	34.6	25	25	1	0	0	1190.69	75	84
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	ELHINLIPNKQDR	99.4%	30.3	25	29.9	2	2	0	1589.88	75	87
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	ELISNSSDALDK	99.7%	83.3	25	65.5	2	0	0	1291.64	47	58
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	ELISNSSDALDKIR	99.7%	86.3	25	77.2	2	1	0	1560.82	47	60
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	FENLCK	97.8%	30.8	25	21.3	3	0	0	810.38	568	573
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	FYEQFSK	99.7%	50.5	25	26.6	4	0	0	948.45	437	443
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	GVVDSEDLPLNISR	99.7%	129	25	0	15	0	0	1513.79	387	400
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	HFSVEGQLEFR	99.7%	73	25	70.6	8	4	0	1348.66	328	338
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	HIYYITGETK	99.7%	48.2	25	46.4	2	0	0	1224.63	490	499
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	HLEINPDHSIIETLR	99.7%	72.5	25	70.9	2	2	0	1786.94	633	647
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	HNDDEQYAWESSAGGSFTVR	99.7%	55.9	25	55.9	0	3	0	2255.96	154	173
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	HSQFIGYPITLFVEK	99.7%	62.7	25	62.7	2	0	0	1778.95	210	224
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	IMKDILEK	99.4%	36.5	25	6.22	1	0	0	989.57	574	581
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	IRYESLTDPSK	99.7%	47.5	25	44.6	2	2	0	1308.68	59	69
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	LGIHEDSQNR	99.7%	39.7	25	32.7	3	0	0	1168.57	447	456
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	LVTSPCCIVTSTYGWTANMER	99.7%	98.2	25	98.2	5	0	0	2462.12	592	612
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	NPDDITNEEYGEFYK	99.7%	98.8	25	91.5	3	0	0	1833.78	300	314
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	RAPFDLFENR	99.7%	47.2	25	39	2	0	0	1264.64	346	355
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	SLTNDWEDHLAVK	99.7%	88	25	79.9	6	3	0	1527.74	315	327
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	TDTGEPMGR	99.5%	37.8	25	37.8	2	0	0	963.42	174	182
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	TLTIVDTGIGMTK	99.7%	118	25	0	27	0	0	1349.73	88	100
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	VILHLKEDQTEYLEER	99.7%	58	25	58	3	6	0	2015.04	186	201
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	YESLTDPSK	99.7%	55.2	25	49.5	4	0	0	1039.49	61	69

Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	YESLTDPSKLDSGK	99.7%	72.2	25	57.5	4	1	0	1539.75	61	74
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	YIDQEELNK	99.7%	60.5	25	40.3	15	0	0	1151.56	284	292
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	YYTSASGDEMVSLK	99.7%	85.8	25	84.3	4	0	0	1550.70	465	478
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	26	59	0.06%	46.3%	YYTSASGDEMVSLKDYCTR	99.7%	41.2	25	41.2	0	2	0	2245.97	465	483
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	ADLINNLGTIAK	99.7%	78.3	25	66.4	21	0	0	1242.71	96	107
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	AKFENLCK	97.9%	31	25	26.9	2	0	0	1009.51	558	565
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	ALLFIPR	99.7%	39.3	25	16	8	0	0	829.53	331	337
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	APFDLFENK	99.7%	45	25	40.8	4	0	0	1080.54	339	347
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	APFDLFENKK	99.7%	46.9	25	40.1	2	0	0	1208.63	339	348
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	CLELFSELAEDKENYK	99.7%	35.3	25	35.3	0	2	0	1987.93	412	427
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	DNSTMGYMMAK	99.7%	84.4	25	80.3	13	0	0	1248.51	613	623
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	EDQTEYLEER	99.7%	62.6	25	57.5	4	0	0	1311.57	187	196
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	EDQTEYLEERR	94.6%	22.1	25	22.1	0	1	0	1467.67	187	197
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	EGLELPEDEEEK	96.8%	29.4	25	28.6	2	0	0	1416.64	539	550
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	EGLELPEDEEEKK	99.7%	51.8	25	49.4	2	0	0	1544.73	539	551
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	EKYIDQEELNK	99.7%	63.2	25	51	2	0	0	1408.70	274	284
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	ELISNASDALDK	99.7%	71.1	25	53.4	7	0	0	1275.64	42	53
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	ELISNASDALDKIR	99.7%	92.6	25	73.4	10	2	0	1544.83	42	55
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	ELKIDIIPNPQER	99.7%	47.1	25	41.9	4	0	0	1564.87	70	82
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	EQVANSAFVER	99.7%	71.4	25	63.1	13	0	0	1249.62	492	502
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	FENLCK	97.8%	30.8	25	21.3	3	0	0	810.38	560	565
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	FYEAFSK	99.3%	35.6	25	30.5	4	0	0	891.42	429	435
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	GFEVVYMTEPIDEYCVQQLK	99.7%	103	25	50.8	7	2	0	2464.14	507	526
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	GVVDSEDLPLNISR	99.7%	129	25	0	15	0	0	1513.79	379	392
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	HFSVEGQLEFR	99.7%	73	25	70.6	8	4	0	1348.66	320	330
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	HLEINPDHPIVETLR	99.7%	86.4	25	80.2	2	4	0	1782.95	625	639
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	HNDDEQYAWESSAGGSFTVR	99.7%	55.9	25	55.9	0	3	0	2255.96	149	168
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	HSQFIGYPITLYLEK	99.7%	47.3	25	0	4	3	0	1808.96	205	219
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	IDIIPNPQER	99.7%	39.8	25	30.7	4	0	0	1194.65	73	82
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	IRYESLTDPSK	99.7%	47.5	25	44.6	2	2	0	1308.68	54	64
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	KFYEAFSK	99.6%	38.4	25	30	2	0	0	1019.52	428	435
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	LGIHEDSTNR	99.7%	51.6	25	47.5	6	0	0	1141.56	439	448
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	LGIHEDSTNRR	99.7%	46.9	25	45.9	0	3	0	1297.66	439	449
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	LVSSPCCIVTSTYGWTANMER	99.7%	106	25	106	6	4	0	2448.10	584	604
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	NPDDITQEEYGEFYK	99.7%	95.5	25	95.5	10	0	0	1847.80	292	306
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	RAPFDLFENK	99.7%	49.6	25	39.2	5	0	0	1236.64	338	347
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	RLSELLR	99.7%	46	25	14.8	4	0	0	886.55	450	456
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	SIYYITGESK	99.7%	73.3	25	69.4	10	0	0	1160.58	482	491
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	SLTNDWEDHLAVK	99.7%	88	25	79.9	6	3	0	1527.74	307	319
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	TLTLVDTGIGMTK	99.7%	118	25	0	27	0	0	1349.73	83	95
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	VFIMDSCDELIPEYLNFIR	99.7%	67.6	25	67.6	1	0	0	2390.14	360	378
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	VILHLKEDQTEYLEER	99.7%	58	25	58	3	6	0	2015.04	181	196
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	YESLTDPSK	99.7%	55.2	25	49.5	4	0	0	1039.49	56	64
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	YESLTDPSKLDSGK	99.7%	72.2	25	57.5	4	1	0	1539.75	56	69
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	YHTSQSGDEMTSLSEYVSR	99.7%	109	25	109	5	9	0	2176.95	457	475
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	60	300	0.31%	53.7%	YIDQEELNK	99.7%	60.5	25	40.3	15	0	0	1151.56	276	284
Helicase SKI2W	SKIV2L	SKIV2_HUMAN	137.8	100.0%	2	2	3	0.00%	2.0%	TQGELFLLLDSR	99.7%	54.2	25	50.7	1	0	0	1391.75	499	510
Helicase SKI2W	SKIV2L	SKIV2_HUMAN	137.8	100.0%	2	2	3	0.00%	2.0%	TVVAEYAIALAQK	99.7%	69.6	25	65.3	2	0	0	1376.78	339	351
Helicase-like transcription factor	HLTF	HLTF_HUMAN	113.9	100.0%	2	2	3	0.00%	1.8%	ASGFVFTR	99.4%	36.4	25	30	1	0	0	884.46	873	880
Helicase-like transcription factor	HLTF	HLTF_HUMAN	113.9	100.0%	2	2	3	0.00%	1.8%	VILDEGHAIR	99.7%	56.3	25	49.4	2	0	0	1122.63	554	563
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	5	5	10	0.01%	10.0%	GQLEQITGK	95.8%	28.4	25	6.51	1	0	0	973.53	312	320

Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	5	5	10	0.01%	10.0%	LEDVLPLAFTR	99.7%	52.7	25	37.3	4	0	0	1273.72	259	269
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	5	5	10	0.01%	10.0%	SGASVVAIR	99.7%	55.1	25	40.8	1	0	0	859.50	176	184
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	5	5	10	0.01%	10.0%	SSAVDPEPQVK	99.7%	49.5	25	38.2	2	0	0	1156.58	248	258
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	5	5	10	0.01%	10.0%	TIPSWATLSASQLAR	99.7%	90.3	25	86.9	2	0	0	1601.86	132	146
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	4	5	9	0.01%	15.7%	DLKDYFTK	99.6%	38.4	25	28.5	2	0	0	1029.53	84	91
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	4	5	9	0.01%	15.7%	EVYQQQQYGSGGR	99.7%	77.7	25	69	2	0	0	1499.69	233	245
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	4	5	9	0.01%	15.7%	FGEVVDCTIK	99.7%	68.5	25	0	7	0	0	1167.57	92	101
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	4	5	9	0.01%	15.7%	GFGFILFK	99.7%	45.2	25	40.1	2	0	0	928.53	111	118
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	4	5	9	0.01%	15.7%	MFVGGLSWDTSKK	99.7%	61.5	25	58.6	3	0	0	1455.73	71	83
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	4	4	10	0.01%	14.4%	AEIIADKQSGK	99.7%	48	25	33.8	2	0	0	1159.63	127	137
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	4	4	10	0.01%	14.4%	AVPKEDIYSGGGGGGSR	99.7%	94.6	25	87	3	0	0	1606.78	173	189
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	4	4	10	0.01%	14.4%	EDIYSGGGGGGSR	99.7%	71.2	25	71.1	1	0	0	1211.53	177	189
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	4	4	10	0.01%	14.4%	LFIGGLNVQTSESGLR	99.7%	104	25	95.6	4	0	0	1690.91	9	24
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	7	9	34	0.04%	22.8%	EDSQRPGAHLTVK	99.7%	59.1	25	44.8	2	0	0	1437.74	93	105
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	7	9	34	0.04%	22.8%	EDSQRPGAHLTVKK	98.2%	26	25	25.6	0	2	0	1565.84	93	106
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	7	9	34	0.04%	22.8%	IEVIEIMTDR	99.7%	69.1	25	57.6	5	0	0	1234.64	131	140
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	7	9	34	0.04%	22.8%	LFIGGLSFETTDESLR	99.7%	82.4	25	77	6	0	0	1784.91	16	31
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	7	9	34	0.04%	22.8%	NQGGYGGSSSSSSYGSGR	99.7%	118	25	118	5	0	0	1694.70	353	370
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	7	9	34	0.04%	22.8%	SESPKEPEQLR	99.7%	46.4	25	35.1	3	2	0	1299.65	4	14
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	7	9	34	0.04%	22.8%	SSGPYGGGGQYFAKPR	99.7%	102	25	102	5	4	0	1628.78	337	352
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	7	9	16	0.02%	27.2%	EDSVKPGAHLTVK	99.7%	47.2	25	40.5	2	0	0	1380.75	114	126
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	7	9	16	0.02%	27.2%	GFAFVTFDDHDTVDK	99.7%	58.8	25	58.8	2	0	0	1713.78	168	182
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	7	9	16	0.02%	27.2%	IETIEVMEDR	99.7%	75.6	25	68.3	4	0	0	1234.60	152	161
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	7	9	16	0.02%	27.2%	IFVGGIKEDTEEYNLR	99.7%	69	25	69	2	1	0	1882.95	128	143
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	7	9	16	0.02%	27.2%	LFIGGLSFETTDDSLR	99.7%	52.4	25	52.4	2	0	0	1770.89	37	52
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	7	9	16	0.02%	27.2%	SSGSPYGGGYGSGGGSGGYGSR	99.7%	136	25	136	2	0	0	1910.79	355	376
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	7	9	16	0.02%	27.2%	WGTLTDCVVMR	97.3%	30.1	25	22.9	1	0	0	1337.63	58	68
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	5	5	20	0.02%	16.1%	FGEVVDCTLK	99.7%	68.5	25	0	7	0	0	1167.57	120	129
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	5	5	20	0.02%	16.1%	FGEVVDCTLKLDPITGR	99.7%	46.2	25	43.9	0	3	0	1919.99	120	136
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	5	5	20	0.02%	16.1%	GFGFVLFK	99.7%	39.3	25	30.8	3	0	0	914.51	139	146
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	5	5	20	0.02%	16.1%	IDASKNEEDEGHSNSSPR	99.7%	46.6	25	46.6	0	2	0	1971.86	68	85
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	5	5	20	0.02%	16.1%	IFVGGLSPDTPEEK	99.7%	77	25	68.7	5	0	0	1488.76	184	197
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	4	7	13	0.01%	21.9%	ATENDIYNFFSPLNPVR	99.7%	78.7	25	78.7	7	2	0	1996.98	300	316
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	4	7	13	0.01%	21.9%	DLSYCLSGMYDHR	99.7%	71.2	25	71.2	4	0	0	1616.68	263	275
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	4	7	13	0.01%	21.9%	HSGPNSADSANDGFVR	99.7%	92.9	25	86.2	2	2	0	1630.72	99	114
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	4	7	13	0.01%	21.9%	QSGEAFVELGSEDDVK	99.7%	111	25	107	2	0	0	1709.79	53	68
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	4	7	13	0.01%	21.9%	VHIEIGPDGR	99.7%	54	25	53.1	8	0	0	1092.58	317	326
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	4	7	13	0.01%	21.9%	YGDSEFTVQSTTGHCVHMR	99.7%	77.1	25	77.1	0	3	0	2211.95	276	294
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	11	15	75	0.08%	39.2%	ATENDIYNFFSPLNPVR	99.7%	78.7	25	78.7	7	2	0	1996.98	300	316
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	11	15	75	0.08%	39.2%	DLNYCFSGMSDHR	99.7%	68.3	25	68.3	8	0	0	1601.65	263	275
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	11	15	75	0.08%	39.2%	EGRPSGEAFVELESEDEVK	99.7%	71.2	25	71.2	0	4	0	2106.98	50	68
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	11	15	75	0.08%	39.2%	GLPWSCSADEVQR	99.7%	81.6	25	78.8	5	0	0	1504.69	17	29
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	11	15	75	0.08%	39.2%	HTGPNSPDTANDGFVR	99.7%	90.5	25	90.5	8	8	0	1684.77	99	114
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	11	15	75	0.08%	39.2%	SNNVEMDWVLK	99.7%	62.2	25	58.7	4	0	0	1334.64	88	98
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	11	15	75	0.08%	39.2%	STGEAFVQFASQEIAEK	99.7%	90.4	25	90.4	8	0	0	1841.89	151	167
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	11	15	75	0.08%	39.2%	VHIEIGPDGR	99.7%	54	25	53.1	8	0	0	1092.58	317	326
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	11	15	75	0.08%	39.2%	VTGEADVEFATHEDAVAAMSK	99.7%	44.9	25	44.9	0	2	0	2194.00	327	347
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	11	15	75	0.08%	39.2%	YGDGGSTFQSTTGHCVHMR	99.7%	58.7	25	58.7	0	7	0	2097.89	276	294
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	11	15	75	0.08%	39.2%	YVELFLNSTAGASGGAYEHR	99.7%	38.9	25	30.4	0	4	0	2142.03	356	375
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	6	11	0.01%	30.1%	ATENDIYNFFSPLNPMR	99.7%	63.1	25	63.1	4	0	0	2028.95	300	316
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	6	11	0.01%	30.1%	DLNYCFSGMSDHR	99.7%	68.3	25	68.3	8	0	0	1601.65	263	275

Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	6	11	0.01%	30.1%	EGRPSGEAFVELESEEEVK	99.6%	31.8	25	23.1	0	1	0	2121.00	50	68
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	6	11	0.01%	30.1%	GLPWSCSADEVMR	99.7%	61.6	25	58.3	2	0	0	1523.66	17	29
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	6	11	0.01%	30.1%	HTGPNSPDTANDGFVR	99.7%	90.5	25	90.5	8	8	0	1684.77	99	114
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	6	11	0.01%	30.1%	SNSVEMDWVLK	99.1%	34.8	25	30.5	1	0	0	1307.63	88	98
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	6	11	0.01%	30.1%	STGEAFVQFASQEIAEK	99.7%	90.4	25	90.4	8	0	0	1841.89	151	167
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	6	11	0.01%	30.1%	VHIEIGPDGR	99.7%	54	25	53.1	8	0	0	1092.58	317	326
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	6	11	0.01%	30.1%	YGDGGSSFQSTTGHCVHMR	99.7%	62.6	25	62.6	0	3	0	2083.87	276	294
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	4	4	7	0.01%	13.9%	ATENDIANFFSPLNPIR	99.7%	47.3	25	47.3	2	0	0	1918.97	206	222
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	4	4	7	0.01%	13.9%	EIAENALGK	99.7%	40.1	25	40.1	1	0	0	944.50	68	76
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	4	4	7	0.01%	13.9%	STGEAFVQFASK	99.7%	68.1	25	64	2	0	0	1271.63	56	67
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	4	4	7	0.01%	13.9%	VHIDIGADGR	99.7%	44	25	28.9	2	0	0	1052.55	223	232
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	22	53	0.05%	42.5%	DLAGSIIGK	99.7%	58	25	32.1	2	0	0	873.50	397	405
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	22	53	0.05%	42.5%	DYDDMSPR	99.7%	41.7	25	41.7	2	0	0	998.39	279	286
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	22	53	0.05%	42.5%	GGDLMAYDR	99.7%	64.6	25	64.6	4	0	0	1013.44	317	325
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	22	53	0.05%	42.5%	GGDLMAYDRR	98.2%	31.7	25	16.2	1	0	0	1153.54	317	326
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	22	53	0.05%	42.5%	GSDFDCELR	99.7%	53.8	25	53	2	0	0	1098.45	140	148
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	22	53	0.05%	42.5%	GSYGDLGGPIITTQVTIPK	99.7%	95.8	25	93.3	2	0	0	1917.03	378	396
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	22	53	0.05%	42.5%	IDEPLEGSEDR	99.7%	78.7	25	69.3	2	0	0	1259.58	423	433
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	22	53	0.05%	42.5%	IILDLISESPIK	99.7%	86.6	25	81.4	10	0	0	1340.80	208	219
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	22	53	0.05%	42.5%	IITITGTQDQIQNAQYLLQNSVK	99.6%	32.2	25	30.9	0	3	0	2589.39	434	456
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	22	53	0.05%	42.5%	ILSISADIETIGEILK	99.7%	45.4	25	45.4	1	0	0	1714.98	87	102
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	22	53	0.05%	42.5%	LFQECCPHSTDR	99.7%	81.1	25	81.1	2	1	0	1549.65	180	191
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	22	53	0.05%	42.5%	LLIHQSLAGGIIGVK	99.7%	66	25	66	2	2	0	1518.94	149	163
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	22	53	0.05%	42.5%	NTDEMVELR	99.7%	79	25	58.2	4	0	0	1106.51	38	46
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	22	53	0.05%	42.5%	RDYDDMSPR	98.2%	31.8	25	28.4	2	0	0	1154.49	278	286
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	22	53	0.05%	42.5%	RPAEDMEEEQAFKR	99.7%	67.4	25	67.4	0	1	0	1735.81	22	35
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	22	53	0.05%	42.5%	SRNTDEMVELR	99.7%	39.2	25	24.8	0	1	0	1349.65	36	46
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	22	53	0.05%	42.5%	TDYNASVSVPDSSGPER	99.7%	90.3	25	90.3	2	0	0	1780.80	70	86
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	22	53	0.05%	42.5%	VVLIGGKPDR	99.7%	63.6	25	40.1	7	0	0	1053.64	192	201
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	9	11	24	0.02%	17.5%	AITHLNNNFMFGQK	99.7%	66.2	25	66.2	2	2	0	1634.81	435	448
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	9	11	24	0.02%	17.5%	ASLNGADIYSGCCTLK	99.7%	68.2	25	63.2	1	0	0	1729.79	249	264
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	9	11	24	0.02%	17.5%	IEYAKPTR	99.7%	42.5	25	36.2	4	0	0	977.54	265	272
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	9	11	24	0.02%	17.5%	ISRPGDSDDSR	99.4%	30.7	25	30.7	2	1	0	1204.56	179	189
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	9	11	24	0.02%	17.5%	LCFSTAQHAS	99.7%	51.2	25	51.2	4	0	0	1121.50	580	589
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	9	11	24	0.02%	17.5%	NPNGPYPYTLK	99.1%	34.6	25	30.1	2	0	0	1263.64	569	579
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	9	11	24	0.02%	17.5%	TPASPVVHIR	99.7%	39.4	25	33.9	1	0	0	1076.62	98	107
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	9	11	24	0.02%	17.5%	VFNVFCLYGNVEK	99.7%	101	25	89.3	4	0	0	1588.78	399	411
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	9	11	24	0.02%	17.5%	YYGGGSEGGR	99.2%	35.5	25	35.5	1	0	0	1002.43	47	56
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	ACQIFVR	97.3%	30.1	25	21	1	0	0	893.47	652	658
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	ADILEDKDGK	99.7%	57.7	25	42.6	3	0	0	1103.56	233	242
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	AFITNIPFDVK	99.7%	69.4	25	54	4	0	0	1264.69	73	83
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	DKFNECGHVLYADIK	99.7%	48.9	25	42.2	1	0	0	1808.86	671	685
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	EVFSMAGVVVR	99.7%	64.4	25	56.8	2	0	0	1193.63	222	232
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	FESPEVAER	99.7%	41.3	25	30.3	3	0	0	1063.51	699	707
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	FGSGMNMGR	99.7%	64.2	25	57.7	9	0	0	956.41	363	371
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	GCAVVEFK	99.7%	48.1	25	31.3	2	0	0	909.45	113	120
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	GGNRFEPYANPTK	99.7%	42.9	25	38.5	2	0	0	1450.71	57	69
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	GIGMGNIGPAGMGMEGIGFGINK	99.7%	109	25	109	8	2	0	2226.04	323	345
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	GNFGGSFAGSFGGAGGHAPGVAR	99.7%	129	25	129	2	2	0	2034.95	628	650
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	INEILSNALK	99.7%	68.1	25	52.3	7	0	0	1114.65	372	381
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	INEILSNALKR	99.7%	51.9	25	48.2	2	0	0	1270.75	372	382

Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	KACQIFVR	99.7%	53.9	25	40.8	2	0	0	1021.56	651	658
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	LGGAGMER	97.3%	30	25	30	1	0	0	806.38	411	418
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	LGSTVFVANLDYK	99.7%	88	25	83.3	5	0	0	1426.76	202	214
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	LKEVFSMAGVVVR	99.7%	89.6	25	84.3	4	2	0	1434.81	220	232
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	MGAGLGHGMDR	99.7%	87.1	25	83.7	6	0	0	1101.49	419	429
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	MGAGMGFGLER	99.7%	84.8	25	59.6	13	0	0	1141.51	486	496
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	MGANNLER	99.7%	74.5	25	66.5	5	0	0	904.43	558	565
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	MGANSLER	99.7%	70.6	25	54.7	5	0	0	877.42	571	578
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	MGGMEGPFGGGMENMGR	99.7%	64.5	25	64.5	5	0	0	1714.68	346	362
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	MGLAMGGGGGASFDR	99.7%	106	25	60.3	10	0	0	1399.61	607	621
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	MGLSMER	99.7%	53.6	25	44.4	5	0	0	823.38	525	531
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	MGLVMDR	99.7%	44.2	25	41.8	5	0	0	821.40	437	443
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	MGPAMGPALGAGIER	99.7%	71.4	25	57.1	8	0	0	1427.71	592	606
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	MGPLGLDHMASSIER	99.7%	80.7	25	80.7	7	4	0	1613.78	457	471
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	MGPVMDR	99.6%	38.1	25	13.8	2	0	0	821.36	544	550
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	MVPAGMGAGLER	99.7%	49.7	25	45.6	6	0	0	1188.59	532	543
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	NLPFDFTWK	98.7%	33.1	25	27.7	1	0	0	1167.58	659	667
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	QGGGGGGGSVPGIER	99.7%	88.5	25	87.2	8	0	0	1284.63	389	403
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	VGEVTYVELLMDAEGK	99.7%	112	25	112	5	0	0	1768.87	95	110
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	53	161	0.17%	48.5%	VGQTIER	99.7%	55.2	25.2	21.9	2	0	0	802.44	504	510
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	13	14	33	0.03%	21.8%	AGPIWDLR	99.7%	57.9	25	44.6	2	0	0	927.50	185	192
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	13	14	33	0.03%	21.8%	DLFEDELVPLFEK	99.7%	102	25	97.3	4	0	0	1593.80	172	184
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	13	14	33	0.03%	21.8%	DSDLSHVQNK	99.5%	37.1	25	22.9	1	0	0	1142.54	82	91
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	13	14	33	0.03%	21.8%	GFCFLEYEDHK	99.7%	42.2	25	42.2	2	0	0	1444.62	287	297
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	13	14	33	0.03%	21.8%	GYAFVTFCTK	99.7%	54.1	25	54.1	1	0	0	1193.57	204	213
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	13	14	33	0.03%	21.8%	HIGVCISVANNR	99.7%	51.5	25	0	1	0	0	1339.69	233	244
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	13	14	33	0.03%	21.8%	LFVGSIPK	96.9%	29.5	25	17	1	0	0	860.52	245	252
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	13	14	33	0.03%	21.8%	LMMDPLTGLNR	99.7%	66	25	61.8	4	0	0	1260.64	193	203
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	13	14	33	0.03%	21.8%	LYNNHEIR	99.7%	41.8	25	26.7	2	0	0	1058.54	222	229
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	13	14	33	0.03%	21.8%	NLANTVTEEILEK	99.7%	114	25	107	5	0	0	1473.78	344	356
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	13	14	33	0.03%	21.8%	SAFLCGVMK	99.5%	37	25	31.9	2	0	0	1012.50	92	100
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	13	14	33	0.03%	21.8%	TGYTLDVTTGQR	99.7%	68.7	25	65.3	6	0	0	1311.65	131	142
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	13	14	33	0.03%	21.8%	TKEQILEEFSK	99.7%	61.8	25	61.8	2	0	0	1351.71	255	265
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	12	13	32	0.03%	35.4%	AGPIWDLR	99.7%	57.9	25	44.6	2	0	0	927.50	188	195
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	12	13	32	0.03%	35.4%	DLYEDELVPLFEK	99.7%	71.7	25	70.5	4	0	0	1609.80	175	187
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	12	13	32	0.03%	35.4%	EFNEEGALSVLQQFK	99.7%	93.1	25	80.2	4	0	0	1738.86	70	84
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	12	13	32	0.03%	35.4%	GFCFLEYEDHK	99.7%	42.2	25	42.2	2	0	0	1444.62	290	300
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	12	13	32	0.03%	35.4%	GYAFITFCGK	99.7%	77.3	25	72.2	2	0	0	1163.56	207	216
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	12	13	32	0.03%	35.4%	HLGVCISVANNR	99.7%	51.5	25	0	1	0	0	1339.69	236	247
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	12	13	32	0.03%	35.4%	LCDSYEIRPGK	99.7%	56.8	25	33.2	2	0	0	1337.65	225	235
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	12	13	32	0.03%	35.4%	LFVGSIPK	96.9%	29.5	25	17	1	0	0	860.52	248	255
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	12	13	32	0.03%	35.4%	LKDYAFVHFEDR	99.7%	54.3	25	53.4	0	2	0	1539.76	373	384
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	12	13	32	0.03%	35.4%	LMMDPLSGQNR	99.7%	50.2	25	32.9	2	0	0	1261.60	196	206
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	12	13	32	0.03%	35.4%	NLATTVTEEILEK	99.7%	108	25	96.2	7	0	0	1460.78	347	359
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	12	13	32	0.03%	35.4%	SAFLCGVMK	99.5%	37	25	31.9	2	0	0	1012.50	95	103
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	12	13	32	0.03%	35.4%	STAYEDYYYHPPPR	99.7%	36.8	25	36.8	0	2	0	1758.78	428	441
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	12	13	32	0.03%	35.4%	TGYTLDVTTGQR	99.7%	68.7	25	65.3	6	0	0	1311.65	134	145
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	12	13	32	0.03%	35.4%	TKENILEEFSK	99.7%	54.8	25	31	2	0	0	1337.69	258	268
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	12	13	32	0.03%	35.4%	VQESTKGPDEAK	99.7%	54.5	25	50	2	0	0	1288.64	115	126
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	12	13	32	0.03%	35.4%	VTEGLVDVILYHQPDDK	99.7%	58	25	58	0	1	0	1941.00	269	285
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	12	13	32	0.03%	35.4%	YGGPPPDSVYSGVQPGIGTEVFVGK	99.7%	44.7	25	44.7	0	2	0	2507.25	147	171

Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	AEGGGGGGRPGAPAAGDGK	99.7%	65.7	25	61.5	2	2	0	1538.73	216	234
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	AEGGGGGGRPGAPAAGDGKTEQK	99.4%	30.6	25	30.6	0	3	0	2024.97	216	238
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	AVVVCPKDEDYK	99.7%	41.2	25	41.2	2	0	0	1422.69	603	614
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	DCEVVMMIGLPGAGK	99.7%	86.8	25	74.7	6	0	0	1576.75	496	510
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	DIDIHEVR	99.7%	47.1	25	38.8	9	0	0	996.51	353	360
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	DLPEHAVLK	99.7%	44.9	25	34.7	4	0	0	1021.57	627	635
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	FIEIAAR	99.7%	43.4	25	29.2	10	0	0	819.47	566	572
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	GKVCFEMK	99.7%	46	25	39.9	3	0	0	998.48	332	339
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	GYFEYIEENK	99.7%	66.5	25	59.1	2	0	0	1291.58	256	265
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	GYFEYIEENKYSR	99.7%	73.2	25	68.3	8	2	0	1697.78	256	268
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	KAEGGGGGGRPGAPAAGDGK	99.7%	35.5	25	35.5	0	3	0	1666.83	215	234
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	KDCEVVMMIGLPGAGK	99.7%	97.3	25	97.3	6	6	0	1704.85	495	510
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	KMCLFAGFQR	99.7%	45.8	25	37	4	0	0	1257.62	592	601
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	LLEQYKEESK	99.7%	62.1	25	55.8	10	0	0	1266.66	665	674
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	LNTLLQR	99.7%	40.5	25	15.4	3	0	0	857.52	552	558
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	LQAALDDEEAGGRPAMEPGNGSLDLGGDSAGR	99.7%	105	25	102	0	4	0	3126.44	38	69
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	LSASSLTMESFAFLWAGGR	99.7%	68.6	25	64.9	2	0	0	2047.00	306	324
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	MCLFAGFQR	99.7%	62.1	25	51.7	11	0	0	1129.53	593	601
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	MMVAGFK	98.8%	33.4	25	19.3	4	0	0	815.38	537	543
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	NFILDQTNVSAAAQR	99.7%	135	25	115	16	2	0	1647.84	576	590
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	NGQDLGVAFK	99.7%	61.6	25	54.4	8	0	0	1048.54	424	433
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	RNFILDQTNVSAAAQR	99.7%	52	25	46.7	0	2	0	1803.95	575	590
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	SSGPTSLFAVTVAPPGAR	99.7%	67.3	25	61.6	11	1	0	1714.91	187	204
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	TCNCETEDYGEK	99.7%	51	25	51	2	0	0	1505.55	388	399
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	VSELKEELK	99.7%	39.7	25	17.7	2	0	0	1074.60	13	21
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	VTEKIPVR	99.7%	55	25	40.8	7	0	0	941.58	340	347
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	39	173	0.18%	32.4%	YNILGTNTIMDK	99.7%	80.3	25	68.2	16	0	0	1398.69	525	536
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	7	7	11	0.01%	10.5%	HLPSTEPDPHVVR	99.7%	35.2	25	33.9	0	3	0	1483.77	271	283
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	7	7	11	0.01%	10.5%	INEEISVK	99.4%	36.2	25	22.8	1	0	0	931.51	263	270
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	7	7	11	0.01%	10.5%	NCAVEFNFGQR	99.7%	57.8	25	57.8	1	0	0	1341.60	376	386
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	7	7	11	0.01%	10.5%	NPPGASTYNK	97.9%	31.1	25	27.4	1	0	0	1048.51	722	731
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	7	7	11	0.01%	10.5%	NYILDQTNVYGSAQR	99.7%	119	25	105	3	0	0	1741.85	501	515
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	7	7	11	0.01%	10.5%	QGAPTSFLPPEASQLKPDR	99.2%	29.2	25	29.2	0	1	0	2039.06	147	165
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	7	7	11	0.01%	10.5%	WDVLIQQATQCLNR	99.7%	71.8	25	67.3	1	0	0	1744.88	477	490
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	8	9	16	0.02%	12.7%	DLLVQQASQCLSK	99.7%	128	25	124	2	0	0	1489.77	509	521
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	8	9	16	0.02%	12.7%	EGCTEVSLLR	99.7%	53.4	25	38.7	2	0	0	1163.57	306	315
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	8	9	16	0.02%	12.7%	GLEEPEMDPK	99.7%	42.4	25	42.4	1	0	0	1160.51	497	506
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	8	9	16	0.02%	12.7%	NCVVELNFGQK	99.7%	62.8	25	50.7	2	0	0	1307.64	407	417
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	8	9	16	0.02%	12.7%	NFILDQCNVYNSGQR	99.7%	78	25	73.9	2	0	0	1827.84	532	546
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	8	9	16	0.02%	12.7%	SGDETPGSEVPGDK	99.7%	49.4	25	49.4	2	0	0	1374.60	161	174
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	8	9	16	0.02%	12.7%	VTQNLPMK	98.5%	32.6	25	16.3	1	0	0	930.51	298	305
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	8	9	16	0.02%	12.7%	YNVLGAETVLNQMR	99.7%	93.9	25	89.2	4	0	0	1607.82	481	494
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	10	11	31	0.03%	35.1%	EESGKPGAHVTVK	98.2%	31.7	25	30.9	1	0	0	1338.70	100	112
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	10	11	31	0.03%	35.1%	GGGGNFGPGPGSNFR	99.7%	77.4	25	77.4	6	0	0	1377.63	214	228
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	10	11	31	0.03%	35.1%	GGNFGFGDSR	99.7%	49.5	25	38.6	4	0	0	1013.44	204	213
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	10	11	31	0.03%	35.1%	IDTIEIITDR	99.7%	96	25	86.8	2	0	0	1188.65	138	147
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	10	11	31	0.03%	35.1%	LFIGGLSFETTEESLR	99.7%	84.6	25	84.6	4	0	0	1798.92	23	38
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	10	11	31	0.03%	35.1%	LTDCVVMR	99.7%	51.2	25	41.2	2	0	0	993.49	47	54
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	10	11	31	0.03%	35.1%	NMGGPYGGGNYGPGGSGGSGGYGGR	99.7%	131	25	131	6	0	0	2205.90	326	350
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	10	11	31	0.03%	35.1%	NYYEQWGK	98.2%	31.7	25	31.7	1	0	0	1087.48	39	46
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	10	11	31	0.03%	35.1%	QEMQEVQSSR	98.0%	31.3	25	30.9	1	0	0	1237.55	191	200

Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	10	11	31	0.03%	35.1%	TLETVPLER	99.7%	44.4	25	43.5	4	0	0	1057.59	4	12
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	9	12	28	0.03%	26.1%	GFAFVQYVNER	99.7%	93.2	25	90.3	4	0	0	1329.66	51	61
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	9	12	28	0.03%	26.1%	KSDVEAIFSK	99.7%	52.2	25	39.2	1	0	0	1123.60	30	39
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	9	12	28	0.03%	26.1%	LKGDDLQAIK	99.4%	36.8	25	29	2	0	0	1100.63	188	197
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	9	12	28	0.03%	26.1%	MIAGQVLDINLAAEPK	99.7%	121	25	121	6	1	0	1682.91	74	89
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	9	12	28	0.03%	26.1%	QKVDSLLENLEK	99.7%	57.3	25	49.1	2	0	0	1415.77	205	216
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	9	12	28	0.03%	26.1%	SDVEAIFSK	99.7%	57.6	25	54.3	2	0	0	995.50	31	39
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	9	12	28	0.03%	26.1%	VFIGNLNTLVVK	99.7%	87.2	25	87.2	6	0	0	1316.79	18	29
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	9	12	28	0.03%	26.1%	VFIGNLNTLVVKK	95.6%	22.8	25	22.8	1	1	0	1444.89	18	30
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	9	12	28	0.03%	26.1%	VPPPPPIAR	99.3%	36	25	34.2	2	0	0	943.57	143	151
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	8	9	17	0.02%	9.4%	ASGVEGADVVK	99.7%	66.6	25	47.7	2	0	0	1031.54	177	187
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	8	9	17	0.02%	9.4%	FLLSESGSGK	99.4%	36.3	25	24.3	2	0	0	1024.53	442	451
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	8	9	17	0.02%	9.4%	FLSQIESDR	99.7%	61.9	25	51.7	2	0	0	1094.55	786	794
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	8	9	17	0.02%	9.4%	GAAMVTAVAYR	99.7%	84.2	25	69.8	2	0	0	1125.57	452	462
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	8	9	17	0.02%	9.4%	HIDLVEGDEGR	99.7%	45.1	25	43.2	2	0	0	1239.60	244	254
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	8	9	17	0.02%	9.4%	LALLQVR	99.7%	40.4	25	21	2	0	0	812.54	795	801
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	8	9	17	0.02%	9.4%	LSDETLIDIMTR	99.7%	58.4	25	51.9	1	0	0	1406.72	31	42
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	8	9	17	0.02%	9.4%	SANLVAATLGAILNR	99.7%	96.4	25	89.7	3	1	0	1483.86	382	396
Hexokinase-2	HK2	HXK2_HUMAN	102.4	100.0%	3	3	4	0.00%	5.2%	FLSQIESDCLALLQVR	99.7%	45.6	25	45.6	1	0	0	1891.99	786	801
Hexokinase-2	HK2	HXK2_HUMAN	102.4	100.0%	3	3	4	0.00%	5.2%	GAAMVTAVAYR	99.7%	84.2	25	69.8	2	0	0	1125.57	452	462
Hexokinase-2	HK2	HXK2_HUMAN	102.4	100.0%	3	3	4	0.00%	5.2%	LSPELLNTGR	99.7%	40.3	25	29.4	2	0	0	1099.61	324	333
Hexokinase-2	HK2	HXK2_HUMAN	102.4	100.0%	3	3	4	0.00%	5.2%	NVELVEGEEGR	99.7%	42	25	42	1	0	0	1230.60	692	702
Histidine triad nucleotide-binding protein 1	HINT1	HINT1_HUMAN	13.8	99.8%	2	2	2	0.00%	18.3%	AQVARPGGDTIFGK	95.4%	28	25	28	1	0	0	1416.76	8	21
Histidine triad nucleotide-binding protein 1	HINT1	HINT1_HUMAN	13.8	99.8%	2	2	2	0.00%	18.3%	CAADLGLNK	99.6%	38.4	25	28.5	1	0	0	961.48	84	92
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	15	0.02%	16.2%	ISICSSDKR	99.5%	37.8	25	25.3	2	0	0	1065.54	405	413
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	15	0.02%	16.2%	LGCFNLTIK	99.7%	53.4	25	38.6	2	0	0	1065.58	271	279
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	15	0.02%	16.2%	LHISPSNMTNQNTNEYLEK	99.7%	41.9	25	41.9	0	1	0	2249.05	343	361
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	15	0.02%	16.2%	SIRPDNMSEYSK	99.7%	45.3	25	26.8	4	0	0	1426.66	78	89
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	15	0.02%	16.2%	VMTVSFHK	99.7%	45.4	25	39.1	2	0	0	948.50	193	200
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	15	0.02%	16.2%	YGEYFPGTGDLR	99.7%	76.1	25	75.1	2	0	0	1374.63	201	212
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	15	0.02%	16.2%	YYAVNYPLR	99.7%	50.2	25	41.7	2	0	0	1158.59	221	229
Histone deacetylase 2	HDAC2	HDAC2_HUMAN	55.4	100.0%	2	2	3	0.00%	10.2%	LGCFNLTVK	99.7%	55.7	25	48.4	2	0	0	1051.56	272	280
Histone deacetylase 2	HDAC2	HDAC2_HUMAN	55.4	100.0%	2	2	3	0.00%	10.2%	SIRPDNMSEYSK	99.7%	45.3	25	26.8	4	0	0	1426.66	79	90
Histone deacetylase 2	HDAC2	HDAC2_HUMAN	55.4	100.0%	2	2	3	0.00%	10.2%	VMTVSFHK	99.7%	45.4	25	39.1	2	0	0	948.50	194	201
Histone deacetylase 2	HDAC2	HDAC2_HUMAN	55.4	100.0%	2	2	3	0.00%	10.2%	YGEYFPGTGDLR	99.7%	76.1	25	75.1	2	0	0	1374.63	202	213
Histone deacetylase 2	HDAC2	HDAC2_HUMAN	55.4	100.0%	2	2	3	0.00%	10.2%	YYAVNFPMR	99.7%	50.3	25	50.3	1	0	0	1160.56	222	230
Histone deacetylase 8	HDAC8	HDAC8_HUMAN	41.8	99.8%	2	2	3	0.00%	7.4%	FSPGFFPGTGDVSDVGLGK	96.7%	29.3	25	23.6	1	0	0	1883.92	203	221
Histone deacetylase 8	HDAC8	HDAC8_HUMAN	41.8	99.8%	2	2	3	0.00%	7.4%	IQQILNYIK	99.2%	35.2	25	24.9	2	0	0	1132.67	362	370
Histone deacetylase complex subunit SAP18	SAP18	SAP18_HUMAN	17.6	99.9%	2	2	4	0.00%	15.7%	KGTDDSMTLQSQK	99.7%	58	25	54.2	2	0	0	1438.68	114	126
Histone deacetylase complex subunit SAP18	SAP18	SAP18_HUMAN	17.6	99.9%	2	2	4	0.00%	15.7%	VKEIGSTMSGR	98.2%	31.7	25	27.8	2	0	0	1164.60	103	113
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	8	10	137	0.14%	24.7%	ALAAAGYDVEK	99.7%	79.1	25	66.2	33	0	0	1107.57	65	75
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	8	10	137	0.14%	24.7%	ALAAAGYDVEKNNSR	99.7%	96.9	25	96.9	9	4	0	1578.79	65	79
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	8	10	137	0.14%	24.7%	ASGPPVSELITK	99.7%	78.8	25	71.3	29	0	0	1198.67	35	46
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	8	10	137	0.14%	24.7%	KALAAAGYDVEK	99.7%	66.3	25	60.9	3	0	0	1235.66	64	75
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	8	10	137	0.14%	24.7%	KASGPPVSELITK	99.7%	82.1	25	77.7	18	2	0	1326.76	34	46
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	8	10	137	0.14%	24.7%	SETAPAAPAAPAPAEK	99.7%	59.5	25	0	1	0	0	1478.75	2	17
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	8	10	137	0.14%	24.7%	SGVSLAALK	99.7%	69	25	37.6	3	0	0	845.51	55	63
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	8	10	137	0.14%	24.7%	SGVSLAALKK	99.7%	76.1	25	71.8	35	0	0	973.60	55	64
Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	3	3	18	0.02%	17.4%	ALVQNDTLLQVK	99.7%	82	25	73.6	6	0	0	1341.77	95	106
Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	3	3	18	0.02%	17.4%	GAPAAATAPAPTAHK	99.7%	77.3	25	71.2	6	0	0	1331.71	129	143
Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	3	3	18	0.02%	17.4%	YSQLVVETIR	99.7%	91	25	70.6	6	0	0	1207.67	48	57

Histone H2A type 1-B/E	HIST1H2AB	H2A1B_HUMAN	14.1	100.0%	3	3	15	0.02%	26.9%	AGLQFPVGR	99.7%	67.5	25	55.4	10	0	0	944.53	22	30
Histone H2A type 1-B/E	HIST1H2AB	H2A1B_HUMAN	14.1	100.0%	3	3	15	0.02%	26.9%	HLQLAIR	98.5%	32.5	25	23.9	2	0	0	850.53	83	89
Histone H2A type 1-B/E	HIST1H2AB	H2A1B_HUMAN	14.1	100.0%	3	3	15	0.02%	26.9%	VTIAQGGVLPNIQAVLLPK	99.7%	40.9	25	40.9	3	0	0	1931.17	101	119
Histone H2B type 1-C/E/F/G/I	HIST1H2BC	H2B1C_HUMAN	13.9	100.0%	4	5	23	0.02%	27.0%	AMGIMNSFVNDIFER	99.7%	89.5	25	43.8	9	0	0	1759.81	59	73
Histone H2B type 1-C/E/F/G/I	HIST1H2BC	H2B1C_HUMAN	13.9	100.0%	4	5	23	0.02%	27.0%	ESYSVYVYK	97.8%	31	25	31	2	0	0	1137.55	36	44
Histone H2B type 1-C/E/F/G/I	HIST1H2BC	H2B1C_HUMAN	13.9	100.0%	4	5	23	0.02%	27.0%	KESYSVYVYK	99.7%	43.7	25	41.5	2	0	0	1265.64	35	44
Histone H2B type 1-C/E/F/G/I	HIST1H2BC	H2B1C_HUMAN	13.9	100.0%	4	5	23	0.02%	27.0%	LLLPGELAK	99.7%	52.4	25	19.6	10	0	0	953.60	101	109
Histone H3.1t	HIST3H3	H31T_HUMAN	15.5	100.0%	3	3	5	0.01%	19.9%	EIAQDFKTDLR	99.7%	40.5	25	30	2	0	0	1335.69	74	84
Histone H3.1t	HIST3H3	H31T_HUMAN	15.5	100.0%	3	3	5	0.01%	19.9%	STELLIR	99.6%	39	25	25.6	2	0	0	831.49	58	64
Histone H3.1t	HIST3H3	H31T_HUMAN	15.5	100.0%	3	3	5	0.01%	19.9%	YRPGTVALR	97.1%	29.8	25	22.4	1	0	0	1032.59	42	50
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	8	26	0.03%	51.5%	DAVTYTEHAK	99.7%	44.4	25	44.4	3	0	0	1134.54	69	78
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	8	26	0.03%	51.5%	DNIQGITKPAIR	99.7%	54.3	25	39.5	6	2	0	1325.75	25	36
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	8	26	0.03%	51.5%	ISGLIYEETR	99.7%	59.8	25	50.5	5	0	0	1180.62	47	56
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	8	26	0.03%	51.5%	TVTAMDVVYALK	99.7%	74.8	25	74.3	4	0	0	1310.70	81	92
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	8	26	0.03%	51.5%	TVTAMDVVYALKR	99.7%	52.9	25	52.9	2	0	0	1466.80	81	93
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	8	26	0.03%	51.5%	VFLENVIR	99.7%	57.5	25	48.7	4	0	0	989.58	61	68
Histone-binding protein RBBP4	RBBP4	RBBP4_HUMAN	47.7	100.0%	2	2	2	0.00%	3.5%	LMIWDTR	98.9%	33.7	25	25.7	1	0	0	934.48	252	258
Histone-binding protein RBBP4	RBBP4	RBBP4_HUMAN	47.7	100.0%	2	2	2	0.00%	3.5%	TVALWDLR	99.4%	36.8	25	22.7	1	0	0	973.55	297	304
Hornerin	HRNR	HORN_HUMAN	282.4	99.8%	2	3	8	0.01%	1.3%	GPYESGSGHSSGLGHR	99.7%	89.7	25	88.3	1	5	0	1584.72	1038	1053
Hornerin	HRNR	HORN_HUMAN	282.4	99.8%	2	3	8	0.01%	1.3%	QSLGHGQHGSGSGQSPSPSR	99.7%	51.2	25	51.2	0	2	0	1947.90	992	1011
Hsp70-binding protein 1	HSPBP1	HPBP1_HUMAN	39.5	99.8%	2	2	4	0.00%	5.5%	ALFAISCLVR	99.7%	66	25	61.7	2	0	0	1149.64	211	220
Hsp70-binding protein 1	HSPBP1	HPBP1_HUMAN	39.5	99.8%	2	2	4	0.00%	5.5%	YLEAGAAGLR	99.7%	44.2	25	34	2	0	0	1020.55	156	165
Huntingtin	HTT	HD_HUMAN	347.6	99.9%	2	2	2	0.00%	0.8%	AALPSLTNPPSLSPIR	97.9%	31.1	25	31.1	1	0	0	1633.93	1167	1182
Huntingtin	HTT	HD_HUMAN	347.6	99.9%	2	2	2	0.00%	0.8%	LFEPLVIK	96.4%	29	25	19.5	1	0	0	958.60	1424	1431
Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	HMGCL_HUMAN	34.4	99.8%	2	2	4	0.00%	8.6%	EVVIFGAASELFTK	99.7%	83.9	25	80.8	2	0	0	1510.82	123	136
Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	HMGCL_HUMAN	34.4	99.8%	2	2	4	0.00%	8.6%	FPGINYPVLTPNLK	99.7%	51.9	25	47	2	0	0	1572.88	98	111
Hydroxysteroid dehydrogenase-like protein 2	HSDL2	HSDL2_HUMAN	45.4	100.0%	3	3	6	0.01%	9.6%	LAGCTVFITGASR	99.7%	95.9	25	75.9	2	0	0	1352.70	8	20
Hydroxysteroid dehydrogenase-like protein 2	HSDL2	HSDL2_HUMAN	45.4	100.0%	3	3	6	0.01%	9.6%	LLGTIYTAAEEIEAVGGK	99.7%	103	25	100	2	0	0	1834.98	50	67
Hydroxysteroid dehydrogenase-like protein 2	HSDL2	HSDL2_HUMAN	45.4	100.0%	3	3	6	0.01%	9.6%	SGAVEETFR	99.7%	57.3	25	50.2	2	0	0	995.48	307	315
Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	HPRT_HUMAN	24.6	100.0%	3	5	8	0.01%	15.6%	TMQTLLSLVR	99.7%	71.8	25	40.6	3	0	0	1161.67	142	151
Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	HPRT_HUMAN	24.6	100.0%	3	5	8	0.01%	15.6%	VFIPHGLIMDR	99.7%	40.8	25	38.2	0	3	0	1297.71	35	45
Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	HPRT_HUMAN	24.6	100.0%	3	5	8	0.01%	15.6%	VIGGDDLSTLTGK	99.7%	98.6	25	92.7	2	0	0	1275.68	116	128
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	23	41	0.04%	22.5%	AANSLEAFIFETQDK	99.7%	89.4	25	72.7	2	1	0	1683.82	739	753
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	23	41	0.04%	22.5%	AEAGPEGVAPAPEGEK	99.7%	90.4	25	77.3	2	0	0	1508.72	670	685
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	23	41	0.04%	22.5%	AEAGPEGVAPAPEGEKK	99.7%	54	25	54	2	2	0	1636.82	670	686
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	23	41	0.04%	22.5%	DAVITVPVFFNQAER	99.7%	62.7	25	53.4	2	0	0	1705.89	171	185
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	23	41	0.04%	22.5%	DAVVYPILVEFTR	99.7%	81.4	25	81.4	3	0	0	1521.83	439	451
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	23	41	0.04%	22.5%	EAGMQPQLQIR	95.1%	27.8	25	22.6	1	0	0	1270.66	252	262
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	23	41	0.04%	22.5%	EVEEEPGIHSLK	99.6%	38	25	31.3	1	0	0	1366.69	452	463
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	23	41	0.04%	22.5%	FFGDSAASMAIK	99.7%	68.5	25	63.4	2	0	0	1244.60	80	91
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	23	41	0.04%	22.5%	KYPDYESK	95.9%	28.4	25	23.8	1	0	0	1029.49	530	537
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	23	41	0.04%	22.5%	LAGLFNEQR	99.7%	65.6	25	53	2	0	0	1047.56	283	291
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	23	41	0.04%	22.5%	LGNTISSLFGGGTTPDAK	99.7%	121	25	119	2	0	0	1735.89	577	594
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	23	41	0.04%	22.5%	LYQPEYQEVSTEEQREEISGK	99.7%	34.7	25	33.2	0	2	0	2542.19	754	774
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	23	41	0.04%	22.5%	TLGGLEMELR	99.7%	67.1	25	63.2	4	0	0	1118.59	269	278
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	23	41	0.04%	22.5%	TPVIVTLK	99.1%	34.6	25	34.6	1	0	0	870.57	68	75
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	23	41	0.04%	22.5%	VAIVKPGVPMEIVLNK	98.7%	27.2	25	27.2	0	3	0	1707.02	47	62
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	23	41	0.04%	22.5%	VEFEELCADLFER	99.7%	83.7	25	82.5	2	0	0	1656.76	346	358
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	23	41	0.04%	22.5%	VLQLINDNTATALSYGVFR	99.7%	130	25	130	2	2	0	2095.12	199	217
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	23	41	0.04%	22.5%	YFQHLLGK	99.3%	36	25	30.1	2	0	0	1005.55	99	106
Ig kappa chain V-I region Lay	IGKV1-13	KV113_HUMAN	11.8	99.8%	2	3	7	0.01%	25.0%	DIQMTQSPSSLSVSVGDR	99.7%	66.1	25	66.1	5	0	0	1922.91	1	18

Ig kappa chain V-I region Lay	IGKV1-13	KV113_HUMAN	11.8	99.8%	2	3	7	0.01%	25.0%	LLIYGASTR	99.7%	73.8	25	18	2	0	0	993.57	46	54
Ig kappa chain V-II region RPMI 6410	IGKV2-30	KV206_HUMAN	14.7	99.8%	2	4	420	0.44%	12.0%	FSGSGSGTDFTLK	99.7%	101	25	0	390	1	0	1303.62	87	99
Ig kappa chain V-II region RPMI 6410	IGKV2-30	KV206_HUMAN	14.7	99.8%	2	4	420	0.44%	12.0%	FSGSGSGTDFTLKISR	99.7%	97.3	25	0	14	15	0	1659.83	87	102
Ig kappa chain V-IV region (Fragment)	IGKV4-1	KV401_HUMAN	13.4	99.8%	2	2	21	0.02%	19.8%	LLIYWASTR	99.7%	62.9	25	47.3	20	0	0	1122.63	72	80
Ig kappa chain V-IV region (Fragment)	IGKV4-1	KV401_HUMAN	13.4	99.8%	2	2	21	0.02%	19.8%	NYLAWYQQKPGQPPK	99.7%	39.2	25	39.2	1	0	0	1817.93	57	71
Immunoglobulin-binding protein 1	IGBP1	IGBP1_HUMAN	39.2	99.8%	2	2	3	0.00%	5.9%	LPELFETGR	99.7%	47.9	25	44.7	2	0	0	1061.56	12	20
Immunoglobulin-binding protein 1	IGBP1	IGBP1_HUMAN	39.2	99.8%	2	2	3	0.00%	5.9%	YGALPDQGIAK	99.7%	47.1	25	41.4	1	0	0	1132.60	277	287
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	7	7	11	0.01%	18.5%	ASLSLIEK	99.6%	38.2	25	28.8	2	0	0	860.51	487	494
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	7	7	11	0.01%	18.5%	GINSSNVENQLQATQAAR	99.7%	107	25	99.6	1	0	0	1900.95	84	101
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	7	7	11	0.01%	18.5%	LLGASELPIVTPALR	99.7%	62.3	25	62.3	3	0	0	1549.93	301	315
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	7	7	11	0.01%	18.5%	NKNPAPPIDAVEQILPTLVR	99.7%	57.3	25	57.3	1	0	0	2185.23	239	258
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	7	7	11	0.01%	18.5%	NNQGTVNWSVDDIVK	99.7%	58.3	25	58.3	1	0	0	1688.82	69	83
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	7	7	11	0.01%	18.5%	NPAPPIDAVEQILPTLVR	99.7%	64.9	25	64.9	1	0	0	1943.10	241	258
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	7	7	11	0.01%	18.5%	QDQIQQVVNHGLVPFLVSVLSK	99.7%	66.3	25	66.3	0	2	0	2448.36	367	388
Importin subunit alpha-5	KPNA1	IMA5_HUMAN	60.2	100.0%	3	3	5	0.01%	8.2%	EAAWAITNATSGGSAEQIK	99.7%	102	25	96.4	2	0	0	1904.93	399	417
Importin subunit alpha-5	KPNA1	IMA5_HUMAN	60.2	100.0%	3	3	5	0.01%	8.2%	EACWTISNITAGNR	99.7%	48.8	25	48.8	1	0	0	1592.75	357	370
Importin subunit alpha-5	KPNA1	IMA5_HUMAN	60.2	100.0%	3	3	5	0.01%	8.2%	NAVWALSNLCR	99.7%	48.9	25	44.7	2	0	0	1303.66	231	241
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	22	47	0.05%	28.0%	AAVENLPTFLVELSR	99.7%	109	25	107	5	0	0	1658.91	28	42
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	22	47	0.05%	28.0%	ANFDKESER	99.7%	41.6	25	35.3	2	0	0	1095.51	207	215
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	22	47	0.05%	28.0%	DTAAWTVGR	99.7%	61	25	48.7	2	0	0	976.48	426	434
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	22	47	0.05%	28.0%	ESCLEAYTGIVQGLK	99.7%	86.3	25	77.6	2	0	0	1667.83	763	777
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	22	47	0.05%	28.0%	GALQYLVPILTQTLTK	99.7%	49.5	25	49.5	2	0	0	1759.04	317	332
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	22	47	0.05%	28.0%	LAATNALLNSLEFTK	99.7%	108	25	104	3	0	0	1605.88	192	206
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	22	47	0.05%	28.0%	LLETTDRPDGHQNNLR	99.7%	42.5	25	38.7	0	2	0	1878.94	510	525
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	22	47	0.05%	28.0%	LQQVLQMESHIQSTSDR	99.7%	43.8	25	41.5	0	2	0	2015.98	558	574
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	22	47	0.05%	28.0%	NSLTSKDPDIK	99.6%	38.6	25	21.8	1	0	0	1217.64	63	73
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	22	47	0.05%	28.0%	SDYDMVDYLNELR	99.7%	86.7	25	86.7	2	0	0	1632.72	750	762
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	22	47	0.05%	28.0%	SNEILTAIIQGMR	99.7%	92.8	25	86	4	0	0	1445.78	170	182
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	22	47	0.05%	28.0%	SSAYESLMEIVK	99.7%	89.9	25	86.6	4	0	0	1356.67	526	537
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	22	47	0.05%	28.0%	TTLVIMER	99.7%	48.5	25	38.6	4	0	0	978.53	550	557
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	22	47	0.05%	28.0%	TVSPDRLELEAAQK	99.7%	55.8	25	45.4	2	0	0	1556.83	10	23
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	22	47	0.05%	28.0%	VAAGLQIK	99.7%	42.6	25	28.6	2	0	0	799.50	55	62
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	22	47	0.05%	28.0%	VAALQNLVK	99.7%	51.1	25	41.6	2	0	0	955.59	235	243
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	22	47	0.05%	28.0%	VLANPGNSQVAR	99.7%	77.7	25	70.7	2	0	0	1225.66	43	54
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	22	47	0.05%	28.0%	YLEVVLNTLQQASQAQVDK	99.7%	118	25	117	2	0	0	2147.13	731	749
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	22	47	0.05%	28.0%	YMEAFKPFLGIGLK	99.7%	58.1	25	58.1	2	0	0	1613.88	646	659
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	5	5	11	0.01%	6.1%	ALLTFYHVTK	99.3%	35.7	25	30.1	3	0	0	1192.67	147	156
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	5	5	11	0.01%	6.1%	IFQNMSPLLELSSENLR	99.7%	80.6	25	76.6	2	0	0	2007.02	688	704
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	5	5	11	0.01%	6.1%	LTVDDFEFR	99.7%	50.6	25	49.7	2	0	0	1141.55	541	549
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	5	5	11	0.01%	6.1%	MAFFTYPTLTEICR	99.7%	49	25	49	1	0	0	1765.83	354	367
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	5	5	11	0.01%	6.1%	SIGTDNVCR	99.7%	39.5	25	36.5	3	0	0	1021.47	255	263
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	27	55	0.06%	22.1%	ACYALENFVENLGPK	99.7%	112	25	103	2	0	0	1724.83	458	472
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	27	55	0.06%	22.1%	AQELQAVLGLS	99.7%	46.2	25	37.5	2	0	0	1128.63	1071	1081
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	27	55	0.06%	22.1%	ATEQLQIVLR	99.7%	70.5	25	42.1	2	0	0	1170.68	24	33
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	27	55	0.06%	22.1%	DNICGALAR	99.7%	52.6	25	44.3	2	0	0	989.48	959	967
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	27	55	0.06%	22.1%	EVMPLLLAYLK	99.7%	63.5	25	49	6	0	0	1289.75	435	445
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	27	55	0.06%	22.1%	GLEDPSQVVR	99.7%	53.5	25	33.8	1	0	0	1099.57	402	411
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	27	55	0.06%	22.1%	ICSLILADNK	99.5%	37.8	25	25.8	1	0	0	1146.62	1026	1035
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	27	55	0.06%	22.1%	ILCCLTFLVK	99.7%	45.4	25	38.4	2	0	0	1266.70	267	276
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	27	55	0.06%	22.1%	LAELCGVLK	99.7%	57.1	25	46	3	0	0	1002.57	793	801
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	27	55	0.06%	22.1%	LIMAMQTLIPIDEAK	99.7%	60.6	25	54.6	6	0	0	1686.92	206	220

Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	27	55	0.06%	22.1%	LLECPHLNVR	99.7%	43.3	25	37.8	2	0	0	1250.67	705	714
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	27	55	0.06%	22.1%	LLMASPTR	99.7%	56.4	25	48.6	2	0	0	904.49	968	975
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	27	55	0.06%	22.1%	LLNETLGEVGSPGLLFYSLR	99.7%	93.5	25	93.5	1	1	0	2178.18	163	182
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	27	55	0.06%	22.1%	LLPVLLSTAQEADPEVR	99.7%	78.7	25	77.6	3	2	0	1851.02	900	916
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	27	55	0.06%	22.1%	NVALGNAIR	99.7%	51.3	25	40.4	1	0	0	927.54	256	264
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	27	55	0.06%	22.1%	QFAAVLTR	99.7%	40.4	25	16.3	2	0	0	905.52	55	62
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	27	55	0.06%	22.1%	QHTDSFQAALGSLPVDK	99.7%	39.7	25	34.6	0	2	0	1813.91	1054	1070
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	27	55	0.06%	22.1%	SLILTALQR	99.7%	57.9	25	43.7	2	0	0	1014.63	82	90
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	27	55	0.06%	22.1%	TLTTMAPYLSTEDVPLAR	99.7%	70.2	25	69.3	4	0	0	1979.02	183	200
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	27	55	0.06%	22.1%	VRDNICGALAR	99.7%	45.4	25	31.5	2	0	0	1244.65	957	967
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	21	27	55	0.06%	22.1%	VVPSYMQAVNR	99.7%	49	25	44.8	4	0	0	1279.65	751	761
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	AKLEEHFK	99.7%	49.6	25	23.4	2	0	0	1001.54	799	806
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	ATAAFILANEHNVALFK	99.7%	101	25	94	2	0	0	1829.99	196	212
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	EFQQYLPVVMGPLMK	99.7%	65.1	25	60.7	2	0	0	1779.92	618	632
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	EGFVEYTEQVVK	99.7%	66.1	25	58	2	0	0	1427.71	694	705
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	FLFDSVSSQNVGLR	99.7%	99.6	25	99.6	6	0	0	1568.81	135	148
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	FMQDASDVMQLLLK	99.7%	114	25	106	7	0	0	1638.82	573	586
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	FVPYYDLFMPSLK	99.7%	54.3	25	0	6	0	0	1635.81	527	539
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	HIVENAVQK	98.5%	32.5	25	30	2	0	0	1037.57	540	548
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	KQAEETYENIPGQSK	99.5%	31.4	25	27.5	0	1	0	1721.83	27	41
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	LQELIQK	99.7%	41.9	25	12.3	3	0	0	871.52	497	503
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	LVLEQVVTSIASVADTAEEK	99.7%	103	25	103	2	4	0	2102.12	507	526
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	MLVQCMQDQEHPSIR	98.0%	25.7	25	18.8	0	1	0	1887.85	176	190
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	NLIDEDGNNQWPEGLK	99.7%	62.1	25	62.1	1	0	0	1841.87	119	134
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	QAEETYENIPGQSK	99.7%	80.8	25	77.1	1	0	0	1593.74	28	41
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	QMAAVLLR	98.3%	31.9	25	12.9	4	0	0	901.53	60	67
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	SELLMIIQMETQSSMR	99.7%	81.6	25	65.8	2	0	0	1928.91	91	106
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	SLLIPYLDNLVK	99.7%	42.3	25	23.9	4	0	0	1387.82	476	487
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	SLVEIADTVPK	99.7%	96.2	25	77.1	8	0	0	1171.66	239	249
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	STACQMLVCYAK	99.7%	62.6	25	62.6	2	0	0	1431.64	679	690
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	TIECISLIGLAVGK	99.7%	103	25	103	8	0	0	1473.83	557	570
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	TKENVNATENCISAVGK	99.7%	79.7	25	79.7	1	0	0	1834.90	962	978
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	VAAAESMPLLLECAR	99.7%	67.3	25	57.9	2	0	0	1630.83	721	735
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	VCDIAAELAR	99.7%	56.8	25	38.3	5	0	0	1117.57	109	118
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	VIAALLQTMEDQGNQR	99.7%	120	25	119	4	0	0	1802.91	442	457
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	VQAHAAAALINFTEDCPK	99.7%	55.8	25	55.8	0	2	0	1955.96	458	475
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	VSDILHSIFSSYK	99.7%	63.7	25	60	2	2	0	1495.78	842	854
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	27	32	90	0.09%	32.5%	YAACNAVGQMATDFAPGFQK	99.7%	61.6	25	44.4	2	0	0	2146.97	417	436
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	21	27	63	0.07%	23.3%	AFAVGVQQVLLK	99.7%	90.6	25	77.9	6	0	0	1272.77	295	306
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	21	27	63	0.07%	23.3%	AIFQTIQNR	99.7%	52.2	25	43.8	4	0	0	1090.60	964	972
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	21	27	63	0.07%	23.3%	DGALHMIGSLAEILLK	98.7%	33.2	25	33.2	3	0	0	1696.93	430	445
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	21	27	63	0.07%	23.3%	ENIVEAIIHSPELIR	99.7%	68.2	25	62.7	3	2	0	1732.96	93	107
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	21	27	63	0.07%	23.3%	ETENDDLTNVIQK	99.7%	73.2	25	70.4	2	0	0	1518.73	552	564
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	21	27	63	0.07%	23.3%	EYNEFAEVFLK	99.7%	68	25	62.7	6	0	0	1388.67	284	294
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	21	27	63	0.07%	23.3%	FIQLLSDQSDQSVLIQK	99.7%	111	25	107	2	0	0	1962.05	185	201
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	21	27	63	0.07%	23.3%	FKSDQNLQTALELTR	98.6%	27	25	27	0	1	0	1763.93	488	502
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	21	27	63	0.07%	23.3%	GIDQCIPLFVEAALER	99.7%	87.5	25	83.8	2	0	0	1830.94	753	768
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	21	27	63	0.07%	23.3%	GTMDPALR	99.7%	51.6	25	41.9	3	0	0	876.42	12	19
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	21	27	63	0.07%	23.3%	LLEVIILQCK	99.7%	78.8	25	78.8	6	0	0	1228.73	741	750
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	21	27	63	0.07%	23.3%	QLQDIATLADQR	99.7%	55.2	25	48.6	2	0	0	1371.72	991	1002
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	21	27	63	0.07%	23.3%	QLQDIATLADQRR	99.7%	38.3	25	38.3	0	1	0	1527.82	991	1003

Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	21	27	63	0.07%	23.3%	SDQNLQTALELTR	99.7%	74.8	25	58.8	3	0	0	1488.77	490	502
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	21	27	63	0.07%	23.3%	SPLVAAMQHFLPVLK	99.7%	80.4	25	80.4	2	1	0	1650.94	168	182
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	21	27	63	0.07%	23.3%	TMGFCYQILTEPNADPR	99.7%	71.6	25	71.6	2	0	0	2012.92	411	427
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	21	27	63	0.07%	23.3%	VLTGVAGEDAECHAAK	99.7%	93.1	25	93.1	2	2	0	1627.77	725	740
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	21	27	63	0.07%	23.3%	VQLTTCIHHIIK	98.1%	25.9	25	22.7	0	1	0	1462.82	108	119
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	21	27	63	0.07%	23.3%	WALHILAR	99.7%	45.9	25	38.2	2	0	0	979.58	263	270
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	21	27	63	0.07%	23.3%	YGSPGNVSK	99.3%	36.1	25	28.1	2	0	0	908.45	275	283
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	21	27	63	0.07%	23.3%	YLEMIYSMCK	99.7%	56.8	25	54.3	3	0	0	1337.59	714	723
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	4	4	6	0.01%	5.3%	EYFEFSEFFLK	99.7%	57.1	25	57.1	1	0	0	1485.69	285	295
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	4	4	6	0.01%	5.3%	IAAENELNQSYK	99.7%	67.7	25	67.2	1	0	0	1379.68	20	31
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	4	4	6	0.01%	5.3%	IINFAPSLLR	99.7%	54.3	25	44.6	2	0	0	1143.69	32	41
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	4	4	6	0.01%	5.3%	LLEVIILQCK	99.7%	78.8	25	78.8	6	0	0	1228.73	741	750
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	4	4	6	0.01%	5.3%	TYAVGIQQVLLK	99.7%	85.7	25	79.4	2	0	0	1332.79	296	307
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	16	33	0.03%	14.8%	AIWGYCDQLK	99.7%	46.7	25	44.4	2	0	0	1253.60	540	549
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	16	33	0.03%	14.8%	EVTDTQMPLVAPVILPEMYK	99.7%	68	25	66.1	4	0	0	2274.18	176	195
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	16	33	0.03%	14.8%	FRPPETTER	97.7%	30.8	25	17.5	2	0	0	1132.57	96	104
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	16	33	0.03%	14.8%	IFTMAEVYGIR	99.7%	93.5	25	86.3	4	0	0	1315.67	196	206
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	16	33	0.03%	14.8%	LIINELSNVMEANAAR	99.7%	112	25	102	5	0	0	1757.92	920	935
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	16	33	0.03%	14.8%	LIPTLVSIMQAPADK	99.7%	63.7	25	52.2	2	0	0	1612.90	647	661
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	16	33	0.03%	14.8%	LLQHGINADDKR	98.3%	32.1	25	28.5	1	0	0	1379.74	866	877
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	16	33	0.03%	14.8%	NSGTEHWWK	96.5%	29.1	25	26.5	1	0	0	1144.52	437	445
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	16	33	0.03%	14.8%	QLASVILK	99.7%	48.5	25	24.6	2	0	0	871.56	75	82
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	16	33	0.03%	14.8%	TSEFTAAFVGR	99.7%	111	25	91.1	2	0	0	1185.59	755	765
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	16	33	0.03%	14.8%	VSSVALCK	99.3%	36	25	21.2	2	0	0	863.47	858	865
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	16	33	0.03%	14.8%	WTNIPLLVK	98.1%	31.5	25	22	2	0	0	1083.66	908	916
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	16	33	0.03%	14.8%	YSNDPVVASLAQDIFK	99.7%	96.9	25	88.9	4	0	0	1766.90	616	631
Inactive hydroxysteroid dehydrogenase-like protein 1	HSDL1	HSDL1_HUMAN	37.0	100.0%	5	5	8	0.01%	15.8%	AYAEELASR	99.7%	54.6	25	48.3	2	0	0	1009.49	82	90
Inactive hydroxysteroid dehydrogenase-like protein 1	HSDL1	HSDL1_HUMAN	37.0	100.0%	5	5	8	0.01%	15.8%	AYLDHFSR	99.5%	37.1	25	30.8	1	0	0	1008.49	223	230
Inactive hydroxysteroid dehydrogenase-like protein 1	HSDL1	HSDL1_HUMAN	37.0	100.0%	5	5	8	0.01%	15.8%	GLNIILISR	99.7%	55.1	25	55.1	2	0	0	998.64	91	99
Inactive hydroxysteroid dehydrogenase-like protein 1	HSDL1	HSDL1_HUMAN	37.0	100.0%	5	5	8	0.01%	15.8%	SITVICDFYSLIR	99.6%	38.9	25	38.5	1	0	0	1586.82	37	49
Inactive hydroxysteroid dehydrogenase-like protein 1	HSDL1	HSDL1_HUMAN	37.0	100.0%	5	5	8	0.01%	15.8%	WAVVSGATDGIGK	99.7%	65.7	25	60.4	2	0	0	1260.66	69	81
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	5	5	8	0.01%	31.4%	ALLELQEYFGSLAA	98.2%	31.7	25	31.7	1	0	0	1524.79	181	194
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	5	5	8	0.01%	31.4%	IDLPEYQGEPDEISIQK	99.7%	83.9	25	79	2	0	0	1973.97	40	56
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	5	5	8	0.01%	31.4%	IVFVTGNAK	98.6%	32.8	25	21.2	2	0	0	948.55	10	18
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	5	5	8	0.01%	31.4%	KIVFVTGNAK	96.0%	28.6	25	28.6	1	0	0	1076.65	9	18
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	5	5	8	0.01%	31.4%	SAYALCTFALSTGDPSQPVR	99.7%	89.5	25	89.5	2	0	0	2141.03	111	130
Inosine-5'-monophosphate dehydrogenase 2	IMPDH2	IMDH2_HUMAN	55.8	100.0%	3	3	4	0.00%	7.2%	LPIVNEDDELVAIIAR	98.8%	33.5	25	33.5	1	0	0	1779.99	209	224
Inosine-5'-monophosphate dehydrogenase 2	IMPDH2	IMDH2_HUMAN	55.8	100.0%	3	3	4	0.00%	7.2%	VAQGVSGAVQDK	99.7%	69.6	25	59	2	0	0	1158.61	439	450
Inosine-5'-monophosphate dehydrogenase 2	IMPDH2	IMDH2_HUMAN	55.8	100.0%	3	3	4	0.00%	7.2%	YFSEADKIK	97.1%	29.8	25	20.3	1	0	0	1100.56	430	438
Inositol 1,4,5-trisphosphate receptor type 2	ITPR2	ITPR2_HUMAN	308.1	99.8%	2	2	2	0.00%	0.8%	EIETFVSLLR	99.7%	61.2	25	56.2	1	0	0	1206.67	614	623
Inositol 1,4,5-trisphosphate receptor type 2	ITPR2	ITPR2_HUMAN	308.1	99.8%	2	2	2	0.00%	0.8%	LFENFLVDMAR	98.0%	31.3	25	23.4	1	0	0	1354.68	1450	1460
Insulin receptor substrate 4	IRS4	IRS4_HUMAN	133.8	100.0%	2	2	2	0.00%	2.5%	GAQDVAGGSNPGAHNPSANLAR	94.9%	22.3	25	22.3	0	1	0	2060.99	1177	1198
Insulin receptor substrate 4	IRS4	IRS4_HUMAN	133.8	100.0%	2	2	2	0.00%	2.5%	LAPSPARPR	95.7%	28.3	25	28.3	1	0	0	964.57	436	444
Insulin-degrading enzyme	IDE	IDE_HUMAN	118.0	99.8%	2	2	2	0.00%	2.8%	NEFIPTNFEILPLEK	98.5%	32.5	25	31	1	0	0	1803.95	528	542
Insulin-degrading enzyme	IDE	IDE_HUMAN	118.0	99.8%	2	2	2	0.00%	2.8%	NLYVTFPIPDLQK	99.3%	35.8	25	35.8	1	0	0	1547.85	312	324
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	20	26	70	0.07%	41.4%	AIETFSGK	99.5%	37.7	25	37.7	2	0	0	852.45	53	60
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	20	26	70	0.07%	41.4%	AISVHSTPEGCSSACK	99.7%	68.5	25	68.5	2	3	0	1690.75	243	258
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	20	26	70	0.07%	41.4%	DQTPDENDQVIVK	99.7%	78.4	25	72	4	0	0	1500.72	526	538
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	20	26	70	0.07%	41.4%	EEVKLETHIR	99.7%	39.3	25	32.3	2	0	0	1253.68	484	493
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	20	26	70	0.07%	41.4%	IIGHFYASQMAQR	99.7%	65.5	25	65.5	4	4	0	1521.76	539	551
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	20	26	70	0.07%	41.4%	ILAHNNFVGR	99.7%	51.5	25	46	4	0	0	1140.63	281	290

Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	20	26	70	0.07%	41.4%	IRDILAQVK	99.7%	48.4	25	27.7	2	0	0	1055.66	553	561
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	20	26	70	0.07%	41.4%	ISYSGQFLVK	99.7%	70.2	25	62.7	2	0	0	1141.63	27	36
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	20	26	70	0.07%	41.4%	ITISSLQDLTLYNPER	99.7%	85	25	84	4	0	0	1862.99	310	325
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	20	26	70	0.07%	41.4%	LKEENFFGPK	99.7%	45.6	25	44.1	2	0	0	1208.63	474	483
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	20	26	70	0.07%	41.4%	LLVPTQYVGAIIGK	99.7%	97.2	25	97.2	5	0	0	1471.89	200	213
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	20	26	70	0.07%	41.4%	LYIGNLNESVTPADLEK	99.7%	111	25	103	2	0	0	1875.97	4	20
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	20	26	70	0.07%	41.4%	MILEIMHK	99.7%	46.1	25	41.2	2	0	0	1014.55	259	266
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	20	26	70	0.07%	41.4%	MVIITGPPEAQFK	99.7%	80.5	25	64.2	8	0	0	1430.77	453	465
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	20	26	70	0.07%	41.4%	QGSPVAAGAPAK	99.7%	71.8	25	69	4	0	0	1053.57	179	190
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	20	26	70	0.07%	41.4%	QQQVDIPLR	99.7%	60.7	25	45.1	4	0	0	1096.61	191	199
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	20	26	70	0.07%	41.4%	RLEIEHSVPK	99.7%	41.4	25	41.4	1	0	0	1207.68	67	76
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	20	26	70	0.07%	41.4%	SGYAFVDCPDEHWAMK	99.7%	71.8	25	71.8	1	0	0	1912.80	37	52
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	20	26	70	0.07%	41.4%	TADEVPLK	99.7%	48.6	25	36.9	2	0	0	872.47	273	280
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	20	26	70	0.07%	41.4%	TVNELQNLTAAEVVVPR	99.7%	107	25	94	4	2	0	1853.01	509	525
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	99.7%	2	2	2	0.00%	8.0%	IAPAEGPDVSER	99.4%	36.6	25	36.6	1	0	0	1240.62	463	474
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	99.7%	2	2	2	0.00%	8.0%	ILVPTQFVGAIIGK	99.7%	62.6	25	0	4	0	0	1455.89	198	211
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	99.7%	2	2	2	0.00%	8.0%	MVIITGPPEAQFK	99.7%	80.5	25	64.2	8	0	0	1430.77	475	487
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	99.7%	2	2	2	0.00%	8.0%	YPQGVASQR	94.9%	27.6	25	20.5	1	0	0	1005.51	589	597
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	13	14	26	0.03%	33.9%	ALQSGPPQSR	98.7%	33.2	25	19.3	1	0	0	1040.55	568	577
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	13	14	26	0.03%	33.9%	DQTPDENDQVVVK	99.4%	36.6	25	34.2	1	0	0	1486.70	526	538
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	13	14	26	0.03%	33.9%	FTEEIPLK	97.3%	30.1	25	10.9	2	0	0	976.54	273	280
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	13	14	26	0.03%	33.9%	IAPAEAPDAK	98.8%	33.6	25	33.6	4	0	0	982.52	441	450
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	13	14	26	0.03%	33.9%	IKEENFVSPK	99.2%	35	25	25.6	1	0	0	1190.64	474	483
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	13	14	26	0.03%	33.9%	ILAHNNFVGR	99.7%	51.5	25	46	4	0	0	1140.63	281	290
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	13	14	26	0.03%	33.9%	IPVSGPFLVK	99.4%	36.2	25	36.2	2	0	0	1056.65	27	36
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	13	14	26	0.03%	33.9%	ITGHFYACQVAQR	96.5%	23.6	25	19.1	0	1	0	1550.75	539	551
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	13	14	26	0.03%	33.9%	ITISPLQELTLYNPER	99.7%	72.7	25	72.7	2	0	0	1887.02	310	325
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	13	14	26	0.03%	33.9%	LLVPTQFVGAIIGK	99.7%	62.6	25	0	4	0	0	1455.89	200	213
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	13	14	26	0.03%	33.9%	LYIGNLSENAAPSDLESIFK	99.7%	72.6	25	72.6	1	0	0	2181.11	4	23
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	13	14	26	0.03%	33.9%	MVIITGPPEAQFK	99.7%	80.5	25	64.2	8	0	0	1430.77	453	465
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	13	14	26	0.03%	33.9%	SITILSTPEGTSAACK	99.7%	74.6	25	70.4	2	0	0	1635.83	243	258
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	13	14	26	0.03%	33.9%	TGYAFVDCPDESWALK	99.7%	85.8	25	85.8	2	0	0	1858.83	37	52
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	13	14	26	0.03%	33.9%	TVNELQNLSSAEVVVPR	99.7%	51.8	25	45.7	2	1	0	1854.99	509	525
Integrator complex subunit 11	CPSF3L	INT11_HUMAN	67.7	100.0%	3	3	6	0.01%	5.7%	VLIPVFALGR	99.7%	55.2	25	55.2	2	0	0	1084.69	235	244
Integrator complex subunit 11	CPSF3L	INT11_HUMAN	67.7	100.0%	3	3	6	0.01%	5.7%	VPIYFSTGLTEK	99.7%	45.9	25	45.9	2	0	0	1354.73	263	274
Integrator complex subunit 11	CPSF3L	INT11_HUMAN	67.7	100.0%	3	3	6	0.01%	5.7%	VTPLGAGQDVGR	99.7%	59	25	55.8	2	0	0	1169.63	6	17
Integrator complex subunit 7	INTS7	INT7_HUMAN	106.8	99.9%	2	2	3	0.00%	2.4%	QIQLLLQYLK	99.7%	45.3	25	44.7	2	0	0	1259.77	252	261
Integrator complex subunit 7	INTS7	INT7_HUMAN	106.8	99.9%	2	2	3	0.00%	2.4%	YPFPILINSAFLK	98.3%	31.9	25	31.9	1	0	0	1522.87	55	67
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	99.8%	2	2	4	0.00%	4.5%	IGDFGLVTSLK	99.7%	60.7	25	54.6	2	0	0	1149.65	430	440
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	99.8%	2	2	4	0.00%	4.5%	LAYLQILSEETSVK	99.7%	79.4	25	79.4	2	0	0	1593.87	160	173
Interferon-related developmental regulator 1	IFRD1	IFRD1_HUMAN	50.3	99.8%	2	2	2	0.00%	8.7%	GSSAGGGGSGAAAATAATAGGQHR	99.7%	38.2	25	37.2	0	1	0	1927.90	13	36
Interferon-related developmental regulator 1	IFRD1	IFRD1_HUMAN	50.3	99.8%	2	2	2	0.00%	8.7%	IAAGESLALLFELAR	99.7%	71.8	25	71.8	1	0	0	1573.89	284	298
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	10	16	33	0.03%	31.0%	GTMTTGHNVADLVVILK	99.7%	78.4	25	66.6	3	4	0	1768.96	111	127
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	10	16	33	0.03%	31.0%	ILITTVPPNLR	99.7%	39.9	25	39.7	3	0	0	1236.77	175	185
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	10	16	33	0.03%	31.0%	ILPTLEAVAALGNK	99.7%	99	25	91.7	4	0	0	1409.84	128	141
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	10	16	33	0.03%	31.0%	KLDPELHLDIK	99.7%	52.6	25	38.1	2	1	0	1320.75	186	196
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	10	16	33	0.03%	31.0%	LDPELHLDIK	99.7%	41.3	25	34.2	2	0	0	1192.66	187	196
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	10	16	33	0.03%	31.0%	NQDLAPNSAEQASILSLVTK	99.7%	128	25	128	2	2	0	2099.10	61	80
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	10	16	33	0.03%	31.0%	QPLALNVAYR	99.7%	54.6	25	37.4	2	0	0	1144.65	260	269
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	10	16	33	0.03%	31.0%	VKPAPDETSFSEALLK	99.7%	81.2	25	68.7	2	2	0	1731.92	44	59
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	10	16	33	0.03%	31.0%	VLQSALAAIR	99.7%	87.7	25	79.3	2	0	0	1041.64	197	206

Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	10	16	33	0.03%	31.0%	WFEENASQSTVK	99.7%	75.5	25	68.5	2	0	0	1425.66	210	221
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	22	26	53	0.05%	28.3%	AVSDWIDEQEK	99.7%	50.3	25	44.1	1	0	0	1319.61	44	54
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	22	26	53	0.05%	28.3%	AYAALAALEK	99.7%	87.5	25	60.3	4	0	0	1020.57	578	587
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	22	26	53	0.05%	28.3%	CLAALASLR	99.7%	48.4	25	40	2	0	0	974.55	203	211
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	22	26	53	0.05%	28.3%	EATDAIGHLDR	99.7%	66.2	25	47.2	2	0	0	1197.59	298	308
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	22	26	53	0.05%	28.3%	EDITQSAQHALR	99.7%	77.4	25	65.1	2	2	0	1368.69	312	323
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	22	26	53	0.05%	28.3%	EPPLSLTIHLTSPVVR	99.7%	47.1	25	47.1	0	2	0	1759.01	162	177
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	22	26	53	0.05%	28.3%	FNYSGSGGR	99.1%	34.8	25	26	1	0	0	944.42	807	815
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	22	26	53	0.05%	28.3%	FVMEVEVDGQK	99.7%	55	25	47.7	2	0	0	1280.62	555	565
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	22	26	53	0.05%	28.3%	GDLDLELVLLCK	99.7%	46.7	25	40.8	1	0	0	1387.75	106	117
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	22	26	53	0.05%	28.3%	GWPLELLCEK	99.7%	53	25	0	2	0	0	1244.63	248	257
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	22	26	53	0.05%	28.3%	IFVNDDRHVMAK	98.9%	27.9	25	24.5	0	1	0	1460.73	6	17
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	22	26	53	0.05%	28.3%	LAAFGQLHK	99.7%	55.4	25	42.7	3	0	0	984.56	324	332
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	22	26	53	0.05%	28.3%	LFPDTPLALDANK	99.7%	64.1	25	56.9	2	0	0	1414.76	588	600
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	22	26	53	0.05%	28.3%	LFPDTPLALDANKK	99.7%	69.1	25	58.4	2	0	0	1542.85	588	601
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	22	26	53	0.05%	28.3%	LNQLKPGLQYK	99.7%	42.3	25	32.1	3	0	0	1301.76	409	419
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	22	26	53	0.05%	28.3%	NPVMELNEK	99.6%	38.3	25	38.3	4	0	0	1073.53	527	535
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	22	26	53	0.05%	28.3%	RPMEEDGEEKSPSK	99.7%	33.4	25	33.4	0	2	0	1634.73	372	385
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	22	26	53	0.05%	28.3%	SIGTANRPMGAGEALRR	99.7%	43.4	25	43.4	0	2	0	1756.92	258	274
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	22	26	53	0.05%	28.3%	VLAGETLSVNDPPDVLDR	99.7%	93.2	25	92.6	2	0	0	1909.99	183	200
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	22	26	53	0.05%	28.3%	VLGMDPLPSK	99.7%	43.8	25	33.8	4	0	0	1056.58	333	342
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	22	26	53	0.05%	28.3%	VLQDMGLPTGAEGR	99.7%	81.1	25	68.7	4	0	0	1443.73	461	474
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	22	26	53	0.05%	28.3%	YELISETGGSHDKR	99.7%	58.6	25	54.6	1	2	0	1591.77	541	554
Iron-sulfur protein NUBPL	NUBPL	NUBPL_HUMAN	34.1	99.8%	2	2	4	0.00%	10.7%	AIGLLDVDVYGPSVPK	99.7%	94.1	25	91.9	3	0	0	1642.91	100	115
Iron-sulfur protein NUBPL	NUBPL	NUBPL_HUMAN	34.1	99.8%	2	2	4	0.00%	10.7%	STTAVNLALALAANDSSK	99.7%	47.8	25	47.8	1	0	0	1746.92	82	99
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	9	12	24	0.02%	27.9%	APIQWEER	99.7%	53.6	25	46.6	2	0	0	1028.52	59	66
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	9	12	24	0.02%	27.9%	CSDFTEEICR	99.7%	69	25	64.7	2	0	0	1316.52	351	360
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	9	12	24	0.02%	27.9%	DMANPTALLLSAVMMLR	99.7%	61.1	25	32	1	0	0	1862.95	300	316
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	9	12	24	0.02%	27.9%	IAEFAFEYAR	99.7%	84.6	25	77.1	2	0	0	1216.60	179	188
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	9	12	24	0.02%	27.9%	IEAACFATIK	99.7%	64.8	25	56.1	2	0	0	1123.58	327	336
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	9	12	24	0.02%	27.9%	MSDGLFLQK	99.7%	53.5	25	23.3	4	0	0	1054.52	206	214
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	9	12	24	0.02%	27.9%	NVTAIQGPGGK	99.7%	56.6	25	56.3	2	0	0	1041.57	67	77
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	9	12	24	0.02%	27.9%	TPIAAGHPSMNLLLR	99.7%	84.3	25	84.3	4	2	0	1590.88	101	115
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	9	12	24	0.02%	27.9%	TPYTDVNIVTIR	99.7%	66.2	25	59.9	3	0	0	1391.75	135	146
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	13	17	32	0.03%	35.1%	DMGGYSTTTDFIK	99.7%	79.6	25	72	4	0	0	1435.64	362	374
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	13	17	32	0.03%	35.1%	EQTEGEYSSLEHESAR	99.7%	71.7	25	68.8	2	2	0	1851.80	165	180
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	13	17	32	0.03%	35.1%	FAFDYATK	99.2%	35.2	25	31.1	2	0	0	962.46	200	207
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	13	17	32	0.03%	35.1%	FAFDYATKK	99.7%	51.4	25	46	2	0	0	1090.56	200	208
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	13	17	32	0.03%	35.1%	GELASYDMR	99.4%	36.9	25	34	3	0	0	1041.47	123	131
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	13	17	32	0.03%	35.1%	GVIECLK	96.0%	28.5	25	11	1	0	0	818.44	181	187
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	13	17	32	0.03%	35.1%	HLNLEYHSSMIADAVK	99.7%	34.4	25	34.4	0	1	0	1843.90	335	350
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	13	17	32	0.03%	35.1%	HNNLDLVIIR	99.7%	72.9	25	62.4	2	0	0	1206.70	155	164
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	13	17	32	0.03%	35.1%	LGDGLFLQCCEEVAELYPK	99.7%	51.7	25	51.7	1	0	0	2241.06	224	242
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	13	17	32	0.03%	35.1%	NIANPTAMLLSASNMLR	99.7%	145	25	138	8	0	0	1816.94	318	334
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	13	17	32	0.03%	35.1%	SLPGYMTR	96.4%	28.9	25	21.2	1	0	0	940.46	147	154
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	13	17	32	0.03%	35.1%	SVIGHLQTK	95.5%	28	25	28	1	0	0	982.57	375	383
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	13	17	32	0.03%	35.1%	TRDMGGYSTTTDFIK	98.8%	33.5	25	29.1	2	0	0	1708.79	360	374
Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G	IDH3G_HUMAN	42.8	100.0%	4	4	7	0.01%	14.0%	ENTEGEYSSLEHESVAGVVESLK	98.2%	26.1	25	26.1	0	1	0	2493.16	168	190
Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G	IDH3G_HUMAN	42.8	100.0%	4	4	7	0.01%	14.0%	LGDGLFLQCCR	99.7%	71.8	25	71.8	2	0	0	1338.63	227	237
Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G	IDH3G_HUMAN	42.8	100.0%	4	4	7	0.01%	14.0%	SLPGVVTR	99.7%	41.1	25	28.1	2	0	0	828.49	150	157
Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G	IDH3G_HUMAN	42.8	100.0%	4	4	7	0.01%	14.0%	TSLDLYANVIHCK	99.7%	64.6	25	62.7	2	0	0	1533.77	137	149

Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	23	44	0.05%	36.5%	ATDFVADR	99.2%	35.2	25	29.3	2	0	0	894.43	181	188
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	23	44	0.05%	36.5%	CATITPDEAR	98.7%	33.2	25	24.6	2	0	0	1133.53	113	122
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	23	44	0.05%	36.5%	CATITPDEARVEEFK	98.0%	25.7	25	25.7	0	1	0	1765.84	113	127
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	23	44	0.05%	36.5%	FKDIFQEIFDK	99.7%	57.1	25	47.5	2	0	0	1429.74	262	272
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	23	44	0.05%	36.5%	GKLDGNQDLIR	99.7%	58.7	25	43.6	2	2	0	1228.66	383	393
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	23	44	0.05%	36.5%	IIWQFIK	99.1%	34.5	25	27.6	2	0	0	947.57	61	67
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	23	44	0.05%	36.5%	LIDDMVAQVLK	99.7%	81.4	25	66.6	4	0	0	1244.69	289	299
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	23	44	0.05%	36.5%	LILPHVDIQLK	99.7%	55.4	25	37.2	2	0	0	1288.80	70	80
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	23	44	0.05%	36.5%	LNEHFLNTTDFLDTIK	99.7%	77.6	25	72.6	2	2	0	1920.97	427	442
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	23	44	0.05%	36.5%	NILGGTVFR	99.3%	35.7	25	29.1	2	0	0	976.56	141	149
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	23	44	0.05%	36.5%	NILGGTVFREPIICK	99.7%	65.8	25	65.8	2	0	0	1716.95	141	155
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	23	44	0.05%	36.5%	SSGGFVWACK	99.7%	71.9	25	63.8	2	0	0	1098.50	300	309
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	23	44	0.05%	36.5%	TIEAEAAHGTVTR	99.7%	96.1	25	88.3	3	0	0	1355.69	341	353
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	23	44	0.05%	36.5%	VAKPVVEMDGDEMTR	99.7%	61.5	25	61.5	3	3	0	1708.79	46	60
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	23	44	0.05%	36.5%	VCVETVESGAMTK	99.7%	120	25	114	4	0	0	1426.66	401	413
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	23	44	0.05%	36.5%	YFDLGLPNR	99.7%	64.3	25	49.8	2	0	0	1094.56	81	89
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	AEPDHMVLGK	98.0%	31.3	25	24.8	1	0	0	1112.54	894	903
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	APLKPYPVSPSDK	99.7%	58.8	25	56	2	2	0	1398.76	1039	1051
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	AVPSWFVR	99.5%	37.6	25	32.7	2	0	0	961.53	411	418
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	CNLVPTDEITVYYK	99.7%	39.7	25	33.5	2	0	0	1714.84	1001	1014
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	DVLLPWYNAYR	99.7%	50.3	25	46.8	2	0	0	1409.72	651	661
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	EFEDAFPADFIAEGIDQTR	99.7%	67.1	25	67.1	2	0	0	2170.99	547	565
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	EIVVIHQDPEALK	99.7%	66.4	25	45.9	2	0	0	1490.82	849	861
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	ESVDHLTIPSR	99.7%	48.5	25	32.7	2	0	0	1253.65	501	511
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	FGWDCHGLPVEYEIDK	98.7%	27.2	25	27.2	0	1	0	1964.89	83	98
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	FLIQNVLR	99.7%	44.4	25	28.9	5	0	0	1002.61	662	669
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	FVDILTNWYVR	99.7%	81	25	74.2	4	0	0	1425.75	726	736
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	GSELEITLTR	99.7%	70.4	25	48.5	2	0	0	1118.61	1062	1071
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	LESDYEILER	99.7%	82.9	25	67.5	2	0	0	1266.62	269	278
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	LFLNETQTQEITEDIPVK	99.7%	116	25	104	2	0	0	2118.10	1227	1244
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	LLILMEAR	99.7%	57.5	25	36.5	4	0	0	974.57	255	262
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	LRAEPDHMVLGK	99.6%	32.7	25	32.7	0	2	0	1365.73	892	903
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	LYLINSPVVR	99.7%	66	25	58.6	5	0	0	1173.70	625	634
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	MGITEYNNQCR	99.7%	67.4	25	67.4	4	0	0	1401.59	111	121
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	NNDLCYWVPELVR	99.7%	81	25	75.7	3	0	0	1677.81	429	441
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	NVIVNGLVLASDGQK	99.7%	105	25	105	2	0	0	1526.85	586	600
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	QLSSEELEQFQK	99.7%	72.3	25	65.9	2	0	0	1465.72	918	929
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	TESAVSQMQSVIELGR	99.7%	111	25	111	4	0	0	1750.86	818	833
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	TGTIVVEGHELHDEDIR	99.7%	41.7	25	41.2	0	2	0	1919.95	930	946
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	TVYVSVLPTTADF	99.6%	38.7	25	29.9	2	0	0	1412.73	1250	1262
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	VCMDFNIIR	99.7%	55.3	25	48.1	2	0	0	1183.56	335	343
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	VENMVDQLLR	99.7%	87.9	25	69.5	4	0	0	1216.64	419	428
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	VLIDPVSVQDK	96.4%	28.9	25	24.3	1	0	0	1212.68	786	796
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	VREELIDK	98.8%	33.6	25	20.4	2	0	0	1001.56	809	816
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	YAHQSGFHVDR	94.8%	22.2	25	22.2	0	1	0	1316.61	71	81
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	YIIEELNVR	99.7%	65.9	25	12.1	2	0	0	1148.63	869	877
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	31	36	76	0.08%	28.3%	YRPLFDYFLK	98.2%	26	25	21.6	0	1	0	1361.73	289	298
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	27	49	0.05%	25.3%	ASPLLPANHVTMAK	97.6%	30.6	25	23.3	1	0	0	1465.78	373	386
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	27	49	0.05%	25.3%	AVLEEGTDVVIK	99.7%	93.6	25	82.2	2	0	0	1272.70	434	445
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	27	49	0.05%	25.3%	CGFSELYSWQR	99.7%	66	25	63.4	1	0	0	1432.63	91	101
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	27	49	0.05%	25.3%	DSFLGSIPGK	99.7%	72.8	25	55.5	2	0	0	1020.54	887	896

Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	27	49	0.05%	25.3%	EAQNLSAMEIR	99.7%	63.1	25	53.5	4	0	0	1261.62	171	181
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	27	49	0.05%	25.3%	ELSNFYFSIIK	99.7%	63.3	25	53.1	2	0	0	1360.71	793	803
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	27	49	0.05%	25.3%	EMTADVIELK	99.7%	54.1	25	39.4	4	0	0	1148.59	948	957
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	27	49	0.05%	25.3%	EPPYGADVLR	99.7%	44.9	25	32.7	2	0	0	1116.57	688	697
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	27	49	0.05%	25.3%	FLINLEGGDIR	99.7%	80.6	25	49.8	2	0	0	1246.68	960	970
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	27	49	0.05%	25.3%	FLINLEGGDIREESSYK	99.7%	46.5	25	42.4	0	2	0	1969.99	960	976
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	27	49	0.05%	25.3%	FPLLKPSPK	99.6%	38	25	30.9	2	0	0	1026.63	273	281
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	27	49	0.05%	25.3%	LVHSYPYDWR	94.9%	27.6	25	18	1	0	0	1335.65	459	468
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	27	49	0.05%	25.3%	QQPDTELEIQQK	99.7%	50.5	25	48.4	2	0	0	1456.73	79	90
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	27	49	0.05%	25.3%	SCQTALVEILDVIVR	99.7%	98.4	25	94.7	2	1	0	1715.94	818	832
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	27	49	0.05%	25.3%	SGDLYVLAADK	99.7%	88.4	25	78.6	2	0	0	1151.59	326	336
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	27	49	0.05%	25.3%	SYKPVFWSPSSR	99.3%	35.5	25	33.1	2	0	0	1440.73	239	250
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	27	49	0.05%	25.3%	TALAEAELEYNPEHVSR	99.7%	65.6	25	65.6	2	2	0	1928.93	251	267
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	27	49	0.05%	25.3%	TGWISTSSIWK	99.7%	51.1	25	43.2	2	0	0	1265.65	861	871
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	27	49	0.05%	25.3%	TKDEYLINSQTTEHIVK	99.7%	55.7	25	54.1	0	2	0	2019.04	539	555
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	27	49	0.05%	25.3%	TVIVHGFTLGEK	99.7%	62	25	48.8	1	2	0	1300.73	650	661
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	27	49	0.05%	25.3%	VWGVPIPVFHHK	98.1%	25.8	25	23.6	0	2	0	1415.79	527	538
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	27	49	0.05%	25.3%	YTAESSDTLCPR	99.7%	93.1	25	87.1	2	0	0	1399.62	993	1004
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	4	4	9	0.01%	5.8%	LAEPSQLLK	99.1%	34.8	25	13.6	2	0	0	998.59	116	124
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	4	4	9	0.01%	5.8%	LLNDEDPVVVTK	99.7%	70.4	25	65.2	4	0	0	1341.73	150	161
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	4	4	9	0.01%	5.8%	LNYGIPAIVK	98.3%	32.1	25	25.4	2	0	0	1087.65	478	487
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	4	4	9	0.01%	5.8%	TMQNTSDLDTAR	99.7%	53.2	25	48.8	1	0	0	1352.61	192	203
Katanin p60 ATPase-containing subunit A1	KATNA1	KTNA1_HUMAN	56.0	100.0%	5	5	12	0.01%	13.2%	DIISQNPNVR	99.7%	60.8	25	52.4	4	0	0	1155.61	198	207
Katanin p60 ATPase-containing subunit A1	KATNA1	KTNA1_HUMAN	56.0	100.0%	5	5	12	0.01%	13.2%	EAVVLPMWMPEFFK	98.6%	32.7	25	32.7	1	0	0	1723.86	223	236
Katanin p60 ATPase-containing subunit A1	KATNA1	KTNA1_HUMAN	56.0	100.0%	5	5	12	0.01%	13.2%	FYSPATIFIDEIDSICSR	99.7%	97.1	25	97.1	2	0	0	2134.02	299	316
Katanin p60 ATPase-containing subunit A1	KATNA1	KTNA1_HUMAN	56.0	100.0%	5	5	12	0.01%	13.2%	SVSAADIER	99.7%	53.3	25	28.2	2	0	0	947.48	472	480
Katanin p60 ATPase-containing subunit A1	KATNA1	KTNA1_HUMAN	56.0	100.0%	5	5	12	0.01%	13.2%	TTFFNVSSSTLTSK	99.7%	66.1	25	63.3	3	0	0	1519.76	268	281
Kinase D-interacting substrate of 220 kDa	KIDINS220	KDIS_HUMAN	196.5	99.8%	2	2	4	0.00%	1.2%	NIEVVELLLDK	99.7%	45	25	42.6	2	0	0	1284.74	347	357
Kinase D-interacting substrate of 220 kDa	KIDINS220	KDIS_HUMAN	196.5	99.8%	2	2	4	0.00%	1.2%	SILTQIFGAR	99.7%	53.5	25	52	2	0	0	1105.64	417	426
Kinesin-like protein KIF11	KIF11	KIF11_HUMAN	119.2	100.0%	3	3	7	0.01%	3.4%	LNLVDLAGSENIGR	99.7%	77	25	77	2	0	0	1470.79	261	274
Kinesin-like protein KIF11	KIF11	KIF11_HUMAN	119.2	100.0%	3	3	7	0.01%	3.4%	NILNKPEVNQK	99.6%	38.6	25	32.9	2	0	0	1296.73	358	368
Kinesin-like protein KIF11	KIF11	KIF11_HUMAN	119.2	100.0%	3	3	7	0.01%	3.4%	TVLQELINVLK	99.7%	50.9	25	36.1	3	0	0	1269.78	619	629
Kinesin-like protein KIF22	KIF22	KIF22_HUMAN	73.3	99.8%	2	2	3	0.00%	3.8%	ALMDLLQLTR	99.7%	60.1	25	40.1	2	0	0	1173.67	150	159
Kinesin-like protein KIF22	KIF22	KIF22_HUMAN	73.3	99.8%	2	2	3	0.00%	3.8%	VLDLLDPASGDLVIR	99.2%	35.4	25	24.5	1	0	0	1595.90	184	198
Kinesin-like protein KIF23	KIF23	KIF23_HUMAN	110.1	100.0%	2	2	3	0.00%	2.6%	ALLQEFDNAVLSK	99.7%	70.6	25	51.3	2	0	0	1447.78	524	536
Kinesin-like protein KIF23	KIF23	KIF23_HUMAN	110.1	100.0%	2	2	3	0.00%	2.6%	NLQQELETQNQK	99.7%	63.8	25	53.2	1	0	0	1472.73	588	599
Kinetochore-associated protein 1	KNTC1	KNTC1_HUMAN	250.8	99.8%	2	2	4	0.00%	1.0%	LGISFQPVFR	99.7%	47.9	25	40.4	2	0	0	1163.66	1414	1423
Kinetochore-associated protein 1	KNTC1	KNTC1_HUMAN	250.8	99.8%	2	2	4	0.00%	1.0%	VLAPELIPSILEK	99.3%	35.8	25	35.8	2	0	0	1421.86	727	739
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	5	5	7	0.01%	14.7%	GLLEESSFATLFPK	99.7%	67.1	25	64.8	2	0	0	1538.81	53	66
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	5	5	7	0.01%	14.7%	ILQDDVACDIIK	99.7%	79.4	25	54.4	2	0	0	1402.73	135	146
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	5	5	7	0.01%	14.7%	LGALTAEEIALK	99.7%	75.7	25	44.9	1	0	0	1228.71	358	369
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	5	5	7	0.01%	14.7%	SVSFEQAVR	98.1%	31.6	25	24	1	0	0	1022.53	126	134
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	5	5	7	0.01%	14.7%	TFDPYIIIR	99.7%	45.2	25	32.5	1	0	0	1137.63	107	115
Kynurenine--oxoglutarate transaminase 3	CCBL2	KAT3_HUMAN	51.4	100.0%	3	3	5	0.01%	8.2%	AIILNTPHNPLGK	99.7%	59.6	25	58.8	2	0	0	1387.81	210	222
Kynurenine--oxoglutarate transaminase 3	CCBL2	KAT3_HUMAN	51.4	100.0%	3	3	5	0.01%	8.2%	IAAIDSLNQYTR	99.7%	58.2	25	58.2	1	0	0	1364.72	88	99
Kynurenine--oxoglutarate transaminase 3	CCBL2	KAT3_HUMAN	51.4	100.0%	3	3	5	0.01%	8.2%	MAGATPVFIPLR	99.7%	71.7	25	44.8	2	0	0	1272.71	168	179
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	10	11	16	0.02%	25.3%	FIPEITISDILR	99.7%	70.6	25	67.4	2	0	0	1416.81	388	399
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	10	11	16	0.02%	25.3%	FPFLGVHFTPR	97.5%	24.8	25	22.9	0	2	0	1317.71	308	318
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	10	11	16	0.02%	25.3%	GDYLLLKPEK	96.0%	28.5	25	24.1	1	0	0	1175.67	283	292
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	10	11	16	0.02%	25.3%	GNIYPVPDSR	99.2%	35.5	25	23.5	1	0	0	1117.56	298	307
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	10	11	16	0.02%	25.3%	HPSLSIGVLEK	99.7%	42.1	25	37.6	1	0	0	1179.67	71	81

L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	10	11	16	0.02%	25.3%	ISELSGCTPDPR	99.7%	58.2	25	46.9	1	0	0	1331.63	266	277
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	10	11	16	0.02%	25.3%	LASQNFSYGVTEMYK	99.7%	77.4	25	77.4	1	0	0	1737.82	360	374
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	10	11	16	0.02%	25.3%	LIQQEDIK	98.7%	33.2	25	9.1	2	0	0	986.55	166	173
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	10	11	16	0.02%	25.3%	LIVAVEQEEIPR	99.7%	75.7	25	39.5	2	0	0	1395.78	137	148
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	10	11	16	0.02%	25.3%	MDGSIWLGPNAVLAFK	99.7%	43.5	25	43.5	3	0	0	1734.89	319	334
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	5	6	11	0.01%	22.8%	DFLLQQTMLR	99.7%	53.9	25	43.3	3	0	0	1264.67	29	38
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	5	6	11	0.01%	22.8%	IAWALSR	99.6%	37.9	25	24.8	2	0	0	816.47	89	95
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	5	6	11	0.01%	22.8%	KSLDFYTR	99.7%	45.3	25	15.4	2	0	0	1029.54	44	51
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	5	6	11	0.01%	22.8%	RFEELGVK	99.7%	48.7	25	26.7	2	0	0	977.54	141	148
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	5	6	11	0.01%	22.8%	VLGMTLIQK	99.7%	57	25	51.4	2	0	0	1002.60	52	60
Lamina-associated polypeptide 2, isoform alpha	TMPO	LAP2A_HUMAN	75.5	99.8%	2	2	4	0.00%	4.2%	SSTPLPTISSSAENTR	99.7%	41.8	25	41.8	1	0	0	1647.82	158	173
Lamina-associated polypeptide 2, isoform alpha	TMPO	LAP2A_HUMAN	75.5	99.8%	2	2	4	0.00%	4.2%	YGVNPGPIVGTTR	99.7%	58.7	25	58.4	3	0	0	1330.71	127	139
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	25	0.03%	13.7%	KFADGEVVR	99.7%	45.3	25	39	2	0	0	1020.55	5	13
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	25	0.03%	13.7%	LTPLILKPFGNSISR	99.7%	48.9	25	48.9	2	1	0	1655.98	117	131
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	25	0.03%	13.7%	NDLSPASSGNAVYDFFIGR	99.7%	87.1	25	87.1	8	0	0	2029.96	354	372
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	25	0.03%	13.7%	NLLVSGWWGFVR	99.7%	71.5	25	71.5	4	0	0	1433.77	533	544
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	25	0.03%	13.7%	TFEVTPIR	98.9%	33.7	25	30.8	2	0	0	962.53	196	203
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	25	0.03%	13.7%	VVEGTPLIDGR	99.7%	57.7	25	48.3	4	0	0	1155.64	280	290
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	25	0.03%	13.7%	YNGEPEHIER	99.7%	47.5	25	34.2	2	0	0	1243.57	132	141
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	AEHDQLLLNYAK	99.3%	35.7	25	35.7	1	1	0	1414.73	112	123
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	AGGPTTPLSPTR	99.7%	65	25	65	4	0	0	1154.62	15	26
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	AKLQIELGK	99.7%	58.6	25	33.2	2	0	0	999.62	101	109
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	ALYETELADAR	99.7%	69.8	25	54.2	4	0	0	1251.62	80	90
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	ALYETELADARR	98.4%	32.2	25	32.2	3	0	0	1407.72	80	91
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	CKAEHDQLLLNYAK	95.8%	22.9	25	22.9	0	1	0	1702.86	110	123
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	CQSLTEDLEFR	99.7%	61.7	25	58.5	1	0	0	1397.64	198	208
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	CQSLTEDLEFRK	99.7%	64.9	25	59.9	2	2	0	1525.73	198	209
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	DAALATALGDK	99.7%	62.9	25	52.9	2	0	0	1045.55	146	156
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	DAALATALGDKK	99.7%	75.7	25	48.7	5	0	0	1173.65	146	157
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	DQMQQQLNDYEQLLDVK	99.7%	104	25	104	2	0	0	2108.00	351	367
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	ESDLNGAQIK	99.7%	44	25	37.3	1	0	0	1074.54	125	134
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	IESLSSQLSNLQK	99.7%	87.8	25	76	2	0	0	1446.78	300	312
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	IGDTSVSYK	99.7%	79.4	25	79.2	2	0	0	969.49	475	483
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	IQELEDLLAK	99.7%	68.6	25	36.1	4	0	0	1171.66	321	330
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	KESDLNGAQIK	99.3%	35.7	25	23	2	0	0	1202.64	124	134
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	KLLEGEEER	99.7%	71.3	25	47.8	2	0	0	1102.57	379	387
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	KQLADETLLK	99.7%	39.7	25	32.2	2	0	0	1158.67	182	191
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	LALDMEISAYR	99.7%	66.8	25	63	2	0	0	1297.65	368	378
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	LALDMEISAYRK	99.7%	47	25	45.1	2	2	0	1425.74	368	379
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	LAQALHEMR	99.7%	76.9	25	66.1	4	0	0	1068.56	242	250
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	LAVYIDK	98.3%	31.9	25	31.9	2	0	0	821.48	43	49
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	LAVYIDKVR	99.2%	35.5	25	34.7	2	0	0	1076.65	43	51
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	LKNTSEQDQPMGGWEMIR	99.6%	31.9	25	31.9	0	1	0	2151.98	456	473
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	LLEGEEER	99.6%	38.1	25	30.1	2	0	0	974.48	380	387
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	LLEGEEERLK	99.7%	50	25	37.3	4	0	0	1215.66	380	389
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	LQEKEELR	99.7%	49.3	25	24.4	2	0	0	1044.57	30	37
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	LQIELGK	99.0%	34.2	25	0	3	0	0	800.49	103	109
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	LREYEAALNSK	99.7%	66.2	25	49.9	4	0	0	1293.68	135	145
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	LSSEMNTSTVNSAR	99.7%	110	25	103	7	0	0	1496.70	277	290
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	LVEVDSGR	98.4%	32.3	25	21.8	1	0	0	874.46	227	234
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	LYKEELEQTYHAK	99.7%	65.5	25	59.7	2	4	0	1651.83	259	271

Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	MRIESLSSQLSNLQK	99.7%	57.9	25	56	2	3	0	1749.92	298	312
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	NQNSWGTGEDVK	99.7%	66.9	25	66.9	2	0	0	1334.60	517	528
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	QIEYEYK	97.4%	30.2	25	23.3	2	0	0	972.47	235	241
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	SLETENSALQLQVTER	99.7%	98.3	25	94.2	1	0	0	1817.92	52	67
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	SLETENSALQLQVTEREEVR	99.7%	61.3	25	61.3	0	4	0	2331.18	52	71
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	SMYEEEINETR	99.7%	69.8	25	69.8	2	0	0	1416.59	210	220
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	39	47	106	0.11%	52.2%	SMYEEEINETRR	95.5%	28	25	22.7	1	0	0	1556.70	210	221
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	19	22	46	0.05%	41.0%	AGGPATPLSPTR	99.7%	52.7	25	47.5	4	0	0	1124.61	9	20
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	19	22	46	0.05%	41.0%	ALELENDRLLLK	99.7%	42.5	25	32.6	1	0	0	1426.83	46	57
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	19	22	46	0.05%	41.0%	ALYESELADAR	99.7%	58.8	25	46.3	2	0	0	1237.61	74	84
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	19	22	46	0.05%	41.0%	ATSSSSGSLSATGR	99.7%	92.4	25	91.9	2	0	0	1268.61	397	410
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	19	22	46	0.05%	41.0%	CQSLQEELDFRK	99.7%	38.8	25	35.5	0	1	0	1552.74	192	203
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	19	22	46	0.05%	41.0%	EGELTVAQGR	99.7%	70.3	25	39.7	4	0	0	1059.54	119	128
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	19	22	46	0.05%	41.0%	GLESDVAELR	99.7%	84.3	25	65.3	2	0	0	1088.56	152	161
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	19	22	46	0.05%	41.0%	ISEKEEVTTR	99.7%	72.2	25	50.7	2	0	0	1191.62	58	67
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	19	22	46	0.05%	41.0%	KLLEGEEER	99.7%	71.3	25	47.8	2	0	0	1102.57	373	381
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	19	22	46	0.05%	41.0%	LESLSYQLSGLQK	99.7%	65	25	54	1	0	0	1465.79	294	306
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	19	22	46	0.05%	41.0%	LLEGEEER	99.6%	38.1	25	30.1	2	0	0	974.48	374	381
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	19	22	46	0.05%	41.0%	LLEGEEERLK	99.7%	50	25	37.3	4	0	0	1215.66	374	383
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	19	22	46	0.05%	41.0%	LQEKEELR	99.7%	49.3	25	24.4	2	0	0	1044.57	24	31
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	19	22	46	0.05%	41.0%	LQIEIGK	99.0%	34.2	25	0	3	0	0	800.49	97	103
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	19	22	46	0.05%	41.0%	LRAELDEVNK	99.7%	40.3	25	22.3	2	0	0	1186.64	104	113
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	19	22	46	0.05%	41.0%	LSSDQNDKAASAAR	99.7%	65.2	25	60.2	2	0	0	1433.70	271	284
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	19	22	46	0.05%	41.0%	LYKLELEQTYQAK	99.7%	82.9	25	78.2	2	0	0	1626.87	253	265
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	19	22	46	0.05%	41.0%	MAQALEELR	98.8%	33.4	25	15.6	1	0	0	1076.54	236	244
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	19	22	46	0.05%	41.0%	NNSDKDQSLGNWR	99.7%	40.4	25	12.9	2	1	0	1533.70	470	482
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	19	22	46	0.05%	41.0%	QVLEGEEIAYK	99.7%	72.9	25	64	2	0	0	1278.66	486	496
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	19	22	46	0.05%	41.0%	RLVEVDSSR	99.7%	51.4	25	37.4	3	0	0	1060.57	220	228
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	19	22	46	0.05%	41.0%	SEVELAAALSDKR	99.7%	79.4	25	70.1	2	0	0	1388.74	139	151
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	19	22	46	0.05%	41.0%	TVLVNADGEEVAMR	99.7%	105	25	105	4	0	0	1503.75	542	555
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	19	22	46	0.05%	41.0%	VKDLESLFHR	99.7%	66.5	25	54.5	2	4	0	1243.68	129	138
Lanosterol synthase	LSS	ERG7_HUMAN	83.3	99.8%	2	2	2	0.00%	3.1%	HPDIEAQER	99.2%	35	25	25.5	1	0	0	1094.52	664	672
Lanosterol synthase	LSS	ERG7_HUMAN	83.3	99.8%	2	2	2	0.00%	3.1%	STVFGTALNYVSLR	99.7%	57.3	25	49.7	1	0	0	1527.82	149	162
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	8	9	17	0.02%	7.6%	ETESAPGSPR	98.5%	32.6	25	29.5	1	0	0	1030.48	514	523
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	8	9	17	0.02%	7.6%	FQQVPTDALANK	99.7%	57.9	25	49.2	2	0	0	1331.70	742	753
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	8	9	17	0.02%	7.6%	FWSFFLR	99.7%	41.5	25	37.3	2	0	0	1002.52	918	924
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	8	9	17	0.02%	7.6%	LFGAPEPSTIAR	97.9%	31.1	25	6.59	2	0	0	1258.68	754	765
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	8	9	17	0.02%	7.6%	LGIGQSQEMNTLFR	99.7%	82.2	25	78.2	4	0	0	1593.81	904	917
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	8	9	17	0.02%	7.6%	LQEYLGK	95.0%	27.6	25	19.5	1	0	0	850.47	1011	1017
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	8	9	17	0.02%	7.6%	SLPTTVPESPNYR	98.9%	34	25	32.4	1	0	0	1460.74	766	778
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	8	9	17	0.02%	7.6%	YGLECLFR	99.7%	59.4	25	55.7	4	0	0	1057.51	949	956
La-related protein 7	LARP7	LARP7_HUMAN	66.9	99.8%	2	2	3	0.00%	5.0%	AIEFLNNPPEEAPR	99.7%	54.9	25	54.9	1	0	0	1596.80	182	195
La-related protein 7	LARP7	LARP7_HUMAN	66.9	99.8%	2	2	3	0.00%	5.0%	VNATGPQFVSGVIVK	99.7%	70.5	25	61.2	2	0	0	1515.85	444	458
Large neutral amino acids transporter small subunit 1	SLC7A5	LAT1_HUMAN	55.0	99.9%	2	3	7	0.01%	6.3%	ALAAPAAEEKEEAR	99.7%	88	25	83.6	4	1	0	1455.74	10	23
Large neutral amino acids transporter small subunit 1	SLC7A5	LAT1_HUMAN	55.0	99.9%	2	3	7	0.01%	6.3%	SADGSAPAGEGEGVTLQR	99.7%	82.2	25	82.2	2	0	0	1701.80	31	48
Lethal(2) giant larvae protein homolog 1	LLGL1	L2GL1_HUMAN	115.4	99.9%	2	2	6	0.01%	2.4%	APVVAIAVLDGR	99.7%	92.2	25	83.7	4	0	0	1180.70	788	799
Lethal(2) giant larvae protein homolog 1	LLGL1	L2GL1_HUMAN	115.4	99.9%	2	2	6	0.01%	2.4%	TGPLPWPAGFQPR	97.5%	30.4	25	27.4	2	0	0	1423.75	578	590
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	AFAETHIK	99.1%	34.8	25	29.3	2	0	0	916.49	1091	1098
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	AGDMENAENILTVMR	99.7%	75.8	25	75.8	8	0	0	1663.78	245	259
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	AGYPQYVSEILEK	99.7%	76.4	25	67.9	2	0	0	1496.76	315	327
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	CVANNQVETLEK	99.7%	68.3	25	58.5	2	0	0	1404.68	930	941

Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	DAGIEPGPDTYLALLNAYAEK	99.7%	47	25	47	1	0	0	2221.10	260	280
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	DAHLLVESK	99.7%	56.2	25	47.8	2	0	0	1011.55	641	649
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	DLPVTEAVFSALVTGHAR	99.7%	79.5	25	79.5	2	0	0	1883.00	227	244
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	DTTALSFFHMLNGAALR	99.7%	42.4	25	41	1	0	0	1864.94	783	799
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	EKDIQEESTFSSR	99.7%	68	25	64.2	2	0	0	1555.72	65	77
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	EQNIVFNAETYSNLIK	99.7%	98.1	25	98.1	2	0	0	1882.95	1060	1075
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	FSPTDFLAK	96.3%	28.8	25	19.9	1	0	0	1025.53	179	187
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	GAYDIFLNAK	99.7%	59.8	25	58.2	2	0	0	1111.58	1050	1059
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	GDLSTALEVAIDCYEK	99.7%	57	25	57	2	0	0	1783.84	836	851
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	GDVENIEVVQK	99.7%	61.8	25	49.9	2	0	0	1229.64	1153	1163
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	GFTLNDAANSR	99.7%	84.2	25	71.5	2	0	0	1165.56	1099	1109
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	IHDVLCK	97.3%	30.1	25	19.6	1	0	0	884.47	858	864
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	IPENIYR	97.0%	29.7	25	17.8	1	0	0	904.49	618	624
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	IQEENVIPR	99.7%	55.5	25	48.1	2	0	0	1097.60	981	989
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	ISIMAER	99.7%	50.8	25	37.4	2	0	0	835.43	1237	1243
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	KGAYDIFLNAK	99.0%	34.5	25	34.5	2	0	0	1239.67	1049	1059
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	KIIETPGIR	99.7%	54.9	25	46.8	2	0	0	1026.63	909	917
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	LDDLFLK	99.3%	35.7	25	13.9	2	0	0	863.49	1351	1357
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	LDDLFLKR	99.7%	54.7	25	41	2	0	0	1019.59	1351	1358
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	LDSSAVLDTGK	99.7%	87	25	78.1	2	0	0	1105.57	740	750
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	LGAVYDVSHYNALLK	99.7%	89.4	25	81	2	2	0	1662.89	156	170
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	LIASYCNVGDIEGASK	99.7%	114	25	110	2	0	0	1696.82	203	218
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	LIITQVR	97.0%	29.6	25	10.3	1	0	0	842.55	1110	1116
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	LLMSEDYFTQAMEVK	99.7%	97.2	25	97.2	8	0	0	1836.84	1076	1090
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	LQDAINILK	99.7%	55.1	25	41.8	2	0	0	1027.61	764	772
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	LVEKGETDLIQK	99.7%	52.3	25	44.3	2	0	0	1372.77	865	876
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	MEEANIQPNR	99.7%	63.4	25	56.8	2	0	0	1201.56	188	197
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	MLNGLEDSIGLSK	99.7%	82.7	25	59.4	5	0	0	1392.70	1164	1176
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	MVFINNIALAQIK	99.7%	94.2	25	93.5	4	0	0	1474.85	1177	1189
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	NLLESYHVPELIK	99.7%	64.3	25	53.1	2	0	0	1554.85	628	640
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	NVQGIIEILK	99.7%	70.6	25	59	2	0	0	1126.68	454	463
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	QLILVLCSEENMQK	99.7%	87.8	25	83.1	2	0	0	1720.86	684	697
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	SCGSLLPELK	99.7%	53.4	25	43.2	2	0	0	1103.58	129	138
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	SEAANGNLDFVLSFLK	99.7%	71.3	25	69.3	1	0	0	1724.89	514	529
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	SGGLGGSHALLLLR	99.7%	79.4	25	72.2	2	2	0	1350.79	115	128
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	SNTLPISLQSIR	99.7%	78.9	25	57.1	2	0	0	1328.75	530	541
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	SVLELIPELNEK	97.1%	29.7	25	27.2	1	0	0	1383.77	1306	1317
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	SYVSEKDVTSAK	99.7%	74.1	25	74.1	2	0	0	1313.66	1327	1338
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	TVLDQQQTPSR	99.7%	66.7	25	49.2	2	0	0	1272.65	1129	1139
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	TVQLTSSELESTLETLK	99.7%	115	25	113	2	0	0	1878.99	656	672
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	VIEPQYFGLAYLFR	99.7%	66.4	25	64.9	2	0	0	1715.92	1210	1223
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	46	52	104	0.11%	38.1%	VYLQNEYK	99.1%	34.7	25	24.4	1	0	0	1056.54	171	178
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	10	10	14	0.01%	17.6%	FLALEGNPLR	99.6%	38.3	25	28.8	1	0	0	1129.64	338	347
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	10	10	14	0.01%	17.6%	FLPEFPSCSLLK	99.6%	38.4	25	21.8	1	0	0	1437.74	257	268
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	10	10	14	0.01%	17.6%	GTAAILEYLR	99.7%	59.9	25	43.2	2	0	0	1106.62	588	597
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	10	10	14	0.01%	17.6%	LQTINLSFNR	99.7%	65.9	25	55.9	2	0	0	1205.66	497	506
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	10	10	14	0.01%	17.6%	NLSEVPQCVWR	99.7%	45.6	25	45.6	1	0	0	1387.68	47	57
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	10	10	14	0.01%	17.6%	QATLIPDEVFDAVK	99.6%	38.8	25	20.3	1	0	0	1545.82	410	423
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	10	10	14	0.01%	17.6%	SLPAEINR	95.9%	28.4	25	21.8	1	0	0	899.49	211	218
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	10	10	14	0.01%	17.6%	SNIVTSINFSK	99.7%	54.3	25	50.6	1	0	0	1209.65	424	434
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	10	10	14	0.01%	17.6%	SVPDEIILLR	99.7%	49.6	25	29.9	2	0	0	1154.68	303	312

Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	10	10	14	0.01%	17.6%	TLLLDGNPFR	99.7%	66.1	25	60.2	2	0	0	1145.63	569	578
Leucine-rich repeat-containing protein 47	LRRC47	LRC47_HUMAN	63.5	99.8%	2	2	3	0.00%	6.4%	APGPGLAQGLPQLHSLVLR	95.3%	22.5	25	22.5	0	1	0	1924.11	65	83
Leucine-rich repeat-containing protein 47	LRRC47	LRC47_HUMAN	63.5	99.8%	2	2	3	0.00%	6.4%	NALGPGLSPELGPLPALR	99.7%	64.6	25	64.6	2	0	0	1772.01	85	102
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	24	27	47	0.05%	23.1%	ANGHLLLNSEK	99.7%	52.5	25	45.6	1	0	0	1195.64	706	716
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	24	27	47	0.05%	23.1%	CEFAVGYQR	99.7%	39.8	25	35	2	0	0	1129.51	70	78
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	24	27	47	0.05%	23.1%	EDKGTGVVTSVPSDSPDDIAALR	99.7%	32.9	25	29.8	0	2	0	2329.15	382	404
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	24	27	47	0.05%	23.1%	ELAVEGMHR	99.1%	34.7	25	28.3	2	0	0	1057.51	837	845
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	24	27	47	0.05%	23.1%	ELMGEEILGASLSAPLTSYK	99.7%	44.4	25	44.4	1	0	0	2109.08	351	370
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	24	27	47	0.05%	23.1%	EVWDYVFFK	99.7%	43.6	25	35.1	2	0	0	1232.60	633	641
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	24	27	47	0.05%	23.1%	FASEAEDKIR	99.7%	64.8	25	55.1	1	0	0	1165.58	1040	1049
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	24	27	47	0.05%	23.1%	FDDPLLGPR	99.7%	72.8	25	57.8	2	0	0	1029.54	1118	1126
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	24	27	47	0.05%	23.1%	GFYEGIMLVDGFK	99.7%	93.6	25	84.9	4	0	0	1475.72	471	483
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	24	27	47	0.05%	23.1%	GTGVVTSVPSDSPDDIAALR	99.7%	69.5	25	69.5	2	0	0	1956.99	385	404
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	24	27	47	0.05%	23.1%	MIDAGDALIYMEPEK	99.7%	63.8	25	63.8	2	0	0	1695.80	498	512
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	24	27	47	0.05%	23.1%	QEFEFWYPVDLR	99.7%	63.1	25	59	2	0	0	1628.77	660	671
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	24	27	47	0.05%	23.1%	QTGEGVGPQEYTLLK	99.7%	59.7	25	53.3	2	0	0	1619.83	254	268
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	24	27	47	0.05%	23.1%	SFITTDVNPYYDSFVR	99.7%	104	25	101	2	0	0	1923.91	204	219
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	24	27	47	0.05%	23.1%	SGPASTFNDR	97.6%	30.6	25	22.2	1	0	0	1051.48	786	795
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	24	27	47	0.05%	23.1%	STGNFLTLTQAIDK	99.7%	90.9	25	80.9	2	0	0	1508.80	720	733
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	24	27	47	0.05%	23.1%	TGFFEFQAAK	99.7%	55.5	25	52	2	0	0	1145.56	823	832
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	24	27	47	0.05%	23.1%	VDIGDTIIYLVH	99.7%	78.4	25	77.6	2	0	0	1357.74	1165	1176
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	24	27	47	0.05%	23.1%	VFASELNAGIIK	99.7%	97	25	85.8	2	0	0	1261.72	796	807
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	24	27	47	0.05%	23.1%	VFEVNASNLEK	99.7%	71.2	25	63.4	2	0	0	1249.64	29	39
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	24	27	47	0.05%	23.1%	VIASELGSMPELK	99.7%	63.4	25	45.8	4	0	0	1373.73	971	983
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	24	27	47	0.05%	23.1%	VIASELGSMPELKK	99.7%	80.1	25	66.8	2	0	0	1501.83	971	984
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	24	27	47	0.05%	23.1%	VIYVLPMLTIK	99.7%	57.6	25	57.6	2	0	0	1289.79	371	381
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	24	27	47	0.05%	23.1%	WQFLTLR	99.4%	36.7	25	30.2	1	0	0	963.54	220	226
Leukotriene A-4 hydrolase	LTA4H	LKHA4_HUMAN	69.3	99.8%	2	2	3	0.00%	3.8%	SAYEFSETESMLK	99.7%	43.8	25	43.8	1	0	0	1521.68	231	243
Leukotriene A-4 hydrolase	LTA4H	LKHA4_HUMAN	69.3	99.8%	2	2	3	0.00%	3.8%	TFGETHPFTK	99.7%	44.1	25	43.4	2	0	0	1164.57	356	365
LINE-1 retrotransposable element ORF1 protein	L1RE1	LORF1_HUMAN	40.1	99.8%	2	2	3	0.00%	6.8%	DFVTTRPALK	99.1%	34.6	25	25.6	2	0	0	1147.65	305	314
LINE-1 retrotransposable element ORF1 protein	L1RE1	LORF1_HUMAN	40.1	99.8%	2	2	3	0.00%	6.8%	LTADLSAETLQAR	99.7%	99	25	92.7	1	0	0	1388.74	249	261
Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	DBT	ODB2_HUMAN	53.5	100.0%	3	4	6	0.01%	7.3%	LREELKPIAFAR	99.2%	29.1	25	28.9	0	1	0	1442.85	290	301
Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	DBT	ODB2_HUMAN	53.5	100.0%	3	4	6	0.01%	7.3%	LSFMPFFLK	99.2%	35	25	28.8	2	0	0	1129.61	305	313
Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	DBT	ODB2_HUMAN	53.5	100.0%	3	4	6	0.01%	7.3%	SYLENPAFMLLDLK	99.7%	77.6	25	70.4	3	0	0	1653.86	469	482
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	6	6	10	0.01%	2.5%	EIFVDFAPFLSR	99.7%	67.4	25	66.1	3	0	0	1440.75	1813	1824
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	6	6	10	0.01%	2.5%	IQNPQILK	97.9%	31.2	25	20.5	1	0	0	953.58	813	820
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	6	6	10	0.01%	2.5%	SAAAIALPPIAK	98.8%	33.6	25	32	1	0	0	1122.69	213	224
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	6	6	10	0.01%	2.5%	SPVDIVTGGISPVR	99.7%	58.1	25	58.1	1	0	0	1396.78	1488	1501
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	6	6	10	0.01%	2.5%	VGVGTSFGLPQTR	99.6%	38.6	25	38.6	2	0	0	1318.71	2183	2195
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	6	6	10	0.01%	2.5%	YGPDAFFNFPGK	99.7%	73.8	25	68.6	2	0	0	1359.64	201	212
LisH domain and HEAT repeat-containing protein KIAA1468	KIAA1468	K1468_HUMAN	134.6	99.8%	2	2	3	0.00%	2.0%	ALNFLVNEFLLK	99.7%	61.3	25	61.3	2	0	0	1420.82	258	269
LisH domain and HEAT repeat-containing protein KIAA1468	KIAA1468	K1468_HUMAN	134.6	99.8%	2	2	3	0.00%	2.0%	LSIDAIAAQLLR	99.0%	34.2	25	27.6	1	0	0	1283.77	92	103
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	17	22	153	0.16%	51.2%	DLADELALVDVIEDK	99.7%	99.6	25	98.2	2	0	0	1657.85	43	57
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	17	22	153	0.16%	51.2%	DQLIYNLLK	99.7%	68.2	25	46.3	7	0	0	1119.64	6	14
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	17	22	153	0.16%	51.2%	DQLIYNLLKEEQTPQNK	99.7%	88.8	25	88.8	4	4	0	2074.08	6	22
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	17	22	153	0.16%	51.2%	DYNVTANSK	99.7%	56.4	25	52.9	3	0	0	1011.47	82	90
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	17	22	153	0.16%	51.2%	FIIPNVVK	99.7%	40.4	25	27.1	5	0	0	929.58	119	126
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	17	22	153	0.16%	51.2%	GEMMDLQHGSLFLR	99.7%	63	25	63	8	2	0	1633.78	60	73
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	17	22	153	0.16%	51.2%	ITVVGVGAVGMACAISILMK	99.7%	53.2	25	47.2	2	0	0	2006.08	23	42
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	17	22	153	0.16%	51.2%	IVSGKDYNVTANSK	99.7%	91.5	25	91	8	2	0	1495.78	77	90
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	17	22	153	0.16%	51.2%	KSADTLWGIQK	98.9%	28	25	23.3	0	2	0	1246.68	318	328

L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	17	22	153	0.16%	51.2%	LLIVSNPVDILTYVAWK	99.7%	123	25	0	5	1	0	1944.12	133	149
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	17	22	153	0.16%	51.2%	LVIITAGAR	99.7%	70.6	25	37.1	22	0	0	913.58	91	99
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	17	22	153	0.16%	51.2%	QVVESAYEVIK	99.7%	71.8	25	64.4	12	0	0	1264.68	233	243
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	17	22	153	0.16%	51.2%	SADTLWGIQK	99.7%	62.5	25	52.5	14	0	0	1118.58	319	328
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	17	22	153	0.16%	51.2%	TLHPDLGTDK	98.9%	33.8	25	33.8	2	0	0	1096.56	213	222
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	17	22	153	0.16%	51.2%	VIGSGCNLDSAR	99.7%	80.3	25	68.4	22	0	0	1248.60	158	169
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	17	22	153	0.16%	51.2%	VTLTSEEEAR	99.7%	68.9	25	62.4	24	0	0	1134.56	306	315
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	17	22	153	0.16%	51.2%	VTLTSEEEARLK	99.7%	46.5	25	41.7	2	0	0	1375.74	306	317
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	23	135	0.14%	47.6%	EKLIAPVAEEEATVPNNK	99.7%	88.4	25	88.4	4	3	0	1952.03	6	23
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	23	135	0.14%	47.6%	FIIPQIVK	99.7%	42	25	38.4	3	0	0	957.61	120	127
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	23	135	0.14%	47.6%	GEMMDLQHGSLFLQTPK	99.7%	46.1	25	46.1	0	6	0	1963.93	61	77
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	23	135	0.14%	47.6%	GLTSVINQK	99.7%	59.6	25	45	12	0	0	959.55	300	308
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	23	135	0.14%	47.6%	HRVIGSGCNLDSAR	99.7%	37.5	25	37.5	0	3	0	1541.76	157	170
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	23	135	0.14%	47.6%	ITVVGVGQVGMACAISILGK	99.7%	113	25	113	5	4	0	1973.09	24	43
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	23	135	0.14%	47.6%	IVADKDYSVTANSK	99.7%	88.7	25	79.1	15	7	0	1510.77	78	91
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	23	135	0.14%	47.6%	IVVVTAGVR	99.7%	78.5	25	67.9	12	0	0	913.58	92	100
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	23	135	0.14%	47.6%	KSADTLWDIQK	99.7%	53.5	25	51.8	2	0	0	1304.68	319	329
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	23	135	0.14%	47.6%	LIAPVAEEEATVPNNK	99.7%	101	25	99.3	13	2	0	1694.90	8	23
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	23	135	0.14%	47.6%	LKDDEVAQLK	99.7%	55.2	25	35.7	2	0	0	1158.64	309	318
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	23	135	0.14%	47.6%	MVVESAYEVIK	99.7%	88.8	25	82.8	26	0	0	1267.66	234	244
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	23	135	0.14%	47.6%	SADTLWDIQK	99.7%	86.8	25	66.2	12	0	0	1176.59	320	329
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	23	135	0.14%	47.6%	SADTLWDIQKDLK	99.7%	53.2	25	41.2	2	0	0	1532.80	320	332
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	23	135	0.14%	47.6%	SLADELALVDVLEDK	99.7%	73	25	62.8	2	0	0	1629.86	44	58
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	23	135	0.14%	47.6%	VIGSGCNLDSAR	99.7%	80.3	25	68.4	22	0	0	1248.60	159	170
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	10	10	17	0.02%	12.9%	DIIALNPLYR	99.7%	64.3	25	58.8	2	0	0	1187.68	302	311
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	10	10	17	0.02%	12.9%	EAEDELSAR	98.5%	32.5	25	23	1	0	0	1019.46	245	253
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	10	10	17	0.02%	12.9%	EIFDIAFPDEQAEALAVER	99.7%	65.1	25	58.4	1	0	0	2163.06	941	959
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	10	10	17	0.02%	12.9%	FSVGGMTDVAEIK	99.7%	44.6	25	40.6	1	0	0	1369.67	547	559
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	10	10	17	0.02%	12.9%	ILCFYGPPGVGK	99.7%	50.5	25	50	1	0	0	1307.68	518	529
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	10	10	17	0.02%	12.9%	ILEFIAVSQLR	99.7%	75.6	25	64.5	3	0	0	1288.76	501	511
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	10	10	17	0.02%	12.9%	LAQPYVGVFLK	99.7%	45.3	25	41.9	2	0	0	1234.72	159	169
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	10	10	17	0.02%	12.9%	LGLLDNHSSEFNVTR	99.1%	28.8	25	27.5	0	1	0	1701.86	445	459
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	10	10	17	0.02%	12.9%	LSSDVLTLLIK	99.7%	80	25	62.2	3	0	0	1201.74	691	701
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	10	10	17	0.02%	12.9%	TENPLILIDEVDK	99.7%	67.8	25	67.8	2	0	0	1498.80	582	594
Long-chain fatty acid transport protein 4	SLC27A4	S27A4_HUMAN	72.1	99.8%	2	2	4	0.00%	3.1%	ILSFVYPIR	98.6%	32.9	25	24.2	1	0	0	1107.66	409	417
Long-chain fatty acid transport protein 4	SLC27A4	S27A4_HUMAN	72.1	99.8%	2	2	4	0.00%	3.1%	TVPILFASTVR	99.7%	50.5	25	50.5	3	0	0	1203.71	75	85
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	10	11	17	0.02%	18.3%	AKPVNSKPDSAYR	99.7%	51.3	25	49.2	2	1	0	1432.75	57	69
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	10	11	17	0.02%	18.3%	IGYSSPQTLADQSSK	99.7%	101	25	100	2	0	0	1581.78	349	363
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	10	11	17	0.02%	18.3%	LKDIVSLVPR	99.7%	55.5	25	49.7	2	0	0	1139.71	221	230
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	10	11	17	0.02%	18.3%	LLLCGGAPLSATTQR	99.7%	92.6	25	83.3	2	0	0	1557.84	447	461
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	10	11	17	0.02%	18.3%	LQAGEYVSLGK	99.0%	34.1	25	30	1	0	0	1164.63	586	596
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	10	11	17	0.02%	18.3%	LSPEPWTPETGLVTDAFK	99.7%	81.9	25	80.1	2	0	0	1988.00	682	699
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	10	11	17	0.02%	18.3%	NTPLCDSFVFR	99.6%	38.9	25	38.2	2	0	0	1355.64	425	435
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	10	11	17	0.02%	18.3%	SVNSLDGLASVLYPGCDTLDK	97.5%	30.5	25	30.5	1	0	0	2224.08	70	90
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	10	11	17	0.02%	18.3%	THYQADIER	96.3%	28.8	25	28.8	1	0	0	1132.54	707	715
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	10	11	17	0.02%	18.3%	VSEMSSFQR	99.7%	64.6	25	60.4	1	0	0	1086.49	398	406
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	7	8	16	0.02%	20.6%	EVTWEVLEGEVEK	99.3%	35.9	25	33.5	1	0	0	1546.76	300	312
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	7	8	16	0.02%	20.6%	GSIFVVFDSIESAK	99.7%	84.8	25	79.9	2	0	0	1498.78	152	165
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	7	8	16	0.02%	20.6%	GSIFVVFDSIESAKK	99.7%	76.7	25	70.2	2	0	0	1626.87	152	166
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	7	8	16	0.02%	20.6%	IIEDQQESLNK	99.7%	85	25	72.8	3	0	0	1316.67	318	328
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	7	8	16	0.02%	20.6%	LDEGWVPLEIMIK	99.7%	46	25	34.3	3	0	0	1542.82	42	54

Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	7	8	16	0.02%	20.6%	LTTDFNVIVEALSK	99.7%	120	25	115	3	0	0	1549.85	61	74
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	7	8	16	0.02%	20.6%	SPSKPLPEVTDEYKNDVK	98.6%	27	25	27	0	2	0	2046.04	92	109
Lys-63-specific deubiquitinase BRCC36	BRCC3	BRCC3_HUMAN	36.1	99.9%	2	2	4	0.00%	7.6%	VCLESAVELPK	99.7%	46.4	25	37	2	0	0	1244.66	227	237
Lys-63-specific deubiquitinase BRCC36	BRCC3	BRCC3_HUMAN	36.1	99.9%	2	2	4	0.00%	7.6%	VLYTCFQSIQAQK	99.7%	78.6	25	73	2	0	0	1585.80	168	180
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	15	0.02%	16.6%	IAPELYHK	99.2%	35	25	11.3	2	0	0	970.54	298	305
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	15	0.02%	16.6%	INMVEELEK	99.7%	39.6	25	19.3	1	0	0	1104.56	394	402
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	15	0.02%	16.6%	LIFYDLR	97.9%	31.1	25	30.5	2	0	0	939.53	142	148
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	15	0.02%	16.6%	LPETNLFETEETRK	99.7%	36.6	25	31.8	0	2	0	1706.86	408	421
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	15	0.02%	16.6%	MLVVGGIDR	99.7%	64.8	25	56.8	2	0	0	959.53	306	314
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	15	0.02%	16.6%	RGDIIGVQGNPGK	99.7%	66.9	25	63.6	2	0	0	1310.72	178	190
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	15	0.02%	16.6%	SEEEFIHINNK	99.7%	65.3	25	64.8	1	0	0	1359.65	165	175
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	15	0.02%	16.6%	VAMFLTDSNNIK	99.3%	35.7	25	34.2	1	0	0	1352.69	554	565
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	15	0.02%	16.6%	YSHLQPGDHLTDITLK	99.5%	30.8	25	28.1	0	2	0	1837.94	112	127
Lysophosphatidylcholine acyltransferase 1	LPCAT1	PCAT1_HUMAN	59.2	100.0%	3	3	4	0.00%	7.7%	ITFADFHR	95.8%	28.4	25	23.3	1	0	0	1006.51	471	478
Lysophosphatidylcholine acyltransferase 1	LPCAT1	PCAT1_HUMAN	59.2	100.0%	3	3	4	0.00%	7.7%	TCLITFKPGAFIPGAPVQPVVLR	98.4%	26.4	25	26.4	0	2	0	2481.41	215	237
Lysophosphatidylcholine acyltransferase 1	LPCAT1	PCAT1_HUMAN	59.2	100.0%	3	3	4	0.00%	7.7%	TLDTIQLAFK	99.7%	55.1	25	28.2	1	0	0	1149.65	417	426
Lysophospholipid acyltransferase 7	MBOAT7	MBOA7_HUMAN	52.8	99.7%	2	2	3	0.00%	5.1%	AASLEYDYETIR	94.7%	27.5	25	19.9	1	0	0	1430.68	289	300
Lysophospholipid acyltransferase 7	MBOAT7	MBOA7_HUMAN	52.8	99.7%	2	2	3	0.00%	5.1%	AASQPTSLAPEK	99.7%	44	25	33.8	2	0	0	1199.63	457	468
Lysosomal protective protein	CTSA	PPGB_HUMAN	54.5	100.0%	3	3	5	0.01%	6.5%	EFSHIAFLTIK	98.9%	34	25	29.3	2	0	0	1305.72	443	453
Lysosomal protective protein	CTSA	PPGB_HUMAN	54.5	100.0%	3	3	5	0.01%	6.5%	FLNKQPY	97.6%	30.6	25	25.2	1	0	0	909.48	474	480
Lysosomal protective protein	CTSA	PPGB_HUMAN	54.5	100.0%	3	3	5	0.01%	6.5%	YGDSGEQIAGFVK	99.7%	78.9	25	73.1	2	0	0	1370.66	430	442
Macrophage migration inhibitory factor	MIF	MIF_HUMAN	12.5	99.8%	2	3	8	0.01%	17.4%	LLCGLLAER	99.7%	68.1	25	53	2	0	0	1044.59	79	87
Macrophage migration inhibitory factor	MIF	MIF_HUMAN	12.5	99.8%	2	3	8	0.01%	17.4%	PMFIVNTNVPR	99.7%	67.9	25	53.4	6	0	0	1287.69	2	12
Magnesium transporter protein 1	MAGT1	MAGT1_HUMAN	38.0	100.0%	3	3	5	0.01%	8.1%	GFSAEQIAR	99.1%	34.9	25	25	2	0	0	978.50	160	168
Magnesium transporter protein 1	MAGT1	MAGT1_HUMAN	38.0	100.0%	3	3	5	0.01%	8.1%	RGDTYELQVR	99.7%	43	25	38.3	1	0	0	1236.63	150	159
Magnesium transporter protein 1	MAGT1	MAGT1_HUMAN	38.0	100.0%	3	3	5	0.01%	8.1%	YSSAFTNR	99.7%	63.4	25	55.7	2	0	0	945.44	106	113
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	7	8	13	0.01%	29.0%	AGAGSATLSMAYAGAR	99.7%	68.2	25	64.5	2	0	0	1470.70	242	257
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	7	8	13	0.01%	29.0%	ANTFVAELK	98.2%	31.7	25	17.6	2	0	0	992.54	177	185
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	7	8	13	0.01%	29.0%	IFGVTTLDIVR	99.7%	46.2	25	38.5	2	0	0	1233.72	166	176
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	7	8	13	0.01%	29.0%	SQETECTYFSTPLLLGK	99.7%	58.1	25	58.1	2	0	0	1973.95	280	296
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	7	8	13	0.01%	29.0%	VAVLGASGGIGQPLSLLLK	99.7%	63.1	25	63.1	2	0	0	1793.09	27	45
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	7	8	13	0.01%	29.0%	VDFPQDQLTALTGR	99.7%	49.5	25	44.6	2	0	0	1560.80	216	229
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	7	8	13	0.01%	29.0%	VNVPVIGGHAGK	99.7%	46.5	25	46.5	1	0	0	1147.66	192	203
Malectin	MLEC	MLEC_HUMAN	32.2	100.0%	4	4	8	0.01%	18.5%	FAEVYFAQSQQK	99.7%	67.7	25	67.7	2	0	0	1445.71	127	138
Malectin	MLEC	MLEC_HUMAN	32.2	100.0%	4	4	8	0.01%	18.5%	LSVQGEVSTFTGK	99.7%	71.7	25	71.7	2	0	0	1352.71	178	190
Malectin	MLEC	MLEC_HUMAN	32.2	100.0%	4	4	8	0.01%	18.5%	SNPEDQILYQTER	99.7%	58.4	25	44.8	2	0	0	1592.76	91	103
Malectin	MLEC	MLEC_HUMAN	32.2	100.0%	4	4	8	0.01%	18.5%	VCALYIMAGTVDDVPK	99.7%	68.7	25	53.5	2	0	0	1751.87	205	220
Malignant T-cell-amplified sequence 1	MCTS1	MCTS1_HUMAN	20.6	99.8%	2	2	2	0.00%	17.1%	FVLSGANIMCPGLTSPGAK	99.7%	52.9	25	52.9	1	0	0	1935.97	104	122
Malignant T-cell-amplified sequence 1	MCTS1	MCTS1_HUMAN	20.6	99.8%	2	2	2	0.00%	17.1%	YPFILPHQQVDK	99.2%	35.5	25	30.6	1	0	0	1484.79	88	99
Malonyl-CoA-acyl carrier protein transacylase, mitochondrial	MCAT	FABD_HUMAN	43.0	99.9%	2	2	2	0.00%	6.4%	LLAQQLVSPVK	99.7%	53.2	25	48.3	1	0	0	1195.74	315	325
Malonyl-CoA-acyl carrier protein transacylase, mitochondrial	MCAT	FABD_HUMAN	43.0	99.9%	2	2	2	0.00%	6.4%	LMEPAVEPLTQALK	99.7%	41.5	25	35.9	1	0	0	1539.85	273	286
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	5	5	8	0.01%	14.0%	GVTVGEGVR	99.4%	36.6	25	24.9	2	0	0	873.48	310	318
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	5	5	8	0.01%	14.0%	LLPAITILGCR	99.7%	50.4	25	50.1	2	0	0	1226.73	380	390
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	5	5	8	0.01%	14.0%	SAGSALYASR	99.7%	41.2	25	37.5	1	0	0	982.50	250	259
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	5	5	8	0.01%	14.0%	VAPSAVLGPNVSIGK	99.7%	59.9	25	58.5	2	0	0	1408.82	295	309
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	5	5	8	0.01%	14.0%	VEGTPSDPNPNDPR	99.7%	48.6	25	32.8	1	0	0	1494.68	353	366
Mannose-1-phosphate guanyltransferase beta	GMPPB	GMPPB_HUMAN	39.8	100.0%	4	4	7	0.01%	14.7%	ALILVGGYGTR	99.7%	72.6	25	64.3	2	0	0	1119.65	3	13
Mannose-1-phosphate guanyltransferase beta	GMPPB	GMPPB_HUMAN	39.8	100.0%	4	4	7	0.01%	14.7%	FVEKPQVFVSNK	99.7%	56.6	25	53.5	2	0	0	1421.78	159	170
Mannose-1-phosphate guanyltransferase beta	GMPPB	GMPPB_HUMAN	39.8	100.0%	4	4	7	0.01%	14.7%	LCSGPGIVGNVLVDPSAR	99.7%	72.4	25	72.4	2	0	0	1810.95	244	261
Mannose-1-phosphate guanyltransferase beta	GMPPB	GMPPB_HUMAN	39.8	100.0%	4	4	7	0.01%	14.7%	YGVVVCEADTGR	99.7%	72.6	25	67.8	1	0	0	1325.62	144	155
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	16	18	46	0.05%	23.4%	DLDELSRYPEDK	99.7%	51.4	25	45.2	1	0	0	1479.70	121	132

Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	16	18	46	0.05%	23.4%	GDADQASNILASFGLSAR	99.7%	105	25	102	4	0	0	1792.88	103	120
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	16	18	46	0.05%	23.4%	GNLGAGNGNLQGPR	99.7%	53.9	25	48.1	3	0	0	1324.67	374	387
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	16	18	46	0.05%	23.4%	GPGPLQER	98.4%	32.1	25	26.5	1	0	0	853.45	256	263
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	16	18	46	0.05%	23.4%	GPLPLSSQHR	99.7%	45.8	25	34.3	4	0	0	1091.60	93	102
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	16	18	46	0.05%	23.4%	GPSLNPVLDYDHGSR	99.7%	37.8	25	37.8	0	1	0	1626.79	193	207
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	16	18	46	0.05%	23.4%	IGPYQPNVPVGIDYVIPK	99.7%	67.8	25	67.8	4	0	0	1969.08	781	798
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	16	18	46	0.05%	23.4%	ITPENLPQILLQLK	99.7%	80	25	77.9	3	0	0	1619.97	133	146
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	16	18	46	0.05%	23.4%	LCSLFYTNEEVAK	99.7%	69.1	25	64	4	0	0	1573.76	805	817
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	16	18	46	0.05%	23.4%	MDYEDDRLR	99.7%	44.3	25	38.1	1	0	0	1212.53	217	225
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	16	18	46	0.05%	23.4%	SFQQSSLSR	99.7%	65.8	25	43.5	2	0	0	1039.52	4	12
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	16	18	46	0.05%	23.4%	SQAFIEMETR	99.7%	60.1	25	46.4	5	0	0	1211.57	533	542
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	16	18	46	0.05%	23.4%	SQESGYYDR	99.7%	44.6	25	44.6	2	0	0	1104.46	208	216
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	16	18	46	0.05%	23.4%	TEEGPTLSYGR	99.7%	62.9	25	52.4	4	0	0	1209.57	150	160
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	16	18	46	0.05%	23.4%	VIHLSNLPHSGYSDSAVLK	99.7%	34.5	25	34.1	0	3	0	2037.08	497	515
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	16	18	46	0.05%	23.4%	VVHIMDFQR	99.1%	34.8	25	26.2	4	0	0	1144.59	399	407
MAU2 chromatid cohesion factor homolog	MAU2	SCC4_HUMAN	69.1	99.8%	2	2	3	0.00%	2.9%	GLFSFFQGR	99.7%	56.3	25	53.1	2	0	0	1058.54	466	474
MAU2 chromatid cohesion factor homolog	MAU2	SCC4_HUMAN	69.1	99.8%	2	2	3	0.00%	2.9%	MSNAEDLNR	98.5%	32.5	25	10.9	1	0	0	1049.47	488	496
MAX gene-associated protein	MGA	MGAP_HUMAN	331.8	100.0%	6	6	10	0.01%	2.7%	ISNPSAFSIVPR	99.7%	65.5	25	55	2	0	0	1287.71	2208	2219
MAX gene-associated protein	MGA	MGAP_HUMAN	331.8	100.0%	6	6	10	0.01%	2.7%	LGNSGASPSSAGK	99.5%	37.8	25	28.5	2	0	0	1132.56	3014	3026
MAX gene-associated protein	MGA	MGAP_HUMAN	331.8	100.0%	6	6	10	0.01%	2.7%	VANPSSDADGQSLK	99.7%	49	25	43.5	1	0	0	1388.67	2957	2970
MAX gene-associated protein	MGA	MGAP_HUMAN	331.8	100.0%	6	6	10	0.01%	2.7%	VGSFIIELASQR	99.7%	74	25	63.3	2	0	0	1319.73	1369	1380
MAX gene-associated protein	MGA	MGAP_HUMAN	331.8	100.0%	6	6	10	0.01%	2.7%	VLQSEGEAVDPEANVIK	99.7%	88.2	25	88.2	2	0	0	1797.92	1954	1970
MAX gene-associated protein	MGA	MGAP_HUMAN	331.8	100.0%	6	6	10	0.01%	2.7%	VTLGPTQVFLANK	99.7%	46.4	25	46.4	1	0	0	1387.79	2672	2684
Mediator of DNA damage checkpoint protein 1	MDC1	MDC1_HUMAN	226.7	100.0%	4	4	5	0.01%	2.7%	EGAQVPTGR	96.4%	28.9	25	18.2	1	0	0	914.47	664	672
Mediator of DNA damage checkpoint protein 1	MDC1	MDC1_HUMAN	226.7	100.0%	4	4	5	0.01%	2.7%	NQLVTPEPTSR	98.5%	32.4	25	17.5	2	0	0	1241.65	1585	1595
Mediator of DNA damage checkpoint protein 1	MDC1	MDC1_HUMAN	226.7	100.0%	4	4	5	0.01%	2.7%	TPEPVVPTAPEPHPTTSTDQPVTPK	99.1%	28.6	25	28.6	0	1	0	2623.33	1608	1632
Mediator of DNA damage checkpoint protein 1	MDC1	MDC1_HUMAN	226.7	100.0%	4	4	5	0.01%	2.7%	TPETLVPTAPK	99.7%	43.2	25	31.6	1	0	0	1153.65	1403	1413
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	7	7	11	0.01%	6.1%	EVGNALLNVVLK	99.7%	39.2	25	13.4	2	0	0	1268.76	1121	1132
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	7	7	11	0.01%	6.1%	FLELLPVSK	99.3%	36	25	35.1	1	0	0	1045.63	974	982
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	7	7	11	0.01%	6.1%	FLTEVLLPIVK	99.7%	59.3	25	59.3	2	0	0	1271.80	1230	1240
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	7	7	11	0.01%	6.1%	GFISQLLPTVFK	98.8%	33.6	25	30	1	0	0	1349.78	583	594
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	7	7	11	0.01%	6.1%	LFDLLYPEK	99.7%	48.3	25	46.6	2	0	0	1137.62	398	406
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	7	7	11	0.01%	6.1%	NACLLPAYFAVTEIR	99.7%	41.1	25	24.2	2	0	0	1737.90	174	188
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	7	7	11	0.01%	6.1%	SSVALAPALVETYSR	99.7%	45.6	25	45.5	1	0	0	1563.84	555	569
Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADM	ACADM_HUMAN	46.6	99.8%	2	2	3	0.00%	5.2%	ANWYFLLAR	99.7%	57.6	25	51.1	2	0	0	1153.62	198	206
Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADM	ACADM_HUMAN	46.6	99.8%	2	2	3	0.00%	5.2%	IYQIYEGTSQIQR	99.7%	48.7	25	39.4	1	0	0	1598.82	396	408
Melanoma-associated antigen D2	MAGED2	MAGD2_HUMAN	65.0	100.0%	3	3	6	0.01%	6.6%	LQSSQEPEAPPPR	99.7%	65.8	25	62.2	2	0	0	1435.72	262	274
Melanoma-associated antigen D2	MAGED2	MAGD2_HUMAN	65.0	100.0%	3	3	6	0.01%	6.6%	SSEAVIWEVLR	99.7%	63.4	25	35.5	2	0	0	1288.69	386	396
Melanoma-associated antigen D2	MAGED2	MAGD2_HUMAN	65.0	100.0%	3	3	6	0.01%	6.6%	VPNSNPPEYEFFWGLR	99.7%	72.2	25	72.2	2	0	0	1951.93	431	446
Metaxin-1	MTX1	MTX1_HUMAN	51.5	100.0%	3	3	5	0.01%	8.4%	ECLTLLSQR	99.3%	35.8	25	6.12	1	0	0	1119.58	325	333
Metaxin-1	MTX1	MTX1_HUMAN	51.5	100.0%	3	3	5	0.01%	8.4%	ISNPWQSPSGTLPALR	99.7%	61.8	25	61.8	2	0	0	1723.91	191	206
Metaxin-1	MTX1	MTX1_HUMAN	51.5	100.0%	3	3	5	0.01%	8.4%	QTPAGPETEEEPYR	99.7%	43	25	43	2	0	0	1603.72	403	416
Metaxin-2	MTX2	MTX2_HUMAN	29.8	100.0%	5	5	7	0.01%	24.7%	GHSLSDGLEEVQK	99.7%	57.9	25	56.7	1	0	0	1398.69	96	108
Metaxin-2	MTX2	MTX2_HUMAN	29.8	100.0%	5	5	7	0.01%	24.7%	LGTQPYFFNK	99.7%	55.2	25	45.1	2	0	0	1214.62	197	206
Metaxin-2	MTX2	MTX2_HUMAN	29.8	100.0%	5	5	7	0.01%	24.7%	NYSNLLAFCR	99.7%	40.1	25	36	1	0	0	1257.60	238	247
Metaxin-2	MTX2	MTX2_HUMAN	29.8	100.0%	5	5	7	0.01%	24.7%	RIEQHYFEDR	99.7%	41.2	25	39.7	0	2	0	1392.67	248	257
Metaxin-2	MTX2	MTX2_HUMAN	29.8	100.0%	5	5	7	0.01%	24.7%	VPFIHVGNQVVSELGPIVQFVK	99.7%	47.1	25	47.1	0	1	0	2406.35	72	93
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	28	59	0.06%	37.3%	ADKNEVAAEVAK	99.7%	66.2	25	39.1	2	0	0	1244.65	864	875
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	28	59	0.06%	37.3%	AEVLISTVGPEDCVVPFLTRPK	99.7%	60.7	25	60.7	0	2	0	2427.30	26	47
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	28	59	0.06%	37.3%	ALTHIDHSLSR	99.3%	29.9	25	27.9	0	2	0	1249.66	120	130
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	28	59	0.06%	37.3%	FFGGYVPEMVLTPDDQR	99.7%	64	25	64	4	0	0	1970.93	664	680

Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	28	59	0.06%	37.3%	FVEGVCPFCGYEEAR	99.7%	68.2	25	68.2	2	0	0	1819.78	400	414
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	28	59	0.06%	37.3%	GFVLQDTVEQLR	99.7%	88.1	25	66.2	3	0	0	1404.75	377	388
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	28	59	0.06%	37.3%	GLESLPPLRPQQNPVLPVAGER	99.7%	36.6	25	36.6	0	2	0	2367.31	243	264
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	28	59	0.06%	37.3%	GVGVFGDMAQDTGIPADIWR	99.7%	102	25	102	4	0	0	2121.01	599	618
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	28	59	0.06%	37.3%	ITQDIFQQLLK	99.7%	69.3	25	52.8	5	0	0	1346.77	365	375
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	28	59	0.06%	37.3%	ITQDIFQQLLKR	99.7%	43.9	25	31	2	0	0	1502.87	365	376
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	28	59	0.06%	37.3%	KGEDVLGSVR	99.7%	58.5	25	50.6	2	0	0	1059.58	109	118
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	28	59	0.06%	37.3%	LENDQIESLR	99.7%	79.3	25	65.4	2	0	0	1216.62	805	814
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	28	59	0.06%	37.3%	LFVSDGVPGCLPVLAAAGR	99.7%	70.9	25	68.8	2	0	0	1899.02	3	21
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	28	59	0.06%	37.3%	LINAVELK	99.7%	39.6	25	27.8	2	0	0	899.56	424	431
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	28	59	0.06%	37.3%	NNSELLNNLGNFINR	99.7%	91.8	25	91.5	2	0	0	1731.88	642	656
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	28	59	0.06%	37.3%	NPEQVDLYQFMAK	99.7%	75.9	25	75.9	4	0	0	1582.76	542	554
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	28	59	0.06%	37.3%	QLAVAEGKPPEAPK	99.7%	65.6	25	58.6	2	0	0	1434.80	882	895
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	28	59	0.06%	37.3%	QPQPSPAEGR	99.7%	54.5	25	50.5	2	0	0	1066.53	205	214
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	28	59	0.06%	37.3%	QQGVLALRPYLQK	99.7%	60.1	25	56.8	2	0	0	1513.89	192	204
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	28	59	0.06%	37.3%	QWNTLYLCGTDEYGTATETK	99.7%	111	25	111	1	0	0	2351.05	302	321
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	28	59	0.06%	37.3%	RLEEWLGR	99.7%	43	25	25.8	2	0	0	1058.57	460	467
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	28	59	0.06%	37.3%	SCPVVQSSQHLFLDLPK	99.7%	85	25	85	2	2	0	1955.01	440	456
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	28	59	0.06%	37.3%	TLPGSDWTPNAQFITR	99.7%	95	25	92.6	2	0	0	1803.90	468	483
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	28	59	0.06%	37.3%	VPVLQLDSGNYLFSTSAICR	99.7%	136	25	136	2	0	0	2240.14	48	67
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	14	21	237	0.25%	46.5%	AHAAQVTCVAASPHK	99.7%	92.3	25	89.2	12	13	0	1547.77	165	179
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	14	21	237	0.25%	46.5%	AHAAQVTCVAASPHKDSVFLSCSEDNR	99.7%	46.5	25	46.5	0	1	0	2957.36	165	191
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	14	21	237	0.25%	46.5%	CWAGSLWLFK	99.7%	42.4	25	36	8	0	0	1267.63	53	62
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	14	21	237	0.25%	46.5%	DPCAAPNEGFCSAGVQTEAGVADLTWVGER	98.5%	26.7	25	26.7	0	1	0	3164.41	63	92
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	14	21	237	0.25%	46.5%	DSVFLSCSEDNR	99.7%	77.2	25	69.1	16	0	0	1428.61	180	191
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	14	21	237	0.25%	46.5%	ETPPPLVPPAAR	99.7%	44.9	25	30.7	7	0	0	1244.70	4	15
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	14	21	237	0.25%	46.5%	EWNLPPNAPACMER	99.7%	75.4	25	75.4	24	0	0	1684.76	16	29
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	14	21	237	0.25%	46.5%	FCKYEHDDIVSTVSVLSSGTQAVSGSK	99.7%	112	25	112	0	2	0	2901.39	119	145
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	14	21	237	0.25%	46.5%	ILLWDTR	99.7%	53.3	25	48.3	17	0	0	916.53	192	198
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	14	21	237	0.25%	46.5%	KETPPPLVPPAAR	99.7%	58.4	25	53.5	4	2	0	1372.79	3	15
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	14	21	237	0.25%	46.5%	SDGALLLGASSLSGR	99.7%	130	25	124	44	2	0	1403.75	38	52
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	14	21	237	0.25%	46.5%	VWDLAQQVVLSSYR	99.7%	111	25	107	27	6	0	1663.88	151	164
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	14	21	237	0.25%	46.5%	YEHDDIVSTVSVLSSGTQAVSGSK	99.7%	129	25	129	10	15	0	2466.20	122	145
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	14	21	237	0.25%	46.5%	YRSDGALLLGASSLSGR	99.7%	110	25	104	9	17	0	1722.91	36	52
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	4	6	45	0.05%	24.1%	GLGTGTLYIAESR	99.7%	101	25	83.2	12	0	0	1337.71	31	43
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	4	6	45	0.05%	24.1%	LEGMLSQSVSSQYNMAGVR	99.7%	117	25	117	18	4	0	2072.97	188	206
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	4	6	45	0.05%	24.1%	QQPDTEAVLNGK	99.7%	66.4	25	64.2	6	0	0	1299.65	19	30
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	4	6	45	0.05%	24.1%	SFPPPGPAEGLLR	99.7%	40	25	40	5	0	0	1337.72	6	18
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	9	10	17	0.02%	30.1%	DLADVAAR	98.6%	32.7	25	14.8	2	0	0	830.44	102	109
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	9	10	17	0.02%	30.1%	EAEREGATEEAVR	99.7%	42.4	25	35.2	1	0	0	1446.68	110	122
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	9	10	17	0.02%	30.1%	EIIIEERPGQELTDVNGVR	99.7%	51.1	25	48.2	0	2	0	2167.14	294	312
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	9	10	17	0.02%	30.1%	GSLQILDQLLLPK	99.7%	69.1	25	52.3	2	0	0	1437.87	11	23
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	9	10	17	0.02%	30.1%	GVSAVVVGADR	99.7%	78.5	25	64.3	2	0	0	1029.57	239	249
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	9	10	17	0.02%	30.1%	TALTTTISSR	99.7%	75.9	25	66.7	2	0	0	1050.58	351	360
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	9	10	17	0.02%	30.1%	VGTYQLAIVAK	99.7%	81.4	25	79	2	0	0	1162.68	260	270
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	9	10	17	0.02%	30.1%	VICCTEDMLEK	96.8%	29.4	25	27.3	1	0	0	1413.61	125	135
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	9	10	17	0.02%	30.1%	YEAVGSVHQAWEAIR	99.7%	66.7	25	58.8	1	2	0	1715.85	27	41
Methyltransferase-like protein 13	METTL13	MET13_HUMAN	78.8	99.8%	2	2	2	0.00%	4.3%	LATPELLETAQALER	99.7%	69	25	57.5	1	0	0	1654.90	660	674
Methyltransferase-like protein 13	METTL13	MET13_HUMAN	78.8	99.8%	2	2	2	0.00%	4.3%	YTLHVVDSPTVKPSR	99.7%	48.5	25	48.3	0	1	0	1698.92	282	296
Microsomal glutathione S-transferase 1	MGST1	MGST1_HUMAN	17.6	100.0%	3	5	14	0.01%	16.8%	KVFANPEDCVAFGK	99.7%	63	25	63	2	1	0	1581.77	42	55
Microsomal glutathione S-transferase 1	MGST1	MGST1_HUMAN	17.6	100.0%	3	5	14	0.01%	16.8%	MMLMSTATAFYR	99.7%	75.1	25	75.1	10	0	0	1422.66	27	38

Microsomal glutathione S-transferase 1	MGST1	MGST1_HUMAN	17.6	100.0%	3	5	14	0.01%	16.8%	VFANPEDCVAFGK	99.0%	34.2	25	34.2	1	0	0	1453.68	43	55
Microsomal glutathione S-transferase 3	MGST3	MGST3_HUMAN	16.5	99.8%	2	2	3	0.00%	18.4%	IASGLGLAWIVGR	99.7%	63.9	25	57.9	2	0	0	1312.77	85	97
Microsomal glutathione S-transferase 3	MGST3	MGST3_HUMAN	16.5	99.8%	2	2	3	0.00%	18.4%	VLYAYGYYTGEPSKR	99.7%	56.7	25	56.5	1	0	0	1766.87	98	112
Microtubule-associated protein 1B	MAP1B	MAP1B_HUMAN	270.6	99.9%	2	2	4	0.00%	1.0%	AVLDALLEGK	99.7%	45.6	25	39.9	2	0	0	1028.60	2400	2409
Microtubule-associated protein 1B	MAP1B	MAP1B_HUMAN	270.6	99.9%	2	2	4	0.00%	1.0%	SVGNTIDPVILFQK	99.7%	52.9	25	52.4	2	0	0	1530.85	401	414
Microtubule-associated protein RP/EB family member 2	MAPRE2	MARE2_HUMAN	37.0	99.8%	2	2	3	0.00%	6.7%	FQDNLDFIQWFK	99.7%	53	25	49.4	1	0	0	1600.78	144	155
Microtubule-associated protein RP/EB family member 2	MAPRE2	MARE2_HUMAN	37.0	99.8%	2	2	3	0.00%	6.7%	LALEGVEKER	99.7%	41.5	25	27.4	2	0	0	1143.64	256	265
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	5	5	8	0.01%	1.3%	ALEFGEPVLLVGDTGCGK	99.7%	69.4	25	69.4	2	0	0	1861.94	1379	1396
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	5	5	8	0.01%	1.3%	FMLFATQNPPGLYGGR	99.3%	35.8	25	32.4	1	0	0	1768.88	1189	1204
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	5	5	8	0.01%	1.3%	GEPVLLVGETGTGK	99.7%	87.4	25	80.5	2	0	0	1356.74	670	683
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	5	5	8	0.01%	1.3%	SLTTLSEQWIILR	99.7%	42.2	25	26.7	1	0	0	1559.88	4242	4254
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	5	5	8	0.01%	1.3%	TSLVEYLAAVTGR	99.7%	61.8	25	61.8	2	0	0	1379.75	336	348
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	17	0.02%	17.3%	AMVEAVQLIADGK	99.7%	87.5	25	72.7	2	0	0	1344.72	197	209
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	17	0.02%	17.3%	ANSTEYGLASGVFTR	99.7%	104	25	97.6	1	0	0	1572.77	848	862
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	17	0.02%	17.3%	DLGEEALNEYLK	99.7%	42.4	25	34.7	1	0	0	1393.68	904	915
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	17	0.02%	17.3%	EESFGPIMVISK	99.7%	47.3	25	42.7	1	0	0	1336.68	824	835
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	17	0.02%	17.3%	FLFPEGIK	97.7%	30.8	25	16.5	1	0	0	950.53	189	196
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	17	0.02%	17.3%	GVINIIPGSGGIAGQR	99.7%	41.9	25	41.9	2	0	0	1508.85	642	657
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	17	0.02%	17.3%	LGFTGSTPIGK	99.7%	60.3	25	55.8	2	0	0	1077.59	667	677
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	17	0.02%	17.3%	SAACLAAGNTLVLKPAQVTPLTALK	98.7%	27.3	25	27.3	0	1	0	2508.42	605	629
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	17	0.02%	17.3%	SPLIIFNDCELDK	99.7%	57.8	25	47.1	2	0	0	1563.77	699	711
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	17	0.02%	17.3%	TDVAAPFGGVK	96.8%	29.4	25	23.8	1	0	0	1061.56	887	897
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	17	0.02%	17.3%	VSYASLADVDK	99.7%	57.5	25	54.1	2	0	0	1167.59	474	484
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	17	0.02%	17.3%	VVGVFTVPDKDGK	95.8%	28.3	25	17	1	0	0	1360.75	48	60
Mitochondrial 2-oxodicarboxylate carrier	SLC25A21	ODC_HUMAN	33.3	99.8%	2	2	3	0.00%	8.7%	IQGPQPVPGEIK	96.8%	29.4	25	24.9	1	0	0	1262.71	235	246
Mitochondrial 2-oxodicarboxylate carrier	SLC25A21	ODC_HUMAN	33.3	99.8%	2	2	3	0.00%	8.7%	NTFAEQPSTVGYAR	99.7%	66.4	25	54.5	2	0	0	1540.74	142	155
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	18	33	0.03%	50.3%	AVIGMTAGATGAFVGTPAEVALIR	99.7%	105	25	105	4	4	0	2273.23	123	146
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	18	33	0.03%	50.3%	AVVVNAAQLASYSQSK	99.7%	119	25	117	2	0	0	1635.87	191	206
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	18	33	0.03%	50.3%	EEGVLTLWR	98.8%	33.3	25	21.3	2	0	0	1102.59	174	182
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	18	33	0.03%	50.3%	FLFGGLAGMGATVFVQPLDLVK	99.7%	69.8	25	69.8	1	0	0	2296.24	25	46
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	18	33	0.03%	50.3%	GIYTGLSAGLLR	99.7%	85.7	25	78.8	2	0	0	1220.70	79	90
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	18	33	0.03%	50.3%	ITREEGVLTLWR	99.7%	41.7	25	34	1	2	0	1472.82	171	182
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	18	33	0.03%	50.3%	LGIYTVLFER	99.7%	67.2	25	67.2	3	0	0	1210.68	99	108
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	18	33	0.03%	50.3%	LTGADGTPPGFLLK	99.7%	69.8	25	61.2	1	0	0	1386.76	109	122
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	18	33	0.03%	50.3%	MTADGRLPADQR	96.3%	28.9	25	22	1	0	0	1330.65	147	158
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	18	33	0.03%	50.3%	NGLDVLFK	99.7%	48.7	25	37.7	2	0	0	905.51	261	268
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	18	33	0.03%	50.3%	NVFNALIR	99.7%	39.4	25	25.3	2	0	0	946.55	163	170
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	18	33	0.03%	50.3%	TSFHALTSILK	99.7%	54.2	25	43.9	2	2	0	1217.69	63	73
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	18	33	0.03%	50.3%	YEGFFSLWK	99.7%	52.1	25	46	2	0	0	1176.57	272	280
Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20	MCAT_HUMAN	32.9	100.0%	4	4	6	0.01%	12.6%	EGITGLYR	99.7%	45.3	25	39.3	1	0	0	908.48	66	73
Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20	MCAT_HUMAN	32.9	100.0%	4	4	6	0.01%	12.6%	ELIRDEGVTSLYK	99.7%	41.7	25	37.7	2	0	0	1522.81	255	267
Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20	MCAT_HUMAN	32.9	100.0%	4	4	6	0.01%	12.6%	GTVLTLMR	99.7%	43.5	25	35	1	0	0	906.51	171	178
Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20	MCAT_HUMAN	32.9	100.0%	4	4	6	0.01%	12.6%	KLYQEFGIR	99.7%	47.9	25	37.1	2	0	0	1153.64	158	166
Mitochondrial carrier homolog 2	MTCH2	MTCH2_HUMAN	33.3	99.8%	2	2	4	0.00%	9.9%	GLFTGLTPR	99.7%	58.4	25	31.7	2	0	0	961.55	69	77
Mitochondrial carrier homolog 2	MTCH2	MTCH2_HUMAN	33.3	99.8%	2	2	4	0.00%	9.9%	VLQHYQESDKGEELGPGNVQK	99.4%	30.5	25	30.5	0	2	0	2355.16	91	111
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	23	0.02%	48.4%	FAIYETVR	99.7%	44.6	25	35.9	2	0	0	998.53	79	86
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	23	0.02%	48.4%	GALVTVGQLSCYDQAK	99.7%	124	25	122	2	0	0	1709.85	171	186
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	23	0.02%	48.4%	GEYQGVFHCAVETAK	99.7%	60.1	25	60.1	2	2	0	1695.78	232	246
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	23	0.02%	48.4%	GSQGPLPFHEK	99.7%	45.9	25	36.9	1	0	0	1196.61	92	102
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	23	0.02%	48.4%	LFSGATMASSR	99.7%	59	25	52	2	0	0	1143.55	160	170
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	23	0.02%	48.4%	LGPLAFYK	99.7%	52.6	25	45.5	2	0	0	908.52	247	254

Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	23	0.02%	48.4%	NYAHALDGLYR	99.7%	62	25	59.3	2	0	0	1292.64	140	150
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	23	0.02%	48.4%	QMTYSLTR	99.7%	43.6	25	33.7	2	0	0	999.49	71	78
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	23	0.02%	48.4%	TDGILALYSGLSASLCR	99.7%	90.5	25	84.8	2	0	0	1796.92	54	70
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	23	0.02%	48.4%	VHLQTQQEVK	98.8%	33.3	25	31.2	1	0	0	1209.66	32	41
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	23	0.02%	48.4%	VLLGSVSGLAGGFVGTPADLVNVR	99.7%	76.5	25	76.5	2	1	0	2298.28	103	126
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	4	4	8	0.01%	21.7%	KLYPTVGKPSSS	99.6%	39	25	35.8	2	0	0	1263.69	155	166
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	4	4	8	0.01%	21.7%	SVDFLLDSSLR	99.7%	77.1	25	58.8	2	0	0	1251.66	144	154
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	4	4	8	0.01%	21.7%	SVDFLLDSSLRK	99.7%	65.5	25	57.2	2	0	0	1379.75	144	155
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	4	4	8	0.01%	21.7%	YLGYANEVGEAFR	99.7%	78.8	25	75.4	2	0	0	1488.71	21	33
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	7	7	13	0.01%	22.3%	GAAVNLTLVTPEK	99.7%	92.1	25	89.2	2	0	0	1312.75	68	80
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	7	7	13	0.01%	22.3%	GLGATLLR	99.4%	36.4	25	14.9	2	0	0	800.50	189	196
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	7	7	13	0.01%	22.3%	GVNEDTYSGILDCAR	99.7%	67.2	25	67.2	2	0	0	1669.75	259	273
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	7	7	13	0.01%	22.3%	HEGPSAFLK	98.7%	33.2	25	31.1	2	0	0	985.51	278	286
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	7	7	13	0.01%	22.3%	IQLQDAGR	99.7%	45.6	25	31.2	2	0	0	900.49	129	136
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	7	7	13	0.01%	22.3%	LAANDFFR	99.7%	54.2	25	41.5	2	0	0	953.48	84	91
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	7	7	13	0.01%	22.3%	VYTSMSDCLIK	99.2%	35	25	33.4	1	0	0	1316.62	45	55
Mitochondrial import inner membrane translocase subunit Tim13	TIMM13	TIM13_HUMAN	10.5	99.9%	2	2	3	0.00%	25.3%	VQIAVANAQELLQR	99.7%	88.7	25	80.2	2	0	0	1552.88	28	41
Mitochondrial import inner membrane translocase subunit Tim13	TIMM13	TIM13_HUMAN	10.5	99.9%	2	2	3	0.00%	25.3%	YMDAWNTVSR	94.9%	27.6	25	27.6	1	0	0	1242.56	73	82
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	11	23	0.02%	27.5%	APDQAAEIGSR	98.0%	31.3	25	27.6	1	0	0	1114.55	33	43
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	11	23	0.02%	27.5%	AQGPQQQPGSEGPSYAK	99.7%	53.3	25	53.3	4	0	0	1729.81	48	64
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	11	23	0.02%	27.5%	IPDEFDNDPILVQQLR	99.7%	112	25	99.2	2	0	0	1911.98	98	113
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	11	23	0.02%	27.5%	QNLFLGSLTSR	99.7%	59.6	25	41.1	2	0	0	1235.67	335	345
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	11	23	0.02%	27.5%	RAPDQAAEIGSR	99.7%	46.7	25	37.3	2	2	0	1270.65	32	43
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	11	23	0.02%	27.5%	SNKQNLFLGSLTSR	99.7%	68.6	25	64.1	2	0	0	1564.84	332	345
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	11	23	0.02%	27.5%	TIALNGVEDVR	99.7%	87.4	25	74.6	2	0	0	1186.64	285	295
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	11	23	0.02%	27.5%	TVLEHYALEDDPLAAFK	99.7%	79.6	25	79.6	2	2	0	1931.98	296	312
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	11	23	0.02%	27.5%	VLLDLSAFLK	99.7%	48.7	25	48.7	2	0	0	1118.68	275	284
Mitochondrial import receptor subunit TOM22 homolog	TOMM22	TOM22_HUMAN	15.5	99.8%	2	4	11	0.01%	16.2%	LQMEQQQQLQQR	99.7%	75.8	25	59	7	0	0	1557.78	106	117
Mitochondrial import receptor subunit TOM22 homolog	TOMM22	TOM22_HUMAN	15.5	99.8%	2	4	11	0.01%	16.2%	LWGLTEMFPER	99.7%	43.5	25	39.4	4	0	0	1394.68	48	58
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	7	12	22	0.02%	21.9%	ELFPIQMEGVK	99.7%	51.4	25	40.3	4	0	0	1290.68	92	102
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	7	12	22	0.02%	21.9%	FQCGFGLTIG	95.9%	28.5	25	22.9	1	0	0	1099.52	352	361
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	7	12	22	0.02%	21.9%	FVNWQVDGEYR	99.7%	62	25	62	2	0	0	1412.66	185	195
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	7	12	22	0.02%	21.9%	GSVDSNWIVGATLEK	99.7%	116	25	105	2	0	0	1575.80	316	330
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	7	12	22	0.02%	21.9%	MQDTSVSFGYQLDLPK	99.7%	105	25	105	4	0	0	1844.87	294	309
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	7	12	22	0.02%	21.9%	NKFQCGFGLTIG	99.7%	45.3	25	43.4	2	0	0	1341.66	350	361
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	7	12	22	0.02%	21.9%	RPGEEGTVMSLAGK	99.7%	69.1	25	59.7	4	3	0	1447.72	240	253
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	17	18	55	0.06%	27.6%	AAMDNSEIAGEKK	99.7%	53.4	25	51.9	4	0	0	1379.65	258	270
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	17	18	55	0.06%	27.6%	AVDEAADALLK	99.7%	61.4	25	50.6	4	0	0	1115.59	287	297
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	17	18	55	0.06%	27.6%	ELDSITPEVLPGWK	99.7%	67.4	25	48.2	4	0	0	1583.83	372	385
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	17	18	55	0.06%	27.6%	ERPPEEVAAR	99.7%	41.8	25	31.3	4	0	0	1153.60	196	205
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	17	18	55	0.06%	27.6%	EVAGAKPHITAAEGK	99.7%	50.1	25	34.6	1	0	0	1478.80	316	330
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	17	18	55	0.06%	27.6%	GIEQAVQSHAVAEEEAR	99.7%	62.7	25	59.9	0	4	0	1823.89	548	564
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	17	18	55	0.06%	27.6%	GVYSEETLR	99.7%	55	25	44.9	2	0	0	1053.52	624	632
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	17	18	55	0.06%	27.6%	ISSVSEVMK	96.1%	28.6	25	15.3	1	0	0	979.51	111	119
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	17	18	55	0.06%	27.6%	LFEMVLGPAAYNVPLPK	99.4%	36.6	25	36.6	2	0	0	1859.01	85	101
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	17	18	55	0.06%	27.6%	LHNMIVDLDNVVK	99.7%	70.8	25	70.8	2	0	0	1509.81	331	343
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	17	18	55	0.06%	27.6%	LSEQELQFR	99.7%	73.8	25	48.6	4	0	0	1149.59	517	525
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	17	18	55	0.06%	27.6%	SEFEQNLSEK	99.7%	52.4	25	43.2	2	0	0	1210.56	507	516
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	17	18	55	0.06%	27.6%	TSSAETPTIPLGSAVEAIK	99.7%	110	25	103	4	0	0	1872.00	582	600
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	17	18	55	0.06%	27.6%	TVEGALKER	99.7%	41.7	25	28.6	2	0	0	1002.56	276	284
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	17	18	55	0.06%	27.6%	VAMIDETR	99.7%	47.6	25	37.2	4	0	0	934.47	645	652

Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	17	18	55	0.06%	27.6%	VVSQYHELVVQAR	99.7%	72.1	25	68.9	4	3	0	1527.83	354	366
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	17	18	55	0.06%	27.6%	YSTSGSSGLTTGK	99.7%	66.7	25	65.6	4	0	0	1245.60	33	45
Mitochondrial inner membrane protein OXA1L	OXA1L	OXA1L_HUMAN	48.5	100.0%	4	4	8	0.01%	9.2%	ASSEMALYQK	99.7%	47.7	25	43.4	2	0	0	1127.54	198	207
Mitochondrial inner membrane protein OXA1L	OXA1L	OXA1L_HUMAN	48.5	100.0%	4	4	8	0.01%	9.2%	CLIFPLIVTGQR	99.7%	74.6	25	58.1	2	0	0	1416.80	153	164
Mitochondrial inner membrane protein OXA1L	OXA1L	OXA1L_HUMAN	48.5	100.0%	4	4	8	0.01%	9.2%	LAGDHIEYYK	99.7%	56.1	25	47.8	2	0	0	1208.59	188	197
Mitochondrial inner membrane protein OXA1L	OXA1L	OXA1L_HUMAN	48.5	100.0%	4	4	8	0.01%	9.2%	NQLELAAR	99.7%	43.7	25	19.8	2	0	0	914.51	387	394
Mitochondrial ornithine transporter 1	SLC25A15	ORNT1_HUMAN	32.7	100.0%	5	5	8	0.01%	15.3%	IQVLSMSGK	99.1%	34.8	25	19.2	2	0	0	962.53	237	245
Mitochondrial ornithine transporter 1	SLC25A15	ORNT1_HUMAN	32.7	100.0%	5	5	8	0.01%	15.3%	LQTMYEMETSGK	99.7%	41	25	41	2	0	0	1449.62	134	145
Mitochondrial ornithine transporter 1	SLC25A15	ORNT1_HUMAN	32.7	100.0%	5	5	8	0.01%	15.3%	SQNTVWSVIK	99.7%	54.8	25	52.4	2	0	0	1161.63	149	158
Mitochondrial ornithine transporter 1	SLC25A15	ORNT1_HUMAN	32.7	100.0%	5	5	8	0.01%	15.3%	TFINVVK	97.1%	29.7	25	13.4	1	0	0	820.49	252	258
Mitochondrial ornithine transporter 1	SLC25A15	ORNT1_HUMAN	32.7	100.0%	5	5	8	0.01%	15.3%	TYSQVGFR	99.2%	35.3	25	24.1	1	0	0	957.48	54	61
Mitochondrial pyruvate carrier 2	MPC2	MPC2_HUMAN	14.3	100.0%	3	4	7	0.01%	23.6%	LLDKVELMLPEK	99.7%	39.7	25	25.5	2	1	0	1427.82	16	27
Mitochondrial pyruvate carrier 2	MPC2	MPC2_HUMAN	14.3	100.0%	3	4	7	0.01%	23.6%	TVFFWAPIMK	99.7%	41.9	25	32	2	0	0	1239.66	40	49
Mitochondrial pyruvate carrier 2	MPC2	MPC2_HUMAN	14.3	100.0%	3	4	7	0.01%	23.6%	YSLVIIPK	99.7%	41.7	25	41.7	2	0	0	932.58	85	92
Mitochondrial Rho GTPase 2	RHOT2	MIRO2_HUMAN	68.1	100.0%	5	5	9	0.01%	8.3%	ILLLGEAQVGK	99.7%	66.1	25	36.5	2	0	0	1140.70	7	17
Mitochondrial Rho GTPase 2	RHOT2	MIRO2_HUMAN	68.1	100.0%	5	5	9	0.01%	8.3%	NISELFYYAQK	99.4%	36.3	25	20.7	2	0	0	1375.69	154	164
Mitochondrial Rho GTPase 2	RHOT2	MIRO2_HUMAN	68.1	100.0%	5	5	9	0.01%	8.3%	SAFLQAFLGR	99.7%	70.6	25	58	2	0	0	1109.61	430	439
Mitochondrial Rho GTPase 2	RHOT2	MIRO2_HUMAN	68.1	100.0%	5	5	9	0.01%	8.3%	SFAHCASVYK	99.7%	46.6	25	37.2	1	0	0	1169.54	500	509
Mitochondrial Rho GTPase 2	RHOT2	MIRO2_HUMAN	68.1	100.0%	5	5	9	0.01%	8.3%	VPIILVGNK	99.7%	46.3	25	0	2	0	0	952.62	111	119
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	11	13	29	0.03%	31.0%	DSIIYLTADSPNVMTTFR	99.7%	101	25	101	5	0	0	2060.00	285	302
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	11	13	29	0.03%	31.0%	EVPEHITEEELK	99.7%	47.3	25	37.7	2	0	0	1452.72	107	118
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	11	13	29	0.03%	31.0%	NLTLDQMIR	99.5%	37.4	25	25.8	1	0	0	1103.59	350	358
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	11	13	29	0.03%	31.0%	NMDIAMGWK	99.7%	44.1	25	32.2	1	0	0	1065.49	186	194
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	11	13	29	0.03%	31.0%	NVDPFHIYFCNLK	99.7%	42.5	25	40	4	0	0	1666.80	237	249
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	11	13	29	0.03%	31.0%	SMQPGTSLAK	99.5%	37.7	25	27.8	2	0	0	1019.52	316	325
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	11	13	29	0.03%	31.0%	SSVQEECVSTISSSK	99.7%	46.4	25	46.4	1	0	0	1627.75	72	86
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	11	13	29	0.03%	31.0%	SSVQEECVSTISSSKDEDPLAATR	99.7%	45.6	25	45.6	0	2	0	2596.20	72	95
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	11	13	29	0.03%	31.0%	TLMECVSNTAK	99.7%	73.9	25	73.9	4	0	0	1253.59	119	129
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	11	13	29	0.03%	31.0%	VYVIGSFVDK	99.7%	55.8	25	49	5	0	0	1126.61	306	315
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	11	13	29	0.03%	31.0%	YLQWEIGNK	99.7%	50.2	25	46.2	2	0	0	1150.59	341	349
Mitochondrial ribonuclease P protein 3	KIAA0391	MRRP3_HUMAN	67.3	100.0%	5	5	9	0.01%	9.3%	DVIDGGDQYRK	99.7%	55.5	25	52.5	2	0	0	1265.61	375	385
Mitochondrial ribonuclease P protein 3	KIAA0391	MRRP3_HUMAN	67.3	100.0%	5	5	9	0.01%	9.3%	EALLLLEDIKK	99.7%	47.6	25	40.5	2	0	0	1284.78	228	238
Mitochondrial ribonuclease P protein 3	KIAA0391	MRRP3_HUMAN	67.3	100.0%	5	5	9	0.01%	9.3%	ESQLLLNVVSQLAK	99.7%	84.8	25	81.1	2	0	0	1541.89	422	435
Mitochondrial ribonuclease P protein 3	KIAA0391	MRRP3_HUMAN	67.3	100.0%	5	5	9	0.01%	9.3%	LLDILSYLR	99.7%	76.8	25	65.5	2	0	0	1105.66	301	309
Mitochondrial ribonuclease P protein 3	KIAA0391	MRRP3_HUMAN	67.3	100.0%	5	5	9	0.01%	9.3%	TWFESVPGK	94.8%	27.5	25	24.1	1	0	0	1050.53	325	333
Mitochondrial-processing peptidase subunit beta	PMPCB	MPPB_HUMAN	54.4	99.9%	2	2	2	0.00%	6.8%	FTGSEIR	99.3%	35.8	25	25.2	1	0	0	809.42	279	285
Mitochondrial-processing peptidase subunit beta	PMPCB	MPPB_HUMAN	54.4	99.9%	2	2	2	0.00%	6.8%	IDAVNAETIR	99.7%	54.4	25	45.3	1	0	0	1101.59	442	451
Mitochondrial-processing peptidase subunit beta	PMPCB	MPPB_HUMAN	54.4	99.9%	2	2	2	0.00%	6.8%	STQAATQVVLNVPETR	99.7%	58.6	25	48	1	0	0	1713.91	44	59
Mitogen-activated protein kinase kinase kinase 7	MAP3K7	M3K7_HUMAN	67.2	99.8%	2	3	5	0.01%	5.8%	DLKPPNLLLVAGGTVLK	99.7%	43.1	25	41.6	2	2	0	1748.07	156	172
Mitogen-activated protein kinase kinase kinase 7	MAP3K7	M3K7_HUMAN	67.2	99.8%	2	3	5	0.01%	5.8%	SIQDLTVTGTEPGQVSSR	99.7%	87.3	25	86.4	1	0	0	1874.95	439	456
Mitotic checkpoint protein BUB3	BUB3	BUB3_HUMAN	37.2	100.0%	5	5	10	0.01%	17.4%	LNQPPEDGISSVK	99.7%	50.8	25	46.3	2	0	0	1383.71	9	21
Mitotic checkpoint protein BUB3	BUB3	BUB3_HUMAN	37.2	100.0%	5	5	10	0.01%	17.4%	TPCNAGTFSQPEK	99.7%	61	25	61	2	0	0	1436.65	127	139
Mitotic checkpoint protein BUB3	BUB3	BUB3_HUMAN	37.2	100.0%	5	5	10	0.01%	17.4%	VAVEYLDPSPEVQK	99.7%	42.8	25	42.8	2	0	0	1573.81	203	216
Mitotic checkpoint protein BUB3	BUB3	BUB3_HUMAN	37.2	100.0%	5	5	10	0.01%	17.4%	VLVWDLR	99.7%	40.3	25	28.3	2	0	0	900.53	159	165
Mitotic checkpoint protein BUB3	BUB3	BUB3_HUMAN	37.2	100.0%	5	5	10	0.01%	17.4%	VYTLSVSGDR	99.7%	71.8	25	59.1	2	0	0	1096.56	140	149
MKI67 FHA domain-interacting nucleolar phosphoprotein	NIFK	MK67I_HUMAN	34.2	100.0%	3	3	4	0.00%	14.0%	GIDYDFPSLILQK	99.7%	68.8	25	68.8	2	0	0	1508.80	180	192
MKI67 FHA domain-interacting nucleolar phosphoprotein	NIFK	MK67I_HUMAN	34.2	100.0%	3	3	4	0.00%	14.0%	GYAFVEFESEDVAK	99.7%	101	25	96	1	0	0	1590.73	87	100
MKI67 FHA domain-interacting nucleolar phosphoprotein	NIFK	MK67I_HUMAN	34.2	100.0%	3	3	4	0.00%	14.0%	IVAETMNNYLFGER	99.7%	60.2	25	58.3	1	0	0	1656.81	101	114
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	8	8	14	0.01%	8.8%	EDLILSLR	99.7%	43.7	25	15.2	2	0	0	958.56	239	246
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	8	8	14	0.01%	8.8%	FAEFLLPLLIEK	99.7%	78.7	25	71.4	4	0	0	1432.85	255	266
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	8	8	14	0.01%	8.8%	GEWFLLGSPGS	99.4%	36.5	25	33.9	1	0	0	1149.56	1020	1030

MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	8	8	14	0.01%	8.8%	GLSHVLNR	99.3%	35.7	25	32.3	2	0	0	895.51	894	901
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	8	8	14	0.01%	8.8%	IVHDLISR	99.1%	34.7	25	34.7	1	0	0	952.56	196	203
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	8	8	14	0.01%	8.8%	LLQAAAGASAR	99.7%	76.1	25	73.1	2	0	0	1028.58	374	384
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	8	8	14	0.01%	8.8%	LPTPVLLPYKPQVIR	99.0%	28.4	25	28.4	0	1	0	1734.07	984	998
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	8	8	14	0.01%	8.8%	VEAEGLAALHSLTACLSR	99.7%	55.6	25	51.1	0	1	0	1897.98	317	334
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	7	9	18	0.02%	29.1%	AYLEPEHTK	95.3%	27.9	25	24.1	1	0	0	1087.54	24	32
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	7	9	18	0.02%	29.1%	CTAPQYVDFVMSSVQK	99.7%	60.3	25	50.8	3	2	0	1875.86	105	120
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	7	9	18	0.02%	29.1%	EFNLLDPK	94.7%	27.4	25	14.2	1	0	0	975.51	188	195
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	7	9	18	0.02%	29.1%	EFPSSFESLVR	99.7%	64.3	25	57.3	3	0	0	1297.64	135	145
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	7	9	18	0.02%	29.1%	ELVVLPR	99.7%	41.3	25	23.2	2	0	0	825.52	42	48
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	7	9	18	0.02%	29.1%	ITDFQFK	99.7%	47.6	25	15.9	2	0	0	898.47	35	41
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	7	9	18	0.02%	29.1%	LVTDEDVFPTK	99.7%	80.1	25	67.6	4	0	0	1263.65	121	131
Monocarboxylate transporter 1	SLC16A1	MOT1_HUMAN	53.9	100.0%	3	4	16	0.02%	8.2%	DLHDANTDLIGR	99.7%	53.6	25	48.6	8	2	0	1339.66	225	236
Monocarboxylate transporter 1	SLC16A1	MOT1_HUMAN	53.9	100.0%	3	4	16	0.02%	8.2%	ESKEEETSIDVAGKPNEVTK	99.7%	51.9	25	51.9	0	4	0	2190.08	460	479
Monocarboxylate transporter 1	SLC16A1	MOT1_HUMAN	53.9	100.0%	3	4	16	0.02%	8.2%	LNDMYGDYK	99.7%	43.7	25	43.2	2	0	0	1118.48	412	420
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	24	46	0.05%	28.4%	AEIDLVCELAK	99.7%	86.7	25	71.7	2	0	0	1260.65	808	818
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	24	46	0.05%	28.4%	ASGLVPNVVVLVATVR	99.7%	59.6	25	59.6	1	0	0	1593.97	730	745
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	24	46	0.05%	28.4%	AVIELLEK	99.7%	58.1	25	28	2	0	0	914.56	206	213
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	24	46	0.05%	28.4%	DFILPISDVR	99.7%	51.7	25	45.3	2	0	0	1174.65	926	935
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	24	46	0.05%	28.4%	DIELSPEAQAK	99.7%	64.8	25	52.3	2	0	0	1200.61	881	891
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	24	46	0.05%	28.4%	DVDGVTDINLGK	99.7%	79.2	25	72.4	2	0	0	1245.63	178	189
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	24	46	0.05%	28.4%	EFSEIQLAR	99.7%	66.5	25	35	2	0	0	1092.57	531	539
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	24	46	0.05%	28.4%	EIGLLADEIEIYGK	99.7%	120	25	117	3	0	0	1562.83	380	393
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	24	46	0.05%	28.4%	EVLSLLQEK	99.7%	50.3	25	42.5	2	0	0	1058.61	84	92
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	24	46	0.05%	28.4%	FQFLYDVQVPIVDK	99.7%	103	25	103	2	0	0	1710.91	855	868
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	24	46	0.05%	28.4%	GDAHECFVSPVAK	99.7%	34.3	25	34.3	0	2	0	1416.66	193	205
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	24	46	0.05%	28.4%	ILHENTQTDK	97.3%	30.1	25	30.1	1	0	0	1198.61	507	516
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	24	46	0.05%	28.4%	IQNMVSSGR	99.7%	48.3	25	42.5	2	0	0	991.50	327	335
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	24	46	0.05%	28.4%	KITIGQGNTEK	99.7%	50.4	25	36.8	2	0	0	1188.66	586	596
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	24	46	0.05%	28.4%	LDIDPSTITWQR	99.7%	81.5	25	70.3	2	0	0	1444.74	564	575
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	24	46	0.05%	28.4%	LQPLSPVPSDIEISR	99.7%	63.1	25	62.4	2	0	0	1650.91	353	367
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	24	46	0.05%	28.4%	LVPLVNGVR	98.3%	31.9	25	31.9	2	0	0	966.61	522	530
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	24	46	0.05%	28.4%	MHGGGPSVTAGVPLKK	99.7%	33.8	25	33	0	3	0	1535.84	749	764
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	24	46	0.05%	28.4%	SGQPVTADDLGVTGALTVLMK	99.7%	91.3	25	91.3	1	0	0	2089.09	639	659
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	24	46	0.05%	28.4%	TDPSTLTEEEVSK	99.7%	72.8	25	63.6	2	0	0	1435.68	548	560
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	24	46	0.05%	28.4%	TIAQAVYGAK	99.7%	64.1	25	54.8	2	0	0	1021.57	871	880
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	24	46	0.05%	28.4%	VLNALKPEK	99.7%	42.6	25	32.8	2	0	0	1011.62	169	177
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	23	24	46	0.05%	28.4%	YVLVAGITPTPLGEGK	99.7%	101	25	96.8	3	0	0	1614.91	414	429
Motile sperm domain-containing protein 2	MOSPD2	MSPD2_HUMAN	59.7	100.0%	4	4	8	0.01%	8.5%	EISVNDLNESSIPR	99.7%	67.4	25	60.1	2	0	0	1572.79	74	87
Motile sperm domain-containing protein 2	MOSPD2	MSPD2_HUMAN	59.7	100.0%	4	4	8	0.01%	8.5%	LIAFWLER	99.7%	51	25	41.2	2	0	0	1047.60	128	135
Motile sperm domain-containing protein 2	MOSPD2	MSPD2_HUMAN	59.7	100.0%	4	4	8	0.01%	8.5%	TLIVLTNVTK	99.7%	61.1	25	61.1	2	0	0	1101.69	348	357
Motile sperm domain-containing protein 2	MOSPD2	MSPD2_HUMAN	59.7	100.0%	4	4	8	0.01%	8.5%	TWLGPEAVSLLK	99.7%	39.9	25	17	2	0	0	1313.75	200	211
mRNA export factor	RAE1	RAE1L_HUMAN	41.0	100.0%	5	5	8	0.01%	18.5%	CWEVQDSGQTIPK	99.7%	71.4	25	67.7	2	0	0	1547.72	68	80
mRNA export factor	RAE1	RAE1L_HUMAN	41.0	100.0%	5	5	8	0.01%	18.5%	CYCADVIYPMAVVATAER	99.7%	89.5	25	89.5	1	0	0	2088.96	173	190
mRNA export factor	RAE1	RAE1L_HUMAN	41.0	100.0%	5	5	8	0.01%	18.5%	NAAEELKPR	94.8%	27.5	25	23.7	1	0	0	1027.55	357	365
mRNA export factor	RAE1	RAE1L_HUMAN	41.0	100.0%	5	5	8	0.01%	18.5%	QNKPTGFALGSIEGR	98.2%	26	25	26	0	2	0	1574.83	225	239
mRNA export factor	RAE1	RAE1L_HUMAN	41.0	100.0%	5	5	8	0.01%	18.5%	SSNPMMVLQLPER	99.7%	42.6	25	40.5	2	0	0	1501.75	160	172
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	5	7	11	0.01%	25.1%	EGDVLTPEQAR	98.9%	33.7	25	31.4	1	0	0	1214.60	178	188
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	5	7	11	0.01%	25.1%	GEVGLLFTNR	99.7%	57.7	25	55.1	2	0	0	1105.60	98	107
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	5	7	11	0.01%	25.1%	GVVTLLSDYEVCK	99.7%	78.6	25	74.8	2	0	0	1482.75	165	177
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	5	7	11	0.01%	25.1%	SPSDEYKDNLHQVSK	99.7%	41.8	25	41.8	1	1	0	1746.83	80	94

mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	5	7	11	0.01%	25.1%	YLFIFSVANMR	99.7%	53.4	25	53.4	4	0	0	1360.71	39	49
Multidrug resistance-associated protein 1	ABCC1	MRP1_HUMAN	171.6	99.8%	2	2	3	0.00%	1.6%	ITIIPQDPVLFSGSLR	99.7%	41.9	25	35	1	0	0	1756.00	1370	1385
Multidrug resistance-associated protein 1	ABCC1	MRP1_HUMAN	171.6	99.8%	2	2	3	0.00%	1.6%	TPSGNLVNR	99.7%	56.5	25	49.7	2	0	0	957.51	1067	1075
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	7	7	12	0.01%	21.6%	ACGNFGIPCELR	99.6%	38.7	25	32.6	2	0	0	1393.64	287	298
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	7	7	12	0.01%	21.6%	ASILNTWISLK	99.7%	74.1	25	61.3	2	0	0	1245.72	404	414
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	7	7	12	0.01%	21.6%	EIVLADVIDNDSWR	99.7%	114	25	109	2	0	0	1644.82	202	215
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	7	7	12	0.01%	21.6%	EVTPEGLQMVK	99.7%	50.6	25	49.6	2	0	0	1230.64	236	246
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	7	7	12	0.01%	21.6%	ITSCIFQLLQEAGIK	99.7%	46.7	25	42.7	1	0	0	1720.93	60	74
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	7	7	12	0.01%	21.6%	TKEVYELLDSPGK	99.7%	88	25	85.5	2	0	0	1478.77	18	30
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	7	7	12	0.01%	21.6%	VVVLMGSTSDLGHCEK	99.7%	59	25	51.8	1	0	0	1731.84	268	283
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	49	0.05%	17.9%	AGALHAQVER	98.9%	33.9	25	24	1	0	0	1051.56	897	906
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	49	0.05%	17.9%	ALVDILSEVSK	99.7%	88.8	25	72.6	2	0	0	1173.67	180	190
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	49	0.05%	17.9%	AQDSSLHMPER	99.7%	42.2	25	42.2	2	0	0	1286.58	433	443
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	49	0.05%	17.9%	ATLQEILPEVLK	99.7%	43.4	25	38.5	2	0	0	1353.80	191	202
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	49	0.05%	17.9%	EIPSATQSPISK	99.7%	55.2	25	42.5	2	0	0	1257.67	1156	1167
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	49	0.05%	17.9%	ELEAHSAEAR	97.8%	30.8	25	27.4	1	0	0	1112.53	582	591
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	49	0.05%	17.9%	EVVEQGLLK	99.7%	52.9	25	40.9	3	0	0	1014.58	287	295
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	49	0.05%	17.9%	GNTAEGCVHETQEK	99.7%	73.3	25	73.3	3	0	0	1559.68	936	949
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	49	0.05%	17.9%	HPFSFPLENQAR	99.4%	30.4	25	25.3	0	1	0	1442.72	499	510
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	49	0.05%	17.9%	HQACLLLQK	96.9%	29.6	25	24.1	2	0	0	1110.61	1028	1036
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	49	0.05%	17.9%	KPTSQIPETK	99.7%	40.6	25	39	3	0	0	1128.63	489	498
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	49	0.05%	17.9%	LITGLGVGR	99.7%	40.5	25	31.9	1	0	0	885.55	77	85
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	49	0.05%	17.9%	LLEYLR	97.4%	30.3	25	17.1	1	0	0	806.48	57	62
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	49	0.05%	17.9%	LLGAALPLLTK	99.7%	59.5	25	59.5	4	0	0	1109.73	308	318
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	49	0.05%	17.9%	LPAIALDLLR	99.7%	63.2	25	56	3	0	0	1094.69	264	273
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	49	0.05%	17.9%	LVGSVNLFSDENVPR	99.7%	89.4	25	86.5	2	0	0	1645.85	232	246
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	49	0.05%	17.9%	QLMGQVLAK	99.7%	40.5	25	27	2	0	0	987.57	1054	1062
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	49	0.05%	17.9%	SPAPGAPTR	99.7%	39.5	25	23.9	2	0	0	853.45	1232	1240
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	49	0.05%	17.9%	SPLSALAR	99.7%	51.8	25	24.1	2	0	0	814.48	1290	1297
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	49	0.05%	17.9%	SPSLLQSGAK	99.3%	35.7	25	26.3	2	0	0	987.55	1308	1317
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	49	0.05%	17.9%	TLGVQRPK	99.4%	36.2	25	32.2	2	0	0	898.55	1141	1148
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	49	0.05%	17.9%	VLDLVEVLVTK	99.7%	101	25	101	2	0	0	1227.76	828	838
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	49	0.05%	17.9%	VYSTALSSFLTK	99.7%	98.9	25	88.3	4	0	0	1316.71	977	988
Myosin light polypeptide 6	MYL6	MYL6_HUMAN	16.9	100.0%	4	5	9	0.01%	27.2%	ALGQNPTNAEVLK	99.7%	51.3	25	48.9	4	0	0	1354.73	38	50
Myosin light polypeptide 6	MYL6	MYL6_HUMAN	16.9	100.0%	4	5	9	0.01%	27.2%	EAFQLFDR	99.7%	39.3	25	39.3	1	0	0	1025.51	14	21
Myosin light polypeptide 6	MYL6	MYL6_HUMAN	16.9	100.0%	4	5	9	0.01%	27.2%	HVLVTLGEK	99.5%	37.5	25	37	1	0	0	995.59	111	119
Myosin light polypeptide 6	MYL6	MYL6_HUMAN	16.9	100.0%	4	5	9	0.01%	27.2%	ILYSQCGDVMR	99.7%	58.6	25	58.6	3	0	0	1357.62	27	37
Myosin-10	MYH10	MYH10_HUMAN	229.0	100.0%	3	3	5	0.01%	2.5%	ALELDPNLYR	99.7%	41.3	25	36.7	2	0	0	1203.64	753	762
Myosin-10	MYH10	MYH10_HUMAN	229.0	100.0%	3	3	5	0.01%	2.5%	LDPHLVLDQLR	99.7%	43.5	25	39.1	2	0	0	1318.75	690	700
Myosin-10	MYH10	MYH10_HUMAN	229.0	100.0%	3	3	5	0.01%	2.5%	QLLQANPILESFGNAK	99.7%	49.3	25	49.3	2	0	0	1742.94	217	232
Myosin-10	MYH10	MYH10_HUMAN	229.0	100.0%	3	3	5	0.01%	2.5%	SDLLLEGFNNYR	99.7%	45.7	25	44.8	1	0	0	1440.71	297	308
Myosin-9	MYH9	MYH9_HUMAN	226.5	100.0%	3	3	5	0.01%	2.0%	EQADFAIEALAK	99.7%	63.7	25	0	1	0	0	1305.67	408	419
Myosin-9	MYH9	MYH9_HUMAN	226.5	100.0%	3	3	5	0.01%	2.0%	LDPHLVLDQLR	99.7%	43.5	25	39.1	2	0	0	1318.75	683	693
Myosin-9	MYH9	MYH9_HUMAN	226.5	100.0%	3	3	5	0.01%	2.0%	QLLQANPILEAFGNAK	99.7%	74	25	73	2	0	0	1726.95	210	225
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	12	12	21	0.02%	12.6%	AGFVPVYLR	98.4%	32.2	25	25	2	0	0	1021.58	726	734
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	12	12	21	0.02%	12.6%	AIEEQMVAAK	99.6%	38	25	34.1	2	0	0	1105.56	913	922
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	12	12	21	0.02%	12.6%	ASEVFLQR	99.7%	63.8	25	42	2	0	0	949.51	521	528
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	12	12	21	0.02%	12.6%	EELEALFLPYDLK	99.7%	67.3	25	64.5	2	0	0	1579.83	811	823
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	12	12	21	0.02%	12.6%	EIELPSGQLMGLFNR	99.7%	49.5	25	47.9	1	0	0	1719.87	883	897
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	12	12	21	0.02%	12.6%	ILIENGVAER	99.7%	58.6	25	46.1	2	0	0	1113.63	12	21
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	12	12	21	0.02%	12.6%	LDYLGVSYGLTPR	99.7%	75.5	25	69.2	2	0	0	1453.77	706	718

N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	12	12	21	0.02%	12.6%	QDDPFELFIAATNIR	99.7%	69.8	25	65.7	1	0	0	1749.88	89	103
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	12	12	21	0.02%	12.6%	QQSAQSQVSTTAENK	99.7%	92.3	25	90.2	2	0	0	1606.77	433	447
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	12	12	21	0.02%	12.6%	SLFVVVGDR	99.7%	57.4	25	48.6	2	0	0	991.56	24	32
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	12	12	21	0.02%	12.6%	TEAHQDVVGR	99.7%	44.5	25	43.6	2	0	0	1111.55	173	182
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	12	12	21	0.02%	12.6%	YRTEAHQDVVGR	94.7%	22.1	25	17	0	1	0	1430.71	171	182
N-acetyltransferase 14	NAT14	NAT14_HUMAN	21.7	100.0%	3	3	4	0.00%	19.4%	APSHLSVR	96.6%	29.2	25	29.2	1	0	0	866.48	2	9
N-acetyltransferase 14	NAT14	NAT14_HUMAN	21.7	100.0%	3	3	4	0.00%	19.4%	AWAGGMGEPR	98.4%	32.2	25	32.2	1	0	0	1031.47	153	162
N-acetyltransferase 14	NAT14	NAT14_HUMAN	21.7	100.0%	3	3	4	0.00%	19.4%	GSGDVCGVLALAPGTNAGDGAR	99.7%	71.5	25	71.5	2	0	0	2014.96	103	124
N-acylneuraminate cytidylyltransferase	CMAS	NEUA_HUMAN	48.4	99.8%	2	2	2	0.00%	6.5%	EVTEPLNLNPAK	98.9%	34	25	31.9	1	0	0	1324.71	189	200
N-acylneuraminate cytidylyltransferase	CMAS	NEUA_HUMAN	48.4	99.8%	2	2	2	0.00%	6.5%	VGLSGAPADACSTAQK	98.1%	31.5	25	31.5	1	0	0	1532.74	384	399
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	7	7	9	0.01%	8.0%	AVVLAANHFGR	99.7%	40	25	40	1	0	0	1154.64	203	213
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	7	7	9	0.01%	8.0%	FFTGQITAAGK	99.7%	44.6	25	42.3	1	0	0	1140.60	214	224
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	7	7	9	0.01%	8.0%	FGIHPVAGR	98.7%	33	25	33	1	0	0	953.53	960	968
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	7	7	9	0.01%	8.0%	GITHIGYTDLPSR	99.7%	46	25	34.6	1	0	0	1429.74	367	379
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	7	7	9	0.01%	8.0%	TSGTLISFIYPAQNPELLNK	99.7%	60.9	25	60.9	2	0	0	2206.18	147	166
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	7	7	9	0.01%	8.0%	VAGAQIQGAK	99.7%	40	25	30.8	1	0	0	942.54	108	117
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	7	7	9	0.01%	8.0%	VALSPAGVQNLVK	99.7%	53.3	25	45.9	2	0	0	1295.77	72	84
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4	NDUFAF4	NDUF4_HUMAN	20.3	99.8%	2	2	4	0.00%	11.4%	EQISLYPEVK	99.7%	42.7	25	34.5	2	0	0	1205.64	42	51
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4	NDUFAF4	NDUF4_HUMAN	20.3	99.8%	2	2	4	0.00%	11.4%	IMQEYQLEQK	99.7%	52.9	25	42.2	2	0	0	1325.64	138	147
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	8	8	12	0.01%	23.7%	FDKGPWLK	95.2%	27.8	25	11.6	1	0	0	990.54	278	285
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	8	8	12	0.01%	23.7%	ITSAYLQDIENAYK	99.7%	87.2	25	83.1	2	0	0	1628.82	229	242
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	8	8	12	0.01%	23.7%	KVVEDIEYLK	99.7%	41.4	25	40	1	0	0	1235.69	268	277
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	8	8	12	0.01%	23.7%	LLQYSDALEHLLTTGQGVVLER	99.7%	48.6	25	48.6	0	1	0	2455.32	140	161
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	8	8	12	0.01%	23.7%	LQSWLYSSR	99.7%	54.2	25	45.4	2	0	0	1139.58	131	139
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	8	8	12	0.01%	23.7%	TFLPEMSEK	99.1%	34.5	25	28.7	1	0	0	1097.52	244	252
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	8	8	12	0.01%	23.7%	VITVDGNICTGK	99.7%	76.9	25	66.2	2	0	0	1276.66	59	70
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	8	8	12	0.01%	23.7%	VVEDIEYLK	99.7%	56.6	25	53.4	2	0	0	1107.59	269	277
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	100.0%	3	4	10	0.01%	26.2%	FNVTGTPEQYVPYSTTR	99.7%	71.6	25	71.6	2	0	0	1959.94	115	131
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	100.0%	3	4	10	0.01%	26.2%	GLQQITGHGGLR	99.7%	64.5	25	59	5	1	0	1236.68	10	21
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	100.0%	3	4	10	0.01%	26.2%	VGTLVGEDK	99.0%	34.3	25	3.61	2	0	0	917.49	35	43
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	NDUAD_HUMAN	16.7	100.0%	3	4	9	0.01%	20.8%	ENLEEEAIIMK	99.7%	72.3	25	68.8	3	0	0	1334.65	89	99
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	NDUAD_HUMAN	16.7	100.0%	3	4	9	0.01%	20.8%	LQIEDFEAR	99.7%	43.2	25	36.5	4	0	0	1120.56	60	68
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	NDUAD_HUMAN	16.7	100.0%	3	4	9	0.01%	20.8%	VGESVFHTTR	99.7%	83.8	25	72.5	2	0	0	1132.57	106	115
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	NDUFA4	NDUA4_HUMAN	9.4	100.0%	3	3	6	0.01%	37.0%	FYSVNVDYSK	99.7%	65.2	25	54.7	2	0	0	1221.58	64	73
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	NDUFA4	NDUA4_HUMAN	9.4	100.0%	3	3	6	0.01%	37.0%	LALFNPDVCWDR	97.7%	30.7	25	30.7	2	0	0	1505.72	36	47
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	NDUFA4	NDUA4_HUMAN	9.4	100.0%	3	3	6	0.01%	37.0%	LGPNDQYK	99.5%	37.7	25	31.6	2	0	0	934.46	56	63
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	NDUA5_HUMAN	13.5	100.0%	4	5	10	0.01%	44.0%	ILDVLEEIPK	99.7%	64.3	25	57	2	0	0	1168.68	31	40
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	NDUA5_HUMAN	13.5	100.0%	4	5	10	0.01%	44.0%	KYTEQITNEK	99.3%	35.9	25	29.4	2	0	0	1253.64	46	55
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	NDUA5_HUMAN	13.5	100.0%	4	5	10	0.01%	44.0%	LWEPLVEEPPADQWK	99.7%	48.7	25	48.7	2	0	0	1836.92	99	113
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	NDUA5_HUMAN	13.5	100.0%	4	5	10	0.01%	44.0%	TTGLVGLAVCNTPHER	99.7%	53.4	25	53.4	2	2	0	1724.88	8	23
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	NDUFA6	NDUA6_HUMAN	17.9	100.0%	3	3	9	0.01%	18.8%	FFHETEAPRPK	98.4%	32.2	25	32.2	3	0	0	1358.69	132	142
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	NDUFA6	NDUA6_HUMAN	17.9	100.0%	3	3	9	0.01%	18.8%	GKIELEETIK	99.7%	50.1	25	34.4	2	0	0	1159.66	112	121
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	NDUFA6	NDUA6_HUMAN	17.9	100.0%	3	3	9	0.01%	18.8%	VVDLLVIK	99.7%	52.6	25	50.9	4	0	0	898.60	104	111
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	7	8	16	0.02%	19.1%	FGPIPLGSLGWK	99.7%	41.2	25	41.2	1	0	0	1271.71	223	234
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	7	8	16	0.02%	19.1%	MGSQVIIPYR	99.7%	47.9	25	40.6	4	0	0	1163.62	76	85
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	7	8	16	0.02%	19.1%	NFDFEDVFVK	99.7%	39.3	25	16.8	2	0	0	1259.59	138	147
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	7	8	16	0.02%	19.1%	QPVYVVDVSK	99.7%	49.9	25	46.5	2	0	0	1133.62	238	247
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	7	8	16	0.02%	19.1%	SFAFVGPSR	99.7%	39.4	25	39.4	2	0	0	967.50	262	270
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	7	8	16	0.02%	19.1%	VFEISPFEPWITR	99.7%	57.4	25	56.2	3	0	0	1620.84	304	316
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	7	8	16	0.02%	19.1%	YVVNHLGR	98.8%	33.5	25	24.6	2	0	0	957.53	68	75
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	NDUFB4	NDUB4_HUMAN	15.2	100.0%	3	3	6	0.01%	31.0%	EYLLQYNDPNRR	99.4%	30.1	25	27.3	0	2	0	1580.78	46	57

NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	NDUFB4	NDUB4_HUMAN	15.2	100.0%	3	3	6	0.01%	31.0%	GLIENPALLR	99.7%	66.2	25	54.7	2	0	0	1095.65	58	67
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	NDUFB4	NDUB4_HUMAN	15.2	100.0%	3	3	6	0.01%	31.0%	TLPETLDPAEYNISPETR	99.7%	42.6	25	41.7	2	0	0	2046.00	13	30
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial	NDUFB5	NDUB5_HUMAN	21.8	100.0%	2	3	4	0.00%	14.3%	NFYDSPEKIYER	98.8%	33.4	25	23.8	2	0	0	1560.73	124	135
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial	NDUFB5	NDUB5_HUMAN	21.8	100.0%	2	3	4	0.00%	14.3%	TMAVLQIEAEKAELR	99.7%	55	25	51.9	1	1	0	1701.92	136	150
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	6	6	9	0.01%	13.6%	EAYEAGLIGK	99.7%	53.6	25	46	2	0	0	1050.55	175	184
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	6	6	9	0.01%	13.6%	GEFYNEASNLQVAIR	99.3%	36.1	25	30.5	1	0	0	1710.84	160	174
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	6	6	9	0.01%	13.6%	GGAGFPTGLK	95.8%	28.3	25	23.9	1	0	0	904.49	89	98
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	6	6	9	0.01%	13.6%	GGTWFAGFGR	99.6%	38.5	25	36.7	2	0	0	1055.51	258	267
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	6	6	9	0.01%	13.6%	GPDWILGEIK	99.7%	50.4	25	48.4	2	0	0	1127.61	72	81
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	6	6	9	0.01%	13.6%	IFTNLYGR	97.8%	31	25	17.8	1	0	0	983.53	41	48
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	5	7	11	0.01%	14.5%	GEFGVYLVSDGSSRPYR	99.7%	45.8	25	45.8	2	1	0	1888.92	405	421
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	5	7	11	0.01%	14.5%	IKAPGFAHLAGLDK	98.4%	26.4	25	25.6	0	1	0	1437.82	424	437
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	5	7	11	0.01%	14.5%	LVMELSGEMVR	99.7%	62.9	25	59.8	3	0	0	1263.64	97	107
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	5	7	11	0.01%	14.5%	MFEFYER	99.3%	36	25	32.1	2	0	0	1021.44	210	216
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	5	7	11	0.01%	14.5%	NITLNFGPQHPAAHGVLR	99.7%	45.3	25	45	0	2	0	1942.04	79	96
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	7	7	13	0.01%	34.1%	AANWYER	99.7%	48.1	25	47.3	2	0	0	909.42	162	168
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	7	7	13	0.01%	34.1%	DFPLSGYVELR	99.7%	78.8	25	60.8	2	0	0	1295.66	201	211
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	7	7	13	0.01%	34.1%	ILTDYGFEGHPFR	99.7%	68.8	25	68.8	2	0	0	1551.76	187	199
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	7	7	13	0.01%	34.1%	QLSAFGEYVAEILPK	99.7%	63	25	57.9	2	0	0	1664.89	57	71
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	7	7	13	0.01%	34.1%	SLVDLTAVDVPTR	99.7%	89.6	25	87.7	2	0	0	1385.76	110	122
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	7	7	13	0.01%	34.1%	TYTDELTPIESAVSVFK	99.7%	43.6	25	43.6	2	0	0	1899.96	145	161
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	7	7	13	0.01%	34.1%	VVAEPVELAQEFRK	99.7%	39.2	25	39.2	1	0	0	1614.89	219	232
NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	NDUFS6	NDUS6_HUMAN	13.7	99.8%	2	2	4	0.00%	21.8%	TGTCGYCGLQFR	96.2%	28.7	25	28.1	2	0	0	1419.61	109	120
NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	NDUFS6	NDUS6_HUMAN	13.7	99.8%	2	2	4	0.00%	21.8%	VIACDGGGGALGHPK	99.7%	53.8	25	53.8	2	0	0	1408.70	84	98
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	NDUS7_HUMAN	23.6	100.0%	3	5	16	0.02%	15.0%	LDDLVNWAR	99.7%	76.8	25	59.3	2	0	0	1101.57	67	75
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	NDUS7_HUMAN	23.6	100.0%	3	5	16	0.02%	15.0%	QSDVMIVAGTLTNK	99.7%	116	25	109	8	0	0	1476.77	116	129
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	NDUS7_HUMAN	23.6	100.0%	3	5	16	0.02%	15.0%	VYDQMPEPR	99.7%	51.3	25	51.3	6	0	0	1134.52	137	145
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	NDUS8_HUMAN	23.7	100.0%	5	6	13	0.01%	29.0%	EPATINYPFEK	99.7%	41.8	25	41.8	1	0	0	1308.65	78	88
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	NDUS8_HUMAN	23.7	100.0%	5	6	13	0.01%	29.0%	GLGMTLSYLFR	99.7%	59.7	25	58.1	4	0	0	1257.67	67	77
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	NDUS8_HUMAN	23.7	100.0%	5	6	13	0.01%	29.0%	LCEAICPAQAITIEAEPR	99.7%	105	25	105	2	0	0	2042.00	116	133
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	NDUS8_HUMAN	23.7	100.0%	5	6	13	0.01%	29.0%	TLLWTELFR	99.7%	75.9	25	71.4	2	0	0	1178.66	58	66
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	NDUS8_HUMAN	23.7	100.0%	5	6	13	0.01%	29.0%	YVNMQDPEMDMK	99.7%	46.7	25	32.2	4	0	0	1532.61	38	49
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	17	20	30	0.03%	28.6%	ALSEIAGMTLPYDTLDQVR	99.7%	70.1	25	67.7	3	0	0	2109.05	625	643
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	17	20	30	0.03%	28.6%	FASEIAGVDDLGTTGR	99.7%	109	25	106	2	0	0	1608.79	185	200
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	17	20	30	0.03%	28.6%	FEAPLFNAR	99.7%	58.5	25	52.5	2	0	0	1064.55	409	417
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	17	20	30	0.03%	28.6%	GLLTYTSWEDALSR	99.7%	95.4	25	94.2	2	0	0	1611.80	312	325
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	17	20	30	0.03%	28.6%	GWNILTNSEK	99.7%	48.1	25	39.5	2	0	0	1161.59	99	108
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	17	20	30	0.03%	28.6%	ILQDIASGSHPFSQVLK	99.7%	48.9	25	48.9	1	2	0	1840.00	451	467
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	17	20	30	0.03%	28.6%	LVNQQLLADPLVPPQLTIK	99.1%	34.7	25	32.2	2	0	0	2100.24	674	692
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	17	20	30	0.03%	28.6%	MTSGVTGDWK	99.5%	37.8	25	37.8	1	0	0	1081.50	502	511
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	17	20	30	0.03%	28.6%	NDGAAILAAVSSIAQK	99.7%	127	25	125	2	0	0	1528.83	484	499
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	17	20	30	0.03%	28.6%	SATYVNTEGR	99.7%	59.5	25	46.7	2	0	0	1097.52	593	602
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	17	20	30	0.03%	28.6%	SWLHNDLK	98.5%	32.5	25	25	1	0	0	1012.52	421	428
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	17	20	30	0.03%	28.6%	VAGMLQSFQGK	99.7%	62.8	25	55.5	2	0	0	1181.60	326	336
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	17	20	30	0.03%	28.6%	VAVTPPGLAR	97.2%	30	25	30	1	0	0	980.59	608	617
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	17	20	30	0.03%	28.6%	VGMQIPR	99.6%	38.8	25	22.2	1	0	0	800.44	56	62
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	17	20	30	0.03%	28.6%	VLFLLGADGGCITR	99.7%	99.9	25	90.7	2	0	0	1491.80	544	557
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	17	20	30	0.03%	28.6%	VMNILHR	99.4%	36.6	25	31.5	1	0	0	882.50	512	518
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	17	20	30	0.03%	28.6%	VVAACAMPVMK	99.7%	61.2	25	58.8	1	0	0	1176.59	88	98
NADH-ubiquinone oxidoreductase chain 1	MT-ND1	NU1M_HUMAN	35.7	99.8%	2	2	3	0.00%	8.5%	GPNVVGPYGLLQPFADAMK	95.4%	28	25	28	1	0	0	1974.02	36	54
NADH-ubiquinone oxidoreductase chain 1	MT-ND1	NU1M_HUMAN	35.7	99.8%	2	2	3	0.00%	8.5%	ILGYMQLR	99.7%	46.9	25	40.8	2	0	0	993.56	27	34

N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	7	10	15	0.02%	26.4%	AMIENFNAK	99.7%	46.3	25	33.7	2	0	0	1037.51	97	105
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	7	10	15	0.02%	26.4%	HVVLGAIENK	99.7%	46.8	25	44.6	2	0	0	1079.62	170	179
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	7	10	15	0.02%	26.4%	HVVLGAIENKVESK	99.7%	52	25	52	1	1	0	1522.86	170	183
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	7	10	15	0.02%	26.4%	MEEDPDDVPHGHITSLAVK	99.7%	44.5	25	40.8	0	3	0	2089.99	60	78
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	7	10	15	0.02%	26.4%	YVSLHVR	99.7%	41.5	25	32	2	0	0	873.49	106	112
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	7	10	15	0.02%	26.4%	YYADGEDAYAMK	99.7%	56	25	56	2	0	0	1396.57	137	148
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	7	10	15	0.02%	26.4%	YYADGEDAYAMKR	99.7%	47.8	25	47.8	2	0	0	1568.67	137	149
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	26	51	0.05%	23.3%	AIELATTLDESLTNR	99.7%	119	25	101	2	0	0	1646.86	783	797
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	26	51	0.05%	23.3%	ALKPANMLER	99.7%	41.1	25	24.2	2	0	0	1142.64	267	276
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	26	51	0.05%	23.3%	DLSLLQIQMR	99.7%	71.6	25	59.2	4	0	0	1216.67	119	128
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	26	51	0.05%	23.3%	EALEHLCTYEK	99.7%	55.7	25	39.7	2	0	0	1392.65	208	218
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	26	51	0.05%	23.3%	EEAYELVR	99.5%	37.8	25	27.1	2	0	0	1008.50	63	70
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	26	51	0.05%	23.3%	FAEHGETLAMK	99.7%	48.3	25	43.7	4	2	0	1233.59	42	52
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	26	51	0.05%	23.3%	FLLMLQSVK	99.7%	59.2	25	40.9	2	0	0	1094.63	688	696
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	26	51	0.05%	23.3%	GCPPVFNTLR	98.6%	32.8	25	20.3	2	0	0	1160.59	321	330
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	26	51	0.05%	23.3%	GLTLNCLGK	99.6%	38.3	25	19.2	1	0	0	975.53	53	61
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	26	51	0.05%	23.3%	IAIEIYLK	99.7%	39.5	25	31.6	2	0	0	962.59	560	567
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	26	51	0.05%	23.3%	ILEEFRK	99.3%	35.8	25	33.2	3	0	0	934.54	170	176
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	26	51	0.05%	23.3%	IYEEAWTK	99.7%	39.2	25	29.5	2	0	0	1039.51	279	286
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	26	51	0.05%	23.3%	KEEAYELVR	99.7%	63.6	25	54.5	2	0	0	1136.59	62	70
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	26	51	0.05%	23.3%	LEDAADVYR	99.7%	73.2	25	72	3	0	0	1051.51	240	248
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	26	51	0.05%	23.3%	LFNTAVCESK	99.7%	63.1	25	54.1	2	0	0	1168.57	715	724
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	26	51	0.05%	23.3%	LPLNFLSGEK	99.3%	35.8	25	23.8	2	0	0	1117.63	296	305
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	26	51	0.05%	23.3%	MVYYLDPSSQK	99.7%	55.6	25	55.6	3	0	0	1330.63	771	781
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	26	51	0.05%	23.3%	NFNETFLKR	99.1%	34.8	25	22.2	2	0	0	1168.61	749	757
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	26	51	0.05%	23.3%	NPENWAYYK	99.7%	39.5	25	32.5	2	0	0	1184.54	254	262
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	26	51	0.05%	23.3%	RLPLNFLSGEK	99.7%	58.8	25	58.8	2	0	0	1273.73	295	305
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	26	51	0.05%	23.3%	VAIIEELVVGYETSLK	99.7%	70.7	25	70.7	2	0	0	1762.98	339	354
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	26	51	0.05%	23.3%	WDKDNLQILR	99.7%	34.1	25	25.6	0	1	0	1300.70	109	118
N-alpha-acetyltransferase 20	NAA20	NAA20_HUMAN	20.4	100.0%	3	5	7	0.01%	17.4%	AFTCDDLFR	96.4%	29	25	17.6	1	0	0	1144.51	6	14
N-alpha-acetyltransferase 20	NAA20	NAA20_HUMAN	20.4	100.0%	3	5	7	0.01%	17.4%	LMELLEEISER	99.7%	84.1	25	65.7	3	0	0	1361.70	92	102
N-alpha-acetyltransferase 20	NAA20	NAA20_HUMAN	20.4	100.0%	3	5	7	0.01%	17.4%	VSNQVAVNMYK	99.7%	60.3	25	60.3	3	0	0	1252.64	114	124
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	17	17	30	0.03%	18.6%	ALQQHLCVVQLTR	99.7%	43	25	40.6	0	2	0	1565.86	410	422
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	17	17	30	0.03%	18.6%	DIQYPFLGPVPTR	99.7%	64.2	25	46.3	2	0	0	1502.80	748	760
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	17	17	30	0.03%	18.6%	DTSEYIIQAYK	99.7%	78.2	25	78.1	2	0	0	1330.65	576	586
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	17	17	30	0.03%	18.6%	FINQLLGVVPLSTPTEDK	99.7%	76	25	76	2	0	0	1971.08	384	401
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	17	17	30	0.03%	18.6%	IPEFIAFR	99.7%	53.4	25	35	2	0	0	992.56	593	600
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	17	17	30	0.03%	18.6%	LALPADIR	99.7%	39.7	25	26	1	0	0	868.53	402	409
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	17	17	30	0.03%	18.6%	LGDPEELMFQYFK	99.7%	49	25	49	1	0	0	1616.77	345	357
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	17	17	30	0.03%	18.6%	LLLQQLEATLETGK	99.7%	88.3	25	88.3	2	0	0	1556.89	729	742
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	17	17	30	0.03%	18.6%	LLLQQLEATLETGKR	99.7%	34	25	30	0	2	0	1712.99	729	743
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	17	17	30	0.03%	18.6%	LNNSLHFAQVR	98.4%	26.5	25	22	0	2	0	1298.70	603	613
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	17	17	30	0.03%	18.6%	LSLEEETLWLR	99.7%	76.6	25	71.4	2	0	0	1388.74	678	688
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	17	17	30	0.03%	18.6%	LTSEIQSR	99.7%	46.3	25	31.6	2	0	0	933.50	224	231
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	17	17	30	0.03%	18.6%	SLLDQLKDVFSK	99.7%	66.3	25	56.5	2	0	0	1392.77	807	818
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	17	17	30	0.03%	18.6%	TMFLPLAER	99.7%	41.4	25	35.2	1	0	0	1093.57	171	179
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	17	17	30	0.03%	18.6%	VFVDLLPATQCTK	99.7%	73.4	25	67.5	2	0	0	1491.79	371	383
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	17	17	30	0.03%	18.6%	YQEALDVIR	99.7%	57	25	46.6	2	0	0	1106.58	209	217
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	17	17	30	0.03%	18.6%	YQHGLEFGK	96.8%	29.4	25	21.5	1	0	0	1078.53	446	454
Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACA	NACAM_HUMAN	205.4	99.8%	2	2	4	0.00%	1.4%	IEDLSQQAQLAAAEK	99.7%	113	25	106	2	0	0	1614.83	1991	2005
Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACA	NACAM_HUMAN	205.4	99.8%	2	2	4	0.00%	1.4%	SPASDTYIVFGEAK	99.7%	83.8	25	79.8	2	0	0	1484.73	1977	1990

Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	14	15	23	0.02%	13.6%	AAEDLFVNIR	99.7%	89.5	25	72.5	2	0	0	1147.61	306	315
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	14	15	23	0.02%	13.6%	ASLGLADHR	99.7%	82.2	25	72.4	2	0	0	939.50	502	510
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	14	15	23	0.02%	13.6%	DEIIWLLR	99.7%	49.2	25	41.6	2	0	0	1057.60	380	387
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	14	15	23	0.02%	13.6%	ELATVLSDQPGLLGPK	99.7%	86.8	25	86.8	2	0	0	1637.91	352	367
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	14	15	23	0.02%	13.6%	EYLTSHLEIR	99.1%	34.9	25	29.2	1	0	0	1260.66	706	715
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	14	15	23	0.02%	13.6%	KFPAVETR	99.1%	34.8	25	13.4	2	0	0	947.53	63	70
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	14	15	23	0.02%	13.6%	LQAYTSVSK	96.0%	28.6	25	25.1	1	0	0	996.54	493	501
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	14	15	23	0.02%	13.6%	LSSVDSVLK	97.8%	31	25	24.7	1	0	0	947.54	897	905
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	14	15	23	0.02%	13.6%	LVVENVDVLTQMR	99.7%	69.1	25	67.8	2	0	0	1531.82	869	881
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	14	15	23	0.02%	13.6%	MFQQCLELPSQSR	94.8%	27.5	25	22.2	1	0	0	1623.76	552	564
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	14	15	23	0.02%	13.6%	NNNQQLAQLQK	99.7%	73.3	25	66.1	2	0	0	1298.68	71	81
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	14	15	23	0.02%	13.6%	QVEDGEVFDFR	99.7%	41.2	25	40.9	1	0	0	1340.61	474	484
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	14	15	23	0.02%	13.6%	SLSELLGPYGMK	97.1%	29.8	25	26	2	0	0	1310.67	838	849
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	14	15	23	0.02%	13.6%	SLSLCNMFLDEMAK	99.7%	56.4	25	56.4	2	0	0	1658.76	595	608
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	7	7	11	0.01%	15.4%	DAAAVGNHVAK	99.7%	64.7	25	54.2	2	0	0	1052.55	353	363
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	7	7	11	0.01%	15.4%	EGQGNLPVR	97.2%	29.9	25	28	1	0	0	969.51	318	326
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	7	7	11	0.01%	15.4%	FTVVVATQLPESTSLR	98.2%	31.8	25	31.8	1	0	0	1747.96	123	138
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	7	7	11	0.01%	15.4%	GTIPDMIADSGK	99.2%	35	25	26	1	0	0	1204.59	327	338
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	7	7	11	0.01%	15.4%	LLCSNSAFLR	99.7%	53.5	25	39.5	2	0	0	1180.61	382	391
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	7	7	11	0.01%	15.4%	TYGLVGYMR	99.7%	49.7	25	37.3	2	0	0	1059.53	155	163
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	7	7	11	0.01%	15.4%	YPGVSNYQVEEDIGK	99.7%	66.9	25	66.9	2	0	0	1697.80	442	456
Negative elongation factor B	NELFB	NELFB_HUMAN	65.7	99.8%	2	2	3	0.00%	4.0%	ALEPTGQSGEAVK	99.1%	34.5	25	27.3	1	0	0	1286.66	526	538
Negative elongation factor B	NELFB	NELFB_HUMAN	65.7	99.8%	2	2	3	0.00%	4.0%	DSPDLLLLLR	99.7%	52.1	25	20.5	2	0	0	1154.68	334	343
Neuroblastoma-amplified sequence	NBAS	NBAS_HUMAN	268.6	99.9%	2	2	3	0.00%	0.8%	AEEIEHYAR	99.7%	39.5	25	33.5	1	0	0	1117.53	850	858
Neuroblastoma-amplified sequence	NBAS	NBAS_HUMAN	268.6	99.9%	2	2	3	0.00%	0.8%	LLGLAELLR	99.7%	45.5	25	2.8	2	0	0	997.64	1262	1270
Neurochondrin	NCDN	NCDN_HUMAN	78.9	100.0%	2	2	3	0.00%	3.6%	IPILSTFLTAR	99.7%	50.6	25	50	2	0	0	1231.74	130	140
Neurochondrin	NCDN	NCDN_HUMAN	78.9	100.0%	2	2	3	0.00%	3.6%	LLSTSPALQGTPASR	99.7%	63.8	25	59.5	1	0	0	1498.82	579	593
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	8	9	13	0.01%	11.0%	ATLEMVNHEK	99.7%	46.8	25	36.8	2	0	0	1171.58	159	168
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	8	9	13	0.01%	11.0%	EIEAEIQALR	99.7%	77.3	25	59.6	2	0	0	1171.63	128	137
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	8	9	13	0.01%	11.0%	EYQDLLNVK	99.7%	52.6	25	46.8	7	0	0	1121.58	383	391
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	8	9	13	0.01%	11.0%	LLEGEETR	98.9%	33.7	25	17.7	2	0	0	946.48	404	411
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	8	9	13	0.01%	11.0%	LRDDTEAAIR	99.7%	57.6	25	42.3	2	0	0	1159.61	195	204
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	8	9	13	0.01%	11.0%	SIELESVR	98.0%	31.2	25	12.8	1	0	0	932.50	328	335
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	8	9	13	0.01%	11.0%	SNEKEQLQGLNDR	99.6%	39.1	25	30.1	1	1	0	1530.75	99	111
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	8	9	13	0.01%	11.0%	VEEHEETFEEK	99.6%	37.9	25	31.1	1	0	0	1405.61	883	893
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	8	9	13	0.01%	11.0%	VQSLQDEVAFLR	99.7%	83.2	25	71	2	0	0	1404.75	224	235
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	8	9	13	0.01%	11.0%	VSGSPSSGFR	96.9%	29.6	25	22.7	1	0	0	980.48	27	36
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	42	0.04%	19.6%	EVLDSFLDLAR	99.7%	92.4	25	84.4	8	0	0	1277.67	179	189
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	42	0.04%	19.6%	GPAGDATVASEK	99.7%	67.9	25	57.7	4	0	0	1102.54	526	537
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	42	0.04%	19.6%	GPAGDATVASEKESVM	99.7%	77.7	25	77.7	2	0	0	1564.72	526	541
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	42	0.04%	19.6%	IVEMEDVGLLFAR	99.7%	86.2	25	82.3	4	0	0	1491.79	289	301
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	42	0.04%	19.6%	LGPEGELLIR	99.7%	80.6	25	68.7	2	0	0	1096.64	248	257
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	42	0.04%	19.6%	LSAFVFPGELLLR	99.7%	73.4	25	65.5	5	0	0	1461.85	86	98
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	42	0.04%	19.6%	NIFPSNLVSAAFR	99.7%	52.7	25	47	6	0	0	1435.77	190	202
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	42	0.04%	19.6%	SELPLDPLPVPTEEGNPLLK	99.7%	89.6	25	89.6	6	0	0	2158.16	503	522
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	42	0.04%	19.6%	STEPELIQVK	99.7%	59.6	25	54.6	5	0	0	1143.63	493	502
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	5	6	8	0.01%	7.5%	EGLGLDVER	96.3%	28.9	25	24.4	1	0	0	987.51	589	597
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	5	6	8	0.01%	7.5%	GAVEDVISR	99.7%	54.9	25	34.2	2	0	0	945.50	525	533
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	5	6	8	0.01%	7.5%	SESHTDLTFSR	99.7%	36.4	25	29	1	2	0	1279.59	616	626
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	5	6	8	0.01%	7.5%	SGEGIREPISVK	97.6%	30.5	25	13.2	1	0	0	1271.70	572	583
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	5	6	8	0.01%	7.5%	TNPEYIYAPLK	99.7%	41.3	25	41.3	1	0	0	1308.68	212	222

Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	7	7	10	0.01%	13.1%	DPEFVFYDQLK	99.7%	53.4	25	53.4	2	0	0	1400.67	501	511
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	7	7	10	0.01%	13.1%	ELETVAAHQFPEVR	99.7%	76.6	25	65.4	2	0	0	1625.83	340	353
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	7	7	10	0.01%	13.1%	IIAEALTR	99.7%	54.3	25	25.2	1	0	0	886.54	417	424
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	7	7	10	0.01%	13.1%	LLDFSYEQYQK	99.7%	47.9	25	47.9	1	0	0	1433.69	89	99
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	7	7	10	0.01%	13.1%	NAVLNTEAR	99.7%	44.6	25	35.9	2	0	0	987.52	65	73
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	7	7	10	0.01%	13.1%	QSAGAVVIILPR	99.7%	53.5	25	37	1	0	0	1223.75	103	114
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	7	7	10	0.01%	13.1%	TMAAEVLSR	98.8%	33.3	25	28.3	1	0	0	977.51	74	82
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	13	17	30	0.03%	36.9%	AVPEGFVIPR	98.8%	33.4	25	25.9	1	0	0	1084.62	118	127
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	13	17	30	0.03%	36.9%	DLLNCSFK	98.4%	32.2	25	29.9	2	0	0	996.48	393	400
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	13	17	30	0.03%	36.9%	DVYKEHFQDDVFNEK	99.7%	81.5	25	74.1	1	2	0	1912.87	85	99
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	13	17	30	0.03%	36.9%	GTDTVAGLALIK	99.7%	104	25	71.3	3	0	0	1158.67	217	228
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	13	17	30	0.03%	36.9%	GVSSQETAGIGASAHLVNFK	99.7%	83.3	25	83.3	1	2	0	1973.01	197	216
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	13	17	30	0.03%	36.9%	GWNYILEK	98.8%	33.6	25	24	2	0	0	1022.53	100	107
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	13	17	30	0.03%	36.9%	MWSIENIAFGSGGGLLQK	99.7%	107	25	101	1	1	0	1923.96	372	389
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	13	17	30	0.03%	36.9%	SYSFDEIRK	99.1%	34.8	25	30.4	2	0	0	1144.56	470	478
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	13	17	30	0.03%	36.9%	TPAGNFVTLEEGKGDLEEYGQDLLHTVFK	99.7%	80.5	25	80.5	0	2	0	3207.58	435	463
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	13	17	30	0.03%	36.9%	VIQGDGVDINTLQEIVEGMK	99.7%	116	25	116	4	0	0	2158.11	350	369
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	13	17	30	0.03%	36.9%	VKYEETVFYGLQYILNK	99.7%	59.5	25	59.5	0	2	0	2107.11	52	68
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	13	17	30	0.03%	36.9%	YEETVFYGLQYILNK	99.7%	80.5	25	74.6	2	0	0	1879.95	54	68
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	13	17	30	0.03%	36.9%	YLLETSGNLDGLEYK	99.7%	101	25	94.2	2	0	0	1714.85	175	189
Nodal modulator 1	NOMO1	NOMO1_HUMAN	134.3	100.0%	3	3	5	0.01%	3.0%	DGENYVVLLDSTLPR	99.7%	56.5	25	51.8	2	0	0	1690.86	1106	1120
Nodal modulator 1	NOMO1	NOMO1_HUMAN	134.3	100.0%	3	3	5	0.01%	3.0%	FLLFSSLVTK	97.2%	30	25	29.6	2	0	0	1154.68	235	244
Nodal modulator 1	NOMO1	NOMO1_HUMAN	134.3	100.0%	3	3	5	0.01%	3.0%	IQSTVTQPGGK	97.4%	30.2	25	20.4	1	0	0	1115.61	160	170
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	14	20	58	0.06%	33.5%	AAPGAEFAPNKR	99.7%	64	25	61	5	0	0	1228.64	457	468
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	14	20	58	0.06%	33.5%	AGEVFIHK	99.7%	55	25	29.8	6	0	0	900.49	100	107
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	14	20	58	0.06%	33.5%	AVVIVDDR	99.7%	42.3	25	31.7	4	0	0	886.50	177	184
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	14	20	58	0.06%	33.5%	DKGFGFIR	99.0%	34.1	25	24	1	0	0	939.50	108	115
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	14	20	58	0.06%	33.5%	EKLEMEMEAAR	99.7%	41.9	25	23.1	1	0	0	1352.62	294	304
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	14	20	58	0.06%	33.5%	FACHSASLTVR	99.7%	62.7	25	54.8	3	6	0	1248.62	143	153
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	14	20	58	0.06%	33.5%	FAQPGSFEYEYAMR	99.7%	68.3	25	68	5	0	0	1695.75	257	270
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	14	20	58	0.06%	33.5%	FGQAATMEGIGAIGGTPPAFNR	99.7%	63.8	25	59.5	1	2	0	2179.06	435	456
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	14	20	58	0.06%	33.5%	GIVEFSGKPAAR	99.7%	42.6	25	42.6	2	1	0	1231.68	191	202
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	14	20	58	0.06%	33.5%	LFVGNLPPDITEEEMR	97.8%	30.8	25	29	1	0	0	1859.92	76	91
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	14	20	58	0.06%	33.5%	MEELHNQEVQK	99.7%	69	25	26.1	5	0	0	1384.65	326	336
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	14	20	58	0.06%	33.5%	MGQMAMGGAMGINNR	99.7%	57.5	25	57	6	0	0	1602.65	384	398
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	14	20	58	0.06%	33.5%	RMEELHNQEVQK	99.7%	35.7	25	30.3	0	2	0	1540.75	325	336
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	14	20	58	0.06%	33.5%	VELDNMPLR	99.7%	68.6	25	49.5	7	0	0	1086.56	127	135
Nuclear autoantigenic sperm protein	NASP	NASP_HUMAN	85.2	100.0%	3	3	3	0.00%	3.7%	EAQLYAAQAHLK	98.6%	32.9	25	27.5	1	0	0	1342.71	536	547
Nuclear autoantigenic sperm protein	NASP	NASP_HUMAN	85.2	100.0%	3	3	3	0.00%	3.7%	MAVLNEQVK	98.9%	33.7	25	28.8	1	0	0	1031.56	618	626
Nuclear autoantigenic sperm protein	NASP	NASP_HUMAN	85.2	100.0%	3	3	3	0.00%	3.7%	SIEVIENR	99.4%	36.6	25	20.5	1	0	0	959.52	610	617
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	8	8	16	0.02%	10.6%	ANNYNEAVYLVR	99.7%	55.3	25	42.5	2	0	0	1425.71	118	129
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	8	8	16	0.02%	10.6%	ATNDEIFSILK	99.7%	66.1	25	58.7	2	0	0	1250.66	512	522
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	8	8	16	0.02%	10.6%	DGVLEEQIER	99.0%	34.1	25	22.6	2	0	0	1187.59	685	694
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	8	8	16	0.02%	10.6%	IFANTESYLK	99.7%	46.9	25	24.8	1	0	0	1185.62	195	204
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	8	8	16	0.02%	10.6%	NLFLVIFQR	99.7%	64.4	25	60.6	4	0	0	1149.68	708	716
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	8	8	16	0.02%	10.6%	NYNFGGEFVEAMIR	99.7%	85.6	25	80.4	3	0	0	1646.76	97	110
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	8	8	16	0.02%	10.6%	SFSHSFSALAK	96.1%	28.6	25	13.3	1	0	0	1181.59	558	568
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	8	8	16	0.02%	10.6%	VMFEVWR	95.7%	28.2	25	26.8	1	0	0	966.49	589	595
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	11	11	17	0.02%	5.9%	AADALEEQQR	99.7%	52.4	25	37.6	2	0	0	1130.54	725	734
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	11	11	17	0.02%	5.9%	AVQAQGGESQQEAQR	99.7%	78.4	25	78.4	2	0	0	1586.75	1574	1588
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	11	11	17	0.02%	5.9%	DSAQTSVTQAQR	99.7%	68.8	25	60.4	2	0	0	1291.62	632	643

Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	11	11	17	0.02%	5.9%	ELVKEPAR	99.4%	36.7	25	30.3	2	0	0	941.54	936	943
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	11	11	17	0.02%	5.9%	HQVEQLSSSLK	99.7%	42	25	42	1	0	0	1255.66	551	561
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	11	11	17	0.02%	5.9%	LADDLSTLQEK	99.7%	67.3	25	53.6	2	0	0	1232.64	898	908
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	11	11	17	0.02%	5.9%	LDFVCSFLQK	98.7%	33.1	25	25.8	1	0	0	1256.63	61	70
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	11	11	17	0.02%	5.9%	LEILQQQLQVANEAR	99.7%	72.7	25	70.8	1	0	0	1752.96	617	631
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	11	11	17	0.02%	5.9%	LGHELQQAGLK	99.7%	39.6	25	32.6	1	0	0	1193.66	1655	1665
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	11	11	17	0.02%	5.9%	LLQAETASNSAR	99.7%	74.9	25	67.5	2	0	0	1260.65	1271	1282
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	11	11	17	0.02%	5.9%	SAPASQASLR	97.0%	29.7	25	18.1	1	0	0	987.52	1840	1849
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	10	10	18	0.02%	13.7%	AIYAALSGNLK	99.7%	66.3	25	52.6	2	0	0	1120.64	426	436
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	10	10	18	0.02%	13.7%	EADLDVATITK	99.7%	70.8	25	62.8	2	0	0	1175.62	627	637
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	10	10	18	0.02%	13.7%	EYLGANWTLEK	99.7%	64.9	25	52.7	1	0	0	1323.66	481	491
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	10	10	18	0.02%	13.7%	GHLDALTADVK	99.7%	57.1	25	52.1	2	0	0	1139.61	804	814
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	10	10	18	0.02%	13.7%	IDVIDWLVFDPAQR	99.7%	41	25	41	1	0	0	1686.89	672	685
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	10	10	18	0.02%	13.7%	IQSALEEESVFAVTAVNASEK	99.7%	69	25	69	1	0	0	2222.12	230	250
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	10	10	18	0.02%	13.7%	SGFGEISSPVIR	98.8%	33.4	25	28.5	2	0	0	1248.66	4	15
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	10	10	18	0.02%	13.7%	TVVEALFQR	99.7%	68.5	25	64.2	2	0	0	1062.59	251	259
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	10	10	18	0.02%	13.7%	VFEELQATDK	99.7%	76.2	25	65.3	3	0	0	1179.59	492	501
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	10	10	18	0.02%	13.7%	VLLQASQDENFGNTTPR	99.7%	101	25	101	2	0	0	1889.94	32	48
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	19	22	37	0.04%	20.2%	AAFLQYCR	99.7%	57.2	25	40	2	0	0	1028.50	524	531
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	19	22	37	0.04%	20.2%	AHATLLGLANMETR	99.5%	31.2	25	31.2	0	1	0	1513.78	949	962
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	19	22	37	0.04%	20.2%	DGIQLSEYLPEVK	99.7%	75.9	25	65.7	2	0	0	1490.77	1111	1123
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	19	22	37	0.04%	20.2%	DLLQADQLGSLK	99.7%	80.4	25	68.3	2	0	0	1300.71	1124	1135
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	19	22	37	0.04%	20.2%	DMLQAASHYR	99.7%	48.2	25	43.8	2	0	0	1191.56	734	743
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	19	22	37	0.04%	20.2%	ENITDAIWGSESNYEAIK	99.7%	51.6	25	51.6	2	0	0	2039.96	318	335
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	19	22	37	0.04%	20.2%	EYEIPSNLTPADVFFR	99.7%	51.8	25	51.8	3	0	0	1897.93	676	691
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	19	22	37	0.04%	20.2%	FLLHQETLPEQLLAEK	99.7%	47.2	25	41.8	0	2	0	1909.04	1001	1016
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	19	22	37	0.04%	20.2%	GLPLGSAVSSPVLFSPVGR	99.7%	80.1	25	80.1	2	0	0	1840.03	36	54
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	19	22	37	0.04%	20.2%	HAYSWDINR	99.7%	44.4	25	37	2	0	0	1161.54	306	314
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	19	22	37	0.04%	20.2%	IEEMAEQER	99.7%	42.8	25	8.78	2	0	0	1150.50	992	1000
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	19	22	37	0.04%	20.2%	LLLCEHAEK	99.7%	43.1	25	34.4	2	0	0	1112.58	638	646
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	19	22	37	0.04%	20.2%	NETIAQEDKIK	99.7%	55	25	38.3	1	0	0	1288.67	510	520
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	19	22	37	0.04%	20.2%	NSGLVSITSR	99.7%	79.9	25	75.9	2	0	0	1033.56	467	476
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	19	22	37	0.04%	20.2%	SNPYFEFVLK	99.7%	43.2	25	35.9	2	0	0	1243.64	1136	1145
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	19	22	37	0.04%	20.2%	SSFYSLTSSNISK	99.7%	90	25	75.9	2	0	0	1420.70	284	296
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	19	22	37	0.04%	20.2%	TFGSSLPVK	99.3%	35.7	25	31.5	2	0	0	935.52	83	91
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	19	22	37	0.04%	20.2%	VAYPQADSNLR	99.7%	50.7	25	45.8	1	0	0	1233.62	788	798
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	19	22	37	0.04%	20.2%	YMTQFADQNFSDFLFR	99.7%	82.7	25	82.7	3	0	0	2045.91	888	903
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	13	13	26	0.03%	11.4%	CYLVTGEGQK	96.2%	28.7	25	19	1	0	0	1154.55	916	925
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	13	13	26	0.03%	11.4%	DLLILQQLLMR	99.7%	72.4	25	71.2	3	0	0	1355.81	733	743
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	13	13	26	0.03%	11.4%	EFTVCSIGTANAVAGAVK	99.7%	68.5	25	63	2	0	0	1794.91	61	78
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	13	13	26	0.03%	11.4%	GFNPAQPLNIR	96.1%	28.6	25	25.2	1	0	0	1226.66	690	700
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	13	13	26	0.03%	11.4%	GQFCIFQLVSTESNR	99.7%	46.4	25	44.6	1	0	0	1785.86	366	380
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	13	13	26	0.03%	11.4%	LLSTYLER	99.7%	56.4	25	38.9	2	0	0	994.56	1291	1298
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	13	13	26	0.03%	11.4%	LLTGWMPTAIR	99.7%	42.1	25	30.4	2	0	0	1258.70	266	276
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	13	13	26	0.03%	11.4%	LPLTPVFEGLAFK	99.7%	41.8	25	22.7	2	0	0	1431.82	1237	1249
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	13	13	26	0.03%	11.4%	LPPYDIPGMVSVVELK	99.7%	39.5	25	36.5	1	0	0	1756.96	243	258
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	13	13	26	0.03%	11.4%	MNLTQLYGSNTAGYIVCR	99.7%	82.6	25	82.6	2	0	0	2060.99	701	718
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	13	13	26	0.03%	11.4%	SEDGEIVSTPR	99.7%	73.7	25	66.2	3	0	0	1189.57	949	959
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	13	13	26	0.03%	11.4%	SFVELSGAER	99.7%	68.6	25	59.4	4	0	0	1094.55	44	53
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	13	13	26	0.03%	11.4%	TAPLLLSYYLIK	99.7%	58.7	25	48.4	2	0	0	1394.83	766	777
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	19	21	34	0.04%	10.6%	AQIEQVIANCEHK	99.7%	76	25	76	2	0	0	1539.76	1207	1219

Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	19	21	34	0.04%	10.6%	ASTEGVAIQGQQGTR	99.7%	101	25	98.2	2	0	0	1502.76	70	84
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	19	21	34	0.04%	10.6%	DACDGHEIGR	99.7%	48.4	25	48.4	2	0	0	1129.47	1484	1493
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	19	21	34	0.04%	10.6%	DLPSADSVQYR	99.7%	47.6	25	36.8	2	0	0	1250.60	572	582
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	19	21	34	0.04%	10.6%	ENLFMDLLR	99.7%	53.5	25	37.6	3	0	0	1150.59	860	868
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	19	21	34	0.04%	10.6%	FQDDNVEGDKVSK	99.0%	28.4	25	26.8	0	1	0	1480.69	1733	1745
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	19	21	34	0.04%	10.6%	FTDELMEQGLTYK	99.7%	63.9	25	63.9	1	0	0	1590.74	173	185
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	19	21	34	0.04%	10.6%	IQQGALELLR	99.7%	70.8	25	60.6	2	0	0	1140.67	1566	1575
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	19	21	34	0.04%	10.6%	KADNVVNIAR	99.7%	47.3	25	34.4	2	0	0	1099.62	892	901
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	19	21	34	0.04%	10.6%	KPVSTTNLQDPGVLGCPR	99.4%	30.3	25	29.5	0	1	0	1939.01	1013	1030
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	19	21	34	0.04%	10.6%	LAWALALR	99.7%	52.6	25	36.3	2	0	0	913.56	331	338
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	19	21	34	0.04%	10.6%	LPGLQATVR	99.7%	66.8	25	64	2	0	0	954.57	322	330
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	19	21	34	0.04%	10.6%	LTAPEDVFSK	99.7%	40.9	25	40.9	2	0	0	1106.57	1452	1461
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	19	21	34	0.04%	10.6%	MLALALLDR	99.7%	64.4	25	55.5	3	0	0	1015.60	1494	1502
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	19	21	34	0.04%	10.6%	QYIATIHSR	96.5%	29	25	21	1	0	0	1088.58	305	313
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	19	21	34	0.04%	10.6%	RQPEAVHLLDK	95.9%	23.1	25	15.1	0	1	0	1305.73	31	41
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	19	21	34	0.04%	10.6%	SVSGFLHFDTATK	99.7%	48.9	25	46.9	2	0	0	1409.71	1165	1177
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	19	21	34	0.04%	10.6%	TLQSLLTPQPPLLK	95.1%	27.8	25	18.8	1	0	0	1548.94	1535	1548
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	19	21	34	0.04%	10.6%	YSFIQALVR	99.7%	65.2	25	59.5	2	0	0	1096.61	1993	2001
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	9	9	14	0.01%	15.5%	AKDAAFATLVSDR	99.7%	66.6	25	63.3	1	0	0	1364.72	493	505
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	9	9	14	0.01%	15.5%	DAAFATLVSDR	99.7%	74.3	25	68.1	2	0	0	1165.58	495	505
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	9	9	14	0.01%	15.5%	DVDVYSQILR	99.7%	74.5	25	65.9	2	0	0	1207.63	60	69
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	9	9	14	0.01%	15.5%	EADASPASAGICR	99.7%	53.9	25	50.8	1	0	0	1304.59	219	231
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	9	9	14	0.01%	15.5%	FADAASLLLSLMTSR	99.7%	79.2	25	77.4	2	0	0	1595.85	553	567
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	9	9	14	0.01%	15.5%	IPLNTEQK	95.5%	28	25	9.09	2	0	0	942.53	442	449
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	9	9	14	0.01%	15.5%	LGSALSWSIR	99.7%	104	25	81.4	2	0	0	1089.61	483	492
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	9	9	14	0.01%	15.5%	SEMVPSCPFIYIIR	96.0%	28.6	25	27.9	1	0	0	1727.85	45	58
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	9	9	14	0.01%	15.5%	TMPILSPGNTQTLTELELK	99.7%	64.9	25	64.9	1	0	0	2086.11	239	257
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	44	0.05%	28.3%	AFDIIER	97.9%	31.1	25	23.2	1	0	0	863.46	710	716
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	44	0.05%	28.3%	AQHQLGEFK	94.6%	27.4	25	22	1	0	0	1057.54	341	349
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	44	0.05%	28.3%	AVYCIIGR	99.7%	40.7	25	22.7	3	0	0	951.51	389	396
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	44	0.05%	28.3%	CGDLLAASQVVNR	99.7%	79.9	25	67.5	2	0	0	1402.71	328	340
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	44	0.05%	28.3%	CVSELVIESR	99.7%	41.9	25	23.1	2	0	0	1191.60	569	578
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	44	0.05%	28.3%	DNALLSAIEESR	99.7%	92.3	25	87.7	2	0	0	1317.66	107	118
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	44	0.05%	28.3%	EALQYFYFLR	99.7%	53.2	25	43	6	0	0	1349.69	546	555
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	44	0.05%	28.3%	ESMLVEWEQVK	99.7%	57.8	25	43.5	2	0	0	1377.67	131	141
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	44	0.05%	28.3%	FTSDTKPIINK	99.7%	60.1	25	52	2	0	0	1263.69	601	611
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	44	0.05%	28.3%	GLDISHISQR	99.7%	65.2	25	63	2	0	0	1125.60	68	77
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	44	0.05%	28.3%	LESLSAATTFEPLEPVKDTDIQGFLK	99.7%	64.8	25	64.8	0	1	0	2849.48	78	103
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	44	0.05%	28.3%	LLMLYTR	99.7%	39.6	25	36.4	2	0	0	909.52	531	537
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	44	0.05%	28.3%	LTLSQFQK	99.7%	57.4	25	48.2	2	0	0	964.55	435	442
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	44	0.05%	28.3%	LVPLNQESVEER	99.7%	64.2	25	59.3	2	0	0	1412.74	719	730
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	44	0.05%	28.3%	NLQEIQQAGER	99.7%	63.1	25	32.4	2	0	0	1285.65	32	42
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	44	0.05%	28.3%	NMALSIAER	99.7%	39.4	25	34	2	0	0	1004.52	665	673
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	44	0.05%	28.3%	QALAYLEQSYK	99.7%	46.9	25	44.5	2	0	0	1313.67	257	267
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	44	0.05%	28.3%	QMTDVLLTPATDALK	99.7%	92.4	25	74.8	2	0	0	1616.86	229	243
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	44	0.05%	28.3%	SSGQSAQLLSHEPGDPPCLR	99.7%	49.7	25	41.6	0	1	0	2136.01	505	524
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	44	0.05%	28.3%	TLITFAGMIPYR	99.7%	87.4	25	76.5	5	0	0	1382.75	791	802
Nuclear pore complex protein Nup98-Nup96	NUP98	NUP98_HUMAN	197.6	100.0%	3	3	10	0.01%	2.2%	LALLLSQFVGSQSVR	99.7%	100	25	93.2	6	0	0	1617.93	1358	1372
Nuclear pore complex protein Nup98-Nup96	NUP98	NUP98_HUMAN	197.6	100.0%	3	3	10	0.01%	2.2%	NSPVEAVFSYLTGK	99.7%	84.6	25	72.7	3	0	0	1511.77	1328	1341
Nuclear pore complex protein Nup98-Nup96	NUP98	NUP98_HUMAN	197.6	100.0%	3	3	10	0.01%	2.2%	SITADPLDYR	95.7%	28.2	25	18.4	1	0	0	1150.57	1514	1523
Nuclear pore membrane glycoprotein 210	NUP210	PO210_HUMAN	205.1	100.0%	5	5	6	0.01%	3.4%	AVDPTSGQLYGLAR	99.6%	38.4	25	28.1	1	0	0	1447.75	1259	1272

Nuclear pore membrane glycoprotein 210	NUP210	PO210_HUMAN	205.1	100.0%	5	5	6	0.01%	3.4%	GVAIGQTSLTASVTNK	99.7%	56.5	25	56.5	1	0	0	1546.84	1048	1063
Nuclear pore membrane glycoprotein 210	NUP210	PO210_HUMAN	205.1	100.0%	5	5	6	0.01%	3.4%	TVSVGLTLLR	99.7%	67	25	57.3	1	0	0	1058.66	1448	1457
Nuclear pore membrane glycoprotein 210	NUP210	PO210_HUMAN	205.1	100.0%	5	5	6	0.01%	3.4%	VFGAPEVLENLEVK	99.7%	82.2	25	73.6	2	0	0	1543.84	1711	1724
Nuclear pore membrane glycoprotein 210	NUP210	PO210_HUMAN	205.1	100.0%	5	5	6	0.01%	3.4%	VGQALELPLR	99.7%	40.7	25	40.7	1	0	0	1095.65	549	558
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	9	9	16	0.02%	16.8%	AQFFVEDASTASALK	99.7%	103	25	94.6	2	0	0	1584.79	159	173
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	9	9	16	0.02%	16.8%	AWLLSMIQSK	99.7%	65.2	25	51.3	2	0	0	1176.64	133	142
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	9	9	16	0.02%	16.8%	DQSTYISAIR	99.7%	55.7	25	31.5	2	0	0	1153.58	333	342
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	9	9	16	0.02%	16.8%	GSYFGTENLK	99.1%	34.6	25	21.6	1	0	0	1115.54	375	384
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	9	9	16	0.02%	16.8%	IIEENIPELLSLNLSNNR	99.7%	68	25	62.8	2	0	0	2081.12	259	276
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	9	9	16	0.02%	16.8%	ILNLSGNELK	99.7%	54.5	25	40.6	2	0	0	1100.63	295	304
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	9	9	16	0.02%	16.8%	LDDMSSIVQK	99.7%	45.2	25	37.7	2	0	0	1151.56	280	289
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	9	9	16	0.02%	16.8%	LNVVAFLNELPK	99.7%	90.9	25	84.9	2	0	0	1356.79	460	471
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	9	9	16	0.02%	16.8%	SAQAFTHLK	99.3%	35.9	25	29.4	1	0	0	1002.54	599	607
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	10	11	23	0.02%	40.4%	AADPPAENSSAPEAEQGGAE	99.7%	43.6	25	43.6	2	0	0	1897.80	305	324
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	10	11	23	0.02%	40.4%	EDGNEEDKENQGDETQGQQPPQR	99.7%	40.2	25	40.2	0	2	0	2628.10	257	279
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	10	11	23	0.02%	40.4%	EDVFVHQTAIK	99.7%	53.8	25	46.9	2	0	0	1286.67	82	92
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	10	11	23	0.02%	40.4%	GAEAANVTGPGGVPVQGSK	99.7%	104	25	104	2	0	0	1695.87	119	137
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	10	11	23	0.02%	40.4%	NDTKEDVFVHQTAIK	99.7%	71.6	25	67.6	2	3	0	1744.89	78	92
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	10	11	23	0.02%	40.4%	NEGSESAPEGQAQQR	99.7%	50.5	25	50.4	2	0	0	1587.70	171	185
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	10	11	23	0.02%	40.4%	NGYGFINR	99.7%	57.7	25	52.8	3	0	0	940.46	70	77
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	10	11	23	0.02%	40.4%	NYQQNYQNSESGEK	99.7%	98.8	25	98.1	2	0	0	1688.71	157	170
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	10	11	23	0.02%	40.4%	NYQQNYQNSESGEKNEGSESAPEGQAQQR	99.7%	84.3	25	84.3	0	1	0	3257.40	157	185
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	10	11	23	0.02%	40.4%	SVGDGETVEFDVVEGEK	99.7%	106	25	92.1	2	0	0	1795.82	102	118
Nucleolar and coiled-body phosphoprotein 1	NOLC1	NOLC1_HUMAN	73.6	99.8%	2	2	5	0.01%	3.4%	DNQLSEVANK	99.7%	45.8	25	34.5	1	0	0	1117.55	24	33
Nucleolar and coiled-body phosphoprotein 1	NOLC1	NOLC1_HUMAN	73.6	99.8%	2	2	5	0.01%	3.4%	VAGGAAPSKPASAK	99.7%	49.8	25	44	4	0	0	1211.67	497	510
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	13	28	0.03%	14.6%	DREIQLEISGK	99.7%	58.6	25	52.7	2	0	0	1287.69	627	637
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	13	28	0.03%	14.6%	EEGTPLTLYYSHWR	99.7%	75.7	25	71.3	2	0	0	1751.84	610	623
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	13	28	0.03%	14.6%	LFHEVVQAFR	99.5%	31.2	25	25.7	2	2	0	1245.67	169	178
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	13	28	0.03%	14.6%	LSNVNLQEK	99.7%	44.9	25	34.2	2	0	0	1044.57	508	516
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	13	28	0.03%	14.6%	MLQPSSSPLWGK	99.7%	56.2	25	44	4	0	0	1330.68	234	245
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	13	28	0.03%	14.6%	NSVPVTVAMVER	99.7%	44.1	25	37.8	2	0	0	1301.69	145	156
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	13	28	0.03%	14.6%	QVQQLLGK	99.2%	35.2	25	26.8	2	0	0	913.55	569	576
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	13	28	0.03%	14.6%	SPDKPGGSPSASR	98.3%	26.2	25	26.2	2	1	0	1242.61	49	61
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	13	28	0.03%	14.6%	VLAFLVLSR	99.7%	76.8	25	76.8	5	0	0	1017.65	311	319
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	13	28	0.03%	14.6%	VQENSAYICSR	99.7%	79.8	25	74.7	2	0	0	1326.61	577	587
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	7	7	12	0.01%	10.2%	DLSSSEPVHAK	99.7%	53.3	25	52.1	2	0	0	1169.58	113	123
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	7	7	12	0.01%	10.2%	FLQGDSFLNEDLNQLIK	99.7%	63.3	25	63.3	2	0	0	1994.02	761	777
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	7	7	12	0.01%	10.2%	FYLENLEQMVK	99.7%	71.5	25	55.3	2	0	0	1413.71	307	317
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	7	7	12	0.01%	10.2%	IRPLTEAEK	97.2%	30	25	17.3	1	0	0	1056.60	275	283
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	7	7	12	0.01%	10.2%	LGQASLGVIK	99.7%	73.9	25	39.3	2	0	0	985.60	394	403
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	7	7	12	0.01%	10.2%	LVIVSLMELFK	99.7%	45.7	25	45.7	1	0	0	1291.77	257	267
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	7	7	12	0.01%	10.2%	SPLLPAVLEGLAK	99.7%	58.6	25	58.6	2	0	0	1307.79	512	524
Nucleolar complex protein 4 homolog	NOC4L	NOC4L_HUMAN	58.5	100.0%	4	5	10	0.01%	8.0%	LFGALLER	99.7%	53	25	26.2	2	0	0	918.54	56	63
Nucleolar complex protein 4 homolog	NOC4L	NOC4L_HUMAN	58.5	100.0%	4	5	10	0.01%	8.0%	LGELLGHPSFQVK	99.7%	41.4	25	38.3	2	2	0	1424.79	103	115
Nucleolar complex protein 4 homolog	NOC4L	NOC4L_HUMAN	58.5	100.0%	4	5	10	0.01%	8.0%	REPTVSSFYVK	99.7%	40.3	25	33.1	2	0	0	1312.69	222	232
Nucleolar complex protein 4 homolog	NOC4L	NOC4L_HUMAN	58.5	100.0%	4	5	10	0.01%	8.0%	RLEAVLASR	99.7%	52.9	25	31	2	0	0	1014.61	17	25
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	5	5	9	0.01%	8.2%	ADVDVQPYAFTTK	99.7%	73.5	25	73.5	2	0	0	1454.72	191	203
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	5	5	9	0.01%	8.2%	FTQQNYHDR	99.7%	43.4	25	35.8	2	0	0	1208.54	53	61
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	5	5	9	0.01%	8.2%	IAELSEDDQK	99.7%	42.2	25	35	2	0	0	1147.55	296	305
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	5	5	9	0.01%	8.2%	LALGQINIAK	99.7%	49.3	25	44.8	2	0	0	1040.65	94	103
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	5	5	9	0.01%	8.2%	QSLEYLEQVR	99.1%	34.8	25	15.9	1	0	0	1264.65	146	155

Nucleolar MIF4G domain-containing protein 1	NOM1	NOM1_HUMAN	96.3	99.8%	2	2	3	0.00%	2.8%	TRPSAAATAAAR	96.4%	28.9	25	21.5	1	0	0	1143.62	160	171
Nucleolar MIF4G domain-containing protein 1	NOM1	NOM1_HUMAN	96.3	99.8%	2	2	3	0.00%	2.8%	TYNPFYAFLASK	98.4%	32.3	25	31	2	0	0	1421.71	702	713
Nucleolar pre-ribosomal-associated protein 1	URB1	NPA1P_HUMAN	254.4	100.0%	2	2	3	0.00%	1.2%	ILLTLVANPYSYTDK	99.7%	51.8	25	51.8	2	0	0	1710.93	703	717
Nucleolar pre-ribosomal-associated protein 1	URB1	NPA1P_HUMAN	254.4	100.0%	2	2	3	0.00%	1.2%	ISTINILLSTLK	99.7%	44.3	25	44.1	1	0	0	1315.82	237	248
Nucleolar protein 16	NOP16	NOP16_HUMAN	21.2	100.0%	4	4	8	0.01%	24.2%	AMEVDIEERPK	99.7%	53.4	25	46.5	2	0	0	1316.65	75	85
Nucleolar protein 16	NOP16	NOP16_HUMAN	21.2	100.0%	4	4	8	0.01%	24.2%	DEKNYYQDTPK	99.2%	35.4	25	34.7	2	0	0	1400.63	136	146
Nucleolar protein 16	NOP16	NOP16_HUMAN	21.2	100.0%	4	4	8	0.01%	24.2%	FGYSVNR	98.3%	31.9	25	22.7	2	0	0	842.42	13	19
Nucleolar protein 16	NOP16	NOP16_HUMAN	21.2	100.0%	4	4	8	0.01%	24.2%	QNLAEMGLAVDPNR	99.7%	53.3	25	53	2	0	0	1543.75	51	64
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	6	8	13	0.01%	11.3%	IINDNATYCR	99.7%	60.5	25	60.5	2	0	0	1239.58	203	212
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	6	8	13	0.01%	11.3%	LLLETHLPSK	98.0%	31.4	25	25.4	1	0	0	1150.68	78	87
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	6	8	13	0.01%	11.3%	LREQVEER	99.7%	39.7	25	19.5	2	0	0	1058.56	397	404
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	6	8	13	0.01%	11.3%	MSQVAPSLSALIGEAVGAR	99.7%	91.9	25	88.8	3	0	0	1872.98	289	307
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	6	8	13	0.01%	11.3%	VVSLSEYR	99.7%	60.6	25	51.8	2	0	0	952.51	271	278
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	6	8	13	0.01%	11.3%	YGLIFHSTFIGR	99.7%	47.3	25	47.3	1	2	0	1410.75	348	359
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	8	9	16	0.02%	19.1%	EAHEPLAVADAK	99.7%	43.4	25	40.4	2	0	0	1250.64	82	93
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	8	9	16	0.02%	19.1%	HAASTVQILGAEK	99.7%	74.6	25	69.7	1	0	0	1324.72	311	323
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	8	9	16	0.02%	19.1%	IISDNLTYCK	99.7%	55	25	55	2	0	0	1226.61	197	206
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	8	9	16	0.02%	19.1%	LIAHAGSLLNLAK	99.7%	51.5	25	51.5	2	2	0	1320.80	298	310
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	8	9	16	0.02%	19.1%	LSELLPEEVEAEVK	99.7%	71	25	68.5	2	0	0	1584.84	222	235
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	8	9	16	0.02%	19.1%	SQMDGLIPGVEPR	99.7%	54.4	25	54.4	2	0	0	1414.70	121	133
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	8	9	16	0.02%	19.1%	TQLYEYLQNR	99.7%	50.3	25	48.5	2	0	0	1327.66	269	278
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	8	9	16	0.02%	19.1%	YGLIYHASLVGQTSPK	99.7%	54.6	25	54.6	0	1	0	1733.92	338	353
Nucleolar protein 9	NOP9	NOP9_HUMAN	69.4	99.8%	2	2	4	0.00%	4.6%	GSSVDGSPLLLFLR	99.7%	69.2	25	60.7	2	0	0	1460.81	311	324
Nucleolar protein 9	NOP9	NOP9_HUMAN	69.4	99.8%	2	2	4	0.00%	4.6%	TLLQVLGGTILESER	99.7%	88.7	25	88.7	2	0	0	1628.92	209	223
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	AAVIGDVIR	99.7%	61.9	25	47.2	7	0	0	913.55	424	432
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	APQVLVLAPTR	99.7%	61.5	25	61.5	6	0	0	1164.71	260	270
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	DFSDITKK	99.3%	35.7	25	23.9	2	0	0	953.49	279	286
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	DSEDNPQTLLFSATCPHWVFNVAK	99.7%	59.3	25	59.3	0	1	0	2776.30	364	387
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	DVESYIHR	99.7%	39.5	25	28	2	0	0	1018.50	517	524
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	EAQELSQNSAIK	99.7%	63.3	25	52.1	5	0	0	1317.66	450	461
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	EEYQLVQVEQK	99.7%	67.4	25	62.3	1	0	0	1392.70	545	555
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	EGAFSNFPISEETIK	99.7%	62.2	25	62.2	8	0	0	1668.81	185	199
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	ELKEQLGEEIDSK	99.7%	68.6	25	59.5	2	0	0	1517.77	656	668
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	GAVEALAAALAHISGATSVDQR	99.7%	56.6	25	56.6	0	2	0	2108.11	606	627
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	GRAPQVLVLAPTR	99.7%	52.5	25	52.5	2	0	0	1377.83	258	270
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	GVTFLFPIQAK	99.7%	64.6	25	43.4	2	0	0	1220.70	205	215
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	IGVPSATEIIK	99.7%	46.7	25	44.8	4	0	0	1127.67	563	573
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	KAEPSEVDMNSPK	99.7%	58.9	25	58.9	2	1	0	1447.67	61	73
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	LGVCFDVPTASVTEIQEK	99.7%	73.3	25	68.7	2	0	0	1992.99	679	696
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	LLDSVPPTAISHFK	99.5%	31.1	25	17.5	1	2	0	1524.84	582	595
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	LSVACFYGGTPYGGQFER	99.7%	93.4	25	90	2	0	0	2008.92	287	304
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	NEEPSEEEIDAPKPK	99.7%	71.5	25	64	2	2	0	1711.80	117	131
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	NGIDILVGTPGR	99.7%	103	25	92.8	3	0	0	1211.67	307	318
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	NGSFGVLVATNVAAR	99.7%	94	25	92.4	2	0	0	1475.80	485	499
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	QDAQSLHGDIPQK	99.7%	61.3	25	58.5	2	1	0	1436.71	462	474
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	SDAGLESDTAMK	99.7%	78.8	25	78.8	4	0	0	1240.54	7	18
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	SDKTEEIAEEEETVFPK	99.7%	36.4	25	34.6	0	1	0	1980.93	38	54
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	STYEQVDLIGK	99.7%	74.7	25	67.4	3	0	0	1252.64	392	402
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	STYEQVDLIGKK	99.7%	67.9	25	53	2	0	0	1380.74	392	403
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	TAITVEHLAIK	99.7%	71.9	25	70.2	5	0	0	1195.70	407	417
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	TFSFAIPLIEK	99.7%	69.2	25	67.1	3	0	0	1265.71	237	247

Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	TIIFCETKK	95.7%	28.2	25	13.3	2	0	0	1139.61	441	449
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	34	88	0.09%	46.4%	WQLSVATEQPELEGPR	99.7%	70.6	25	70.6	2	0	0	1839.92	703	718
Nucleolar transcription factor 1	UBTF	UBF1_HUMAN	89.4	99.8%	2	2	3	0.00%	3.4%	FLESLPEEEQQR	99.7%	52	25	47.2	2	0	0	1504.73	361	372
Nucleolar transcription factor 1	UBTF	UBF1_HUMAN	89.4	99.8%	2	2	3	0.00%	3.4%	TLTELILDAQEHVK	99.7%	56.7	25	50.3	1	0	0	1609.88	84	97
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	175	0.18%	32.5%	ALELTGLK	99.7%	51.7	25	35.9	6	0	0	844.51	363	370
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	175	0.18%	32.5%	EAMEDGEIDGNK	97.6%	30.5	25	30.5	1	0	0	1323.54	628	639
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	175	0.18%	32.5%	EAMEDGEIDGNKVTLDWAKPK	99.7%	76.4	25	76.4	0	8	0	2346.13	628	648
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	175	0.18%	32.5%	ESFDGSVR	95.9%	28.4	25	21.1	1	0	0	896.41	590	597
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	175	0.18%	32.5%	EVFEDAAEIR	99.7%	71	25	56.7	6	0	0	1178.57	411	420
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	175	0.18%	32.5%	FGYVDFESAEDLEK	99.7%	95.8	25	88.1	9	0	0	1648.74	349	362
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	175	0.18%	32.5%	GFGFVDFNSEEDAK	99.7%	87.5	25	87.5	11	0	0	1561.68	611	624
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	175	0.18%	32.5%	GIAYIEFK	99.7%	45.2	25	38.3	8	0	0	940.51	430	437
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	175	0.18%	32.5%	GLSEDTTEETLK	99.7%	89.7	25	82.5	5	0	0	1322.63	578	589
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	175	0.18%	32.5%	GLSEDTTEETLKESFDGSVR	99.7%	109	25	107	5	6	0	2200.03	578	597
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	175	0.18%	32.5%	GYAFIEFASFEDAK	99.7%	114	25	107	12	0	0	1594.74	524	537
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	175	0.18%	32.5%	KFGYVDFESAEDLEK	99.7%	96.1	25	80.4	3	4	0	1776.83	348	362
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	175	0.18%	32.5%	KVAVATPAK	96.0%	28.5	25	23.4	1	0	0	884.56	71	79
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	175	0.18%	32.5%	LELQGPR	99.7%	40	25	31.7	10	0	0	812.46	555	561
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	175	0.18%	32.5%	NDLAVVDVR	99.7%	77	25	65.6	11	0	0	1000.54	334	342
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	175	0.18%	32.5%	QKVEGTEPTTAFNLFVGNLNFNK	99.3%	29.9	25	29.9	0	1	0	2568.31	296	318
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	175	0.18%	32.5%	SISLYYTGEK	99.7%	58.6	25	46.5	11	0	0	1160.58	458	467
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	175	0.18%	32.5%	TEADAEKTFEEK	99.7%	70.8	25	63.9	8	0	0	1397.64	438	449
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	175	0.18%	32.5%	TGISDVFAK	99.7%	72.3	25	54.5	12	0	0	937.50	325	333
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	175	0.18%	32.5%	TLVLSNLSYSATEETLQEVFEK	99.7%	125	25	125	5	2	0	2501.27	487	508
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	175	0.18%	32.5%	VAVATPAKK	96.6%	29.2	25	17.5	1	0	0	884.56	72	80
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	175	0.18%	32.5%	VEGTEPTTAFNLFVGNLNFNK	99.7%	85.8	25	85.8	7	4	0	2312.16	298	318
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	175	0.18%	32.5%	VFGNEIK	99.0%	34.3	25	11.4	4	0	0	806.44	371	377
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	175	0.18%	32.5%	VFGNEIKLEKPK	96.9%	24	25	21.1	0	1	0	1401.81	371	382
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	175	0.18%	32.5%	VTLDWAKPK	99.7%	51.9	25	49	2	0	0	1057.60	640	648
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	175	0.18%	32.5%	VTQDELKEVFEDAAEIR	99.7%	97.4	25	89.3	4	6	0	1991.99	404	420
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	8	14	53	0.05%	31.6%	DELHIVEAEAMNYEGSPIK	99.7%	62.1	25	61.5	0	3	0	2145.02	55	73
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	8	14	53	0.05%	31.6%	GPSSVEDIK	99.7%	65.6	25	57.8	7	0	0	931.47	240	248
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	8	14	53	0.05%	31.6%	GPSSVEDIKAK	99.7%	87.9	25	77.6	11	0	0	1130.61	240	250
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	8	14	53	0.05%	31.6%	LLSISGKR	99.7%	48.5	25	39.9	4	0	0	873.55	135	142
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	8	14	53	0.05%	31.6%	MQASIEK	96.7%	29.3	25	12.3	1	0	0	806.41	251	257
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	8	14	53	0.05%	31.6%	MSVQPTVSLGGFEITPPVVLR	99.7%	96.4	25	95.9	10	3	0	2227.22	81	101
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	8	14	53	0.05%	31.6%	MTDQEAIQDLWQWR	99.7%	69.8	25	68.2	5	0	0	1835.84	278	291
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	8	14	53	0.05%	31.6%	VDNDENEHQLSLR	99.7%	81.8	25	77.9	8	1	0	1568.73	33	45
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	7	7	10	0.01%	4.8%	ALLLVPASVNCLR	99.7%	42.9	25	42.9	2	0	0	1425.82	1142	1154
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	7	7	10	0.01%	4.8%	CTLLLILLR	99.7%	64.4	25	62.2	2	0	0	1114.70	1160	1168
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	7	7	10	0.01%	4.8%	HTLNPEETSSVVR	96.2%	28.7	25	26.3	1	0	0	1468.74	331	343
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	7	7	10	0.01%	4.8%	LAFSVTNNVIR	99.7%	57	25	49.9	2	0	0	1233.69	816	826
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	7	7	10	0.01%	4.8%	LSMSLMEQLLK	97.3%	30.1	25	25.6	1	0	0	1292.70	1399	1409
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	7	7	10	0.01%	4.8%	QLFLDVLDGTK	99.4%	36.7	25	27.6	1	0	0	1248.68	1131	1141
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	7	7	10	0.01%	4.8%	VQRPPSAASAAPSSSK	99.5%	37.4	25	30.8	1	0	0	1540.81	1518	1533
Nucleoporin NUP53	NUP35	NUP53_HUMAN	34.8	100.0%	2	2	2	0.00%	7.7%	ASTSDYQVISDR	99.5%	37.1	25	35.8	1	0	0	1341.63	295	306
Nucleoporin NUP53	NUP35	NUP53_HUMAN	34.8	100.0%	2	2	2	0.00%	7.7%	TLGTPTQPGSTPR	99.7%	68.7	25	59	1	0	0	1312.69	270	282
Nucleoside diphosphate kinase 6	NME6	NDK6_HUMAN	21.1	100.0%	4	4	7	0.01%	22.0%	DAIQLWR	98.1%	31.5	25	17.6	1	0	0	901.49	90	96
Nucleoside diphosphate kinase 6	NME6	NDK6_HUMAN	21.1	100.0%	4	4	7	0.01%	22.0%	GSFGLTDTR	99.7%	67.7	25	56.9	2	0	0	953.47	117	125
Nucleoside diphosphate kinase 6	NME6	NDK6_HUMAN	21.1	100.0%	4	4	7	0.01%	22.0%	LVEFMASGPIR	99.7%	58.3	25	58.3	2	0	0	1235.65	72	82
Nucleoside diphosphate kinase 6	NME6	NDK6_HUMAN	21.1	100.0%	4	4	7	0.01%	22.0%	NTTHGSDSVVSASR	99.7%	51.3	25	44.4	2	0	0	1417.67	126	139

Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	11	32	0.03%	46.7%	DRPFFAGLVK	99.7%	48.6	25	31.1	2	0	0	1149.64	57	66
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	11	32	0.03%	46.7%	GDFCIQVGR	99.7%	66.2	25	57.4	4	0	0	1051.50	106	114
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	11	32	0.03%	46.7%	GLVGEIIK	99.7%	41.5	25	32.8	2	0	0	828.52	19	26
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	11	32	0.03%	46.7%	GLVGEIIKR	99.7%	45.5	25	34.4	4	0	0	984.62	19	27
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	11	32	0.03%	46.7%	NIIHGSDSVESAEK	99.7%	47	25	33.4	1	0	0	1485.72	115	128
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	11	32	0.03%	46.7%	TFIAIKPDGVQR	99.7%	55.9	25	55.5	4	1	0	1344.76	7	18
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	11	32	0.03%	46.7%	VMLGETNPADSKPGTIR	99.7%	62.7	25	55.2	8	6	0	1801.91	89	105
Nucleoside diphosphate kinase, mitochondrial	NME4	NDKM_HUMAN	20.7	100.0%	3	3	4	0.00%	20.3%	AMIGHTDSAEAAPGTIR	97.5%	24.8	25	24.1	0	1	0	1713.82	122	138
Nucleoside diphosphate kinase, mitochondrial	NME4	NDKM_HUMAN	20.7	100.0%	3	3	4	0.00%	20.3%	GDFSVHISR	96.7%	29.3	25	21	1	0	0	1017.51	139	147
Nucleoside diphosphate kinase, mitochondrial	NME4	NDKM_HUMAN	20.7	100.0%	3	3	4	0.00%	20.3%	TLVAVKPDGVQR	99.7%	42.4	25	42.4	2	0	0	1282.75	40	51
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	4	4	11	0.01%	17.1%	FYEEVHDLER	99.7%	44.8	25	39.8	6	0	0	1336.62	95	104
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	4	4	11	0.01%	17.1%	GIPEFWLTVFK	99.7%	60.9	25	50.1	3	0	0	1336.73	166	176
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	4	4	11	0.01%	17.1%	LDGLVETPTGYIESLPR	99.7%	92.1	25	86.4	5	0	0	1859.98	56	72
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	4	4	11	0.01%	17.1%	NVDLLSDMVQEHDEPILK	98.6%	26.9	25	24	0	1	0	2095.04	177	194
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	4	4	11	0.01%	17.1%	YAVLYQPLFDK	99.7%	51.2	25	51.2	2	0	0	1356.72	106	116
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	5	5	14	0.01%	13.3%	AAATAEEPDPK	99.7%	46.6	25	46.6	2	0	0	1099.53	147	157
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	5	5	14	0.01%	13.3%	FYEEVHDLER	99.7%	44.8	25	39.8	6	0	0	1336.62	84	93
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	5	5	14	0.01%	13.3%	GIPEFWFTIFR	99.7%	53.5	25	51.5	1	0	0	1412.74	158	168
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	5	5	14	0.01%	13.3%	LTDQVMQNPR	99.7%	59.1	25	53.3	3	0	0	1201.60	27	36
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	5	5	14	0.01%	13.3%	VLAALQER	99.7%	42.5	25	31.2	2	0	0	899.53	37	44
Oligosaccharyltransferase complex subunit OSTC	OSTC	OSTC_HUMAN	16.8	99.8%	2	2	6	0.01%	14.1%	MKLPGYLMG	99.7%	40.3	25	32.1	2	0	0	1025.52	141	149
Oligosaccharyltransferase complex subunit OSTC	OSTC	OSTC_HUMAN	16.8	99.8%	2	2	6	0.01%	14.1%	VPFLVLECPNLK	99.7%	70.3	25	69.4	4	0	0	1428.79	7	18
Origin recognition complex subunit 3	ORC3	ORC3_HUMAN	82.3	100.0%	5	6	9	0.01%	9.1%	AVSELELLGFIKPTK	99.7%	84.3	25	83.5	2	0	0	1644.96	683	697
Origin recognition complex subunit 3	ORC3	ORC3_HUMAN	82.3	100.0%	5	6	9	0.01%	9.1%	ENVVNFIDCLVR	99.7%	64.1	25	63.7	1	0	0	1477.75	553	564
Origin recognition complex subunit 3	ORC3	ORC3_HUMAN	82.3	100.0%	5	6	9	0.01%	9.1%	LLLTTQFPFK	99.7%	42.8	25	35.6	2	0	0	1207.71	292	301
Origin recognition complex subunit 3	ORC3	ORC3_HUMAN	82.3	100.0%	5	6	9	0.01%	9.1%	SKEEESVHVTQR	99.7%	48.6	25	48.6	1	2	0	1428.71	164	175
Origin recognition complex subunit 3	ORC3	ORC3_HUMAN	82.3	100.0%	5	6	9	0.01%	9.1%	TTSSQWQSPPVVVILK	99.7%	46.9	25	43.4	1	0	0	1769.98	205	220
Origin recognition complex subunit 4	ORC4	ORC4_HUMAN	50.4	100.0%	4	4	5	0.01%	10.6%	LDILELLEK	99.7%	53.7	25	47.5	1	0	0	1085.65	196	204
Origin recognition complex subunit 4	ORC4	ORC4_HUMAN	50.4	100.0%	4	4	5	0.01%	10.6%	LLLDNTQIMNALQK	99.7%	99.1	25	94.5	2	0	0	1614.89	404	417
Origin recognition complex subunit 4	ORC4	ORC4_HUMAN	50.4	100.0%	4	4	5	0.01%	10.6%	QSPHSNLFGVQVQYK	99.7%	33.7	25	33.7	0	1	0	1731.88	31	45
Origin recognition complex subunit 4	ORC4	ORC4_HUMAN	50.4	100.0%	4	4	5	0.01%	10.6%	SVQEVLQK	97.0%	29.7	25	4.89	1	0	0	930.53	261	268
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	5	5	6	0.01%	11.3%	AMQTVYLR	95.5%	28	25	16.8	1	0	0	981.52	264	271
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	5	5	6	0.01%	11.3%	CTVSLDFIR	95.9%	28.5	25	22.8	1	0	0	1110.56	409	417
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	5	5	6	0.01%	11.3%	ESQVSILQSLFGER	99.7%	100	25	95.7	2	0	0	1592.83	12	25
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	5	5	6	0.01%	11.3%	LLLEQILNK	99.7%	45.3	25	27.6	1	0	0	1083.68	71	79
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	5	5	6	0.01%	11.3%	TYVTQTLLK	99.2%	35	25	34.5	1	0	0	1066.61	44	52
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	21	28	65	0.07%	50.3%	AFYNNVLGEYEEYITK	99.7%	85.2	25	81.4	2	0	0	1952.93	114	129
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	21	28	65	0.07%	50.3%	DNGLLAKPTHGDIIR	99.7%	39.9	25	39.9	0	2	0	1619.89	399	413
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	21	28	65	0.07%	50.3%	EDELRESIEIINK	99.7%	55.7	25	41.6	1	0	0	1587.82	422	434
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	21	28	65	0.07%	50.3%	FAPPLVIKEDELR	99.7%	49.5	25	47.3	2	2	0	1526.86	414	426
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	21	28	65	0.07%	50.3%	GIYLWDVEGR	99.7%	62.2	25	48.7	3	0	0	1207.61	67	76
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	21	28	65	0.07%	50.3%	GIYLWDVEGRK	99.7%	48.6	25	48.6	2	0	0	1335.71	67	77
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	21	28	65	0.07%	50.3%	GKGLLNAIVIK	98.7%	33.1	25	33.1	1	0	0	1125.74	373	383
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	21	28	65	0.07%	50.3%	GLLNAIVIK	99.7%	58.4	25	48	4	0	0	940.62	375	383
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	21	28	65	0.07%	50.3%	HQVLFIADEIQTGLAR	99.7%	105	25	99.7	2	2	0	1810.98	256	271
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	21	28	65	0.07%	50.3%	IVFAAGNFWGR	99.7%	72.6	25	67.3	7	0	0	1237.65	170	180
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	21	28	65	0.07%	50.3%	KTVQGPPTSDDIFER	99.7%	72.7	25	72.7	1	2	0	1689.84	32	46
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	21	28	65	0.07%	50.3%	KWGYTVK	95.0%	27.7	25	17.1	1	0	0	881.49	155	161
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	21	28	65	0.07%	50.3%	LPSDVVTAVR	99.7%	80	25	70.1	7	0	0	1056.60	363	372
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	21	28	65	0.07%	50.3%	NELMKLPSDVVTAVR	99.7%	50.3	25	45.7	1	2	0	1687.90	358	372
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	21	28	65	0.07%	50.3%	SQVDKLTLTSR	99.7%	65.9	25	59.1	4	2	0	1247.70	103	113

Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	21	28	65	0.07%	50.3%	TVQGPPTSDDIFER	99.7%	101	25	87.9	2	0	0	1561.75	33	46
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	21	28	65	0.07%	50.3%	TVQGPPTSDDIFEREYK	97.8%	25.3	25	22.2	0	1	0	1981.95	33	49
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	21	28	65	0.07%	50.3%	VAIAALEVLEEENLAENADK	99.7%	108	25	101	2	0	0	2141.10	332	351
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	21	28	65	0.07%	50.3%	VLPMNTGVEAGETACK	99.7%	103	25	103	4	0	0	1692.79	136	151
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	21	28	65	0.07%	50.3%	WLAVDYENVRPDIVLLGK	99.7%	88.5	25	88.5	2	2	0	2100.15	275	292
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	21	28	65	0.07%	50.3%	YGAHNYHPLPVALER	99.7%	55.3	25	55.3	2	0	0	1736.89	50	64
Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	CPOX	HEM6_HUMAN	50.2	100.0%	3	4	7	0.01%	8.8%	AGVSISVVHGNLSEEAAK	95.7%	22.8	25	22.8	0	1	0	1767.92	203	220
Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	CPOX	HEM6_HUMAN	50.2	100.0%	3	4	7	0.01%	8.8%	FGLFTPGSR	99.6%	38.9	25	35.4	2	0	0	981.52	405	413
Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	CPOX	HEM6_HUMAN	50.2	100.0%	3	4	7	0.01%	8.8%	IESILMSLPLTAR	99.7%	62.7	25	62.7	4	0	0	1459.82	414	426
Oxysterol-binding protein-related protein 8	OSBPL8	OSBL8_HUMAN	101.2	100.0%	3	3	6	0.01%	5.1%	FYGNSLSAILEGEAR	99.7%	93	25	85.1	1	0	0	1626.81	542	556
Oxysterol-binding protein-related protein 8	OSBPL8	OSBL8_HUMAN	101.2	100.0%	3	3	6	0.01%	5.1%	GEAVGSITQPLPSSYLIIR	99.7%	42.6	25	42.6	1	0	0	2001.10	228	246
Oxysterol-binding protein-related protein 8	OSBPL8	OSBL8_HUMAN	101.2	100.0%	3	3	6	0.01%	5.1%	VVLPTFILEPR	99.7%	79.2	25	79.2	4	0	0	1283.77	423	433
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	13	15	27	0.03%	34.5%	AGTEPSDAIR	97.0%	29.6	25	22.6	1	0	0	1016.50	266	275
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	13	15	27	0.03%	34.5%	CQIIYPR	98.3%	32	25	18.8	2	0	0	949.49	341	347
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	13	15	27	0.03%	34.5%	ELEMIGFIENNVSK	99.7%	85.5	25	74.4	2	0	0	1622.81	355	368
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	13	15	27	0.03%	34.5%	HSNVVILTTSNITEK	99.7%	35.6	25	35.6	0	1	0	1655.90	290	304
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	13	15	27	0.03%	34.5%	IDVAFVDR	99.7%	50.8	25	31.5	1	0	0	934.50	305	312
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	13	15	27	0.03%	34.5%	IYLSCLEELMK	99.7%	56.9	25	48.9	2	0	0	1398.70	330	340
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	13	15	27	0.03%	34.5%	LSLLLNDISR	99.7%	70.1	25	47.5	2	0	0	1143.67	369	378
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	13	15	27	0.03%	34.5%	NVQSVSIIDTELK	99.7%	69.2	25	61.7	2	0	0	1445.78	69	81
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	13	15	27	0.03%	34.5%	QQLLTLR	99.7%	45	25	27.7	2	0	0	871.54	348	354
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	13	15	27	0.03%	34.5%	QYIGPPSAAAIFK	99.7%	68	25	64	2	0	0	1362.74	317	329
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	13	15	27	0.03%	34.5%	VVLLHGPPGTGK	99.7%	65.8	25	65.6	2	0	0	1174.69	174	185
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	13	15	27	0.03%	34.5%	VVNAVLTQIDQIKR	99.7%	78.8	25	78.8	2	2	0	1596.94	276	289
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	13	15	27	0.03%	34.5%	YGQLIEINSHSLFSK	99.7%	78	25	78	2	2	0	1735.90	206	220
Paired amphipathic helix protein Sin3a	SIN3A	SIN3A_HUMAN	145.2	100.0%	2	2	3	0.00%	1.7%	AELVQLVSPFLGK	99.6%	39.1	25	39.1	1	0	0	1400.81	498	510
Paired amphipathic helix protein Sin3a	SIN3A	SIN3A_HUMAN	145.2	100.0%	2	2	3	0.00%	1.7%	SLLESTYQR	99.7%	42.5	25	35.2	2	0	0	1096.56	1044	1052
Pantothenate kinase 4	PANK4	PANK4_HUMAN	86.0	100.0%	2	2	4	0.00%	2.9%	GLLAGNVFDWGAK	99.7%	44.2	25	35.3	2	0	0	1347.71	560	572
Pantothenate kinase 4	PANK4	PANK4_HUMAN	86.0	100.0%	2	2	4	0.00%	2.9%	VYFGGFFIR	99.7%	59.5	25	52.2	2	0	0	1105.58	319	327
Parafibromin	CDC73	CDC73_HUMAN	60.6	99.8%	2	2	2	0.00%	3.8%	NIFAILQSVK	99.7%	42.3	25	42.3	1	0	0	1132.67	248	257
Parafibromin	CDC73	CDC73_HUMAN	60.6	99.8%	2	2	2	0.00%	3.8%	SAPLEIGLQR	99.7%	43.8	25	36.2	1	0	0	1083.62	111	120
PAX3- and PAX7-binding protein 1	PAXBP1	PAXB1_HUMAN	104.8	100.0%	2	2	2	0.00%	2.6%	LEGSSGGIGER	99.6%	38.7	25	24.9	1	0	0	1061.52	430	440
PAX3- and PAX7-binding protein 1	PAXBP1	PAXB1_HUMAN	104.8	100.0%	2	2	2	0.00%	2.6%	TLQELSIDGLLNR	99.7%	74.2	25	74	1	0	0	1471.81	794	806
PCI domain-containing protein 2	PCID2	PCID2_HUMAN	46.0	100.0%	5	5	10	0.01%	13.5%	CGIFLILEK	99.5%	37.4	25	22.2	2	0	0	1092.61	308	316
PCI domain-containing protein 2	PCID2	PCID2_HUMAN	46.0	100.0%	5	5	10	0.01%	13.5%	CQTVIVQSFLR	99.7%	49.8	25	36.8	2	0	0	1350.72	83	93
PCI domain-containing protein 2	PCID2	PCID2_HUMAN	46.0	100.0%	5	5	10	0.01%	13.5%	DGASCAELVSFK	99.7%	45.3	25	45.3	2	0	0	1283.59	21	32
PCI domain-containing protein 2	PCID2	PCID2_HUMAN	46.0	100.0%	5	5	10	0.01%	13.5%	MILIYLLPVK	99.7%	59.5	25	59.5	3	0	0	1202.76	250	259
PCI domain-containing protein 2	PCID2	PCID2_HUMAN	46.0	100.0%	5	5	10	0.01%	13.5%	VFANNADQQLVK	97.7%	30.7	25	25.9	1	0	0	1346.71	117	128
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	8	8	13	0.01%	14.1%	AIGIEPSLATYHHIIR	96.7%	23.8	25	21.5	0	1	0	1790.99	362	377
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	8	8	13	0.01%	14.1%	AYEQALNLYTELLNNR	99.7%	41.7	25	41.7	1	0	0	1924.98	271	286
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	8	8	13	0.01%	14.1%	FIGPDQHR	96.8%	29.5	25	19.8	2	0	0	969.49	447	454
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	8	8	13	0.01%	14.1%	SAYESQPIR	99.7%	42.3	25	26.5	1	0	0	1050.52	557	565
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	8	8	13	0.01%	14.1%	SELLNELMDSAK	99.7%	80	25	78.5	2	0	0	1349.66	608	619
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	8	8	13	0.01%	14.1%	SPALQVLR	99.7%	64.2	25	58.8	2	0	0	883.54	351	358
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	8	8	13	0.01%	14.1%	VEGTDVTGIEEVVIPK	99.7%	100	25	90.4	2	0	0	1684.90	46	61
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	8	8	13	0.01%	14.1%	VMSDFAINQEQK	99.7%	96.4	25	90.4	2	0	0	1409.67	649	660
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	15	26	0.03%	58.2%	EGMNIVEAMER	99.7%	42.7	25	42.7	2	0	0	1278.58	134	144
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	15	26	0.03%	58.2%	IIPGFMCQGGDFTR	99.7%	43.7	25	43.7	3	0	0	1598.75	56	69
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	15	26	0.03%	58.2%	ITIADCGQLE	99.6%	38	25	37.9	1	0	0	1119.54	156	165
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	15	26	0.03%	58.2%	KITIADCGQLE	99.7%	60.9	25	48.1	2	0	0	1247.63	155	165
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	15	26	0.03%	58.2%	SIYGEKFEDENFILK	99.7%	76.9	25	72.3	2	2	0	1831.91	77	91

Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	15	26	0.03%	58.2%	TEWLDGKHVVFGK	99.5%	31	25	28	0	1	0	1515.80	119	131
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	15	26	0.03%	58.2%	VKEGMNIVEAMER	99.7%	76.5	25	72.5	5	1	0	1505.75	132	144
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	15	26	0.03%	58.2%	VNPTVFFDIAVDGEPLGR	99.7%	95.9	25	91.3	2	1	0	1946.00	2	19
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	15	26	0.03%	58.2%	VSFELFADK	99.7%	59.8	25	56.4	2	0	0	1055.54	20	28
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	15	26	0.03%	58.2%	VSFELFADKVPK	99.7%	58.3	25	49.6	2	0	0	1379.76	20	31
Peptidyl-prolyl cis-trans isomerase H	PPIH	PPIH_HUMAN	19.2	99.8%	2	2	4	0.00%	13.0%	IIDGLLVMR	99.7%	51.6	25	42.6	2	0	0	1029.61	144	152
Peptidyl-prolyl cis-trans isomerase H	PPIH	PPIH_HUMAN	19.2	99.8%	2	2	4	0.00%	13.0%	KIENVPTGPNNKPK	99.6%	32	25	32	0	2	0	1535.85	153	166
Peptidyl-tRNA hydrolase ICT1, mitochondrial	ICT1	ICT1_HUMAN	23.6	100.0%	3	3	4	0.00%	15.0%	IRDMITEASQTPK	97.7%	30.8	25	30.8	1	0	0	1489.77	154	166
Peptidyl-tRNA hydrolase ICT1, mitochondrial	ICT1	ICT1_HUMAN	23.6	100.0%	3	3	4	0.00%	15.0%	NLADCLQK	99.7%	39.3	25	31.5	1	0	0	961.48	146	153
Peptidyl-tRNA hydrolase ICT1, mitochondrial	ICT1	ICT1_HUMAN	23.6	100.0%	3	3	4	0.00%	15.0%	QADSDIPLDR	99.7%	51	25	36.6	2	0	0	1129.55	67	76
Periodic tryptophan protein 1 homolog	PWP1	PWP1_HUMAN	55.8	99.8%	2	2	2	0.00%	4.6%	IWDILGDRPSLVHSR	99.1%	29	25	29	0	1	0	1763.96	412	426
Periodic tryptophan protein 1 homolog	PWP1	PWP1_HUMAN	55.8	99.8%	2	2	2	0.00%	4.6%	SVALYDCR	97.2%	30	25	25.2	1	0	0	983.46	323	330
Periodic tryptophan protein 2 homolog	PWP2	PWP2_HUMAN	102.5	99.8%	2	2	3	0.00%	2.6%	AGTLLPVIQFLQK	99.7%	54	25	52.7	2	0	0	1427.86	838	850
Periodic tryptophan protein 2 homolog	PWP2	PWP2_HUMAN	102.5	99.8%	2	2	3	0.00%	2.6%	LVQEALEAVPR	97.9%	31.1	25	23.5	1	0	0	1224.69	774	784
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	33	0.03%	49.7%	ADEGISFR	99.7%	55.4	25	41.5	2	0	0	894.43	121	128
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	33	0.03%	49.7%	ATAVMPDGQFK	99.7%	43.6	25	38.7	4	0	0	1164.57	17	27
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	33	0.03%	49.7%	ATAVMPDGQFKDISLSDYK	99.7%	45.1	25	45.1	2	3	0	2086.02	17	35
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	33	0.03%	49.7%	DISLSDYKGK	99.7%	47.2	25	41.5	2	0	0	1125.58	28	37
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	33	0.03%	49.7%	GLFIIDDKGILR	99.7%	56.7	25	53.8	3	2	0	1359.80	129	140
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	33	0.03%	49.7%	IGHPAPNFK	99.1%	34.8	25	32	1	0	0	980.53	8	16
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	33	0.03%	49.7%	KQGGLGPMNIPLVSDPK	99.1%	28.6	25	28.4	0	3	0	1766.95	93	109
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	33	0.03%	49.7%	LVQAFQFTDK	99.7%	63.6	25	56.6	2	0	0	1196.63	159	168
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	33	0.03%	49.7%	QGGLGPMNIPLVSDPK	99.7%	86.9	25	78.6	2	0	0	1638.85	94	109
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	33	0.03%	49.7%	QGGLGPMNIPLVSDPKR	99.7%	39.2	25	39.2	0	2	0	1794.95	94	110
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	33	0.03%	49.7%	QITVNDLPVGR	99.7%	76.5	25	68.7	2	0	0	1211.67	141	151
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	33	0.03%	49.7%	TIAQDYGVLK	99.7%	68.2	25	61.2	3	0	0	1107.60	111	120
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	6	6	11	0.01%	26.3%	ATAVVDGAFK	99.7%	52.3	25	44	2	0	0	978.53	17	26
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	6	6	11	0.01%	26.3%	ATAVVDGAFKEVK	99.7%	69.3	25	58.2	2	0	0	1334.73	17	29
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	6	6	11	0.01%	26.3%	EGGLGPLNIPLLADVTR	99.7%	80	25	80	2	0	0	1734.98	93	109
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	6	6	11	0.01%	26.3%	KEGGLGPLNIPLLADVTR	99.0%	28.4	25	26.9	0	1	0	1863.07	92	109
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	6	6	11	0.01%	26.3%	LSEDYGVLK	99.7%	58.7	25	47.5	2	0	0	1023.54	111	119
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	6	6	11	0.01%	26.3%	QITVNDLPVGR	99.7%	76.5	25	68.7	2	0	0	1211.67	140	150
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	6	6	11	0.01%	26.3%	RLSEDYGVLK	99.7%	45	25	31.5	2	0	0	1179.64	110	119
Peroxiredoxin-4	PRDX4	PRDX4_HUMAN	30.5	99.8%	2	2	3	0.00%	13.3%	DYGVYLEDSGHTLR	99.7%	51.8	25	47.5	1	0	0	1624.76	187	200
Peroxiredoxin-4	PRDX4	PRDX4_HUMAN	30.5	99.8%	2	2	3	0.00%	13.3%	GLFIIDDKGILR	99.7%	56.7	25	53.8	3	2	0	1359.80	201	212
Peroxiredoxin-4	PRDX4	PRDX4_HUMAN	30.5	99.8%	2	2	3	0.00%	13.3%	LVQAFQYTDK	99.7%	41.7	25	41.7	2	0	0	1212.63	231	240
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	11	12	23	0.02%	53.1%	DFTPVCTTELGR	99.7%	82.9	25	75.5	4	0	0	1395.66	42	53
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	11	12	23	0.02%	53.1%	DGDSVMVLPTIPEEEAK	99.7%	41.5	25	37.4	1	0	0	1845.88	183	199
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	11	12	23	0.02%	53.1%	DINAYNCEEPTEK	99.7%	69.7	25	69.7	2	0	0	1582.67	85	97
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	11	12	23	0.02%	53.1%	ELAILLGMLDPAEKDEK	98.9%	34	25	34	1	0	0	1885.00	109	125
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	11	12	23	0.02%	53.1%	LPFPIIDDR	99.7%	59.2	25	46.2	2	0	0	1085.60	98	106
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	11	12	23	0.02%	53.1%	LPFPIIDDRNR	98.3%	26.2	25	16.5	0	2	0	1355.74	98	108
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	11	12	23	0.02%	53.1%	LSILYPATTGR	99.7%	53.7	25	35.3	2	0	0	1191.67	145	155
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	11	12	23	0.02%	53.1%	NFDEILR	99.7%	46.6	25	22.1	2	0	0	906.47	156	162
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	11	12	23	0.02%	53.1%	PGGLLLGDVAPNFEANTTVGR	99.7%	94.8	25	93.5	2	1	0	2098.09	2	22
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	11	12	23	0.02%	53.1%	VVFVFGPDK	99.7%	48.6	25	45	2	0	0	1007.56	133	141
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	11	12	23	0.02%	53.1%	VVFVFGPDKK	99.7%	41.8	25	39.5	2	0	0	1135.65	133	142
Peroxisomal biogenesis factor 3	PEX3	PEX3_HUMAN	42.1	99.8%	2	2	4	0.00%	5.6%	EAAEYIAQAR	99.7%	64.6	25	56	2	0	0	1121.56	44	53
Peroxisomal biogenesis factor 3	PEX3	PEX3_HUMAN	42.1	99.8%	2	2	4	0.00%	5.6%	HSLSLLDLEQK	99.3%	35.6	25	29.6	2	0	0	1282.70	198	208
Peroxisomal membrane protein PMP34	SLC25A17	PM34_HUMAN	34.6	99.8%	2	2	3	0.00%	10.4%	AIATTVTYPLQTVQSILR	99.7%	53	25	53	2	0	0	1975.12	214	231
Peroxisomal membrane protein PMP34	SLC25A17	PM34_HUMAN	34.6	99.8%	2	2	3	0.00%	10.4%	LSSLDVFIIGAVAK	99.7%	72.8	25	72.8	1	0	0	1432.84	200	213

Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	8	8	13	0.01%	14.1%	EALAFIIR	97.7%	30.8	25	20.8	1	0	0	932.56	341	348
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	8	8	13	0.01%	14.1%	GSATNYITR	99.7%	67.3	25	57.5	2	0	0	982.50	12	20
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	8	8	13	0.01%	14.1%	ITHQIVDRPGQQTSVIGR	99.7%	35.1	25	35.1	0	1	0	2005.09	373	390
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	8	8	13	0.01%	14.1%	LAALEEQR	99.7%	48.8	25	35.3	2	0	0	929.51	496	503
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	8	8	13	0.01%	14.1%	LAQEEESEAKR	99.7%	46.2	25	41.3	2	0	0	1289.63	524	534
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	8	8	13	0.01%	14.1%	LEGQAQAEAK	99.7%	55.5	25	39	2	0	0	1044.53	250	259
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	8	8	13	0.01%	14.1%	LQLSLADFR	99.7%	55.7	25	44.3	2	0	0	1062.59	27	35
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	8	8	13	0.01%	14.1%	SFGGEVSWDK	99.7%	45.5	25	45.3	1	0	0	1111.51	349	358
PHD finger protein 6	PHF6	PHF6_HUMAN	41.3	100.0%	3	3	4	0.00%	8.5%	AEFGDFDIK	97.1%	29.7	25	23.6	1	0	0	1041.49	258	266
PHD finger protein 6	PHF6	PHF6_HUMAN	41.3	100.0%	3	3	4	0.00%	8.5%	DKECGQLLISENQK	99.7%	47.2	25	42.6	1	0	0	1661.82	25	38
PHD finger protein 6	PHF6	PHF6_HUMAN	41.3	100.0%	3	3	4	0.00%	8.5%	TVLQEIKR	99.7%	46.1	25	14.8	2	0	0	986.60	267	274
PHD finger-like domain-containing protein 5A	PHF5A	PHF5A_HUMAN	12.4	99.8%	2	2	2	0.00%	18.2%	ICDECNYGSYQGR	99.7%	61.4	25	61.4	1	0	0	1621.64	45	57
PHD finger-like domain-containing protein 5A	PHF5A	PHF5A_HUMAN	12.4	99.8%	2	2	2	0.00%	18.2%	TDLFYER	97.3%	30.1	25	19.3	1	0	0	943.45	96	102
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	9	11	18	0.02%	25.0%	DQHDTFFLRDPAEALQLPMDYVQR	99.7%	55	25	54.7	0	2	0	2905.39	272	295
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	9	11	18	0.02%	25.0%	FKPAYNPYTEPSMEVFSYHQGLK	99.7%	45	25	43.3	0	1	0	2733.30	405	427
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	9	11	18	0.02%	25.0%	HWELTAEGEEIAR	99.7%	64.6	25	62.8	1	1	0	1540.74	60	72
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	9	11	18	0.02%	25.0%	LDAEPRPPPTQEAA	99.7%	51.3	25	45.2	2	0	0	1491.74	495	508
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	9	11	18	0.02%	25.0%	LGITQLR	99.7%	53.5	25	32.5	2	0	0	800.50	398	404
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	9	11	18	0.02%	25.0%	LLAEVTLK	99.4%	36.8	25	20.1	2	0	0	886.56	164	171
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	9	11	18	0.02%	25.0%	SLQALGEVIEAELR	99.7%	103	25	98	2	0	0	1527.84	43	56
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	9	11	18	0.02%	25.0%	VNLQMVYDSPLCR	99.7%	50.2	25	50.2	1	0	0	1594.77	482	494
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	9	11	18	0.02%	25.0%	VVDSMEDEVQR	99.7%	88.1	25	88.1	4	0	0	1306.59	128	138
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	24	0.02%	19.9%	ALVAIGTHDLDTLSGPFTYTAK	99.2%	29.4	25	29.4	0	2	0	2291.19	155	176
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	24	0.02%	19.9%	ASEGPAFFPGR	99.7%	77	25	60.6	3	0	0	1135.55	537	547
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	24	0.02%	19.9%	DLLFQALGR	99.7%	63.5	25	42.2	3	0	0	1032.58	9	17
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	24	0.02%	19.9%	DRYDSFIELQEK	99.7%	59.5	25	55.6	2	0	0	1542.74	134	145
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	24	0.02%	19.9%	LFEISDIVIK	99.7%	53.6	25	36.7	4	0	0	1176.69	474	483
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	24	0.02%	19.9%	LGVLHPDVITK	99.7%	50.2	25	50.2	2	0	0	1191.71	561	571
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	24	0.02%	19.9%	LIITEETAK	99.7%	42.2	25	32.3	2	0	0	1017.58	108	116
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	24	0.02%	19.9%	NIFIECTGTDFTK	99.7%	93.2	25	89.2	2	0	0	1545.73	250	262
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	24	0.02%	19.9%	TTLLPGLLK	99.0%	34.1	25	26.1	2	0	0	955.62	452	460
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	24	0.02%	19.9%	YDLLCLEGLVR	99.7%	60.5	25	57.3	2	0	0	1350.71	72	82
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	14	18	68	0.07%	34.5%	FACFER	98.9%	33.9	25	29.5	4	0	0	829.37	235	240
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	14	18	68	0.07%	34.5%	FGFYEVFK	99.3%	35.8	25	26.4	4	0	0	1036.51	138	145
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	14	18	68	0.07%	34.5%	GIFNGFSVTLK	99.7%	73.8	25	65.1	4	0	0	1182.65	102	112
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	14	18	68	0.07%	34.5%	GSSASLVLK	99.4%	36.3	25	25.2	2	0	0	861.50	296	304
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	14	18	68	0.07%	34.5%	GSSASLVLKR	99.7%	53.2	25	38.1	6	0	0	1017.61	296	305
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	14	18	68	0.07%	34.5%	GVAPLWMR	99.7%	48	25	26	12	0	0	929.50	219	226
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	14	18	68	0.07%	34.5%	GWAPTFLGYSMQGLCK	99.7%	76.7	25	76.7	6	0	0	1815.86	122	137
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	14	18	68	0.07%	34.5%	IQTQPGYANTLR	99.7%	76.9	25	61.9	11	0	0	1361.72	190	201
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	14	18	68	0.07%	34.5%	LPRPPPPEMPESLK	99.7%	34.1	25	32.4	0	1	0	1587.86	342	355
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	14	18	68	0.07%	34.5%	MQVDPQK	99.5%	37.1	25	26.1	2	0	0	845.42	93	99
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	14	18	68	0.07%	34.5%	MQVDPQKYK	99.7%	42.4	25	32.3	2	0	0	1136.58	93	101
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	14	18	68	0.07%	34.5%	MYKEEGLK	99.7%	50.3	25	38.6	5	0	0	997.50	207	214
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	14	18	68	0.07%	34.5%	TVEALYK	99.2%	35.4	25	16.2	3	0	0	823.46	241	247
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	14	18	68	0.07%	34.5%	VLYSNMLGEENTYLWR	99.7%	103	25	103	6	0	0	2003.95	146	161
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	6	7	14	0.01%	34.8%	AATALLEAGLAR	99.7%	87.8	25	72.7	2	0	0	1156.67	2	13
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	6	7	14	0.01%	34.8%	GVITMNEEYETR	99.7%	67.1	25	63.4	4	0	0	1441.66	67	78
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	6	7	14	0.01%	34.8%	IDPTVLLGALPLR	99.7%	89.3	25	88.2	2	0	0	1377.85	41	53
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	6	7	14	0.01%	34.8%	LGVEQLR	99.7%	45.4	25	21.1	2	0	0	814.48	90	96
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	6	7	14	0.01%	34.8%	LSTVDMTGIPTLDNLQK	99.7%	56.3	25	56.3	2	0	0	1845.96	97	113

Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	6	7	14	0.01%	34.8%	QLVQDENVR	99.7%	44.8	25	36.7	2	0	0	1100.57	58	66
Phosphatidylinositide phosphatase SAC1	SACM1L	SAC1_HUMAN	67.0	100.0%	4	4	6	0.01%	6.6%	ELSAQPEVHR	99.7%	44.3	25	29.3	1	0	0	1165.60	175	184
Phosphatidylinositide phosphatase SAC1	SACM1L	SAC1_HUMAN	67.0	100.0%	4	4	6	0.01%	6.6%	LEEQDEFEK	99.7%	39.1	25	21.3	2	0	0	1166.52	424	432
Phosphatidylinositide phosphatase SAC1	SACM1L	SAC1_HUMAN	67.0	100.0%	4	4	6	0.01%	6.6%	QVIINLINQK	99.7%	50	25	34.8	1	0	0	1182.72	302	311
Phosphatidylinositide phosphatase SAC1	SACM1L	SAC1_HUMAN	67.0	100.0%	4	4	6	0.01%	6.6%	TNVIQSLLAR	99.7%	55.1	25	32.9	2	0	0	1114.66	396	405
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	100.0%	8	9	28	0.03%	13.6%	ALYSTAMESIQGGAAR	99.7%	86.9	25	86.9	3	0	0	1625.80	352	367
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	100.0%	8	9	28	0.03%	13.6%	DCLVLESFK	99.7%	52.2	25	39.8	3	0	0	1110.55	305	313
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	100.0%	8	9	28	0.03%	13.6%	FYGLYCVQSGGK	99.7%	58.5	25	44.6	4	0	0	1378.65	220	231
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	100.0%	8	9	28	0.03%	13.6%	GVDASGETTYK	96.9%	29.6	25	29.6	1	0	0	1127.52	62	72
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	100.0%	8	9	28	0.03%	13.6%	GVDASGETTYKK	99.7%	60.7	25	53.7	5	0	0	1255.62	62	73
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	100.0%	8	9	28	0.03%	13.6%	LLPGYYMNLNQNPR	99.7%	67.3	25	55.4	4	0	0	1692.85	201	214
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	100.0%	8	9	28	0.03%	13.6%	QAQGAQSTSDEKRPVGQK	99.7%	43.8	25	42.4	0	4	0	1914.96	334	351
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	100.0%	8	9	28	0.03%	13.6%	VVVMNNILPR	99.7%	73.5	25	62.7	4	0	0	1154.67	235	244
Phosphatidylserine decarboxylase proenzyme	PISD	PISD_HUMAN	46.7	99.8%	2	2	2	0.00%	5.1%	GVTYSLESFLGPR	99.7%	56.4	25	42.5	1	0	0	1425.74	210	222
Phosphatidylserine decarboxylase proenzyme	PISD	PISD_HUMAN	46.7	99.8%	2	2	2	0.00%	5.1%	ILNFGQVK	99.5%	37.6	25	14.2	1	0	0	918.54	194	201
Phosphatidylserine synthase 1	PTDSS1	PTSS1_HUMAN	55.5	99.8%	2	2	4	0.00%	5.7%	AVLQFTPASWTYVR	99.7%	56.4	25	56.4	2	0	0	1638.86	263	276
Phosphatidylserine synthase 1	PTDSS1	PTSS1_HUMAN	55.5	99.8%	2	2	4	0.00%	5.7%	ILFIGGITAPTVR	99.7%	58.9	25	58.9	2	0	0	1357.82	324	336
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	6	7	14	0.01%	12.7%	AFVRPSGTEDVVR	99.7%	51.5	25	43.1	1	3	0	1432.75	493	505
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	6	7	14	0.01%	12.7%	LNHLCGADFVK	99.7%	42.7	25	29.6	2	0	0	1273.64	245	255
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	6	7	14	0.01%	12.7%	MGLLAVLR	99.7%	74.4	25	55.8	4	0	0	872.54	42	49
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	6	7	14	0.01%	12.7%	QAVTPPGLQEAINDLVK	95.0%	27.7	25	25.8	1	0	0	1792.98	470	486
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	6	7	14	0.01%	12.7%	VDCANGIGALK	99.2%	35.5	25	27.4	1	0	0	1117.57	210	220
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	6	7	14	0.01%	12.7%	VISTTDAER	99.7%	57.6	25	51.2	2	0	0	991.51	461	469
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	21	23	52	0.05%	37.8%	AIDTTQLFSLPK	99.7%	82.5	25	68.4	2	0	0	1333.74	589	600
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	21	23	52	0.05%	37.8%	DEAGHFLWPGFGENAR	99.7%	33.7	25	33.7	0	2	0	1802.82	538	553
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	21	23	52	0.05%	37.8%	DFVEHSAR	99.7%	41	25	36.2	2	0	0	960.45	46	53
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	21	23	52	0.05%	37.8%	DFWEQEVR	99.3%	35.9	25	25	2	0	0	1108.51	601	608
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	21	23	52	0.05%	37.8%	EGALDLSGLR	99.7%	44.2	25	41.2	1	0	0	1030.55	579	588
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	21	23	52	0.05%	37.8%	EIISFGSGYGGNSLLGK	99.7%	112	25	112	4	0	0	1698.87	245	261
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	21	23	52	0.05%	37.8%	ETPIGLVPK	98.9%	33.6	25	33.6	1	0	0	953.57	570	578
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	21	23	52	0.05%	37.8%	EVLAELEALER	99.7%	79.2	25	68.6	2	0	0	1271.68	625	635
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	21	23	52	0.05%	37.8%	GQLGNWMSPADFQR	99.7%	76.7	25	76.1	4	0	0	1622.74	129	142
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	21	23	52	0.05%	37.8%	GVPLVYEAFNWR	99.7%	62.8	25	50.3	3	0	0	1450.75	458	469
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	21	23	52	0.05%	37.8%	HGVFVGSAMR	95.2%	27.8	25	22.1	1	0	0	1060.54	470	479
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	21	23	52	0.05%	37.8%	IFHVNWFR	97.4%	30.2	25	19.1	2	0	0	1118.59	529	536
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	21	23	52	0.05%	37.8%	LGTPVLQALGDGDFVK	99.7%	108	25	101	6	0	0	1629.89	194	209
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	21	23	52	0.05%	37.8%	SYLTEQVNQDLPK	99.7%	111	25	105	2	0	0	1534.77	612	624
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	21	23	52	0.05%	37.8%	TLIGHVPDQR	99.7%	41.7	25	30.3	2	0	0	1135.62	235	244
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	21	23	52	0.05%	37.8%	TMYVLPFSMGPVGSPLSR	99.7%	84.2	25	81.6	8	0	0	1938.98	156	173
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	21	23	52	0.05%	37.8%	TVIVTPSQR	94.6%	27.4	25	22.9	1	0	0	1000.58	109	117
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	21	23	52	0.05%	37.8%	VLDWICR	99.7%	47.2	25	42.8	2	0	0	961.49	554	560
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	21	23	52	0.05%	37.8%	VLSGDLGQLPTGIR	99.7%	99.3	25	91.7	2	0	0	1425.81	32	45
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	21	23	52	0.05%	37.8%	YNNCWLAR	97.1%	29.8	25	23.5	2	0	0	1096.50	89	96
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	21	23	52	0.05%	37.8%	YVAAAFPSACGK	99.6%	38.6	25	38.6	1	0	0	1241.60	297	308
Phosphoglycerate kinase 1	PGK1	PGK1_HUMAN	44.6	100.0%	3	3	6	0.01%	10.3%	ALESPERPFLAILGGAK	99.6%	32.2	25	32.2	0	2	0	1769.00	200	216
Phosphoglycerate kinase 1	PGK1	PGK1_HUMAN	44.6	100.0%	3	3	6	0.01%	10.3%	LGDVYVNDAFGTAHR	99.7%	54.8	25	54.6	0	2	0	1634.79	157	171
Phosphoglycerate kinase 1	PGK1	PGK1_HUMAN	44.6	100.0%	3	3	6	0.01%	10.3%	VLPGVDALSNI	99.7%	49.8	25	49.8	2	0	0	1097.62	407	417
Phosphoglycerate mutase 1	PGAM1	PGAM1_HUMAN	28.8	99.8%	2	2	4	0.00%	9.8%	ALPFWNEEIVPQIK	99.7%	49.1	25	30.5	2	0	0	1683.91	163	176
Phosphoglycerate mutase 1	PGAM1	PGAM1_HUMAN	28.8	99.8%	2	2	4	0.00%	9.8%	VLIAAHGNSLR	99.7%	40.2	25	40.2	2	0	0	1150.67	181	191
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	7	7	10	0.01%	25.5%	AVEMAAQR	99.5%	37.3	25	9.5	1	0	0	875.44	221	228
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	7	7	10	0.01%	25.5%	FIAGTGCLVR	99.7%	48.9	25	23	2	0	0	1093.58	211	220

Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	7	7	10	0.01%	25.5%	FIFDCVSQEYGINPER	99.7%	51.7	25	51.7	1	0	0	1973.91	239	254
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	7	7	10	0.01%	25.5%	GETAVPGAPEALR	99.7%	60.7	25	43.3	2	0	0	1267.66	42	54
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	7	7	10	0.01%	25.5%	LGFITNNSSK	99.7%	44	25	26.9	2	0	0	1080.57	63	72
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	7	7	10	0.01%	25.5%	QADIIGKPSR	98.5%	32.4	25	24.7	1	0	0	1084.61	229	238
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	7	7	10	0.01%	25.5%	TILTLTGVSTLGDVK	99.7%	77.7	25	77.7	1	0	0	1517.88	276	290
Phosphoinositide 3-kinase regulatory subunit 4	PIK3R4	PI3R4_HUMAN	153.1	100.0%	2	2	3	0.00%	1.9%	GVIDLAALGITGR	99.0%	34.4	25	34.4	2	0	0	1255.74	817	829
Phosphoinositide 3-kinase regulatory subunit 4	PIK3R4	PI3R4_HUMAN	153.1	100.0%	2	2	3	0.00%	1.9%	VVTLLSDPENIVK	99.7%	49.1	25	38.8	1	0	0	1426.82	541	553
Phospholipase A-2-activating protein	PLAA	PLAP_HUMAN	87.2	99.8%	2	2	2	0.00%	4.3%	AINCPEDIVFPALDILR	99.7%	40	25	40	1	0	0	1956.03	602	618
Phospholipase A-2-activating protein	PLAA	PLAP_HUMAN	87.2	99.8%	2	2	2	0.00%	4.3%	IGDVVGSSGANQQTSGK	99.7%	72.7	25	67.8	1	0	0	1604.79	377	393
Phosphomannomutase 2	PMM2	PMM2_HUMAN	28.1	99.8%	2	2	3	0.00%	8.9%	IGVVGGSDFEK	99.7%	48.3	25	42.6	2	0	0	1107.57	41	51
Phosphomannomutase 2	PMM2	PMM2_HUMAN	28.1	99.8%	2	2	3	0.00%	8.9%	NGMLNVSPIGR	98.8%	33.3	25	24.7	1	0	0	1173.60	124	134
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	5	5	10	0.01%	26.4%	AGLTHIITMDLHQK	99.7%	59.2	25	0	0	3	0	1577.85	125	138
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	5	5	10	0.01%	26.4%	EIQGFFSFPVDNLR	99.7%	69.6	25	69.6	2	0	0	1668.84	139	152
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	5	5	10	0.01%	26.4%	EKPPITVVGDVGGR	99.7%	41.3	25	41.3	2	2	0	1423.79	237	250
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	5	5	10	0.01%	26.4%	GQDIFIIQTIPR	99.7%	106	25	94	2	0	0	1400.79	57	68
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	5	5	10	0.01%	26.4%	NIIGVIPYFPYSK	99.7%	66.8	25	66.4	2	0	0	1510.83	91	103
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	5	5	10	0.01%	26.4%	SVVYQETNGETR	99.7%	72.7	25	66.4	2	0	0	1382.65	37	48
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	5	5	10	0.01%	26.4%	VFSANSTAACTELAK	99.7%	79.3	25	79.3	2	0	0	1569.76	10	24
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	9	17	29	0.03%	32.0%	AGLTHLITMDLHQK	99.7%	59.2	25	0	0	3	0	1577.85	137	150
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	9	17	29	0.03%	32.0%	EIQGFFNIPVDNLR	99.7%	72.8	25	59.9	2	0	0	1661.86	151	164
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	9	17	29	0.03%	32.0%	EKPPITVVGDVGGR	99.7%	41.3	25	41.3	2	2	0	1423.79	250	263
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	9	17	29	0.03%	32.0%	IFVMATHGLLSSDAPR	99.7%	97.6	25	90.1	4	4	0	1714.89	293	308
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	9	17	29	0.03%	32.0%	LLASMMCK	99.7%	39.9	25	32.2	2	0	0	953.46	129	136
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	9	17	29	0.03%	32.0%	SIIGVIPYFPYSK	99.7%	53.3	25	49.2	2	0	0	1483.82	103	115
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	9	17	29	0.03%	32.0%	SVAAIHPSLEIPMLIPK	99.7%	33.6	25	33.6	2	1	0	1816.04	233	249
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	9	17	29	0.03%	32.0%	TVDISMILSEAIR	99.7%	69.2	25	66.4	3	0	0	1463.78	338	350
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	9	17	29	0.03%	32.0%	VQVYQEPNR	98.7%	33.2	25	18	2	0	0	1132.57	49	57
Phosphoribosylformylglycinamidine synthase	PFAS	PUR4_HUMAN	144.7	99.8%	2	2	2	0.00%	2.4%	ELSDPAGAIIYTSR	99.7%	62.2	25	56.5	1	0	0	1492.76	528	541
Phosphoribosylformylglycinamidine synthase	PFAS	PUR4_HUMAN	144.7	99.8%	2	2	2	0.00%	2.4%	GVAFVGGFSYADVLGSAK	99.7%	80	25	77.7	1	0	0	1744.89	1110	1127
Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform	PHKA1	KPB1_HUMAN	137.3	100.0%	3	3	3	0.00%	2.7%	AALEALDELDLFGVK	99.7%	58.2	25	54.5	1	0	0	1603.86	207	221
Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform	PHKA1	KPB1_HUMAN	137.3	100.0%	3	3	3	0.00%	2.7%	AYELEQSVVK	99.7%	44.5	25	39.3	1	0	0	1165.61	74	83
Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform	PHKA1	KPB1_HUMAN	137.3	100.0%	3	3	3	0.00%	2.7%	RLDGALNR	97.9%	31.1	25	0	1	0	0	914.52	1059	1066
Phosphoserine aminotransferase	PSAT1	SERC_HUMAN	40.4	100.0%	8	8	12	0.01%	24.6%	ALELNMLSLK	99.7%	63.1	25	60.3	2	0	0	1131.64	324	333
Phosphoserine aminotransferase	PSAT1	SERC_HUMAN	40.4	100.0%	8	8	12	0.01%	24.6%	ASLYNAVTIEDVQK	99.7%	102	25	97.8	1	0	0	1550.81	343	356
Phosphoserine aminotransferase	PSAT1	SERC_HUMAN	40.4	100.0%	8	8	12	0.01%	24.6%	ELLAVPDNYK	99.4%	36.4	25	29.6	2	0	0	1161.62	62	71
Phosphoserine aminotransferase	PSAT1	SERC_HUMAN	40.4	100.0%	8	8	12	0.01%	24.6%	FGTINIVHPK	99.7%	51.3	25	45	2	0	0	1125.64	118	127
Phosphoserine aminotransferase	PSAT1	SERC_HUMAN	40.4	100.0%	8	8	12	0.01%	24.6%	GVGISVLEMSHR	99.0%	34.2	25	31.7	1	0	0	1284.67	34	45
Phosphoserine aminotransferase	PSAT1	SERC_HUMAN	40.4	100.0%	8	8	12	0.01%	24.6%	LPHSVLLEIQK	99.7%	34.6	25	24.7	0	2	0	1276.76	17	27
Phosphoserine aminotransferase	PSAT1	SERC_HUMAN	40.4	100.0%	8	8	12	0.01%	24.6%	NVGSAGVTVVIVR	99.7%	59.9	25	57	1	0	0	1270.75	201	213
Phosphoserine aminotransferase	PSAT1	SERC_HUMAN	40.4	100.0%	8	8	12	0.01%	24.6%	QVVNFGPGPAK	97.7%	30.7	25	20.2	1	0	0	1113.61	6	16
Plasma membrane calcium-transporting ATPase 1	ATP2B1	AT2B1_HUMAN	138.8	100.0%	2	2	3	0.00%	2.4%	EASDIILTDDNFTSIVK	99.7%	74.1	25	65.7	2	0	0	1880.95	824	840
Plasma membrane calcium-transporting ATPase 1	ATP2B1	AT2B1_HUMAN	138.8	100.0%	2	2	3	0.00%	2.4%	SSLYEGLEKPESR	99.7%	42.6	25	35.4	1	0	0	1494.74	1164	1176
Plasminogen activator inhibitor 1 RNA-binding protein	SERBP1	PAIRB_HUMAN	45.0	100.0%	2	2	2	0.00%	6.6%	EETQPPVALKK	97.5%	30.5	25	24	1	0	0	1239.69	93	103
Plasminogen activator inhibitor 1 RNA-binding protein	SERBP1	PAIRB_HUMAN	45.0	100.0%	2	2	2	0.00%	6.6%	FDQLFDDESDPFEVLK	96.9%	29.5	25	22	1	0	0	1943.89	17	32
Plastin-3	PLS3	PLST_HUMAN	70.8	100.0%	2	2	2	0.00%	3.3%	ALENDPDCR	99.3%	36	25	36	1	0	0	1089.46	136	144
Plastin-3	PLS3	PLST_HUMAN	70.8	100.0%	2	2	2	0.00%	3.3%	INNFSADIKDSK	99.7%	56.3	25	49	1	0	0	1351.69	289	300
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	AALAHSEEVTASQVAATK	99.7%	40.2	25	35	0	1	0	1783.92	2744	2761
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	APVPASELLASGVLSR	99.7%	90.7	25	90.7	2	0	0	1566.89	3447	3462
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	AQLEPVASPAK	99.7%	42.9	25	42.7	1	0	0	1110.62	1428	1438
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	AQVEQELTTLR	99.7%	54.7	25	48.2	1	0	0	1287.69	2319	2329
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	DLSELGSVR	99.7%	42.3	25	28	1	0	0	975.51	3477	3485

Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	ELEQLGR	98.3%	32	25	0	1	0	0	844.45	1338	1344
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	GGAEGELQALR	99.6%	38.8	25	32.1	1	0	0	1100.57	1606	1616
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	GIYQSLEGAVQAGQLK	99.7%	68.5	25	65.1	1	0	0	1661.89	478	493
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	GLLSAEVAR	94.9%	27.6	25	11.1	1	0	0	915.53	3850	3858
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	IIITVVEEQEQK	99.7%	71.2	25	69.8	2	0	0	1428.79	3095	3106
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	IISLETYNLLR	99.7%	59.5	25	53.4	1	0	0	1334.77	3794	3804
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	LAAIGEATR	99.7%	43.1	25	24.7	1	0	0	901.51	1976	1984
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	LGFHLPLEVAYQR	99.0%	28.5	25	28.5	0	2	0	1542.84	3951	3963
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	LKAEATEAAR	99.3%	35.7	25	29.7	1	0	0	1059.58	2349	2358
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	LKQSAEEQAQAR	95.7%	28.3	25	28.3	1	0	0	1358.70	2254	2265
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	LLEAAAQSTK	97.9%	31.1	25	27.7	1	0	0	1031.57	4600	4609
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	LLEAQIATGGVIDPVHSHR	99.7%	52.3	25	52.1	0	1	0	2013.09	2942	2960
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	LQAEEVAQQK	99.7%	66.5	25	52.4	2	0	0	1143.60	1783	1792
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	LQEAGILSAEELQR	99.7%	98.5	25	98.5	2	0	0	1556.83	2795	2808
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	LQLEACETR	99.7%	47.8	25	40.4	2	0	0	1119.55	1131	1139
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	LRAETEQGEQQR	99.7%	56.7	25	48.1	1	0	0	1444.71	1855	1866
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	LSVAAQEAAR	99.7%	73.1	25	48.6	2	0	0	1015.55	2420	2429
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	LSVYAALQR	99.7%	71.9	25	64.4	2	0	0	1020.58	2847	2855
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	LTVDEAVR	99.3%	36	25	21.6	2	0	0	902.49	3213	3220
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	QSSEAEIQAK	99.2%	35.2	25	23.8	1	0	0	1090.54	1564	1573
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	SAEAELQSKR	98.7%	33.1	25	14.1	1	0	0	1118.58	1710	1719
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	SIQEELQQLR	99.7%	64.6	25	50.7	2	0	0	1243.66	1554	1563
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	SKEQAELEAAR	99.7%	58.6	25	45.8	2	0	0	1231.63	2098	2108
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	SLSAIYLEK	94.7%	27.4	25	25.9	1	0	0	1023.57	1216	1224
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	SLVPAAELLESR	99.7%	50.2	25	41.3	2	0	0	1284.72	3116	3127
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	SQVEEELFSVR	99.7%	74.9	25	64.5	2	0	0	1322.66	2361	2371
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	SSIAGLLLK	99.7%	40.3	25	24.9	1	0	0	901.57	2833	2841
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	TPVEVPVGGFK	98.8%	33.6	25	27.6	2	0	0	1129.63	3374	3384
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	VLADPSDDTK	94.6%	27.4	25	21.9	1	0	0	1060.52	2979	2988
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	VLALPEPSPAAPTLR	99.5%	37.1	25	37.1	2	0	0	1531.88	1187	1201
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	VPDVQDGVR	96.2%	28.8	25	24.3	1	0	0	984.51	402	410
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	VPVDVAYQR	96.0%	28.5	25	23.7	1	0	0	1046.56	3620	3628
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	VPVDVAYR	99.7%	39.7	25	29.3	2	0	0	918.50	2961	2968
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	39	39	56	0.06%	9.3%	VQSGSESVIQEYVDLR	99.7%	86.4	25	86.4	2	0	0	1808.90	1442	1457
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	99.8%	2	2	3	0.00%	5.6%	ASVHTLSGHTNAVATVR	99.7%	33.3	25	27	0	2	0	1720.91	321	337
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	99.8%	2	2	3	0.00%	5.6%	GPQNATDSYVHK	99.3%	35.8	25	34.6	1	0	0	1316.62	69	80
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	7	7	18	0.02%	9.1%	KGDEVDGVDEVAK	99.7%	43.6	25	26.8	1	0	0	1360.66	209	221
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	7	7	18	0.02%	9.1%	KPPLLNNADSVQAK	99.7%	59.6	25	52.8	1	0	0	1494.83	748	761
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	7	7	18	0.02%	9.1%	QQVPSGESAILDR	99.7%	49.2	25	48.7	3	0	0	1399.72	270	282
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	7	7	18	0.02%	9.1%	TLGDFAAEYAK	99.7%	59.5	25	45.4	3	0	0	1185.58	109	119
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	7	7	18	0.02%	9.1%	TTNFAGILSQGLR	99.7%	89.3	25	76.7	4	0	0	1377.75	866	878
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	7	7	18	0.02%	9.1%	VFSATLGLVDIVK	99.7%	85.9	25	64.8	2	0	0	1361.80	552	564
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	7	7	18	0.02%	9.1%	VVSEDFLQDVSASTK	99.7%	110	25	103	4	0	0	1624.81	453	467
Poly(A) RNA polymerase, mitochondrial	MTPAP	PAPD1_HUMAN	66.2	100.0%	3	3	4	0.00%	5.2%	NVSQSQLQK	97.8%	30.9	25	17.3	1	0	0	1031.55	489	497
Poly(A) RNA polymerase, mitochondrial	MTPAP	PAPD1_HUMAN	66.2	100.0%	3	3	4	0.00%	5.2%	SPPILPTLDSLK	99.7%	39.3	25	39.3	2	0	0	1280.75	392	403
Poly(A) RNA polymerase, mitochondrial	MTPAP	PAPD1_HUMAN	66.2	100.0%	3	3	4	0.00%	5.2%	TVLIHCPEK	99.3%	35.9	25	33.7	1	0	0	1096.58	77	85
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	6	7	17	0.02%	22.5%	AITIAGVPQSVTECVK	99.7%	46.3	25	45.5	2	0	0	1672.89	145	160
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	6	7	17	0.02%	22.5%	ESTGAQVQVAGDMLPNSTER	99.7%	107	25	107	6	0	0	2089.98	125	144
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	6	7	17	0.02%	22.5%	IANPVEGSSGR	99.7%	78.6	25	73.9	2	0	0	1086.55	315	325
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	6	7	17	0.02%	22.5%	IITLTGPTNAIFK	99.7%	66.9	25	65.5	2	0	0	1388.82	58	70
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	6	7	17	0.02%	22.5%	INISEGNCPER	99.7%	49.1	25	42.9	4	0	0	1288.60	47	57

Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	6	7	17	0.02%	22.5%	QGANINEIR	99.7%	54	25	40.5	1	0	0	1014.53	298	306
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	18	0.02%	23.3%	AITIAGIPQSIIECVK	99.7%	65.8	25	62.8	4	0	0	1712.96	145	160
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	18	0.02%	23.3%	ESTGAQVQVAGDMLPNSTER	99.7%	107	25	107	6	0	0	2089.98	125	144
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	18	0.02%	23.3%	IANPVEGSTDR	99.7%	53.1	25	53.1	2	0	0	1158.58	323	333
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	18	0.02%	23.3%	IITLAGPTNAIFK	99.7%	64.7	25	64.7	6	0	0	1358.80	58	70
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	18	0.02%	23.3%	INISEGNCPER	99.7%	49.1	25	42.9	4	0	0	1288.60	47	57
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	18	0.02%	23.3%	LVVPASQCGSLIGK	99.7%	67.9	25	66.6	6	0	0	1428.79	102	115
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	18	0.02%	16.8%	GYGFIEYEK	99.7%	47.7	25	46.5	2	0	0	1105.52	268	276
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	18	0.02%	16.8%	KQESTVMVLR	99.7%	49.4	25	44.9	4	0	0	1206.65	458	467
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	18	0.02%	16.8%	KVVAEVYDQER	99.7%	71.9	25	66.8	1	0	0	1335.69	541	551
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	18	0.02%	16.8%	LGLPPLTPEQQEALQK	99.7%	56.6	25	54.8	2	0	0	1761.97	54	69
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	18	0.02%	16.8%	QGEEEDAEIIVK	99.7%	77.3	25	65.3	2	0	0	1359.66	503	514
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	18	0.02%	16.8%	SIDMSWDSVTMK	99.7%	56.6	25	56.6	1	0	0	1399.62	157	168
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	18	0.02%	16.8%	VVAEVYDQER	99.7%	76.8	25	70.4	2	0	0	1207.60	542	551
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	18	0.02%	16.8%	VYVGSIYYELGEDTIR	99.7%	73.4	25	73.4	2	0	0	1876.93	131	146
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	18	0.02%	16.8%	YAMEQSIK	99.7%	54.9	25	37.4	2	0	0	969.47	73	80
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	23	31	104	0.11%	35.8%	AKEFTNVYIK	99.6%	38.8	25	35.4	2	0	0	1212.66	187	196
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	23	31	104	0.11%	35.8%	ALDTMNFDVIK	99.7%	87.2	25	79.8	7	0	0	1266.64	68	78
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	23	31	104	0.11%	35.8%	ALYDTFSAFGNILSCK	99.7%	94.9	25	93.2	6	0	0	1806.87	114	129
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	23	31	104	0.11%	35.8%	EFSPFGTITSAK	99.7%	60.7	25	50.6	6	0	0	1284.65	313	324
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	23	31	104	0.11%	35.8%	EFTNVYIK	99.7%	40.3	25	25.4	2	0	0	1013.53	189	196
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	23	31	104	0.11%	35.8%	FGPALSVK	99.7%	50.9	25	12.6	6	0	0	818.48	214	221
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	23	31	104	0.11%	35.8%	FSPAGPILSIR	99.7%	59	25	44.1	5	0	0	1157.67	31	41
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	23	31	104	0.11%	35.8%	GFGFVCFSSPEEATK	99.7%	82.9	25	82.9	6	0	0	1662.75	334	348
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	23	31	104	0.11%	35.8%	GFGFVSFER	99.7%	54.8	25	37.6	8	0	0	1045.51	232	240
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	23	31	104	0.11%	35.8%	GYGFVHFETQEAAER	99.7%	59.8	25	57.9	4	5	0	1740.80	139	153
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	23	31	104	0.11%	35.8%	IMWSQR	98.1%	31.4	25	0	1	0	0	820.41	84	89
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	23	31	104	0.11%	35.8%	IVATKPLYVALAQR	99.7%	88.6	25	88.6	3	4	0	1542.94	357	370
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	23	31	104	0.11%	35.8%	KEFSPFGTITSAK	99.7%	70	25	69.2	2	2	0	1412.74	312	324
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	23	31	104	0.11%	35.8%	LFPLIQAMHPTLAGK	99.7%	84.4	25	83.7	2	0	0	1636.92	566	580
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	23	31	104	0.11%	35.8%	MNGMLLNDRK	98.3%	32	25	3.62	1	0	0	1191.60	158	167
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	23	31	104	0.11%	35.8%	NLDDGIDDER	99.7%	54.6	25	40.9	2	0	0	1161.50	300	309
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	23	31	104	0.11%	35.8%	NLDDGIDDERLR	99.7%	53.4	25	39.5	2	1	0	1430.69	300	311
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	23	31	104	0.11%	35.8%	QAHLTNQYMQR	99.7%	60.5	25	57.2	4	2	0	1405.66	375	385
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	23	31	104	0.11%	35.8%	RSLGYAYVNFQQPADAER	99.7%	53.2	25	47.4	0	1	0	2085.01	50	67
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	23	31	104	0.11%	35.8%	SGVGNIFIK	99.7%	74.9	25	48	7	0	0	934.54	96	104
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	23	31	104	0.11%	35.8%	SKVDEAVAVLQAHQAK	99.7%	111	25	107	2	2	0	1693.92	605	620
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	23	31	104	0.11%	35.8%	SLGYAYVNFQQPADAER	99.7%	83.7	25	83.7	4	0	0	1928.91	51	67
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	23	31	104	0.11%	35.8%	YQGVNLYVK	99.7%	47.3	25	39.7	5	0	0	1083.58	291	299
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	7	8	14	0.01%	26.9%	AKEFTNVYIK	99.6%	38.8	25	35.4	2	0	0	1212.66	187	196
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	7	8	14	0.01%	26.9%	ALDTMNFDVIK	99.7%	87.2	25	79.8	7	0	0	1266.64	68	78
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	7	8	14	0.01%	26.9%	ALYDTFSAFGNILSCK	99.7%	94.9	25	93.2	6	0	0	1806.87	114	129
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	7	8	14	0.01%	26.9%	EFSPFGSITSAK	99.7%	72.5	25	71.8	2	0	0	1270.63	313	324
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	7	8	14	0.01%	26.9%	EFTNVYIK	99.7%	40.3	25	25.4	2	0	0	1013.53	189	196
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	7	8	14	0.01%	26.9%	FSPAGPVLSIR	99.7%	58.7	25	45.2	3	0	0	1143.65	31	41
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	7	8	14	0.01%	26.9%	GFGFVCFSSPEEATK	99.7%	82.9	25	82.9	6	0	0	1662.75	334	348
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	7	8	14	0.01%	26.9%	GFGFVSYEKHEDANK	99.7%	41	25	36.1	0	2	0	1727.80	232	246
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	7	8	14	0.01%	26.9%	GYAFVHFETQEAADK	99.7%	41.4	25	41.4	1	0	0	1712.79	139	153
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	7	8	14	0.01%	26.9%	IMWSQR	98.1%	31.4	25	0	1	0	0	820.41	84	89
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	7	8	14	0.01%	26.9%	IVGSKPLYVALAQR	99.7%	64.6	25	53.3	1	2	0	1514.91	357	370
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	7	8	14	0.01%	26.9%	KAHLTNQYMQR	99.5%	31.4	25	31.4	0	1	0	1405.70	375	385

Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	7	8	14	0.01%	26.9%	MNGMLLNDRK	98.3%	32	25	3.62	1	0	0	1191.60	158	167
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	7	8	14	0.01%	26.9%	RSLGYAYVNFQQPADAER	99.7%	53.2	25	47.4	0	1	0	2085.01	50	67
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	7	8	14	0.01%	26.9%	SLGYAYVNFQQPADAER	99.7%	83.7	25	83.7	4	0	0	1928.91	51	67
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	7	8	14	0.01%	26.9%	YQGVNLYIK	99.7%	45.9	25	33.7	2	0	0	1097.60	291	299
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	4	4	7	0.01%	12.5%	GVVLFPWQAR	97.1%	29.7	25	21.6	1	0	0	1172.66	92	101
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	4	4	7	0.01%	12.5%	IFSLSGTLETVR	99.7%	65.7	25	52.5	2	0	0	1322.73	286	297
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	4	4	7	0.01%	12.5%	LENLDSDVVQLR	99.7%	66.3	25	66.3	2	0	0	1400.74	269	280
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	4	4	7	0.01%	12.5%	VLETVGVFEVPK	99.7%	70.7	25	64.3	2	0	0	1316.75	61	72
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	6	8	11	0.01%	16.8%	GQPIYIQFSNHK	99.5%	37.2	25	36.7	1	0	0	1431.74	123	134
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	6	8	11	0.01%	16.8%	HQNVQLPR	99.7%	40.9	25	34	2	0	0	991.54	411	418
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	6	8	11	0.01%	16.8%	IAIPGLAGAGNSVLLVSNLNPER	99.7%	109	25	109	2	1	0	2275.28	326	348
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	6	8	11	0.01%	16.8%	KLPIDVTEGEVISLGLPFGK	99.7%	39.9	25	39.1	0	2	0	2112.20	65	84
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	6	8	11	0.01%	16.8%	VTNLLMLK	99.7%	45.8	25	0	2	0	0	947.56	85	92
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	6	8	11	0.01%	16.8%	VTPQSLFILFGVYGDVQR	99.6%	32.5	25	32.5	0	1	0	2039.10	349	366
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	5	7	19	0.02%	48.0%	GTAYVVYEDIFDAK	99.7%	58	25	56.9	4	0	0	1590.77	58	71
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	5	7	19	0.02%	48.0%	ITAEEMYDIFGK	99.7%	75.7	25	70.1	8	0	0	1416.67	30	41
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	5	7	19	0.02%	48.0%	NACDHLSGFNVCNR	99.3%	35.9	25	35.9	1	1	0	1663.71	72	85
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	5	7	19	0.02%	48.0%	YGINTDPPK	95.4%	28	25	28	1	0	0	1004.50	117	125
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	5	7	19	0.02%	48.0%	YLVVLYYNANR	99.7%	76.6	25	69.5	4	0	0	1387.74	86	96
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	10	11	20	0.02%	27.0%	FIASTGMDR	99.7%	57.9	25	46.3	2	0	0	997.48	489	497
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	10	11	20	0.02%	27.0%	ILTGGADKNVVVFDK	99.7%	73.6	25	69	2	2	0	1575.87	237	251
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	10	11	20	0.02%	27.0%	IWSVPNASCVQVVR	99.7%	62.1	25	54.2	2	0	0	1614.84	290	303
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	10	11	20	0.02%	27.0%	KVTSVVFHPSQDLVFSASPDATIR	99.7%	98.9	25	98.9	0	2	0	2601.37	266	289
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	10	11	20	0.02%	27.0%	QELSHALYQHDAACR	99.7%	55.5	25	55.5	0	2	0	1798.83	101	115
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	10	11	20	0.02%	27.0%	SSEQILATLK	99.7%	69.8	25	51.3	2	0	0	1089.62	252	261
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	10	11	20	0.02%	27.0%	TLQLDNNFEVK	99.7%	52.8	25	45.1	2	0	0	1320.68	429	439
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	10	11	20	0.02%	27.0%	TVPEELVKPEELSK	99.7%	68.7	25	61	2	0	0	1597.87	193	206
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	10	11	20	0.02%	27.0%	VTSVVFHPSQDLVFSASPDATIR	96.7%	23.9	25	23.9	0	1	0	2473.27	267	289
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	10	11	20	0.02%	27.0%	YIAENGTDPINNQPLSEEQLIDIK	99.7%	40	25	40	1	0	0	2714.35	33	56
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	25.7%	AAELETDIR	99.7%	53.3	25	29.2	2	0	0	1017.52	379	387
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	25.7%	AAQDLCEEALR	99.7%	43.9	25	35.3	1	0	0	1275.60	693	703
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	25.7%	AAVELEEPEDAR	99.7%	70.1	25	61.5	2	0	0	1328.63	409	420
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	25.7%	AEVLWLMGAK	99.7%	70.6	25	58.6	2	0	0	1117.61	607	616
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	25.7%	AGSVATCQAVMR	99.7%	68.3	25	55.3	4	0	0	1250.60	516	527
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	25.7%	AIYAYALQVFPSK	99.7%	45.8	25	34.4	1	0	0	1470.80	561	573
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	25.7%	AIYAYALQVFPSKK	99.7%	70	25	58.6	1	0	0	1598.89	561	574
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	25.7%	AVIGIGIEEEDRK	99.7%	72.9	25	72.9	2	0	0	1428.77	528	540
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	25.7%	AVVAQAVR	99.7%	46.9	25	44.2	2	0	0	813.49	360	367
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	25.7%	ESLEALLQR	99.7%	54	25	24.6	2	0	0	1058.58	591	599
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	25.7%	FELQHGTEEQQEEVR	99.7%	39.9	25	31.7	0	1	0	1858.86	884	898
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	25.7%	HGELWCAVSK	99.0%	34.2	25	30.2	2	0	0	1186.57	908	917
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	25.7%	HIWITAAK	99.7%	40.6	25	23.6	1	0	0	939.54	465	472
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	25.7%	HLQTGENHTSVDPR	95.4%	28	25	28	1	0	0	1590.76	190	203
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	25.7%	HYEDFPK	99.2%	35.2	25	24.3	2	0	0	935.43	704	710
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	25.7%	IDSDLGDAWAFFYK	99.7%	103	25	99.8	2	0	0	1647.77	870	883
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	25.7%	IQQQFSDLKR	99.7%	33.2	25	23.9	1	2	0	1262.69	138	147
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	25.7%	LESENDEYER	99.7%	50.9	25	50.9	2	0	0	1283.54	651	660
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	25.7%	LEWVQDNIR	99.7%	46	25	30.5	2	0	0	1172.61	684	692
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	25.7%	LSQVSDSVSGQTVVDPK	99.7%	120	25	108	1	0	0	1745.89	255	271
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	25.7%	NPGLWLESVR	99.7%	53.5	25	47.1	2	0	0	1170.63	776	785
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	25.7%	SEDVWLEAAR	99.7%	62.5	25	52.2	1	0	0	1175.57	342	351

Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	25.7%	WLAGDVPAAR	99.3%	36	25	33.6	2	0	0	1055.56	619	628
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	26	27	47	0.05%	11.9%	AISAANLHLR	99.7%	65.9	25	55.4	2	0	0	1065.62	2077	2086
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	26	27	47	0.05%	11.9%	ALDIPLVK	96.3%	28.9	25	23.9	2	0	0	868.55	421	428
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	26	27	47	0.05%	11.9%	AQIAGYLYGVSPPDNPQVK	99.7%	49.9	25	42.5	1	0	0	2017.04	2122	2140
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	26	27	47	0.05%	11.9%	DNPNLLFNMCGFECR	99.7%	77.7	25	75.2	2	0	0	1886.80	1181	1195
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	26	27	47	0.05%	11.9%	EAVVNTQELLDLLVK	99.7%	53.4	25	50.9	1	0	0	1683.95	1276	1290
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	26	27	47	0.05%	11.9%	EQSQLTATQTR	99.7%	74.6	25	61.2	2	0	0	1262.63	2035	2045
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	26	27	47	0.05%	11.9%	FGDLILK	99.7%	47.2	25	27.7	2	0	0	805.48	1902	1908
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	26	27	47	0.05%	11.9%	FICISDLR	99.7%	40	25	30.3	2	0	0	1023.53	2114	2121
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	26	27	47	0.05%	11.9%	FNTGPVGK	98.2%	31.7	25	13.1	2	0	0	819.44	616	623
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	26	27	47	0.05%	11.9%	FSPIPFPPLSYK	96.5%	29	25	26.3	1	0	0	1392.76	822	833
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	26	27	47	0.05%	11.9%	GSELQLPFQACLK	99.7%	65.2	25	55.5	2	0	0	1490.77	1886	1898
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	26	27	47	0.05%	11.9%	GYLPSHYER	96.8%	29.4	25	29.4	1	0	0	1121.54	2250	2258
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	26	27	47	0.05%	11.9%	IDLTLLNR	99.7%	58.2	25	37	2	0	0	957.57	988	995
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	26	27	47	0.05%	11.9%	ISLIQIFR	99.7%	67.9	25	63.7	4	0	0	989.61	1571	1578
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	26	27	47	0.05%	11.9%	LIVDHNIADYMTAK	99.7%	63	25	63	2	0	0	1603.82	999	1012
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	26	27	47	0.05%	11.9%	LLILALER	99.7%	55.3	25	55.3	4	0	0	940.62	838	845
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	26	27	47	0.05%	11.9%	QILMASGSTTFTK	99.7%	51	25	49.3	3	0	0	1384.71	1246	1258
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	26	27	47	0.05%	11.9%	QTDVGITHFR	99.7%	53	25	42.2	2	0	0	1173.60	1345	1354
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	26	27	47	0.05%	11.9%	RALDIPLVK	97.7%	30.8	25	26.3	1	0	0	1024.65	420	428
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	26	27	47	0.05%	11.9%	TIIITCSFTPGSCTLTAYK	99.7%	56.1	25	56.1	1	0	0	2134.06	2211	2229
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	26	27	47	0.05%	11.9%	TISSYTAFSR	99.7%	41.8	25	37.9	2	0	0	1132.56	1926	1935
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	26	27	47	0.05%	11.9%	TSYEEFTHK	97.0%	29.7	25	27.2	1	0	0	1141.52	1202	1210
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	26	27	47	0.05%	11.9%	VPGLPTPIENMILR	99.5%	37	25	37	1	0	0	1565.87	728	741
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	26	27	47	0.05%	11.9%	VQMLLSDR	99.7%	40.7	25	32.1	2	0	0	961.51	2259	2266
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	26	27	47	0.05%	11.9%	YIQPWESEFIDSQR	99.7%	65.9	25	64.2	1	0	0	1797.84	1371	1384
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	26	27	47	0.05%	11.9%	YYVLNALK	97.7%	30.8	25	26.8	1	0	0	983.56	453	460
Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16	DHX38	PRP16_HUMAN	140.5	100.0%	3	3	6	0.01%	2.8%	DATSDLAIIAR	99.7%	57.9	25	42.2	2	0	0	1145.62	435	445
Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16	DHX38	PRP16_HUMAN	140.5	100.0%	3	3	6	0.01%	2.8%	SLNTDVLFGLLR	99.7%	72.1	25	61.4	2	0	0	1347.76	658	669
Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16	DHX38	PRP16_HUMAN	140.5	100.0%	3	3	6	0.01%	2.8%	TNLANVVLLLK	99.7%	62.5	25	54.7	2	0	0	1197.76	889	899
Pre-mRNA-splicing factor SPF27	BCAS2	SPF27_HUMAN	26.1	100.0%	3	3	4	0.00%	16.9%	EAAAALVEEETRR	95.7%	28.3	25	16.2	1	0	0	1444.74	30	42
Pre-mRNA-splicing factor SPF27	BCAS2	SPF27_HUMAN	26.1	100.0%	3	3	4	0.00%	16.9%	EMESNWVSLVSK	98.4%	32.3	25	27.8	1	0	0	1408.68	180	191
Pre-mRNA-splicing factor SPF27	BCAS2	SPF27_HUMAN	26.1	100.0%	3	3	4	0.00%	16.9%	TIVQLENEIYQIK	99.7%	66	25	47.3	2	0	0	1590.87	198	210
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	7	7	11	0.01%	12.6%	DSPPEVAGAR	99.4%	36.4	25	25.5	2	0	0	998.49	543	552
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	7	7	11	0.01%	12.6%	IVVEFSSPNVAK	99.7%	53.8	25	37.3	2	0	0	1289.71	127	138
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	7	7	11	0.01%	12.6%	LLGITPVCR	98.0%	31.4	25	26.4	1	0	0	1028.59	569	577
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	7	7	11	0.01%	12.6%	SELFSGLPQK	99.7%	40.7	25	36.2	1	0	0	1105.59	116	125
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	7	7	11	0.01%	12.6%	SSQDFQPR	99.7%	41	25	30.5	1	0	0	964.45	512	519
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	7	7	11	0.01%	12.6%	TVLQQVIEDGSK	99.7%	60.5	25	58	2	0	0	1316.71	100	111
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	7	7	11	0.01%	12.6%	VGLAALIIQDFK	99.7%	72.5	25	65.1	2	0	0	1287.77	427	438
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	21	0.02%	30.2%	APILIATDVASR	99.7%	95.5	25	95.5	6	0	0	1226.71	469	480
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	21	0.02%	30.2%	APLPDLYPFGTMR	99.7%	39.9	25	39.9	2	0	0	1477.75	69	81
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	21	0.02%	30.2%	DMVGIAQTGSGK	99.7%	59.8	25	57.5	2	0	0	1179.57	210	221
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	21	0.02%	30.2%	ELAQQVQQVADDYGK	99.7%	108	25	108	2	0	0	1691.82	255	269
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	21	0.02%	30.2%	FVINYDYPNSSEDYVHR	95.7%	22.9	25	15.4	0	1	0	2117.96	489	505
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	21	0.02%	30.2%	GDGPICLVLAPTR	99.7%	45.1	25	40.8	2	0	0	1368.73	242	254
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	21	0.02%	30.2%	GLDVEDVK	99.4%	36.8	25	30.4	4	0	0	874.45	481	488
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	21	0.02%	30.2%	GTAYTFFTPGNLK	99.7%	58.8	25	57.2	2	0	0	1416.72	516	528
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	21	0.02%	30.2%	GVEICIATPGR	99.7%	89.2	25	64.4	2	0	0	1172.61	294	304
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	21	0.02%	30.2%	IVDQIRPDR	98.7%	33	25	24.3	2	0	0	1111.62	342	350
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	21	0.02%	30.2%	LIDFLESGK	99.7%	51.5	25	47	2	0	0	1021.56	305	313

Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	21	0.02%	30.2%	LTPYEVDELRR	98.7%	33.1	25	28.1	1	0	0	1390.73	144	154
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	21	0.02%	30.2%	MLDMGFEPQIR	99.7%	72.6	25	66.5	6	0	0	1336.64	330	340
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	21	0.02%	30.2%	NFYVEHPEVAR	99.7%	53.8	25	49.9	2	0	0	1360.66	133	143
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	21	0.02%	30.2%	QLAEDFLR	99.7%	43.9	25	0	2	0	0	991.52	365	372
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	21	0.02%	30.2%	QTLMWSATWPK	99.7%	59	25	50.9	2	0	0	1348.67	351	361
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	21	0.02%	30.2%	SSQSSSQQFSGIGR	99.7%	110	25	105	2	0	0	1455.68	671	684
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	21	0.02%	30.2%	STCIYGGAPK	99.7%	58.2	25	48.6	4	0	0	1053.50	275	284
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	11	11	21	0.02%	30.2%	VLEEANQAINPK	99.7%	75	25	62.7	3	0	0	1325.71	536	547
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	3	3	5	0.01%	3.9%	EAVVQEPER	99.4%	36.3	25	34	1	0	0	1056.53	642	650
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	3	3	5	0.01%	3.9%	IFVNSNTDVAPFLR	99.7%	66.7	25	52.6	2	0	0	1592.84	423	436
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	3	3	5	0.01%	3.9%	VLVLVPTR	98.2%	31.6	25	31.6	2	0	0	896.59	292	299
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	5	5	6	0.01%	11.5%	GSFADLGLEPR	99.7%	50.8	25	50	1	0	0	1161.59	126	136
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	5	5	6	0.01%	11.5%	LLGQPSLDSLPIPAPR	99.7%	43.1	25	43.1	1	0	0	1673.96	190	205
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	5	5	6	0.01%	11.5%	SPDEPLPVVR	99.7%	42.1	25	41.9	1	0	0	1108.60	28	37
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	5	5	6	0.01%	11.5%	TLSYLLPLLQR	99.7%	40.8	25	40.8	2	0	0	1316.79	179	189
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	5	5	6	0.01%	11.5%	VASPDAVTTITSSK	99.7%	59.1	25	56.3	1	0	0	1376.73	344	357
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	6	6	8	0.01%	10.1%	DVLVATDVASK	99.7%	57.5	25	42.8	2	0	0	1117.61	484	494
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	6	6	8	0.01%	10.1%	ILESVAEGR	98.1%	31.6	25	15.4	1	0	0	973.53	116	124
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	6	6	8	0.01%	10.1%	MVYLLECLQK	99.7%	48.2	25	40.6	1	0	0	1296.67	421	430
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	6	6	8	0.01%	10.1%	SALVKPVTINVGR	99.5%	30.8	25	30.8	0	2	0	1353.82	388	400
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	6	6	8	0.01%	10.1%	TPPPVLIFAEK	97.0%	29.7	25	29.7	1	0	0	1211.70	431	441
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	6	6	8	0.01%	10.1%	YLALDEADR	99.5%	37.6	25	27.3	1	0	0	1065.52	340	348
Probable ATP-dependent RNA helicase DDX46	DDX46	DDX46_HUMAN	117.4	100.0%	3	3	7	0.01%	2.7%	LLVATSVAAR	99.7%	64.5	25	43.5	2	0	0	1000.61	672	681
Probable ATP-dependent RNA helicase DDX46	DDX46	DDX46_HUMAN	117.4	100.0%	3	3	7	0.01%	2.7%	LNYVPLEK	97.9%	31.1	25	23.8	1	0	0	975.55	908	915
Probable ATP-dependent RNA helicase DDX46	DDX46	DDX46_HUMAN	117.4	100.0%	3	3	7	0.01%	2.7%	TIAFLLPMFR	99.7%	49.1	25	46.1	4	0	0	1208.69	423	432
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	4	4	8	0.01%	11.6%	IQIEAIPLALQGR	99.7%	98	25	87.3	2	0	0	1421.85	50	62
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	4	4	8	0.01%	11.6%	LQQYYIFIPSK	99.7%	53	25	37.8	2	0	0	1399.76	238	248
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	4	4	8	0.01%	11.6%	SILLATDVASR	99.7%	49.5	25	34.7	1	0	0	1145.65	315	325
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	4	4	8	0.01%	11.6%	TGAFALPILNALLETPQR	99.7%	79.2	25	79.2	3	0	0	1925.09	75	92
Probable ATP-dependent RNA helicase DDX49	DDX49	DDX49_HUMAN	54.2	99.8%	2	2	2	0.00%	4.4%	ILIATDVASR	99.7%	55.2	25	38.9	1	0	0	1058.62	301	310
Probable ATP-dependent RNA helicase DDX49	DDX49	DDX49_HUMAN	54.2	99.8%	2	2	2	0.00%	4.4%	TAAFVLPILQK	99.7%	43	25	36.2	1	0	0	1200.74	53	63
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	22	23	61	0.06%	37.5%	APILIATDVASR	99.7%	95.5	25	95.5	6	0	0	1226.71	392	403
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	22	23	61	0.06%	37.5%	DGWPAMGIHGDK	99.7%	40.7	25	35	2	0	0	1283.58	364	375
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	22	23	61	0.06%	37.5%	DRGFGAPR	95.4%	28	25	18.1	1	0	0	875.45	13	20
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	22	23	61	0.06%	37.5%	ELAQQVQQVAAEYCR	99.7%	86.7	25	86.7	2	0	0	1792.86	178	192
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	22	23	61	0.06%	37.5%	FVINYDYPNSSEDYIHR	99.7%	41.6	25	41.6	0	2	0	2131.97	412	428
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	22	23	61	0.06%	37.5%	GDGPICLVLAPTR	99.7%	45.1	25	40.8	2	0	0	1368.73	165	177
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	22	23	61	0.06%	37.5%	GLDVEDVK	99.4%	36.8	25	30.4	4	0	0	874.45	404	411
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	22	23	61	0.06%	37.5%	GVEICIATPGR	99.7%	89.2	25	64.4	2	0	0	1172.61	217	227
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	22	23	61	0.06%	37.5%	IVDQIRPDR	98.7%	33	25	24.3	2	0	0	1111.62	265	273
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	22	23	61	0.06%	37.5%	LIDFLECGK	99.7%	64.5	25	62	4	0	0	1094.56	228	236
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	22	23	61	0.06%	37.5%	LLQLVEDR	99.7%	65.4	25	50	4	0	0	985.57	471	478
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	22	23	61	0.06%	37.5%	LMEEIMSEKENK	99.7%	45.4	25	35.1	2	0	0	1480.70	332	343
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	22	23	61	0.06%	37.5%	MLDMGFEPQIR	99.7%	72.6	25	66.5	6	0	0	1336.64	253	263
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	22	23	61	0.06%	37.5%	NFYQEHPDLAR	99.7%	55.6	25	43.3	1	0	0	1389.65	57	67
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	22	23	61	0.06%	37.5%	QTLMWSATWPK	99.7%	59	25	50.9	2	0	0	1348.67	274	284
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	22	23	61	0.06%	37.5%	QVSDLISVLR	99.7%	84.9	25	68.2	4	0	0	1129.66	452	461
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	22	23	61	0.06%	37.5%	STCIYGGAPK	99.7%	58.2	25	48.6	4	0	0	1053.50	198	207
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	22	23	61	0.06%	37.5%	TAQEVETYR	99.7%	72.8	25	61.2	2	0	0	1096.53	69	77
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	22	23	61	0.06%	37.5%	TGTAYTFFTPNNIK	99.7%	86.8	25	79.6	4	0	0	1574.79	438	451
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	22	23	61	0.06%	37.5%	TIVFVETK	96.7%	29.2	25	21.9	2	0	0	936.54	344	351

Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	22	23	61	0.06%	37.5%	TIVFVETKR	99.7%	50.3	25	50.3	1	0	0	1092.64	344	352
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	22	23	61	0.06%	37.5%	TTYLVLDEADR	99.7%	88.4	25	82.8	2	0	0	1295.65	242	252
Probable ATP-dependent RNA helicase DDX52	DDX52	DDX52_HUMAN	67.5	100.0%	4	5	7	0.01%	8.0%	ELASQIHR	98.3%	31.9	25	14.5	1	0	0	953.52	245	252
Probable ATP-dependent RNA helicase DDX52	DDX52	DDX52_HUMAN	67.5	100.0%	4	5	7	0.01%	8.0%	ELLASAPTGSGK	98.6%	32.7	25	27	2	0	0	1130.61	204	215
Probable ATP-dependent RNA helicase DDX52	DDX52	DDX52_HUMAN	67.5	100.0%	4	5	7	0.01%	8.0%	GFNPPVLVFVQSIER	99.7%	82.9	25	82.9	2	0	0	1701.93	410	424
Probable ATP-dependent RNA helicase DDX52	DDX52	DDX52_HUMAN	67.5	100.0%	4	5	7	0.01%	8.0%	TLAFSIPILMQLK	99.7%	63.7	25	58.2	2	0	0	1474.87	216	228
Probable ATP-dependent RNA helicase DHX36	DHX36	DHX36_HUMAN	114.8	100.0%	4	4	8	0.01%	5.5%	ASLLDDYQLPEILR	99.7%	83.1	25	70.8	3	0	0	1645.88	620	633
Probable ATP-dependent RNA helicase DHX36	DHX36	DHX36_HUMAN	114.8	100.0%	4	4	8	0.01%	5.5%	AVICAGLYPK	99.7%	39.3	25	32.4	2	0	0	1091.59	833	842
Probable ATP-dependent RNA helicase DHX36	DHX36	DHX36_HUMAN	114.8	100.0%	4	4	8	0.01%	5.5%	ISAISVAER	99.7%	58.9	25	44.4	1	0	0	945.54	267	275
Probable ATP-dependent RNA helicase DHX36	DHX36	DHX36_HUMAN	114.8	100.0%	4	4	8	0.01%	5.5%	LGGIAYFLSR	99.7%	76.8	25	73.9	2	0	0	1096.62	648	657
Probable ATP-dependent RNA helicase DHX36	DHX36	DHX36_HUMAN	114.8	100.0%	4	4	8	0.01%	5.5%	NLQSDVLMTVVK	99.7%	45.1	25	38.2	1	0	0	1346.73	340	351
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	6	6	11	0.01%	5.7%	DSPTLSNSGIR	99.7%	48.4	25	41	2	0	0	1146.58	898	908
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	6	6	11	0.01%	5.7%	GFQEDSEIR	99.6%	39	25	27.6	2	0	0	1080.50	208	216
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	6	6	11	0.01%	5.7%	LGDASIAAPFTSK	99.7%	85.7	25	82	2	0	0	1277.67	951	963
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	6	6	11	0.01%	5.7%	SIDGSIVLPLAR	99.7%	58.1	25	55.7	2	0	0	1240.73	786	797
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	6	6	11	0.01%	5.7%	SPQENLVPCDVLLLR	99.7%	43.4	25	43.4	2	0	0	1752.93	328	342
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	6	6	11	0.01%	5.7%	VLDLQADSR	99.7%	44.1	25	35.5	1	0	0	1016.54	372	380
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	9	9	17	0.02%	16.3%	DSKPHFTTVFQNSVYK	99.7%	36.1	25	36.1	0	2	0	1897.94	653	668
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	9	9	17	0.02%	16.3%	IFGIADDAHIGNLLTSK	99.7%	72.8	25	72.7	1	0	0	1784.95	361	377
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	9	9	17	0.02%	16.3%	IMDLIGIQTK	99.7%	55.7	25	43.9	2	0	0	1131.64	123	132
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	9	9	17	0.02%	16.3%	IVYSMYSR	99.7%	48.8	25	40	2	0	0	1018.50	587	594
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	9	9	17	0.02%	16.3%	LTEYPLVINTLK	99.7%	52.2	25	44.7	2	0	0	1403.81	92	103
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	9	9	17	0.02%	16.3%	TEMGLYYSYFK	99.7%	58.9	25	58.9	2	0	0	1401.64	62	72
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	9	9	17	0.02%	16.3%	TPLCNLLVK	99.7%	53.1	25	46.9	3	0	0	1057.61	644	652
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	9	9	17	0.02%	16.3%	VLEVVKE	99.7%	42.6	25	6.84	2	0	0	815.49	669	675
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	9	9	17	0.02%	16.3%	YSTKPDAVFAGAMPTMASVK	99.7%	37.6	25	30.2	0	1	0	2104.01	544	563
Probable cytosolic iron-sulfur protein assembly protein CIAO1	CIAO1	CIAO1_HUMAN	37.8	100.0%	3	3	5	0.01%	11.5%	CICTLSGFHSR	98.7%	33.1	25	24.8	1	0	0	1337.61	243	253
Probable cytosolic iron-sulfur protein assembly protein CIAO1	CIAO1	CIAO1_HUMAN	37.8	100.0%	3	3	5	0.01%	11.5%	EPGLLASCSDDGEVAFWK	99.7%	66	25	66	2	0	0	1980.90	315	332
Probable cytosolic iron-sulfur protein assembly protein CIAO1	CIAO1	CIAO1_HUMAN	37.8	100.0%	3	3	5	0.01%	11.5%	MKDSLVLLGR	99.7%	61.8	25	54.9	2	0	0	1131.66	1	10
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	5	5	8	0.01%	16.0%	LQVLVGDVLK	99.7%	57	25	26.9	2	0	0	1083.68	107	116
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	5	5	8	0.01%	16.0%	LSINTQLLAR	99.7%	86.4	25	74.7	2	0	0	1128.67	175	184
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	5	5	8	0.01%	16.0%	NPLIINSIIDK	99.7%	54.2	25	54.2	2	0	0	1239.73	41	51
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	5	5	8	0.01%	16.0%	SMDIDDFIR	96.0%	28.5	25	23.4	1	0	0	1111.51	292	300
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	5	5	8	0.01%	16.0%	SSAVQQLLEK	99.7%	49.7	25	33.8	1	0	0	1102.61	244	253
Probable global transcription activator SNF2L1	SMARCA1	SMCA1_HUMAN	122.6	100.0%	2	2	2	0.00%	10.0%	ANYAVDAYFR	99.7%	48.8	25	40.2	1	0	0	1189.56	755	764
Probable global transcription activator SNF2L1	SMARCA1	SMCA1_HUMAN	122.6	100.0%	2	2	2	0.00%	10.0%	APFHQLR	97.5%	30.4	25	26.5	1	0	0	868.48	945	951
Probable global transcription activator SNF2L1	SMARCA1	SMCA1_HUMAN	122.6	100.0%	2	2	2	0.00%	10.0%	CNELQDIEK	99.7%	49	25	27	1	0	0	1148.53	906	914
Probable global transcription activator SNF2L1	SMARCA1	SMCA1_HUMAN	122.6	100.0%	2	2	2	0.00%	10.0%	DFNQFIK	96.8%	29.4	25	10.1	2	0	0	911.46	864	870
Probable global transcription activator SNF2L1	SMARCA1	SMCA1_HUMAN	122.6	100.0%	2	2	2	0.00%	10.0%	ESELTDEDITTILER	99.3%	36.1	25	32.2	1	0	0	1763.85	681	695
Probable global transcription activator SNF2L1	SMARCA1	SMCA1_HUMAN	122.6	100.0%	2	2	2	0.00%	10.0%	IMAQIER	98.8%	33.5	25	13.3	2	0	0	876.46	915	921
Probable global transcription activator SNF2L1	SMARCA1	SMCA1_HUMAN	122.6	100.0%	2	2	2	0.00%	10.0%	KANYAVDAYFR	99.7%	41.7	25	41.7	2	0	0	1317.66	754	764
Probable global transcription activator SNF2L1	SMARCA1	SMCA1_HUMAN	122.6	100.0%	2	2	2	0.00%	10.0%	LDSIVIQQGR	99.7%	87.3	25	74.5	2	0	0	1128.64	642	651
Probable global transcription activator SNF2L1	SMARCA1	SMCA1_HUMAN	122.6	100.0%	2	2	2	0.00%	10.0%	LITDNTVEER	99.7%	66.7	25	51.9	1	0	0	1189.61	622	631
Probable global transcription activator SNF2L1	SMARCA1	SMCA1_HUMAN	122.6	100.0%	2	2	2	0.00%	10.0%	LLNILMQLR	99.7%	76.4	25	61.2	6	0	0	1113.68	449	457
Probable global transcription activator SNF2L1	SMARCA1	SMCA1_HUMAN	122.6	100.0%	2	2	2	0.00%	10.0%	LRLDSIVIQQGR	99.2%	29	25	29	0	2	0	1397.82	640	651
Probable global transcription activator SNF2L1	SMARCA1	SMCA1_HUMAN	122.6	100.0%	2	2	2	0.00%	10.0%	VLIFSQMTR	99.7%	66.6	25	62	4	0	0	1094.60	505	513
Probable global transcription activator SNF2L1	SMARCA1	SMCA1_HUMAN	122.6	100.0%	2	2	2	0.00%	10.0%	YLVIDEAHR	99.7%	46.7	25	43.4	2	0	0	1115.58	307	315
Probable glutamate--tRNA ligase, mitochondrial	EARS2	SYEM_HUMAN	58.7	100.0%	3	3	4	0.00%	5.5%	GGPAGPYQQSQR	99.7%	48.2	25	48.2	2	0	0	1245.60	109	120
Probable glutamate--tRNA ligase, mitochondrial	EARS2	SYEM_HUMAN	58.7	100.0%	3	3	4	0.00%	5.5%	TALYNYIFAK	97.6%	30.6	25	20.4	1	0	0	1203.64	56	65
Probable glutamate--tRNA ligase, mitochondrial	EARS2	SYEM_HUMAN	58.7	100.0%	3	3	4	0.00%	5.5%	VLGLLER	99.5%	37	25	27.7	1	0	0	799.50	449	455
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	10	11	19	0.02%	12.2%	AMQDALADLPEWYGIK	99.7%	50.3	25	49.2	1	0	0	1820.89	251	266

Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	10	11	19	0.02%	12.2%	EEVDLTGSVPVHAK	99.7%	65.1	25	54.7	2	0	0	1480.76	615	628
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	10	11	19	0.02%	12.2%	FYVLSMFPYPSGK	99.7%	88.7	25	84	3	0	0	1535.76	84	96
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	10	11	19	0.02%	12.2%	IPVPQQVAR	98.8%	33.6	25	33.6	2	0	0	1007.60	853	861
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	10	11	19	0.02%	12.2%	LPSGQYLQR	99.7%	66.8	25	56.6	2	0	0	1061.57	606	614
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	10	11	19	0.02%	12.2%	QDAFLALTQK	99.7%	64.7	25	44.6	2	0	0	1134.62	420	429
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	10	11	19	0.02%	12.2%	SPQPQLLSNK	95.1%	27.7	25	25.5	1	0	0	1111.61	711	720
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	10	11	19	0.02%	12.2%	TALINFLVQD	99.7%	61.8	25	61.8	2	0	0	1133.62	894	903
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	10	11	19	0.02%	12.2%	TDALPGVLR	99.7%	46.7	25	42.4	2	0	0	941.54	682	690
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	10	11	19	0.02%	12.2%	VYTISDTIAR	99.7%	47.7	25	38.5	2	0	0	1138.61	104	113
Probable methyltransferase-like protein 15	METTL15	MET15_HUMAN	46.1	99.8%	2	2	4	0.00%	7.1%	AMLGQFSQAEALLMK	99.7%	51.4	25	51.4	2	0	0	1637.84	141	155
Probable methyltransferase-like protein 15	METTL15	MET15_HUMAN	46.1	99.8%	2	2	4	0.00%	7.1%	VLSPQDQDVQDNPR	99.7%	76.1	25	73.1	2	0	0	1610.78	382	395
Probable proline--tRNA ligase, mitochondrial	PARS2	SYPM_HUMAN	53.3	99.8%	2	2	4	0.00%	4.6%	FGYPFVIIAGK	99.7%	46.5	25	39.3	2	0	0	1211.68	428	438
Probable proline--tRNA ligase, mitochondrial	PARS2	SYPM_HUMAN	53.3	99.8%	2	2	4	0.00%	4.6%	QLPFLLYQVTR	99.7%	46	25	44.1	2	0	0	1377.79	176	186
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	5	7	11	0.01%	19.0%	AVDPEDDFQR	99.7%	61.3	25	61.3	2	0	0	1191.53	95	104
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	5	7	11	0.01%	19.0%	ESYDDVSSFR	99.7%	60.5	25	60.5	2	0	0	1204.51	263	272
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	5	7	11	0.01%	19.0%	GLLKPGLNVVLEGPK	95.9%	23	25	23	1	1	0	1533.94	30	44
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	5	7	11	0.01%	19.0%	QAQAAVLAVLPR	99.7%	77.5	25	77.3	2	0	0	1236.74	111	122
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	5	7	11	0.01%	19.0%	RPTDYFAEMAK	99.7%	54.6	25	47.7	3	0	0	1328.63	132	142
Probable serine carboxypeptidase CPVL	CPVL	CPVL_HUMAN	54.2	100.0%	3	3	7	0.01%	6.7%	FLSLPEVR	99.7%	45.4	25	36.5	2	0	0	960.55	332	339
Probable serine carboxypeptidase CPVL	CPVL	CPVL_HUMAN	54.2	100.0%	3	3	7	0.01%	6.7%	NNDFYVTGESYAGK	99.7%	88.3	25	88.3	4	0	0	1564.69	195	208
Probable serine carboxypeptidase CPVL	CPVL	CPVL_HUMAN	54.2	100.0%	3	3	7	0.01%	6.7%	SDSEVAGYIR	99.7%	76.3	25	66.8	1	0	0	1096.53	424	433
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	4	4	6	0.01%	16.7%	GPGMGAPLVSVAVVAR	99.7%	45.3	25	40.6	1	0	0	1496.83	79	94
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	4	4	6	0.01%	16.7%	PAVLGFEGSANK	99.7%	87.4	25	80.6	2	0	0	1189.62	2	13
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	4	4	6	0.01%	16.7%	TPLSDSGVTQR	99.7%	40.6	25	24.1	2	0	0	1160.59	313	323
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	4	4	6	0.01%	16.7%	TYVTPPGTGFLPGDTAR	99.7%	49.9	25	44.9	1	0	0	1749.88	31	47
Probable tRNA pseudouridine synthase 1	TRUB1	TRUB1_HUMAN	37.3	99.8%	2	2	3	0.00%	6.6%	AAAAVVAAAAR	99.7%	58.6	25	58.6	1	0	0	941.55	39	49
Probable tRNA pseudouridine synthase 1	TRUB1	TRUB1_HUMAN	37.3	99.8%	2	2	3	0.00%	6.6%	GVLVVGIGSGTK	99.7%	58.2	25	51.4	2	0	0	1086.65	126	137
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	15	16	26	0.03%	6.9%	EIYTNLGPR	99.7%	55	25	42	2	0	0	1062.56	795	803
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	15	16	26	0.03%	6.9%	ELDMEPYTVAGVAK	98.9%	34	25	31.2	1	0	0	1522.75	1821	1834
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	15	16	26	0.03%	6.9%	ELLAFQTSEK	99.7%	52.2	25	44.2	2	0	0	1165.61	1436	1445
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	15	16	26	0.03%	6.9%	FNDYFEFPR	99.7%	57.5	25	49.3	2	0	0	1234.55	1812	1820
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	15	16	26	0.03%	6.9%	FSEYLLECPSAEVR	99.7%	50.4	25	50.4	1	0	0	1699.80	2100	2113
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	15	16	26	0.03%	6.9%	GDLLEGANAYHCEK	99.7%	60.3	25	60.3	2	0	0	1576.71	1760	1773
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	15	16	26	0.03%	6.9%	HSGDYFTLLR	99.3%	36.1	25	32.9	1	0	0	1208.61	1371	1380
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	15	16	26	0.03%	6.9%	IIEDCSNSEETVK	99.4%	36.8	25	13.9	1	0	0	1523.69	2289	2301
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	15	16	26	0.03%	6.9%	LPPVLAIQLK	98.5%	32.5	25	30.1	1	0	0	1091.72	1789	1798
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	15	16	26	0.03%	6.9%	LYSVVSQLIR	99.7%	81.1	25	69.3	2	0	0	1177.69	2228	2237
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	15	16	26	0.03%	6.9%	SGGLPLVLSMLTR	99.7%	55.3	25	49.9	4	0	0	1359.77	1120	1132
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	15	16	26	0.03%	6.9%	TGETGIEETILEGHLGVTK	99.1%	28.8	25	28.8	0	1	0	1984.02	1417	1435
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	15	16	26	0.03%	6.9%	VISSVSYYTHR	99.7%	61.4	25	56.9	2	0	0	1311.67	361	371
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	15	16	26	0.03%	6.9%	VLGGSFADQK	99.0%	34.5	25	26.1	2	0	0	1021.53	1713	1722
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	15	16	26	0.03%	6.9%	VVIQSNDDIASR	99.7%	72	25	70.1	2	0	0	1316.68	777	788
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	100.0%	2	2	2	0.00%	3.2%	FLLEYIAPMTEK	99.7%	44.6	25	44.6	1	0	0	1454.76	615	626
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	100.0%	2	2	2	0.00%	3.2%	SEDYVDIVQGR	99.7%	64.9	25	57.9	1	0	0	1280.61	431	441
Profilin-1	PFN1	PROF1_HUMAN	15.1	100.0%	3	4	9	0.01%	31.4%	DSLLQDGEFSMDLR	99.7%	99.8	25	95.3	4	0	0	1641.74	76	89
Profilin-1	PFN1	PROF1_HUMAN	15.1	100.0%	3	4	9	0.01%	31.4%	STGGAPTFNVTVTK	99.7%	68.2	25	57.1	4	0	0	1379.72	92	105
Profilin-1	PFN1	PROF1_HUMAN	15.1	100.0%	3	4	9	0.01%	31.4%	TFVNITPAEVGVLVGK	98.1%	31.6	25	26.4	1	0	0	1643.94	39	54
Profilin-2	PFN2	PROF2_HUMAN	15.0	99.8%	2	2	5	0.01%	19.3%	EGFFTNGLTLGAK	99.7%	55.7	25	51.7	2	0	0	1354.70	57	69
Profilin-2	PFN2	PROF2_HUMAN	15.0	99.8%	2	2	5	0.01%	19.3%	SQGGEPTYNVAVGR	99.7%	56.8	25	56.5	3	0	0	1434.70	92	105
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	13	13	23	0.02%	18.2%	DLQQSIAR	99.7%	39.1	25	21.4	1	0	0	930.50	708	715
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	13	13	23	0.02%	18.2%	DTIVLLCKPEPELNAAIPSANPAK	98.8%	27.6	25	27.6	0	1	0	2561.36	518	541

Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	13	13	23	0.02%	18.2%	ELPELLQR	99.7%	44.3	25	33	2	0	0	997.57	439	446
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	13	13	23	0.02%	18.2%	ETVLSALSR	99.7%	62.1	25	38	1	0	0	975.55	165	173
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	13	13	23	0.02%	18.2%	FYNELTEILVR	99.7%	80.6	25	70.7	3	0	0	1396.75	676	686
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	13	13	23	0.02%	18.2%	LANQAADYFGDAFK	99.7%	74.3	25	65.2	1	0	0	1530.72	216	229
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	13	13	23	0.02%	18.2%	NIQVSHQEFSK	99.4%	36.7	25	27.7	2	0	0	1316.66	628	638
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	13	13	23	0.02%	18.2%	SLLSNLDEVKK	99.7%	58.8	25	30.4	2	0	0	1245.71	554	564
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	13	13	23	0.02%	18.2%	STPVNVPISQK	99.6%	38.7	25	38.7	2	0	0	1169.65	340	350
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	13	13	23	0.02%	18.2%	SVIEQGGIQTVDQLIK	99.7%	98.5	25	90.3	3	0	0	1727.95	423	438
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	13	13	23	0.02%	18.2%	TMQGSEVVNVLK	99.7%	52.4	25	44.3	1	0	0	1320.68	542	553
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	13	13	23	0.02%	18.2%	TSEVDLAKPLVK	99.5%	37.2	25	33.1	2	0	0	1299.75	12	23
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	13	13	23	0.02%	18.2%	YYDQICSIEPK	99.7%	56.8	25	54.5	2	0	0	1415.65	71	81
Programmed cell death protein 10	PDCD10	PDC10_HUMAN	24.7	100.0%	5	5	9	0.01%	21.2%	AEKENPGLTQDIIMK	99.7%	58.7	25	53.8	1	0	0	1686.87	51	65
Programmed cell death protein 10	PDCD10	PDC10_HUMAN	24.7	100.0%	5	5	9	0.01%	21.2%	AINVFVSANR	99.7%	40.2	25	32.1	2	0	0	1090.60	187	196
Programmed cell death protein 10	PDCD10	PDC10_HUMAN	24.7	100.0%	5	5	9	0.01%	21.2%	ENPGLTQDIIMK	99.7%	40.6	25	32.8	2	0	0	1358.70	54	65
Programmed cell death protein 10	PDCD10	PDC10_HUMAN	24.7	100.0%	5	5	9	0.01%	21.2%	IPDEINDR	99.7%	44.2	25	37.6	2	0	0	971.48	117	124
Programmed cell death protein 10	PDCD10	PDC10_HUMAN	24.7	100.0%	5	5	9	0.01%	21.2%	SVEVNFTESLLR	99.7%	78.3	25	74.1	2	0	0	1393.73	71	82
Programmed cell death protein 6	PDCD6	PDCD6_HUMAN	21.9	100.0%	5	7	13	0.01%	28.3%	AGVNFSEFTGVWK	99.7%	66.8	25	56.7	2	0	0	1441.71	78	90
Programmed cell death protein 6	PDCD6	PDCD6_HUMAN	21.9	100.0%	5	7	13	0.01%	28.3%	LSDQFHDILIR	99.7%	61.1	25	53.3	2	2	0	1356.73	126	136
Programmed cell death protein 6	PDCD6	PDCD6_HUMAN	21.9	100.0%	5	7	13	0.01%	28.3%	QALSGFGYR	99.7%	76.8	25	68.3	2	0	0	998.51	117	125
Programmed cell death protein 6	PDCD6	PDCD6_HUMAN	21.9	100.0%	5	7	13	0.01%	28.3%	SIISMFDRENK	99.7%	51.2	25	50.4	3	0	0	1339.67	67	77
Programmed cell death protein 6	PDCD6	PDCD6_HUMAN	21.9	100.0%	5	7	13	0.01%	28.3%	YITDWQNVFR	99.7%	54.3	25	45.3	2	0	0	1341.66	91	100
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	13	15	68	0.07%	57.0%	AAELIANSLATAGDGLIELR	99.7%	108	25	91.4	8	2	0	1998.09	220	239
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	13	15	68	0.07%	57.0%	AAIISAEGDSK	99.7%	68.2	25	61.1	4	0	0	1061.55	209	219
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	13	15	68	0.07%	57.0%	AATFGLILDDVSLTHLTFGK	99.7%	56.1	25	56.1	1	0	0	2119.14	158	177
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	13	15	68	0.07%	57.0%	DLQNVNITLR	99.7%	73.8	25	57.8	4	0	0	1185.66	84	93
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	13	15	68	0.07%	57.0%	EFTEAVEAK	99.7%	46.2	25	38.1	4	0	0	1023.50	178	186
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	13	15	68	0.07%	57.0%	FDAGELITQR	99.7%	75	25	60.8	12	0	0	1149.59	134	143
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	13	15	68	0.07%	57.0%	IFTSIGEDYDER	99.7%	89.2	25	81.4	6	0	0	1444.66	106	117
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	13	15	68	0.07%	57.0%	ILFRPVASQLPR	99.7%	56.8	25	44.3	4	6	0	1396.84	94	105
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	13	15	68	0.07%	57.0%	KLEAAEDIAYQLSR	99.7%	131	25	129	4	0	0	1606.84	240	253
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	13	15	68	0.07%	57.0%	LEAAEDIAYQLSR	99.7%	71	25	62.2	2	0	0	1478.75	241	253
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	13	15	68	0.07%	57.0%	NITYLPAGQSVLLQLPQ	99.7%	98.9	25	95.8	3	0	0	1855.03	256	272
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	13	15	68	0.07%	57.0%	QVSDDLTER	99.7%	54.5	25	47.7	4	0	0	1062.51	149	157
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	13	15	68	0.07%	57.0%	VLPSITTEILK	99.7%	60.5	25	48	4	0	0	1213.74	118	128
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	17	25	94	0.10%	61.9%	AQFLVEK	99.6%	38.8	25	20	2	0	0	834.47	210	216
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	17	25	94	0.10%	61.9%	AQVSLLIR	99.7%	65.9	25	53.3	4	0	0	899.57	158	165
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	17	25	94	0.10%	61.9%	DLAGRLPAGPR	99.1%	34.8	25	32.7	2	0	0	1122.64	7	17
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	17	25	94	0.10%	61.9%	DLQMVNISLR	99.7%	71.4	25	47.7	8	0	0	1188.64	98	107
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	17	25	94	0.10%	61.9%	ESVFTVEGGHR	99.7%	96.5	25	84.2	2	2	0	1217.59	38	48
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	17	25	94	0.10%	61.9%	EYTAAVEAK	99.7%	49.7	25	39.8	2	0	0	981.49	192	200
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	17	25	94	0.10%	61.9%	FNASQLITQR	99.7%	83.4	25	73.4	9	0	0	1177.63	148	157
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	17	25	94	0.10%	61.9%	IGGVQQDTILAEGLHFR	99.7%	88.3	25	88.3	4	4	0	1853.99	55	71
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	17	25	94	0.10%	61.9%	IPWFQYPIIYDIR	99.7%	62.1	25	62.1	4	0	0	1723.92	72	84
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	17	25	94	0.10%	61.9%	IVQAEGEAEAAK	99.7%	99.1	25	91.4	2	0	0	1215.62	225	236
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	17	25	94	0.10%	61.9%	IYLTADNLVLNLQDESFTR	99.7%	51.6	25	51.6	2	0	0	2225.15	271	289
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	17	25	94	0.10%	61.9%	LGLDYEER	99.7%	63.7	25	50.4	9	0	0	994.48	124	131
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	17	25	94	0.10%	61.9%	LLLGAGAVAYGVR	99.7%	98.5	25	82	11	0	0	1259.75	25	37
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	17	25	94	0.10%	61.9%	MLGEALSK	99.7%	40.6	25	21.3	4	0	0	848.45	237	244
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	17	25	94	0.10%	61.9%	QKIVQAEGEAEAAK	99.7%	70.9	25	61.4	4	2	0	1471.78	223	236
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	17	25	94	0.10%	61.9%	VLPSIVNEVLK	99.7%	57	25	47.8	4	0	0	1210.74	132	142
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	17	25	94	0.10%	61.9%	VLSRPNAQELPSMYQR	99.7%	52.3	25	44.1	5	8	0	1888.97	108	123

Prolactin-inducible protein	PIP	PIP_HUMAN	16.6	100.0%	3	3	8	0.01%	26.0%	FYTIEILKVE	99.7%	42.5	25	34.1	4	0	0	1254.70	137	146
Prolactin-inducible protein	PIP	PIP_HUMAN	16.6	100.0%	3	3	8	0.01%	26.0%	TVQIAAVVDVIR	99.7%	71.2	25	61.8	3	0	0	1283.77	107	118
Prolactin-inducible protein	PIP	PIP_HUMAN	16.6	100.0%	3	3	8	0.01%	26.0%	TYLISSIPLQGAFNYK	99.3%	35.7	25	35.7	1	0	0	1814.97	70	85
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	11	15	36	0.04%	47.1%	AEDNADTLALVFEAPNQEK	99.7%	104	25	104	2	0	0	2074.99	92	110
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	11	15	36	0.04%	47.1%	ATPLSSTVTLSMSADVPLVVEYK	99.7%	60	25	60	2	1	0	2424.26	218	240
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	11	15	36	0.04%	47.1%	DLSHIGDAVVISCAK	99.7%	84	25	84	4	2	0	1584.81	150	164
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	11	15	36	0.04%	47.1%	FSASGELGNGNIK	99.7%	114	25	107	5	0	0	1293.64	169	181
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	11	15	36	0.04%	47.1%	IADMGHLK	99.7%	50.7	25	42.8	2	0	0	884.47	241	248
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	11	15	36	0.04%	47.1%	LVQGSILK	98.9%	33.9	25	14.3	2	0	0	857.55	6	13
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	11	15	36	0.04%	47.1%	LVQGSILKK	99.7%	50.1	25	17	2	0	0	985.64	6	14
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	11	15	36	0.04%	47.1%	MPSGEFAR	99.7%	41.2	25	34.3	3	0	0	894.41	139	146
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	11	15	36	0.04%	47.1%	NLAMGVNLTSMSK	99.7%	107	25	105	7	0	0	1365.69	65	77
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	11	15	36	0.04%	47.1%	SEGFDTYR	99.7%	39.3	25	33.5	3	0	0	974.42	54	61
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	11	15	36	0.04%	47.1%	VSDYEMK	95.2%	27.8	25	22.8	1	0	0	871.39	111	117
Prolyl 3-hydroxylase 1	LEPRE1	P3H1_HUMAN	83.4	100.0%	4	4	6	0.01%	6.4%	DLSFFGGLLR	99.7%	71	25	52.8	2	0	0	1124.61	106	115
Prolyl 3-hydroxylase 1	LEPRE1	P3H1_HUMAN	83.4	100.0%	4	4	6	0.01%	6.4%	LTNVAATSGDGYR	99.7%	83.5	25	82.3	2	0	0	1324.65	489	501
Prolyl 3-hydroxylase 1	LEPRE1	P3H1_HUMAN	83.4	100.0%	4	4	6	0.01%	6.4%	SPYNYLQVAYFK	99.7%	75.7	25	63.3	1	0	0	1492.75	144	155
Prolyl 3-hydroxylase 1	LEPRE1	P3H1_HUMAN	83.4	100.0%	4	4	6	0.01%	6.4%	TVTAEVQPQCGR	99.7%	48.3	25	40.4	1	0	0	1345.65	636	647
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	7	7	13	0.01%	16.3%	DPEGFVGHPVNAFK	99.7%	65.3	25	58.9	2	0	0	1513.74	73	86
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	7	7	13	0.01%	16.3%	GVAVDYLPER	99.7%	61.7	25	50.3	2	0	0	1118.58	277	286
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	7	7	13	0.01%	16.3%	HAACPVLVGNK	99.7%	57.3	25	45	2	0	0	1165.61	500	510
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	7	7	13	0.01%	16.3%	LLELDPEHQR	99.5%	37.1	25	37.1	2	0	0	1249.65	231	240
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	7	7	13	0.01%	16.3%	LQDTYNLDTDTISK	99.7%	102	25	94.7	2	0	0	1626.79	137	150
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	7	7	13	0.01%	16.3%	QYFPNDEDQVGAAK	99.5%	37.1	25	34.6	1	0	0	1581.72	119	132
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	7	7	13	0.01%	16.3%	SAWLSGYENPVVSR	99.7%	78.9	25	74.7	2	0	0	1564.78	383	396
Proteasomal ATPase-associated factor 1	PAAF1	PAAF1_HUMAN	42.2	99.8%	2	2	5	0.01%	5.9%	GGILDTAIVDR	95.8%	28.4	25	28.2	1	0	0	1129.62	177	187
Proteasomal ATPase-associated factor 1	PAAF1	PAAF1_HUMAN	42.2	99.8%	2	2	5	0.01%	5.9%	SGAPVLSLLSVR	99.7%	74.6	25	71.1	4	0	0	1198.72	321	332
Proteasome activator complex subunit 3	PSME3	PSME3_HUMAN	29.5	100.0%	5	5	8	0.01%	24.0%	ITSEAEDLVANFFPK	99.7%	62.2	25	53.7	2	0	0	1680.85	22	36
Proteasome activator complex subunit 3	PSME3	PSME3_HUMAN	29.5	100.0%	5	5	8	0.01%	24.0%	MWVQLLIPR	98.1%	31.4	25	13	1	0	0	1171.67	138	146
Proteasome activator complex subunit 3	PSME3	PSME3_HUMAN	29.5	100.0%	5	5	8	0.01%	24.0%	NQYVTLHDMILK	99.1%	34.6	25	34.6	1	0	0	1490.77	226	237
Proteasome activator complex subunit 3	PSME3	PSME3_HUMAN	29.5	100.0%	5	5	8	0.01%	24.0%	SNQQLVDIIEK	99.7%	69.7	25	62.4	2	0	0	1286.70	111	121
Proteasome activator complex subunit 3	PSME3	PSME3_HUMAN	29.5	100.0%	5	5	8	0.01%	24.0%	TVTEIDEKEYISLR	99.7%	51.2	25	51.2	2	0	0	1695.88	205	218
Proteasome assembly chaperone 3	PSMG3	PSMG3_HUMAN	13.1	99.8%	2	2	4	0.00%	18.0%	AVLLAVAVK	99.7%	45.1	25	30.4	2	0	0	883.60	94	102
Proteasome assembly chaperone 3	PSMG3	PSMG3_HUMAN	13.1	99.8%	2	2	4	0.00%	18.0%	NLVAFVSQEAGNR	99.7%	85.4	25	64.5	2	0	0	1404.72	81	93
Proteasome subunit alpha type-1	PSMA1	PSA1_HUMAN	29.6	99.8%	2	2	2	0.00%	10.6%	AQPAQPADEPAEK	99.4%	36.2	25	36.2	1	0	0	1351.65	244	256
Proteasome subunit alpha type-1	PSMA1	PSA1_HUMAN	29.6	99.8%	2	2	2	0.00%	10.6%	NQYDNDVTVWSPQGR	99.5%	37.2	25	37.2	1	0	0	1778.81	4	18
Proteasome subunit alpha type-3	PSMA3	PSA3_HUMAN	28.4	100.0%	3	3	6	0.01%	11.8%	CKDGVVFGVEK	97.9%	31.1	25	21.3	1	0	0	1237.62	42	52
Proteasome subunit alpha type-3	PSMA3	PSA3_HUMAN	28.4	100.0%	3	3	6	0.01%	11.8%	SNFGYNIPLK	99.7%	40.8	25	37.1	3	0	0	1152.60	101	110
Proteasome subunit alpha type-3	PSMA3	PSA3_HUMAN	28.4	100.0%	3	3	6	0.01%	11.8%	VFQVEYAMK	99.7%	53.4	25	49.1	2	0	0	1114.56	21	29
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	8	10	23	0.02%	35.2%	ATCIGNNSAAAVSMLK	99.7%	103	25	98.1	8	0	0	1623.78	161	176
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	8	10	23	0.02%	35.2%	LLDEVFFSEK	99.7%	62.7	25	51.8	4	0	0	1226.63	55	64
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	8	10	23	0.02%	35.2%	LNEDMACSVAGITSDANVLTNELR	99.7%	72.8	25	72.8	1	0	0	2593.22	68	91
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	8	10	23	0.02%	35.2%	LSAEKVEIATLTR	99.7%	102	25	92.4	2	2	0	1430.82	206	218
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	8	10	23	0.02%	35.2%	QAYTQFGGK	99.4%	36.9	25	28	1	0	0	999.49	119	127
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	8	10	23	0.02%	35.2%	QDYKEGEMTLK	99.7%	48.7	25	44.8	1	0	0	1341.64	177	187
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	8	10	23	0.02%	35.2%	TTIFSPEGR	99.7%	46.2	25	36.9	2	0	0	1007.52	9	17
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	8	10	23	0.02%	35.2%	VEIATLTR	99.7%	72.2	25	51.4	2	0	0	902.53	211	218
Proteasome subunit alpha type-5	PSMA5	PSA5_HUMAN	26.4	100.0%	4	6	12	0.01%	22.4%	AIGSASEGAQSSLQEVYHK	99.7%	109	25	109	2	2	0	1961.96	169	187
Proteasome subunit alpha type-5	PSMA5	PSA5_HUMAN	26.4	100.0%	4	6	12	0.01%	22.4%	GVNTFSPEGR	98.7%	33.1	25	17.4	2	0	0	1063.52	11	20
Proteasome subunit alpha type-5	PSMA5	PSA5_HUMAN	26.4	100.0%	4	6	12	0.01%	22.4%	ITSPLMEPSSIEK	99.7%	64.2	25	62	4	0	0	1431.74	54	66
Proteasome subunit alpha type-5	PSMA5	PSA5_HUMAN	26.4	100.0%	4	6	12	0.01%	22.4%	LFQVEYAIEAIK	99.7%	77.3	25	66.1	2	0	0	1423.78	21	32

Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	4	5	10	0.01%	19.4%	ALLEVVQSGGK	99.7%	73.2	25	62	2	0	0	1100.63	194	204
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	4	5	10	0.01%	19.4%	LTVEDPVTVEYITR	99.7%	99.6	25	91.5	2	0	0	1634.86	96	109
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	4	5	10	0.01%	19.4%	NIELAVMR	99.7%	52	25	41.2	4	0	0	961.51	205	212
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	4	5	10	0.01%	19.4%	NYTDEAIETDDLTIK	99.7%	101	25	95.1	2	0	0	1740.82	175	189
Proteasome subunit beta type-2	PSMB2	PSB2_HUMAN	22.8	99.9%	2	2	3	0.00%	12.9%	FILNLPTFSVR	99.7%	47.9	25	37.9	2	0	0	1306.75	171	181
Proteasome subunit beta type-2	PSMB2	PSB2_HUMAN	22.8	99.9%	2	2	3	0.00%	12.9%	NGYELSPTAAANFTR	99.7%	54.2	25	54.2	1	0	0	1611.78	71	85
Proteasome subunit beta type-5	PSMB5	PSB5_HUMAN	28.5	100.0%	4	4	7	0.01%	18.6%	ATAGAYIASQTVK	99.7%	76.2	25	69.6	2	0	0	1280.68	79	91
Proteasome subunit beta type-5	PSMB5	PSB5_HUMAN	28.5	100.0%	4	4	7	0.01%	18.6%	DAYSGGAVNLYHVR	99.7%	55.7	25	55.7	2	0	0	1521.74	226	239
Proteasome subunit beta type-5	PSMB5	PSB5_HUMAN	28.5	100.0%	4	4	7	0.01%	18.6%	LLANMVYQYK	99.7%	50.2	25	49.8	2	0	0	1242.66	141	150
Proteasome subunit beta type-5	PSMB5	PSB5_HUMAN	28.5	100.0%	4	4	7	0.01%	18.6%	VSSDNVADLHEK	99.7%	50.8	25	47.6	1	0	0	1313.63	246	257
Proteasome subunit beta type-6	PSMB6	PSB6_HUMAN	25.4	100.0%	3	3	6	0.01%	13.0%	LAAIAESGVER	99.7%	95	25	82.3	2	0	0	1115.61	210	220
Proteasome subunit beta type-6	PSMB6	PSB6_HUMAN	25.4	100.0%	3	3	6	0.01%	13.0%	QVLLGDQIPK	99.7%	50.3	25	42.6	2	0	0	1110.65	221	230
Proteasome subunit beta type-6	PSMB6	PSB6_HUMAN	25.4	100.0%	3	3	6	0.01%	13.0%	TTTGSYIANR	99.7%	59.2	25	58.1	2	0	0	1083.54	54	63
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	38	0.04%	11.5%	AGEQLAPFLPQLVPR	99.7%	48.7	25	46.5	3	0	0	1635.92	1112	1126
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	38	0.04%	11.5%	AIACVVTACSAELEK	99.7%	100	25	96.4	2	0	0	1621.79	1591	1605
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	38	0.04%	11.5%	AQGAIAMASIAK	99.7%	48	25	42	2	0	0	1131.62	1545	1556
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	38	0.04%	11.5%	EGAVLKPELK	98.2%	31.9	25	21.1	1	0	0	1083.64	316	325
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	38	0.04%	11.5%	FQEFSNIVIPLIK	99.7%	47.3	25	46.7	3	0	0	1547.88	1651	1663
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	38	0.04%	11.5%	HSVATAADLELK	99.7%	46.3	25	43.4	1	0	0	1254.67	274	285
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	38	0.04%	11.5%	IVAISCAADILK	99.7%	70.7	25	63.1	2	0	0	1273.72	1633	1644
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	38	0.04%	11.5%	LLSMAYSAVGK	99.7%	73.8	25	64	3	0	0	1139.61	415	425
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	38	0.04%	11.5%	LMSALLSGLTDR	99.7%	89.9	25	77.4	2	0	0	1276.69	1401	1412
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	38	0.04%	11.5%	LSSTQEGVR	99.7%	43.7	25	22.4	2	0	0	976.51	47	55
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	38	0.04%	11.5%	MSEQQDLER	99.7%	39.3	25	33.4	1	0	0	1151.50	771	779
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	38	0.04%	11.5%	SASPFNLAEKPK	99.5%	37.1	25	29.6	1	0	0	1288.69	157	168
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	38	0.04%	11.5%	TEALSVIELLLK	99.7%	81.1	25	72.5	4	0	0	1328.80	1785	1796
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	38	0.04%	11.5%	TIAALLPCLLDK	99.7%	48.2	25	34.1	3	0	0	1327.77	1250	1261
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	38	0.04%	11.5%	TLMSSGQMAPSSSNK	99.7%	64.6	25	64.6	2	0	0	1557.69	632	646
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	38	0.04%	11.5%	TPDGQGLSTYK	99.7%	48.2	25	40.8	2	0	0	1166.57	1057	1067
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	38	0.04%	11.5%	VYLGDIPLK	97.6%	30.5	25	25.8	2	0	0	1017.60	305	313
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	18	19	38	0.04%	11.5%	YLLLLAAGDPR	99.7%	72.6	25	69.4	2	0	0	1201.69	517	527
Protein AAR2 homolog	AAR2	AAR2_HUMAN	43.5	99.8%	2	2	2	0.00%	7.8%	QICAFSDVLPVLSMK	99.7%	44	25	30.3	1	0	0	1723.88	154	168
Protein AAR2 homolog	AAR2	AAR2_HUMAN	43.5	99.8%	2	2	2	0.00%	7.8%	WISLTNFISEATVEK	99.1%	34.6	25	34.6	1	0	0	1737.91	133	147
Protein arginine N-methyltransferase 1	PRMT1	ANM1_HUMAN	41.5	100.0%	4	4	6	0.01%	13.3%	ATLYVTAIEDR	99.7%	63	25	59.3	1	0	0	1251.66	186	196
Protein arginine N-methyltransferase 1	PRMT1	ANM1_HUMAN	41.5	100.0%	4	4	6	0.01%	13.3%	GKVEEVELPVEK	99.7%	58.2	25	53.7	2	0	0	1355.74	134	145
Protein arginine N-methyltransferase 1	PRMT1	ANM1_HUMAN	41.5	100.0%	4	4	6	0.01%	13.3%	QLVTNACLIK	97.9%	31	25	20.1	1	0	0	1159.65	234	243
Protein arginine N-methyltransferase 1	PRMT1	ANM1_HUMAN	41.5	100.0%	4	4	6	0.01%	13.3%	VEDLTFTSPFCLQVK	99.7%	53	25	53	2	0	0	1783.89	252	266
Protein arginine N-methyltransferase 3	PRMT3	ANM3_HUMAN	59.9	100.0%	3	3	4	0.00%	6.6%	AVIPEAVVEVLDPK	99.7%	58.7	25	58.7	2	0	0	1478.85	397	410
Protein arginine N-methyltransferase 3	PRMT3	ANM3_HUMAN	59.9	100.0%	3	3	4	0.00%	6.6%	TLISEPCGIK	99.6%	38.9	25	18.8	1	0	0	1117.59	411	420
Protein arginine N-methyltransferase 3	PRMT3	ANM3_HUMAN	59.9	100.0%	3	3	4	0.00%	6.6%	VVFSTGPQSTK	99.3%	35.9	25	35.1	1	0	0	1150.61	467	477
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	AAILPTSIFLTNK	99.7%	108	25	108	35	0	0	1388.81	228	240
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	AAILPTSIFLTNKK	99.7%	71.1	25	69.8	6	3	0	1516.91	228	241
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	ADIIVSELLGSFADNELSPECLDGAQHFLK	99.7%	117	25	109	0	2	0	3288.61	429	458
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	DDGVSIPGEYTSFLAPISSSK	99.7%	83.4	25	83.4	16	0	0	2170.06	459	479
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	DDIIENAPTTHTEEYSGEEK	99.7%	86.4	25	86.4	4	4	0	2278.00	165	184
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	DLNCVPEIADTLGAVAK	99.7%	104	25	101	33	2	0	1785.91	19	35
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	DPEAQFEMPYVVR	99.7%	74.3	25	74.3	6	0	0	1580.74	493	505
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	DPIKYSQYQQAIYK	99.7%	69.6	25	62.7	2	2	0	1744.89	330	343
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	DPMIDNNR	99.7%	41.8	25	33.4	9	0	0	974.44	527	534
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	DRDPEAQFEMPYVVR	99.7%	54.4	25	52.2	4	8	0	1851.87	491	505
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	DTNVQVLMVLGAGR	99.7%	103	25	88.5	6	0	0	1488.78	355	368

Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	DWNTLIVGK	99.7%	65.3	25	49.7	15	0	0	1045.57	77	85
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	EFCSYLQYLEYLSQNRPPPNAYELFAK	99.7%	43.3	25	43.3	0	3	0	3340.60	276	302
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	EFIQEPAK	99.7%	48	25	24.2	20	0	0	961.50	53	60
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	EGQTICVR	99.7%	44.1	25	36.7	14	0	0	962.47	594	601
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	EWVAPEK	95.8%	28.3	25	18.8	1	0	0	858.44	422	428
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	GPLVNASLR	99.7%	68.4	25	59.1	11	0	0	926.54	369	377
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	GYEDYLQSPLQPLMDNLESQTYEVFEKDPIK	99.7%	88.1	25	87.3	0	8	0	3705.75	303	333
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	IAVALEIGADLPSNHVIDR	99.7%	112	25	112	6	10	0	2003.09	202	220
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	IKLYAVEK	99.7%	44.5	25	23.1	7	0	0	963.59	386	393
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	KGFPVLSK	99.7%	49.2	25	25.2	14	0	0	875.54	241	248
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	KVWYEWAVTAPVCSAIHNPTGR	99.7%	79.5	25	79.5	0	2	0	2542.27	610	631
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	LEVQFIITGTNHHSEK	99.7%	34.1	25	34.1	0	2	0	1852.96	260	275
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	LHNFHQLSAPQPCFTFSHPNR	99.7%	79.2	25	67.6	0	2	0	2535.21	506	526
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	LSPWIRPDSK	99.1%	34.7	25	27.2	2	0	0	1198.66	86	95
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	QGFDFLCMPVFHPR	99.7%	63.4	25	60.2	12	23	0	1750.82	36	49
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	REFIQEPAK	99.7%	42.9	25	30.8	2	0	0	1117.60	52	60
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	RIAVALEIGADLPSNHVIDR	99.7%	52	25	52	0	1	0	2159.19	201	220
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	SDLLLSGR	99.7%	66.5	25	51.9	7	0	0	860.48	69	76
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	SDLLLSGRDWNTLIVGK	99.7%	83.2	25	83.2	8	7	0	1887.03	69	85
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	TLCDYSK	99.2%	35.5	25	35.5	1	0	0	886.40	194	200
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	TLCDYSKR	99.7%	55.2	25	41	3	0	0	1042.50	194	201
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	TWMWWHNFR	99.7%	43.7	25	35.1	11	3	0	1363.62	185	193
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	VPEEEKDTNVQVLMVLGAGR	99.7%	116	25	116	4	11	0	2184.13	349	368
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	VPLVAPEDLR	99.7%	57.7	25	52.3	15	0	0	1108.64	155	164
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	VPLVAPEDLRDDIIENAPTTHTEEYSGEEK	99.7%	86.2	25	86.2	0	3	0	3367.62	155	184
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	VWYEWAVTAPVCSAIHNPTGR	99.7%	75.3	25	75.3	2	2	0	2414.17	611	631
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	WLGEPIK	98.8%	33.5	25	23.5	4	0	0	842.48	221	227
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	39	61	402	0.42%	65.0%	YSQYQQAIYK	99.7%	66.1	25	66.1	24	0	0	1291.63	334	343
Protein CIP2A	KIAA1524	CIP2A_HUMAN	102.2	100.0%	3	3	6	0.01%	3.7%	ALALAQADR	99.7%	55.5	25	43.2	2	0	0	928.52	648	656
Protein CIP2A	KIAA1524	CIP2A_HUMAN	102.2	100.0%	3	3	6	0.01%	3.7%	LITPLAFALTSDNR	99.7%	93.7	25	93.7	2	0	0	1531.85	509	522
Protein CIP2A	KIAA1524	CIP2A_HUMAN	102.2	100.0%	3	3	6	0.01%	3.7%	SLLLTVSQYK	99.7%	58.1	25	56.8	2	0	0	1151.67	9	18
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	4	5	10	0.01%	12.0%	LLASANLEEVTMK	99.7%	72.2	25	66.8	4	0	0	1418.76	332	344
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	4	5	10	0.01%	12.0%	NVGQFSGFPFEK	99.7%	54.7	25	54.7	2	0	0	1356.66	126	137
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	4	5	10	0.01%	12.0%	SGVNSELVKR	99.6%	39	25	27.3	2	0	0	1088.61	169	178
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	4	5	10	0.01%	12.0%	SICEVLDLER	99.7%	71.7	25	58.9	2	0	0	1233.61	159	168
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	4	4	9	0.01%	4.3%	ELGEYFLFDPK	99.7%	49.2	25	39.6	4	0	0	1357.67	1117	1127
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	4	4	9	0.01%	4.3%	LLSALCILPQPEDMNER	99.7%	39.3	25	39.3	1	0	0	1999.00	262	278
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	4	4	9	0.01%	4.3%	NAGAFGFNISFLCK	99.7%	43.9	25	43.9	1	0	0	1545.75	993	1006
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	4	4	9	0.01%	4.3%	TAQNLSIFLGSFR	99.7%	72.1	25	72.1	3	0	0	1453.78	856	868
Protein diaphanous homolog 3	DIAPH3	DIAP3_HUMAN	136.9	100.0%	3	3	5	0.01%	2.8%	FFCIVEGLR	99.7%	49.1	25	43.1	1	0	0	1140.59	323	331
Protein diaphanous homolog 3	DIAPH3	DIAP3_HUMAN	136.9	100.0%	3	3	5	0.01%	2.8%	IAQNLSIFLSSFR	99.7%	84.4	25	84.4	2	0	0	1495.83	719	731
Protein diaphanous homolog 3	DIAPH3	DIAP3_HUMAN	136.9	100.0%	3	3	5	0.01%	2.8%	LAESMIQNLIK	99.7%	60.7	25	53.8	2	0	0	1259.70	749	759
Protein disulfide-isomerase A6	PDIA6	PDIA6_HUMAN	48.1	99.8%	2	2	3	0.00%	6.1%	GSFSEQGINEFLR	99.7%	59.1	25	44.5	1	0	0	1483.72	374	386
Protein disulfide-isomerase A6	PDIA6	PDIA6_HUMAN	48.1	99.8%	2	2	3	0.00%	6.1%	TGEAIVDAALSALR	99.7%	101	25	87.8	2	0	0	1386.76	119	132
Protein DJ-1	PARK7	PARK7_HUMAN	19.9	100.0%	3	5	9	0.01%	30.2%	EGPYDVVVLPGGNLGAQNLSESAAVK	99.7%	51.6	25	51.6	0	2	0	2584.33	64	89
Protein DJ-1	PARK7	PARK7_HUMAN	19.9	100.0%	3	5	9	0.01%	30.2%	GAEEMETVIPVDVMR	99.7%	53.4	25	48.2	3	0	0	1675.80	13	27
Protein DJ-1	PARK7	PARK7_HUMAN	19.9	100.0%	3	5	9	0.01%	30.2%	VTVAGLAGKDPVQCSR	99.7%	65.9	25	65.9	2	2	0	1657.87	33	48
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	8	8	16	0.02%	7.6%	ADLTALFLPR	99.7%	77.2	25	67.4	4	0	0	1116.64	875	884
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	8	8	16	0.02%	7.6%	AVQGAQQPSLYQIR	99.7%	58.7	25	54.8	2	0	0	1558.83	1047	1060
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	8	8	16	0.02%	7.6%	GAQATLSSTTK	99.7%	63	25	52.4	2	0	0	1064.56	661	671
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	8	8	16	0.02%	7.6%	KFESLFPGK	99.7%	41.4	25	40.4	1	0	0	1052.58	1007	1015

Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	8	8	16	0.02%	7.6%	LLQSLLDTR	99.7%	49.5	25	40.6	3	0	0	1058.62	765	773
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	8	8	16	0.02%	7.6%	TGLCYLPEELAALQK	99.1%	34.6	25	27.4	1	0	0	1705.88	43	57
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	8	8	16	0.02%	7.6%	VGLGLGYLELPQINYK	99.7%	67.3	25	67.3	2	0	0	1776.99	731	746
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	8	8	16	0.02%	7.6%	VPECLYTLPSLR	99.7%	51.4	25	48.3	1	0	0	1447.76	238	249
Protein FRG1	FRG1	FRG1_HUMAN	29.2	99.8%	2	2	2	0.00%	11.2%	EVDEGPSPPEQFTAVK	99.4%	36.9	25	36.9	1	0	0	1729.83	86	101
Protein FRG1	FRG1	FRG1_HUMAN	29.2	99.8%	2	2	2	0.00%	11.2%	YLGINSDGLVVGR	99.7%	82.1	25	67.6	1	0	0	1362.74	116	128
Protein jagunal homolog 1	JAGN1	JAGN1_HUMAN	21.1	100.0%	4	4	8	0.01%	17.5%	AAGTDGSDFQHR	99.7%	60.2	25	49.8	2	0	0	1261.56	9	20
Protein jagunal homolog 1	JAGN1	JAGN1_HUMAN	21.1	100.0%	4	4	8	0.01%	17.5%	LLDSWFTSTQEK	99.7%	90.6	25	90.6	2	0	0	1454.72	169	180
Protein jagunal homolog 1	JAGN1	JAGN1_HUMAN	21.1	100.0%	4	4	8	0.01%	17.5%	LLDSWFTSTQEKK	99.7%	42.2	25	37.2	2	0	0	1582.81	169	181
Protein jagunal homolog 1	JAGN1	JAGN1_HUMAN	21.1	100.0%	4	4	8	0.01%	17.5%	MSVGHLR	97.8%	30.8	25	20.6	2	0	0	799.42	55	61
Protein KRI1 homolog	KRI1	KRI1_HUMAN	82.6	100.0%	4	4	4	0.00%	7.8%	AFVEDSEDEDGAGEGGSSLLQK	98.2%	31.8	25	8.18	1	0	0	2239.98	166	187
Protein KRI1 homolog	KRI1	KRI1_HUMAN	82.6	100.0%	4	4	4	0.00%	7.8%	FEEPDSASVK	95.3%	27.9	25	22.5	1	0	0	1108.52	302	311
Protein KRI1 homolog	KRI1	KRI1_HUMAN	82.6	100.0%	4	4	4	0.00%	7.8%	LQAFGLNPK	95.5%	28	25	8.59	1	0	0	987.56	674	682
Protein KRI1 homolog	KRI1	KRI1_HUMAN	82.6	100.0%	4	4	4	0.00%	7.8%	LQETSSQSYVEEQK	99.7%	79.4	25	73.3	1	0	0	1655.78	145	158
Protein MON2 homolog	MON2	MON2_HUMAN	190.5	100.0%	3	3	4	0.00%	1.8%	LQLLLLNPLK	99.7%	42.4	25	42.4	2	0	0	1164.77	862	871
Protein MON2 homolog	MON2	MON2_HUMAN	190.5	100.0%	3	3	4	0.00%	1.8%	VLSIGLPVAR	99.7%	51.4	25	50.2	1	0	0	1024.65	1470	1479
Protein MON2 homolog	MON2	MON2_HUMAN	190.5	100.0%	3	3	4	0.00%	1.8%	YLLQPLGDFSR	96.3%	28.8	25	27.7	1	0	0	1308.69	1132	1142
Protein NipSnap homolog 1	NIPSNAP1	NIPS1_HUMAN	33.3	100.0%	3	4	7	0.01%	13.0%	FSGGYPALMDCMNK	99.6%	38.8	25	38.8	2	0	0	1590.68	128	141
Protein NipSnap homolog 1	NIPSNAP1	NIPS1_HUMAN	33.3	100.0%	3	4	7	0.01%	13.0%	GWDENVYYTVPLVR	99.7%	60.6	25	58.6	1	0	0	1710.85	255	268
Protein NipSnap homolog 1	NIPSNAP1	NIPS1_HUMAN	33.3	100.0%	3	4	7	0.01%	13.0%	MGPNIYELR	99.7%	72.8	25	57.8	4	0	0	1092.55	180	188
Protein NipSnap homolog 2	GBAS	NIPS2_HUMAN	33.7	100.0%	3	4	8	0.01%	10.8%	ICQEVLPK	99.4%	36.8	25	17.7	2	0	0	986.53	92	99
Protein NipSnap homolog 2	GBAS	NIPS2_HUMAN	33.7	100.0%	3	4	8	0.01%	10.8%	SGPNIYELR	99.7%	70.2	25	63.4	2	0	0	1048.54	182	190
Protein NipSnap homolog 2	GBAS	NIPS2_HUMAN	33.7	100.0%	3	4	8	0.01%	10.8%	YEGGYPALTEVMNK	99.7%	46.9	25	46.9	4	0	0	1587.74	130	143
Protein Njmu-R1	C17orf75	NJMU_HUMAN	44.6	99.8%	2	2	4	0.00%	4.8%	GGNPFLFR	99.7%	46.8	25	23.7	2	0	0	907.48	309	316
Protein Njmu-R1	C17orf75	NJMU_HUMAN	44.6	99.8%	2	2	4	0.00%	4.8%	NVIAVLEEFMK	99.7%	70.5	25	67.3	2	0	0	1292.69	379	389
Protein odr-4 homolog	ODR4	ODR4_HUMAN	51.1	100.0%	5	5	8	0.01%	13.7%	AFVSGLLIGQCSSQK	99.7%	50.9	25	46.3	2	0	0	1594.83	24	38
Protein odr-4 homolog	ODR4	ODR4_HUMAN	51.1	100.0%	5	5	8	0.01%	13.7%	DYVILATR	99.7%	44.6	25	36.6	2	0	0	950.53	39	46
Protein odr-4 homolog	ODR4	ODR4_HUMAN	51.1	100.0%	5	5	8	0.01%	13.7%	STATVQICSGSVNLK	99.7%	96	25	86.6	1	0	0	1564.80	268	282
Protein odr-4 homolog	ODR4	ODR4_HUMAN	51.1	100.0%	5	5	8	0.01%	13.7%	TPPKEEQSENLK	99.1%	34.9	25	28.6	1	0	0	1399.71	47	58
Protein odr-4 homolog	ODR4	ODR4_HUMAN	51.1	100.0%	5	5	8	0.01%	13.7%	VLTQLLLNSDHR	99.7%	61.9	25	53.3	2	0	0	1408.79	256	267
Protein pelota homolog	PELO	PELO_HUMAN	43.4	100.0%	3	3	5	0.01%	9.1%	FYEQVVQAIQR	99.7%	70.3	25	58.6	2	0	0	1380.73	185	195
Protein pelota homolog	PELO	PELO_HUMAN	43.4	100.0%	3	3	5	0.01%	9.1%	KQWDSVVLER	99.7%	41.5	25	34.7	1	0	0	1259.67	115	124
Protein pelota homolog	PELO	PELO_HUMAN	43.4	100.0%	3	3	5	0.01%	9.1%	VQTESSTGSVGSNR	99.7%	61.1	25	57.7	2	0	0	1408.67	47	60
Protein phosphatase 1B	PPM1B	PPM1B_HUMAN	52.6	100.0%	6	7	12	0.01%	15.2%	DNMSIVLVCFSNAPK	99.7%	47.3	25	42.5	1	0	0	1710.82	286	300
Protein phosphatase 1B	PPM1B	PPM1B_HUMAN	52.6	100.0%	6	7	12	0.01%	15.2%	HIYFINCGDSR	99.7%	54.8	25	54.8	1	0	0	1381.63	143	153
Protein phosphatase 1B	PPM1B	PPM1B_HUMAN	52.6	100.0%	6	7	12	0.01%	15.2%	IQNAGGSVMIQR	99.7%	72.9	25	63.8	1	0	0	1273.67	180	191
Protein phosphatase 1B	PPM1B	PPM1B_HUMAN	52.6	100.0%	6	7	12	0.01%	15.2%	NVIEAVYSR	99.7%	47.2	25	43	4	0	0	1050.56	361	369
Protein phosphatase 1B	PPM1B	PPM1B_HUMAN	52.6	100.0%	6	7	12	0.01%	15.2%	SGSALELSVENVK	99.7%	82	25	72.1	2	0	0	1332.70	91	103
Protein phosphatase 1B	PPM1B	PPM1B_HUMAN	52.6	100.0%	6	7	12	0.01%	15.2%	SGSTAVGVMISPK	99.7%	54.7	25	51.1	3	0	0	1249.65	130	142
Protein QIL1	QIL1	QIL1_HUMAN	13.1	99.8%	2	2	2	0.00%	9.3%	EGWEYVK	96.5%	29	25	21.7	1	0	0	910.43	108	114
Protein QIL1	QIL1	QIL1_HUMAN	13.1	99.8%	2	2	2	0.00%	9.3%	EYSKEGWEYVK	96.7%	29.2	25	26.3	1	0	0	1417.66	104	114
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	9	9	18	0.02%	5.6%	AINIGQLVDVK	99.7%	77.8	25	64.1	2	0	0	1169.69	632	642
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	9	9	18	0.02%	5.6%	FAQLEFQLGDAER	99.7%	90.3	25	84.3	2	0	0	1523.75	1767	1779
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	9	9	18	0.02%	5.6%	IPLLLTSLSFK	99.7%	50.5	25	50.5	4	0	0	1231.77	1178	1188
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	9	9	18	0.02%	5.6%	LGPSVVGLAR	99.7%	83.1	25	75.7	2	0	0	968.59	1343	1352
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	9	9	18	0.02%	5.6%	LKDGVLAYAR	98.1%	31.5	25	23.9	2	0	0	1105.64	386	395
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	9	9	18	0.02%	5.6%	TSIIEAQYLR	99.7%	57.1	25	48.2	2	0	0	1193.65	437	446
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	9	9	18	0.02%	5.6%	TTEPGVTGLLLAVEGPAAK	99.7%	89.7	25	89.7	2	0	0	1824.01	982	1000
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	9	9	18	0.02%	5.6%	VLCLSQSEGR	97.1%	29.8	25	23.9	1	0	0	1148.57	692	701
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	9	9	18	0.02%	5.6%	WLEVEIAPDIR	99.2%	35.5	25	22.3	1	0	0	1340.72	1165	1175
Protein S100-A8	S100A8	S10A8_HUMAN	10.8	99.8%	2	2	7	0.01%	23.7%	ALNSIIDVYHK	99.7%	50.5	25	47	3	0	0	1272.69	8	18

Protein S100-A8	S100A8	S10A8_HUMAN	10.8	99.8%	2	2	7	0.01%	23.7%	LLETECPQYIR	99.7%	56.9	25	47.9	4	0	0	1421.71	37	47
Protein SAAL1	SAAL1	SAAL1_HUMAN	53.6	100.0%	3	4	6	0.01%	7.6%	KPENSAESNTEETKR	99.7%	51.8	25	51.8	0	2	0	1719.81	369	383
Protein SAAL1	SAAL1	SAAL1_HUMAN	53.6	100.0%	3	4	6	0.01%	7.6%	VDLPLIDSLIR	99.7%	52.7	25	48.4	1	0	0	1253.75	348	358
Protein SAAL1	SAAL1	SAAL1_HUMAN	53.6	100.0%	3	4	6	0.01%	7.6%	VLQNMEQCQK	99.7%	64.2	25	56.8	3	0	0	1277.60	359	368
Protein SCO2 homolog, mitochondrial	SCO2	SCO2_HUMAN	29.8	99.8%	2	2	4	0.00%	10.5%	QGPAETGGQGQPQGPGLR	99.7%	40	25	40	2	0	0	1734.85	41	58
Protein SCO2 homolog, mitochondrial	SCO2	SCO2_HUMAN	29.8	99.8%	2	2	4	0.00%	10.5%	SAEQISDSVR	99.7%	50	25	33.4	2	0	0	1091.53	246	255
Protein SEC13 homolog	SEC13	SEC13_HUMAN	35.5	100.0%	4	4	5	0.01%	19.3%	DVAWAPSIGLPTSTIASCSQDGR	99.7%	66.2	25	66.2	1	0	0	2389.15	217	239
Protein SEC13 homolog	SEC13	SEC13_HUMAN	35.5	100.0%	4	4	5	0.01%	19.3%	FASGGCDNLIK	99.7%	49.9	25	39.1	1	0	0	1181.56	182	192
Protein SEC13 homolog	SEC13	SEC13_HUMAN	35.5	100.0%	4	4	5	0.01%	19.3%	GQGSVSASVTEGQQNEQ	96.3%	28.9	25	28.9	1	0	0	1705.76	306	322
Protein SEC13 homolog	SEC13	SEC13_HUMAN	35.5	100.0%	4	4	5	0.01%	19.3%	NGGQILIADLR	99.7%	59.8	25	56	2	0	0	1169.66	44	54
Protein SET	SET	SET_HUMAN	33.5	100.0%	4	4	7	0.01%	15.5%	EFHLNESGDPSSK	99.7%	48	25	41.3	2	0	0	1446.65	155	167
Protein SET	SET	SET_HUMAN	33.5	100.0%	4	4	7	0.01%	15.5%	IDFYFDENPYFENK	99.7%	79.9	25	79.9	2	0	0	1840.81	137	150
Protein SET	SET	SET_HUMAN	33.5	100.0%	4	4	7	0.01%	15.5%	LRQPFFQK	98.0%	31.2	25	22.7	1	0	0	1063.60	76	83
Protein SET	SET	SET_HUMAN	33.5	100.0%	4	4	7	0.01%	15.5%	VEVTEFEDIK	99.7%	65.6	25	60	2	0	0	1208.60	123	132
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	5	6	11	0.01%	8.7%	DVLLDVAYAYGK	99.7%	93.2	25	93.2	2	0	0	1326.69	293	304
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	5	6	11	0.01%	8.7%	ELQSVEQEVR	99.7%	64.5	25	51.1	1	0	0	1216.62	164	173
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	5	6	11	0.01%	8.7%	LLGSLYALGIPK	99.7%	74.7	25	72.1	2	0	0	1244.76	149	160
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	5	6	11	0.01%	8.7%	LSFHQTQVSQR	99.7%	52.3	25	41.5	2	0	0	1330.69	305	315
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	5	6	11	0.01%	8.7%	VLVMLAAQSR	99.7%	83	25	69.5	4	0	0	1103.62	261	270
Protein THEM6	THEM6	THEM6_HUMAN	23.9	100.0%	3	3	3	0.00%	13.9%	DGFVCALLR	99.5%	37.7	25	9.73	1	0	0	1050.54	142	150
Protein THEM6	THEM6	THEM6_HUMAN	23.9	100.0%	3	3	3	0.00%	13.9%	LLEPFEVR	99.2%	35.5	25	18.9	1	0	0	1002.56	113	120
Protein THEM6	THEM6	THEM6_HUMAN	23.9	100.0%	3	3	3	0.00%	13.9%	MESGLSDVTKDQ	99.5%	37.5	25	35.3	1	0	0	1325.59	197	208
Protein timeless homolog	TIMELESS	TIM_HUMAN	138.7	99.8%	2	2	2	0.00%	2.3%	IQDCLLAGQAPQALTLLR	99.7%	41.5	25	41.3	1	0	0	1981.09	603	620
Protein timeless homolog	TIMELESS	TIM_HUMAN	138.7	99.8%	2	2	2	0.00%	2.3%	LLALGLVAER	99.7%	82.8	25	81.5	1	0	0	1054.66	931	940
Protein transport protein Sec23B	SEC23B	SC23B_HUMAN	86.5	99.8%	2	2	2	0.00%	3.1%	AESEEGPDVLR	99.7%	40.5	25	31.4	1	0	0	1201.57	536	546
Protein transport protein Sec23B	SEC23B	SC23B_HUMAN	86.5	99.8%	2	2	2	0.00%	3.1%	MVVPLACLLTPLK	99.7%	40.2	25	40.2	1	0	0	1454.85	34	46
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	7	18	0.02%	10.9%	AFSPTTVNTGR	99.7%	68.7	25	58.1	4	0	0	1150.59	195	205
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	7	18	0.02%	10.9%	ETSMVHELNR	99.6%	38.7	25	29.3	1	0	0	1231.57	406	415
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	7	18	0.02%	10.9%	GQYNTYPIK	99.7%	51.8	25	39.2	5	0	0	1083.55	274	282
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	7	18	0.02%	10.9%	IIEVGDTPK	99.7%	52.7	25	43.8	4	0	0	971.54	99	107
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	7	18	0.02%	10.9%	IIEVGDTPKDR	99.7%	43.3	25	28.1	2	1	0	1242.67	99	109
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	7	18	0.02%	10.9%	TWIEVSGSSAK	99.1%	34.6	25	26.1	1	0	0	1164.59	378	388
Protein transport protein Sec61 subunit beta	SEC61B	SC61B_HUMAN	10.0	99.8%	2	2	3	0.00%	21.9%	FYTEDSPGLK	95.5%	28	25	17.5	1	0	0	1156.55	58	67
Protein transport protein Sec61 subunit beta	SEC61B	SC61B_HUMAN	10.0	99.8%	2	2	3	0.00%	21.9%	TTSAGTGGMWR	99.7%	59.7	25	46.8	2	0	0	1124.52	47	57
Protein tyrosine phosphatase type IVA 1	PTP4A1	TP4A1_HUMAN	19.8	100.0%	3	3	4	0.00%	20.8%	FLITHNPTNATLNK	99.7%	52	25	48.1	2	0	0	1583.85	19	32
Protein tyrosine phosphatase type IVA 1	PTP4A1	TP4A1_HUMAN	19.8	100.0%	3	3	4	0.00%	20.8%	VCEATYDTTLVEK	99.4%	36.3	25	36.3	1	0	0	1528.72	48	60
Protein tyrosine phosphatase type IVA 1	PTP4A1	TP4A1_HUMAN	19.8	100.0%	3	3	4	0.00%	20.8%	YEDAVQFIR	99.5%	37.4	25	24.9	1	0	0	1140.57	126	134
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	7	7	13	0.01%	9.1%	ALIPLALEGTDVGQTK	99.7%	102	25	102	4	0	0	1625.91	692	707
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	7	7	13	0.01%	9.1%	LDQAVLDLQR	99.7%	74.4	25	58.5	1	0	0	1170.65	108	117
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	7	7	13	0.01%	9.1%	LLVLYSGEDDELLQR	99.7%	80.4	25	65.7	2	0	0	1762.92	822	836
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	7	7	13	0.01%	9.1%	QFAEGSTLK	96.3%	28.8	25	16	1	0	0	980.50	517	525
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	7	7	13	0.01%	9.1%	TESPVLTSSCR	99.7%	41.7	25	41.7	1	0	0	1236.59	654	664
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	7	7	13	0.01%	9.1%	TVATLSILGTR	99.7%	74.9	25	70	2	0	0	1131.67	230	240
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	7	7	13	0.01%	9.1%	VEQMFQILLDPEEK	99.7%	55.6	25	38.8	2	0	0	1718.87	153	166
Protein virilizer homolog	KIAA1429	VIR_HUMAN	202.0	100.0%	3	3	4	0.00%	2.0%	DTGELASSFLEFMR	99.7%	39.3	25	39.3	1	0	0	1602.75	1389	1402
Protein virilizer homolog	KIAA1429	VIR_HUMAN	202.0	100.0%	3	3	4	0.00%	2.0%	LLELILLDQTVR	99.7%	63.9	25	63.9	2	0	0	1425.87	534	545
Protein virilizer homolog	KIAA1429	VIR_HUMAN	202.0	100.0%	3	3	4	0.00%	2.0%	VVTAGSAILQK	96.4%	29	25	22.1	1	0	0	1086.65	546	556
Protein VPRBP	VPRBP	VPRBP_HUMAN	169.0	100.0%	4	4	5	0.01%	3.1%	SALQIIINCVCGPDNR	99.6%	38.7	25	38.7	2	0	0	1829.90	680	695
Protein VPRBP	VPRBP	VPRBP_HUMAN	169.0	100.0%	4	4	5	0.01%	3.1%	VLLSLLSIK	99.5%	37.8	25	37.8	1	0	0	985.67	737	745
Protein VPRBP	VPRBP	VPRBP_HUMAN	169.0	100.0%	4	4	5	0.01%	3.1%	VNSTTKPEDGGLKK	99.6%	31.9	25	31.6	0	1	0	1473.79	253	266
Protein VPRBP	VPRBP	VPRBP_HUMAN	169.0	100.0%	4	4	5	0.01%	3.1%	YAAELIER	96.5%	29	25	9.44	1	0	0	964.51	808	815

Protein YIF1A	YIF1A	YIF1A_HUMAN	32.0	99.8%	2	2	4	0.00%	9.2%	TAALGPDSMGGPVPR	99.7%	75.4	25	75.4	2	0	0	1441.71	251	265
Protein YIF1A	YIF1A	YIF1A_HUMAN	32.0	99.8%	2	2	4	0.00%	9.2%	YFFAVDTAYVAK	99.7%	77	25	67.5	2	0	0	1394.70	93	104
Protein zwilch homolog	ZWILCH	ZWILC_HUMAN	67.2	99.8%	2	2	3	0.00%	4.1%	FLLVLADGLR	99.7%	66.7	25	62.7	2	0	0	1116.68	271	280
Protein zwilch homolog	ZWILCH	ZWILC_HUMAN	67.2	99.8%	2	2	3	0.00%	4.1%	INLPVTALPPLWVR	98.6%	32.8	25	28.8	1	0	0	1588.96	126	139
Pumilio homolog 1	PUM1	PUM1_HUMAN	126.5	100.0%	5	5	8	0.01%	5.0%	DQYANYVVQK	99.7%	45.9	25	32.1	1	0	0	1227.60	1118	1127
Pumilio homolog 1	PUM1	PUM1_HUMAN	126.5	100.0%	5	5	8	0.01%	5.0%	FFEFGSLEQK	99.7%	51.4	25	36	2	0	0	1231.60	905	914
Pumilio homolog 1	PUM1	PUM1_HUMAN	126.5	100.0%	5	5	8	0.01%	5.0%	GIFLGDQWR	99.7%	42.5	25	36.6	1	0	0	1091.56	165	173
Pumilio homolog 1	PUM1	PUM1_HUMAN	126.5	100.0%	5	5	8	0.01%	5.0%	GNVLVLSQHK	99.7%	54.8	25	54.8	2	0	0	1094.63	1067	1076
Pumilio homolog 1	PUM1	PUM1_HUMAN	126.5	100.0%	5	5	8	0.01%	5.0%	SASSASSLFSPSSTLFSSSR	99.7%	77.6	25	77.6	2	0	0	1992.95	797	816
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	AFFESHPAPSAER	99.7%	45.8	25	45.2	2	1	0	1445.68	870	882
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	AFPCWDEPAIK	98.8%	33.3	25	30.6	2	0	0	1333.62	187	197
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	AGIISTVEVLK	99.7%	76.8	25	62.2	2	0	0	1129.68	628	638
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	ATFDISLVVPK	99.7%	73.6	25	63.8	2	0	0	1189.68	198	208
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	DAESIHQYLLQR	99.7%	78.4	25	64.2	2	0	0	1472.75	901	912
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	DNWEELYNR	99.7%	50.1	25	43.6	1	0	0	1238.54	833	841
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	DVFSPIGER	97.7%	30.7	25	22.6	1	0	0	1019.52	681	689
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	DYFNVPYPLPK	99.7%	61	25	56.2	3	0	0	1352.69	294	304
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	ETALLIDPK	99.7%	45.9	25	45	2	0	0	999.57	328	336
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	FALEVAAK	99.6%	38.6	25	21.3	2	0	0	848.49	280	287
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	GMNMYLTK	98.9%	33.8	25	27.2	2	0	0	957.45	460	467
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	HGDGTTLDIMLK	99.7%	57.1	25	52.5	2	0	0	1316.65	754	765
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	IDFVGELNDK	99.7%	59.1	25	41.1	2	0	0	1149.58	146	155
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	IDFVGELNDKMK	99.7%	43.7	25	40.3	1	0	0	1424.71	146	157
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	ILMDKPEMNVVLK	99.7%	49	25	45.8	1	0	0	1529.84	559	571
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	KPYPDDENLVEVK	99.7%	87	25	77.4	2	0	0	1545.78	222	234
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	LEAAAQVR	99.7%	41.2	25	26.2	2	0	0	857.48	80	87
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	LGLQNDLFSLAR	99.7%	92.8	25	79.8	4	0	0	1346.74	616	627
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	LNLGTVGFYR	99.7%	67.9	25	50.4	2	0	0	1139.62	581	590
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	LSVEGFAVDK	99.7%	47.8	25	40.9	2	0	0	1064.56	854	863
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	NVKPDQWVK	99.5%	37.5	25	23.9	2	0	0	1113.61	572	580
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	QILSADLR	99.7%	59.5	25	40.6	2	0	0	915.53	737	744
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	SKYTTPSGEVR	96.3%	28.9	25	24	1	0	0	1224.62	162	172
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	SPVYLTVLK	99.7%	59.8	25	53.9	3	0	0	1019.61	745	753
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	TIQQCCENILLNAAWLK	99.7%	58.5	25	57.6	2	0	0	2075.04	883	899
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	TQYSSAMLESLLPGIR	99.7%	71.6	25	56.8	4	0	0	1765.92	591	606
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	VALSNMNVIDR	99.7%	72.3	25	62.6	4	0	0	1231.65	211	221
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	VLGATLLPDLIQK	99.7%	93.7	25	93.7	5	0	0	1380.85	782	794
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	VTLSFPSTLQTGTGTLK	99.7%	59.8	25	59	2	0	0	1750.96	129	145
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	YAAVTQFEATDAR	99.7%	105	25	103	2	0	0	1442.69	173	185
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	YAAVTQFEATDARR	99.7%	51.1	25	47.5	1	0	0	1598.79	173	186
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	32	36	70	0.07%	36.6%	YQGGFLISR	99.7%	62.2	25	56.9	2	0	0	1040.55	842	850
Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial	CLPP	CLPP_HUMAN	30.2	100.0%	5	6	9	0.01%	28.5%	AYDIYSR	96.7%	29.3	25	12.2	1	0	0	887.43	72	78
Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial	CLPP	CLPP_HUMAN	30.2	100.0%	5	6	9	0.01%	28.5%	GQATDIAIQAEEIMK	99.7%	97.1	25	90.7	4	0	0	1633.81	186	200
Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial	CLPP	CLPP_HUMAN	30.2	100.0%	5	6	9	0.01%	28.5%	IMIHQPSGGAR	98.3%	32	25	32	1	0	0	1166.61	175	185
Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial	CLPP	CLPP_HUMAN	30.2	100.0%	5	6	9	0.01%	28.5%	QSLQVIESAMER	99.7%	64.1	25	63.7	2	0	0	1390.70	215	226
Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial	CLPP	CLPP_HUMAN	30.2	100.0%	5	6	9	0.01%	28.5%	VLVHPPQDGEDEPTLVQKEPVEAAPAAEPVPAST	99.7%	50.4	25	48.8	0	1	0	3517.77	244	277
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	AIFQQPPVGVR	99.7%	58	25	58	2	0	0	1211.69	715	725
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	AIVLAAIFR	99.7%	64.6	25	64.6	4	0	0	973.62	886	894
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	ALTQFPLPK	97.5%	30.4	25	23.6	1	0	0	1014.60	238	246
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	ATISLSDSDLLR	99.7%	86.1	25	73.4	2	0	0	1290.69	1116	1127
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	AVAGWEEVLR	99.7%	65.4	25	55.7	2	0	0	1129.60	942	951

Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	CNVIITQPR	99.7%	42.6	25	34.1	2	0	0	1100.59	484	492
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	DPFSSSLQNR	99.7%	55.1	25	47.8	2	0	0	1150.55	909	918
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	DVNTDFLLILLK	99.7%	65.9	25	47.9	4	0	0	1403.81	565	576
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	ENYLEENLLYAPSLR	99.7%	59.2	25	55	2	0	0	1823.92	959	973
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	EYLTTLGQR	99.7%	49.8	25	43.5	2	0	0	1080.57	865	873
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	FKPNSVTYR	99.5%	37.4	25	30.3	2	0	0	1111.59	1041	1049
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	GEPGGILCFLPGWQEIK	99.6%	38.8	25	35.7	1	0	0	1900.96	666	682
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	GGALLFCTVGILLR	99.7%	78.1	25	68.3	2	0	0	1489.86	529	542
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	GSSFEMTDDDSAIR	99.7%	80.4	25	77.4	2	0	0	1530.64	224	237
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	GVLMAGLYPNLIQVR	99.7%	47.5	25	36.7	2	0	0	1659.93	1017	1031
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	IPQLLLER	99.7%	57.9	25	41.2	2	0	0	981.61	467	474
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	ISAVSVAQR	99.7%	70.5	25	29.4	2	0	0	930.54	494	502
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	LQEALGMHESK	99.7%	41.1	25	36.2	3	0	0	1242.61	688	698
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	LQSDDILPLGK	99.7%	51.5	25	39.2	2	0	0	1198.67	378	388
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	LSQSLLELWR	99.7%	76.9	25	69.5	2	0	0	1244.70	413	422
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	LVLMSATGDNER	99.7%	71.8	25	62.1	4	0	0	1321.64	587	598
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	NLLNSVIGR	99.7%	54.9	25	41.6	2	0	0	985.58	55	63
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	NLMQFHTVGTK	99.7%	42	25	36.8	3	0	0	1291.65	264	274
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	NVGFQVR	94.7%	27.4	25	18.6	1	0	0	819.45	514	520
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	RISAVSVAQR	99.7%	44.6	25	22.5	2	0	0	1086.64	493	502
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	RPCTIQVPEPILR	96.2%	23.3	25	23.1	0	2	0	1578.88	344	356
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	SGNILLHK	99.7%	44.7	25	27	2	0	0	881.52	1052	1059
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	SVEVEGYGSK	99.7%	51.4	25	51.2	2	0	0	1054.51	96	105
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	TPLENLVLQAK	99.7%	69.3	25	69.3	2	0	0	1225.72	814	824
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	VIQIATSSSTAK	99.7%	74.4	25	66.7	3	0	0	1205.67	252	263
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	31	35	68	0.07%	27.6%	VSCLETVWVSR	99.7%	75.9	25	70.7	2	0	0	1335.67	763	773
Putative ATP-dependent RNA helicase DHX57	DHX57	DHX57_HUMAN	155.6	99.8%	2	2	3	0.00%	1.6%	ISAISVAER	99.7%	58.9	25	44.4	1	0	0	945.54	604	612
Putative ATP-dependent RNA helicase DHX57	DHX57	DHX57_HUMAN	155.6	99.8%	2	2	3	0.00%	1.6%	QFTELLSDIGFAR	99.7%	55.1	25	47.1	2	0	0	1496.77	1165	1177
Putative deoxyribose-phosphate aldolase	DERA	DEOC_HUMAN	35.2	100.0%	3	3	5	0.01%	13.5%	ETVNATFPVAIVMLR	98.9%	34	25	26.2	1	0	0	1660.91	224	238
Putative deoxyribose-phosphate aldolase	DERA	DEOC_HUMAN	35.2	100.0%	3	3	5	0.01%	13.5%	IGASTLLSDIER	99.7%	69.8	25	56.8	3	0	0	1274.70	288	299
Putative deoxyribose-phosphate aldolase	DERA	DEOC_HUMAN	35.2	100.0%	3	3	5	0.01%	13.5%	TILATGELGTLTNVYK	99.7%	43.7	25	43.7	1	0	0	1693.94	189	204
Putative GTP-binding protein 6	GTPBP6	GTPB6_HUMAN	56.9	99.8%	2	2	2	0.00%	4.3%	ALTGDAAIQPR	99.7%	60.8	25	48.3	1	0	0	1112.61	313	323
Putative GTP-binding protein 6	GTPBP6	GTPB6_HUMAN	56.9	99.8%	2	2	2	0.00%	4.3%	DVSHPEAELQK	97.7%	30.8	25	29.5	1	0	0	1252.62	383	393
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	99.8%	2	2	2	0.00%	3.2%	EGNSPSFFNPEEAATVTSYLK	99.7%	57.3	25	57.3	1	0	0	2288.07	788	808
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	99.8%	2	2	2	0.00%	3.2%	VLITTLITAGR	99.7%	80.8	25	77.2	1	0	0	1157.73	618	628
Putative methyltransferase NSUN5	NSUN5	NSUN5_HUMAN	46.7	99.8%	2	2	5	0.01%	6.1%	VLVYELLLGK	99.7%	67.3	25	54.1	4	0	0	1146.71	73	82
Putative methyltransferase NSUN5	NSUN5	NSUN5_HUMAN	46.7	99.8%	2	2	5	0.01%	6.1%	YSAVLDAVIASAGLLR	99.7%	61.4	25	61.4	1	0	0	1618.92	46	61
Putative mitochondrial import inner membrane translocase subunit Tim23B	TIMM23B	TI23B_HUMAN	21.9	100.0%	3	4	7	0.01%	14.8%	ETQNMAWSKPR	99.7%	42.8	25	31.2	2	0	0	1347.65	102	112
Putative mitochondrial import inner membrane translocase subunit Tim23B	TIMM23B	TI23B_HUMAN	21.9	100.0%	3	4	7	0.01%	14.8%	NVQILNMVTR	99.7%	77.4	25	50.1	4	0	0	1187.66	113	122
Putative mitochondrial import inner membrane translocase subunit Tim23B	TIMM23B	TI23B_HUMAN	21.9	100.0%	3	4	7	0.01%	14.8%	YLVQDTDEFILPTGANK	99.7%	67.3	25	60.5	1	0	0	1923.97	52	68
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	7	9	18	0.02%	16.8%	ALDQSDNDMSAVYR	99.7%	83.8	25	83.8	4	0	0	1584.70	536	549
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	7	9	18	0.02%	16.8%	CDLFIQEGAR	99.7%	55.4	25	38.7	2	0	0	1208.57	303	312
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	7	9	18	0.02%	16.8%	DLVLGPSGVLQGIRPGK	99.7%	62.6	25	62.6	2	0	0	1706.00	339	355
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	7	9	18	0.02%	16.8%	FQQAVDAVEEFLR	99.7%	77.2	25	69.3	2	0	0	1551.78	79	91
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	7	9	18	0.02%	16.8%	GLYEDCSSCFQAMGK	99.7%	95.8	25	95.8	4	0	0	1752.70	408	422
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	7	9	18	0.02%	16.8%	GMMAGPMAAFK	99.6%	38.5	25	17.3	2	0	0	1111.51	191	201
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	7	9	18	0.02%	16.8%	TSFFLGEVGNAAK	99.7%	88.5	25	84.5	2	0	0	1340.68	423	435
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	6	8	20	0.02%	8.3%	EAMNDPLLER	94.7%	27.4	25	22.3	1	0	0	1187.57	244	253
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	6	8	20	0.02%	8.3%	FTDILVR	99.7%	40.6	25	26.2	1	0	0	863.50	146	152
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	6	8	20	0.02%	8.3%	HQSFVLVGETGSGK	99.5%	31.5	25	31.5	0	1	0	1445.74	153	166
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	6	8	20	0.02%	8.3%	SNLGSVVLQLK	99.7%	83.4	25	74.8	3	0	0	1157.69	505	515

Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	6	8	20	0.02%	8.3%	TLATDILMGVLK	99.7%	97.5	25	82.7	10	0	0	1290.73	266	277
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	6	8	20	0.02%	8.3%	YGVIILDEAHER	99.7%	63.3	25	54	3	1	0	1414.73	254	265
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	27	0.03%	16.1%	DLAQALINR	99.7%	45.3	25	40.2	2	0	0	1013.57	323	331
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	27	0.03%	16.1%	ELLLSAIDSVNATSK	99.7%	113	25	110	4	0	0	1560.85	493	507
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	27	0.03%	16.1%	GADSELSTVPSVTK	99.7%	40	25	14.4	2	0	0	1390.71	656	669
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	27	0.03%	16.1%	GISAGAVQTAGK	99.7%	65.5	25	54.9	3	0	0	1059.58	80	91
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	27	0.03%	16.1%	GVNLDPLGK	99.1%	34.7	25	32.1	1	0	0	912.52	332	340
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	27	0.03%	16.1%	IQDIVGILR	99.7%	67.6	25	51.1	4	0	0	1026.63	243	251
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	27	0.03%	16.1%	LVPTGLDFGQEGFTR	99.7%	97.2	25	94	4	0	0	1636.83	539	553
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	27	0.03%	16.1%	NTGVILANDANAER	99.7%	90.2	25	85.7	1	0	0	1457.73	408	421
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	27	0.03%	16.1%	SPEAKPLPGK	99.1%	34.6	25	33.9	1	0	0	1023.58	67	76
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	27	0.03%	16.1%	SVVGNLHR	99.0%	34.1	25	15.6	3	0	0	881.50	424	431
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	27	0.03%	16.1%	TQASSSFQDSSQPAGK	99.7%	96.9	25	96.3	2	0	0	1625.74	670	685
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	5	5	6	0.01%	6.6%	ISHLSGSGSGDER	99.7%	39.2	25	29.5	2	0	0	1301.61	204	216
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	5	5	6	0.01%	6.6%	LQQLALGR	99.7%	50.1	25	27.8	1	0	0	898.55	307	314
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	5	5	6	0.01%	6.6%	QDGGTAPVASASPK	98.8%	33.3	25	30.6	1	0	0	1285.64	770	783
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	5	5	6	0.01%	6.6%	SSGAASSAPGGGDGAEYK	98.9%	33.9	25	28	1	0	0	1568.68	153	170
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	5	5	6	0.01%	6.6%	VGAGAGAAPFR	99.7%	50.2	25	38.8	1	0	0	973.52	349	359
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	99.8%	2	2	2	0.00%	7.7%	LAETQEEISAEVAAK	99.7%	85.5	25	80.6	1	0	0	1588.81	108	122
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	99.8%	2	2	2	0.00%	7.7%	VEQLGAEGNVEESQK	99.7%	64.4	25	57.5	1	0	0	1616.78	140	154
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	9	16	39	0.04%	36.7%	CMTNTPVVVR	99.7%	54.6	25	43.6	5	0	0	1176.59	120	129
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	9	16	39	0.04%	36.7%	EGATVYATGTHAQVEDGR	99.7%	63.3	25	60.9	1	2	0	1861.87	130	147
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	9	16	39	0.04%	36.7%	ELQSMADQEQVSPAAIK	99.7%	53.2	25	36.9	2	0	0	1860.90	267	283
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	9	16	39	0.04%	36.7%	ELQSMADQEQVSPAAIKK	99.7%	46.2	25	44.8	1	4	0	1973.00	267	284
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	9	16	39	0.04%	36.7%	GFTAAGVLAAHK	99.7%	73.4	25	64.9	4	0	0	1142.63	18	29
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	9	16	39	0.04%	36.7%	IMASSPDMDLATVSALR	99.7%	72.3	25	69.4	3	0	0	1777.88	30	46
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	9	16	39	0.04%	36.7%	LDSPAGTALSPSGHTK	99.7%	75	25	72.7	4	3	0	1538.78	292	307
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	9	16	39	0.04%	36.7%	LGAQALLGAAK	99.7%	99.5	25	91.1	5	0	0	1012.62	205	215
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	9	16	39	0.04%	36.7%	SLLINAVEASCIR	99.7%	92	25	87.3	6	0	0	1445.78	252	264
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	9	16	39	0.04%	36.7%	VKLDSPAGTALSPSGHTK	99.7%	37.3	25	22.3	1	4	0	1765.94	290	307
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	10	12	29	0.03%	29.7%	ELQSMADQEK	99.7%	50.4	25	44.3	4	0	0	1178.54	267	276
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	10	12	29	0.03%	29.7%	GFTAAGILSAHK	99.7%	65.6	25	55.8	4	0	0	1172.64	18	29
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	10	12	29	0.03%	29.7%	IIASSPEMNLPTVSALR	99.7%	133	25	128	4	0	0	1798.97	30	46
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	10	12	29	0.03%	29.7%	ISPAALKK	98.6%	32.8	25	28.2	2	0	0	827.54	277	284
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	10	12	29	0.03%	29.7%	KLMAFQPAPK	99.7%	47.9	25	29.7	1	0	0	1130.64	107	116
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	10	12	29	0.03%	29.7%	LESPTVSTLTPSSPGK	99.7%	74.7	25	56.1	2	0	0	1600.84	292	307
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	10	12	29	0.03%	29.7%	LMAFQPAPK	99.7%	64.4	25	53.6	2	0	0	1002.54	108	116
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	10	12	29	0.03%	29.7%	MGVNLTR	99.7%	42.7	25	16.2	2	0	0	806.42	48	54
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	10	12	29	0.03%	29.7%	SLLINAVEASCIR	99.7%	92	25	87.3	6	0	0	1445.78	252	264
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	10	12	29	0.03%	29.7%	VKLESPTVSTLTPSSPGK	99.7%	82.1	25	74.3	2	0	0	1828.01	290	307
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	5	7	13	0.01%	21.5%	AATMSAVEAATCR	99.7%	76.4	25	76.4	2	0	0	1354.61	255	267
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	5	7	13	0.01%	21.5%	IAAQTLLGTAK	99.7%	94.8	25	94.8	2	0	0	1086.65	208	218
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	5	7	13	0.01%	21.5%	MAGAIAQGLIR	99.7%	77.6	25	69.9	4	0	0	1116.62	19	29
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	5	7	13	0.01%	21.5%	MGMPSSLAHR	99.7%	42.7	25	34.1	2	0	0	1086.52	198	207
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	5	7	13	0.01%	21.5%	VEAQHILASAPTDR	99.7%	79.6	25	78.2	2	1	0	1507.79	33	46
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	9	9	13	0.01%	10.8%	AEAEAQAEELSFPR	99.7%	99.3	25	98.2	2	0	0	1547.73	929	942
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	9	9	13	0.01%	10.8%	DAHQSLLATR	99.7%	42.9	25	33.3	1	0	0	1111.59	572	581
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	9	9	13	0.01%	10.8%	DFTATFGPLDSLNTR	99.7%	60.8	25	34.4	1	0	0	1654.81	1022	1036
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	9	9	13	0.01%	10.8%	GANAVGYTNYPDNVVFK	99.7%	79.4	25	78.8	2	0	0	1828.89	645	661
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	9	9	13	0.01%	10.8%	GQIGAPMPGK	96.7%	29.3	25	25.4	1	0	0	971.50	1110	1119
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	9	9	13	0.01%	10.8%	GTPLDTEVPMER	99.0%	34.3	25	32.8	1	0	0	1344.65	819	830

Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	9	9	13	0.01%	10.8%	LDNASAFQGAVISPHYDSLLVK	99.7%	62.2	25	62.2	0	2	0	2345.21	407	428
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	9	9	13	0.01%	10.8%	TSTAPAASPNVR	99.7%	47.7	25	32.7	2	0	0	1171.61	19	30
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	9	9	13	0.01%	10.8%	VVEIAPAAHLDPQLR	99.3%	29.8	25	26.3	0	1	0	1628.91	274	288
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	13	15	33	0.03%	33.1%	AAASTDYYKR	99.7%	49.1	25	49.1	2	0	0	1145.56	236	245
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	13	15	33	0.03%	33.1%	AHGFTFTR	96.7%	29.3	25	29.3	1	0	0	936.47	120	127
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	13	15	33	0.03%	33.1%	EILAELTGR	99.7%	56.4	25	46	2	0	0	1001.56	133	141
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	13	15	33	0.03%	33.1%	GANQWIK	99.6%	38.6	25	25.3	1	0	0	816.44	379	385
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	13	15	33	0.03%	33.1%	GDFIPGLR	96.9%	29.5	25	15.1	1	0	0	874.48	246	253
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	13	15	33	0.03%	33.1%	GPILMELQTYR	99.7%	60.2	25	60.2	4	0	0	1320.70	278	288
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	13	15	33	0.03%	33.1%	LEEGPPVTTVLTR	99.7%	73	25	69.6	3	0	0	1411.78	46	58
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	13	15	33	0.03%	33.1%	LPCIFICENNR	99.7%	71.2	25	71.2	3	0	0	1435.68	216	226
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	13	15	33	0.03%	33.1%	NFYGGNGIVGAQVPLGAGIALACK	99.7%	38.5	25	38.5	0	3	0	2347.22	159	182
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	13	15	33	0.03%	33.1%	RGDFIPGLR	98.9%	33.8	25	18.9	2	0	0	1030.58	245	253
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	13	15	33	0.03%	33.1%	TREEIQEVR	99.4%	36.2	25	13.3	4	0	0	1159.61	303	311
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	13	15	33	0.03%	33.1%	VDGMDILCVR	99.7%	61.6	25	54.5	4	0	0	1177.57	254	263
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	13	15	33	0.03%	33.1%	YGMGTSVER	99.7%	51	25	46.5	3	0	0	999.46	227	235
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	9	12	38	0.04%	30.4%	DFLIPIGK	99.4%	36.8	25	23.6	1	0	0	902.53	220	227
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	9	12	38	0.04%	30.4%	DIIFAIKK	99.7%	46.1	25	32.9	2	0	0	947.59	348	355
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	9	12	38	0.04%	30.4%	EGVECEVINMR	99.7%	67.2	25	67.2	6	0	0	1335.60	259	269
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	9	12	38	0.04%	30.4%	ILEDNSIPQVK	99.7%	83.4	25	66.4	4	0	0	1255.69	337	347
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	9	12	38	0.04%	30.4%	IMEGPAFNFLDAPAVR	99.7%	91.8	25	85.2	9	0	0	1747.88	309	324
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	9	12	38	0.04%	30.4%	TYYMSGGLQPVPIVFR	99.7%	78.1	25	76.9	8	0	0	1843.94	130	145
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	9	12	38	0.04%	30.4%	VFLLGEEVAQYDGAYK	99.7%	123	25	120	4	0	0	1801.90	53	68
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	9	12	38	0.04%	30.4%	VTGADVPMPYAK	99.7%	46.4	25	36.6	2	0	0	1248.63	325	336
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	9	12	38	0.04%	30.4%	VVSPWNSEDAK	98.7%	33.2	25	13.3	2	0	0	1231.60	174	184
Pyruvate dehydrogenase protein X component, mitochondrial	PDHX	ODPX_HUMAN	54.1	99.8%	2	2	5	0.01%	4.6%	HSLDASQGTATGPR	99.7%	61	25	59.7	4	0	0	1397.68	195	208
Pyruvate dehydrogenase protein X component, mitochondrial	PDHX	ODPX_HUMAN	54.1	99.8%	2	2	5	0.01%	4.6%	VVDDELATR	95.1%	27.7	25	21.7	1	0	0	1017.52	477	485
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	AEGSDVANAVLDGADCIMLSGETAK	99.7%	126	25	126	6	1	0	2494.14	343	367
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	AGKPVICATQMLESMIK	99.7%	55.4	25	55.4	1	4	0	1908.96	320	336
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	CCSGAIIVLTK	99.7%	81.1	25	74.6	3	0	0	1221.63	423	433
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	CDENILWLDYK	99.7%	80.8	25	79	2	0	0	1468.68	152	162
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	DPVQEAWAEDVDLR	99.7%	96.2	25	92.5	2	0	0	1642.77	476	489
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	FDEILEASDGIMVAR	99.7%	98.4	25	98.4	2	0	0	1681.81	280	294
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	FGVEQDVDMVFASFIR	99.7%	127	25	127	15	3	0	1859.90	231	246
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	GADFLVTEVENGGSLGSK	99.7%	125	25	121	6	0	0	1779.88	189	206
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	GADFLVTEVENGGSLGSKK	99.7%	36.4	25	24.8	0	2	0	1907.97	189	207
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	GDLGIEIPAEK	99.7%	61.2	25	30.6	15	0	0	1141.61	295	305
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	GDYPLEAVR	99.7%	65.3	25	57.2	17	0	0	1019.52	368	376
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	GIFPVLCK	97.1%	29.8	25	13.2	2	0	0	933.52	468	475
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	GIFPVLCKDPVQEAWAEDVDLR	99.7%	52.7	25	52.7	0	2	0	2557.28	468	489
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	GSGTAEVELK	99.7%	64.8	25	44.5	2	0	0	990.51	126	135
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	GSGTAEVELKK	99.7%	53	25	37.5	10	0	0	1118.61	126	136
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	GVNLPGAAVDLPAVSEK	99.7%	139	25	135	2	0	0	1636.89	208	224
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	GVNLPGAAVDLPAVSEKDIQDLK	98.2%	26	25	26	0	3	0	2349.27	208	230
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	ITLDNAYMEK	99.7%	62.3	25	44.2	9	0	0	1197.58	142	151
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	IYVDDGLISLQVK	99.7%	102	25	102	9	0	0	1462.82	174	186
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	KGVNLPGAAVDLPAVSEK	99.7%	42.9	25	42.9	2	1	0	1764.99	207	224
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	LAPITSDPTEATAVGAVEASFK	99.7%	173	25	173	5	4	0	2175.12	401	422
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	LDIDSPPITAR	99.7%	69.8	25	61.6	18	0	0	1197.65	33	43
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	LNFSHGTHEYHAETIK	99.7%	47.7	25	43.7	0	2	0	1883.90	74	89
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	MQHLIAR	99.7%	41.2	25	31.9	5	0	0	868.48	377	383

Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	NTGIICTIGPASR	99.7%	97.2	25	91.8	14	0	0	1359.71	44	56
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	RFDEILEASDGIMVAR	99.7%	80.2	25	80.2	5	4	0	1821.92	279	294
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	SVETLKEMIK	99.7%	48.8	25	39.2	7	0	0	1177.65	57	66
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	TATESFASDPILYRPVAVALDTK	99.7%	47.1	25	47.1	0	7	0	2465.29	93	115
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	45	201	0.21%	61.2%	VNFAMNVGK	99.7%	57.8	25	53.4	9	0	0	979.50	490	498
Queuine tRNA-ribosyltransferase subunit QTRTD1	QTRTD1	QTRD1_HUMAN	46.7	100.0%	5	5	7	0.01%	15.2%	GVDLFESFFPYQVTER	99.7%	61.1	25	60.1	1	0	0	1933.93	267	282
Queuine tRNA-ribosyltransferase subunit QTRTD1	QTRTD1	QTRD1_HUMAN	46.7	100.0%	5	5	7	0.01%	15.2%	LISGVSRPDEVLECIER	96.0%	23.1	25	23.1	0	1	0	1972.02	250	266
Queuine tRNA-ribosyltransferase subunit QTRTD1	QTRTD1	QTRD1_HUMAN	46.7	100.0%	5	5	7	0.01%	15.2%	LQEESEVLQK	99.7%	53	25	41.4	2	0	0	1202.63	177	186
Queuine tRNA-ribosyltransferase subunit QTRTD1	QTRTD1	QTRD1_HUMAN	46.7	100.0%	5	5	7	0.01%	15.2%	SLLFLDNCLR	99.7%	44.5	25	28.8	2	0	0	1250.66	167	176
Queuine tRNA-ribosyltransferase subunit QTRTD1	QTRTD1	QTRD1_HUMAN	46.7	100.0%	5	5	7	0.01%	15.2%	SVSVWSVAGR	99.7%	57.1	25	51.7	1	0	0	1047.56	112	121
Rab3 GTPase-activating protein non-catalytic subunit	RAB3GAP2	RBGPR_HUMAN	156.0	100.0%	4	4	5	0.01%	3.2%	VAQFLVIYAPR	99.7%	51.3	25	51.3	1	0	0	1276.74	461	471
Rab3 GTPase-activating protein non-catalytic subunit	RAB3GAP2	RBGPR_HUMAN	156.0	100.0%	4	4	5	0.01%	3.2%	VILLDVAR	94.9%	27.6	25	11.4	1	0	0	898.57	408	415
Rab3 GTPase-activating protein non-catalytic subunit	RAB3GAP2	RBGPR_HUMAN	156.0	100.0%	4	4	5	0.01%	3.2%	VSSLQAEPLPR	99.7%	63.8	25	51.1	2	0	0	1196.66	914	924
Rab3 GTPase-activating protein non-catalytic subunit	RAB3GAP2	RBGPR_HUMAN	156.0	100.0%	4	4	5	0.01%	3.2%	VVSAAVQAQHSATK	99.7%	77	25	73	1	0	0	1396.75	1220	1233
Rab-like protein 2A	RABL2A	RBL2A_HUMAN	26.1	99.8%	2	2	3	0.00%	11.0%	IICLGDSAVGK	99.5%	37.5	25	37.5	1	0	0	1132.60	24	34
Rab-like protein 2A	RABL2A	RBL2A_HUMAN	26.1	99.8%	2	2	3	0.00%	11.0%	TILVDFWDTAGQER	99.7%	60.6	25	60.6	2	0	0	1650.81	69	82
Rab-like protein 3	RABL3	RABL3_HUMAN	26.4	99.8%	2	2	4	0.00%	8.1%	WSLEALNR	99.7%	49.7	25	32.1	2	0	0	988.52	109	116
Rab-like protein 3	RABL3	RABL3_HUMAN	26.4	99.8%	2	2	4	0.00%	8.1%	YLAAGSSNAVK	99.7%	52.1	25	37.5	2	0	0	1080.57	185	195
Rac GTPase-activating protein 1	RACGAP1	RGAP1_HUMAN	71.0	99.9%	2	2	3	0.00%	2.9%	NLFEQLVR	97.0%	29.6	25	19.2	1	0	0	1018.57	10	17
Rac GTPase-activating protein 1	RACGAP1	RGAP1_HUMAN	71.0	99.9%	2	2	3	0.00%	2.9%	TPSSSSLSQR	99.7%	47.8	25	44.4	2	0	0	1049.52	588	597
Ragulator complex protein LAMTOR1	LAMTOR1	LTOR1_HUMAN	17.7	99.8%	2	2	4	0.00%	16.1%	IAAYAYSALSQIR	99.7%	60.1	25	50.7	2	0	0	1426.77	135	147
Ragulator complex protein LAMTOR1	LAMTOR1	LTOR1_HUMAN	17.7	99.8%	2	2	4	0.00%	16.1%	TDEQALLSSILAK	99.7%	113	25	111	2	0	0	1388.76	48	60
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	17	38	0.04%	32.7%	AFNSSSFNSNTFLTR	99.7%	102	25	89	3	0	0	1692.80	501	515
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	17	38	0.04%	32.7%	GAVAIADAIR	99.7%	83.6	25	73.8	4	0	0	956.55	280	289
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	17	38	0.04%	32.7%	GAVAMAETLK	99.7%	55.4	25	43.4	3	0	0	990.53	252	261
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	17	38	0.04%	32.7%	ILAAALTECHR	99.7%	53.6	25	50.1	2	0	0	1254.66	161	171
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	17	38	0.04%	32.7%	LENDGATALAEAFR	99.7%	70.6	25	64.6	2	0	0	1477.73	192	205
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	17	38	0.04%	32.7%	LLVHMGLLK	95.8%	28.4	25	28.4	1	0	0	1023.64	516	524
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	17	38	0.04%	32.7%	LNNCGMGIGGGK	99.7%	51.7	25	50.5	2	0	0	1177.55	149	160
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	17	38	0.04%	32.7%	LNTAEDAKDVIK	99.7%	69.7	25	53.8	2	0	0	1316.71	32	43
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	17	38	0.04%	32.7%	MAVQDAVDALMQK	99.7%	76.9	25	75.1	3	0	0	1419.70	488	500
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	17	38	0.04%	32.7%	QVEVINFGDCLVR	99.7%	86	25	84.5	3	0	0	1548.78	265	277
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	17	38	0.04%	32.7%	SSACFTLQELK	99.7%	55.5	25	46.3	2	0	0	1283.63	138	148
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	17	38	0.04%	32.7%	SSAQGKPLALK	98.7%	33	25	21.9	1	0	0	1099.65	173	183
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	17	38	0.04%	32.7%	SSVLIAQQTDTSDPEK	99.7%	99.8	25	90.1	2	0	0	1718.84	453	468
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	17	38	0.04%	32.7%	TQVAGGQLSFK	99.7%	62.6	25	55.6	4	0	0	1135.61	16	26
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	17	38	0.04%	32.7%	VINLNDNTFTEK	99.7%	66.1	25	59.3	2	0	0	1407.71	240	251
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	17	38	0.04%	32.7%	VSSVFKDEATVR	99.7%	76	25	64	2	0	0	1337.71	476	487
Ran-specific GTPase-activating protein	RANBP1	RANG_HUMAN	23.3	99.8%	2	2	3	0.00%	10.9%	FASENDLPEWK	99.6%	38.2	25	24.9	1	0	0	1335.62	58	68
Ran-specific GTPase-activating protein	RANBP1	RANG_HUMAN	23.3	99.8%	2	2	3	0.00%	10.9%	TLEEDEEELFK	99.7%	63.7	25	63.2	2	0	0	1381.64	40	50
Ras GTPase-activating protein-binding protein 1	G3BP1	G3BP1_HUMAN	52.2	99.8%	2	2	3	0.00%	5.8%	EAGEQGDIEPR	99.7%	67.9	25	67.9	2	0	0	1200.55	321	331
Ras GTPase-activating protein-binding protein 1	G3BP1	G3BP1_HUMAN	52.2	99.8%	2	2	3	0.00%	5.8%	FMQTFVLAPEGSVANK	99.7%	43.5	25	43.5	1	0	0	1738.88	108	123
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	13	13	23	0.02%	10.3%	ALQSPALGLR	99.5%	37.4	25	28.1	2	0	0	1025.61	327	336
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	13	13	23	0.02%	10.3%	ATFYGEQVDYYK	99.7%	54	25	54	2	0	0	1483.67	1517	1528
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	13	13	23	0.02%	10.3%	EEIQSSISGVTAAYNR	99.7%	87.1	25	87.1	1	0	0	1724.84	723	738
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	13	13	23	0.02%	10.3%	GVLLEIEDLQVNQFK	97.0%	29.6	25	29.6	1	0	0	1744.95	1572	1586
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	13	13	23	0.02%	10.3%	ILAIGLINEALDEGDAQK	99.7%	72.8	25	72.8	3	0	0	1883.01	539	556
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	13	13	23	0.02%	10.3%	ITLQDVVSHSK	99.6%	38.2	25	30.4	2	0	0	1226.67	925	935
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	13	13	23	0.02%	10.3%	LAAVALINAAIQK	99.7%	65.1	25	42.5	2	0	0	1295.80	389	401
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	13	13	23	0.02%	10.3%	LGNFFSPK	99.7%	40.6	25	40.6	2	0	0	909.48	81	88
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	13	13	23	0.02%	10.3%	LPYDVTPEQALAHEEVK	99.0%	28.3	25	19.7	0	1	0	1938.98	1112	1128

Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	13	13	23	0.02%	10.3%	LQQTYAALNSK	99.7%	56.1	25	47.6	2	0	0	1236.66	1506	1516
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	13	13	23	0.02%	10.3%	NVIFEISPTEEVGDFEVK	99.7%	57.9	25	57.9	2	0	0	2052.02	1587	1604
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	13	13	23	0.02%	10.3%	TLQALQIPAAK	99.7%	71.7	25	67.1	2	0	0	1153.69	557	567
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	13	13	23	0.02%	10.3%	YGIQMPAFSK	99.5%	37.3	25	23.6	1	0	0	1141.57	192	201
Ras-associating and dilute domain-containing protein	RADIL	RADIL_HUMAN	117.5	99.8%	2	2	3	0.00%	2.2%	SVLATGTSSAR	99.7%	40.6	25	35.3	1	0	0	1049.56	80	90
Ras-associating and dilute domain-containing protein	RADIL	RADIL_HUMAN	117.5	99.8%	2	2	3	0.00%	2.2%	VVSVYQAALDLLR	99.7%	61.2	25	57.1	2	0	0	1446.83	612	624
Ras-related protein Rab-10	RAB10	RAB10_HUMAN	22.5	99.9%	2	2	4	0.00%	17.0%	AFLTLAEDILR	99.7%	64.7	25	54.8	2	0	0	1261.72	162	172
Ras-related protein Rab-10	RAB10	RAB10_HUMAN	22.5	99.9%	2	2	4	0.00%	17.0%	LQIWDTAGQER	99.7%	72.3	25	0	6	0	0	1316.66	60	70
Ras-related protein Rab-10	RAB10	RAB10_HUMAN	22.5	99.9%	2	2	4	0.00%	17.0%	NIDEHANEDVER	99.7%	63.8	25	58.9	2	0	0	1440.64	106	117
Ras-related protein Rab-13	RAB13	RAB13_HUMAN	22.8	100.0%	4	4	7	0.01%	21.7%	SFENIQNWMK	97.1%	29.8	25	29.8	1	0	0	1312.60	95	104
Ras-related protein Rab-13	RAB13	RAB13_HUMAN	22.8	100.0%	4	4	7	0.01%	21.7%	SIKENASAGVER	99.7%	56.9	25	50.1	2	0	0	1260.65	105	116
Ras-related protein Rab-13	RAB13	RAB13_HUMAN	22.8	100.0%	4	4	7	0.01%	21.7%	SSMNVDEAFSSLAR	99.7%	121	25	116	2	0	0	1513.70	154	167
Ras-related protein Rab-13	RAB13	RAB13_HUMAN	22.8	100.0%	4	4	7	0.01%	21.7%	TITTAYYR	98.7%	33	25	21	2	0	0	988.51	72	79
Ras-related protein Rab-18	RAB18	RAB18_HUMAN	23.0	100.0%	4	4	7	0.01%	26.2%	GAQGVILVYDVTR	99.7%	57.7	25	50.6	2	0	0	1390.77	80	92
Ras-related protein Rab-18	RAB18	RAB18_HUMAN	23.0	100.0%	4	4	7	0.01%	26.2%	IIQTPGLWESENQNK	99.7%	58.5	25	57.2	2	0	0	1756.89	169	183
Ras-related protein Rab-18	RAB18	RAB18_HUMAN	23.0	100.0%	4	4	7	0.01%	26.2%	ILIIGESGVGK	99.7%	50.6	25	30.6	2	0	0	1085.66	11	21
Ras-related protein Rab-18	RAB18	RAB18_HUMAN	23.0	100.0%	4	4	7	0.01%	26.2%	TCDGVQCAFEELVEK	96.0%	28.5	25	28.5	1	0	0	1784.78	154	168
Ras-related protein Rab-1A	RAB1A	RAB1A_HUMAN	22.7	99.8%	2	3	6	0.01%	44.4%	EFADSLGIPFLETSAK	99.7%	54	25	46.8	2	0	0	1724.87	141	156
Ras-related protein Rab-1A	RAB1A	RAB1A_HUMAN	22.7	99.8%	2	3	6	0.01%	44.4%	FADDTYTESYISTIGVDFK	99.7%	80.7	25	80.7	2	0	0	2172.00	31	49
Ras-related protein Rab-1A	RAB1A	RAB1A_HUMAN	22.7	99.8%	2	3	6	0.01%	44.4%	LQIWDTAGQER	99.7%	72.3	25	0	6	0	0	1316.66	62	72
Ras-related protein Rab-1A	RAB1A	RAB1A_HUMAN	22.7	99.8%	2	3	6	0.01%	44.4%	MGPGATAGGAEK	99.7%	42.7	25	35.8	2	0	0	1046.49	176	187
Ras-related protein Rab-1A	RAB1A	RAB1A_HUMAN	22.7	99.8%	2	3	6	0.01%	44.4%	NATNVEQSFMTMAAEIK	99.7%	59.3	25	1.63	4	0	0	1884.88	157	173
Ras-related protein Rab-1A	RAB1A	RAB1A_HUMAN	22.7	99.8%	2	3	6	0.01%	44.4%	QWLQEIDR	99.7%	47.1	25	25	2	0	0	1087.55	104	111
Ras-related protein Rab-1A	RAB1A	RAB1A_HUMAN	22.7	99.8%	2	3	6	0.01%	44.4%	QWLQEIDRYASENVNK	95.9%	23	25	23	0	2	0	1992.98	104	119
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	7	10	25	0.03%	46.8%	EFADSLGIPFLETSAK	99.7%	54	25	46.8	2	0	0	1724.87	138	153
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	7	10	25	0.03%	46.8%	FADDTYTESYISTIGVDFK	99.7%	80.7	25	80.7	2	0	0	2172.00	28	46
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	7	10	25	0.03%	46.8%	LQIWDTAGQER	99.7%	72.3	25	0	6	0	0	1316.66	59	69
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	7	10	25	0.03%	46.8%	MGPGAASGGERPNLK	99.7%	56.5	25	50.4	4	5	0	1457.72	173	187
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	7	10	25	0.03%	46.8%	NATNVEQAFMTMAAEIK	99.7%	62.2	25	14.7	2	0	0	1900.88	154	170
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	7	10	25	0.03%	46.8%	QWLQEIDR	99.7%	47.1	25	25	2	0	0	1087.55	101	108
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	7	10	25	0.03%	46.8%	QWLQEIDRYASENVNK	95.9%	23	25	23	0	2	0	1992.98	101	116
Ras-related protein Rab-23	RAB23	RAB23_HUMAN	26.7	99.8%	2	2	3	0.00%	10.5%	TIGVDFLER	98.9%	34	25	34	1	0	0	1049.56	41	49
Ras-related protein Rab-23	RAB23	RAB23_HUMAN	26.7	99.8%	2	2	3	0.00%	10.5%	VVAEVGDIPTVLVQNK	99.7%	63.2	25	60	2	0	0	1680.95	107	122
Ras-related protein Rab-32	RAB32	RAB32_HUMAN	25.0	100.0%	3	3	5	0.01%	18.7%	AGGGAGDPGLGAAAAPAPETR	99.7%	40.3	25	19.5	1	0	0	1763.87	2	22
Ras-related protein Rab-32	RAB32	RAB32_HUMAN	25.0	100.0%	3	3	5	0.01%	18.7%	DNINIEEAAR	99.7%	67.7	25	59.5	2	0	0	1144.56	177	186
Ras-related protein Rab-32	RAB32	RAB32_HUMAN	25.0	100.0%	3	3	5	0.01%	18.7%	LQLWDIAGQER	99.7%	55.6	25	47.3	2	0	0	1328.70	77	87
Ras-related protein Rab-5C	RAB5C	RAB5C_HUMAN	23.5	100.0%	4	4	6	0.01%	23.6%	GVDLQENNPASR	99.7%	45.5	25	41.3	1	0	0	1299.63	199	210
Ras-related protein Rab-5C	RAB5C	RAB5C_HUMAN	23.5	100.0%	4	4	6	0.01%	23.6%	LVLLGESAVGK	99.5%	37.3	25	21.6	3	0	0	1085.66	24	34
Ras-related protein Rab-5C	RAB5C	RAB5C_HUMAN	23.5	100.0%	4	4	6	0.01%	23.6%	QASPNIVIALAGNK	97.8%	30.9	25	30.9	1	0	0	1395.80	122	135
Ras-related protein Rab-5C	RAB5C	RAB5C_HUMAN	23.5	100.0%	4	4	6	0.01%	23.6%	TAMNVNEIFMAIAK	99.4%	36.2	25	1.69	1	0	0	1568.78	167	180
Ras-related protein Rab-6A	RAB6A	RAB6A_HUMAN	23.6	100.0%	3	4	7	0.01%	22.1%	ELNVMFIETSAK	99.7%	71.8	25	61	3	0	0	1381.70	147	158
Ras-related protein Rab-6A	RAB6A	RAB6A_HUMAN	23.6	100.0%	3	4	7	0.01%	22.1%	GSDVIIMLVGNK	99.7%	77.8	25	68.2	2	0	0	1245.69	116	127
Ras-related protein Rab-6A	RAB6A	RAB6A_HUMAN	23.6	100.0%	3	4	7	0.01%	22.1%	LQLWDTAGQER	99.7%	72.3	25	0	6	0	0	1316.66	64	74
Ras-related protein Rab-6A	RAB6A	RAB6A_HUMAN	23.6	100.0%	3	4	7	0.01%	22.1%	LVFLGEQSVGK	99.7%	64.7	25	51	2	0	0	1176.66	16	26
Ras-related protein Rab-7a	RAB7A	RAB7A_HUMAN	23.5	100.0%	3	3	6	0.01%	18.4%	DPENFPFVVLGNK	99.7%	64.7	25	64.7	2	0	0	1475.75	114	126
Ras-related protein Rab-7a	RAB7A	RAB7A_HUMAN	23.5	100.0%	3	3	6	0.01%	18.4%	EAINVEQAFQTIAR	99.7%	78.6	25	78.6	2	0	0	1589.83	158	171
Ras-related protein Rab-7a	RAB7A	RAB7A_HUMAN	23.5	100.0%	3	3	6	0.01%	18.4%	VIILGDSGVGK	98.1%	31.6	25	18.5	2	0	0	1057.63	11	21
Ras-related protein Rab-9A	RAB9A	RAB9A_HUMAN	22.8	99.8%	2	2	4	0.00%	12.4%	DATNVAAAFEEAVR	99.7%	94.1	25	86.7	2	0	0	1463.71	157	170
Ras-related protein Rab-9A	RAB9A	RAB9A_HUMAN	22.8	99.8%	2	2	4	0.00%	12.4%	VILLGDGGVGK	99.7%	56.7	25	38.2	2	0	0	1027.61	10	20
Ras-related protein Rap-2b	RAP2B	RAP2B_HUMAN	20.5	99.8%	2	2	3	0.00%	17.5%	ASVDELFAEIVR	99.7%	49.3	25	40.3	2	0	0	1348.71	151	162
Ras-related protein Rap-2b	RAP2B	RAP2B_HUMAN	20.5	99.8%	2	2	3	0.00%	17.5%	VPMILVGNK	97.8%	30.8	25	27.5	1	0	0	970.58	109	117

Ras-related protein Rap-2b	RAP2B	RAP2B_HUMAN	20.5	99.8%	2	2	3	0.00%	17.5%	VVVLGSGGVGK	99.7%	58.9	25	44.7	2	0	0	971.59	6	16
Ras-related protein Rap-2c	RAP2C	RAP2C_HUMAN	20.7	100.0%	2	2	3	0.00%	17.5%	SMVDELFAEIVR	96.8%	29.4	25	29.4	1	0	0	1424.71	151	162
Ras-related protein Rap-2c	RAP2C	RAP2C_HUMAN	20.7	100.0%	2	2	3	0.00%	17.5%	VPLILVGNK	99.7%	46.3	25	0	2	0	0	952.62	109	117
Ras-related protein Rap-2c	RAP2C	RAP2C_HUMAN	20.7	100.0%	2	2	3	0.00%	17.5%	VVVLGSGGVGK	99.7%	58.9	25	44.7	2	0	0	971.59	6	16
Ras-related protein R-Ras2	RRAS2	RRAS2_HUMAN	23.4	100.0%	3	3	6	0.01%	17.2%	LVVVGGGGVGK	98.7%	33.3	25	32.1	2	0	0	941.58	17	27
Ras-related protein R-Ras2	RRAS2	RRAS2_HUMAN	23.4	100.0%	3	3	6	0.01%	17.2%	MNVDQAFHELVR	99.7%	62.7	25	56.1	2	0	0	1458.72	162	173
Ras-related protein R-Ras2	RRAS2	RRAS2_HUMAN	23.4	100.0%	3	3	6	0.01%	17.2%	QVTQEEGQQLAR	99.7%	64.8	25	57.7	2	0	0	1386.70	136	147
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	22	22	35	0.04%	24.6%	ADSVVVLLCR	99.7%	49.5	25	41.8	2	0	0	1131.62	201	210
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	22	22	35	0.04%	24.6%	AGAKPDQIGIITPYEGQR	98.8%	27.5	25	20.4	0	2	0	1914.01	794	811
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	22	22	35	0.04%	24.6%	AGLSQSLFER	99.7%	74	25	50.3	2	0	0	1107.58	689	698
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	22	22	35	0.04%	24.6%	AYQHGGVTGLSQY	99.5%	37	25	37	2	0	0	1380.65	1117	1129
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	22	22	35	0.04%	24.6%	CFLSWLVK	96.4%	29	25	19.7	2	0	0	1052.56	237	244
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	22	22	35	0.04%	24.6%	EAIDSPVSFLALHNQIR	99.7%	50.8	25	47.6	2	0	0	1910.01	561	577
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	22	22	35	0.04%	24.6%	EKDFIILSCVR	99.7%	58.3	25	52.7	2	0	0	1379.74	844	854
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	22	22	35	0.04%	24.6%	FTAQGLPDLNHSQVYAVK	99.2%	29.2	25	29.2	0	1	0	1988.02	474	491
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	22	22	35	0.04%	24.6%	IAYFTLPK	99.7%	46.2	25	43.6	2	0	0	952.55	342	349
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	22	22	35	0.04%	24.6%	KLVNTINPGAR	99.7%	62.1	25	52.8	2	0	0	1182.70	929	939
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	22	22	35	0.04%	24.6%	LEADYDKK	98.2%	31.8	25	13.6	1	0	0	981.49	312	319
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	22	22	35	0.04%	24.6%	LKESQTQDNITVR	99.3%	29.8	25	23.4	0	1	0	1531.81	320	332
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	22	22	35	0.04%	24.6%	LMQGDEICLR	99.7%	54.4	25	40.6	1	0	0	1234.59	367	376
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	22	22	35	0.04%	24.6%	LQVQYR	98.1%	31.4	25	0	1	0	0	806.45	709	714
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	22	22	35	0.04%	24.6%	LYQEVEIASVDAFQGR	99.7%	95.9	25	95.9	2	0	0	1824.91	828	843
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	22	22	35	0.04%	24.6%	TDSGNEDLVIIWLR	97.6%	30.5	25	30.4	1	0	0	1630.84	350	363
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	22	22	35	0.04%	24.6%	TFAVDETSVSGYIYHK	99.7%	64.9	25	64.9	1	0	0	1816.88	440	455
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	22	22	35	0.04%	24.6%	TVLQRPLSLIQGPPGTGK	99.7%	39.3	25	39.3	0	2	0	1862.09	492	509
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	22	22	35	0.04%	24.6%	TVTSATIVYHLAR	99.7%	96.2	25	89	2	0	0	1431.80	510	522
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	22	22	35	0.04%	24.6%	VPDNYGDEIAIELR	99.7%	50.3	25	50.3	1	0	0	1603.80	394	407
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	22	22	35	0.04%	24.6%	YEDAYQYQNIFGPLVK	99.7%	82.6	25	82.6	2	0	0	1947.95	296	311
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	22	22	35	0.04%	24.6%	YGVIIVGNPK	99.7%	59.8	25	59.8	1	0	0	1059.62	879	888
Regulator of nonsense transcripts 3B	UPF3B	REN3B_HUMAN	57.8	99.9%	2	2	3	0.00%	5.0%	FLESYATDNEK	99.7%	45.4	25	41	1	0	0	1316.60	163	173
Regulator of nonsense transcripts 3B	UPF3B	REN3B_HUMAN	57.8	99.9%	2	2	3	0.00%	5.0%	KAESTESIGSSEK	99.7%	72.3	25	69.3	2	0	0	1352.65	406	418
Regulatory-associated protein of mTOR	RPTOR	RPTOR_HUMAN	149.0	100.0%	5	5	7	0.01%	3.9%	ALETIGANLQK	99.7%	53.6	25	40.2	1	0	0	1157.65	98	108
Regulatory-associated protein of mTOR	RPTOR	RPTOR_HUMAN	149.0	100.0%	5	5	7	0.01%	3.9%	LDDQIFLNR	99.7%	56.5	25	44.8	1	0	0	1133.60	1013	1021
Regulatory-associated protein of mTOR	RPTOR	RPTOR_HUMAN	149.0	100.0%	5	5	7	0.01%	3.9%	LYSLLSDPIPEVR	99.7%	57.2	25	40.7	2	0	0	1501.83	604	616
Regulatory-associated protein of mTOR	RPTOR	RPTOR_HUMAN	149.0	100.0%	5	5	7	0.01%	3.9%	QDLLVASLFR	99.7%	51.3	25	36.2	2	0	0	1161.66	339	348
Regulatory-associated protein of mTOR	RPTOR	RPTOR_HUMAN	149.0	100.0%	5	5	7	0.01%	3.9%	SVSSYGNIR	99.2%	35.3	25	28.4	1	0	0	982.50	719	727
Replication factor C subunit 1	RFC1	RFC1_HUMAN	128.3	100.0%	5	5	9	0.01%	5.1%	AALLSGPPGVGK	99.5%	37.5	25	32.8	2	0	0	1066.63	646	657
Replication factor C subunit 1	RFC1	RFC1_HUMAN	128.3	100.0%	5	5	9	0.01%	5.1%	AIVAESLNNTSIK	99.7%	46.2	25	41.8	1	0	0	1359.75	688	700
Replication factor C subunit 1	RFC1	RFC1_HUMAN	128.3	100.0%	5	5	9	0.01%	5.1%	GGIQELIGLIK	99.7%	46.4	25	37.4	3	0	0	1140.70	732	742
Replication factor C subunit 1	RFC1	RFC1_HUMAN	128.3	100.0%	5	5	9	0.01%	5.1%	IIDEDGLLNLIR	99.7%	52.1	25	36.5	2	0	0	1383.78	469	480
Replication factor C subunit 1	RFC1	RFC1_HUMAN	128.3	100.0%	5	5	9	0.01%	5.1%	TVNMDYLSLLR	99.7%	50.4	25	50.4	1	0	0	1324.69	993	1003
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	11	12	21	0.02%	39.8%	APGSAGHYELPWVEK	99.7%	35.8	25	35.7	0	2	0	1640.81	27	41
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	11	12	21	0.02%	39.8%	DAMLELNASNDR	99.7%	64.3	25	57.4	1	0	0	1348.62	100	111
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	11	12	21	0.02%	39.8%	EGNVPNIIIAGPPGTGK	99.7%	73.2	25	66.1	2	0	0	1633.89	66	82
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	11	12	21	0.02%	39.8%	FALACNASDKIIEPIQSR	99.7%	44.6	25	44.2	0	2	0	2033.05	167	184
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	11	12	21	0.02%	39.8%	IAEGVNSLLQMAGLLAR	99.7%	91.4	25	86.4	4	0	0	1755.98	327	343
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	11	12	21	0.02%	39.8%	IIILDEADSMTDGAQQALR	99.7%	91.2	25	83.2	1	0	0	2060.03	137	155
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	11	12	21	0.02%	39.8%	IIILDEADSMTDGAQQALRR	99.7%	35.3	25	33	0	1	0	2232.13	137	156
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	11	12	21	0.02%	39.8%	LNEIVGNEDTVSR	99.7%	91.5	25	91.5	2	0	0	1445.72	47	59
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	11	12	21	0.02%	39.8%	LTDAQILTR	99.7%	73	25	64.6	2	0	0	1030.59	193	201
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	11	12	21	0.02%	39.8%	TTSILCLAR	99.7%	43.9	25	30.4	2	0	0	1034.57	83	91

Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	11	12	21	0.02%	39.8%	VCDEPHPLLVK	99.7%	51.5	25	37	2	0	0	1306.68	254	264
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	10	11	20	0.02%	32.0%	AIYHLEAFVAK	99.7%	55	25	36	2	0	0	1261.69	328	338
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	10	11	20	0.02%	32.0%	ALLMCEACR	99.7%	45.9	25	45.9	4	0	0	1123.51	226	234
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	10	11	20	0.02%	32.0%	EGLNLPSQLAHR	99.7%	59.8	25	52.5	2	0	0	1334.72	203	214
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	10	11	20	0.02%	32.0%	ELYGVGVEK	94.5%	27.3	25	18.9	1	0	0	993.53	58	66
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	10	11	20	0.02%	32.0%	ETANAIVSQQTPQR	99.7%	98.1	25	92.2	2	0	0	1542.79	257	270
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	10	11	20	0.02%	32.0%	LDYHKEQAAQLR	99.0%	34.5	25	26.4	1	0	0	1471.77	16	27
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	10	11	20	0.02%	32.0%	NLVQCGDFPHLLVYGPSGAGK	99.2%	29.2	25	29	0	2	0	2229.11	28	48
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	10	11	20	0.02%	32.0%	TVAQSQQLETNSQR	99.7%	95.4	25	87.8	2	0	0	1589.79	114	127
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	10	11	20	0.02%	32.0%	VVLLTEVDK	99.7%	41.9	25	41.9	2	0	0	1015.60	131	139
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	10	11	20	0.02%	32.0%	VVLLTEVDKLTK	99.7%	70.7	25	70.7	2	0	0	1357.83	131	142
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	10	10	17	0.02%	31.1%	AITFLQSATR	99.7%	90.6	25	82.5	2	0	0	1107.62	241	250
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	10	10	17	0.02%	31.1%	ELFGPELFR	99.7%	52.5	25	32.6	2	0	0	1107.58	94	102
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	10	10	17	0.02%	31.1%	GTSISTKPPLTK	99.7%	65.8	25	40.5	2	0	0	1229.71	7	18
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	10	10	17	0.02%	31.1%	IIEPLTSR	99.1%	34.7	25	9.13	1	0	0	928.55	186	193
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	10	10	17	0.02%	31.1%	ISDEGIAYLVK	99.7%	76.4	25	70.8	2	0	0	1207.66	222	232
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	10	10	17	0.02%	31.1%	NFAQLTVSGSR	99.7%	48.9	25	20.8	1	0	0	1179.61	125	135
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	10	10	17	0.02%	31.1%	SLEGADLPNLLFYGPPGTGK	99.7%	63.8	25	63.8	2	0	0	2046.05	65	84
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	10	10	17	0.02%	31.1%	TSTILAAAR	99.7%	57.4	25	49.5	2	0	0	903.53	85	93
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	10	10	17	0.02%	31.1%	VITDIAGVIPAEK	99.7%	58.2	25	53.2	1	0	0	1325.77	261	273
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	10	10	17	0.02%	31.1%	VLELNASDER	99.7%	70.2	25	63.3	2	0	0	1145.58	105	114
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	9	11	23	0.02%	31.2%	ALNILQSTNMAFGK	99.7%	89.6	25	78.7	4	0	0	1523.79	216	229
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	9	11	23	0.02%	31.2%	ALVTLSSGDMR	99.7%	46.8	25	37.5	1	0	0	1149.59	204	214
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	9	11	23	0.02%	31.2%	FCLICNYLSK	99.7%	44.7	25	40.8	2	0	0	1317.63	151	160
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	9	11	23	0.02%	31.2%	FGPLTPELMVPR	99.6%	38.9	25	33.9	5	0	0	1356.73	174	185
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	9	11	23	0.02%	31.2%	GPILSFASTR	99.7%	66.9	25	65.3	6	0	0	1048.58	103	112
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	9	11	23	0.02%	31.2%	IQLSSLIAAFQVTR	99.7%	84.5	25	84.5	2	0	0	1546.90	320	333
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	9	11	23	0.02%	31.2%	LVILDEADAMTQDAQNALR	99.7%	99.2	25	96.4	1	0	0	2103.04	121	139
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	9	11	23	0.02%	31.2%	MADIEYR	99.7%	46.2	25	38.3	1	0	0	897.41	305	311
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	9	11	23	0.02%	31.2%	TSTILACAK	99.6%	38.5	25	32.3	1	0	0	964.51	67	75
Required for meiotic nuclear division protein 1 homolog	RMND1	RMND1_HUMAN	51.6	100.0%	4	4	7	0.01%	10.7%	DAANILVMGVENSAK	99.7%	96.1	25	93.3	2	0	0	1531.78	205	219
Required for meiotic nuclear division protein 1 homolog	RMND1	RMND1_HUMAN	51.6	100.0%	4	4	7	0.01%	10.7%	EGDPGTIFFFR	99.6%	38.9	25	38.9	1	0	0	1285.62	220	230
Required for meiotic nuclear division protein 1 homolog	RMND1	RMND1_HUMAN	51.6	100.0%	4	4	7	0.01%	10.7%	IGELFALR	99.7%	53.1	25	42.3	2	0	0	918.54	353	360
Required for meiotic nuclear division protein 1 homolog	RMND1	RMND1_HUMAN	51.6	100.0%	4	4	7	0.01%	10.7%	LNSELDLDDAILEK	99.7%	65.6	25	59.9	2	0	0	1587.81	289	302
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	7	12	0.01%	23.3%	AEELHYPLGER	99.6%	38	25	34.8	1	0	0	1313.65	25	35
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	7	12	0.01%	23.3%	EALLGVQEDVDEYVK	99.7%	87.2	25	87.2	2	0	0	1706.85	42	56
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	7	12	0.01%	23.3%	QLHDDYFYHDEL	99.7%	52.2	25	41.8	2	1	0	1594.68	306	317
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	7	12	0.01%	23.3%	VIDFDENTALDDAEEESFR	99.7%	102	25	102	2	0	0	2214.97	130	148
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	7	12	0.01%	23.3%	VIDFDENTALDDAEEESFRK	99.6%	32	25	30	0	2	0	2343.06	130	149
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	7	12	0.01%	23.3%	WDPTANEDPEWILVEK	99.7%	64	25	63.5	2	0	0	1941.92	217	232
Retinoid-inducible serine carboxypeptidase	SCPEP1	RISC_HUMAN	50.8	100.0%	3	3	4	0.00%	6.4%	MAAGIGLELYK	99.7%	48.5	25	46.5	1	0	0	1165.63	172	182
Retinoid-inducible serine carboxypeptidase	SCPEP1	RISC_HUMAN	50.8	100.0%	3	3	4	0.00%	6.4%	NLAFYWILK	99.7%	47.6	25	27.7	2	0	0	1167.66	420	428
Retinoid-inducible serine carboxypeptidase	SCPEP1	RISC_HUMAN	50.8	100.0%	3	3	4	0.00%	6.4%	SLETSAFVK	98.1%	31.5	25	25.2	1	0	0	981.53	408	416
Rho-related GTP-binding protein RhoC	RHOC	RHOC_HUMAN	22.0	99.9%	2	2	4	0.00%	10.9%	ISAFGYLECSAK	99.7%	72.8	25	68.6	2	0	0	1345.65	151	162
Rho-related GTP-binding protein RhoC	RHOC	RHOC_HUMAN	22.0	99.9%	2	2	4	0.00%	10.9%	TCLLIVFSK	99.7%	39.7	25	32.7	2	0	0	1080.61	19	27
Rho-related GTP-binding protein RhoG	RHOG	RHOG_HUMAN	21.3	100.0%	3	3	3	0.00%	19.4%	AVLNPTPIKR	96.8%	29.5	25	16.9	1	0	0	1108.68	175	184
Rho-related GTP-binding protein RhoG	RHOG	RHOG_HUMAN	21.3	100.0%	3	3	3	0.00%	19.4%	TCLLICYTTNAFPK	99.7%	49	25	49	1	0	0	1701.83	17	30
Rho-related GTP-binding protein RhoG	RHOG	RHOG_HUMAN	21.3	100.0%	3	3	3	0.00%	19.4%	YLECSALQQDGVK	95.1%	27.7	25	25.5	1	0	0	1510.72	154	166
Ribonuclease P protein subunit p14	RPP14	RPP14_HUMAN	13.7	100.0%	3	3	5	0.01%	26.6%	ICSSGLVK	98.8%	33.6	25	21.5	1	0	0	863.47	77	84
Ribonuclease P protein subunit p14	RPP14	RPP14_HUMAN	13.7	100.0%	3	3	5	0.01%	26.6%	PAPAATYER	99.7%	39.7	25	37.7	2	0	0	975.49	2	10
Ribonuclease P protein subunit p14	RPP14	RPP14_HUMAN	13.7	100.0%	3	3	5	0.01%	26.6%	VIQVSPFLLALSGNSR	99.7%	78.4	25	72.2	2	0	0	1700.97	104	119

Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	4	4	6	0.01%	20.9%	ADLHGAIISVTK	99.5%	37.8	25	34	1	0	0	1224.69	133	144
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	4	4	6	0.01%	20.9%	EANDSDVQPSGAQR	99.7%	45.8	25	45.8	2	0	0	1473.66	13	26
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	4	4	6	0.01%	20.9%	LFDIKPEQQR	99.6%	38.8	25	32.2	2	0	0	1273.69	86	95
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	4	4	6	0.01%	20.9%	SVIYHALSQK	97.4%	30.3	25	21.1	1	0	0	1145.63	3	12
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	6	6	16	0.02%	27.2%	GLAFELVYSPAIK	99.7%	63.8	25	61.1	2	0	0	1407.79	149	161
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	6	6	16	0.02%	27.2%	KTAFGIISTVK	99.7%	52.9	25	52.9	2	0	0	1164.70	236	246
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	6	6	16	0.02%	27.2%	LYDVVAVFPK	99.7%	72.2	25	72.1	5	0	0	1150.65	99	108
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	6	6	16	0.02%	27.2%	NVIISSAAERPLEIR	99.7%	43.9	25	34.9	2	0	0	1667.94	184	198
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	6	6	16	0.02%	27.2%	RPPINVAIDR	99.4%	36.6	25	24.3	3	0	0	1150.67	139	148
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	6	6	16	0.02%	27.2%	YTISSALNLMQICK	99.7%	44.1	25	44.1	2	0	0	1641.83	168	181
Ribonuclease P protein subunit p38	RPP38	RPP38_HUMAN	31.8	100.0%	4	4	7	0.01%	14.1%	ELLLVLVCK	99.7%	40	25	40	2	0	0	1086.66	128	136
Ribonuclease P protein subunit p38	RPP38	RPP38_HUMAN	31.8	100.0%	4	4	7	0.01%	14.1%	NTTDFVDEVR	99.7%	42.7	25	32.3	2	0	0	1195.56	185	194
Ribonuclease P protein subunit p38	RPP38	RPP38_HUMAN	31.8	100.0%	4	4	7	0.01%	14.1%	QLAIGVNEVTR	99.7%	47.5	25	35	2	0	0	1199.67	112	122
Ribonuclease P protein subunit p38	RPP38	RPP38_HUMAN	31.8	100.0%	4	4	7	0.01%	14.1%	TSLNNPYIIR	99.7%	55.3	25	46.8	1	0	0	1190.65	23	32
Ribonuclease P/MRP protein subunit POP5	POP5	POP5_HUMAN	18.8	100.0%	3	4	5	0.01%	22.7%	LSLDDRVLSSLVR	99.3%	29.8	25	28.1	1	1	0	1472.84	22	34
Ribonuclease P/MRP protein subunit POP5	POP5	POP5_HUMAN	18.8	100.0%	3	4	5	0.01%	22.7%	YLLCELVSDDPR	96.8%	29.4	25	26.6	1	0	0	1479.72	8	19
Ribonuclease P/MRP protein subunit POP5	POP5	POP5_HUMAN	18.8	100.0%	3	4	5	0.01%	22.7%	YLNAYTGIVLLR	99.7%	59.5	25	51.4	2	0	0	1395.80	57	68
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	8	8	12	0.01%	9.8%	AASVHTVGEDTEETPHR	99.4%	30.3	25	30.3	0	1	0	1835.85	449	465
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	8	8	12	0.01%	9.8%	AGPEGTSQEIPK	99.7%	54.4	25	43.9	2	0	0	1213.61	89	100
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	8	8	12	0.01%	9.8%	EMLGPVTFIWK	99.7%	41.8	25	41.8	2	0	0	1320.70	303	313
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	8	8	12	0.01%	9.8%	ISDQDLNR	99.7%	51.1	25	31.8	2	0	0	960.47	567	574
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	8	8	12	0.01%	9.8%	LGWGSGWDVLLPK	99.7%	48	25	43.6	1	0	0	1427.77	612	624
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	8	8	12	0.01%	9.8%	NQPTNVTLSSGFVADR	99.7%	57.4	25	57.4	1	0	0	1705.85	15	30
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	8	8	12	0.01%	9.8%	SSNSLVFQTLPR	99.7%	39.1	25	23.5	1	0	0	1348.72	126	137
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	8	8	12	0.01%	9.8%	YITASTFAQAR	99.7%	51.2	25	44.9	2	0	0	1228.63	101	111
Ribonucleoside-diphosphate reductase subunit M2 B	RRM2B	RIR2B_HUMAN	40.7	100.0%	3	3	4	0.00%	11.4%	EFLFNAIETMPYVK	99.6%	38.1	25	38.1	1	0	0	1701.86	153	166
Ribonucleoside-diphosphate reductase subunit M2 B	RRM2B	RIR2B_HUMAN	40.7	100.0%	3	3	4	0.00%	11.4%	FSQEVQVPEAR	99.7%	59.2	25	46.2	2	0	0	1289.65	111	121
Ribonucleoside-diphosphate reductase subunit M2 B	RRM2B	RIR2B_HUMAN	40.7	100.0%	3	3	4	0.00%	11.4%	GLMPGLTFSNELISR	99.1%	34.7	25	33.3	1	0	0	1634.86	212	226
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	7	8	16	0.02%	29.2%	ENISEWR	99.7%	46.3	25	39.8	1	0	0	933.44	157	163
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	7	8	16	0.02%	29.2%	IFSGSSHQDLSQK	99.7%	66.3	25	64.8	2	0	0	1433.70	6	18
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	7	8	16	0.02%	29.2%	MVLVGDVKDR	99.7%	69.2	25	55.1	4	0	0	1147.61	205	214
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	7	8	16	0.02%	29.2%	NCTIVSPDAGGAK	99.7%	61.1	25	51.3	2	0	0	1289.62	164	176
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	7	8	16	0.02%	29.2%	VAILVDDMADTCGTICHAADK	99.3%	30.1	25	30.1	0	1	0	2292.03	215	235
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	7	8	16	0.02%	29.2%	VTAVIPCFPYAR	99.7%	49.1	25	44.9	4	0	0	1393.73	85	96
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	7	8	16	0.02%	29.2%	VYAILTHGIFSGPAISR	98.8%	27.8	25	27.8	0	2	0	1802.00	244	260
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	2	2	3	0.00%	28.9%	FSNQETSVEIGESVR	99.7%	48	25	48	1	0	0	1681.80	35	49
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	2	2	3	0.00%	28.9%	MVLVGDVKDR	99.7%	69.2	25	55.1	4	0	0	1147.61	205	214
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	2	2	3	0.00%	28.9%	PNIVLFSGSSHQDLSQR	99.7%	45.9	25	41.4	0	2	0	1884.96	2	18
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	2	2	3	0.00%	28.9%	VAILVDDMADTCGTICHAADK	99.3%	30.1	25	30.1	0	1	0	2292.03	215	235
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	2	2	3	0.00%	28.9%	VTAVIPCFPYAR	99.7%	49.1	25	44.9	4	0	0	1393.73	85	96
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	2	2	3	0.00%	28.9%	VYAILTHGIFSGPAISR	98.8%	27.8	25	27.8	0	2	0	1802.00	244	260
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	5	5	9	0.01%	8.0%	FVNLISER	99.7%	53.5	25	33.8	2	0	0	977.54	122	129
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	5	5	9	0.01%	8.0%	GCYFVLDWLQK	99.7%	79.4	25	79.4	2	0	0	1428.70	172	182
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	5	5	9	0.01%	8.0%	LLDVTGGLGTDELR	99.7%	108	25	103	2	0	0	1458.78	99	112
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	5	5	9	0.01%	8.0%	SGNELPLAVASTADLIR	99.7%	92.2	25	91.8	2	0	0	1726.93	80	96
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	5	5	9	0.01%	8.0%	VECVLAELK	99.5%	37.3	25	24.1	1	0	0	1060.57	304	312
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	26	0.03%	30.8%	AAESETPGKSPEK	99.7%	45.3	25	35.5	2	0	0	1330.65	418	430
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	26	0.03%	30.8%	ATNESEDEIPQLVPIGK	99.7%	51.5	25	46.7	2	0	0	1839.93	357	373
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	26	0.03%	30.8%	DDVAPESGDTTVK	97.7%	30.7	25	30.7	1	0	0	1333.61	319	331
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	26	0.03%	30.8%	EINDCIGGTVLNISK	99.7%	101	25	97.1	2	0	0	1632.83	193	207
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	26	0.03%	30.8%	KVPVSVNLLSK	99.7%	44.3	25	44.3	2	0	0	1183.74	178	188

Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	26	0.03%	30.8%	LLPSLIGR	99.5%	37.2	25	28	2	0	0	868.56	164	171
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	26	0.03%	30.8%	LLSSFDFFLTDAR	99.7%	98.3	25	93.6	2	0	0	1531.78	148	160
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	26	0.03%	30.8%	LPEKWESVK	97.2%	30	25	10.5	1	0	0	1115.61	241	249
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	26	0.03%	30.8%	LTLPHSIR	99.6%	38.9	25	38.9	2	0	0	936.56	82	89
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	26	0.03%	30.8%	RLLPSLIGR	99.7%	42.2	25	37	1	0	0	1024.66	163	171
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	26	0.03%	30.8%	SAALPIFSSFVSNWDEATK	99.7%	77.6	25	77.2	1	0	0	2070.02	258	276
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	26	0.03%	30.8%	TPANEKVEIQK	99.7%	39.3	25	27.2	2	0	0	1256.68	375	385
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	26	0.03%	30.8%	TVSQIISLQTLK	99.7%	79.9	25	79.9	2	0	0	1330.79	125	136
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	26	0.03%	30.8%	TVSQIISLQTLKK	99.7%	49	25	49	2	0	0	1458.89	125	137
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	26	0.03%	30.8%	VPVSVNLLSK	99.7%	49.5	25	45.4	2	0	0	1055.65	179	188
Ribosomal protein S6 kinase alpha-1	RPS6KA1	KS6A1_HUMAN	82.7	99.8%	2	2	2	0.00%	7.4%	APQAPLHSVVQQLHGK	99.7%	34.5	25	34.5	0	1	0	1709.94	395	410
Ribosomal protein S6 kinase alpha-1	RPS6KA1	KS6A1_HUMAN	82.7	99.8%	2	2	2	0.00%	7.4%	DLKPENILLDEEGHIK	99.7%	52	25	48.1	0	2	0	1862.99	187	202
Ribosomal protein S6 kinase alpha-1	RPS6KA1	KS6A1_HUMAN	82.7	99.8%	2	2	2	0.00%	7.4%	EASFVLHTIGK	99.4%	36.8	25	35.3	1	0	0	1201.66	511	521
Ribosomal protein S6 kinase alpha-1	RPS6KA1	KS6A1_HUMAN	82.7	99.8%	2	2	2	0.00%	7.4%	YGQHPNIITLK	99.2%	35.5	25	30.3	1	0	0	1283.71	466	476
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	5	5	6	0.01%	8.9%	DLKPENILLDEEGHIK	99.7%	52	25	48.1	0	2	0	1862.99	193	208
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	5	5	6	0.01%	8.9%	GAMAATYSALNR	99.7%	58.6	25	51.2	1	0	0	1241.59	701	712
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	5	5	6	0.01%	8.9%	LGMPQFLSPEAQSLLR	99.1%	34.5	25	34.5	1	0	0	1786.95	285	300
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	5	5	6	0.01%	8.9%	NQSPVLEPVGR	97.3%	30.1	25	25.9	1	0	0	1195.64	713	723
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	5	5	6	0.01%	8.9%	YGQHPNIITLK	99.2%	35.5	25	30.3	1	0	0	1283.71	470	480
Ribosomal RNA processing protein 1 homolog A	RRP1	RRP1_HUMAN	52.8	99.8%	2	2	3	0.00%	5.4%	TKDSLVLNNITR	99.7%	61.2	25	56.8	1	0	0	1373.77	204	215
Ribosomal RNA processing protein 1 homolog A	RRP1	RRP1_HUMAN	52.8	99.8%	2	2	3	0.00%	5.4%	VGAEELTADQNLK	99.7%	56.2	25	44.1	2	0	0	1387.71	180	192
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	7	7	13	0.01%	12.1%	ELLADQNLK	99.3%	35.6	25	31.1	1	0	0	1043.57	183	191
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	7	7	13	0.01%	12.1%	ETGGFSQEELLK	99.7%	54.6	25	36.3	2	0	0	1337.66	42	53
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	7	7	13	0.01%	12.1%	GVFEAIVDQSPFVPEETMEEQK	99.7%	38.9	25	38.9	0	2	0	2525.18	215	236
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	7	7	13	0.01%	12.1%	SILVSPTGPSR	97.3%	30.1	25	14.4	2	0	0	1113.63	702	712
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	7	7	13	0.01%	12.1%	SSTATHPPGPAVQLNK	99.7%	47.4	25	44	2	0	0	1604.84	661	676
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	7	7	13	0.01%	12.1%	TPTSSPASSPLVAK	99.7%	70	25	69.3	2	0	0	1342.72	728	741
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	7	7	13	0.01%	12.1%	VFLDVLMK	99.5%	37.5	25	34.3	2	0	0	964.55	144	151
Ribosome biogenesis protein BMS1 homolog	BMS1	BMS1_HUMAN	145.8	100.0%	3	3	5	0.01%	2.3%	AFAVQSAVR	99.7%	39.7	25	30.2	1	0	0	948.53	44	52
Ribosome biogenesis protein BMS1 homolog	BMS1	BMS1_HUMAN	145.8	100.0%	3	3	5	0.01%	2.3%	IAATGVVLDLDK	99.7%	87.5	25	76.9	2	0	0	1214.70	1008	1019
Ribosome biogenesis protein BMS1 homolog	BMS1	BMS1_HUMAN	145.8	100.0%	3	3	5	0.01%	2.3%	STLIQCLIR	99.7%	43.7	25	30.9	2	0	0	1103.62	96	104
Ribosome biogenesis protein BRX1 homolog	BRIX1	BRX1_HUMAN	41.4	99.7%	2	2	3	0.00%	5.7%	FLVQNIHTLAELK	99.7%	67.9	25	56.6	2	0	0	1525.87	141	153
Ribosome biogenesis protein BRX1 homolog	BRIX1	BRX1_HUMAN	41.4	99.7%	2	2	3	0.00%	5.7%	FVLNLIK	95.0%	27.6	25	27.6	1	0	0	846.54	236	242
Ribosome biogenesis regulatory protein homolog	RRS1	RRS1_HUMAN	41.2	99.7%	2	2	3	0.00%	4.9%	AEQDEAEKLQR	99.7%	45.9	25	38.6	2	0	0	1316.64	13	23
Ribosome biogenesis regulatory protein homolog	RRS1	RRS1_HUMAN	41.2	99.7%	2	2	3	0.00%	4.9%	LPEPTTR	94.5%	27.3	25	10.1	1	0	0	813.45	92	98
Ribosome production factor 2 homolog	RPF2	RPF2_HUMAN	35.6	100.0%	3	3	3	0.00%	10.1%	GPTVSNIR	98.8%	33.3	25	17	1	0	0	843.47	169	176
Ribosome production factor 2 homolog	RPF2	RPF2_HUMAN	35.6	100.0%	3	3	3	0.00%	10.1%	NISHDTFGTTYGR	99.7%	47.7	25	45.8	1	0	0	1468.68	253	265
Ribosome production factor 2 homolog	RPF2	RPF2_HUMAN	35.6	100.0%	3	3	3	0.00%	10.1%	THLASDDLYK	99.7%	42.6	25	37.3	1	0	0	1162.57	228	237
RING finger protein 219	RNF219	RN219_HUMAN	81.1	100.0%	2	2	3	0.00%	2.9%	IQSSLSSASPSK	96.9%	29.5	25	20.3	1	0	0	1191.62	711	722
RING finger protein 219	RNF219	RN219_HUMAN	81.1	100.0%	2	2	3	0.00%	2.9%	NLSLESQIK	99.0%	34.2	25	14.3	2	0	0	1031.57	117	125
RNA 3'-terminal phosphate cyclase	RTCA	RTCA_HUMAN	39.3	100.0%	4	4	11	0.01%	12.8%	AFVAGVLPFK	99.7%	58.1	25	49.5	4	0	0	1048.62	196	205
RNA 3'-terminal phosphate cyclase	RTCA	RTCA_HUMAN	39.3	100.0%	4	4	11	0.01%	12.8%	DLYVNIQPVQEPK	99.7%	58.3	25	52.5	2	0	0	1542.82	224	236
RNA 3'-terminal phosphate cyclase	RTCA	RTCA_HUMAN	39.3	100.0%	4	4	11	0.01%	12.8%	FGFIFNCDIK	99.7%	50.9	25	41.6	2	0	0	1260.61	147	156
RNA 3'-terminal phosphate cyclase	RTCA	RTCA_HUMAN	39.3	100.0%	4	4	11	0.01%	12.8%	VSTALSCLLGLPLR	99.7%	62.4	25	54.6	3	0	0	1499.86	22	35
RNA 3'-terminal phosphate cyclase-like protein	RCL1	RCL1_HUMAN	40.8	100.0%	2	2	4	0.00%	6.2%	LLLEEIYR	99.6%	39.1	25	39.1	2	0	0	1048.60	282	289
RNA 3'-terminal phosphate cyclase-like protein	RCL1	RCL1_HUMAN	40.8	100.0%	2	2	4	0.00%	6.2%	VLLGPLSPYTIEFLR	99.3%	36	25	36	2	0	0	1717.99	315	329
RNA polymerase II-associated factor 1 homolog	PAF1	PAF1_HUMAN	60.0	100.0%	5	5	6	0.01%	11.9%	AGVQSGTNALLVVK	99.7%	67.5	25	60.5	1	0	0	1356.78	339	352
RNA polymerase II-associated factor 1 homolog	PAF1	PAF1_HUMAN	60.0	100.0%	5	5	6	0.01%	11.9%	EGDGVYYNELETR	99.7%	47.2	25	47.2	1	0	0	1544.69	317	329
RNA polymerase II-associated factor 1 homolog	PAF1	PAF1_HUMAN	60.0	100.0%	5	5	6	0.01%	11.9%	GYEENYFFIFR	99.7%	49.3	25	42.2	2	0	0	1484.68	306	316
RNA polymerase II-associated factor 1 homolog	PAF1	PAF1_HUMAN	60.0	100.0%	5	5	6	0.01%	11.9%	VTPVEVMPVFPDFK	99.6%	38.6	25	37.2	1	0	0	1604.84	199	212
RNA polymerase II-associated factor 1 homolog	PAF1	PAF1_HUMAN	60.0	100.0%	5	5	6	0.01%	11.9%	YGISNEKPEVK	99.3%	35.7	25	29.9	1	0	0	1263.66	144	154

RNA pseudouridylate synthase domain-containing protein 3	RPUSD3	RUSD3_HUMAN	38.5	99.8%	2	2	4	0.00%	6.6%	SGPLGDQPFAGLLPK	99.7%	53.7	25	53.7	2	0	0	1496.81	54	68
RNA pseudouridylate synthase domain-containing protein 3	RPUSD3	RUSD3_HUMAN	38.5	99.8%	2	2	4	0.00%	6.6%	TLQCLGLR	99.0%	34.5	25	13.2	2	0	0	960.53	342	349
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	8	9	16	0.02%	22.8%	AIKVEQATKPSFESGR	99.7%	55.9	25	55.9	0	2	0	1747.93	78	93
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	8	9	16	0.02%	22.8%	DRDYSDHPSGGSYR	99.5%	37.5	25	37.5	2	0	0	1611.68	269	282
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	8	9	16	0.02%	22.8%	DSYESYGNSR	99.7%	58.6	25	58.6	1	0	0	1177.48	283	292
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	8	9	16	0.02%	22.8%	DYGHSSSRDDYPSR	99.7%	32.8	25	32.8	0	1	0	1641.69	245	258
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	8	9	16	0.02%	22.8%	GFAFVTFESPADAK	99.7%	87	25	54	2	0	0	1486.72	50	63
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	8	9	16	0.02%	22.8%	IVEVLLMK	99.7%	43.9	25	40.8	4	0	0	944.59	34	41
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	8	9	16	0.02%	22.8%	LFIGGLNTETNEK	99.7%	95.6	25	82.8	2	0	0	1435.74	10	22
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	8	9	16	0.02%	22.8%	VEQATKPSFESGR	99.7%	64.9	25	60.3	2	0	0	1435.72	81	93
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	AHLSENELEALEK	99.7%	87.6	25	87.2	2	1	0	1482.74	794	806
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	AQPGAAPGIYQQSAEASSSQGTAANSQSYTIMSPAVLK	99.7%	74.7	25	74.7	0	4	0	3783.81	499	536
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	ASNIVMLR	99.7%	70.9	25	53.5	2	0	0	903.51	127	134
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	DGDYRDQDYR	99.2%	29.1	25	29.1	0	2	0	1302.53	99	108
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	DGLGSDNIGSR	99.7%	55.9	25	48	7	0	0	1090.51	854	864
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	EKYGIPEPPEPK	99.7%	45.8	25	37.5	2	0	0	1383.72	823	834
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	ESATADAGYAILEK	99.7%	111	25	104	7	0	0	1438.71	686	699
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	GDPTGAGPEASLEPGADSVSMQAFSR	99.7%	109	25	108	4	5	0	2534.15	473	498
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	GFAFVEFSHLQDATR	99.7%	114	25	114	8	9	0	1724.84	172	186
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	GLVAAYSGESDSEEEQER	99.7%	138	25	132	4	0	0	1955.85	727	744
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	GQLQSHGVQAR	99.7%	69.9	25	58.4	9	0	0	1180.62	147	157
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	GSSYGVTSTESYK	99.7%	69.3	25	69.3	2	0	0	1365.62	903	915
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	GSSYGVTSTESYKETLHK	99.7%	63.6	25	63.6	2	0	0	1973.95	903	920
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	HQQLSGLHK	99.6%	38.2	25	32.5	2	0	0	1047.57	777	785
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	INEDWLCNK	99.7%	63.7	25	37.5	6	0	0	1191.55	213	221
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	KQGIVTPIEAQTR	99.7%	50.5	25	50.5	2	2	0	1440.82	881	893
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	KYGGISTASVDFEQPTR	99.7%	132	25	132	2	2	0	1855.92	837	853
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	LACLLCR	99.7%	46.4	25	37.6	2	0	0	905.47	759	765
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	LDQQTLPLGGR	99.7%	86.1	25	73.5	6	0	0	1197.66	253	263
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	MLPQAATEDDIR	99.7%	74.1	25	65.1	8	0	0	1359.66	135	146
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	MLPQAATEDDIRGQLQSHGVQAR	99.7%	43.1	25	40.9	0	1	0	2537.25	135	157
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	MLQAMGWK	99.7%	46.9	25	37.4	6	0	0	964.47	865	872
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	NSFQPISSLR	99.7%	51.8	25	19.9	4	0	0	1148.61	671	680
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	QGIVTPIEAQTR	99.7%	64	25	49.6	4	0	0	1312.72	882	893
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	QNLEIHR	98.3%	31.9	25	19.5	2	0	0	909.49	786	792
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	RESATADAGYAILEK	99.7%	50.3	25	45.9	0	2	0	1594.81	685	699
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	RTYVPALEQSADGHK	99.7%	40.7	25	40.7	0	2	0	1671.85	613	627
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	SEAEQKLPLGTR	99.7%	71.2	25	52.1	10	2	0	1328.72	241	252
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	TINVEFAK	99.7%	44.5	25	35.8	2	0	0	921.50	376	383
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	TYVPALEQSADGHK	99.7%	76.9	25	69.6	4	0	0	1515.74	614	627
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	TYVPALEQSADGHKETGAPSK	98.4%	26.4	25	26.4	0	3	0	2186.07	614	634
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	VSMHYSDPKPK	99.6%	32.4	25	29.2	0	5	0	1304.63	202	212
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	WMEANQHSLNILGQK	99.7%	35.9	25	34.8	1	1	0	1768.88	187	201
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	YGGISTASVDFEQPTR	99.7%	93.8	25	93.8	3	0	0	1727.82	838	853
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	YGGISTASVDFEQPTRDGLGSDNIGSR	99.7%	70.4	25	70.4	0	1	0	2799.32	838	864
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	36	49	157	0.16%	39.4%	YGIPEPPEPK	97.4%	30.3	25	22	2	0	0	1126.58	825	834
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	10	22	0.02%	17.6%	AQPSVSLGAPYR	98.8%	33.4	25	33	3	0	0	1245.66	275	286
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	10	22	0.02%	17.6%	ASYDDPYKK	97.9%	31.2	25	29.5	1	0	0	1086.51	586	594
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	10	22	0.02%	17.6%	ASYVAPLTAQPATYR	99.7%	80.7	25	68.4	3	0	0	1608.84	224	238
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	10	22	0.02%	17.6%	GPGLAVQSGDK	99.5%	37.4	25	37.4	1	0	0	1028.54	154	164
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	10	22	0.02%	17.6%	IFVGNVSAACTSQELR	99.7%	121	25	121	4	0	0	1751.87	81	96

RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	10	22	0.02%	17.6%	INVELSTK	99.5%	37.4	25	27.7	4	0	0	903.51	142	149
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	10	22	0.02%	17.6%	KGPGLAVQSGDK	97.8%	30.9	25	21.7	1	0	0	1156.63	153	164
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	10	22	0.02%	17.6%	TQPMTAQAASYR	99.3%	35.6	25	35	1	0	0	1324.63	263	274
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	10	22	0.02%	17.6%	TQSSASLAASYAAQQHPQAAASYR	99.7%	75.8	25	75.8	0	2	0	2465.18	518	541
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	10	22	0.02%	17.6%	YSGSYNDYLR	99.7%	62.3	25	62.3	2	0	0	1237.55	648	657
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	9	16	0.02%	13.0%	AKENDENCGPTTTVFVGNISEK	99.2%	29.5	25	29.5	0	1	0	2410.12	76	97
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	9	16	0.02%	13.0%	EKEELEEIR	99.7%	44.2	25	23.6	2	0	0	1174.60	539	547
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	9	16	0.02%	13.0%	EYSSELNAPSQESDSHPR	99.0%	28.5	25	28.5	0	1	0	2032.88	217	234
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	9	16	0.02%	13.0%	FPVAPLIPYPLITK	99.7%	48.8	25	48.8	2	0	0	1568.95	248	261
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	9	16	0.02%	13.0%	GAIEVLIR	99.7%	53.9	25	36.6	2	0	0	870.54	209	216
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	9	16	0.02%	13.0%	LGASNSPGQPNSVK	99.7%	55	25	55	2	0	0	1355.69	672	685
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	9	16	0.02%	13.0%	LLAEGHPDPDAELQR	99.7%	53	25	53	2	2	0	1660.83	550	564
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	9	16	0.02%	13.0%	LLHDLQIGEK	99.2%	35.4	25	32.2	2	0	0	1165.66	146	155
RNA-binding protein 26	RBM26	RBM26_HUMAN	113.6	100.0%	4	4	4	0.00%	3.9%	AEAEAAAVHGAR	99.7%	45.3	25	39.5	1	0	0	1152.58	936	947
RNA-binding protein 26	RBM26	RBM26_HUMAN	113.6	100.0%	4	4	4	0.00%	3.9%	AISSTEAVLNNR	99.7%	65.3	25	59.4	1	0	0	1274.67	586	597
RNA-binding protein 26	RBM26	RBM26_HUMAN	113.6	100.0%	4	4	4	0.00%	3.9%	EGSTQQLQTTSPK	98.2%	31.8	25	30	1	0	0	1404.70	606	618
RNA-binding protein 26	RBM26	RBM26_HUMAN	113.6	100.0%	4	4	4	0.00%	3.9%	TRAEAEAAAVHGAR	98.5%	26.7	25	26.7	0	1	0	1409.72	934	947
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	9	9	13	0.01%	13.0%	AAEGVSAADMAK	99.7%	69.8	25	67.1	2	0	0	1136.53	454	465
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	9	9	13	0.01%	13.0%	FNQLVEQYK	99.7%	45.5	25	22.6	1	0	0	1168.60	730	738
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	9	9	13	0.01%	13.0%	GFGFVQFK	99.4%	36.7	25	25.4	1	0	0	929.49	155	162
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	9	9	13	0.01%	13.0%	IVLHPDTEHSK	97.4%	24.7	25	23	0	1	0	1275.67	366	376
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	9	9	13	0.01%	13.0%	KLLLSATSGEK	98.1%	31.5	25	11.6	1	0	0	1146.67	505	515
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	9	9	13	0.01%	13.0%	LINNNPEIFGPLK	99.7%	42.7	25	40.2	2	0	0	1468.82	559	571
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	9	9	13	0.01%	13.0%	QQLSSEQVSR	99.5%	37	25	30.7	2	0	0	1161.59	709	718
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	9	9	13	0.01%	13.0%	SEQLEELFSQVGPVK	99.7%	87.9	25	77.6	2	0	0	1689.87	17	31
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	9	9	13	0.01%	13.0%	TVAVDWAVAK	99.7%	46.8	25	30	1	0	0	1059.58	183	192
RNA-binding protein 39	RBM39	RBM39_HUMAN	59.4	100.0%	3	3	10	0.01%	6.8%	DLEEFFSTVGK	99.7%	59.6	25	47.3	4	0	0	1271.62	168	178
RNA-binding protein 39	RBM39	RBM39_HUMAN	59.4	100.0%	3	3	10	0.01%	6.8%	TGIDLGTTGR	99.7%	53.9	25	46.9	2	0	0	990.52	347	356
RNA-binding protein 39	RBM39	RBM39_HUMAN	59.4	100.0%	3	3	10	0.01%	6.8%	VLGVPIIVQASQAEK	99.7%	108	25	108	4	0	0	1551.91	218	232
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	7	8	11	0.01%	17.6%	AEDAVEAIR	99.7%	58.6	25	22.4	2	0	0	973.49	121	129
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	7	8	11	0.01%	17.6%	GLDNTEFQGK	99.7%	47.9	25	42.9	2	0	0	1108.53	130	139
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	7	8	11	0.01%	17.6%	GLDNTEFQGKR	99.7%	45.8	25	42.1	1	0	0	1264.63	130	140
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	7	8	11	0.01%	17.6%	LFIGNLPR	99.5%	37.6	25	18.8	1	0	0	929.56	4	11
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	7	8	11	0.01%	17.6%	LHGVNINVEASK	99.7%	52.9	25	42.4	1	1	0	1280.70	60	71
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	7	8	11	0.01%	17.6%	VADLTEQYNEQYGAVR	99.7%	89.6	25	85.9	2	0	0	1855.88	183	198
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	7	8	11	0.01%	17.6%	VLECDIIK	99.2%	35.2	25	20.4	1	0	0	989.53	28	35
RNA-binding protein FUS	FUS	FUS_HUMAN	53.4	100.0%	3	4	7	0.01%	6.3%	AAIDWFDGKEFSGNPIK	99.7%	75.9	25	74.6	1	2	0	1894.93	349	365
RNA-binding protein FUS	FUS	FUS_HUMAN	53.4	100.0%	3	4	7	0.01%	6.3%	GEATVSFDDPPSAK	99.7%	102	25	93.8	2	0	0	1420.66	335	348
RNA-binding protein FUS	FUS	FUS_HUMAN	53.4	100.0%	3	4	7	0.01%	6.3%	LKGEATVSFDDPPSAK	99.7%	35.3	25	35.3	0	2	0	1661.84	333	348
RNA-binding protein Musashi homolog 1	MSI1	MSI1H_HUMAN	39.1	100.0%	3	4	7	0.01%	13.0%	GFGFVTFESEDIVEK	99.7%	62.8	25	56.4	2	0	0	1703.82	151	165
RNA-binding protein Musashi homolog 1	MSI1	MSI1H_HUMAN	39.1	100.0%	3	4	7	0.01%	13.0%	GFGFVTFMDQAGVDK	99.7%	93.6	25	88.2	4	0	0	1618.76	62	76
RNA-binding protein Musashi homolog 1	MSI1	MSI1H_HUMAN	39.1	100.0%	3	4	7	0.01%	13.0%	SYTGLAPGYTYQFPEFR	99.7%	50.6	25	50.6	1	0	0	1996.94	231	247
RNA-binding protein PNO1	PNO1	PNO1_HUMAN	27.9	99.9%	2	2	3	0.00%	9.5%	AEEGFTQVTR	99.7%	46.4	25	35	2	0	0	1137.55	12	21
RNA-binding protein PNO1	PNO1	PNO1_HUMAN	27.9	99.9%	2	2	3	0.00%	9.5%	TAICNLILGNPPSK	99.2%	35	25	24.8	1	0	0	1497.81	223	236
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	3	3	7	0.01%	10.5%	GYAFVQYSNER	99.7%	57.1	25	50.2	2	0	0	1333.62	56	66
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	3	3	7	0.01%	10.5%	SNIDALLSR	99.7%	57	25	37.7	2	0	0	988.54	199	207
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	3	3	7	0.01%	10.5%	VFIGNLNTALVK	99.7%	86.6	25	0	3	0	0	1288.76	23	34
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	9	10	19	0.02%	31.2%	ANCIDSTASAEAVFASEVK	99.7%	80.2	25	80.2	2	0	0	1969.92	266	284
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	9	10	19	0.02%	31.2%	ANCIDSTASAEAVFASEVKK	98.3%	26.2	25	26.2	0	1	0	2098.01	266	285
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	9	10	19	0.02%	31.2%	DHAVVVGVYRPPPK	96.0%	23.1	25	23.1	0	2	0	1533.85	305	318
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	9	10	19	0.02%	31.2%	IVALNAHTFLR	97.4%	30.3	25	24.1	2	0	0	1254.73	245	255

rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	9	10	19	0.02%	31.2%	NLVPGESVYGEKR	99.7%	54.9	25	45.4	2	0	0	1447.75	110	122
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	9	10	19	0.02%	31.2%	NVMVEPHR	96.1%	28.7	25	28.6	1	0	0	997.49	85	92
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	9	10	19	0.02%	31.2%	SGRDLINLAK	98.0%	31.3	25	13.6	1	0	0	1086.63	196	205
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	9	10	19	0.02%	31.2%	TNIIPVIEDAR	99.7%	67.9	25	0	4	0	0	1240.69	208	218
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	9	10	19	0.02%	31.2%	VSISEGDDKIEYR	99.7%	66.9	25	64.1	2	2	0	1510.74	123	135
RRP12-like protein	RRP12	RRP12_HUMAN	143.7	100.0%	4	4	5	0.01%	2.6%	FCIQEIEK	97.5%	30.4	25	22.2	1	0	0	1066.52	287	294
RRP12-like protein	RRP12	RRP12_HUMAN	143.7	100.0%	4	4	5	0.01%	2.6%	RAVLETIR	98.5%	32.6	25	12.1	1	0	0	957.58	711	718
RRP12-like protein	RRP12	RRP12_HUMAN	143.7	100.0%	4	4	5	0.01%	2.6%	SWLLPVIR	99.2%	35.5	25	11.2	1	0	0	983.60	567	574
RRP12-like protein	RRP12	RRP12_HUMAN	143.7	100.0%	4	4	5	0.01%	2.6%	VLATQPGPGR	99.7%	43.6	25	35.8	2	0	0	995.56	1129	1138
RUN and FYVE domain-containing protein 1	RUFY1	RUFY1_HUMAN	79.8	99.8%	2	2	3	0.00%	3.1%	AQNAESSLQQK	99.0%	34.1	25	25.3	1	0	0	1203.60	470	480
RUN and FYVE domain-containing protein 1	RUFY1	RUFY1_HUMAN	79.8	99.8%	2	2	3	0.00%	3.1%	SFFGPLELVEK	98.6%	32.9	25	32.2	2	0	0	1265.68	172	182
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	14	0.01%	19.3%	ALESSIAPIVIFASNR	99.7%	61.5	25	61.5	2	1	0	1687.94	318	333
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	14	0.01%	19.3%	AVLLAGPPGTGK	99.7%	42.9	25	34.2	1	0	0	1080.64	65	76
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	14	0.01%	19.3%	EACGVIVELIK	99.7%	41.7	25	31	2	0	0	1230.68	47	57
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	14	0.01%	19.3%	GLGLDESGLAK	99.7%	55.6	25	48.2	2	0	0	1059.57	23	33
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	14	0.01%	19.3%	LDPSIFESLQK	99.7%	50.5	25	40.3	2	0	0	1276.68	172	182
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	14	0.01%	19.3%	QAASGLVGQENAR	99.7%	76.8	25	69.9	2	0	0	1300.66	34	46
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	14	0.01%	19.3%	TALALAIAQELGSK	99.7%	106	25	106	2	0	0	1385.80	77	90
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	12	23	0.02%	28.9%	AAGVVLEMIR	99.7%	64.6	25	50.8	2	0	0	1058.60	55	64
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	12	23	0.02%	28.9%	ALESDMAPVLIMATNR	99.7%	81.8	25	73.4	2	0	0	1731.88	315	330
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	12	23	0.02%	28.9%	AVLIAGQPGTGK	99.7%	66.1	25	50.2	2	0	0	1111.65	72	83
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	12	23	0.02%	28.9%	DKVQAGDVITIDK	99.7%	66.8	25	52.8	2	0	0	1401.76	185	197
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	12	23	0.02%	28.9%	EVVHTVSLHEIDVINSR	99.7%	52.7	25	52.7	0	2	0	1947.03	237	253
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	12	23	0.02%	28.9%	FVQCPDGELQK	99.6%	38.4	25	30.3	2	0	0	1320.63	224	234
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	12	23	0.02%	28.9%	GTEVQVDDIKR	99.7%	54.7	25	41	2	0	0	1259.66	418	428
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	12	23	0.02%	28.9%	LLIVSTTPYSEK	97.9%	31.1	25	25.1	1	0	0	1350.75	354	365
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	12	23	0.02%	28.9%	LLIVSTTPYSEKDTK	99.7%	66.1	25	66.1	2	0	0	1694.92	354	368
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	12	23	0.02%	28.9%	TQGFLALFSGDTGEIK	99.7%	102	25	94.8	2	0	0	1683.86	254	269
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	12	23	0.02%	28.9%	TTEMETIYDLGTK	99.7%	94	25	94	4	0	0	1501.71	165	177
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	6	8	15	0.02%	18.5%	DLDLKKPIYQR	99.2%	35.4	25	33.7	1	0	0	1388.79	363	373
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	6	8	15	0.02%	18.5%	ELLEIVKK	99.7%	39.7	25	34.9	2	0	0	971.61	344	351
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	6	8	15	0.02%	18.5%	FVIGGPQGDAGLTGR	99.7%	105	25	98.1	2	0	0	1444.75	250	264
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	6	8	15	0.02%	18.5%	TGMILLAGEITSR	99.7%	86.1	25	79.3	4	0	0	1377.74	62	74
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	6	8	15	0.02%	18.5%	TQVTVQYMQDR	99.7%	52.1	25	49.2	2	0	0	1368.66	182	192
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	6	8	15	0.02%	18.5%	YLDEDTIYHLQPSGR	99.7%	74.4	25	74.4	2	2	0	1806.87	235	249
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	33	73	0.08%	25.0%	AEIGIAMGSGTAVAK	99.7%	70.5	25	66.8	4	0	0	1375.73	713	727
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	33	73	0.08%	25.0%	AMGVVVATGVNTEIGK	99.7%	82	25	62.7	3	0	0	1561.83	219	234
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	33	73	0.08%	25.0%	ANACNSVIK	99.1%	34.8	25	22.3	2	0	0	976.49	468	476
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	33	73	0.08%	25.0%	EEMHLEDSANFIK	98.1%	31.5	25	30.5	1	0	0	1562.72	573	585
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	33	73	0.08%	25.0%	EFDELNPSAQR	99.7%	64	25	59.8	2	0	0	1305.61	656	666
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	33	73	0.08%	25.0%	EFTLEFSR	99.7%	50.1	25	35.2	3	0	0	1028.50	482	489
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	33	73	0.08%	25.0%	GAPEGVIDR	99.7%	49.1	25	45.4	2	0	0	913.47	515	523
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	33	73	0.08%	25.0%	GTAVAICR	98.1%	31.4	25	18.8	1	0	0	847.45	629	636
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	33	73	0.08%	25.0%	IGIFGQDEDVTSK	99.7%	76.8	25	70.7	4	0	0	1408.70	638	650
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	33	73	0.08%	25.0%	IRDEMVATEQER	99.7%	59.2	25	50.7	4	0	0	1476.71	235	246
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	33	73	0.08%	25.0%	ISLPVILMDETLK	99.7%	78.9	25	69.3	7	0	0	1471.84	972	984
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	33	73	0.08%	25.0%	KAEIGIAMGSGTAVAK	99.7%	67.9	25	62.8	2	1	0	1519.82	712	727
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	33	73	0.08%	25.0%	KSMSVYCTPNKPSR	98.9%	28.1	25	28.1	0	1	0	1670.80	492	505
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	33	73	0.08%	25.0%	LDEFGEQLSK	99.7%	55.9	25	37.4	3	0	0	1165.57	253	262
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	33	73	0.08%	25.0%	MNVFDTELK	99.7%	46.9	25	31	5	0	0	1112.53	452	460
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	33	73	0.08%	25.0%	NMLFSGTNIAAGK	99.7%	77.4	25	61.2	4	0	0	1339.67	206	218

Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	33	73	0.08%	25.0%	NYLEPGKECVQPATK	99.6%	39.1	25	32.8	1	0	0	1733.85	989	1003
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	33	73	0.08%	25.0%	RIGIFGQDEDVTSK	99.7%	33.7	25	33.7	0	1	0	1564.80	637	650
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	33	73	0.08%	25.0%	SLPSVETLGCTSVICSDK	99.7%	94.5	25	94.5	2	0	0	1952.93	335	352
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	33	73	0.08%	25.0%	SMSVYCTPNKPSR	99.7%	43.8	25	43.8	2	0	0	1526.71	493	505
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	33	73	0.08%	25.0%	TGTLTTNQMSVCR	99.7%	51.7	25	49.6	4	0	0	1468.69	353	365
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	33	73	0.08%	25.0%	VDQSILTGESVSVIK	99.7%	85.4	25	78.2	6	0	0	1574.86	175	189
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	33	73	0.08%	25.0%	VGEATETALTCLVEK	99.7%	119	25	108	4	0	0	1620.82	437	451
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	33	73	0.08%	25.0%	VIMITGDNK	99.7%	41.5	25	13.9	3	0	0	990.53	620	628
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	33	73	0.08%	25.0%	VIMITGDNKGTAVAICR	99.7%	35	25	35	0	1	0	1818.96	620	636
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	20	23	64	0.07%	26.5%	DQIIDSLKR	99.7%	48.9	25	29.2	4	0	0	1087.61	80	88
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	20	23	64	0.07%	26.5%	EPAVLMGILGIYK	99.7%	64.8	25	64.8	2	0	0	1403.80	539	551
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	20	23	64	0.07%	26.5%	GVQQLTR	97.1%	29.8	25	13.6	1	0	0	801.46	89	95
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	20	23	64	0.07%	26.5%	IMGFDFCVSSTNPSEQEPK	99.7%	76.3	25	76.3	1	0	0	2172.96	194	212
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	20	23	64	0.07%	26.5%	LGSSSLTNIPEEVR	99.7%	77.8	25	62.7	3	0	0	1501.79	288	301
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	20	23	64	0.07%	26.5%	LGSSSLTNIPEEVREHVK	99.7%	46.2	25	44.7	0	4	0	1995.05	288	305
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	20	23	64	0.07%	26.5%	LILPELGPVFK	99.7%	51.7	25	41.5	4	0	0	1225.76	408	418
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	20	23	64	0.07%	26.5%	LLLNVTPTVRPDADQMTK	97.9%	25.5	25	25.5	0	1	0	2012.08	306	323
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	20	23	64	0.07%	26.5%	LLTVQHPLEESR	99.7%	62.1	25	56.8	4	0	0	1421.77	101	112
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	20	23	64	0.07%	26.5%	LYDVETK	99.7%	40.1	25	34.1	2	0	0	867.45	149	155
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	20	23	64	0.07%	26.5%	MVHGNITPENIILNK	99.7%	38.8	25	38.8	0	2	0	1692.91	174	188
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	20	23	64	0.07%	26.5%	NACLQTSSLAVR	99.7%	85.7	25	68.9	4	0	0	1319.67	494	505
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	20	23	64	0.07%	26.5%	NSVLPMVYR	98.7%	33.2	25	24.4	2	0	0	1078.57	447	455
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	20	23	64	0.07%	26.5%	QEVAVFVFDKK	99.7%	46.4	25	38.4	3	0	0	1309.72	59	69
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	20	23	64	0.07%	26.5%	QQEPIQILLIFLQK	99.7%	63	25	63	3	1	0	1711.02	419	432
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	20	23	64	0.07%	26.5%	SQQPLKPQVHTPVATVK	96.3%	23.5	25	23.5	0	1	0	1858.05	698	714
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	20	23	64	0.07%	26.5%	VNSLVCLGK	99.7%	44.8	25	35.6	3	0	0	989.54	506	514
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	20	23	64	0.07%	26.5%	VTADVTSAVMGNPVTR	99.7%	118	25	101	9	0	0	1633.82	15	30
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	20	23	64	0.07%	26.5%	VTNIGNQQIDK	99.7%	62.6	25	47.1	4	0	0	1229.65	637	647
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	20	23	64	0.07%	26.5%	YGLLQVSEGLSFLHSSVK	99.7%	69.6	25	69.6	4	2	0	1964.05	156	173
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	8	9	15	0.02%	16.8%	FGQDIISPLLSVK	99.7%	76.1	25	72.6	4	0	0	1416.81	51	63
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	8	9	15	0.02%	16.8%	GTAAEMVAVK	99.7%	69	25	55.7	1	0	0	976.51	215	224
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	8	9	15	0.02%	16.8%	LIDLHTNVATAVLEHIK	99.4%	30.1	25	30.1	0	1	0	1887.07	398	414
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	8	9	15	0.02%	16.8%	LTSAVSSLPELLEK	99.7%	77.8	25	62.2	2	0	0	1486.84	382	395
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	8	9	15	0.02%	16.8%	QQNLPVTR	95.8%	28.3	25	21.2	1	0	0	955.53	542	549
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	8	9	15	0.02%	16.8%	SYDLTPVDKFWQK	99.7%	53.9	25	53.9	2	0	0	1626.82	316	328
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	8	9	15	0.02%	16.8%	VMNTGSQFVMEGVK	99.7%	56	25	56	1	0	0	1558.72	523	536
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	8	9	15	0.02%	16.8%	VNLEESSGVENSPAGARPK	99.7%	110	25	110	2	1	0	1940.97	292	310
Sentrin-specific protease 3	SENP3	SENP3_HUMAN	65.0	100.0%	4	5	7	0.01%	7.7%	GLVLQLIQSYQR	99.7%	39.4	25	34.4	2	0	0	1417.82	358	369
Sentrin-specific protease 3	SENP3	SENP3_HUMAN	65.0	100.0%	4	5	7	0.01%	7.7%	LGLLGALMAEDGVR	99.7%	90.6	25	88.4	3	0	0	1430.77	197	210
Sentrin-specific protease 3	SENP3	SENP3_HUMAN	65.0	100.0%	4	5	7	0.01%	7.7%	STSLTFHWK	99.7%	39.2	25	27	1	0	0	1106.56	141	149
Sentrin-specific protease 3	SENP3	SENP3_HUMAN	65.0	100.0%	4	5	7	0.01%	7.7%	YLQAEAVKK	95.1%	27.8	25	18.6	1	0	0	1049.60	498	506
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	7	7	16	0.02%	13.8%	FINDQYEK	98.9%	33.8	25	24.5	2	0	0	1056.50	382	389
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	7	7	16	0.02%	13.8%	LEPKPQPPVAEATPR	99.7%	50.6	25	50.6	0	2	0	1629.90	223	237
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	7	7	16	0.02%	13.8%	QVENAGAIGPSR	99.7%	57.9	25	46.8	2	0	0	1198.62	118	129
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	7	7	16	0.02%	13.8%	RTELSIDISSK	97.8%	31	25	15.1	1	0	0	1248.68	107	117
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	7	7	16	0.02%	13.8%	VPEVPTAPATDAAPK	99.7%	60.3	25	58.9	4	0	0	1463.77	172	186
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	7	7	16	0.02%	13.8%	VVNIVPVIAK	99.1%	34.7	25	34.7	2	0	0	1051.69	436	445
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	7	7	16	0.02%	13.8%	YLQEEVNINR	99.7%	66.4	25	58.1	3	0	0	1277.65	390	399
Serine hydroxymethyltransferase, mitochondrial	SHMT2	GLYM_HUMAN	56.0	99.7%	2	2	2	0.00%	4.4%	AALEALGSCLNNK	99.7%	46.6	25	39.7	1	0	0	1360.69	83	95
Serine hydroxymethyltransferase, mitochondrial	SHMT2	GLYM_HUMAN	56.0	99.7%	2	2	2	0.00%	4.4%	YSEGYPGKR	94.9%	27.6	25	24.3	1	0	0	1056.51	96	104
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	7	7	11	0.01%	21.1%	AACFAIQK	99.7%	49.2	25	36.5	2	0	0	908.47	190	197

Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	7	7	11	0.01%	21.1%	DHPALNYNIVSGPPSHK	99.7%	39.3	25	39.3	0	2	0	1845.92	76	92
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	7	7	11	0.01%	21.1%	ECINFASFNFLGLLDNPR	99.7%	82.3	25	82.3	1	0	0	2127.03	99	116
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	7	7	11	0.01%	21.1%	EQEIEDQKNPR	99.7%	56.1	25	48.1	2	0	0	1385.67	223	233
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	7	7	11	0.01%	21.1%	TEEAIIYSYGFATIASAIPAYSK	99.7%	109	25	109	1	0	0	2466.24	158	180
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	7	7	11	0.01%	21.1%	VVVTVEQTEEELER	99.7%	101	25	101	2	0	0	1659.84	446	459
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	7	7	11	0.01%	21.1%	YGVGTCGPR	99.7%	45.7	25	39.3	1	0	0	966.45	128	136
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	9	9	22	0.02%	41.1%	DGTGVVEFVR	99.7%	57.9	25	38.7	3	0	0	1078.55	155	164
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	9	9	22	0.02%	41.1%	DGYDYDGYR	97.3%	30	25	30	2	0	0	1123.43	75	83
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	9	9	22	0.02%	41.1%	EAGDVCYADVYR	99.7%	69.2	25	69.2	3	0	0	1417.61	143	154
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	9	9	22	0.02%	41.1%	GGPPFAFVEFEDPR	99.7%	55.1	25	55.1	2	0	0	1564.74	52	65
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	9	9	22	0.02%	41.1%	IYVGNLPPDIR	99.7%	58.7	25	50.8	4	0	0	1256.70	18	28
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	9	9	22	0.02%	41.1%	KEDMTYAVR	99.7%	49.7	25	41.5	2	0	0	1112.54	165	173
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	9	9	22	0.02%	41.1%	LRVEFPR	99.0%	34.4	25	15.6	6	0	0	916.54	84	90
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	9	9	22	0.02%	41.1%	SHEGETAYIR	98.6%	32.9	25	31.7	3	0	0	1162.55	182	191
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	9	9	22	0.02%	41.1%	TKDIEDVFYK	99.7%	53.4	25	52	2	0	0	1257.64	29	38
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	9	9	22	0.02%	41.1%	YGAIRDIDLK	96.8%	29.4	25	12.3	1	0	0	1163.64	39	48
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	6	7	13	0.01%	32.9%	AFGYYGPLR	99.7%	47.7	25	42.7	4	0	0	1043.53	29	37
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	6	7	13	0.01%	32.9%	DSCPLDCK	96.5%	29	25	29	1	0	0	994.40	4	11
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	6	7	13	0.01%	32.9%	NRGPPPSWGR	99.5%	37.5	25	35.5	1	0	0	1123.58	89	98
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	6	7	13	0.01%	32.9%	VRVELSNGEK	99.6%	38.7	25	27.3	2	0	0	1130.62	76	85
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	6	7	13	0.01%	32.9%	VYVGNLGNNGNK	99.7%	53.5	25	51	2	0	0	1248.63	12	23
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	6	7	13	0.01%	32.9%	VYVGNLGNNGNKTELER	99.7%	62.5	25	46	1	2	0	1876.95	12	28
Serine/arginine-rich splicing factor 5	SRSF5	SRSF5_HUMAN	31.3	99.8%	2	2	5	0.01%	8.8%	LIVENLSSR	99.7%	65.2	25	50.3	2	0	0	1030.59	110	118
Serine/arginine-rich splicing factor 5	SRSF5	SRSF5_HUMAN	31.3	99.8%	2	2	5	0.01%	8.8%	LNEGVVEFASYGDLK	99.7%	128	25	127	3	0	0	1640.82	144	158
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	8	9	20	0.02%	35.3%	DAEDAIYGR	96.9%	29.5	25	29.5	1	0	0	1009.46	64	72
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	8	9	20	0.02%	35.3%	DGVGMVEYLR	99.7%	61.1	25	38.6	4	0	0	1138.56	145	154
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	8	9	20	0.02%	35.3%	EAGDVCYADVQK	99.7%	69.1	25	69.1	2	0	0	1354.59	133	144
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	8	9	20	0.02%	35.3%	EKDLEDLFYK	99.6%	38.1	25	31.1	2	0	0	1299.65	27	36
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	8	9	20	0.02%	35.3%	HGLVPFAFVR	98.5%	32.4	25	31.4	2	0	0	1142.65	49	58
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	8	9	20	0.02%	35.3%	IYVGNLPTDVR	99.7%	59.7	25	47	2	0	0	1246.68	16	26
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	8	9	20	0.02%	35.3%	KEDMEYALR	99.4%	36.4	25	36.4	1	0	0	1154.55	155	163
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	8	9	20	0.02%	35.3%	LRVEFPR	99.0%	34.4	25	15.6	6	0	0	916.54	82	88
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	15	26	0.03%	39.1%	AERDILVEADSLWVVK	99.7%	48.9	25	48.9	0	1	0	1843.00	136	151
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	15	26	0.03%	39.1%	AKDLILR	98.4%	32.4	25	19	2	0	0	828.53	353	359
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	15	26	0.03%	39.1%	DIKPDNLLLDSK	99.7%	40.7	25	37.7	2	1	0	1370.75	212	223
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	15	26	0.03%	39.1%	DILVEADSLWVVK	99.7%	81.1	25	80	3	0	0	1486.82	139	151
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	15	26	0.03%	39.1%	DWVFINYTYK	99.7%	49.8	25	0	4	0	0	1348.66	437	446
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	15	26	0.03%	39.1%	FCCEWEHR	99.7%	40.7	25	40.7	1	0	0	1223.47	360	367
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	15	26	0.03%	39.1%	IGAPGVEEIK	99.7%	69.3	25	55.9	2	0	0	1012.57	368	377
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	15	26	0.03%	39.1%	LGLEDFESLK	99.7%	60.7	25	57.9	2	0	0	1150.60	84	93
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	15	26	0.03%	39.1%	LSDFGLCTGLK	99.7%	76.7	25	70.5	4	0	0	1210.61	228	238
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	15	26	0.03%	39.1%	LSDFGLCTGLKK	99.7%	69.5	25	61.2	4	2	0	1338.71	228	239
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	15	26	0.03%	39.1%	NLNHSLPSDFTFQNMNSK	95.8%	23	25	23	0	1	0	2093.97	248	265
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	15	26	0.03%	39.1%	QLAFSTVGTPDYIAPEVFMQTGYNK	99.7%	54.5	25	54.5	0	2	0	2777.35	277	301
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	15	26	0.03%	39.1%	RFEGLTAR	99.7%	43.7	25	36.2	2	0	0	949.52	447	454
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	15	26	0.03%	39.1%	SNSFFEGVDWEHIR	99.7%	39	25	39	0	1	0	1722.79	378	391
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	15	26	0.03%	39.1%	VMEEEGLKDEEK	99.7%	66.3	25	51.3	5	0	0	1435.66	51	62
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	15	26	0.03%	39.1%	VTLENFYSNLIAQHEER	97.6%	25	25	23.8	0	2	0	2063.02	25	41
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	15	26	0.03%	39.1%	VTLENFYSNLIAQHEEREMR	99.1%	28.6	25	27.6	0	1	0	2495.20	25	44
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	19	54	0.06%	32.8%	AKDLILR	98.4%	32.4	25	19	2	0	0	828.53	354	360
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	19	54	0.06%	32.8%	DIKPDNLLLDAK	99.7%	49.8	25	45.3	4	0	0	1354.76	213	224

Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	19	54	0.06%	32.8%	DTGHIYAMK	99.4%	36.4	25	25	3	0	0	1035.49	111	119
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	19	54	0.06%	32.8%	DWVFLNYTYK	99.7%	49.8	25	0	4	0	0	1348.66	435	444
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	19	54	0.06%	32.8%	ERPAAIPIEIK	99.7%	47.9	25	36.7	4	0	0	1236.73	393	403
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	19	54	0.06%	32.8%	ETLVFPPEVPISEK	97.0%	29.6	25	29.6	1	0	0	1584.85	340	353
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	19	54	0.06%	32.8%	FCIDSENR	99.7%	41.1	25	39.6	4	0	0	1040.45	361	368
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	19	54	0.06%	32.8%	FEGLTQR	99.2%	35	25	19.1	2	0	0	850.44	446	452
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	19	54	0.06%	32.8%	GHPFFEGVDWEHIR	99.7%	61.1	25	61.1	0	2	0	1725.81	379	392
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	19	54	0.06%	32.8%	LGLDDFESLK	99.7%	53.6	25	50.8	4	0	0	1136.58	85	94
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	19	54	0.06%	32.8%	LSDFGLCTGLK	99.7%	76.7	25	70.5	4	0	0	1210.61	229	239
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	19	54	0.06%	32.8%	LSDFGLCTGLKK	99.7%	69.5	25	61.2	4	2	0	1338.71	229	240
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	19	54	0.06%	32.8%	LTLENFYSNLILQHEER	99.7%	87.2	25	87.2	1	2	0	2119.08	26	42
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	19	54	0.06%	32.8%	NLTHNPPSDFSFQNMNSK	99.7%	58.8	25	58.8	0	5	0	2077.94	249	266
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	19	54	0.06%	32.8%	RFEGLTQR	99.2%	35.3	25	21.6	4	0	0	1006.54	445	452
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	16	19	54	0.06%	32.8%	TRLGLDDFESLK	99.7%	41	25	32.9	2	0	0	1393.73	83	94
Serine/threonine-protein kinase D1	PRKD1	KPCD1_HUMAN	101.7	99.8%	2	2	4	0.00%	5.3%	EIPLSEILSLEPVK	99.7%	44.1	25	44.1	2	0	0	1566.90	465	478
Serine/threonine-protein kinase D1	PRKD1	KPCD1_HUMAN	101.7	99.8%	2	2	4	0.00%	5.3%	FLITQILVALR	99.7%	70.8	25	70.8	2	0	0	1286.82	685	695
Serine/threonine-protein kinase D1	PRKD1	KPCD1_HUMAN	101.7	99.8%	2	2	4	0.00%	5.3%	LCDFGFAR	99.7%	50.8	25	36.9	2	0	0	985.46	725	732
Serine/threonine-protein kinase D1	PRKD1	KPCD1_HUMAN	101.7	99.8%	2	2	4	0.00%	5.3%	SVVGTPAYLAPEVLR	99.7%	66.1	25	62.4	2	0	0	1571.88	742	756
Serine/threonine-protein kinase D2	PRKD2	KPCD2_HUMAN	96.8	100.0%	3	3	5	0.01%	3.9%	EFVLLPAASELAHVK	96.0%	28.5	25	28.5	1	0	0	1623.91	56	70
Serine/threonine-protein kinase D2	PRKD2	KPCD2_HUMAN	96.8	100.0%	3	3	5	0.01%	3.9%	FLITQILVALR	99.7%	70.8	25	70.8	2	0	0	1286.82	653	663
Serine/threonine-protein kinase D2	PRKD2	KPCD2_HUMAN	96.8	100.0%	3	3	5	0.01%	3.9%	LCDFGFAR	99.7%	50.8	25	36.9	2	0	0	985.46	693	700
Serine/threonine-protein kinase D3	PRKD3	KPCD3_HUMAN	100.5	99.8%	2	3	4	0.00%	4.9%	FMVTQILVALR	99.7%	65.5	25	60.2	2	0	0	1306.76	678	688
Serine/threonine-protein kinase D3	PRKD3	KPCD3_HUMAN	100.5	99.8%	2	3	4	0.00%	4.9%	LCDFGFAR	99.7%	50.8	25	36.9	2	0	0	985.46	718	725
Serine/threonine-protein kinase D3	PRKD3	KPCD3_HUMAN	100.5	99.8%	2	3	4	0.00%	4.9%	SVVGTPAYLAPEVLR	99.7%	66.1	25	62.4	2	0	0	1571.88	735	749
Serine/threonine-protein kinase D3	PRKD3	KPCD3_HUMAN	100.5	99.8%	2	3	4	0.00%	4.9%	YITHESDDAR	96.2%	28.7	25	10.7	2	0	0	1206.54	852	861
Serine/threonine-protein kinase MST4	MST4	MST4_HUMAN	46.5	100.0%	5	5	8	0.01%	15.4%	AANVLLSEQGDVK	99.7%	81.1	25	81.1	2	0	0	1343.72	147	159
Serine/threonine-protein kinase MST4	MST4	MST4_HUMAN	46.5	100.0%	5	5	8	0.01%	15.4%	ADIWSLGITAIELAK	99.7%	110	25	98.9	2	0	0	1600.89	200	214
Serine/threonine-protein kinase MST4	MST4	MST4_HUMAN	46.5	100.0%	5	5	8	0.01%	15.4%	AGPFDEFQIATMLK	98.8%	33.6	25	29.7	1	0	0	1567.78	113	126
Serine/threonine-protein kinase MST4	MST4	MST4_HUMAN	46.5	100.0%	5	5	8	0.01%	15.4%	SIAVAEAACPGITDK	99.7%	62.8	25	62.8	1	0	0	1502.75	384	398
Serine/threonine-protein kinase MST4	MST4	MST4_HUMAN	46.5	100.0%	5	5	8	0.01%	15.4%	VLFLIPK	96.7%	29.3	25	28.3	2	0	0	829.55	227	233
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	4	4	8	0.01%	2.0%	DASAVSLSESK	99.7%	55.3	25	45.1	1	0	0	1093.54	911	921
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	4	4	8	0.01%	2.0%	STAMDTLSSLVFQLGK	99.7%	41.4	25	36.8	1	0	0	1697.88	1171	1186
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	4	4	8	0.01%	2.0%	TLVLLLGVDPSR	99.7%	67.4	25	51.7	2	0	0	1282.77	1672	1683
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	4	4	8	0.01%	2.0%	VLGLLGALDPYK	99.7%	41.1	25	41.1	4	0	0	1258.74	887	898
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	4	4	8	0.01%	9.3%	IPISLVLR	99.7%	56.6	25	56.6	2	0	0	910.61	432	439
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	4	4	8	0.01%	9.3%	LLSGGSVLDIIK	99.7%	67.4	25	47.7	2	0	0	1214.74	94	105
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	4	4	8	0.01%	9.3%	SGVLDESTIATILR	99.7%	84.2	25	79.9	2	0	0	1474.81	115	128
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	4	4	8	0.01%	9.3%	TAQALSSGSGSQETK	99.7%	72.9	25	68	2	0	0	1451.70	417	431
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	29	138	0.14%	39.4%	AMEIASQR	99.7%	61.3	25	35.1	6	0	0	905.45	402	409
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	29	138	0.14%	39.4%	ATVEQVLDPR	99.7%	68.8	25	59.7	12	0	0	1127.61	156	165
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	29	138	0.14%	39.4%	DCANVNDFFMR	99.7%	74	25	69.6	9	0	0	1404.57	360	370
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	29	138	0.14%	39.4%	DKYVSGEFR	98.8%	33.5	25	27	3	0	0	1100.54	221	229
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	29	138	0.14%	39.4%	DMDIIMK	99.1%	34.9	25	26.7	2	0	0	865.42	443	449
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	29	138	0.14%	39.4%	EANVYHASTANGESR	99.7%	102	25	101	7	1	0	1605.73	191	205
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	29	138	0.14%	39.4%	ELFEFVTDPSITHENMDAYLSK	99.6%	32.3	25	32.3	0	5	0	2602.20	380	401
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	29	138	0.14%	39.4%	ELYLQVIQYMR	99.7%	89.3	25	79	12	0	0	1455.77	302	312
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	29	138	0.14%	39.4%	GIITEINGCISTGK	99.7%	77.3	25	70.5	4	0	0	1462.76	177	190
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	29	138	0.14%	39.4%	GYVWNGGSNPQANR	99.7%	68.8	25	68.8	3	0	0	1519.70	82	95
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	29	138	0.14%	39.4%	HSVAVMTVR	99.7%	50	25	33.1	11	0	0	999.54	371	379
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	29	138	0.14%	39.4%	INLDKLNVTDSVINK	99.7%	89.9	25	89.9	6	7	0	1685.94	120	134
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	29	138	0.14%	39.4%	KDCANVNDFFMR	98.7%	27.2	25	27.2	0	1	0	1532.66	359	370

Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	29	138	0.14%	39.4%	LNTAEIPCPEPIMLR	99.7%	59.5	25	36.9	7	0	0	1753.90	257	271
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	29	138	0.14%	39.4%	LNVTDSVINK	99.7%	83.6	25	65.6	8	0	0	1102.61	125	134
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	29	138	0.14%	39.4%	NVQLSESK	98.1%	31.6	25	17.9	2	0	0	904.47	292	299
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	29	138	0.14%	39.4%	NYERDMDIIMK	96.0%	28.5	25	10.2	2	0	0	1459.66	439	449
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	29	138	0.14%	39.4%	SSQDHVDEEVFKR	99.7%	70.2	25	65.2	5	7	0	1575.74	415	427
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	29	138	0.14%	39.4%	TSILVFK	99.7%	40.3	25	32.5	4	0	0	807.50	212	218
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	29	138	0.14%	39.4%	TSILVFKDR	99.7%	51.3	25	48.7	1	0	0	1078.63	212	220
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	29	138	0.14%	39.4%	VPALLENQVEER	99.7%	86.9	25	86.9	11	0	0	1396.74	482	493
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	22	29	138	0.14%	39.4%	VVPGQFDDADSSDSENR	99.7%	94.1	25	94.1	2	0	0	1837.78	11	27
Serine/threonine-protein kinase VRK1	VRK1	VRK1_HUMAN	45.5	99.8%	2	2	4	0.00%	5.6%	TVLQLSLR	99.7%	39.6	25	22.5	2	0	0	929.58	153	160
Serine/threonine-protein kinase VRK1	VRK1	VRK1_HUMAN	45.5	99.8%	2	2	4	0.00%	5.6%	VEPSDNGPLFTELK	98.7%	33	25	29.4	2	0	0	1545.78	72	85
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	4	4	7	0.01%	8.1%	ESSLTEPVIVGLLK	99.4%	36.5	25	36.5	2	0	0	1484.86	354	367
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	4	4	7	0.01%	8.1%	FLESPDFQPNIAK	99.7%	62.8	25	55.3	1	0	0	1505.76	220	232
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	4	4	7	0.01%	8.1%	TVETEAVQMLK	99.7%	41.2	25	37.3	1	0	0	1248.65	550	560
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	4	4	7	0.01%	8.1%	VLPIMFPALYR	99.7%	49	25	49	3	0	0	1319.75	442	452
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	8	9	14	0.01%	16.8%	ELVSDANQHVK	99.7%	46.6	25	40.2	2	0	0	1239.63	332	342
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	8	9	14	0.01%	16.8%	LSTIALALGVER	99.7%	76	25	70.2	2	0	0	1242.74	35	46
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	8	9	14	0.01%	16.8%	LTQDQDVDVK	99.7%	52.8	25	42.5	2	0	0	1160.58	567	576
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	8	9	14	0.01%	16.8%	MAGDPVANVR	99.7%	68.7	25	55.5	4	0	0	1045.51	528	537
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	8	9	14	0.01%	16.8%	SEIIPMFSNLASDEQDSVR	99.1%	34.6	25	34.6	1	0	0	2138.01	203	221
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	8	9	14	0.01%	16.8%	TDLVPAFQNLMK	95.0%	27.7	25	26.6	1	0	0	1376.72	281	292
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	8	9	14	0.01%	16.8%	TSACGLFSVCYPR	99.7%	51.7	25	51.7	1	0	0	1517.69	145	157
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	8	9	14	0.01%	16.8%	YMVADKFTELQK	99.7%	43.8	25	43.8	1	0	0	1472.75	261	272
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	5	5	11	0.01%	22.3%	GAGWLFGAK	99.7%	46.9	25	30.2	2	0	0	906.48	211	219
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	5	5	11	0.01%	22.3%	LVTVWSAPNYCYR	99.6%	38.1	25	38.1	2	0	0	1628.79	252	264
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	5	5	11	0.01%	22.3%	QITQVYGFYDECQTK	99.7%	65.3	25	65.3	2	0	0	1879.85	118	132
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	5	5	11	0.01%	22.3%	TGGQVPDTNYIFMGDFVDR	99.7%	39.7	25	39.7	2	0	0	2131.98	67	85
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	5	5	11	0.01%	22.3%	VTNEFVHINNLK	99.7%	65.4	25	65.4	3	0	0	1427.76	220	231
Serine/threonine-protein phosphatase 6 regulatory subunit 1	PPP6R1	PP6R1_HUMAN	96.7	99.7%	2	2	2	0.00%	2.2%	LGQPPGVR	94.8%	27.5	25	18.5	1	0	0	823.48	656	663
Serine/threonine-protein phosphatase 6 regulatory subunit 1	PPP6R1	PP6R1_HUMAN	96.7	99.7%	2	2	2	0.00%	2.2%	VAGALVQNTEK	99.7%	39.7	25	12.8	1	0	0	1129.62	470	480
Serine/threonine-protein phosphatase 6 regulatory subunit 3	PPP6R3	PP6R3_HUMAN	97.7	99.8%	2	2	4	0.00%	2.3%	GPNSALVQQLIK	99.7%	55.6	25	40.1	2	0	0	1267.74	475	486
Serine/threonine-protein phosphatase 6 regulatory subunit 3	PPP6R3	PP6R3_HUMAN	97.7	99.8%	2	2	4	0.00%	2.3%	VLSILISR	99.7%	56.7	25	56.7	2	0	0	900.59	127	134
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	9	9	25	0.03%	34.9%	AIETTDIISR	99.7%	71.2	25	56.9	6	0	0	1118.61	153	162
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	9	9	25	0.03%	34.9%	ALQFPPEGWLR	96.3%	28.9	25	18.1	1	0	0	1313.70	241	251
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	9	9	25	0.03%	34.9%	EPLSLINVR	99.7%	49.2	25	45.1	2	0	0	1040.61	66	74
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	9	9	25	0.03%	34.9%	EQAELTGLR	99.7%	59.9	25	39.6	6	0	0	1016.54	126	134
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	9	9	25	0.03%	34.9%	HSQYHVDGSLEKDR	97.4%	24.7	25	24.7	0	1	0	1670.79	105	118
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	9	9	25	0.03%	34.9%	NVESGEEELASK	99.7%	69	25	67.5	5	0	0	1291.60	77	88
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	9	9	25	0.03%	34.9%	QEEDSYEIFICHANVIR	99.5%	31.4	25	31.4	0	1	0	2122.99	219	235
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	9	9	25	0.03%	34.9%	TLGDTGFMPPDK	99.7%	60.3	25	55.3	2	0	0	1278.60	274	285
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	9	9	25	0.03%	34.9%	VSTDLLR	99.6%	38.3	25	25.3	1	0	0	803.46	170	176
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	PP1G_HUMAN	37.0	100.0%	3	3	5	0.01%	11.5%	IYGFYDECK	99.7%	42	25	31.4	2	0	0	1194.51	133	141
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	PP1G_HUMAN	37.0	100.0%	3	3	5	0.01%	11.5%	NVQLQENEIR	99.7%	53.9	25	48.8	2	0	0	1242.64	27	36
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	PP1G_HUMAN	37.0	100.0%	3	3	5	0.01%	11.5%	TFTDCFNCLPIAAIVDEK	99.3%	36.2	25	36.2	1	0	0	2113.99	151	168
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	7	8	11	0.01%	27.1%	FSPDGELYASGSEDGTLR	99.7%	79.3	25	72.8	1	0	0	1900.86	273	290
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	7	8	11	0.01%	27.1%	IYDLNKPEAEPK	99.7%	48.5	25	45.1	2	1	0	1416.74	126	137
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	7	8	11	0.01%	27.1%	LWDHATMTEVK	96.8%	29.4	25	29.4	1	0	0	1330.65	168	178
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	7	8	11	0.01%	27.1%	LWQTVVGK	99.4%	36.9	25	27.7	1	0	0	930.54	291	298
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	7	8	11	0.01%	27.1%	QGDTGDWIGTFLGHK	99.7%	36.2	25	34.3	0	2	0	1631.78	45	59
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	7	8	11	0.01%	27.1%	TVDFTQDSNYLLTGGQDK	99.7%	84.7	25	84.7	1	0	0	2001.94	105	122
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	7	8	11	0.01%	27.1%	YDYNSGEELESYK	99.7%	76.8	25	76.8	2	0	0	1596.67	250	262

Serpin B12	SERPINB12	SPB12_HUMAN	46.3	100.0%	3	3	4	0.00%	8.4%	ADLTGISPSPNLYLSK	98.6%	32.8	25	17.1	1	0	0	1675.89	328	343
Serpin B12	SERPINB12	SPB12_HUMAN	46.3	100.0%	3	3	4	0.00%	8.4%	IGFIEEVK	97.2%	30	25	15.5	1	0	0	934.52	232	239
Serpin B12	SERPINB12	SPB12_HUMAN	46.3	100.0%	3	3	4	0.00%	8.4%	TDYTLSIANR	99.6%	37.9	25	36.4	2	0	0	1153.58	108	117
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	9	9	18	0.02%	32.1%	DQAVENILVSPVVVASSLGLVSLGGK	99.7%	32.8	25	32.8	0	1	0	2551.43	61	86
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	9	9	18	0.02%	32.1%	DTQSGSLLFIGR	99.7%	86.8	25	73.1	3	0	0	1293.68	394	405
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	9	9	18	0.02%	32.1%	GVVEVTHDLQK	99.7%	53.8	25	41.7	2	0	0	1224.66	309	319
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	9	9	18	0.02%	32.1%	HLAGLGLTEAIDKNK	99.7%	56.1	25	56.1	0	2	0	1579.88	320	334
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	9	9	18	0.02%	32.1%	LFYADHPFIFLVR	99.7%	68.6	25	68.6	2	0	0	1637.88	381	393
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	9	9	18	0.02%	32.1%	LSSLIILMPHHVEPLER	99.7%	47.9	25	47.7	0	2	0	1984.11	264	280
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	9	9	18	0.02%	32.1%	LYGPSSVSFADDFVR	99.7%	85.2	25	84.1	2	0	0	1659.80	134	148
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	9	9	18	0.02%	32.1%	SAGLAFSLYQAMAK	99.7%	88.5	25	81.7	2	0	0	1457.75	47	60
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	9	9	18	0.02%	32.1%	SYTVGVMMMHR	99.7%	40.4	25	40.4	2	0	0	1311.60	229	239
Serrate RNA effector molecule homolog	SRRT	SRRT_HUMAN	100.7	100.0%	8	8	11	0.01%	10.3%	AEIISLCK	99.7%	40.3	25	33.6	1	0	0	933.51	435	442
Serrate RNA effector molecule homolog	SRRT	SRRT_HUMAN	100.7	100.0%	8	8	11	0.01%	10.3%	EICWNLQNIR	99.6%	38.9	25	33.5	1	0	0	1345.67	477	486
Serrate RNA effector molecule homolog	SRRT	SRRT_HUMAN	100.7	100.0%	8	8	11	0.01%	10.3%	ESLSEEEAQK	99.7%	52.1	25	46.1	2	0	0	1149.53	678	687
Serrate RNA effector molecule homolog	SRRT	SRRT_HUMAN	100.7	100.0%	8	8	11	0.01%	10.3%	EVAFFNNFLTDAK	99.7%	60.7	25	59.2	2	0	0	1515.75	746	758
Serrate RNA effector molecule homolog	SRRT	SRRT_HUMAN	100.7	100.0%	8	8	11	0.01%	10.3%	ILEQEEEEEQAGKPGEPSK	99.7%	50.1	25	48.2	0	1	0	2127.01	267	285
Serrate RNA effector molecule homolog	SRRT	SRRT_HUMAN	100.7	100.0%	8	8	11	0.01%	10.3%	LIHTLDDR	99.6%	38.4	25	22.3	1	0	0	982.53	527	534
Serrate RNA effector molecule homolog	SRRT	SRRT_HUMAN	100.7	100.0%	8	8	11	0.01%	10.3%	LRECELSPGVNR	99.7%	54.8	25	54.8	1	0	0	1429.72	487	498
Serrate RNA effector molecule homolog	SRRT	SRRT_HUMAN	100.7	100.0%	8	8	11	0.01%	10.3%	VALSEPQPER	99.7%	41.4	25	30	2	0	0	1125.59	450	459
Serum albumin	ALB	ALBU_HUMAN	69.4	100.0%	3	3	4	0.00%	6.1%	KVPQVSTPTLVEVSR	96.6%	23.8	25	23.8	0	1	0	1639.94	438	452
Serum albumin	ALB	ALBU_HUMAN	69.4	100.0%	3	3	4	0.00%	6.1%	LVNEVTEFAK	99.6%	37.9	25	28.3	1	0	0	1149.62	66	75
Serum albumin	ALB	ALBU_HUMAN	69.4	100.0%	3	3	4	0.00%	6.1%	YICENQDSISSK	99.6%	38.2	25	38.1	2	0	0	1443.64	287	298
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	10	11	20	0.02%	30.3%	ADKEGDYYVLNGSK	99.2%	35.1	25	33.7	1	0	0	1558.74	192	205
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	10	11	20	0.02%	30.3%	ASSTCPLTFENVK	99.7%	76.9	25	67.4	2	0	0	1453.70	257	269
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	10	11	20	0.02%	30.3%	ATYLPQLTTEK	99.7%	50	25	50	2	0	0	1264.68	160	170
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	10	11	20	0.02%	30.3%	FAQEQIAPLVSTMDENSK	99.7%	52.9	25	50.4	2	0	0	2007.97	71	88
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	10	11	20	0.02%	30.3%	GITSFLVDR	98.0%	31.3	25	25.5	1	0	0	1007.55	231	239
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	10	11	20	0.02%	30.3%	IGTIYEGASNIQLNTIAK	99.7%	96.2	25	92.8	2	0	0	1906.03	409	426
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	10	11	20	0.02%	30.3%	LLEAGKPFIK	99.7%	44.6	25	28.1	2	0	0	1115.68	356	365
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	10	11	20	0.02%	30.3%	VPEANILGQIGHGYK	99.7%	61.9	25	60.6	2	2	0	1595.85	270	284
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	10	11	20	0.02%	30.3%	YAIGSLNEGR	99.7%	63.4	25	50.4	2	0	0	1079.55	285	294
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	10	11	20	0.02%	30.3%	YYASEIAGQTTSK	99.7%	119	25	111	2	0	0	1418.68	372	384
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	12	14	39	0.04%	36.6%	ANHFFTVTDPR	96.3%	28.8	25	26.9	1	0	0	1304.64	25	35
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	12	14	39	0.04%	36.6%	HVSPLIGR	99.7%	39.8	25	33.3	2	0	0	878.52	171	178
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	12	14	39	0.04%	36.6%	IQESHPELR	99.7%	49.5	25	36.9	2	0	0	1108.57	306	314
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	12	14	39	0.04%	36.6%	IQESHPELRR	99.6%	31.9	25	29.6	0	1	0	1264.68	306	315
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	12	14	39	0.04%	36.6%	NILLTNEQLESAR	99.7%	107	25	98	4	0	0	1500.80	36	48
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	12	14	39	0.04%	36.6%	NILLTNEQLESARK	99.7%	82.9	25	78.8	2	0	0	1628.90	36	49
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	12	14	39	0.04%	36.6%	QAITQVVVSR	99.7%	80.1	25	72.1	2	0	0	1100.64	224	233
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	12	14	39	0.04%	36.6%	QGIVPPGLTENELWR	99.7%	55.6	25	47.5	4	0	0	1708.90	56	70
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	12	14	39	0.04%	36.6%	SSMSVTSLEAELQAK	99.7%	88.2	25	88.2	6	0	0	1596.78	291	305
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	12	14	39	0.04%	36.6%	VGIPVTDENGNR	99.7%	72.4	25	69.4	4	0	0	1270.64	203	214
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	12	14	39	0.04%	36.6%	WDQSTFIGR	99.7%	61.9	25	0	4	0	0	1109.54	16	24
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	12	14	39	0.04%	36.6%	YIYDSAFHPDTGEK	99.7%	83.6	25	81.3	4	3	0	1642.74	73	86
Sideroflexin-2	SFXN2	SFXN2_HUMAN	36.2	100.0%	2	2	4	0.00%	7.8%	AAAIGITQVVISR	99.7%	72.6	25	57.1	2	0	0	1298.78	220	232
Sideroflexin-2	SFXN2	SFXN2_HUMAN	36.2	100.0%	2	2	4	0.00%	7.8%	YGELEPYVYFNK	99.7%	56.6	25	55.2	2	0	0	1521.73	309	320
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	100.0%	3	3	5	0.01%	13.4%	DAVPAFIEPNVR	99.7%	45.6	25	39	2	0	0	1327.70	19	30
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	100.0%	3	3	5	0.01%	13.4%	QLLCTNEDVSSPASADQR	99.7%	73.8	25	70.6	2	0	0	1990.91	67	84
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	100.0%	3	3	5	0.01%	13.4%	SLATVHPDSSNLIPK	96.8%	29.5	25	28.1	1	0	0	1578.85	92	106
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	8	12	25	0.03%	33.0%	EIPIVHR	97.8%	30.9	25	19.6	1	0	0	863.51	91	97

Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	8	12	25	0.03%	33.0%	GDLLFLTNR	99.7%	69.6	25	51.9	3	0	0	1048.58	64	72
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	8	12	25	0.03%	33.0%	GDLLFLTNRVEDPIR	99.7%	37	25	37	0	2	0	1757.95	64	78
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	8	12	25	0.03%	33.0%	GDNNAVDDRGLYK	99.7%	53	25	52.8	2	1	0	1436.68	115	127
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	8	12	25	0.03%	33.0%	MLSLDFLDDVR	99.7%	43.2	25	32.3	2	0	0	1323.66	1	11
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	8	12	25	0.03%	33.0%	MLSLDFLDDVRR	99.7%	34.3	25	30.1	3	2	0	1495.76	1	12
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	8	12	25	0.03%	33.0%	VGEIVVFR	99.7%	71.3	25	66.5	6	0	0	918.54	79	86
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	8	12	25	0.03%	33.0%	VGEIVVFRIEGR	99.5%	37	25	32.3	2	1	0	1373.79	79	90
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	9	11	20	0.02%	43.4%	DPTGMDPDDIWQLSSSLK	99.7%	64.3	25	64.3	1	0	0	2020.92	147	164
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	9	11	20	0.02%	43.4%	FDDKYTLK	99.4%	36.2	25	20.1	2	0	0	1029.53	166	173
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	9	11	20	0.02%	43.4%	FFDHSGTLVMDAYEPEISR	99.7%	69.8	25	69.8	1	4	0	2214.02	196	214
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	9	11	20	0.02%	43.4%	IDDKPVKIDK	99.7%	43.3	25	34.3	2	0	0	1170.67	41	50
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	9	11	20	0.02%	43.4%	IDKWDGSAVK	99.7%	51.8	25	33.7	2	0	0	1118.58	48	57
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	9	11	20	0.02%	43.4%	LHDSLAIER	99.7%	52	25	46.5	2	0	0	1053.57	215	223
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	9	11	20	0.02%	43.4%	SGLLDKWK	99.7%	47.7	25	33.4	2	0	0	946.54	33	40
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	9	11	20	0.02%	43.4%	SIFLVAHR	99.7%	51.3	25	43.7	2	0	0	942.55	138	145
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	9	11	20	0.02%	43.4%	YVENFGLIDGR	99.7%	74.1	25	66.8	2	0	0	1282.64	74	84
Signal peptidase complex subunit 3	SPCS3	SPCS3_HUMAN	20.3	100.0%	4	4	12	0.01%	21.7%	MNTVLSR	99.1%	34.8	25	9.68	2	0	0	820.43	1	7
Signal peptidase complex subunit 3	SPCS3	SPCS3_HUMAN	20.3	100.0%	4	4	12	0.01%	21.7%	NNALNQVVLWDK	99.7%	63.4	25	48.1	3	0	0	1413.75	97	108
Signal peptidase complex subunit 3	SPCS3	SPCS3_HUMAN	20.3	100.0%	4	4	12	0.01%	21.7%	NVEDFTGPR	99.7%	45.2	25	37.5	3	0	0	1034.49	50	58
Signal peptidase complex subunit 3	SPCS3	SPCS3_HUMAN	20.3	100.0%	4	4	12	0.01%	21.7%	YFFFDDGNGLK	99.7%	47.5	25	30.3	4	0	0	1322.61	127	137
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	6	8	14	0.01%	38.2%	EVNKFQMAYSNLLR	99.7%	62.4	25	55.4	2	1	0	1712.88	75	88
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	6	8	14	0.01%	38.2%	FQMAYSNLLR	99.7%	60.1	25	48.3	3	0	0	1242.63	79	88
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	6	8	14	0.01%	38.2%	GTVEGFEPADNK	99.7%	50.4	25	50.4	2	0	0	1263.59	44	55
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	6	8	14	0.01%	38.2%	KGTVEGFEPADNK	99.7%	44.9	25	38.6	2	0	0	1391.68	43	55
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	6	8	14	0.01%	38.2%	TSGSVYITLKK	99.7%	61.2	25	61.2	2	0	0	1196.69	22	32
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	6	8	14	0.01%	38.2%	VLLESEQFLTELTR	99.7%	81.5	25	80.8	2	0	0	1677.91	2	15
Signal recognition particle 19 kDa protein	SRP19	SRP19_HUMAN	16.2	99.8%	2	3	4	0.00%	18.8%	SVMLYAAEMIPK	99.0%	34.2	25	34	2	0	0	1352.70	103	114
Signal recognition particle 19 kDa protein	SRP19	SRP19_HUMAN	16.2	99.8%	2	3	4	0.00%	18.8%	TGGADQSLQQGEGSK	99.7%	63.6	25	61.3	2	0	0	1462.68	122	136
Signal recognition particle 9 kDa protein	SRP9	SRP09_HUMAN	10.1	100.0%	3	4	6	0.01%	34.9%	LYLADPMK	99.2%	35	25	21.7	3	0	0	950.50	17	24
Signal recognition particle 9 kDa protein	SRP9	SRP09_HUMAN	10.1	100.0%	3	4	6	0.01%	34.9%	PQYQTWEEFSR	99.7%	57.5	25	57.5	1	0	0	1470.66	2	12
Signal recognition particle 9 kDa protein	SRP9	SRP09_HUMAN	10.1	100.0%	3	4	6	0.01%	34.9%	VTDDLVCLVYK	99.7%	60.7	25	52	2	0	0	1324.68	42	52
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	5	6	8	0.01%	8.2%	AGAVEQLR	99.5%	37.6	25	20.9	2	0	0	843.47	459	466
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	5	6	8	0.01%	8.2%	ALADHSMAQTPR	99.7%	46.2	25	41.4	1	0	0	1297.63	569	580
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	5	6	8	0.01%	8.2%	DAAGIAMEAIAFAR	99.7%	99.8	25	83.9	2	0	0	1406.71	497	510
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	5	6	8	0.01%	8.2%	MLDFFTIFSK	99.7%	53.8	25	50.1	2	0	0	1248.63	1	10
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	5	6	8	0.01%	8.2%	TMVQLFEK	98.9%	34	25	29.7	1	0	0	995.52	485	492
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	12	13	26	0.03%	51.3%	AIVFVVDSAAFQR	99.7%	76.4	25	73.4	5	0	0	1422.77	138	150
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	12	13	26	0.03%	51.3%	AVLLVGLCDSGK	99.7%	84.2	25	77.5	2	0	0	1231.67	66	77
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	12	13	26	0.03%	51.3%	DTQTSITDSCAVYR	99.7%	46.3	25	46.3	1	0	0	1616.72	91	104
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	12	13	26	0.03%	51.3%	GDVGSADIQDLEK	99.7%	90.4	25	79.5	2	0	0	1346.64	253	265
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	12	13	26	0.03%	51.3%	GNSLTLIDLPGHESLR	99.7%	52.7	25	52.7	1	2	0	1721.92	110	125
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	12	13	26	0.03%	51.3%	LIQQQLEK	99.2%	35	25	9.17	2	0	0	999.58	192	199
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	12	13	26	0.03%	51.3%	LLTGLYR	99.7%	50.5	25	15.1	2	0	0	835.50	84	90
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	12	13	26	0.03%	51.3%	LQFLER	98.5%	32.6	25	0	2	0	0	805.46	126	131
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	12	13	26	0.03%	51.3%	NTPSFLIACNK	99.7%	54.2	25	47.5	2	0	0	1264.64	171	181
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	12	13	26	0.03%	51.3%	SAAPSTLDSSSTAPAQLGK	99.7%	88.4	25	88.4	2	0	0	1788.90	209	227
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	12	13	26	0.03%	51.3%	SAAPSTLDSSSTAPAQLGKK	99.4%	36.9	25	34.3	1	0	0	1916.99	209	228
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	12	13	26	0.03%	51.3%	VADGGGAGGTFQPYLDTLR	99.7%	114	25	114	2	0	0	1894.93	9	27
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	8	8	16	0.02%	17.5%	AAIEAFNK	97.4%	30.3	25	17.3	2	0	0	863.46	206	213
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	8	8	16	0.02%	17.5%	DLPDVQELITQVR	99.7%	66.9	25	62.1	3	0	0	1525.82	509	521
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	8	8	16	0.02%	17.5%	FETFCLDPSLVTK	99.7%	68.8	25	57.8	2	0	0	1556.77	558	570

Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	8	8	16	0.02%	17.5%	LASAFTEEQAVLYNQR	99.7%	81.1	25	78.6	2	0	0	1839.92	221	236
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	8	8	16	0.02%	17.5%	LFESMLSECR	99.7%	58.7	25	47.6	2	0	0	1271.58	336	345
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	8	8	16	0.02%	17.5%	QVPGGGGGGGSGGGGGSGGGGSGGGR	99.7%	60	25	60	2	0	0	1843.80	6	31
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	8	8	16	0.02%	17.5%	VEEISPNIR	99.7%	46	25	45.6	2	0	0	1056.57	237	245
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	8	8	16	0.02%	17.5%	VSNLQYLHSYLTYIK	98.9%	27.9	25	27.9	0	1	0	1841.98	373	387
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	8	8	12	0.01%	15.4%	AIELLQEFSDQHPENAAEIK	99.7%	37.4	25	37.4	0	2	0	2282.13	357	376
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	8	8	12	0.01%	15.4%	EALNVINTHTK	95.8%	28.4	25	19.8	1	0	0	1239.67	63	73
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	8	8	12	0.01%	15.4%	GTQGATAGASSELDASK	99.7%	77	25	77	1	0	0	1550.73	601	617
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	8	8	12	0.01%	15.4%	SPAHLSLIR	99.7%	58.2	25	50.2	2	0	0	993.58	443	451
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	8	8	12	0.01%	15.4%	TEEALQLYNQIIK	99.7%	64.3	25	55.2	2	0	0	1562.84	242	254
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	8	8	12	0.01%	15.4%	TIESANQQTDKLK	99.7%	70.3	25	56.6	1	0	0	1475.77	100	112
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	8	8	12	0.01%	15.4%	VLANNSLSFEK	99.7%	60.3	25	47	2	0	0	1221.65	74	84
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	8	8	12	0.01%	15.4%	YDECLAVYR	99.7%	39.7	25	33.5	1	0	0	1188.54	125	133
Signal transducer and activator of transcription 1-alpha/beta	STAT1	STAT1_HUMAN	87.3	99.8%	2	2	2	0.00%	3.7%	LLGPNASPDGLIPWTR	99.7%	45.8	25	45.8	1	0	0	1706.92	526	541
Signal transducer and activator of transcription 1-alpha/beta	STAT1	STAT1_HUMAN	87.3	99.8%	2	2	2	0.00%	3.7%	NLSFFLTPPCAR	99.1%	34.9	25	32.6	1	0	0	1422.72	483	494
Signal transducer and activator of transcription 3	STAT3	STAT3_HUMAN	88.1	100.0%	3	3	5	0.01%	6.5%	GLSIEQLTTLAEK	99.7%	89.2	25	79.7	2	0	0	1402.78	519	531
Signal transducer and activator of transcription 3	STAT3	STAT3_HUMAN	88.1	100.0%	3	3	5	0.01%	6.5%	LLQTAATAAQQGGQANHPTAAVVTEK	99.7%	87.6	25	87.6	0	2	0	2576.34	115	140
Signal transducer and activator of transcription 3	STAT3	STAT3_HUMAN	88.1	100.0%	3	3	5	0.01%	6.5%	TQIQSVEPYTK	99.7%	47.3	25	16.3	1	0	0	1293.67	632	642
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	3	3	5	0.01%	20.9%	DVAYQYVK	99.4%	36.8	25	25.9	1	0	0	985.50	96	103
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	3	3	5	0.01%	20.9%	SGDSEVYQLGDVSQK	99.7%	95.2	25	93.9	2	0	0	1611.75	67	81
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	3	3	5	0.01%	20.9%	VGQDPVLR	99.7%	56.7	25	50.5	2	0	0	883.50	39	46
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	14	14	28	0.03%	13.0%	DIFLFITR	99.4%	36.8	25	36.8	1	0	0	1024.58	115	122
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	14	14	28	0.03%	13.0%	DLALVNDQLLGFVR	99.7%	88.8	25	80.8	3	0	0	1572.87	391	404
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	14	14	28	0.03%	13.0%	EVQLAQIFEPLSR	99.7%	73.3	25	64	2	0	0	1529.83	751	763
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	14	14	28	0.03%	13.0%	FNDIHVPVR	99.7%	41.8	25	36.3	2	0	0	1096.59	332	340
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	14	14	28	0.03%	13.0%	IAPVHIDSEAISALVK	99.2%	29.3	25	28	0	2	0	1662.94	618	633
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	14	14	28	0.03%	13.0%	IETDLPQIR	99.7%	50.6	25	43.9	2	0	0	1084.60	709	717
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	14	14	28	0.03%	13.0%	IFAQYLVPHNLETEER	99.7%	43.2	25	43.2	0	2	0	1959.00	468	483
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	14	14	28	0.03%	13.0%	LLVACCLADIFR	99.7%	59.2	25	55.8	4	0	0	1450.75	88	99
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	14	14	28	0.03%	13.0%	LYTVCDVALCVINSK	99.7%	76.3	25	72.8	2	0	0	1754.88	1075	1089
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	14	14	28	0.03%	13.0%	NDDLNKPINK	99.7%	48.8	25	38.9	2	0	0	1170.61	1285	1294
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	14	14	28	0.03%	13.0%	SHDPEEAIR	94.9%	27.6	25	25.9	1	0	0	1053.50	369	377
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	14	14	28	0.03%	13.0%	SIEGTADDEEEGVSPDTAIR	99.7%	68.4	25	59.2	2	0	0	2090.94	638	657
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	14	14	28	0.03%	13.0%	STLIPILHQK	99.7%	39.7	25	13.7	1	0	0	1149.70	718	727
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	14	14	28	0.03%	13.0%	TVTAAGAENIQQK	99.7%	92.8	25	77.2	2	0	0	1330.70	1240	1252
Small nuclear ribonucleoprotein E	SNRPE	RUXE_HUMAN	10.8	100.0%	4	5	10	0.01%	42.4%	GDNITLLQSVSN	99.7%	51	25	48.5	2	0	0	1260.64	81	92
Small nuclear ribonucleoprotein E	SNRPE	RUXE_HUMAN	10.8	100.0%	4	5	10	0.01%	42.4%	IMLKGDNITLLQSVSN	99.3%	35.8	25	35.8	2	0	0	1761.94	77	92
Small nuclear ribonucleoprotein E	SNRPE	RUXE_HUMAN	10.8	100.0%	4	5	10	0.01%	42.4%	IQVWLYEQVNMR	99.7%	62	25	62	2	0	0	1594.80	31	42
Small nuclear ribonucleoprotein E	SNRPE	RUXE_HUMAN	10.8	100.0%	4	5	10	0.01%	42.4%	VMVQPINLIFR	99.7%	45.7	25	37.6	4	0	0	1345.77	13	23
Small nuclear ribonucleoprotein F	SNRPF	RUXF_HUMAN	9.7	99.7%	2	2	3	0.00%	18.6%	CNNVLYIR	99.7%	52.8	25	38.6	2	0	0	1051.54	66	73
Small nuclear ribonucleoprotein F	SNRPF	RUXF_HUMAN	9.7	99.7%	2	2	3	0.00%	18.6%	LKWGMEYK	94.9%	27.6	25	20.4	1	0	0	1054.54	23	30
Small nuclear ribonucleoprotein Sm D1	SNRPD1	SMD1_HUMAN	13.3	100.0%	4	5	14	0.01%	37.8%	EPVQLETLSIR	99.7%	47.1	25	35	1	0	0	1284.72	51	61
Small nuclear ribonucleoprotein Sm D1	SNRPD1	SMD1_HUMAN	13.3	100.0%	4	5	14	0.01%	37.8%	LSHETVTIELK	99.7%	53.9	25	45.9	6	2	0	1269.71	10	20
Small nuclear ribonucleoprotein Sm D1	SNRPD1	SMD1_HUMAN	13.3	100.0%	4	5	14	0.01%	37.8%	NGTQVHGTITGVDVSMNTHLK	99.6%	32.6	25	32.6	0	1	0	2209.10	21	41
Small nuclear ribonucleoprotein Sm D1	SNRPD1	SMD1_HUMAN	13.3	100.0%	4	5	14	0.01%	37.8%	NREPVQLETLSIR	99.7%	81	25	74.2	4	0	0	1554.86	49	61
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	6	8	19	0.02%	40.7%	EMWTEVPK	96.2%	28.7	25	20.5	2	0	0	1019.49	72	79
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	6	8	19	0.02%	40.7%	GDSVIVVLR	99.7%	77.3	25	61.8	5	0	0	957.57	103	111
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	6	8	19	0.02%	40.7%	HCNMVLENVK	99.7%	60.1	25	60.1	4	0	0	1243.59	62	71
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	6	8	19	0.02%	40.7%	NNTQVLINCR	99.7%	65.7	25	54.7	4	0	0	1231.62	38	47
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	6	8	19	0.02%	40.7%	SEMTPEELQK	99.7%	59.2	25	51.7	3	0	0	1191.56	9	18
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	6	8	19	0.02%	40.7%	SEMTPEELQKR	99.7%	41.4	25	32.2	1	0	0	1347.66	9	19

Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN	24.6	100.0%	3	4	11	0.01%	12.5%	GENLVSMTVEGPPPK	99.7%	75.2	25	64.1	4	0	0	1554.78	74	88
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN	24.6	100.0%	3	4	11	0.01%	12.5%	IFIGTFK	98.6%	32.7	25	22	2	0	0	825.49	26	32
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN	24.6	100.0%	3	4	11	0.01%	12.5%	VLGLVLLR	99.7%	63.8	25	63.8	5	0	0	882.61	66	73
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.08%	29.6%	ADIGVAMGIAGSDVSK	99.7%	115	25	111	4	0	0	1490.75	728	743
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.08%	29.6%	AVAGDASESALLK	99.7%	99.7	25	86.8	5	0	0	1231.65	446	458
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.08%	29.6%	AVFQANQENLPILK	99.7%	72.7	25	53.7	4	0	0	1584.87	431	444
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.08%	29.6%	DGPNALTPPPTTPEWIK	99.7%	45.7	25	45.7	2	0	0	1833.94	75	91
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.08%	29.6%	GIVVYTGDR	99.7%	50.8	25	48.1	3	0	0	979.52	256	264
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.08%	29.6%	GVGIISEGNETVEDIAAR	99.7%	132	25	121	4	0	0	1829.92	630	647
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.08%	29.6%	IAGLCNR	96.1%	29.1	25.5	14.7	1	0	0	803.42	424	430
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.08%	29.6%	IVEIPFNSTNK	99.7%	40.7	25	32.5	1	0	0	1261.68	477	487
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.08%	29.6%	LIFDNLKK	99.7%	39.4	25	27.9	2	0	0	990.60	767	774
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.08%	29.6%	LIIVEGCQR	99.7%	55.2	25	46.9	4	0	0	1087.59	699	707
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.08%	29.6%	LNIPVSQVNPR	99.7%	66.4	25	57.6	6	0	0	1236.71	648	658
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.08%	29.6%	LSLDELHR	99.7%	54.6	25	50.4	1	0	0	982.53	46	53
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.08%	29.6%	MSINAEEVVVGDLVEVK	99.7%	99.8	25	94.3	3	0	0	1846.95	178	194
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.08%	29.6%	NIAFFSTNCVEGTAR	99.7%	105	25	105	3	0	0	1686.79	241	255
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.08%	29.6%	NLEAVETLGSTSTICSDK	99.7%	105	25	105	2	0	0	1924.92	360	377
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.08%	29.6%	NMVPQQALVIR	99.7%	51.8	25	44	3	0	0	1284.71	163	173
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.08%	29.6%	NPNTSEPQHLLVMK	99.7%	78.9	25	71.9	3	0	0	1607.82	495	508
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.08%	29.6%	QGAIVAVTGDGVNDSPALK	99.7%	99.1	25	99.1	2	0	0	1811.95	708	726
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.08%	29.6%	QGAIVAVTGDGVNDSPALKK	99.7%	46.2	25	46.2	0	2	0	1940.05	708	727
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.08%	29.6%	SPDFTNENPLETR	99.7%	82.9	25	72.2	4	0	0	1519.70	228	240
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.08%	29.6%	TSATWLALSR	99.7%	81.6	25	59	4	0	0	1105.60	414	423
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.08%	29.6%	VDNSSLTGESEPQTR	99.7%	83.2	25	69.9	3	0	0	1619.75	213	227
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.08%	29.6%	VIMVTGDHPITAK	99.7%	72.1	25	68	4	1	0	1381.75	613	625
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.08%	29.6%	YGTDLSR	98.1%	31.4	25	20.2	2	0	0	811.39	55	61
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.08%	29.6%	YHTEIVFAR	99.4%	36.4	25	25.6	2	0	0	1135.59	684	692
Sorting and assembly machinery component 50 homolog	SAMM50	SAM50_HUMAN	52.0	99.8%	2	2	3	0.00%	4.9%	SSLSHAMVIDSR	99.7%	54.7	25	43.3	1	0	0	1302.65	256	267
Sorting and assembly machinery component 50 homolog	SAMM50	SAM50_HUMAN	52.0	99.8%	2	2	3	0.00%	4.9%	VTGQFPWSSLR	99.7%	50.1	25	45.8	2	0	0	1277.66	195	205
Sorting nexin-2	SNX2	SNX2_HUMAN	58.5	100.0%	3	3	5	0.01%	6.7%	AVNTQALSGAGILR	99.7%	46.9	25	36.8	2	0	0	1370.78	270	283
Sorting nexin-2	SNX2	SNX2_HUMAN	58.5	100.0%	3	3	5	0.01%	6.7%	ELSANTAAFAK	99.7%	66.5	25	60.2	2	0	0	1122.58	336	346
Sorting nexin-2	SNX2	SNX2_HUMAN	58.5	100.0%	3	3	5	0.01%	6.7%	QFLESSELPR	99.7%	41.7	25	32.9	1	0	0	1205.62	260	269
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	SPTN1_HUMAN	284.5	100.0%	8	8	12	0.01%	3.4%	DLAALEDKVK	99.7%	44.1	25	34.1	1	0	0	1101.62	303	312
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	SPTN1_HUMAN	284.5	100.0%	8	8	12	0.01%	3.4%	DLASVQALLR	99.7%	84.5	25	66.3	1	0	0	1085.63	286	295
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	SPTN1_HUMAN	284.5	100.0%	8	8	12	0.01%	3.4%	DVTGAEALLER	99.7%	50.7	25	40.6	2	0	0	1173.61	1370	1380
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	SPTN1_HUMAN	284.5	100.0%	8	8	12	0.01%	3.4%	EANQQQQFNR	97.9%	31.1	25	24.3	1	0	0	1262.59	676	685
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	SPTN1_HUMAN	284.5	100.0%	8	8	12	0.01%	3.4%	ELPTAFDYVEFTR	97.7%	30.7	25	30.7	1	0	0	1587.77	2455	2467
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	SPTN1_HUMAN	284.5	100.0%	8	8	12	0.01%	3.4%	LFGAAEVQR	99.7%	54.8	25	29.8	2	0	0	990.54	251	259
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	SPTN1_HUMAN	284.5	100.0%	8	8	12	0.01%	3.4%	SQLLGSAHEVQR	99.7%	46.8	25	37.5	2	0	0	1324.70	1226	1237
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	SPTN1_HUMAN	284.5	100.0%	8	8	12	0.01%	3.4%	SSEEIESAFR	99.7%	54.8	25	46.7	2	0	0	1154.53	2405	2414
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	8	8	11	0.01%	4.3%	ALVADSHPESER	99.7%	42.7	25	42.7	2	0	0	1310.63	1657	1668
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	8	8	11	0.01%	4.3%	DQNTVETLQR	99.7%	52.2	25	30.1	1	0	0	1203.60	1835	1844
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	8	8	11	0.01%	4.3%	EIGQSVDEVEK	99.7%	41.2	25	35.9	1	0	0	1232.60	2044	2054
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	8	8	11	0.01%	4.3%	GNLEVLLFTIQSK	99.7%	62.1	25	62	2	0	0	1461.83	360	372
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	8	8	11	0.01%	4.3%	LVSQDNFGFDLPAVEAATK	99.7%	59.4	25	59.4	2	0	0	2022.02	444	462
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	8	8	11	0.01%	4.3%	SQNIVTDSSSLSAEAIR	99.7%	107	25	101	1	0	0	1777.89	1548	1564
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	8	8	11	0.01%	4.3%	VLDNAIETEK	99.6%	38	25	31	1	0	0	1131.59	293	302
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	8	8	11	0.01%	4.3%	VQAVVAVAR	99.1%	34.8	25	23.5	1	0	0	912.56	478	486
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	4	4	8	0.01%	12.9%	AAFVLPEFAR	99.7%	42.7	25	38.2	2	0	0	1120.61	286	295
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	4	4	8	0.01%	12.9%	FLPGMAIGYSSSK	99.7%	52	25	35.2	2	0	0	1357.68	136	148

Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	4	4	8	0.01%	12.9%	YQDILVFR	99.7%	52.3	25	52.2	2	0	0	1053.57	48	55
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	4	4	8	0.01%	12.9%	YYNSDVHR	99.7%	45.8	25	44.2	2	0	0	1053.47	278	285
Sphingomyelin phosphodiesterase 4	SMPD4	NSMA3_HUMAN	93.4	100.0%	3	3	3	0.00%	2.9%	LAQLITQAK	99.7%	43.4	25	32.4	1	0	0	985.60	557	565
Sphingomyelin phosphodiesterase 4	SMPD4	NSMA3_HUMAN	93.4	100.0%	3	3	3	0.00%	2.9%	LFVGFLNR	99.6%	39	25	32	1	0	0	965.56	444	451
Sphingomyelin phosphodiesterase 4	SMPD4	NSMA3_HUMAN	93.4	100.0%	3	3	3	0.00%	2.9%	LSEAQLR	99.7%	44.5	25	3.86	1	0	0	816.46	632	638
Sphingosine-1-phosphate lyase 1	SGPL1	SGPL1_HUMAN	63.5	100.0%	3	3	3	0.00%	7.4%	AFEPYLEILEVYSTK	99.7%	51	25	51	1	0	0	1801.93	11	25
Sphingosine-1-phosphate lyase 1	SGPL1	SGPL1_HUMAN	63.5	100.0%	3	3	3	0.00%	7.4%	GIFVFGNPQLSVIALGSR	99.7%	74.6	25	74.6	1	0	0	1875.05	439	456
Sphingosine-1-phosphate lyase 1	SGPL1	SGPL1_HUMAN	63.5	100.0%	3	3	3	0.00%	7.4%	PSTDLLMLK	99.5%	37	25	26.2	1	0	0	1017.57	2	10
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	4	6	19	0.02%	20.2%	GTVLDQVPVNPSLYLIK	99.7%	83.9	25	64.3	4	0	0	1856.05	74	90
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	4	6	19	0.02%	20.2%	ISDAHLADTMIGK	99.7%	70.8	25	67.8	3	0	0	1371.69	123	135
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	4	6	19	0.02%	20.2%	SSVGPSKPVSQPR	99.7%	45.4	25	31.8	4	4	0	1325.72	38	50
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	4	6	19	0.02%	20.2%	VSALEVLPDR	99.7%	84.5	25	66.5	4	0	0	1098.62	108	117
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	AAGLATMISTMRPDIDNMDEYVR	99.7%	39.9	25	39.9	0	1	0	2618.19	603	625
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	AIVNVIGMHK	99.6%	38.6	25	38.6	6	0	0	1097.61	999	1008
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	ATVNTFGYIAK	99.7%	63.3	25	57.3	1	0	0	1184.63	1076	1086
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	DTPGHGSGWAETPR	96.3%	23.4	25	21.4	0	1	0	1467.66	302	315
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	EIISNLAK	99.3%	36.1	25	18.8	2	0	0	887.52	595	602
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	EVMLILIR	99.7%	76.3	25	56.7	8	0	0	986.61	768	775
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	GAEYVSAR	99.1%	34.9	25	13.5	2	0	0	852.42	1046	1053
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	GDTPGHATPGHGGATSSAR	99.7%	73.6	25	73.6	0	4	0	1733.80	271	289
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	GGDSIGETPTPGASK	99.7%	59.8	25	53.8	4	0	0	1373.65	319	333
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	GSETPGATPGSK	98.6%	32.7	25	32.7	1	0	0	1088.52	241	252
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	ICFELLELLK	99.7%	59.7	25	55.4	4	0	0	1277.72	1058	1067
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	ILVVIEPLLIDEDYYAR	99.7%	54.7	25	54.7	1	0	0	2034.12	574	590
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	IYNDDKNTYIR	99.7%	67.1	25	62.2	4	3	0	1414.70	1287	1297
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	IYNSIYIGSQDALIAHYPR	99.7%	40.7	25	40.7	0	2	0	2194.13	1268	1286
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	LLVDVDESTLSPEEQK	97.1%	29.8	25	19.2	1	0	0	1801.91	478	493
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	LLVDVDESTLSPEEQKER	99.7%	38.5	25	36.3	0	4	0	2087.05	478	495
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	MLQYCLQGLFHPAR	99.7%	34.4	25	34.4	0	1	0	1733.86	1246	1259
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	QCCGTDGVEANYIK	99.6%	38.9	25	32.7	1	0	0	1614.69	794	807
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	QLVDTTVELANK	99.7%	93.4	25	83.3	4	0	0	1330.72	832	843
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	QQAADLISR	99.7%	54.8	25	37.3	4	0	0	1001.54	949	957
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	SLVEIIEHGLVDEQQK	99.7%	71.3	25	68.9	4	0	0	1836.97	685	700
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	SVNDQPSGNLPFLKPDDIQYFDK	99.7%	39.9	25	39	0	2	0	2637.28	455	477
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	TDRGGDSIGETPTPGASK	99.7%	41.8	25	41.8	0	1	0	1745.83	316	333
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	TEILPPFFK	99.7%	39.6	25	24.9	3	0	0	1091.61	808	816
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	THEDIEAQIR	99.7%	59.2	25	53.4	4	0	0	1211.60	7	16
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	TMIISPER	99.7%	41.7	25	31.1	2	0	0	962.50	125	132
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	VGAAEIISR	99.7%	81.4	25	42.6	4	0	0	915.53	844	852
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	VPELNVQNGVLK	99.7%	63.2	25	57.3	3	0	0	1309.75	1138	1149
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	VQENCIDLVGR	99.7%	66.6	25	60.5	4	0	0	1302.65	1031	1041
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	VVNGAAASQPPSKR	99.2%	35.2	25	35.2	2	0	0	1381.75	183	196
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	31	34	89	0.09%	29.2%	WDQTADQTPGATPK	99.7%	60.2	25	51.8	1	0	0	1515.71	200	213
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	7	7	12	0.01%	8.8%	AAVLLEQER	99.7%	46.5	25	40.7	2	0	0	1028.57	184	192
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	7	7	12	0.01%	8.8%	KPGDLSDELR	99.7%	49	25	35.7	2	0	0	1129.59	605	614
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	7	7	12	0.01%	8.8%	LAEIGAPIQGNR	99.7%	55.8	25	55.8	2	0	0	1238.69	36	47
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	7	7	12	0.01%	8.8%	LAEIGAPIQGNREELVER	99.7%	36.5	25	29.6	0	2	0	1994.07	36	53
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	7	7	12	0.01%	8.8%	SSLGQSASETEEDTVSVSK	99.7%	79.2	25	79.2	1	0	0	1940.89	302	320
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	7	7	12	0.01%	8.8%	VGEPVALSEEER	99.7%	69.1	25	60	2	0	0	1314.65	135	146
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	7	7	12	0.01%	8.8%	VPPPWLIAMQR	99.2%	35.4	25	35.4	1	0	0	1307.73	628	638
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	19	21	53	0.05%	19.6%	DYIVVGSDSGR	99.7%	76.6	25	64.2	2	0	0	1167.56	76	86

Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	19	21	53	0.05%	19.6%	FGNICVVR	99.7%	57.1	25	47.2	2	0	0	964.50	1050	1057
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	19	21	53	0.05%	19.6%	FLAVGLVDNTVR	99.7%	80.1	25	67.7	4	0	0	1303.74	604	615
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	19	21	53	0.05%	19.6%	FSNTGEDWYVLVGVAK	99.7%	85	25	81.4	4	0	0	1784.89	896	911
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	19	21	53	0.05%	19.6%	ITLETDEDMVTEIR	99.7%	56	25	56	1	0	0	1680.80	313	326
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	19	21	53	0.05%	19.6%	IVILEYQPSK	99.7%	73.4	25	61.5	2	0	0	1189.68	87	96
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	19	21	53	0.05%	19.6%	LGAVFNQVAFPLQYTPR	99.7%	91.7	25	91.7	7	0	0	1921.03	770	786
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	19	21	53	0.05%	19.6%	MFLYNLTLQR	99.7%	57	25	53.7	3	0	0	1298.69	1	10
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	19	21	53	0.05%	19.6%	MQGQEAVLAMSSR	99.7%	84.1	25	76.7	3	0	0	1423.67	706	718
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	19	21	53	0.05%	19.6%	NENQLIIFADDTYPR	99.7%	96.9	25	96.9	2	1	0	1808.88	1017	1031
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	19	21	53	0.05%	19.6%	NFGDQPDIR	99.7%	47.5	25	39.4	2	0	0	1061.50	260	268
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	19	21	53	0.05%	19.6%	QQEIVVSR	99.5%	37	25	12	2	0	0	958.53	27	34
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	19	21	53	0.05%	19.6%	SMFFFLAQTEQGDIFK	99.7%	68.9	25	68.9	2	0	0	1924.92	297	312
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	19	21	53	0.05%	19.6%	SVAGGFVYTYK	99.7%	60.9	25	54.7	4	0	0	1191.60	919	929
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	19	21	53	0.05%	19.6%	SWLSYSYQSR	99.7%	43.9	25	40.4	2	0	0	1276.60	719	728
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	19	21	53	0.05%	19.6%	TPVEEVPAAIAPFQGR	99.7%	78.3	25	71.5	2	0	0	1681.89	943	958
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	19	21	53	0.05%	19.6%	TVLDPVTGDLSDTR	99.7%	93	25	92.1	4	0	0	1488.75	677	690
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	19	21	53	0.05%	19.6%	VIVSDVQESFIWVR	99.7%	63.5	25	55.5	2	0	0	1676.90	1000	1013
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	19	21	53	0.05%	19.6%	YFDTVPVAAAMCVLK	99.5%	37.7	25	37.7	2	0	0	1684.84	329	343
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	3	3	6	0.01%	12.5%	AVIDLNNR	99.7%	52.5	25	36.3	2	0	0	914.51	126	133
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	3	3	6	0.01%	12.5%	NPQNSSQSADGLR	99.7%	73.2	25	68	2	0	0	1373.64	54	66
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	3	3	6	0.01%	12.5%	QYEMGECTR	99.7%	45.2	25	36.9	2	0	0	1173.47	157	165
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	8	12	22	0.02%	24.6%	ELLTSFGPLK	99.7%	40.6	25	28.4	2	0	0	1104.63	277	286
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	8	12	22	0.02%	24.6%	IFVEFTSVFDCQK	99.7%	74.9	25	74.9	2	0	0	1619.78	432	444
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	8	12	22	0.02%	24.6%	LFIGGLPNYLNDDQVK	99.7%	46.3	25	33.1	2	0	0	1805.94	261	276
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	8	12	22	0.02%	24.6%	LGGLTQAPGNPVLAVQINQDK	99.7%	58.2	25	58.2	2	2	0	2133.17	175	195
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	8	12	22	0.02%	24.6%	NFAFLEFR	99.7%	47.8	25	41.3	2	0	0	1043.53	196	203
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	8	12	22	0.02%	24.6%	SIEIPRPVDGVEVPGCGK	99.7%	84.9	25	76	2	2	0	1908.99	414	431
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	8	12	22	0.02%	24.6%	SVDETTQAMAFDGIIFQGQSLK	99.7%	66.1	25	66.1	3	0	0	2386.16	204	225
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	8	12	22	0.02%	24.6%	YCDPDSYHR	99.7%	44.5	25	44.5	2	1	0	1212.47	463	471
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	5	5	8	0.01%	10.2%	AELDDTPMR	99.3%	36	25	30.1	1	0	0	1063.47	350	358
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	5	5	8	0.01%	10.2%	AVVIVDDR	99.7%	42.3	25	31.7	4	0	0	886.50	400	407
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	5	5	8	0.01%	10.2%	FGQGGAGPVGGQGPR	99.7%	53.8	25	53.8	2	0	0	1341.67	667	681
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	5	5	8	0.01%	10.2%	GIVEFASKPAAR	99.0%	34.3	25	34.3	1	0	0	1245.70	414	425
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	5	5	8	0.01%	10.2%	LFVGNLPADITEDEFKR	99.7%	44	25	39.7	0	2	0	1964.01	299	315
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	5	5	8	0.01%	10.2%	YGEPGEVFINK	99.7%	62.8	25	57.6	2	0	0	1252.62	320	330
SRA stem-loop-interacting RNA-binding protein, mitochondrial	SLIRP	SLIRP_HUMAN	12.3	100.0%	3	3	6	0.01%	35.8%	GLGWVQFSSEEGLR	99.7%	76.4	25	74.7	2	0	0	1564.78	61	74
SRA stem-loop-interacting RNA-binding protein, mitochondrial	SLIRP	SLIRP_HUMAN	12.3	100.0%	3	3	6	0.01%	35.8%	IPWTAASSQLK	98.1%	31.6	25	23	2	0	0	1201.66	26	36
SRA stem-loop-interacting RNA-binding protein, mitochondrial	SLIRP	SLIRP_HUMAN	12.3	100.0%	3	3	6	0.01%	35.8%	NALQQENHIIDGVK	99.7%	64.3	25	64.2	2	0	0	1578.82	75	88
SRSF protein kinase 1	SRPK1	SRPK1_HUMAN	74.3	100.0%	4	4	7	0.01%	7.0%	EMVVQLLDDFK	99.7%	45.5	25	45.5	1	0	0	1336.68	142	152
SRSF protein kinase 1	SRPK1	SRPK1_HUMAN	74.3	100.0%	4	4	7	0.01%	7.0%	HFTEDIQTR	99.7%	44.4	25	43.1	3	0	0	1146.55	507	515
SRSF protein kinase 1	SRPK1	SRPK1_HUMAN	74.3	100.0%	4	4	7	0.01%	7.0%	IADLGNACWVHK	99.6%	38.8	25	8.42	1	0	0	1383.68	495	506
SRSF protein kinase 1	SRPK1	SRPK1_HUMAN	74.3	100.0%	4	4	7	0.01%	7.0%	STAGNFLVNPLEPK	99.7%	54.7	25	48.6	2	0	0	1486.79	473	486
Sterile alpha and TIR motif-containing protein 1	SARM1	SARM1_HUMAN	79.4	100.0%	2	2	2	0.00%	4.3%	SGTLALVEPLVASLDPGR	99.7%	48.9	25	48.9	1	0	0	1795.00	290	307
Sterile alpha and TIR motif-containing protein 1	SARM1	SARM1_HUMAN	79.4	100.0%	2	2	2	0.00%	4.3%	SNLADWLGSLDPR	99.7%	65.2	25	65.2	1	0	0	1443.72	485	497
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	8	16	0.02%	32.0%	AEQINQAAGEASAVLAK	99.7%	129	25	127	2	0	0	1670.87	234	250
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	8	16	0.02%	32.0%	APVPGTPDSLSSGSSR	99.7%	63	25	54.8	2	0	0	1514.74	322	337
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	8	16	0.02%	32.0%	ASYGVEDPEYAVTQLAQTTMR	99.7%	93	25	88	2	0	0	2330.10	115	135
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	8	16	0.02%	32.0%	DVQGTDASLDEELDRVK	99.7%	102	25	91.7	2	0	0	1889.91	338	354
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	8	16	0.02%	32.0%	ESAINVAEGK	97.9%	31.2	25	30.5	1	0	0	1017.52	212	221
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	8	16	0.02%	32.0%	ESAINVAEGKK	99.7%	44	25	37.3	2	0	0	1145.62	212	222
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	8	16	0.02%	32.0%	ILEPGLNILIPVLDR	99.7%	85.1	25	85.1	3	0	0	1675.02	58	72

Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	8	16	0.02%	32.0%	NTVVLFVPQQEAWVVER	99.7%	67.8	25	66.2	2	0	0	2014.08	35	51
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	20	24	57	0.06%	39.3%	AQFEGIVTDLIR	99.7%	93.7	25	85	5	0	0	1361.74	349	360
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	20	24	57	0.06%	39.3%	ASNGDAWVEAHGK	99.7%	62.7	25	62.7	2	0	0	1341.62	147	159
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	20	24	57	0.06%	39.3%	DAGQISGLNVLR	99.7%	79.4	25	63.7	3	0	0	1242.68	207	218
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	20	24	57	0.06%	39.3%	EQQIVIQSSGGLSK	99.7%	47.4	25	39.1	1	0	0	1473.79	542	555
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	20	24	57	0.06%	39.3%	EQQIVIQSSGGLSKDDIENMVK	99.7%	56.9	25	56.9	0	3	0	2418.22	542	563
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	20	24	57	0.06%	39.3%	ETGVDLTKDNMALQR	98.4%	32.3	25	24.2	1	1	0	1706.84	293	307
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	20	24	57	0.06%	39.3%	LLGQFTLIGIPPAPR	99.7%	71.1	25	71.1	5	0	0	1592.95	499	513
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	20	24	57	0.06%	39.3%	LYSPSQIGAFVLMK	99.7%	64.4	25	64.4	2	2	0	1569.83	160	173
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	20	24	57	0.06%	39.3%	MKETAENYLGHTAK	99.7%	81.6	25	72.2	1	0	0	1592.77	174	187
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	20	24	57	0.06%	39.3%	NAVITVPAYFNDSQR	99.7%	65.4	25	65.4	2	0	0	1694.85	188	202
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	20	24	57	0.06%	39.3%	QAASSLQQASLK	99.7%	96.1	25	88.2	4	0	0	1231.66	635	646
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	20	24	57	0.06%	39.3%	QAVTNPNNTFYATK	99.7%	88.8	25	88.3	2	0	0	1568.77	108	121
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	20	24	57	0.06%	39.3%	RYDDPEVQK	99.7%	45.3	25	35.7	2	0	0	1149.55	127	135
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	20	24	57	0.06%	39.3%	SDIGEVILVGGMTR	99.7%	85.9	25	82.1	4	0	0	1446.76	378	391
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	20	24	57	0.06%	39.3%	SQVFSTAADGQTQVEIK	99.7%	120	25	116	4	0	0	1808.90	469	485
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	20	24	57	0.06%	39.3%	STNGDTFLGGEDFDQALLR	99.7%	95.8	25	91.9	2	0	0	2055.96	266	284
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	20	24	57	0.06%	39.3%	TTPSVVAFTADGER	99.7%	113	25	112	3	0	0	1450.72	86	99
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	20	24	57	0.06%	39.3%	VINEPTAAALAYGLDK	99.7%	106	25	104	4	0	0	1645.88	219	234
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	20	24	57	0.06%	39.3%	VLENAEGAR	99.7%	54.9	25	43.6	2	0	0	958.50	77	85
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	20	24	57	0.06%	39.3%	VQQTVQDLFGR	99.7%	77.6	25	71.8	2	0	0	1290.68	395	405
Stress-induced-phosphoprotein 1	STIP1	STIP1_HUMAN	62.6	100.0%	2	2	2	0.00%	3.1%	ELIEQLR	99.7%	45	25	16.3	1	0	0	900.52	154	160
Stress-induced-phosphoprotein 1	STIP1	STIP1_HUMAN	62.6	100.0%	2	2	2	0.00%	3.1%	LMDVGLIAIR	99.7%	67.4	25	54.3	1	0	0	1100.65	534	543
Striatin-interacting protein 1	STRIP1	STRP1_HUMAN	95.6	100.0%	5	5	8	0.01%	6.0%	FFNQNIMSYITAK	99.7%	69.8	25	68.9	2	0	0	1576.78	616	628
Striatin-interacting protein 1	STRIP1	STRP1_HUMAN	95.6	100.0%	5	5	8	0.01%	6.0%	ILLAAAPTSK	99.7%	58	25	46.4	2	0	0	984.61	527	536
Striatin-interacting protein 1	STRIP1	STRP1_HUMAN	95.6	100.0%	5	5	8	0.01%	6.0%	LLDGLEVTAR	99.7%	70.7	25	58	1	0	0	1086.62	129	138
Striatin-interacting protein 1	STRIP1	STRP1_HUMAN	95.6	100.0%	5	5	8	0.01%	6.0%	NLFSCINLLR	99.7%	46.6	25	33.6	2	0	0	1249.67	664	673
Striatin-interacting protein 1	STRIP1	STRP1_HUMAN	95.6	100.0%	5	5	8	0.01%	6.0%	VLLLLWK	95.4%	28	25	5.04	1	0	0	884.60	286	292
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	26	30	66	0.07%	24.1%	ADQDRLDLEER	97.8%	31	25	29.8	1	0	0	1359.65	402	412
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	26	30	66	0.07%	24.1%	AEEDTQFNYHR	99.7%	54.6	25	44.6	2	0	0	1409.61	178	188
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	26	30	66	0.07%	24.1%	AFVSMVYSEEGAEDR	99.7%	90.1	25	85.3	1	0	0	1689.74	78	92
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	26	30	66	0.07%	24.1%	DKFQETSDEFEAAR	99.7%	79.9	25	79.9	2	0	0	1672.75	1036	1049
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	26	30	66	0.07%	24.1%	DLIHGAPVGKPAANR	99.6%	31.6	25	31.6	0	3	0	1515.84	63	77
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	26	30	66	0.07%	24.1%	DLTLEENQVK	99.7%	41.8	25	30.4	2	0	0	1188.61	364	373
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	26	30	66	0.07%	24.1%	FNACFESVATNIDEIYK	99.7%	55.7	25	55.7	1	0	0	2020.93	1070	1086
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	26	30	66	0.07%	24.1%	HLALNLQEK	99.3%	35.8	25	31	1	0	0	1065.61	726	734
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	26	30	66	0.07%	24.1%	IIDETMAQLQDLK	99.7%	59.8	25	58.1	1	0	0	1533.78	862	874
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	26	30	66	0.07%	24.1%	LGIQLDFEK	99.7%	44.2	25	38.7	3	0	0	1062.58	817	825
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	26	30	66	0.07%	24.1%	LNEQQSVLQR	99.7%	75.5	25	62.3	4	0	0	1214.65	1010	1019
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	26	30	66	0.07%	24.1%	LREIEENQK	98.3%	31.9	25	20.5	1	0	0	1158.61	425	433
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	26	30	66	0.07%	24.1%	LTEELKEQMK	99.7%	43.8	25	29.6	1	0	0	1248.65	681	690
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	26	30	66	0.07%	24.1%	LVIDVIR	98.6%	32.7	25	14.3	2	0	0	827.54	593	599
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	26	30	66	0.07%	24.1%	LYHNEVEIEK	99.7%	40.1	25	29.9	3	1	0	1273.64	228	237
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	26	30	66	0.07%	24.1%	NFLVFQGAVESIAMK	99.7%	83.9	25	82.6	6	0	0	1653.87	132	146
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	26	30	66	0.07%	24.1%	NMDAIIVDSEK	99.7%	40.8	25	30.7	3	0	0	1250.59	541	551
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	26	30	66	0.07%	24.1%	QIIGPFQR	98.5%	32.4	25	24.5	2	0	0	958.55	19	26
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	26	30	66	0.07%	24.1%	SGELAQEYDKR	99.7%	48.5	25	48.3	3	0	0	1295.62	161	171
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	26	30	66	0.07%	24.1%	SGVISGGASDLK	99.7%	44.4	25	29.5	4	0	0	1090.57	649	660
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	26	30	66	0.07%	24.1%	SKLESELANFGPR	99.7%	76	25	66.7	2	0	0	1447.75	735	747
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	26	30	66	0.07%	24.1%	SNLMDAISFVLGEK	99.7%	70.5	25	57	8	0	0	1523.78	39	52
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	26	30	66	0.07%	24.1%	TALFEEISR	99.7%	68.4	25	62.2	2	0	0	1065.56	152	160

Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	26	30	66	0.07%	24.1%	TVALDGTLFQK	99.7%	58.2	25	41.9	3	0	0	1192.66	638	648
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	26	30	66	0.07%	24.1%	VVQLHEYSEELEK	99.7%	68.4	25	68.4	1	0	0	1602.80	111	123
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	26	30	66	0.07%	24.1%	YSQSDLEQTK	99.7%	54.6	25	42.8	3	0	0	1198.56	714	723
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	ALNHEIEELEK	99.7%	41.6	25	37.7	2	1	0	1324.67	276	286
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	AMNVLTEAEER	99.7%	53	25	40	2	0	0	1278.60	987	997
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	ASNLQDLVYK	99.7%	41.9	25	27.8	1	0	0	1150.61	59	68
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	ASVSITFDNSDKK	99.7%	52.3	25	40.2	1	0	0	1411.71	77	89
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	DQEALEAVKR	99.7%	46.9	25	37.3	2	0	0	1158.61	447	456
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	DTSATTALELVAGER	99.7%	88.1	25	71.6	2	0	0	1533.78	534	548
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	EGMFNNANVLFK	97.2%	30	25	29.4	1	0	0	1383.67	1147	1158
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	ENLTELSGGQR	99.7%	100	25	83.9	2	0	0	1203.60	1080	1090
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	FQELKDVQDELR	99.7%	62.4	25	55.8	2	1	0	1519.78	678	689
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	FVDGVSTVAR	99.7%	81.9	25	70.5	2	0	0	1050.56	1161	1170
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	GLVASLISVK	99.7%	63.9	25	62.3	2	0	0	986.62	524	533
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	HLFGQPNSAYDFK	99.7%	54.5	25	49.3	2	0	0	1523.73	946	958
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	IKELDHNISK	99.7%	53.4	25	39.2	2	0	0	1196.66	910	919
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	ILTTIEDLDQKK	99.7%	73.9	25	59.8	2	0	0	1416.79	1015	1026
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	ITDGLHALQEASNK	98.8%	33.6	25	30.5	1	0	0	1496.77	355	368
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	LKETYEALLAR	99.7%	54.7	25	43.9	2	0	0	1306.74	492	502
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	LQEELSENDKK	99.7%	50.7	25	45.5	2	0	0	1332.66	263	273
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	LYNVVVDTEVTGK	99.7%	83.6	25	78.8	2	0	0	1436.76	549	561
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	LYNVVVDTEVTGKK	99.7%	63.4	25	55.3	2	0	0	1564.86	549	562
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	QKEVITAQDTVIK	99.1%	34.6	25	28.1	1	0	0	1472.83	878	890
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	QQLEAVNEAIK	99.7%	51.3	25	43.3	2	0	0	1242.67	838	848
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	SAEELKEMQDK	99.7%	63.5	25	51.1	3	0	0	1307.61	249	259
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	SIILEGFK	99.6%	38.7	25	38.7	2	0	0	906.53	5	12
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	SLEDALAEAQR	99.7%	90	25	74.1	2	0	0	1202.60	298	308
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	SQAASILTK	99.7%	44.7	25	31.5	2	0	0	918.53	669	677
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	SQSAFDLKK	98.8%	33.3	25	26.5	2	0	0	1023.55	313	321
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	SSYLEYQK	99.7%	47.1	25	41.9	2	0	0	1017.49	215	222
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	SYESQIEVMAAEVAK	99.7%	72.1	25	35.6	2	0	0	1654.80	849	863
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	TEEADLLQTK	99.7%	52.5	25	46.3	2	0	0	1147.58	723	732
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	TIEESEETLK	99.7%	55.6	25	44.1	2	0	0	1178.58	751	760
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	TILEEEITPTIQK	99.7%	78.2	25	64.2	2	0	0	1514.83	197	209
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	TVTLGGDVFDPHGTLSGGAR	99.7%	44	25	44	0	2	0	1956.98	649	668
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	33	37	64	0.07%	30.9%	YLINGVNANNTR	99.7%	57.8	25	47.5	2	0	0	1348.70	115	126
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	AILNGIDSINK	94.6%	27.3	25	18	1	0	0	1157.65	504	514
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	AKDLQDELAGNSEQR	99.7%	89.3	25	88.9	1	1	0	1673.81	309	323
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	AKLDELSAK	99.7%	43.2	25	25.3	2	0	0	974.55	237	245
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	ALDQFVNFSEQK	99.7%	86.3	25	81.6	2	0	0	1425.70	986	997
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	ALEYTIYNQELNETR	99.7%	97.8	25	85.1	2	0	0	1856.90	222	236
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	DLEDTEANKEK	99.7%	54.8	25	31	2	0	0	1291.60	419	429
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	DLQDELAGNSEQR	99.7%	55.6	25	44.1	1	0	0	1474.68	311	323
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	DQTIVDPFSSK	99.7%	43.9	25	17.5	2	0	0	1236.61	16	26
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	DTAYPETNDAIPMISK	99.7%	59.2	25	59.2	4	0	0	1781.83	597	612
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	EENAEQQALAAK	99.7%	87.4	25	74.6	2	0	0	1301.63	475	486
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	ELGSLPQEAFEK	99.7%	43.8	25	38.4	2	0	0	1347.68	945	956
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	EMQQLSGGQK	99.6%	38.8	25	23.7	2	0	0	1105.53	1111	1120
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	GALTGGYYDTR	99.7%	66.1	25	58.5	2	0	0	1173.55	662	672
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	GSQFTSKEER	99.7%	45.6	25	29.6	2	0	0	1168.56	382	391
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	IKLEGIITR	99.3%	35.7	25	11.8	1	0	0	1042.66	819	827

Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	ILMEFNK	97.4%	30.2	25	12.9	1	0	0	910.47	572	578
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	INQMATAPDSQR	99.7%	57.7	25	48	4	0	0	1331.64	144	155
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	KAEEELGELEAK	99.7%	102	25	91.3	2	0	0	1345.68	684	695
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	KEESISLMK	96.5%	29	25	19	1	0	0	1064.57	172	180
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	KYEAIQLTFK	99.5%	37.1	25	36.3	2	0	0	1240.69	1025	1034
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	LALLHEGTGPR	99.7%	63.1	25	60.4	2	0	0	1163.65	62	72
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	LFYHIVDSDEVSTK	99.7%	67.7	25	60.8	2	2	0	1652.82	558	571
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	MNLPGEVTFLPLNK	99.7%	84.5	25	74.7	4	0	0	1588.84	579	592
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	NDVMNLLESAGFSR	99.7%	122	25	122	4	0	0	1552.74	119	132
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	NFSEVFQK	99.7%	39.1	25	17.9	2	0	0	998.49	1039	1046
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	NLEQYNKLDQDLNEVK	99.5%	30.8	25	23.9	0	1	0	1962.98	430	445
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	QVIIQGFR	99.3%	35.9	25	22.9	2	0	0	960.56	5	12
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	SEDLDNSIDKTEAGIK	99.7%	76.1	25	72.3	2	0	0	1734.84	880	895
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	SIMELMNVLELR	99.7%	51.8	25	21.3	4	0	0	1463.76	1013	1024
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	SLDQAINDK	99.7%	44.9	25	32.6	2	0	0	1003.51	401	409
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	SMEVSTQLAR	99.7%	48.6	25	40.7	4	0	0	1137.56	635	644
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	SYRDQTIVDPFSSK	99.7%	42.5	25	30.7	1	0	0	1642.81	13	26
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	VDALNDEIR	99.7%	59.5	25	37.3	1	0	0	1044.53	797	805
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	VETYLNENLR	99.7%	55	25	30.8	2	0	0	1250.64	828	837
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	35	43	76	0.08%	31.3%	VSHIDVITAEMAK	99.7%	72	25	66.5	2	0	0	1413.74	1195	1207
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	22	22	36	0.04%	18.8%	DTLVADNLDQATR	99.7%	59.3	25	54.4	2	0	0	1431.71	714	726
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	22	22	36	0.04%	18.8%	EALIAASETLK	98.8%	33.6	25	31.1	1	0	0	1145.64	525	535
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	22	22	36	0.04%	18.8%	FTASIQR	99.4%	36.4	25	27.1	2	0	0	822.45	821	827
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	22	22	36	0.04%	18.8%	FTQLDLEDVQVR	99.7%	98.5	25	93.9	2	0	0	1462.75	390	401
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	22	22	36	0.04%	18.8%	HNTAVSQLTK	99.7%	43.8	25	38.5	2	0	0	1098.59	513	522
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	22	22	36	0.04%	18.8%	IAEMETQKEK	97.2%	30	25	20.3	1	0	0	1206.60	334	343
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	22	22	36	0.04%	18.8%	IFNLSGGEK	99.7%	41.8	25	25.9	2	0	0	964.51	1188	1196
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	22	22	36	0.04%	18.8%	IHEDTKEINEK	99.7%	47.6	25	42.3	2	0	0	1355.68	344	354
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	22	22	36	0.04%	18.8%	LHNTIVEINNHK	99.2%	29	25	29	0	1	0	1431.77	887	898
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	22	22	36	0.04%	18.8%	LLEENVSAFK	99.7%	43.8	25	36.5	1	0	0	1149.62	858	867
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	22	22	36	0.04%	18.8%	LTQEETNFK	99.7%	54.4	25	51.6	2	0	0	1109.55	565	573
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	22	22	36	0.04%	18.8%	NAQFIIISLR	99.7%	60.3	25	47.7	2	0	0	1174.69	1243	1252
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	22	22	36	0.04%	18.8%	NTNAAEESLPEIQK	99.7%	84.5	25	83.2	2	0	0	1543.76	975	988
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	22	22	36	0.04%	18.8%	QAFYFALR	99.4%	36.7	25	20.4	1	0	0	1015.54	706	713
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	22	22	36	0.04%	18.8%	QLDECASAITK	99.7%	44.5	25	43.3	2	0	0	1235.59	912	922
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	22	22	36	0.04%	18.8%	QNIGVATFIGLDK	99.7%	66.7	25	59.7	2	0	0	1375.76	661	673
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	22	22	36	0.04%	18.8%	SLVHDLFQK	98.9%	33.7	25	32.5	1	0	0	1086.59	574	582
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	22	22	36	0.04%	18.8%	SNNIINETTTR	99.7%	65.4	25	59.2	2	0	0	1262.63	435	445
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	22	22	36	0.04%	18.8%	VAELDKITYER	99.7%	54.5	25	48.3	1	0	0	1336.71	1107	1117
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	22	22	36	0.04%	18.8%	VIQENEHALQK	99.7%	67	25	64.3	2	0	0	1308.69	999	1009
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	22	22	36	0.04%	18.8%	VLDAIIQEK	99.7%	46.8	25	30.2	2	0	0	1028.60	599	607
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	22	22	36	0.04%	18.8%	VVTLQGQIIEQSGTMTGGGSK	99.7%	61.4	25	61.4	1	0	0	2107.07	737	757
Structural maintenance of chromosomes protein 6	SMC6	SMC6_HUMAN	126.3	100.0%	4	4	6	0.01%	4.0%	LYFDNLLSQR	99.7%	51.4	25	45.5	2	0	0	1268.66	943	952
Structural maintenance of chromosomes protein 6	SMC6	SMC6_HUMAN	126.3	100.0%	4	4	6	0.01%	4.0%	SATGSVVSTR	99.4%	36.8	25	23.9	1	0	0	964.51	158	167
Structural maintenance of chromosomes protein 6	SMC6	SMC6_HUMAN	126.3	100.0%	4	4	6	0.01%	4.0%	SAVLTALIVGLGGR	99.7%	45.2	25	42.8	2	0	0	1326.81	83	96
Structural maintenance of chromosomes protein 6	SMC6	SMC6_HUMAN	126.3	100.0%	4	4	6	0.01%	4.0%	YYSSENTRPK	96.5%	29.1	25	21.8	1	0	0	1244.59	649	658
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	SDHB	SDHB_HUMAN	31.6	100.0%	3	3	6	0.01%	11.8%	IKNEVDSTLTFR	99.7%	53.2	25	53.2	2	0	0	1422.76	79	90
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	SDHB	SDHB_HUMAN	31.6	100.0%	3	3	6	0.01%	11.8%	LQDPFSLYR	99.2%	35.4	25	27	2	0	0	1138.59	234	242
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	SDHB	SDHB_HUMAN	31.6	100.0%	3	3	6	0.01%	11.8%	YLGPAVLMQAYR	99.7%	54.1	25	40.7	2	0	0	1381.73	206	217
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	5	7	19	0.02%	19.4%	GGQTHLGLPVFNTVK	99.7%	48.7	25	48.7	3	0	0	1567.86	91	105
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	5	7	19	0.02%	19.4%	IICQGFTGK	99.7%	46.6	25	39.9	2	0	0	1023.53	58	66

Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	5	7	19	0.02%	19.4%	LIGPNCPGVINPGECK	99.7%	71	25	62.5	4	0	0	1724.85	167	182
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	5	7	19	0.02%	19.4%	MGHAGAIIAGGK	99.7%	50.4	25	49.1	4	0	0	1098.57	297	308
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	5	7	19	0.02%	19.4%	QGTFHSQQALEYGTK	99.7%	52	25	48.1	2	4	0	1694.81	67	81
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	10	11	20	0.02%	23.3%	CDVIAQGIVMAVK	99.7%	96.8	25	83.9	2	0	0	1403.74	384	396
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	10	11	20	0.02%	23.3%	DLEIKIPVVVR	99.7%	50	25	50	2	1	0	1280.79	397	407
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	10	11	20	0.02%	23.3%	EQALQLAQK	97.2%	29.9	25	27.5	1	0	0	1028.57	217	225
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	10	11	20	0.02%	23.3%	ICNQVLVCER	99.7%	50.9	25	48.5	2	0	0	1290.63	151	160
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	10	11	20	0.02%	23.3%	ILACDDLDEAAR	99.7%	83.4	25	72	2	0	0	1361.64	427	438
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	10	11	20	0.02%	23.3%	INFDSNSAYR	99.7%	61.9	25	57.1	2	0	0	1186.55	275	284
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	10	11	20	0.02%	23.3%	LSEIVTLAK	99.7%	57.2	25	39.8	2	0	0	973.59	443	451
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	10	11	20	0.02%	23.3%	LYSLFLK	99.4%	36.8	25	25.9	2	0	0	883.53	243	249
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	10	11	20	0.02%	23.3%	MGFPPNIVESAAENMVK	99.7%	72.5	25	69	2	0	0	1833.89	226	242
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	10	11	20	0.02%	23.3%	SPDEAYAIAK	99.7%	77.1	25	73.2	2	0	0	1064.53	79	88
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	10	11	31	0.03%	26.4%	DPNVVGQLAK	99.3%	35.6	25	23.3	1	0	0	1040.57	109	118
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	10	11	31	0.03%	26.4%	EAQVYQAFK	98.4%	32.3	25	24.1	2	0	0	1083.55	339	347
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	10	11	31	0.03%	26.4%	ETYLAILMDR	99.4%	36.7	25	36.5	2	0	0	1224.63	151	160
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	10	11	31	0.03%	26.4%	FFVADTANEALEAAK	99.7%	116	25	104	4	0	0	1596.79	59	73
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	10	11	31	0.03%	26.4%	ILNNSGLPITSAIDLEDAAK	99.7%	84.3	25	84.3	4	0	0	2055.10	404	423
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	10	11	31	0.03%	26.4%	INFDDNAEFR	99.7%	79.2	25	70.8	4	0	0	1240.56	260	269
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	10	11	31	0.03%	26.4%	LYNLFLK	99.3%	36.1	25	26.2	3	0	0	910.54	228	234
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	10	11	31	0.03%	26.4%	MAENLGFVGPLK	99.7%	76.9	25	67.1	5	0	0	1275.68	207	218
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	10	11	31	0.03%	26.4%	QMIGYNLATK	99.7%	51.8	25	34.6	2	0	0	1138.59	119	128
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	10	11	31	0.03%	26.4%	VMVAEALDISR	99.7%	93.8	25	82	4	0	0	1203.64	140	150
SUMO-activating enzyme subunit 2	UBA2	SAE2_HUMAN	71.2	100.0%	3	3	6	0.01%	5.8%	ELAEAVAGGR	99.1%	34.7	25	18.9	2	0	0	972.51	10	19
SUMO-activating enzyme subunit 2	UBA2	SAE2_HUMAN	71.2	100.0%	3	3	6	0.01%	5.8%	QFILVMNALDNR	99.7%	73.3	25	64.6	2	0	0	1433.76	108	119
SUMO-activating enzyme subunit 2	UBA2	SAE2_HUMAN	71.2	100.0%	3	3	6	0.01%	5.8%	VLVVGAGGIGCELLK	99.7%	111	25	102	2	0	0	1484.85	20	34
SUMO-conjugating enzyme UBC9	UBE2I	UBC9_HUMAN	18.0	99.9%	2	2	2	0.00%	8.2%	DHPFGFVAVPTK	97.5%	30.5	25	30.5	1	0	0	1314.68	19	30
SUMO-conjugating enzyme UBC9	UBE2I	UBC9_HUMAN	18.0	99.9%	2	2	2	0.00%	8.2%	KDHPFGFVAVPTK	99.5%	31	25	22.8	0	1	0	1442.78	18	30
SUN domain-containing protein 2	SUN2	SUN2_HUMAN	80.3	100.0%	7	7	11	0.01%	12.6%	AEHQQDSEDLFKK	99.5%	31.5	25	30.6	0	2	0	1574.74	364	376
SUN domain-containing protein 2	SUN2	SUN2_HUMAN	80.3	100.0%	7	7	11	0.01%	12.6%	DSSPHFQAEQR	99.7%	48.4	25	44.3	2	0	0	1301.59	265	275
SUN domain-containing protein 2	SUN2	SUN2_HUMAN	80.3	100.0%	7	7	11	0.01%	12.6%	IGLADYALESGGASVISTR	99.7%	122	25	122	2	0	0	1879.98	544	562
SUN domain-containing protein 2	SUN2	SUN2_HUMAN	80.3	100.0%	7	7	11	0.01%	12.6%	ILTHVAEMQGK	99.7%	43	25	43	1	0	0	1242.65	492	502
SUN domain-containing protein 2	SUN2	SUN2_HUMAN	80.3	100.0%	7	7	11	0.01%	12.6%	LLYWWAGTTWYR	99.7%	65.2	25	65.2	1	0	0	1615.81	179	190
SUN domain-containing protein 2	SUN2	SUN2_HUMAN	80.3	100.0%	7	7	11	0.01%	12.6%	LTTAASLLDVFVLTR	99.7%	94.2	25	94.2	1	0	0	1619.94	191	205
SUN domain-containing protein 2	SUN2	SUN2_HUMAN	80.3	100.0%	7	7	11	0.01%	12.6%	RPDEGWEAR	99.3%	36	25	32.4	2	0	0	1115.52	256	264
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	37	0.04%	18.9%	AIGNTELENK	99.7%	46.4	25	36.7	2	0	0	1088.56	1013	1022
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	37	0.04%	18.9%	DVDFEGTDEPIFGK	99.7%	83.2	25	83.2	2	0	0	1568.71	65	78
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	37	0.04%	18.9%	EAIQCVDNNQSVLVSAHTSAGK	96.4%	23.6	25	23.6	0	1	0	2328.12	146	167
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	37	0.04%	18.9%	EIEEYIHKPK	99.7%	40.4	25	25.2	1	0	0	1285.68	639	648
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	37	0.04%	18.9%	EYPFILDAFQR	99.7%	57.4	25	48.4	4	0	0	1398.71	135	145
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	37	0.04%	18.9%	GIVILMVDEK	99.7%	56.7	25	56.7	4	0	0	1132.63	533	542
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	37	0.04%	18.9%	IVIPNEESVVIYYK	99.7%	48.1	25	47.2	2	0	0	1665.91	615	628
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	37	0.04%	18.9%	KAQIAIDIK	99.7%	43.1	25	25	1	0	0	999.62	825	833
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	37	0.04%	18.9%	LDFNTDEEKK	99.0%	34.2	25	26.4	1	0	0	1238.59	409	418
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	37	0.04%	18.9%	LGFATSSDVIEMK	99.7%	83.5	25	59.6	4	0	0	1413.69	861	873
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	37	0.04%	18.9%	LTEQLAGPLR	99.7%	71.5	25	62.1	2	0	0	1097.63	924	933
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	37	0.04%	18.9%	MTDVFEGSIIR	99.7%	77.1	25	68.1	3	0	0	1267.64	985	995
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	37	0.04%	18.9%	NFQPVIIFSFSK	99.7%	55.9	25	50.8	4	0	0	1426.77	385	396
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	37	0.04%	18.9%	SFYQFQHYR	99.7%	39.2	25	29.7	2	0	0	1275.59	588	596
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	37	0.04%	18.9%	TVLQMDELK	98.8%	33.5	25	24.3	1	0	0	1076.57	844	852
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	37	0.04%	18.9%	WISSGEYIQMSGR	99.7%	39.5	25	39.3	1	0	0	1513.71	511	523

Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	37	0.04%	18.9%	YCLPFLQPGR	99.7%	48.8	25	48.5	2	0	0	1250.64	649	658
Suppressor of SWI4 1 homolog	PPAN	SSF1_HUMAN	53.2	100.0%	4	4	7	0.01%	9.9%	LPGGPTLTFQVK	99.7%	50.3	25	48.6	2	0	0	1257.72	102	113
Suppressor of SWI4 1 homolog	PPAN	SSF1_HUMAN	53.2	100.0%	4	4	7	0.01%	9.9%	TEEELQAILEAK	99.7%	78.1	25	67	2	0	0	1373.72	304	315
Suppressor of SWI4 1 homolog	PPAN	SSF1_HUMAN	53.2	100.0%	4	4	7	0.01%	9.9%	VGGSDEEASGIPSR	99.7%	87.9	25	79.5	2	0	0	1360.63	356	369
Suppressor of SWI4 1 homolog	PPAN	SSF1_HUMAN	53.2	100.0%	4	4	7	0.01%	9.9%	VMEPLTASR	95.6%	28.2	25	23.7	1	0	0	1003.52	53	61
Surfeit locus protein 4	SURF4	SURF4_HUMAN	30.4	100.0%	3	3	8	0.01%	15.2%	GQNDLMGTAEDFADQFLR	99.7%	73.6	25	73.6	2	0	0	2043.91	2	19
Surfeit locus protein 4	SURF4	SURF4_HUMAN	30.4	100.0%	3	3	8	0.01%	15.2%	LCLISTFLEDGIR	99.7%	90	25	83.8	3	0	0	1536.81	31	43
Surfeit locus protein 4	SURF4	SURF4_HUMAN	30.4	100.0%	3	3	8	0.01%	15.2%	SMFAGVPTMR	99.1%	34.9	25	30.8	3	0	0	1112.52	140	149
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	9	10	14	0.01%	10.0%	ALNIVDQEGSLLGK	99.7%	88.6	25	87.5	1	0	0	1456.80	215	228
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	9	10	14	0.01%	10.0%	APSSLSDAVPQR	99.7%	47.7	25	47.3	2	0	0	1227.63	570	581
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	9	10	14	0.01%	10.0%	ATTGTQTLLSSGTR	99.7%	41.8	25	7.87	1	0	0	1393.73	696	709
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	9	10	14	0.01%	10.0%	FGIEIIK	98.7%	33	25	15.6	2	0	0	819.50	328	334
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	9	10	14	0.01%	10.0%	GADQKPTSADCAVR	98.8%	33.4	25	26.7	1	0	0	1475.69	646	659
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	9	10	14	0.01%	10.0%	IPLGLDLK	97.4%	30.2	25	16.1	1	0	0	868.55	298	305
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	9	10	14	0.01%	10.0%	SLALLGQTFSLASSFR	99.7%	82.5	25	82.5	1	0	0	1697.92	479	494
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	9	10	14	0.01%	10.0%	VDNEFLNMLLDK	99.7%	65	25	58.8	3	0	0	1450.72	398	409
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	9	10	14	0.01%	10.0%	YSLSGSVAHSR	99.7%	67.9	25	67.3	2	0	0	1163.58	63	73
Survival motor neuron protein	SMN1	SMN_HUMAN	31.8	100.0%	2	2	3	0.00%	9.5%	GTGQSDDSDIWDDTALIK	99.7%	69.5	25	66.8	1	0	0	1936.88	24	41
Survival motor neuron protein	SMN1	SMN_HUMAN	31.8	100.0%	2	2	3	0.00%	9.5%	NTAASLQQWK	99.7%	47.8	25	42.2	2	0	0	1146.59	84	93
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	ANYAVDAYFR	99.7%	48.8	25	40.2	1	0	0	1189.56	740	749
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	APFHQLR	97.5%	30.4	25	26.5	1	0	0	868.48	930	936
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	CNELQDIEK	99.7%	49	25	27	1	0	0	1148.53	891	899
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	CNTLITLIER	99.7%	68	25	53.4	2	0	0	1232.67	1001	1010
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	DFNQFIK	96.8%	29.4	25	10.1	2	0	0	911.46	849	855
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	DIDILNSAGK	99.7%	68.8	25	38.8	2	0	0	1045.55	431	440
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	EIQEPDPTYEEK	99.7%	58.7	25	50.3	1	0	0	1477.67	72	83
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	ESEITDEDIDGILER	99.7%	87	25	87	2	0	0	1733.81	666	680
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	FITDNTVEER	99.7%	54.2	25	46	2	0	0	1223.59	607	616
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	FVFMLSTR	99.5%	37	25	28.4	1	0	0	1016.52	553	560
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	IMAQIER	98.8%	33.5	25	13.3	2	0	0	876.46	900	906
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	KANYAVDAYFR	99.7%	41.7	25	41.7	2	0	0	1317.66	739	749
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	LDGQTPHDER	99.7%	40.5	25	36.2	2	0	0	1167.54	529	538
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	LDSIVIQQGR	99.7%	87.3	25	74.5	2	0	0	1128.64	627	636
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	LLNILMQLR	99.7%	76.4	25	61.2	6	0	0	1113.68	446	454
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	LLTQGFTNWNK	99.7%	45.9	25	45	1	0	0	1321.69	837	847
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	LRLDSIVIQQGR	99.2%	29	25	29	0	2	0	1397.82	625	636
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	LVDQNLNK	95.7%	28.3	25	23.4	1	0	0	943.52	637	644
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	NPELPNAAQAQK	99.7%	60.5	25	55.2	2	0	0	1280.66	803	814
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	QNLLSVGDYR	99.7%	57.9	25	37.7	2	0	0	1164.60	133	142
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	QTELFAHFIQPAAQK	97.5%	30.5	25	27.9	1	0	0	1728.91	98	112
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	SVCLIGDKEQR	99.7%	51.4	25	28	2	0	0	1304.66	257	267
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	TLQTISLLGYMK	99.7%	49.7	25	49	1	0	0	1383.76	212	223
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	TPEEVIEYSAVFWER	99.7%	59.2	25	59.2	1	0	0	1854.89	876	890
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	VLDILEDYCMWR	99.7%	59	25	58.3	2	0	0	1612.75	511	522
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	VLIFSQMTR	99.7%	66.6	25	62	4	0	0	1094.60	502	510
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	27	29	50	0.05%	24.8%	YLVIDEAHR	99.7%	46.7	25	43.4	2	0	0	1115.58	304	312
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	SMARCD2	SMRD2_HUMAN	58.9	100.0%	4	4	7	0.01%	10.2%	AEGDSAGTAGTPGGTPAGDK	99.7%	68.2	25	67.7	1	0	0	1716.77	207	226
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	SMARCD2	SMRD2_HUMAN	58.9	100.0%	4	4	7	0.01%	10.2%	IITDVIGNPEEERR	99.4%	30.5	25	27.8	0	2	0	1640.86	481	494
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	SMARCD2	SMRD2_HUMAN	58.9	100.0%	4	4	7	0.01%	10.2%	IYISNTFSPSK	98.7%	33.2	25	24.7	2	0	0	1256.65	196	206
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	SMARCD2	SMRD2_HUMAN	58.9	100.0%	4	4	7	0.01%	10.2%	LLGVHTQTR	99.4%	36.8	25	25.2	2	0	0	1024.59	320	328
Symplekin	SYMPK	SYMPK_HUMAN	141.2	100.0%	7	7	13	0.01%	7.0%	ATNLCFAER	99.7%	42.4	25	24.1	2	0	0	1081.51	965	973

Symplekin	SYMPK	SYMPK_HUMAN	141.2	100.0%	7	7	13	0.01%	7.0%	ETAAGGLTLKEER	99.7%	51.5	25	51	1	0	0	1374.72	1230	1242
Symplekin	SYMPK	SYMPK_HUMAN	141.2	100.0%	7	7	13	0.01%	7.0%	LGGFVMNILSR	99.7%	40.9	25	31.5	2	0	0	1206.67	1012	1022
Symplekin	SYMPK	SYMPK_HUMAN	141.2	100.0%	7	7	13	0.01%	7.0%	LLSGLQEKPDQK	99.3%	35.7	25	25.6	1	0	0	1355.75	649	660
Symplekin	SYMPK	SYMPK_HUMAN	141.2	100.0%	7	7	13	0.01%	7.0%	TVIQSLTMYPR	99.7%	41.6	25	41.6	1	0	0	1324.69	1001	1011
Symplekin	SYMPK	SYMPK_HUMAN	141.2	100.0%	7	7	13	0.01%	7.0%	VVDLLNQAALITNDSK	99.7%	77.8	25	77.8	2	0	0	1713.94	36	51
Symplekin	SYMPK	SYMPK_HUMAN	141.2	100.0%	7	7	13	0.01%	7.0%	VVLEAPLITESALEVVR	99.7%	82.1	25	82.1	4	0	0	1838.06	667	683
Syntaxin-binding protein 2	STXBP2	STXB2_HUMAN	66.5	100.0%	3	3	4	0.00%	6.4%	ADTPSLGEGPEK	99.7%	43	25	36.7	1	0	0	1200.57	214	225
Syntaxin-binding protein 2	STXBP2	STXB2_HUMAN	66.5	100.0%	3	3	4	0.00%	6.4%	LIVPVLLDAAVPAYDK	99.7%	45.5	25	45.5	1	0	0	1696.99	388	403
Syntaxin-binding protein 2	STXBP2	STXB2_HUMAN	66.5	100.0%	3	3	4	0.00%	6.4%	YETTGLSEAR	99.7%	72.6	25	62.2	2	0	0	1126.54	266	275
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	5	5	12	0.01%	15.2%	FGGNPGGFGNQGGFGNSR	99.7%	102	25	98.5	2	0	0	1726.77	276	293
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	5	5	12	0.01%	15.2%	FTEYETQVK	99.7%	47.5	25	30.5	2	0	0	1144.55	152	160
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	5	5	12	0.01%	15.2%	GISVHISNAEPK	99.7%	52.2	25	43.4	2	0	0	1251.67	252	263
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	5	5	12	0.01%	15.2%	KMDETDASSAVK	99.1%	34.9	25	28.9	2	0	0	1281.60	84	95
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	5	5	12	0.01%	15.2%	TSDLIVLGLPWK	99.7%	79.1	25	70.5	4	0	0	1341.78	103	114
Target of EGR1 protein 1	TOE1	TOE1_HUMAN	56.5	100.0%	4	4	6	0.01%	8.4%	AARPEIADR	95.1%	27.8	25	9.03	1	0	0	998.54	409	417
Target of EGR1 protein 1	TOE1	TOE1_HUMAN	56.5	100.0%	4	4	6	0.01%	8.4%	ALLNLPGTQTSGEAK	99.7%	53.1	25	47.9	1	0	0	1499.81	348	362
Target of EGR1 protein 1	TOE1	TOE1_HUMAN	56.5	100.0%	4	4	6	0.01%	8.4%	SILSLGLACFK	99.7%	46.7	25	33	2	0	0	1208.67	96	106
Target of EGR1 protein 1	TOE1	TOE1_HUMAN	56.5	100.0%	4	4	6	0.01%	8.4%	YAAEFHAR	99.7%	43.2	25	37.1	2	0	0	964.46	231	238
TATA-binding protein-associated factor 172	BTAF1	BTAF1_HUMAN	206.9	100.0%	4	4	5	0.01%	2.7%	FGDFVSDEVVAPVR	96.6%	29.1	25	25.3	1	0	0	1536.77	355	368
TATA-binding protein-associated factor 172	BTAF1	BTAF1_HUMAN	206.9	100.0%	4	4	5	0.01%	2.7%	IAAGQAVEAIVK	99.7%	84.2	25	72.3	2	0	0	1169.69	60	71
TATA-binding protein-associated factor 172	BTAF1	BTAF1_HUMAN	206.9	100.0%	4	4	5	0.01%	2.7%	LFILLDTGTTPVTR	99.7%	72.5	25	65.5	1	0	0	1546.88	9	22
TATA-binding protein-associated factor 172	BTAF1	BTAF1_HUMAN	206.9	100.0%	4	4	5	0.01%	2.7%	LLCVFALDR	98.3%	31.9	25	27.8	1	0	0	1106.60	346	354
TBC1 domain family member 15	TBC1D15	TBC15_HUMAN	79.5	99.8%	2	2	3	0.00%	2.8%	EFSFLDILR	99.7%	51.7	25	35.6	2	0	0	1139.61	539	547
TBC1 domain family member 15	TBC1D15	TBC15_HUMAN	79.5	99.8%	2	2	3	0.00%	2.8%	VTNYIFDSLR	99.7%	49.6	25	32.2	1	0	0	1227.64	253	262
TBC1 domain family member 4	TBC1D4	TBCD4_HUMAN	146.6	100.0%	3	3	7	0.01%	3.1%	FEINLISPDTK	99.7%	51.6	25	50.4	1	0	0	1276.68	364	374
TBC1 domain family member 4	TBC1D4	TBCD4_HUMAN	146.6	100.0%	3	3	7	0.01%	3.1%	IQALESNLENLLTR	99.7%	91.5	25	79.4	3	0	0	1613.89	1227	1240
TBC1 domain family member 4	TBC1D4	TBCD4_HUMAN	146.6	100.0%	3	3	7	0.01%	3.1%	LLPADALVNCDLLLR	99.7%	58.2	25	53.9	3	0	0	1695.95	1268	1282
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	AFHNEAQVNPER	99.7%	67.6	25	67.6	4	4	0	1411.67	469	480
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	AFHNEAQVNPERK	99.7%	50.5	25	43.7	3	4	0	1539.77	469	481
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	DCLINAAK	99.7%	53.4	25	35.8	2	0	0	904.46	146	153
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	DDKHGSYEDAVHSGALND	99.7%	59.7	25	59.7	2	3	0	1929.82	539	556
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	EQLAIAEFAR	99.7%	68.4	25	51.5	11	0	0	1147.61	434	443
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	EVGDGTTSVVIIAAELLK	99.7%	51.3	25	51.3	2	0	0	1815.01	85	102
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	FATEAAITILR	99.7%	92	25	62.2	13	0	0	1205.69	516	526
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	GANDFMCDEMER	99.7%	78.1	25	78.1	9	0	0	1474.54	379	390
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	HGSYEDAVHSGALND	99.7%	86.6	25	77	2	0	0	1571.67	542	556
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	IACLDFSLQK	99.7%	69.2	25	66.2	5	0	0	1194.62	234	243
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	ICDDELILIK	99.7%	60.2	25	48.8	4	0	0	1231.66	356	365
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	IHPTSVISGYR	99.7%	51.4	25	48	2	0	0	1229.66	112	122
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	ILATGANVILTTGGIDDMCLK	99.7%	63.1	25	63.1	1	0	0	2192.13	278	298
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	LGVQVVITDPEK	99.7%	72.4	25	67.9	2	0	0	1297.74	248	259
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	LGVQVVITDPEKLDQIR	99.7%	78.2	25	77.7	2	3	0	1923.09	248	264
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	LLEVEHPAAK	99.7%	70.8	25	61.1	7	0	0	1106.62	64	73
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	MLVDDIGDVTITNDGATILK	99.7%	127	25	124	5	0	0	2120.08	44	63
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	QAGVFEPTIVK	99.7%	65	25	49.8	3	0	0	1188.66	500	510
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	SLHDALCVVK	99.7%	45.4	25	41.8	3	0	0	1141.60	391	400
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	SLHDALCVVKR	99.7%	48.5	25	47.1	1	0	0	1297.70	391	401
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	SLLVIPNTLAVNAAQDSTDLVAK	99.7%	102	25	102	9	1	0	2353.30	444	466
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	SQNVMAAASIANIVK	99.7%	137	25	131	4	1	0	1532.81	19	33
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	SSLGPVGLDK	99.7%	68.4	25	44.8	3	0	0	972.54	34	43
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	TSASIILR	99.7%	66.9	25	52.2	2	0	0	860.52	371	378

T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	VLCELADLQDK	99.7%	80.1	25	71.7	2	0	0	1303.66	74	84
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	VLCELADLQDKEVGDGTTSVVIIAAELLK	99.7%	73.5	25	73.5	0	2	0	3099.65	74	102
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	WIGLDLSNGKPR	99.7%	36.8	25	16.9	2	2	0	1355.74	485	496
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	YFVEAGAMAVR	99.7%	79.1	25	69.4	7	0	0	1213.60	299	309
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	29	40	134	0.14%	55.9%	YPVNSVNILK	99.7%	60.5	25	42.5	2	0	0	1146.65	190	199
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	24	37	0.04%	50.5%	AAHSEGNTTAGLDMR	99.7%	56.8	25	52	3	1	0	1530.70	467	481
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	24	37	0.04%	50.5%	DASLMVTNDGATILK	99.7%	63.8	25	55.5	1	0	0	1548.79	58	72
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	24	37	0.04%	50.5%	EALLSSAVDHGSDEVK	99.7%	95.4	25	94.3	2	1	0	1656.81	139	154
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	24	37	0.04%	50.5%	EAVAMESYAK	99.7%	40.8	25	40.8	1	0	0	1098.51	432	441
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	24	37	0.04%	50.5%	EGTIGDMAILGITESFQVK	99.7%	84.5	25	84.5	1	0	0	2009.03	482	500
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	24	37	0.04%	50.5%	GATQQILDEAER	99.7%	88.1	25	81.5	2	0	0	1330.66	377	388
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	24	37	0.04%	50.5%	HGINCFINR	99.7%	49.5	25	43.4	2	0	0	1130.55	285	293
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	24	37	0.04%	50.5%	ILIANTGMDTDKIK	99.7%	90.6	25	77.3	2	1	0	1532.84	237	250
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	24	37	0.04%	50.5%	KIHPQTIIAGWR	99.7%	43.1	25	43.1	0	2	0	1419.82	120	131
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	24	37	0.04%	50.5%	LALVTGGEIASTFDHPELVK	97.3%	24.5	25	24.5	0	1	0	2097.12	323	342
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	24	37	0.04%	50.5%	LAVEAVLR	96.4%	28.9	25	0.69	1	0	0	870.54	182	189
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	24	37	0.04%	50.5%	LKGSGNLEAIHIIK	99.7%	48.9	25	37.7	0	2	0	1492.88	190	203
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	24	37	0.04%	50.5%	LTSFIGAIAIGDLVK	99.7%	110	25	101	2	0	0	1517.89	26	40
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	24	37	0.04%	50.5%	MLPTIIADNAGYDSADLVAQLR	99.7%	133	25	133	3	2	0	2347.20	445	466
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	24	37	0.04%	50.5%	QLIYNYPEQLFGAAGVMAIEHADFAGVER	99.2%	29.5	25	29.5	0	1	0	3225.57	294	322
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	24	37	0.04%	50.5%	VAEIEHAEKEK	99.7%	47.5	25	37.6	2	0	0	1282.66	264	274
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	24	37	0.04%	50.5%	VLVDMSR	99.7%	40.3	25	26.4	2	0	0	819.44	83	89
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	24	37	0.04%	50.5%	VQDDEVGDGTTSVTVLAAELLR	99.7%	135	25	135	2	0	0	2288.16	90	111
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	21	27	92	0.10%	59.2%	AFADAMEVIPSTLAENAGLNPISTVTELR	99.7%	39.2	25	37.4	0	1	0	3030.55	453	481
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	21	27	92	0.10%	59.2%	ALIAGGGAPEIELALR	99.7%	92.2	25	92.2	10	0	0	1550.89	420	435
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	21	27	92	0.10%	59.2%	AQDIEAGDGTTSVVIIAGSLLDSCTK	99.7%	98.8	25	98.8	1	1	0	2621.30	97	122
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	21	27	92	0.10%	59.2%	AYILNLVK	99.7%	44.2	25	36.4	4	0	0	933.58	281	288
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	21	27	92	0.10%	59.2%	DALSDLALHFLNK	99.7%	102	25	89.9	10	2	0	1456.78	307	319
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	21	27	92	0.10%	59.2%	DIEREDIEFICK	99.7%	48.6	25	48.6	2	0	0	1566.75	327	338
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	21	27	92	0.10%	59.2%	GAYQDRDKPAQIR	99.7%	37.8	25	35.4	0	2	0	1517.78	22	34
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	21	27	92	0.10%	59.2%	GIEILTDMSRPVELSDRETLLNSATTSLNSK	99.7%	45.7	25	45.7	0	2	0	3406.74	144	174
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	21	27	92	0.10%	59.2%	GIHPTIISESFQK	99.7%	40.1	25	38.3	1	2	0	1456.78	127	139
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	21	27	92	0.10%	59.2%	IDDVVNTR	99.7%	54.6	25	48.7	2	0	0	931.48	532	539
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	21	27	92	0.10%	59.2%	IGLIQFCLSAPK	99.7%	73.3	25	68.5	10	0	0	1346.75	246	257
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	21	27	92	0.10%	59.2%	KTGCNVLLIQK	99.7%	41.9	25	34	2	0	0	1273.73	292	302
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	21	27	92	0.10%	59.2%	LGGTIDDCELVEGLVLTQK	99.7%	108	25	108	2	0	0	2060.06	214	232
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	21	27	92	0.10%	59.2%	LVIEEAER	99.7%	55.6	25	48.2	5	0	0	958.52	396	403
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	21	27	92	0.10%	59.2%	MIQDGKGDVTITNDGATILK	99.7%	62.6	25	55.7	1	4	0	2106.08	60	79
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	21	27	92	0.10%	59.2%	QMQVLHPAAR	99.6%	38.7	25	31.9	2	0	0	1150.62	80	89
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	21	27	92	0.10%	59.2%	SIHDALCVIR	99.7%	59.5	25	0	4	0	0	1183.63	404	413
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	21	27	92	0.10%	59.2%	TDMDNQIVVSDYAQMDR	99.7%	74.9	25	74.9	3	0	0	2032.86	258	274
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	21	27	92	0.10%	59.2%	TGCNVLLIQK	99.7%	52.4	25	39.9	5	0	0	1145.63	293	302
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	21	27	92	0.10%	59.2%	TLSGMESYCVR	99.7%	65.4	25	57.9	8	0	0	1302.58	442	452
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	21	27	92	0.10%	59.2%	VIDPATATSVDLR	99.7%	89.3	25	79.6	8	0	0	1357.73	194	206
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	21	27	92	0.10%	59.2%	VVSQYSSLLSPMSVNAVMK	99.7%	86.6	25	86.6	2	0	0	2072.04	175	193
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	AVTIFIR	99.7%	54	25	24.8	4	0	0	819.51	382	388
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	CPTLEQYAMR	99.7%	45.4	25	44.1	3	0	0	1268.58	440	449
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	DKMLVIEQCK	99.7%	42.8	25	33.3	2	0	0	1279.64	369	378
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	DTEPLIQTAK	99.7%	42.8	25	41.4	2	0	0	1115.59	161	170
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	DVDFELIK	99.6%	38.1	25	18.3	2	0	0	978.51	203	210
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	DVDFELIKVEGK	99.7%	68.2	25	60.3	2	0	0	1391.74	203	214

T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	EKFEEMIQQIK	99.7%	47.4	25	41.2	2	2	0	1438.72	283	293
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	EMNPALGIDCLHK	99.7%	85.1	25	78.8	4	3	0	1513.71	484	496
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	FEEMIQQIK	99.7%	51.9	25	36.8	4	0	0	1165.59	285	293
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	FSELTAEK	99.7%	61.1	25	50.1	2	0	0	924.47	345	352
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	GVIVDKDFSHPQMPK	99.7%	63	25	59.7	4	4	0	1697.87	227	241
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	HKLDVTSVEDYK	95.9%	23	25	23	0	1	0	1433.73	264	275
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	IADGYEQAAR	99.7%	87.8	25	81.1	6	0	0	1093.53	133	142
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	IAILTCPFEPPKPK	99.7%	67.4	25	67.4	2	0	0	1610.90	248	261
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	IDDIRKPGESEE	99.7%	50	25	41.6	2	0	0	1387.67	530	541
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	ISDSVLVDIK	99.7%	54.7	25	44.2	1	0	0	1088.62	151	160
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	ISDSVLVDIKDTEPLIQTAK	99.7%	34.8	25	30.6	0	2	0	2185.20	151	170
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	KQQISLATQMVR	99.7%	67.1	25	59.9	4	4	0	1402.78	514	525
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	LDVTSVEDYK	99.7%	69.5	25	63.2	2	0	0	1168.57	266	275
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	LGFAGLVQEISFGTTK	99.7%	124	25	124	10	0	0	1667.90	353	368
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	LMGLEALK	99.4%	36.8	25	17.9	3	0	0	874.51	28	35
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	LMVELSK	99.7%	41.8	25	12.1	4	0	0	835.46	90	96
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	MIIEEAKR	99.7%	59.3	25	41.2	3	0	0	989.54	393	400
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	MLVIEQCK	99.7%	43	25	27.1	2	0	0	1036.52	371	378
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	QQHVIETLIGK	99.7%	43.6	25	40.7	2	1	0	1265.72	503	513
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	QQISLATQMVR	99.7%	66.2	25	54.6	4	0	0	1274.69	515	525
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	RDVDFELIK	99.7%	44.6	25	7.97	2	0	0	1134.62	202	210
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	SLHDALCVIR	99.7%	59.5	25	0	4	0	0	1183.63	401	410
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	TSLGPNGLDK	99.7%	59.3	25	49.5	2	0	0	1001.53	50	59
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	VAIEHLDK	99.7%	55.5	25	36.3	2	0	0	924.52	143	150
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	31	48	109	0.11%	48.4%	WVGGPEIELIAIATGGR	99.7%	91.6	25	84.5	6	0	0	1738.95	324	340
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	20	24	63	0.07%	44.4%	ALEIIPR	99.7%	41.1	25	35.2	4	0	0	811.50	441	447
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	20	24	63	0.07%	44.4%	ATISNDGATILK	99.7%	49.6	25	36.8	2	0	0	1203.66	56	67
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	20	24	63	0.07%	44.4%	CQVFEETQIGGER	99.7%	75.9	25	69.7	3	0	0	1552.71	345	357
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	20	24	63	0.07%	44.4%	GGAEQFMEETER	99.7%	72.9	25	72.9	5	0	0	1383.58	376	387
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	20	24	63	0.07%	44.4%	IALLNVELELK	99.7%	68.7	25	52.5	2	0	0	1254.77	237	247
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	20	24	63	0.07%	44.4%	INALTAASEAACLIVSVDETIK	99.7%	117	25	117	2	3	0	2289.20	500	521
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	20	24	63	0.07%	44.4%	INALTAASEAACLIVSVDETIKNPR	99.7%	77	25	77	0	2	0	2656.40	500	524
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	20	24	63	0.07%	44.4%	LLDVVHPAAK	99.7%	57.4	25	48.3	4	0	0	1062.63	68	77
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	20	24	63	0.07%	44.4%	LPIGDVATQYFADR	99.7%	90.9	25	89.4	4	0	0	1565.80	293	306
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	20	24	63	0.07%	44.4%	MVVDAVMMLDDLLQLK	99.7%	112	25	54.5	2	0	0	1849.95	178	193
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	20	24	63	0.07%	44.4%	QLCDNAGFDATNILNK	99.7%	63.7	25	57.7	1	0	0	1793.85	448	463
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	20	24	63	0.07%	44.4%	QQLLIGAYAK	99.7%	57.3	25	54.4	1	0	0	1104.64	431	440
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	20	24	63	0.07%	44.4%	SLHDAIMIVR	99.2%	35	25	32.9	2	0	0	1170.63	388	397
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	20	24	63	0.07%	44.4%	SQDAEVGDGTTSVTLLAAEFLK	99.7%	150	25	150	4	1	0	2252.13	85	106
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	20	24	63	0.07%	44.4%	TATQLAVNK	99.7%	54.1	25	44.5	2	0	0	945.54	127	135
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	20	24	63	0.07%	44.4%	TCTFILR	99.7%	39.6	25	21	3	0	0	910.48	369	375
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	20	24	63	0.07%	44.4%	TFSYAGFEMQPK	99.7%	79.7	25	79.7	6	0	0	1405.65	219	230
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	20	24	63	0.07%	44.4%	VPEEDLKR	99.7%	51.2	25	35.9	4	0	0	985.53	314	321
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	20	24	63	0.07%	44.4%	VQGGALEDSQLVAGVAFK	99.7%	96.2	25	96.2	2	0	0	1788.95	200	217
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	20	24	63	0.07%	44.4%	YNFFTGCPK	99.7%	55.8	25	37	4	0	0	1133.51	358	366
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	ACTILLR	99.7%	45.5	25	27.2	2	0	0	846.49	371	377
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	ALDDMISTLK	99.7%	69	25	62.5	5	0	0	1106.58	129	138
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	ALDDMISTLKK	99.7%	58.2	25	52.9	4	1	0	1234.67	129	139
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	AMTGVEQWPYR	99.7%	70.9	25	69.1	4	0	0	1337.63	428	438
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	AVAQALEVIPR	99.7%	88.3	25	74.6	15	0	0	1166.69	439	449
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	EILSEVER	99.7%	67.3	25	22.3	5	0	0	974.52	382	389

T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	EIQVQHPAAK	99.7%	52.1	25	38.9	11	0	0	1120.61	69	78
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	ELGIWEPLAVK	99.7%	58	25	52.6	3	0	0	1254.71	492	502
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	GISDLAQHYLMR	99.7%	76.7	25	73.7	12	3	0	1403.71	295	306
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	IDDIVSGHK	99.7%	55.2	25	41	5	0	0	983.52	519	527
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	IDDIVSGHKK	99.5%	37	25	29	2	0	0	1111.61	519	528
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	IGDEYFTFITDCK	99.7%	66.6	25	63.8	2	0	0	1608.73	355	367
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	IGDEYFTFITDCKDPK	99.7%	42.4	25	42.4	2	0	0	1948.90	355	370
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	IPGGIIEDSCVLR	99.7%	90.7	25	80.9	6	0	0	1428.75	204	216
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	IVLLDSSLEYK	99.7%	79.2	25	72.4	6	0	0	1279.71	238	248
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	IVLLDSSLEYKK	99.7%	54.3	25	50.1	2	1	0	1407.81	238	249
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	IVSRPEELR	98.8%	33.3	25	12.4	1	0	0	1098.63	331	339
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	KGESQTDIEITR	99.7%	87.1	25	55.2	2	2	0	1376.70	249	260
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	MLLDPMGGIVMTNDGNAILR	99.7%	108	25	108	12	6	0	2131.07	49	68
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	MVQFEENGR	99.7%	49.9	25	43.5	2	0	0	1109.50	182	190
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	MVQFEENGRK	99.7%	44.4	25	32.9	4	0	0	1237.60	182	191
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	NLQDAMQVCR	99.7%	78	25	65	8	0	0	1234.57	390	399
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	NVLLDPQLVPGGGASEMAVAHALTEK	99.7%	33	25	30.4	0	7	0	2617.37	400	425
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	SMIEISR	99.7%	43.2	25	23.2	2	0	0	835.43	79	85
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	TAVETAVLLLR	99.7%	107	25	92.6	6	0	0	1185.72	508	518
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	TLIQNCGASTIR	99.7%	70.3	25	57.4	5	0	0	1333.69	450	461
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	42	150	0.16%	48.1%	WSSLACNIALDAVK	99.7%	94.2	25	75.8	2	0	0	1547.79	168	181
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	10	10	16	0.02%	21.2%	AIADTGANVVVTGGK	99.7%	86.2	25	77.1	2	0	0	1372.74	282	296
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	10	10	16	0.02%	21.2%	APGFAQMLK	98.3%	32.1	25	25.8	1	0	0	962.51	8	16
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	10	10	16	0.02%	21.2%	AVDDGVNTFK	99.7%	65.7	25	58.1	2	0	0	1065.52	391	400
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	10	10	16	0.02%	21.2%	DIDEVSSLLR	99.7%	63.6	25	49.9	2	0	0	1146.60	156	165
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	10	10	16	0.02%	21.2%	ETEGDVTSVK	99.7%	41.6	25	38.8	2	0	0	1064.51	226	235
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	10	10	16	0.02%	21.2%	FAEAFEAIPR	99.7%	91.8	25	81.3	2	0	0	1150.59	441	450
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	10	10	16	0.02%	21.2%	IAVYSCPFDGMITETK	99.7%	53	25	53	1	0	0	1831.86	239	254
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	10	10	16	0.02%	21.2%	LFVTNDAATILR	99.7%	82.6	25	76.7	2	0	0	1333.75	63	74
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	10	10	16	0.02%	21.2%	LVPGGGATEIELAK	95.1%	27.7	25	17.7	1	0	0	1354.76	408	421
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	10	10	16	0.02%	21.2%	LYAVHQEGNK	99.3%	35.8	25	26.4	1	0	0	1158.59	467	476
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	31	91	0.09%	48.2%	ALQFLEEVK	99.7%	55.7	25	49	2	0	0	1076.60	130	138
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	31	91	0.09%	48.2%	AQAALAVNISAAR	99.7%	102	25	97.2	5	0	0	1255.71	16	28
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	31	91	0.09%	48.2%	AQLGVQAFADALLIIPK	99.7%	81.9	25	78.9	5	0	0	1768.04	433	449
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	31	91	0.09%	48.2%	DGNVLLHEMQIQHPTASLIAK	99.7%	36.9	25	36.7	0	2	0	2331.21	59	79
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	31	91	0.09%	48.2%	EGIVALRR	98.6%	32.9	25	18.1	3	0	0	913.56	308	315
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	31	91	0.09%	48.2%	EMDRETLIDVAR	99.7%	47.7	25	32.4	3	4	0	1447.72	142	153
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	31	91	0.09%	48.2%	ETLIDVAR	99.7%	45.5	25	37.3	2	0	0	916.51	146	153
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	31	91	0.09%	48.2%	GFVVINQK	99.7%	42	25	27.3	2	0	0	904.53	288	295
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	31	91	0.09%	48.2%	GIDPFSLDALSK	99.7%	86.8	25	37.8	9	0	0	1262.66	296	307
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	31	91	0.09%	48.2%	GLQDVLR	99.7%	43.7	25	17.1	2	0	0	800.46	29	35
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	31	91	0.09%	48.2%	GLVLDHGAR	99.7%	56.8	25	42.3	9	0	0	937.52	209	217
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	31	91	0.09%	48.2%	HKSETDTSLIR	99.6%	32	25	23.6	2	2	0	1286.67	198	208
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	31	91	0.09%	48.2%	HTLTQIK	96.4%	28.9	25	9.13	1	0	0	840.49	382	388
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	31	91	0.09%	48.2%	IITEGFEAAK	99.7%	63.5	25	33.2	5	0	0	1078.58	118	127
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	31	91	0.09%	48.2%	KFIEDR	99.4%	36.6	25	12.8	1	0	0	807.44	265	270
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	31	91	0.09%	48.2%	MLVSGAGDIK	99.7%	74.6	25	49.2	5	0	0	990.53	46	55
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	31	91	0.09%	48.2%	NAIDDGCVVPGAGAVEVAMAEALIK	99.7%	62.1	25	55.5	0	1	0	2470.23	400	424
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	31	91	0.09%	48.2%	QADLYISEGLHPR	99.7%	84.3	25	77.3	3	2	0	1498.77	105	117
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	31	91	0.09%	48.2%	SETDTSLIR	99.7%	79	25	64.5	2	0	0	1021.52	200	208
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	31	91	0.09%	48.2%	TEVNSGFFYK	99.7%	62.4	25	60.2	2	0	0	1191.57	242	251

T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	31	91	0.09%	48.2%	VATAQDDITGDGTTSNVLIIGELLK	99.7%	94.2	25	94.2	3	2	0	2544.34	80	104
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	31	91	0.09%	48.2%	VCGDSDKGFVVINQK	99.7%	72.5	25	72.5	2	2	0	1665.83	281	295
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	31	91	0.09%	48.2%	VLAQNSGFDLQETLVK	99.7%	98.9	25	98.9	8	0	0	1761.94	450	465
Telomere length regulation protein TEL2 homolog	TELO2	TELO2_HUMAN	91.7	99.8%	2	2	2	0.00%	2.8%	AVLICLAQLGEPELR	96.3%	28.8	25	28.2	1	0	0	1681.93	363	377
Telomere length regulation protein TEL2 homolog	TELO2	TELO2_HUMAN	91.7	99.8%	2	2	2	0.00%	2.8%	LVEQVPDR	98.5%	32.5	25	25.5	1	0	0	955.52	255	262
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	13	13	23	0.02%	7.7%	GATALEMGMPLLLQK	99.2%	35.2	25	19	1	0	0	1572.85	203	217
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	13	13	23	0.02%	7.7%	GLEEIPVFDISEK	99.5%	37.7	25	26.6	1	0	0	1475.76	2370	2382
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	13	13	23	0.02%	7.7%	IGISDISSLSEK	99.7%	71.1	25	59.3	2	0	0	1248.67	1700	1711
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	13	13	23	0.02%	7.7%	ITSELSEANALELLSK	99.7%	89.8	25	85.4	4	0	0	1717.92	88	103
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	13	13	23	0.02%	7.7%	LIAEQTLQENLIEK	99.7%	95.6	25	95.6	2	0	0	1641.91	1468	1481
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	13	13	23	0.02%	7.7%	LVIPLVVHSAQK	98.1%	31.5	25	31.5	1	0	0	1303.81	187	198
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	13	13	23	0.02%	7.7%	LVSDIIDPVALEIPLSK	99.7%	45	25	45	3	0	0	1822.06	2399	2415
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	13	13	23	0.02%	7.7%	NTENNDVEISETK	99.2%	35.3	25	35.3	1	0	0	1492.68	1751	1763
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	13	13	23	0.02%	7.7%	SLIDNFALNPDILCSAK	99.7%	71.6	25	65.6	3	0	0	1890.96	299	315
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	13	13	23	0.02%	7.7%	SNESVDIQDQEEK	99.7%	40.9	25	40.9	1	0	0	1520.67	1576	1588
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	13	13	23	0.02%	7.7%	TIGDLSTLTASEIK	99.7%	103	25	99.9	1	0	0	1448.78	2329	2342
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	13	13	23	0.02%	7.7%	TLGETSANAETEQNKK	99.7%	61.4	25	61.4	2	0	0	1720.83	1489	1504
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	13	13	23	0.02%	7.7%	YAEYSFTSLPVPESNLR	99.7%	57.6	25	56.8	1	0	0	1972.97	1659	1675
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	6	6	10	0.01%	8.1%	LAAVQLLQFLAPK	99.7%	70.7	25	67.6	2	0	0	1411.87	116	128
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	6	6	10	0.01%	8.1%	LLLQHAPLR	99.7%	40.9	25	36.1	1	0	0	1060.66	866	874
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	6	6	10	0.01%	8.1%	LQNATPTNFK	99.3%	36.2	25	29.9	2	0	0	1133.60	25	34
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	6	6	10	0.01%	8.1%	SQNFDILQSAISK	99.7%	80.3	25	73.8	2	0	0	1450.75	747	759
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	6	6	10	0.01%	8.1%	VGPEELPVVGQLLR	99.7%	59.5	25	59.5	2	0	0	1505.87	852	865
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	6	6	10	0.01%	8.1%	VLDILLEQYPALITGR	99.7%	67.3	25	67.3	1	0	0	1814.04	163	178
Tetratricopeptide repeat protein 19, mitochondrial	TTC19	TTC19_HUMAN	42.5	99.8%	2	2	4	0.00%	5.5%	GQLENAEQLFK	99.7%	44.4	25	32.4	2	0	0	1276.65	150	160
Tetratricopeptide repeat protein 19, mitochondrial	TTC19	TTC19_HUMAN	42.5	99.8%	2	2	4	0.00%	5.5%	LASIYAAQNR	99.7%	65.9	25	55.5	2	0	0	1106.60	185	194
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	8	8	13	0.01%	6.6%	ASELNPESIYSVFK	99.7%	61.1	25	61.1	2	0	0	1583.80	624	637
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	8	8	13	0.01%	6.6%	CLLTSAIYALQGR	99.7%	74.3	25	74.1	1	0	0	1465.78	1162	1174
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	8	8	13	0.01%	6.6%	DDYELIDVLVNNAK	99.7%	44.9	25	21.1	2	0	0	1620.81	1534	1547
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	8	8	13	0.01%	6.6%	LSDYDSSEEAIR	99.7%	58.5	25	54	1	0	0	1384.62	363	374
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	8	8	13	0.01%	6.6%	SGPGLIGLGIK	99.7%	57.1	25	44.6	2	0	0	1011.62	271	281
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	8	8	13	0.01%	6.6%	SNPDQPAVILLLR	99.7%	49.6	25	49.6	1	0	0	1435.83	1355	1367
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	8	8	13	0.01%	6.6%	TLDQISDADNIPGLLVLK	99.7%	66.4	25	66.4	2	0	0	1925.06	375	392
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	8	8	13	0.01%	6.6%	VVAQYAQR	99.7%	39.7	25	33.9	2	0	0	934.51	1202	1209
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	26	0.03%	26.4%	HEDMTLLVR	99.6%	38.3	25	33.9	3	0	0	1113.57	355	363
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	26	0.03%	26.4%	IHSDTFASGGER	99.7%	74.7	25	63	2	0	0	1276.59	337	348
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	26	0.03%	26.4%	LSQLGLDAGK	99.7%	60.8	25	47.5	2	0	0	1001.56	218	227
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	26	0.03%	26.4%	LWSVDHGEQSVVTAP	99.7%	40.4	25	38.9	2	0	0	1624.80	490	504
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	26	0.03%	26.4%	QTSLDAVAQAVVDR	99.7%	104	25	89.5	2	0	0	1472.77	320	333
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	26	0.03%	26.4%	QVGIICGQESTR	99.7%	45	25	43.7	2	0	0	1347.67	230	241
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	26	0.03%	26.4%	SFLESIDDALAEK	99.7%	78.1	25	69.8	3	0	0	1437.71	116	128
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	26	0.03%	26.4%	VLLQAFDVVER	99.7%	84.8	25	75.1	4	0	0	1288.73	105	115
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	26	0.03%	26.4%	VTNFVAQR	99.7%	54.9	25	37.5	2	0	0	934.51	76	83
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	26	0.03%	26.4%	VYPVSVPYSSAQSTSK	99.7%	55.6	25	55.6	2	0	0	1699.85	387	402
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	26	0.03%	26.4%	YGYTDIDLLSAAK	99.7%	85.2	25	85.2	2	0	0	1429.72	250	262
Thioredoxin	TXN	THIO_HUMAN	11.7	100.0%	3	3	4	0.00%	19.0%	EKLEATINELV	99.7%	69.9	25	69.9	2	0	0	1258.69	95	105
Thioredoxin	TXN	THIO_HUMAN	11.7	100.0%	3	3	4	0.00%	19.0%	LEATINELV	96.8%	29.4	25	29.4	1	0	0	1001.55	97	105
Thioredoxin	TXN	THIO_HUMAN	11.7	100.0%	3	3	4	0.00%	19.0%	VGEFSGANK	99.6%	37.9	25	31.5	1	0	0	908.45	86	94
Thioredoxin domain-containing protein 5	TXNDC5	TXND5_HUMAN	47.6	99.8%	2	2	2	0.00%	4.4%	GYPTLLWFR	98.1%	31.4	25	31.4	1	0	0	1152.62	261	269
Thioredoxin domain-containing protein 5	TXNDC5	TXND5_HUMAN	47.6	99.8%	2	2	2	0.00%	4.4%	IAEVDCTAER	99.4%	36.5	25	36.5	1	0	0	1163.54	376	385
Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3	PRDX3_HUMAN	27.7	100.0%	2	2	8	0.01%	10.2%	DYGVLLEGSGLALR	99.7%	82.9	25	79.3	4	0	0	1462.79	171	184

Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3	PRDX3_HUMAN	27.7	100.0%	2	2	8	0.01%	10.2%	GLFIIDPNGVIK	99.7%	54.4	25	45.5	4	0	0	1285.75	185	196
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	12.1%	AEGGYFGQIR	99.7%	53.1	25	47.4	1	0	0	1097.54	711	720
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	12.1%	CIFSAIDAVYCAR	99.7%	89.8	25	83.3	1	0	0	1545.72	986	998
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	12.1%	ECGNYPGFLTILR	98.0%	31.4	25	26.7	1	0	0	1539.76	1063	1075
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	12.1%	EKTPATTPEAR	99.5%	37.8	25	24.3	1	0	0	1200.62	1283	1293
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	12.1%	FLCCMLETVTR	99.7%	55	25	50.4	2	0	0	1429.66	1042	1052
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	12.1%	FLQLCIFPR	99.7%	46.1	25	35.6	2	0	0	1193.65	977	985
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	12.1%	FVELVHQQK	99.7%	42.5	25	41	2	0	0	1127.62	999	1007
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	12.1%	FYQEPNGETPSSLYR	99.7%	50.2	25	50	1	0	0	1787.82	254	268
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	12.1%	GEFLHLCR	99.7%	46.8	25	38.1	1	0	0	1031.51	22	29
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	12.1%	LDPETLESLGLIK	99.7%	66.6	25	55	4	0	0	1427.80	127	139
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	12.1%	LGLLEALLK	99.7%	50.3	25	44.5	4	0	0	969.63	346	354
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	12.1%	NETYNSHPLLVK	99.6%	38.7	25	26.2	1	0	0	1414.73	529	540
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	12.1%	NGVIFQEGGEK	99.7%	39.5	25	36.2	1	0	0	1177.58	751	761
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	12.1%	SFDLLILK	99.7%	43.9	25	35	2	0	0	948.58	673	680
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	12.1%	TPNFSTLLCYDR	99.7%	59.3	25	59.3	2	0	0	1486.70	1008	1019
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	12.1%	VFSDIIYTVASCTENEASR	99.7%	83.2	25	78	2	0	0	2162.01	1020	1038
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	12.1%	VLNLGQALER	99.7%	52.3	25	43.1	4	0	0	1112.64	1137	1146
THO complex subunit 3	THOC3	THOC3_HUMAN	38.8	100.0%	2	4	7	0.01%	6.0%	TASVFLLEKDR	99.7%	52.1	25	52.1	2	1	0	1278.71	78	88
THO complex subunit 3	THOC3	THOC3_HUMAN	38.8	100.0%	2	4	7	0.01%	6.0%	YVLGMQELFR	99.7%	60.5	25	56.2	4	0	0	1271.65	34	43
THO complex subunit 4	ALYREF	THOC4_HUMAN	26.9	99.8%	2	3	7	0.01%	11.3%	QQLSAEELDAQLDAYNAR	99.7%	101	25	100	2	1	0	2034.97	236	253
THO complex subunit 4	ALYREF	THOC4_HUMAN	26.9	99.8%	2	3	7	0.01%	11.3%	SLGTADVHFER	99.7%	65.8	25	56.9	4	0	0	1231.61	145	155
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	5	5	7	0.01%	8.7%	FLGDIEVWDQAEK	99.7%	58.2	25	50.2	1	0	0	1549.75	505	517
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	5	5	7	0.01%	8.7%	GAYIYNALIEFIR	99.7%	44.9	25	44.9	1	0	0	1542.83	349	361
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	5	5	7	0.01%	8.7%	GFQEVVTPNIFNSR	99.7%	49.4	25	49.1	1	0	0	1607.82	368	381
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	5	5	7	0.01%	8.7%	NELSGALTGLTR	99.7%	90.6	25	73.1	2	0	0	1231.66	443	454
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	5	5	7	0.01%	8.7%	TVYSVFGFSFK	99.2%	35.2	25	35.2	2	0	0	1281.65	485	495
Threonine--tRNA ligase, mitochondrial	TARS2	SYTM_HUMAN	81.0	100.0%	3	3	4	0.00%	3.8%	LADFGALHR	99.7%	66.9	25	53.2	2	0	0	999.54	430	438
Threonine--tRNA ligase, mitochondrial	TARS2	SYTM_HUMAN	81.0	100.0%	3	3	4	0.00%	3.8%	LVELQNTR	99.7%	42.4	25	34.9	1	0	0	972.55	703	710
Threonine--tRNA ligase, mitochondrial	TARS2	SYTM_HUMAN	81.0	100.0%	3	3	4	0.00%	3.8%	VYNALVAFIR	99.7%	71.8	25	67.9	1	0	0	1165.67	331	340
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	6	7	11	0.01%	13.6%	AANNIASLLTK	99.7%	50.5	25	37.3	2	0	0	1115.64	359	369
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	6	7	11	0.01%	13.6%	AAVYVLIR	98.6%	32.7	25	22.4	1	0	0	904.56	477	484
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	6	7	11	0.01%	13.6%	AVLLTQDTK	99.6%	38.8	25	29.3	2	0	0	988.57	441	449
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	6	7	11	0.01%	13.6%	NITHFGPTTLR	95.2%	27.8	25	21.9	1	0	0	1256.67	294	304
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	6	7	11	0.01%	13.6%	TGSVDIIVTDLPFGK	99.7%	44.8	25	44.8	2	0	0	1561.85	397	411
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	6	7	11	0.01%	13.6%	TPQAFVHPSEQDGER	99.7%	36.1	25	36.1	1	2	0	1697.79	485	499
Thymidine kinase, cytosolic	TK1	KITH_HUMAN	25.5	99.8%	2	3	5	0.01%	11.5%	GQIQVILGPMFSGK	99.7%	46.6	25	46.6	3	0	0	1490.80	19	32
Thymidine kinase, cytosolic	TK1	KITH_HUMAN	25.5	99.8%	2	3	5	0.01%	11.5%	TVIVAALDGTFQR	99.7%	75	25	67.6	2	0	0	1390.77	118	130
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	9	10	20	0.02%	10.4%	ASAVSELSPR	99.7%	75.3	25	68.7	3	0	0	1016.54	236	245
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	9	10	20	0.02%	10.4%	EESAASGGAAYTK	99.7%	57.8	25	57.8	3	0	0	1241.56	334	346
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	9	10	20	0.02%	10.4%	EQTFSGGTSQDTK	99.7%	57.8	25	54	2	0	0	1385.62	203	215
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	9	10	20	0.02%	10.4%	GSFSDTGLGDGK	99.7%	55.5	25	51.4	3	0	0	1140.52	376	387
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	9	10	20	0.02%	10.4%	SIFQHIQSAQSQR	99.7%	77.2	25	67	1	3	0	1529.78	609	621
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	9	10	20	0.02%	10.4%	SPLQSVVVR	99.7%	41.3	25	30.8	2	0	0	984.58	253	261
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	9	10	20	0.02%	10.4%	TDSEKPFR	96.1%	28.6	25	15.4	1	0	0	979.48	397	404
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	9	10	20	0.02%	10.4%	VIGANKNQEEEK	99.2%	35.2	25	28.2	1	0	0	1358.69	456	467
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	9	10	20	0.02%	10.4%	YKDDPVDLR	97.7%	30.7	25	17.6	1	0	0	1120.56	710	718
Tight junction protein ZO-1	TJP1	ZO1_HUMAN	195.5	99.8%	2	2	3	0.00%	1.4%	EEAVLFLLDLPK	99.7%	46.8	25	40.9	2	0	0	1386.79	481	492
Tight junction protein ZO-1	TJP1	ZO1_HUMAN	195.5	99.8%	2	2	3	0.00%	1.4%	SVASSQPAKPTK	99.5%	37.5	25	27	1	0	0	1200.66	175	186
Torsin-1A-interacting protein 1	TOR1AIP1	TOIP1_HUMAN	66.2	99.8%	2	2	7	0.01%	4.3%	SELGNQSPSTSSR	99.7%	51.4	25	51.4	4	0	0	1349.63	309	321
Torsin-1A-interacting protein 1	TOR1AIP1	TOIP1_HUMAN	66.2	99.8%	2	2	7	0.01%	4.3%	SQPAILLLTAAR	99.7%	63.2	25	63.2	3	0	0	1253.76	405	416

Torsin-1A-interacting protein 2	TOR1AIP2	TOIP2_HUMAN	51.3	99.8%	2	2	3	0.00%	5.5%	LLAPEAGSHPQQTQK	95.7%	28.2	25	21.2	1	0	0	1604.84	181	195
Torsin-1A-interacting protein 2	TOR1AIP2	TOIP2_HUMAN	51.3	99.8%	2	2	3	0.00%	5.5%	VSPIQIDGAGR	99.7%	49.2	25	46.5	2	0	0	1112.61	325	335
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	4	5	8	0.01%	20.2%	ATTPADGEEPAPEAEALAAAR	99.7%	81.8	25	81.8	2	1	0	2037.97	6	26
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	4	5	8	0.01%	20.2%	DYIQSTMETEK	99.7%	39.3	25	39.2	1	0	0	1360.59	124	134
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	4	5	8	0.01%	20.2%	FLSGLELVK	97.9%	31	25	17.6	2	0	0	1005.60	32	40
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	4	5	8	0.01%	20.2%	TPQGLSNLAK	99.7%	58.8	25	51.5	2	0	0	1028.57	135	144
TraB domain-containing protein	TRABD	TRABD_HUMAN	42.3	99.8%	2	2	3	0.00%	5.9%	AIAALSFWQK	99.7%	44.8	25	40.2	1	0	0	1134.63	200	209
TraB domain-containing protein	TRABD	TRABD_HUMAN	42.3	99.8%	2	2	3	0.00%	5.9%	TVTQLVAEDGSR	99.7%	74.9	25	60.8	2	0	0	1275.65	63	74
Trafficking protein particle complex subunit 1	TRAPPC1	TPPC1_HUMAN	16.8	100.0%	3	3	5	0.01%	19.3%	DGFLAFQTSR	99.7%	52.1	25	42	2	0	0	1141.56	59	68
Trafficking protein particle complex subunit 1	TRAPPC1	TPPC1_HUMAN	16.8	100.0%	3	3	5	0.01%	19.3%	SRLDSYVR	98.9%	33.7	25	23.2	2	0	0	995.53	128	135
Trafficking protein particle complex subunit 1	TRAPPC1	TPPC1_HUMAN	16.8	100.0%	3	3	5	0.01%	19.3%	TVHNLYLFDR	97.9%	31.1	25	25.8	1	0	0	1277.66	2	11
Trafficking protein particle complex subunit 5	TRAPPC5	TPPC5_HUMAN	20.8	99.8%	2	2	3	0.00%	11.7%	EADKLEQANDDAR	97.8%	31	25	29	2	0	0	1474.68	101	113
Trafficking protein particle complex subunit 5	TRAPPC5	TPPC5_HUMAN	20.8	99.8%	2	2	3	0.00%	11.7%	VLGALLFVK	99.7%	39.5	25	39.5	1	0	0	959.63	82	90
Transaldolase	TALDO1	TALDO_HUMAN	37.5	99.8%	2	2	3	0.00%	7.1%	ALAGCDFLTISPK	99.7%	46.3	25	46.3	1	0	0	1392.72	246	258
Transaldolase	TALDO1	TALDO_HUMAN	37.5	99.8%	2	2	3	0.00%	7.1%	LLGELLQDNAK	99.7%	55.6	25	55.6	2	0	0	1213.68	259	269
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	10	10	17	0.02%	7.0%	AVATYHANTER	99.7%	43.2	25	35.6	2	0	0	1232.60	503	513
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	10	10	17	0.02%	7.0%	DSDAGSSTPTTSTR	99.7%	50.2	25	50.2	2	0	0	1382.60	1416	1429
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	10	10	17	0.02%	7.0%	DTALETALNAK	99.7%	68	25	56.9	2	0	0	1146.60	427	437
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	10	10	17	0.02%	7.0%	ELPEYYELIR	99.7%	62.9	25	59.9	2	0	0	1324.68	1493	1502
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	10	10	17	0.02%	7.0%	GLDPVEILQER	99.7%	69.1	25	62.1	2	0	0	1268.68	360	370
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	10	10	17	0.02%	7.0%	IQELENLPGSLAGDLR	99.7%	72.4	25	72.4	2	0	0	1724.92	382	397
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	10	10	17	0.02%	7.0%	LCTVNSVEEK	99.2%	35.1	25	23	1	0	0	1178.57	1204	1213
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	10	10	17	0.02%	7.0%	LLLTGTPLQNK	99.1%	34.9	25	0	1	0	0	1197.72	907	917
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	10	10	17	0.02%	7.0%	QLSEVFIQLPSR	99.7%	39.8	25	39	1	0	0	1416.78	1480	1491
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	10	10	17	0.02%	7.0%	VIQAGMFDQK	99.7%	45.4	25	39.6	2	0	0	1136.58	1228	1237
Transcription elongation factor B polypeptide 1	TCEB1	ELOC_HUMAN	12.5	99.8%	2	2	4	0.00%	23.2%	LISSDGHEFIVK	99.6%	38.2	25	38.2	2	0	0	1344.72	21	32
Transcription elongation factor B polypeptide 1	TCEB1	ELOC_HUMAN	12.5	99.8%	2	2	4	0.00%	23.2%	TYGGCEGPDAMYVK	99.7%	49.5	25	49.5	2	0	0	1563.65	7	20
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	4	5	10	0.01%	15.9%	AEWQVYKEEISR	99.7%	49.3	25	48.1	2	2	0	1537.76	105	116
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	4	5	10	0.01%	15.9%	ELTLLGKPK	98.9%	34	25	33.5	1	0	0	998.62	148	156
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	4	5	10	0.01%	15.9%	SAYNVYVAER	99.7%	53.8	25	45.8	3	0	0	1171.57	160	169
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	4	5	10	0.01%	15.9%	WRELPDSK	97.6%	30.5	25	18.7	2	0	0	1030.53	88	95
Transcription initiation factor TFIID subunit 4	TAF4	TAF4_HUMAN	110.1	100.0%	3	3	10	0.01%	4.0%	ALSAVSAQAAAAQK	99.7%	100	25	85.8	4	0	0	1286.71	804	817
Transcription initiation factor TFIID subunit 4	TAF4	TAF4_HUMAN	110.1	100.0%	3	3	10	0.01%	4.0%	ELNSSPQPYLVPFLK	99.7%	41.3	25	41.3	4	0	0	1731.93	644	658
Transcription initiation factor TFIID subunit 4	TAF4	TAF4_HUMAN	110.1	100.0%	3	3	10	0.01%	4.0%	ILATNSELVGTLTR	99.7%	90.7	25	90.7	2	0	0	1487.84	852	865
Transcriptional activator protein Pur-alpha	PURA	PURA_HUMAN	34.9	100.0%	3	3	4	0.00%	18.0%	FFFDVGSNK	99.7%	49.4	25	49.4	2	0	0	1060.51	231	239
Transcriptional activator protein Pur-alpha	PURA	PURA_HUMAN	34.9	100.0%	3	3	4	0.00%	18.0%	GPGLGSTQGQTIALPAQGLIEFR	99.7%	57.4	25	57.4	1	0	0	2311.24	177	199
Transcriptional activator protein Pur-alpha	PURA	PURA_HUMAN	34.9	100.0%	3	3	4	0.00%	18.0%	LIDDYGVEEEPAELPEGTSLTVDNKR	99.7%	68.2	25	66.9	0	1	0	2889.40	205	230
Transcriptional activator protein Pur-beta	PURB	PURB_HUMAN	33.2	100.0%	3	3	4	0.00%	10.3%	FFFDVGCNK	99.7%	41.7	25	41.7	2	0	0	1133.51	232	240
Transcriptional activator protein Pur-beta	PURB	PURB_HUMAN	33.2	100.0%	3	3	4	0.00%	10.3%	GGGGGPCGFQPASR	98.2%	31.9	25	31.9	1	0	0	1304.58	11	24
Transcriptional activator protein Pur-beta	PURB	PURB_HUMAN	33.2	100.0%	3	3	4	0.00%	10.3%	VSEVKPSYR	97.7%	30.7	25	23.9	1	0	0	1064.57	247	255
Transducin beta-like protein 3	TBL3	TBL3_HUMAN	89.0	100.0%	3	3	4	0.00%	5.0%	ALLLAQWAWQEGSVTR	99.7%	55	25	55	1	0	0	1828.97	87	102
Transducin beta-like protein 3	TBL3	TBL3_HUMAN	89.0	100.0%	3	3	4	0.00%	5.0%	LWALQDFSCLK	99.7%	43.3	25	37.2	1	0	0	1380.70	547	557
Transducin beta-like protein 3	TBL3	TBL3_HUMAN	89.0	100.0%	3	3	4	0.00%	5.0%	VNILEVASGAVLR	99.7%	93.3	25	85.6	2	0	0	1340.79	47	59
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	14	14	25	0.03%	23.0%	AAAEVAGQFVIK	99.5%	37.3	25	29.6	1	0	0	1203.67	589	600
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	14	14	25	0.03%	23.0%	DSAQNSVIIVDK	99.7%	84.2	25	77.8	2	0	0	1288.67	194	205
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	14	14	25	0.03%	23.0%	GFVEPDHYVVVGAQR	99.7%	46.9	25	37.5	0	1	0	1672.84	395	409
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	14	14	25	0.03%	23.0%	ILNIFGVIK	99.7%	55.6	25	41.1	2	0	0	1016.65	386	394
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	14	14	25	0.03%	23.0%	LAQMFSDMVLK	99.7%	39.7	25	33.2	1	0	0	1282.65	429	439
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	14	14	25	0.03%	23.0%	LAVDEEENADNNTK	99.7%	95	25	75.2	2	0	0	1561.70	40	53
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	14	14	25	0.03%	23.0%	LLNENSYVPR	99.7%	58.3	25	51	2	0	0	1204.63	146	155
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	14	14	25	0.03%	23.0%	LVYLVENPGGYVAYSK	99.7%	103	25	103	2	0	0	1771.93	209	224

Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	14	14	25	0.03%	23.0%	SAFSNLFGGEPLSYTR	99.7%	90.5	25	90.2	2	0	0	1745.85	7	22
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	14	14	25	0.03%	23.0%	SGVGTALLLK	99.7%	58.4	25	39.9	2	0	0	958.59	419	428
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	14	14	25	0.03%	23.0%	SSGLPNIPVQTISR	99.7%	64	25	52.1	2	0	0	1468.81	326	339
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	14	14	25	0.03%	23.0%	VEYHFLSPYVSPK	99.7%	42.5	25	41	0	2	0	1565.80	681	693
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	14	14	25	0.03%	23.0%	VSASPLLYTLIEK	99.7%	99.8	25	99.7	2	0	0	1433.83	496	508
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	14	14	25	0.03%	23.0%	YNSQLLSFVR	99.7%	64	25	54.9	2	0	0	1226.65	614	623
Transformation/transcription domain-associated protein	TRRAP	TRRAP_HUMAN	437.6	99.8%	2	2	2	0.00%	0.6%	ACQLPLFSYIVER	99.7%	48.9	25	39.5	1	0	0	1595.83	1132	1144
Transformation/transcription domain-associated protein	TRRAP	TRRAP_HUMAN	437.6	99.8%	2	2	2	0.00%	0.6%	TIPNVIISHR	99.7%	40.3	25	39.7	1	0	0	1149.67	997	1006
Transgelin-2	TAGLN2	TAGL2_HUMAN	22.4	100.0%	4	4	7	0.01%	23.6%	DDGLFSGDPNWFPK	96.1%	28.7	25	28.7	1	0	0	1594.72	140	153
Transgelin-2	TAGLN2	TAGL2_HUMAN	22.4	100.0%	4	4	7	0.01%	23.6%	GASQAGMTGYGMPR	99.7%	48.1	25	44.2	2	0	0	1415.60	183	196
Transgelin-2	TAGLN2	TAGL2_HUMAN	22.4	100.0%	4	4	7	0.01%	23.6%	GPAYGLSR	98.8%	33.3	25	18.4	2	0	0	820.43	5	12
Transgelin-2	TAGLN2	TAGL2_HUMAN	22.4	100.0%	4	4	7	0.01%	23.6%	NFSDNQLQEGK	99.7%	61.5	25	55.8	2	0	0	1279.59	161	171
Transitional endoplasmic reticulum ATPase	VCP	TERA_HUMAN	89.3	100.0%	3	3	5	0.01%	5.2%	GILLYGPPGTGK	99.7%	40.3	25	0	1	0	0	1172.67	240	251
Transitional endoplasmic reticulum ATPase	VCP	TERA_HUMAN	89.3	100.0%	3	3	5	0.01%	5.2%	LDQLIYIPLPDEK	99.1%	34.8	25	34.8	2	0	0	1556.86	639	651
Transitional endoplasmic reticulum ATPase	VCP	TERA_HUMAN	89.3	100.0%	3	3	5	0.01%	5.2%	NAPAIIFIDELDAIAPK	99.7%	56.4	25	48.5	2	0	0	1811.00	296	312
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	5	5	8	0.01%	20.0%	DGATILTHAYSR	99.7%	58.9	25	58	2	0	0	1304.66	121	132
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	5	5	8	0.01%	20.0%	DKGETIQGLR	99.7%	50.7	25	41.8	2	0	0	1116.60	37	46
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	5	5	8	0.01%	20.0%	FISLASLEYSDYSK	99.7%	95.6	25	82.2	1	0	0	1622.79	75	88
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	5	5	8	0.01%	20.0%	FSVYVTESQPDLSGKK	99.7%	75.2	25	75.2	1	0	0	1784.91	148	163
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	5	5	8	0.01%	20.0%	VLEAAVAAK	99.7%	39.9	25	22.2	2	0	0	871.52	137	145
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	4	4	7	0.01%	17.1%	AVTGTHTLALAAK	99.7%	60.9	25	58.6	2	0	0	1253.72	247	259
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	4	4	7	0.01%	17.1%	FVAPEEVLPFTEGDILEK	99.7%	46.5	25	40.5	2	0	0	2033.05	288	305
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	4	4	7	0.01%	17.1%	LMSELYHPDDHVL	97.3%	30.1	25	29.5	1	0	0	1568.74	339	351
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	4	4	7	0.01%	17.1%	MTAAQPSETTVGNMVR	99.7%	76.1	25	76	2	0	0	1724.79	68	83
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	8	8	12	0.01%	17.0%	AELPPGPGAVGR	98.4%	32.3	25	26	2	0	0	1120.61	18	29
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	8	8	12	0.01%	17.0%	ASPSTAGETPSGVK	99.7%	62.2	25	58.5	2	0	0	1288.64	129	142
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	8	8	12	0.01%	17.0%	ASPSTAGETPSGVKR	99.7%	41.1	25	35.5	1	0	0	1444.74	129	143
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	8	8	12	0.01%	17.0%	ILQEAWTEGR	99.7%	51.6	25	38.9	1	0	0	1202.62	345	354
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	8	8	12	0.01%	17.0%	LGLQYSQGLVSGSNAR	99.7%	83.9	25	83.2	2	0	0	1649.86	210	225
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	8	8	12	0.01%	17.0%	LPEYPQVDDLLLR	96.6%	29.2	25	29.2	1	0	0	1570.85	144	156
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	8	8	12	0.01%	17.0%	VGTAQLALVAR	99.7%	97.9	25	84.2	2	0	0	1098.66	418	428
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	8	8	12	0.01%	17.0%	VSLFSHLPQYSR	99.4%	30.2	25	28.4	0	1	0	1433.75	177	188
Translation initiation factor eIF-2B subunit epsilon	EIF2B5	EI2BE_HUMAN	80.4	100.0%	4	4	7	0.01%	5.8%	GYNPAEVGAAGK	99.7%	58.2	25	45.2	1	0	0	1133.56	482	493
Translation initiation factor eIF-2B subunit epsilon	EIF2B5	EI2BE_HUMAN	80.4	100.0%	4	4	7	0.01%	5.8%	IITSELYR	99.7%	42.1	25	11.5	2	0	0	994.56	122	129
Translation initiation factor eIF-2B subunit epsilon	EIF2B5	EI2BE_HUMAN	80.4	100.0%	4	4	7	0.01%	5.8%	VFQNEVLGTLQR	99.7%	64.2	25	59.3	1	0	0	1403.76	552	563
Translation initiation factor eIF-2B subunit epsilon	EIF2B5	EI2BE_HUMAN	80.4	100.0%	4	4	7	0.01%	5.8%	YCALLLPLLK	99.7%	50.7	25	50.7	3	0	0	1203.72	617	626
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	4	4	6	0.01%	10.0%	DFIGVDSTGKR	99.7%	51.5	25	47.4	1	0	0	1194.61	156	166
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	4	4	6	0.01%	10.0%	KGQDSIEPVPGQK	99.7%	75.6	25	74.4	2	0	0	1382.73	134	146
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	4	4	6	0.01%	10.0%	SELIPYLVR	99.7%	46.7	25	39.9	2	0	0	1089.63	226	234
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	4	4	6	0.01%	10.0%	VGFEEVIVVTTR	99.7%	66.8	25	58.2	1	0	0	1348.75	46	57
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	AALLETLSLLLAK	99.7%	81.6	25	81.6	2	0	0	1355.85	2324	2336
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	ADYTSHLR	99.7%	48.3	25	33.9	2	0	0	962.47	2184	2191
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	AGSVELLGAMAYCAPK	99.7%	87.2	25	82.8	2	0	0	1637.80	1515	1530
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	AIITALGVER	99.7%	63.9	25	43.3	2	0	0	1042.63	1872	1881
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	ALADENEFVR	99.7%	57.9	25	49.3	2	0	0	1163.57	1785	1794
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	ALCDPLEEVR	97.1%	29.8	25	24.8	1	0	0	1201.59	2013	2022
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	ALGTLVSHVTLR	99.7%	68.5	25	58.2	2	1	0	1266.75	915	926
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	ALQAAIQQLAEAQPEATAK	99.7%	77.8	25	77.8	1	0	0	1952.04	69	87
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	ALVAVLLSR	99.7%	75.5	25	63.8	4	0	0	941.61	568	576
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	AVMSNLSAHGVK	99.7%	58.8	25	51.9	2	0	0	1213.64	1485	1496
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	AYSDQAIVNLLK	99.7%	94.8	25	70.8	2	0	0	1334.73	2610	2621

Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	EDAGGMIQR	98.9%	33.8	25	19.5	1	0	0	976.45	1372	1380
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	EEFAIMQTPAGELYDK	99.6%	38.7	25	38.7	1	0	0	1841.86	761	776
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	FTPYVGPIIPCILK	98.4%	32.1	25	32.1	2	0	0	1617.91	1771	1784
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	GAAYGLAGLVK	99.7%	64	25	54.1	2	0	0	1019.59	1396	1406
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	GIKEEVQLTSK	99.7%	54.3	25	39.8	2	0	0	1231.69	819	829
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	GVTSILPVLR	99.7%	43.8	25	40.5	2	0	0	1054.66	2260	2269
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	HLDQIIPR	99.7%	41.5	25	33.5	2	0	0	991.57	705	712
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	HLFAILGGSEGK	96.0%	28.5	25	27.5	1	0	0	1228.67	341	352
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	ILPEIIPILEEGLR	99.7%	41.2	25	41.2	2	0	0	1604.96	1960	1973
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	IVVSNTPR	99.6%	38.2	25	33.9	1	0	0	885.52	1910	1917
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	KGVTSILPVLR	99.5%	37.2	25	30.3	1	0	0	1182.76	2259	2269
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	LMDEAVLALR	99.7%	64.2	25	48.9	4	0	0	1130.62	314	323
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	LMEIYQEK	98.0%	31.3	25	26.5	1	0	0	1053.53	1201	1208
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	LMPEIVATASK	97.7%	30.8	25	22.5	1	0	0	1159.64	1735	1745
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	LTEVLTDSHVK	99.7%	50.9	25	41.7	1	0	0	1241.67	1543	1553
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	LTSADALRPSVVSITGPLIR	98.3%	26.2	25	26.2	0	2	0	2066.20	2293	2312
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	LYRPPPVLDALGR	99.7%	50.8	25	46.7	1	2	0	1466.85	1209	1221
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	MTTETASEDDNFGTAQSNK	99.7%	66.1	25	63.9	1	0	0	2062.85	1853	1871
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	NAPNDASYDAVR	99.7%	67	25	64.2	2	0	0	1292.59	1305	1316
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	NLLHSLQSSGIGSK	99.7%	67	25	60.3	2	2	0	1440.78	88	101
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	QAAAIILNIYCSR	99.7%	77.5	25	72.8	1	0	0	1492.79	2169	2181
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	QAGAEALSQAVAR	99.7%	80.9	25	65.5	2	0	0	1271.67	1177	1189
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	QGEEVFQSLSK	96.2%	28.7	25	8.2	1	0	0	1251.62	2624	2634
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	QLSSCLPNIVPK	99.7%	44.6	25	36.6	2	0	0	1355.74	1531	1542
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	SALLDFYMK	99.7%	47.2	25	42	3	0	0	1087.55	221	229
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	SDTQLVVR	99.6%	38.1	25	7.77	2	0	0	917.51	1894	1901
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	SGAAQGLAEVMAGLGVEK	99.7%	86.2	25	76.6	2	0	0	1687.87	1714	1731
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	SIIQSAQQDSIK	99.7%	55.6	25	43.6	1	0	0	1317.70	777	788
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	SIIQSAQQDSIKK	99.7%	47.8	25	36	1	0	0	1445.80	777	789
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	SLVSGLIR	99.5%	37	25	11.6	1	0	0	844.53	2192	2199
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	VDENGPELLPR	99.7%	55.8	25	51.7	2	0	0	1238.64	1027	1037
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	VDPLFTELLNGIR	99.7%	45.6	25	41.3	1	0	0	1486.83	2381	2393
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	VISESPPDQWEAR	99.7%	54.9	25	53.3	1	0	0	1513.73	1222	1234
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	VLAFLSSVAGDALTR	99.7%	80.1	25	80.1	5	0	0	1519.85	2093	2107
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	VLAGLYMGR	99.7%	47.4	25	40.4	2	0	0	979.54	1885	1893
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	VLPLEALVTDAGEVTEAGK	99.7%	86.9	25	86.9	2	2	0	1912.03	617	635
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	54	92	0.10%	20.9%	YLLDSCAPLLR	99.7%	57.1	25	56.8	2	0	0	1320.70	241	251
Translocation protein SEC63 homolog	SEC63	SEC63_HUMAN	88.0	100.0%	4	4	5	0.01%	5.5%	AYAALTDEESR	99.7%	56	25	48.3	1	0	0	1225.57	148	158
Translocation protein SEC63 homolog	SEC63	SEC63_HUMAN	88.0	100.0%	4	4	5	0.01%	5.5%	LSQMAVQGLQQFK	99.7%	62.6	25	54.3	1	0	0	1493.78	369	381
Translocation protein SEC63 homolog	SEC63	SEC63_HUMAN	88.0	100.0%	4	4	5	0.01%	5.5%	VLLLSHLAR	99.7%	59	25	59	2	0	0	1021.65	303	311
Translocation protein SEC63 homolog	SEC63	SEC63_HUMAN	88.0	100.0%	4	4	5	0.01%	5.5%	YSGDQILIR	99.7%	49.8	25	28.6	1	0	0	1064.57	218	226
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	8	10	21	0.02%	41.6%	FFDEESYSLLR	99.7%	78.9	25	74.9	4	0	0	1405.66	106	116
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	8	10	21	0.02%	41.6%	FFDEESYSLLRK	99.7%	56	25	49.7	2	0	0	1533.76	106	117
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	8	10	21	0.02%	41.6%	GQDVGRYQVSWSLDHK	98.0%	25.7	25	25.7	0	2	0	1874.91	80	95
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	8	10	21	0.02%	41.6%	NNEDISIIPPLFTVSVDHR	99.7%	35.9	25	35.9	2	2	0	2166.12	121	139
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	8	10	21	0.02%	41.6%	NRVQNMALYADVGGK	99.7%	35	25	28.6	0	2	0	1635.83	59	73
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	8	10	21	0.02%	41.6%	SAHAGTYEVR	98.6%	32.7	25	31.1	1	0	0	1090.53	96	105
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	8	10	21	0.02%	41.6%	VQNMALYADVGGK	99.7%	86	25	77.1	4	0	0	1365.68	61	73
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	8	10	21	0.02%	41.6%	YQVSWSLDHK	99.7%	40	25	25.4	2	0	0	1262.62	86	95
Transmembrane 9 superfamily member 3	TM9SF3	TM9S3_HUMAN	67.9	100.0%	3	3	6	0.01%	5.4%	NLSGQPNFPCR	99.7%	46.3	25	43	1	0	0	1289.61	419	429
Transmembrane 9 superfamily member 3	TM9SF3	TM9S3_HUMAN	67.9	100.0%	3	3	6	0.01%	5.4%	YFSLPFCVGSK	99.7%	44	25	32.8	3	0	0	1304.63	60	70

Transmembrane 9 superfamily member 3	TM9SF3	TM9S3_HUMAN	67.9	100.0%	3	3	6	0.01%	5.4%	YLDPSFFQHR	99.7%	50	25	39.8	2	0	0	1309.63	211	220
Transmembrane and coiled-coil domain-containing protein 1	TMCO1	TMCO1_HUMAN	21.2	100.0%	3	3	5	0.01%	16.5%	ETITESAGR	99.7%	40.6	25	28.6	1	0	0	963.47	55	63
Transmembrane and coiled-coil domain-containing protein 1	TMCO1	TMCO1_HUMAN	21.2	100.0%	3	3	5	0.01%	16.5%	ILGLAPSR	99.7%	43.4	25	37.4	2	0	0	826.51	161	168
Transmembrane and coiled-coil domain-containing protein 1	TMCO1	TMCO1_HUMAN	21.2	100.0%	3	3	5	0.01%	16.5%	QAGGFLGPPPPSGK	99.7%	62.8	25	55	2	0	0	1309.69	173	186
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	6	9	14	0.01%	33.8%	DLLVTGAYEISDQSGGAGGLR	99.7%	86.6	25	86.2	2	0	0	2079.04	51	71
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	6	9	14	0.01%	33.8%	IPDQLVILDMK	99.7%	69.3	25	59.4	4	0	0	1284.72	117	127
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	6	9	14	0.01%	33.8%	ITDSAGHILYSK	99.7%	73.1	25	60.3	2	1	0	1304.68	76	87
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	6	9	14	0.01%	33.8%	ITDSAGHILYSKEDATK	99.7%	42.4	25	40.8	1	2	0	1848.93	76	92
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	6	9	14	0.01%	33.8%	LEDLSESIVNDFAYMK	99.7%	43	25	40.5	1	0	0	1889.88	154	169
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	6	9	14	0.01%	33.8%	LKPLEVELR	98.6%	32.8	25	29.9	1	0	0	1096.67	144	152
Transmembrane emp24 domain-containing protein 2	TMED2	TMED2_HUMAN	22.8	100.0%	2	4	8	0.01%	12.4%	IVMFTIDIGEAPK	99.7%	69.3	25	66.5	4	0	0	1449.77	105	117
Transmembrane emp24 domain-containing protein 2	TMED2	TMED2_HUMAN	22.8	100.0%	2	4	8	0.01%	12.4%	YTFAAHMDGTYK	99.7%	42.2	25	42.2	4	0	0	1420.62	80	91
Transmembrane protein 11, mitochondrial	TMEM11	TMM11_HUMAN	21.5	100.0%	4	5	7	0.01%	21.4%	KIYELYAV	94.7%	27.5	25	21.8	1	0	0	998.56	185	192
Transmembrane protein 11, mitochondrial	TMEM11	TMM11_HUMAN	21.5	100.0%	4	5	7	0.01%	21.4%	LPLHTLTSSTPVVLVR	99.7%	61.9	25	61.9	2	2	0	1733.03	146	161
Transmembrane protein 11, mitochondrial	TMEM11	TMM11_HUMAN	21.5	100.0%	4	5	7	0.01%	21.4%	YIVIEPTR	99.5%	37.8	25	31.7	1	0	0	990.56	59	66
Transmembrane protein 11, mitochondrial	TMEM11	TMM11_HUMAN	21.5	100.0%	4	5	7	0.01%	21.4%	YQVEYDAYK	99.7%	46.7	25	35.9	1	0	0	1178.54	134	142
Transmembrane protein 126A	TMEM126A	T126A_HUMAN	21.5	100.0%	5	5	11	0.01%	27.7%	ALQLSEPGKEIH	99.7%	40.7	25	40.7	2	0	0	1321.71	184	195
Transmembrane protein 126A	TMEM126A	T126A_HUMAN	21.5	100.0%	5	5	11	0.01%	27.7%	GNILSYWIR	99.7%	47.4	25	35	3	0	0	1121.61	142	150
Transmembrane protein 126A	TMEM126A	T126A_HUMAN	21.5	100.0%	5	5	11	0.01%	27.7%	KINQLPEAER	99.7%	47.1	25	28.1	2	0	0	1197.66	20	29
Transmembrane protein 126A	TMEM126A	T126A_HUMAN	21.5	100.0%	5	5	11	0.01%	27.7%	SNNKENITIVDISR	99.7%	69.1	25	55.1	2	0	0	1602.84	6	19
Transmembrane protein 126A	TMEM126A	T126A_HUMAN	21.5	100.0%	5	5	11	0.01%	27.7%	YQSALLPHK	99.7%	41	25	40.5	2	0	0	1056.58	133	141
Transmembrane protein 201	TMEM201	TM201_HUMAN	72.2	100.0%	3	4	6	0.01%	5.0%	ALLLSHQFK	99.6%	38.5	25	33.7	1	0	0	1056.62	184	192
Transmembrane protein 201	TMEM201	TM201_HUMAN	72.2	100.0%	3	4	6	0.01%	5.0%	EADQTHAQNFSSAVK	99.7%	47.6	25	43.4	2	1	0	1632.76	195	209
Transmembrane protein 201	TMEM201	TM201_HUMAN	72.2	100.0%	3	4	6	0.01%	5.0%	SPVQVILLR	99.7%	65.1	25	59	2	0	0	1024.65	210	218
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	5	6	15	0.02%	22.7%	ALLANALTSALR	99.7%	112	25	105	4	0	0	1213.73	58	69
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	5	6	15	0.02%	22.7%	GSNSLPLLR	99.7%	39.8	25	27.8	2	0	0	956.55	135	143
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	5	6	15	0.02%	22.7%	LCLQSIAFISR	99.7%	69.1	25	61.4	2	0	0	1307.71	231	241
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	5	6	15	0.02%	22.7%	LDTAMWLSR	99.7%	65.2	25	50.1	3	0	0	1092.55	23	31
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	5	6	15	0.02%	22.7%	SVLDKLSANQQNILK	99.7%	77.3	25	73.1	2	2	0	1670.94	144	158
Transmembrane protein 97	TMEM97	TMM97_HUMAN	20.8	99.8%	2	2	3	0.00%	13.1%	EFKDPLLQEPPAWFK	99.7%	46.3	25	44.4	1	0	0	1844.96	53	67
Transmembrane protein 97	TMEM97	TMM97_HUMAN	20.8	99.8%	2	2	3	0.00%	13.1%	ELYPVEFR	99.7%	39.7	25	28.4	2	0	0	1052.54	37	44
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	23	0.02%	15.3%	ALVMLLEVR	99.7%	66.2	25	59.9	4	0	0	1059.62	246	254
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	23	0.02%	15.3%	ATVGILITTIASK	99.7%	115	25	115	2	0	0	1287.79	116	128
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	23	0.02%	15.3%	DNEEKDSAFR	98.5%	32.4	25	27.5	1	0	0	1210.53	814	823
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	23	0.02%	15.3%	ESQSPDTTIQR	99.7%	51.6	25	44.3	2	0	0	1261.60	29	39
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	23	0.02%	15.3%	FSDQFPLPLK	99.7%	47.6	25	47.6	1	0	0	1191.64	880	889
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	23	0.02%	15.3%	GELQNWPDLLPK	99.7%	49.7	25	39	2	0	0	1409.74	129	140
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	23	0.02%	15.3%	QSSFALLGDLTK	99.7%	78.4	25	70.4	2	0	0	1279.69	693	704
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	23	0.02%	15.3%	SECLNNIGDSSPLIR	99.7%	86.1	25	86.1	2	0	0	1674.81	101	115
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	23	0.02%	15.3%	SITCWTLSR	99.7%	39.9	25	10.5	2	0	0	1123.56	464	472
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	23	0.02%	15.3%	SNILTLMYQCMQDK	99.7%	107	25	100	1	0	0	1744.81	674	687
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	23	0.02%	15.3%	TLLENTAITIGR	99.7%	73.1	25	63.1	2	0	0	1301.74	774	785
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	23	0.02%	15.3%	YSDIDIILLK	99.7%	60.5	25	57.8	2	0	0	1192.68	318	327
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	17	0.02%	13.4%	ASFWLGELQR	99.7%	52.5	25	37.8	2	0	0	1206.63	30	39
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	17	0.02%	13.4%	ETTVGAVTVTHK	99.7%	55.5	25	45.6	2	0	0	1242.67	882	893
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	17	0.02%	13.4%	GTALVLAR	99.7%	56.8	25	31.1	2	0	0	800.50	564	571
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	17	0.02%	13.4%	IFTELCETFLEK	99.7%	65.1	25	55	1	0	0	1529.76	298	309
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	17	0.02%	13.4%	IVCTPGQGLGDLR	99.7%	63.3	25	59.4	2	0	0	1385.72	310	322
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	17	0.02%	13.4%	LGEHLYK	99.1%	35	25	19.4	1	0	0	859.47	349	355
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	17	0.02%	13.4%	SLDSFLLSPEAAVGLLK	99.7%	78.7	25	78.5	2	0	0	1759.98	547	563
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	17	0.02%	13.4%	SVDPENNPTLVEVLEGVVR	99.7%	79.4	25	79	2	0	0	2066.08	450	468

Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	17	0.02%	13.4%	TNDEVIHGIFK	98.9%	33.8	25	12.6	1	0	0	1272.66	356	366
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	17	0.02%	13.4%	VIQEIWPVLSETLNK	99.3%	35.8	25	35	2	0	0	1768.98	637	651
Treacle protein	TCOF1	TCOF_HUMAN	152.1	100.0%	2	2	3	0.00%	1.7%	GSLGQGTAPVLPGK	99.6%	39	25	37.3	2	0	0	1281.72	733	746
Treacle protein	TCOF1	TCOF_HUMAN	152.1	100.0%	2	2	3	0.00%	1.7%	KAEEDAALQAK	95.3%	27.9	25	15.5	1	0	0	1173.61	64	74
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	9	12	21	0.02%	28.9%	FFVMTSLR	99.7%	55.4	25	29.8	4	0	0	1000.53	199	206
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	9	12	21	0.02%	28.9%	FGMFEFLSNHMR	99.7%	45.5	25	39.2	1	1	0	1531.68	102	113
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	9	12	21	0.02%	28.9%	FIHDQTSPNPK	99.7%	46.6	25	35.8	2	2	0	1283.64	150	160
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	9	12	21	0.02%	28.9%	GFFHGVR	95.5%	28.1	25	21.3	1	0	0	819.43	163	169
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	9	12	21	0.02%	28.9%	GLSSLLYGSIPK	99.7%	74.4	25	59.1	2	0	0	1234.70	86	97
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	9	12	21	0.02%	28.9%	GTYQGLTATVLK	99.7%	64.3	25	56.7	2	0	0	1251.69	179	190
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	9	12	21	0.02%	28.9%	NTWDCGLQILK	99.7%	61.4	25	51.5	2	0	0	1347.67	258	268
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	9	12	21	0.02%	28.9%	SHGVLGLYR	98.9%	33.7	25	33.7	2	0	0	1001.55	77	85
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	9	12	21	0.02%	28.9%	TQLQLDER	99.7%	53.6	25	34.7	2	0	0	1002.52	51	58
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	32	61	0.06%	42.7%	ADMVIEAVFEDLSLK	99.7%	103	25	102	2	0	0	1679.86	441	455
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	32	61	0.06%	42.7%	ALMGLYHGQVLCK	99.7%	58.9	25	58.9	2	0	0	1489.77	338	350
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	32	61	0.06%	42.7%	ALTSFER	99.7%	39.6	25	17.9	2	0	0	823.43	416	422
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	32	61	0.06%	42.7%	DATLTALDR	99.7%	92.2	25	53.4	2	0	0	975.51	391	399
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	32	61	0.06%	42.7%	DGPGFYTTR	99.7%	44.1	25	38.2	1	0	0	1013.47	541	549
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	32	61	0.06%	42.7%	DLNSDMDSILASLK	99.7%	102	25	101	1	0	0	1521.75	647	660
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	32	61	0.06%	42.7%	DSIFSNLTGQLDYQGFEK	99.7%	97.6	25	97.6	2	0	0	2061.98	423	440
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	32	61	0.06%	42.7%	DTSASAVAVGLK	99.7%	74.2	25	59.2	2	0	0	1118.61	520	531
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	32	61	0.06%	42.7%	EVEAVIPDHCIFASNTSALPISEIAAVSK	99.7%	46.4	25	46.4	0	2	0	3068.56	461	489
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	32	61	0.06%	42.7%	FGELVMTK	99.7%	51.3	25	33.3	2	0	0	940.48	327	334
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	32	61	0.06%	42.7%	FGGGNPELLTQMVSK	99.7%	90.9	25	87.7	4	0	0	1577.80	611	625
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	32	61	0.06%	42.7%	FVDLYGAQK	99.0%	34.4	25	30	1	0	0	1040.54	720	728
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	32	61	0.06%	42.7%	GFYIYQEGVK	99.7%	71.1	25	65.8	2	0	0	1203.60	635	644
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	32	61	0.06%	42.7%	KALTSFER	98.4%	32.3	25	24	2	0	0	951.53	415	422
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	32	61	0.06%	42.7%	LTAYAMTIPFVR	99.7%	60.7	25	59.3	6	0	0	1382.75	268	279
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	32	61	0.06%	42.7%	MGLVDQLVEPLGPGLKPPEER	99.7%	61.9	25	61.3	0	4	0	2290.21	215	235
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	32	61	0.06%	42.7%	MQLLEIITTEK	99.7%	78.9	25	66.6	5	0	0	1318.73	506	516
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	32	61	0.06%	42.7%	MVGVPAALDMMLTGR	99.7%	102	25	102	2	0	0	1561.79	191	205
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	32	61	0.06%	42.7%	SEVSSDEDIQFR	99.7%	78.8	25	76.4	2	0	0	1411.63	665	676
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	32	61	0.06%	42.7%	TGIEQGSDAGYLCESQK	99.7%	97.4	25	93.8	2	0	0	1842.82	310	326
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	32	61	0.06%	42.7%	THINYGVK	96.8%	29.4	25	22.3	1	0	0	931.50	39	46
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	32	61	0.06%	42.7%	TIEYLEEVAITFAK	99.7%	84.3	25	84.3	2	0	0	1626.86	236	249
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	32	61	0.06%	42.7%	TLQEVTQLSQEAQR	99.7%	101	25	91.7	2	2	0	1630.84	112	125
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	32	61	0.06%	42.7%	TVLGTPEVLLGALPGAGGTQR	99.7%	89.4	25	89.4	2	2	0	2007.12	167	187
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	25	32	61	0.06%	42.7%	VIGMHYFSPVDK	99.7%	41.4	25	33.1	2	0	0	1392.70	494	505
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	43.2%	AALTGLLHR	99.7%	50.6	25	39.9	2	0	0	951.57	82	90
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	43.2%	ALAMGYKPK	98.2%	31.8	25	26.1	1	0	0	994.54	326	334
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	43.2%	AMDSDWFAENYMGR	99.7%	62	25	62	1	0	0	1692.68	392	405
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	43.2%	DFMYVSQDPKDQLLLGPTYATPK	99.7%	33	25	30.1	0	1	0	2627.31	339	361
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	43.2%	DLMPHDLAR	96.2%	28.7	25	23.5	2	0	0	1083.53	73	81
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	43.2%	DNGIRPSSLEQMAK	99.7%	58.5	25	47.5	2	0	0	1545.77	278	291
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	43.2%	DQLLLGPTYATPK	99.7%	53.7	25	53.5	2	0	0	1416.77	349	361
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	43.2%	EAALGAGFSDK	99.7%	61	25	55.1	2	0	0	1065.52	118	128
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	43.2%	EGGQYGLVAACAAGGQGHAMIVEAYPK	99.7%	74.2	25	74.2	0	2	0	2705.28	448	474
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	43.2%	EVVDYIIFGTVIQEVK	99.7%	96.4	25	93.1	3	1	0	1852.01	96	111
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	43.2%	FNNWGGSLSLGHPFGATGCR	99.7%	59.6	25	56.6	0	2	0	2134.99	417	436
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	43.2%	KLMLDLNK	99.7%	41.1	25	11.1	2	0	0	990.57	181	188
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	43.2%	LAAAFAVSR	99.7%	75.1	25	61.4	3	0	0	905.52	230	238

Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	43.2%	LMLDLNK	97.4%	30.3	25	18.2	1	0	0	862.47	182	188
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	43.2%	LVMAAANR	99.7%	54.7	25.1	45.6	2	0	0	845.47	437	444
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	43.2%	NVVVVDGVR	99.7%	52.3	25	44.8	2	0	0	956.55	53	61
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	43.2%	TPFLLSGTSYK	99.7%	53.8	25	48.7	2	0	0	1213.65	62	72
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	43.2%	TPFLLSGTSYKDLMPHDLAR	99.7%	46.4	25	46.4	0	3	0	2262.16	62	81
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	43.2%	VGLPPLEK	99.6%	39	25	35	2	0	0	852.52	409	416
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	22	28	64	0.07%	28.2%	AAGFKDPLLASGTDGVGTK	99.7%	88.9	25	84.4	1	0	0	1804.94	481	499
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	22	28	64	0.07%	28.2%	AFAHITGGGLLENIPR	99.7%	106	25	98.7	2	2	0	1665.91	677	692
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	22	28	64	0.07%	28.2%	AIAFLQQPR	99.7%	51	25	31.8	4	0	0	1043.60	425	433
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	22	28	64	0.07%	28.2%	AVQEIMQEK	99.1%	34.5	25	31.4	3	0	0	1091.54	170	178
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	22	28	64	0.07%	28.2%	ENLISALEEAKK	99.7%	75.1	25	57.5	3	0	0	1344.74	394	405
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	22	28	64	0.07%	28.2%	EQTEQILR	98.7%	33	25	23	1	0	0	1016.54	744	751
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	22	28	64	0.07%	28.2%	ESGVDIAAGNMLVK	99.7%	91.3	25	87.7	4	0	0	1403.72	439	452
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	22	28	64	0.07%	28.2%	FGDPECQVILPLLK	99.7%	72	25	64.2	4	0	0	1628.87	293	306
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	22	28	64	0.07%	28.2%	GDTVATLSER	99.7%	44.5	25	19.3	2	0	0	1048.53	966	975
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	22	28	64	0.07%	28.2%	IKDTVLQR	99.7%	46.2	25	15.8	3	0	0	972.58	250	257
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	22	28	64	0.07%	28.2%	ILSGPFVQK	99.7%	45.3	25	9.82	2	0	0	988.58	898	906
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	22	28	64	0.07%	28.2%	ISNTAISISDHTALAQFCK	99.7%	52.6	25	52.6	0	3	0	2077.04	45	63
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	22	28	64	0.07%	28.2%	ITEGDVVVGIASSGLHSNGFSLVR	99.7%	48.3	25	48.3	0	1	0	2414.27	605	628
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	22	28	64	0.07%	28.2%	IYSHSLLPVLR	99.7%	47.1	25	40.7	2	2	0	1297.76	661	671
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	22	28	64	0.07%	28.2%	LGVDLDAQTWR	99.5%	37.7	25	32.3	1	0	0	1273.65	698	708
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	22	28	64	0.07%	28.2%	MLNIHPSLLPSFK	99.7%	51.3	25	41.5	4	2	0	1496.83	911	923
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	22	28	64	0.07%	28.2%	QVLVAPGNAGTACSEK	99.7%	78.8	25	78.7	2	0	0	1601.80	29	44
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	22	28	64	0.07%	28.2%	SAGVQCFGPTAEAAQLESSKR	99.7%	32.7	25	32.7	0	2	0	2194.06	88	108
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	22	28	64	0.07%	28.2%	TFNCGVGAVLVVSK	99.7%	90.7	25	90.7	3	0	0	1450.77	730	743
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	22	28	64	0.07%	28.2%	VDLGGFAGLFDLK	99.7%	102	25	102	4	0	0	1351.73	468	480
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	22	28	64	0.07%	28.2%	VLAVTAIR	99.7%	58.3	25	28.6	4	0	0	842.55	386	393
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	22	28	64	0.07%	28.2%	VLEFNCR	99.7%	42.4	25	36.4	3	0	0	937.46	286	292
Triosephosphate isomerase	TPI1	TPIS_HUMAN	30.8	99.8%	2	2	3	0.00%	9.8%	TATPQQAQEVHEK	99.7%	60.4	25	59	1	0	0	1466.72	213	225
Triosephosphate isomerase	TPI1	TPIS_HUMAN	30.8	99.8%	2	2	3	0.00%	9.8%	VVLAYEPVWAIGTGK	99.7%	61.9	25	58.1	2	0	0	1602.89	198	212
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	13	14	30	0.03%	21.1%	FYALDPSFPR	99.7%	44.3	25	40.5	2	0	0	1212.60	536	545
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	13	14	30	0.03%	21.1%	GAEQLAEGGR	99.7%	83.7	25	72.1	2	0	0	987.49	306	315
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	13	14	30	0.03%	21.1%	IITVSMEDVK	99.7%	59.8	25	51.4	4	0	0	1134.61	619	628
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	13	14	30	0.03%	21.1%	ILCDVPCSGDGTMR	99.7%	59.8	25	54.5	1	0	0	1580.69	265	278
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	13	14	30	0.03%	21.1%	ILLTQENPFFR	99.7%	79.2	25	78.1	4	0	0	1377.75	629	639
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	13	14	30	0.03%	21.1%	KLSSETYSQAK	99.7%	60.8	25	59.2	2	0	0	1241.64	640	650
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	13	14	30	0.03%	21.1%	LAQEGIYTLYPFINSR	99.7%	84.1	25	84.1	3	0	0	1884.99	603	618
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	13	14	30	0.03%	21.1%	LQQQQRPEDAEDGAEGGGK	99.7%	35.6	25	35.6	0	1	0	2012.93	10	28
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	13	14	30	0.03%	21.1%	LSSETYSQAK	99.7%	58.1	25	49.3	2	0	0	1113.54	641	650
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	13	14	30	0.03%	21.1%	MMGLEVLGEK	99.7%	39.6	25	32.5	2	0	0	1106.56	701	710
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	13	14	30	0.03%	21.1%	NNSGEEFDCAFR	99.7%	76.9	25	76.9	2	0	0	1445.58	591	602
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	13	14	30	0.03%	21.1%	SEGALELADVSNELPGLK	99.7%	93.2	25	88.9	4	0	0	1841.95	339	356
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	13	14	30	0.03%	21.1%	YEPDSANPDALQCPIVLCGWR	99.7%	60.3	25	60.3	1	0	0	2461.13	661	681
tRNA pseudouridine synthase A, mitochondrial	PUS1	TRUA_HUMAN	47.5	100.0%	3	3	6	0.01%	7.7%	APGLGLVLER	97.2%	29.9	25	29.9	1	0	0	1024.62	328	337
tRNA pseudouridine synthase A, mitochondrial	PUS1	TRUA_HUMAN	47.5	100.0%	3	3	6	0.01%	7.7%	LSAETLQQVNR	99.7%	52.3	25	43.5	2	0	0	1258.68	224	234
tRNA pseudouridine synthase A, mitochondrial	PUS1	TRUA_HUMAN	47.5	100.0%	3	3	6	0.01%	7.7%	TIEDDLVSALVR	99.7%	75.3	25	69.2	3	0	0	1330.72	111	122
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	6	7	11	0.01%	15.0%	GGGVGGFLPAMK	99.7%	42.7	25	31.5	2	0	0	1090.57	56	67
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	6	7	11	0.01%	15.0%	GQVCVMIHSGSR	99.7%	70.6	25	70.6	2	0	0	1330.64	252	263
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	6	7	11	0.01%	15.0%	LMFEELR	99.7%	41.5	25	31.3	2	0	0	937.48	45	51
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	6	7	11	0.01%	15.0%	LVMEEAPESYK	99.7%	51.9	25	46	2	0	0	1311.61	466	476
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	6	7	11	0.01%	15.0%	SYNDELQFLEK	99.7%	60.7	25	32.2	2	0	0	1385.66	4	14

tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	6	7	11	0.01%	15.0%	VFNTTPDDLDLHVIYDVSHNIAK	99.7%	39.6	25	36	0	1	0	2626.32	335	357
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	68.5%	AFVHWYVGEGMEEGEFSEAR	99.7%	85.4	25	85.4	2	4	0	2330.02	403	422
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	68.5%	AFVHWYVGEGMEEGEFSEAREDMAALEK	99.7%	63	25	63	0	4	0	3217.42	403	430
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	68.5%	AVCMLSNTTAIAEAWAR	99.7%	117	25	109	25	8	0	1880.90	374	390
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	68.5%	AVFVDLEPTVIDEVR	99.7%	111	25	108	39	7	0	1701.91	65	79
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	68.5%	AYHEQLSVAEITNACFEPANQMVK	99.7%	104	25	104	2	9	0	2750.29	281	304
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	68.5%	DVNAAIATIK	99.7%	78.4	25	61.2	18	0	0	1015.58	327	336
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	68.5%	EDMAALEK	99.2%	35.5	25	20.4	3	0	0	906.42	423	430
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	68.5%	EIIDLVLDR	99.7%	79.7	25	76.1	35	0	0	1085.62	113	121
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	68.5%	EIIDLVLDRIR	98.4%	32.1	25	23.6	2	0	0	1354.81	113	123
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	68.5%	FDGALNVDLTEFQTNLVPYPR	99.7%	124	25	124	10	2	0	2409.21	244	264
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	68.5%	FDLMYAK	99.7%	45.8	25	32.1	6	0	0	887.43	395	401
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	68.5%	GDVVPKDVNAAIATIK	97.3%	30.1	25	30.1	1	0	0	1610.91	321	336
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	68.5%	IHFPLATYAPVISAEK	99.7%	75.7	25	68.1	7	10	0	1756.96	265	280
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	68.5%	LADQCTGLQGFLVFHSFGGGTGSGFTSLLMER	99.7%	115	25	115	0	21	0	3390.63	125	156
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	68.5%	LDHKFDLMYAK	99.7%	49.9	25	32	8	9	0	1380.70	391	401
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	68.5%	LIGQIVSSITASLR	99.7%	99.1	25	98.4	2	0	0	1457.87	230	243
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	68.5%	LSVDYGKK	99.7%	54.9	25	42.5	10	0	0	909.50	157	164
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	68.5%	NLDIERPTYTNLNR	99.7%	76.3	25	66.1	9	10	0	1718.88	216	229
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	68.5%	QLFHPEQLITGK	99.7%	38.9	25	0	3	2	0	1410.77	85	96
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	68.5%	QLFHPEQLITGKEDAANNYAR	99.7%	85.4	25	83.9	2	6	0	2415.21	85	105
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	68.5%	RNLDIERPTYTNLNR	98.3%	26.2	25	22.4	0	4	0	1874.98	215	229
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	68.5%	TIGGGDDSFNTFFSETGAGK	99.7%	104	25	104	26	0	0	2007.89	41	60
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	68.5%	TIQFVDWCPTGFK	99.7%	74	25	65.6	17	0	0	1598.77	340	352
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	68.5%	VGINYQPPTVVPGGDLAK	99.7%	65.5	25	65.5	22	0	0	1824.99	353	370
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	19	0.02%	68.5%	YMACCLLYR	99.7%	53.7	25	51.3	24	0	0	1249.55	312	320
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	26	47	389	0.40%	68.7%	AFVHWYVGEGMEEGEFSEAR	99.7%	85.4	25	85.4	2	4	0	2330.02	403	422
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	26	47	389	0.40%	68.7%	AFVHWYVGEGMEEGEFSEAREDMAALEK	99.7%	63	25	63	0	4	0	3217.42	403	430
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	26	47	389	0.40%	68.7%	AVCMLSNTTAIAEAWAR	99.7%	117	25	109	25	8	0	1880.90	374	390
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	26	47	389	0.40%	68.7%	AVFVDLEPTVIDEVR	99.7%	111	25	108	39	7	0	1701.91	65	79
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	26	47	389	0.40%	68.7%	AYHEQLSVAEITNACFEPANQMVK	99.7%	104	25	104	2	9	0	2750.29	281	304
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	26	47	389	0.40%	68.7%	DVNAAIATIK	99.7%	78.4	25	61.2	18	0	0	1015.58	327	336
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	26	47	389	0.40%	68.7%	EDMAALEK	99.2%	35.5	25	20.4	3	0	0	906.42	423	430
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	26	47	389	0.40%	68.7%	EIIDLVLDR	99.7%	79.7	25	76.1	35	0	0	1085.62	113	121
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	26	47	389	0.40%	68.7%	EIIDLVLDRIR	98.4%	32.1	25	23.6	2	0	0	1354.81	113	123
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	26	47	389	0.40%	68.7%	FDGALNVDLTEFQTNLVPYPR	99.7%	124	25	124	10	2	0	2409.21	244	264
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	26	47	389	0.40%	68.7%	FDLMYAK	99.7%	45.8	25	32.1	6	0	0	887.43	395	401
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	26	47	389	0.40%	68.7%	GDVVPKDVNAAIATIK	97.3%	30.1	25	30.1	1	0	0	1610.91	321	336
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	26	47	389	0.40%	68.7%	IHFPLATYAPVISAEK	99.7%	75.7	25	68.1	7	10	0	1756.96	265	280
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	26	47	389	0.40%	68.7%	LADQCTGLQGFLVFHSFGGGTGSGFTSLLMER	99.7%	115	25	115	0	21	0	3390.63	125	156
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	26	47	389	0.40%	68.7%	LDHKFDLMYAK	99.7%	49.9	25	32	8	9	0	1380.70	391	401
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	26	47	389	0.40%	68.7%	LISQIVSSITASLR	99.7%	111	25	111	13	3	0	1487.88	230	243
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	26	47	389	0.40%	68.7%	LSVDYGKK	99.7%	54.9	25	42.5	10	0	0	909.50	157	164
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	26	47	389	0.40%	68.7%	NLDIERPTYTNLNR	99.7%	76.3	25	66.1	9	10	0	1718.88	216	229
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	26	47	389	0.40%	68.7%	QLFHPEQLITGK	99.7%	38.9	25	0	3	2	0	1410.77	85	96
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	26	47	389	0.40%	68.7%	QLFHPEQLITGKEDAANNYAR	99.7%	85.4	25	83.9	2	6	0	2415.21	85	105
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	26	47	389	0.40%	68.7%	RNLDIERPTYTNLNR	98.3%	26.2	25	22.4	0	4	0	1874.98	215	229
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	26	47	389	0.40%	68.7%	RSIQFVDWCPTGFK	98.7%	27.4	25	27.4	0	1	0	1740.85	339	352
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	26	47	389	0.40%	68.7%	SIQFVDWCPTGFK	99.7%	91.8	25	83.8	22	0	0	1584.75	340	352
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	26	47	389	0.40%	68.7%	TIGGGDDSFNTFFSETGAGK	99.7%	104	25	104	26	0	0	2007.89	41	60
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	26	47	389	0.40%	68.7%	VGINYQPPTVVPGGDLAK	99.7%	65.5	25	65.5	22	0	0	1824.99	353	370

Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	26	47	389	0.40%	68.7%	YMACCLLYR	99.7%	53.7	25	51.3	24	0	0	1249.55	312	320
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	6	11	0.01%	68.8%	AFVHWYVGEGMEEGEFSEAR	99.7%	85.4	25	85.4	2	4	0	2330.02	403	422
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	6	11	0.01%	68.8%	AFVHWYVGEGMEEGEFSEAREDMAALEK	99.7%	63	25	63	0	4	0	3217.42	403	430
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	6	11	0.01%	68.8%	AVCMLSNTTAVAEAWAR	99.7%	110	25	109	3	4	0	1850.89	374	390
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	6	11	0.01%	68.8%	AVFVDLEPTVIDEVR	99.7%	111	25	108	39	7	0	1701.91	65	79
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	6	11	0.01%	68.8%	AYHEQLTVAEITNACFEPANQMVK	96.1%	23.2	25	23.2	0	4	0	2764.31	281	304
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	6	11	0.01%	68.8%	DVNAAIATIK	99.7%	78.4	25	61.2	18	0	0	1015.58	327	336
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	6	11	0.01%	68.8%	EDMAALEK	99.2%	35.5	25	20.4	3	0	0	906.42	423	430
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	6	11	0.01%	68.8%	EIIDLVLDR	99.7%	79.7	25	76.1	35	0	0	1085.62	113	121
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	6	11	0.01%	68.8%	EIIDLVLDRIR	98.4%	32.1	25	23.6	2	0	0	1354.81	113	123
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	6	11	0.01%	68.8%	FDGALNVDLTEFQTNLVPYPR	99.7%	124	25	124	10	2	0	2409.21	244	264
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	6	11	0.01%	68.8%	FDLMYAK	99.7%	45.8	25	32.1	6	0	0	887.43	395	401
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	6	11	0.01%	68.8%	GDVVPKDVNAAIATIK	97.3%	30.1	25	30.1	1	0	0	1610.91	321	336
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	6	11	0.01%	68.8%	IHFPLATYAPVISAEK	99.7%	75.7	25	68.1	7	10	0	1756.96	265	280
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	6	11	0.01%	68.8%	LADQCTGLQGFLVFHSFGGGTGSGFTSLLMER	99.7%	115	25	115	0	21	0	3390.63	125	156
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	6	11	0.01%	68.8%	LDHKFDLMYAK	99.7%	49.9	25	32	8	9	0	1380.70	391	401
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	6	11	0.01%	68.8%	LISQIVSSITASLR	99.7%	111	25	111	13	3	0	1487.88	230	243
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	6	11	0.01%	68.8%	LSVDYGKK	99.7%	54.9	25	42.5	10	0	0	909.50	157	164
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	6	11	0.01%	68.8%	NLDIERPTYTNLNR	99.7%	76.3	25	66.1	9	10	0	1718.88	216	229
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	6	11	0.01%	68.8%	QLFHPEQLITGK	99.7%	38.9	25	0	3	2	0	1410.77	85	96
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	6	11	0.01%	68.8%	QLFHPEQLITGKEDAANNYAR	99.7%	85.4	25	83.9	2	6	0	2415.21	85	105
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	6	11	0.01%	68.8%	RNLDIERPTYTNLNR	98.3%	26.2	25	22.4	0	4	0	1874.98	215	229
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	6	11	0.01%	68.8%	TIGGGDDSFNTFFSETGAGK	99.7%	104	25	104	26	0	0	2007.89	41	60
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	6	11	0.01%	68.8%	TIQFVDWCPTGFK	99.7%	74	25	65.6	17	0	0	1598.77	340	352
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	6	11	0.01%	68.8%	VGINYQPPTVVPGGDLAK	99.7%	65.5	25	65.5	22	0	0	1824.99	353	370
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	6	11	0.01%	68.8%	YMACCLLYR	99.7%	53.7	25	51.3	24	0	0	1249.55	312	320
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	AILVDLEPGTMDSVR	99.7%	103	25	96.4	37	0	0	1631.83	63	77
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	ALTVPELTQQVFDAK	99.7%	76.8	25	76.8	18	4	0	1659.90	283	297
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	97.7	25	0	0	8	0	3311.53	123	154
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	EIVHIQAGQCGNQIGAK	99.7%	89.8	25	0	5	4	0	1822.92	3	19
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	EVDEQMLNVQNK	99.7%	89.8	25	77.8	20	0	0	1446.69	325	336
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	FPGQLNADLR	99.7%	67.6	25	55.7	14	0	0	1130.60	242	251
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	FPGQLNADLRK	99.7%	41.5	25	33.3	7	4	0	1258.69	242	252
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	FWEVISDEHGIDPTGTYHGDSDLQLDR	99.7%	89.2	25	43.1	0	4	0	3102.41	20	46
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	GHYTEGAELVDSVLDVVR	99.7%	141	25	135	4	7	0	1958.98	104	121
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	GHYTEGAELVDSVLDVVRK	99.7%	118	25	104	2	4	0	2087.08	104	122
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	IMNTFSVVPSPK	99.7%	98.6	25	89.5	28	0	0	1319.70	163	174
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	IREEYPDR	98.6%	32.9	25	21.2	3	0	0	1077.53	155	162
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	ISEQFTAMFR	99.7%	81	25	72.3	24	0	0	1229.60	381	390
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	ISVYYNEATGGK	99.7%	79.1	25	78.1	26	0	0	1301.64	47	58
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	KEAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	87.4	25	0	0	2	0	3439.63	122	154
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	KLAVNMVPFPR	99.7%	62.8	25	61.8	6	1	0	1271.73	252	262
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	LAVNMVPFPR	99.7%	84.3	25	72.7	27	0	0	1143.63	253	262
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	LHFFMPGFAPLTSR	99.7%	60	25	48.5	17	18	0	1620.84	263	276
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	LTTPTYGDLNHLVSATMSGVTTCLR	99.7%	97.5	25	97.5	4	12	0	2708.34	217	241
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	MAVTFIGNSTAIQELFK	99.7%	136	25	133	17	3	0	1885.97	363	379
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	MAVTFIGNSTAIQELFKR	99.7%	121	25	121	6	12	0	2026.08	363	380
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	MREIVHIQAGQCGNQIGAK	99.7%	75.5	25	0	0	8	0	2110.06	1	19
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	MSMKEVDEQMLNVQNK	99.7%	76.4	25	76.4	12	22	0	1923.90	321	336
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	NMMAACDPR	99.7%	57.1	25	57.1	17	0	0	1065.43	298	306
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	NSSYFVEWIPNNVK	99.7%	82.8	25	71.4	16	0	0	1696.83	337	350

Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	RISEQFTAMFR	99.7%	61.3	25	57.3	2	1	0	1385.70	380	390
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	SGPFGQIFRPDNFVFGQSGAGNNWAK	99.7%	99.1	25	99.1	2	7	0	2798.34	78	103
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	TAVCDIPPR	99.7%	58.8	25	39.8	35	0	0	1028.52	351	359
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	97.8%	25.2	25	25.2	0	2	0	4593.11	175	213
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	61	480	0.50%	83.1%	YLTVAAVFR	99.7%	83.8	25	75.4	8	0	0	1039.59	310	318
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	AILVDLEPGTMDSVR	99.7%	103	25	96.4	37	0	0	1631.83	63	77
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	ALTVPELTQQMFDSK	99.7%	87.4	25	37.7	7	0	0	1707.86	283	297
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	EIVHIQAGQCGNQIGAK	99.7%	89.8	25	0	5	4	0	1822.92	3	19
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	ESESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	67	25	67	0	1	0	3343.52	123	154
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	EVDEQMLNVQNK	99.7%	89.8	25	77.8	20	0	0	1446.69	325	336
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	FPGQLNADLR	99.7%	67.6	25	55.7	14	0	0	1130.60	242	251
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	FPGQLNADLRK	99.7%	41.5	25	33.3	7	4	0	1258.69	242	252
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	GHYTEGAELVDSVLDVVR	99.7%	141	25	135	4	7	0	1958.98	104	121
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	GHYTEGAELVDSVLDVVRK	99.7%	118	25	104	2	4	0	2087.08	104	122
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	IMNTFSVMPSPK	99.7%	94.8	25	84.9	10	0	0	1351.67	163	174
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	INVYYNEATGNK	99.7%	80.1	25	75.6	4	0	0	1385.67	47	58
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	IREEYPDR	98.6%	32.9	25	21.2	3	0	0	1077.53	155	162
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	ISEQFTAMFR	99.7%	81	25	72.3	24	0	0	1229.60	381	390
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	KLAVNMVPFPR	99.7%	62.8	25	61.8	6	1	0	1271.73	252	262
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	LAVNMVPFPR	99.7%	84.3	25	72.7	27	0	0	1143.63	253	262
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	LHFFMPGFAPLTSR	99.7%	60	25	48.5	17	18	0	1620.84	263	276
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	LTTPTYGDLNHLVSATMSGVTTCLR	99.7%	97.5	25	97.5	4	12	0	2708.34	217	241
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	MREIVHIQAGQCGNQIGAK	99.7%	75.5	25	0	0	8	0	2110.06	1	19
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	MSATFIGNSTAIQELFK	99.7%	133	25	0	8	0	0	1873.94	363	379
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	MSATFIGNSTAIQELFKR	99.7%	88.1	25	0	3	9	0	2014.04	363	380
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	MSMKEVDEQMLNVQNK	99.7%	76.4	25	76.4	12	22	0	1923.90	321	336
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	NMMAACDPR	99.7%	57.1	25	57.1	17	0	0	1065.43	298	306
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	NSSYFVEWIPNNVK	99.7%	82.8	25	71.4	16	0	0	1696.83	337	350
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	RISEQFTAMFR	99.7%	61.3	25	57.3	2	1	0	1385.70	380	390
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	SGPFGQIFRPDNFVFGQSGAGNNWAK	99.7%	99.1	25	99.1	2	7	0	2798.34	78	103
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	TAVCDIPPR	99.7%	58.8	25	39.8	35	0	0	1028.52	351	359
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	97.8%	25.2	25	25.2	0	2	0	4593.11	175	213
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	28	0.03%	76.9%	YLTVAAIFR	99.7%	80.6	25	68.6	6	0	0	1053.61	310	318
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	13	0.01%	77.7%	ALTVPELTQQMFDAK	99.7%	88.8	25	87	14	1	0	1691.87	283	297
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	13	0.01%	77.7%	AVLVDLEPGTMDSVR	99.7%	105	25	83.9	19	0	0	1601.82	63	77
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	13	0.01%	77.7%	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	97.7	25	0	0	8	0	3311.53	123	154
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	13	0.01%	77.7%	EIVHLQAGQCGNQIGAK	99.7%	89.8	25	0	5	4	0	1822.92	3	19
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	13	0.01%	77.7%	EVDEQMLSVQSK	99.7%	48.7	25	42	1	0	0	1392.67	325	336
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	13	0.01%	77.7%	FPGQLNADLR	99.7%	67.6	25	55.7	14	0	0	1130.60	242	251
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	13	0.01%	77.7%	FPGQLNADLRK	99.7%	41.5	25	33.3	7	4	0	1258.69	242	252
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	13	0.01%	77.7%	FWEVISDEHGIDPTGTYHGDSDLQLER	99.7%	74.9	25	74.9	0	2	0	3116.42	20	46
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	13	0.01%	77.7%	GHYTEGAELVDAVLDVVR	99.7%	56.4	25	53.8	0	2	0	1942.99	104	121
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	13	0.01%	77.7%	IMNTFSVVPSPK	99.7%	98.6	25	89.5	28	0	0	1319.70	163	174
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	13	0.01%	77.7%	ISEQFTAMFR	99.7%	81	25	72.3	24	0	0	1229.60	381	390
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	13	0.01%	77.7%	KEAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	87.4	25	0	0	2	0	3439.63	122	154
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	13	0.01%	77.7%	KLAVNMVPFPR	99.7%	62.8	25	61.8	6	1	0	1271.73	252	262
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	13	0.01%	77.7%	LAVNMVPFPR	99.7%	84.3	25	72.7	27	0	0	1143.63	253	262
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	13	0.01%	77.7%	LHFFMPGFAPLTSR	99.7%	60	25	48.5	17	18	0	1620.84	263	276
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	13	0.01%	77.7%	LTTPTYGDLNHLVSATMSGVTTCLR	99.7%	97.5	25	97.5	4	12	0	2708.34	217	241
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	13	0.01%	77.7%	MAATFIGNSTAIQELFK	99.7%	94	25	2.21	6	0	0	1857.94	363	379
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	13	0.01%	77.7%	MAATFIGNSTAIQELFKR	99.7%	63	25	0.25	4	0	0	2014.04	363	380

Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	13	0.01%	77.7%	MREIVHLQAGQCGNQIGAK	99.7%	75.5	25	0	0	8	0	2110.06	1	19
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	13	0.01%	77.7%	NMMAACDPR	99.7%	57.1	25	57.1	17	0	0	1065.43	298	306
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	13	0.01%	77.7%	NSSYFVEWIPNNVK	99.7%	82.8	25	71.4	16	0	0	1696.83	337	350
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	13	0.01%	77.7%	RISEQFTAMFR	99.7%	61.3	25	57.3	2	1	0	1385.70	380	390
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	13	0.01%	77.7%	SGPFGQIFRPDNFVFGQSGAGNNWAK	99.7%	99.1	25	99.1	2	7	0	2798.34	78	103
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	13	0.01%	77.7%	TAVCDIPPR	99.7%	58.8	25	39.8	35	0	0	1028.52	351	359
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	13	0.01%	77.7%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	97.8%	25.2	25	25.2	0	2	0	4593.11	175	213
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	13	0.01%	77.7%	YLTVAAVFR	99.7%	83.8	25	75.4	8	0	0	1039.59	310	318
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	ALTVPELTQQMFDAK	99.7%	88.8	25	87	14	1	0	1691.87	283	297
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	AVLVDLEPGTMDSVR	99.7%	105	25	83.9	19	0	0	1601.82	63	77
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	97.7	25	0	0	8	0	3311.53	123	154
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	EIVHLQAGQCGNQIGAK	99.7%	89.8	25	0	5	4	0	1822.92	3	19
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	EVDEQMLNVQNK	99.7%	89.8	25	77.8	20	0	0	1446.69	325	336
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	FPGQLNADLR	99.7%	67.6	25	55.7	14	0	0	1130.60	242	251
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	FPGQLNADLRK	99.7%	41.5	25	33.3	7	4	0	1258.69	242	252
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	FWEVISDEHGIDPTGTYHGDSDLQLER	99.7%	74.9	25	74.9	0	2	0	3116.42	20	46
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	GHYTEGAELVDSVLDVVR	99.7%	141	25	135	4	7	0	1958.98	104	121
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	GHYTEGAELVDSVLDVVRK	99.7%	118	25	104	2	4	0	2087.08	104	122
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	IMNTFSVVPSPK	99.7%	98.6	25	89.5	28	0	0	1319.70	163	174
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	INVYYNEATGGK	99.7%	81.4	25	65.7	8	0	0	1328.65	47	58
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	IREEYPDR	98.6%	32.9	25	21.2	3	0	0	1077.53	155	162
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	ISEQFTAMFR	99.7%	81	25	72.3	24	0	0	1229.60	381	390
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	KEAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	87.4	25	0	0	2	0	3439.63	122	154
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	KLAVNMVPFPR	99.7%	62.8	25	61.8	6	1	0	1271.73	252	262
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	LAVNMVPFPR	99.7%	84.3	25	72.7	27	0	0	1143.63	253	262
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	LHFFMPGFAPLTSR	99.7%	60	25	48.5	17	18	0	1620.84	263	276
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	LTTPTYGDLNHLVSATMSGVTTCLR	99.7%	97.5	25	97.5	4	12	0	2708.34	217	241
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	MREIVHLQAGQCGNQIGAK	99.7%	75.5	25	0	0	8	0	2110.06	1	19
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	MSATFIGNSTAIQELFK	99.7%	133	25	0	8	0	0	1873.94	363	379
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	MSATFIGNSTAIQELFKR	99.7%	88.1	25	0	3	9	0	2014.04	363	380
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	MSMKEVDEQMLNVQNK	99.7%	76.4	25	76.4	12	22	0	1923.90	321	336
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	NMMAACDPR	99.7%	57.1	25	57.1	17	0	0	1065.43	298	306
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	NSSYFVEWIPNNVK	99.7%	82.8	25	71.4	16	0	0	1696.83	337	350
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	RISEQFTAMFR	99.7%	61.3	25	57.3	2	1	0	1385.70	380	390
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	SGPFGQIFRPDNFVFGQSGAGNNWAK	99.7%	99.1	25	99.1	2	7	0	2798.34	78	103
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	TAVCDIPPR	99.7%	58.8	25	39.8	35	0	0	1028.52	351	359
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	97.8%	25.2	25	25.2	0	2	0	4593.11	175	213
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	64	0.07%	82.9%	YLTVAAVFR	99.7%	83.8	25	75.4	8	0	0	1039.59	310	318
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	11	0.01%	44.8%	AALVDLEPGTMDSVR	99.7%	64.8	25	64.8	4	0	0	1573.79	63	77
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	11	0.01%	44.8%	ALTVPELTQQMFDAR	99.7%	59	25	59	4	0	0	1719.87	283	297
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	11	0.01%	44.8%	FPGQLNADLR	99.7%	67.6	25	55.7	14	0	0	1130.60	242	251
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	11	0.01%	44.8%	FPGQLNADLRK	99.7%	41.5	25	33.3	7	4	0	1258.69	242	252
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	11	0.01%	44.8%	GHYTEGAELVDAVLDVVR	99.7%	56.4	25	53.8	0	2	0	1942.99	104	121
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	11	0.01%	44.8%	IMNTFSVMPSPK	99.7%	94.8	25	84.9	10	0	0	1351.67	163	174
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	11	0.01%	44.8%	KLAVNMVPFPR	99.7%	62.8	25	61.8	6	1	0	1271.73	252	262
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	11	0.01%	44.8%	LAVNMVPFPR	99.7%	84.3	25	72.7	27	0	0	1143.63	253	262
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	11	0.01%	44.8%	LHFFMPGFAPLTSR	99.7%	60	25	48.5	17	18	0	1620.84	263	276
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	11	0.01%	44.8%	LTTPTYGDLNHLVSATMSGVTTSLR	97.6%	25	25	25	0	1	0	2635.34	217	241
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	11	0.01%	44.8%	MASTFIGNSTAIQELFK	99.7%	145	25	14.8	9	0	0	1873.94	363	379
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	11	0.01%	44.8%	MASTFIGNSTAIQELFKR	99.7%	69	25	0	2	0	0	2014.04	363	380
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	11	0.01%	44.8%	NMMAACDPR	99.7%	57.1	25	57.1	17	0	0	1065.43	298	306

Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	11	0.01%	44.8%	NSSYFVEWIPNNVK	99.7%	82.8	25	71.4	16	0	0	1696.83	337	350
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	11	0.01%	44.8%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	97.8%	25.2	25	25.2	0	2	0	4593.11	175	213
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	4	4	8	0.01%	10.6%	AVLLDLEPR	98.6%	32.7	25	27.5	2	0	0	1025.60	64	72
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	4	4	8	0.01%	10.6%	KTTVLDVMR	99.7%	40.5	25	28.8	2	0	0	1062.60	287	295
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	4	4	8	0.01%	10.6%	LTQNADCVVVLDNTALNR	99.7%	95.2	25	95.2	2	0	0	2016.02	195	212
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	4	4	8	0.01%	10.6%	VIHSILNSPYAK	99.7%	42.5	25	35	2	0	0	1341.75	73	84
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	11	11	20	0.02%	10.8%	AAMTSLMDLTLLLAR	99.7%	44	25	25	2	0	0	1651.88	874	888
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	11	11	20	0.02%	10.8%	AVTHTSPEDVSFAESR	99.7%	34.9	25	25.5	0	1	0	1732.81	800	815
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	11	11	20	0.02%	10.8%	DAAAVLVSR	99.7%	57.4	25	43	2	0	0	901.51	205	213
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	11	11	20	0.02%	10.8%	GACSVGTNVR	98.5%	32.4	25	23.8	2	0	0	1020.49	455	464
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	11	11	20	0.02%	10.8%	ILQIAESYLIVSDK	99.7%	90.1	25	90.1	2	0	0	1591.89	189	202
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	11	11	20	0.02%	10.8%	IMCCVAQQASEK	99.7%	43.1	25	43.1	2	0	0	1440.63	902	913
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	11	11	20	0.02%	10.8%	ITQLLGLPTYR	99.7%	50.3	25	50.3	2	0	0	1274.75	969	979
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	11	11	20	0.02%	10.8%	LDGNLLTQPGQAR	99.7%	66.9	25	60.2	2	0	0	1382.74	170	182
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	11	11	20	0.02%	10.8%	LPESNQTLLR	99.2%	35.4	25	23.1	1	0	0	1170.65	285	294
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	11	11	20	0.02%	10.8%	LQQVLTGLR	99.7%	56	25	42.8	2	0	0	1027.63	791	799
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	11	11	20	0.02%	10.8%	VIEQLLVGLK	99.7%	67.1	25	67.1	2	0	0	1111.71	361	370
Tyrosine-protein kinase CSK	CSK	CSK_HUMAN	50.7	100.0%	3	3	6	0.01%	8.4%	EASSTQDTGKLPVK	99.7%	64.4	25	48.4	2	0	0	1460.76	338	351
Tyrosine-protein kinase CSK	CSK	CSK_HUMAN	50.7	100.0%	3	3	6	0.01%	8.4%	LLYPPETGLFLVR	99.5%	37	25	34.5	2	0	0	1517.87	95	107
Tyrosine-protein kinase CSK	CSK	CSK_HUMAN	50.7	100.0%	3	3	6	0.01%	8.4%	NVLVSEDNVAK	99.7%	50.8	25	45.5	2	0	0	1187.63	319	329
Tyrosine-protein kinase JAK1	JAK1	JAK1_HUMAN	133.3	100.0%	2	2	2	0.00%	2.3%	NVLVESEHQVK	98.1%	31.6	25	31.6	1	0	0	1281.68	1008	1018
Tyrosine-protein kinase JAK1	JAK1	JAK1_HUMAN	133.3	100.0%	2	2	2	0.00%	2.3%	YDPEGDNTGEQVAVK	99.7%	53.4	25	53.4	1	0	0	1621.73	894	908
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	AFCEPGNVENNGVLSFIK	99.7%	75.3	25	67.4	2	0	0	1994.96	248	265
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	AMLESIGVPLEK	99.7%	73.5	25	64.1	4	0	0	1302.70	103	114
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	APWELLELR	99.7%	56.3	25	42	7	0	0	1126.63	85	93
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	DFAAEVVHPGDLK	99.7%	78.2	25	58.4	2	0	0	1397.71	298	310
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	EYTLDVYR	99.7%	50.3	25	42.5	2	0	0	1058.52	128	135
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	GQPDEELKPK	99.7%	39.8	25	36.6	2	0	0	1140.59	475	484
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	GTDYQLSK	99.7%	45	25	29.6	2	0	0	911.45	120	127
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	GVESQGMLLCASIEGINR	99.7%	93.2	25	90.2	3	0	0	1933.95	433	450
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	HPDADSLYVEK	99.7%	54.7	25	45.7	2	0	0	1273.61	381	391
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	HVLFPLK	99.2%	35.5	25	27.5	2	0	0	853.53	266	272
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	IDVGEAEPR	99.7%	72.3	25	57.5	4	0	0	985.50	392	400
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	IFTFAEK	94.5%	27.3	25	10.1	1	0	0	855.46	191	197
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	IITVEKHPDADSLYVEK	99.7%	36	25	34.8	0	2	0	1957.03	375	391
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	ISEECIAQWK	99.7%	75	25	71.7	2	0	0	1263.60	497	506
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	KIFTFAEK	99.6%	38.6	25	29.1	1	0	0	983.56	190	197
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	KLASAAYPDPSK	99.7%	62.5	25	57	2	0	0	1247.66	335	346
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	LASAAYPDPSK	99.7%	71	25	57.4	2	0	0	1119.57	336	346
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	LLDPIREK	99.4%	36.9	25	19.6	2	0	0	983.59	320	327
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	LSSVVTQHDSK	99.7%	62.7	25	59.8	2	0	0	1200.62	136	146
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	LSSVVTQHDSKK	99.7%	71.9	25	69.7	2	2	0	1328.72	136	147
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	LVVVLCNLKPQK	99.7%	61.5	25	61.5	2	0	0	1410.85	419	430
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	MSSSEEESKIDLLDR	99.7%	62.1	25	59.2	3	0	0	1738.82	223	237
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	NLQEVLGEEK	99.7%	63.8	25	48.2	2	0	0	1158.60	17	26
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	NSEPEEVIPSR	99.7%	74.6	25	59.3	2	0	0	1256.61	357	367
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	NSVEVALNK	99.7%	71.4	25	48.5	2	0	0	973.53	311	319
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	QVEPLDPPAGSAPGEHVFVK	99.7%	49.4	25	49.4	0	2	0	2074.06	451	470
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	SEFVILRDEK	99.7%	47.3	25	35	2	0	0	1235.66	273	282
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	TVVSGLVQFVPK	99.7%	88.7	25	76.6	2	0	0	1273.75	401	412
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	TYTAYVDLEK	99.7%	49	25	41	2	0	0	1202.59	288	297

Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	VDAQFGGIDQR	99.7%	82	25	68.9	2	0	0	1205.59	179	189
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	VSYYENVIK	99.7%	48.3	25	39.1	1	0	0	1114.58	94	102
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	32	36	73	0.08%	60.0%	YLPALGYSK	99.7%	41.1	25	26.3	1	0	0	1011.55	198	206
U1 small nuclear ribonucleoprotein A	SNRPA	SNRPA_HUMAN	31.3	99.8%	2	2	4	0.00%	6.4%	EVSSATNALR	99.7%	60.2	25	39	2	0	0	1047.54	61	70
U1 small nuclear ribonucleoprotein A	SNRPA	SNRPA_HUMAN	31.3	99.8%	2	2	4	0.00%	6.4%	GQAFVIFK	99.7%	48.2	25	39.2	2	0	0	909.52	53	60
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	4	4	8	0.01%	20.0%	GLLQSGQIPGR	99.7%	60.9	25	20.4	2	0	0	1125.64	222	232
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	4	4	8	0.01%	20.0%	KLDGFPLLR	99.7%	49.8	25	33.6	2	0	0	1058.64	56	64
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	4	4	8	0.01%	20.0%	LTAELIEQAAQYTNAVR	99.7%	85.4	25	74.5	2	0	0	1890.99	4	20
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	4	4	8	0.01%	20.0%	NAIANASTLAEVER	99.7%	112	25	106	2	0	0	1458.75	206	219
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	28	80	0.08%	46.1%	ASEVMGPVEAAPEYR	99.7%	93	25	93	8	0	0	1605.76	77	91
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	28	80	0.08%	46.1%	IEEYISK	99.6%	38.9	25	28.4	2	0	0	881.46	67	73
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	28	80	0.08%	46.1%	IMGVAGGLTNLSK	99.7%	94.5	25	78.2	7	0	0	1260.70	231	243
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	28	80	0.08%	46.1%	IYEYVESR	99.7%	60.4	25	51.6	7	0	0	1058.52	204	211
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	28	80	0.08%	46.1%	LEEACDMALELNASK	99.7%	82.7	25	71.2	4	0	0	1709.77	187	201
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	28	80	0.08%	46.1%	LGLTEIR	99.7%	60.1	25	20.5	2	0	0	801.48	366	372
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	28	80	0.08%	46.1%	LGLTEIRK	99.7%	61.5	25	49	6	0	0	929.58	366	373
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	28	80	0.08%	46.1%	MFAEIMMK	98.6%	32.8	25	32.8	3	0	0	1032.46	59	66
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	28	80	0.08%	46.1%	MPACNIMLLGAQR	99.7%	89.1	25	71.4	6	0	0	1490.73	244	256
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	28	80	0.08%	46.1%	MSFGEIEEDAYQEDLGFSLGHLGK	99.7%	47.8	25	47.8	0	2	0	2672.22	378	401
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	28	80	0.08%	46.1%	MSFIAPNLSIIIGASTAAK	99.7%	58.5	25	58.5	3	0	0	1905.05	212	230
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	28	80	0.08%	46.1%	QVKPLPAPLDGQR	99.7%	33	25	33	1	3	0	1418.81	339	351
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	28	80	0.08%	46.1%	SSGTASSVAFTPLQGLEIVNPQAAEK	99.7%	53.5	25	53.5	2	3	0	2602.34	445	470
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	28	80	0.08%	46.1%	VDSFHESTEGK	99.7%	67.2	25	67.2	4	1	0	1235.55	305	315
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	28	80	0.08%	46.1%	VGYELKDEIER	99.7%	52.8	25	32.4	7	2	0	1350.69	316	326
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	28	80	0.08%	46.1%	VIVDANNLTVEIENELNIIHK	99.7%	44.3	25	40.6	0	2	0	2390.29	92	112
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	28	80	0.08%	46.1%	WQEPPPVK	96.6%	29.2	25	17.3	1	0	0	980.52	331	338
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	18	28	80	0.08%	46.1%	YFSSMAEFLK	99.7%	59.2	25	58.6	4	0	0	1238.58	479	488
U4/U6 small nuclear ribonucleoprotein Prp4	PRPF4	PRP4_HUMAN	58.5	100.0%	2	2	3	0.00%	4.8%	ALGEPITLFGEGPAER	99.7%	57.4	25	57.4	2	0	0	1656.86	114	129
U4/U6 small nuclear ribonucleoprotein Prp4	PRPF4	PRP4_HUMAN	58.5	100.0%	2	2	3	0.00%	4.8%	FLGTTCYDR	97.1%	29.9	25	23.2	1	0	0	1132.51	337	345
U4/U6.U5 tri-snRNP-associated protein 1	SART1	SNUT1_HUMAN	90.3	100.0%	3	3	6	0.01%	5.4%	EAAGTTAAAGTGGATEQPPR	99.7%	80.4	25	80.4	2	0	0	1813.87	12	31
U4/U6.U5 tri-snRNP-associated protein 1	SART1	SNUT1_HUMAN	90.3	100.0%	3	3	6	0.01%	5.4%	LEQGGTADGLR	99.7%	45.5	25	34.8	1	0	0	1116.56	351	361
U4/U6.U5 tri-snRNP-associated protein 1	SART1	SNUT1_HUMAN	90.3	100.0%	3	3	6	0.01%	5.4%	LQAQSLSTVGPR	99.7%	70.5	25	67.5	3	0	0	1256.70	374	385
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	AALETDENLLLCAPTGAGK	99.7%	110	25	98.5	2	0	0	1943.97	491	509
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	ANSNLVLQADR	99.7%	68.6	25	52.8	2	0	0	1200.63	15	25
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	DEPTGEVLSLVGK	99.7%	88.2	25	77	2	0	0	1343.71	34	46
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	DIDAFWLQR	99.7%	64.1	25	45.5	2	0	0	1163.58	262	270
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	DILCGAADEVLAVLK	99.7%	48.5	25	34.5	1	0	0	1586.85	130	144
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	DTLGLFLR	99.7%	54.4	25	30.6	2	0	0	934.54	746	753
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	EEGWWVVIGDAK	99.7%	54.6	25	37.5	2	0	0	1388.68	2061	2072
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	EGSASTEVLR	99.7%	48.8	25	33.9	2	0	0	1048.53	754	763
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	FQIMNEIVYEK	99.7%	73.8	25	57.6	3	0	0	1413.71	701	711
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	FYDDAIVSQK	99.7%	54	25	39.8	2	0	0	1185.58	275	284
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	GTQVYSPEK	96.8%	29.4	25	24.8	1	0	0	1008.50	830	838
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	HLILPEK	97.5%	30.4	25	18.8	2	0	0	849.52	1288	1294
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	IIYIAPMR	99.4%	36.6	25	19.6	4	0	0	976.56	538	545
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	IVALSSSLSNAK	99.7%	96.7	25	92.1	2	0	0	1189.68	1487	1498
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	KADEVLEILK	99.7%	51.2	25	39.1	2	0	0	1157.68	285	294
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	KPVIVFVPSR	99.7%	65.4	25	63.1	2	0	0	1141.71	1557	1566
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	LELSVHLQPITR	99.7%	47.4	25	47.4	2	1	0	1405.82	1184	1195
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	LIGLSATLPNYEDVATFLR	99.7%	58.8	25	58.8	1	0	0	2093.13	648	666
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	LTAIDILTTCAADIQR	99.7%	87.8	25	78.2	2	0	0	1774.94	1571	1586

U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	LYDLNHNEIGELIR	99.7%	77.6	25	69.9	2	2	0	1698.88	1153	1166
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	MTQNPNYYNLQGISHR	99.2%	29.4	25	29.4	0	3	0	1951.91	1764	1779
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	NALLQLTDSQIADVAR	99.7%	117	25	114	2	0	0	1727.93	1994	2009
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	NIEMTQEDVR	99.7%	62.2	25	40.5	4	0	0	1234.57	638	647
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	NQVLVFVHSR	99.7%	62.5	25	59	2	1	0	1198.67	719	728
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	SGGPVVVLVQLER	99.7%	50.2	25	50.2	2	0	0	1352.79	2031	2043
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	SLVQEMVGSFGK	99.7%	98.7	25	94.9	6	0	0	1281.65	546	557
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	TGNFQVTELGR	99.7%	72.2	25	68.2	1	0	0	1221.62	976	986
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	TICAEFAILR	99.7%	79.4	25	69.9	2	0	0	1193.63	1357	1366
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	TNLLLQAHLSR	99.7%	71.6	25	63.7	2	0	0	1265.73	1891	1901
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	TYTQLVR	99.4%	36.8	25	19.6	1	0	0	880.49	604	610
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	VELTITPDFQWDEK	99.4%	36.5	25	30.7	1	0	0	1720.84	1200	1213
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	VFSLSSEFK	99.5%	37.7	25	30	2	0	0	1043.54	1017	1025
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	VPIPVKESIEEPSAK	97.2%	24.4	25	21.6	0	1	0	1622.90	1044	1058
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	VVLLTGETSTDLK	99.7%	101	25	96.7	2	0	0	1375.77	1405	1417
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	WLSCETQLPVSFR	99.7%	75.4	25	66.2	2	0	0	1622.80	1275	1287
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	36	44	79	0.08%	19.9%	YAQAGFEGFK	99.7%	60.1	25	60.1	2	0	0	1117.53	470	479
Ubiquinol-cytochrome-c reductase complex assembly factor 1	UQCC1	UQCC1_HUMAN	34.6	100.0%	4	5	8	0.01%	16.4%	IIEAMGFTGPLK	99.7%	78.9	25	74.1	4	0	0	1276.70	96	107
Ubiquinol-cytochrome-c reductase complex assembly factor 1	UQCC1	UQCC1_HUMAN	34.6	100.0%	4	5	8	0.01%	16.4%	NPQSILKPHSPTYNDEGL	97.2%	29.9	25	27.7	1	0	0	2009.99	282	299
Ubiquinol-cytochrome-c reductase complex assembly factor 1	UQCC1	UQCC1_HUMAN	34.6	100.0%	4	5	8	0.01%	16.4%	TDFEEFFLR	99.7%	67.6	25	54.7	2	0	0	1203.57	128	136
Ubiquinol-cytochrome-c reductase complex assembly factor 1	UQCC1	UQCC1_HUMAN	34.6	100.0%	4	5	8	0.01%	16.4%	VMGVNPYILK	97.3%	30	25	27.9	1	0	0	1133.64	189	198
Ubiquitin carboxyl-terminal hydrolase 15	USP15	UBP15_HUMAN	112.4	100.0%	4	4	6	0.01%	4.1%	FSYVTPR	99.2%	35.2	25	25.4	2	0	0	869.45	354	360
Ubiquitin carboxyl-terminal hydrolase 15	USP15	UBP15_HUMAN	112.4	100.0%	4	4	6	0.01%	4.1%	QDTFSGTGFFPLDR	99.7%	52.5	25	47.3	2	0	0	1587.74	933	946
Ubiquitin carboxyl-terminal hydrolase 15	USP15	UBP15_HUMAN	112.4	100.0%	4	4	6	0.01%	4.1%	STLVCPECAK	98.6%	32.7	25	28.5	1	0	0	1164.54	444	453
Ubiquitin carboxyl-terminal hydrolase 15	USP15	UBP15_HUMAN	112.4	100.0%	4	4	6	0.01%	4.1%	VEVYLTELK	99.7%	45.3	25	44	1	0	0	1093.61	129	137
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	7	7	9	0.01%	3.4%	IFLLECNVR	95.7%	28.3	25	21.8	1	0	0	1163.62	2224	2232
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	7	7	9	0.01%	3.4%	LEAASSALGGPTLTHAVTR	99.7%	40.9	25	40.9	0	2	0	1851.99	877	895
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	7	7	9	0.01%	3.4%	LVSIPELLSAVK	95.7%	28.2	25	28.2	1	0	0	1268.78	358	369
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	7	7	9	0.01%	3.4%	SSQLNNPQFVWVVPALR	99.4%	36.3	25	36.3	1	0	0	1955.05	621	637
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	7	7	9	0.01%	3.4%	VAVATILEK	98.8%	33.5	25	30.5	1	0	0	943.58	2236	2244
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	7	7	9	0.01%	3.4%	VLYNLEVLSSK	99.7%	71.7	25	71.7	2	0	0	1264.71	1174	1184
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	7	7	9	0.01%	3.4%	YVITIEDFYSVPR	99.7%	42.8	25	42.8	1	0	0	1601.82	934	946
Ubiquitin conjugation factor E4 A	UBE4A	UBE4A_HUMAN	122.6	100.0%	3	3	6	0.01%	3.8%	DAQQSSSPAADNLR	99.7%	63.3	25	61.5	2	0	0	1459.68	545	558
Ubiquitin conjugation factor E4 A	UBE4A	UBE4A_HUMAN	122.6	100.0%	3	3	6	0.01%	3.8%	IFLITLDNSDPSLK	99.7%	87.8	25	80	2	0	0	1575.86	91	104
Ubiquitin conjugation factor E4 A	UBE4A	UBE4A_HUMAN	122.6	100.0%	3	3	6	0.01%	3.8%	LLTFNPTYCALK	98.3%	31.9	25	31.7	2	0	0	1440.76	457	468
Ubiquitin conjugation factor E4 B	UBE4B	UBE4B_HUMAN	146.2	100.0%	5	5	6	0.01%	5.4%	DENPFASLTATSQPIAAAAR	99.7%	102	25	102	1	0	0	2031.01	218	237
Ubiquitin conjugation factor E4 B	UBE4B	UBE4B_HUMAN	146.2	100.0%	5	5	6	0.01%	5.4%	ELFEEVISK	99.7%	53.6	25	38.1	2	0	0	1093.58	1181	1189
Ubiquitin conjugation factor E4 B	UBE4B	UBE4B_HUMAN	146.2	100.0%	5	5	6	0.01%	5.4%	ILDPAYPDITLPLNSDVPK	99.7%	44.3	25	44.3	1	0	0	2081.12	857	875
Ubiquitin conjugation factor E4 B	UBE4B	UBE4B_HUMAN	146.2	100.0%	5	5	6	0.01%	5.4%	ITLPNDETR	99.2%	35.1	25	25	1	0	0	1058.55	718	726
Ubiquitin conjugation factor E4 B	UBE4B	UBE4B_HUMAN	146.2	100.0%	5	5	6	0.01%	5.4%	YFSGPAITLENTR	99.7%	45	25	39	1	0	0	1468.74	611	623
Ubiquitin thioesterase OTUB1	OTUB1	OTUB1_HUMAN	31.3	99.8%	2	2	3	0.00%	8.9%	IQQEIAVQNPLVSER	99.7%	46.5	25	34	1	0	0	1723.93	37	51
Ubiquitin thioesterase OTUB1	OTUB1	OTUB1_HUMAN	31.3	99.8%	2	2	3	0.00%	8.9%	LLTSGYLQR	99.7%	62.2	25	55.8	2	0	0	1050.59	177	185
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	7	44	0.05%	56.4%	CCLTYCFNKPEDK	99.7%	56	25	56	4	0	0	1734.73	144	156
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	7	44	0.05%	56.4%	ECPSDECGAGVFMASHFDR	95.3%	22.6	25	22.6	0	1	0	2187.85	120	138
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	7	44	0.05%	56.4%	ESTLHLVLR	99.7%	71.1	25	52.2	2	0	0	1067.62	64	72
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	7	44	0.05%	56.4%	IQDKEGIPPDQQR	99.7%	53.4	25	52	4	0	0	1523.78	30	42
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	7	44	0.05%	56.4%	TITLEVEPSDTIENVK	99.7%	114	25	110	17	0	0	1787.93	12	27
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	7	44	0.05%	56.4%	TLSDYNIQK	99.7%	54.9	25	40.1	14	0	0	1081.55	55	63
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	7	44	0.05%	56.4%	YYKVDENGK	99.2%	35.2	25	21.6	2	0	0	1115.54	105	113
Ubiquitin-like modifier-activating enzyme 1	UBA1	UBA1_HUMAN	117.9	100.0%	5	5	8	0.01%	7.0%	AAVATFLQSVQVPEFTPK	99.7%	54.2	25	54.2	2	0	0	1933.04	785	802
Ubiquitin-like modifier-activating enzyme 1	UBA1	UBA1_HUMAN	117.9	100.0%	5	5	8	0.01%	7.0%	LAGTQPLEVLEAVQR	99.7%	88.7	25	88.7	2	0	0	1623.91	679	693

Ubiquitin-like modifier-activating enzyme 1	UBA1	UBA1_HUMAN	117.9	100.0%	5	5	8	0.01%	7.0%	LKSDTAAAAVR	95.0%	27.7	25	17.3	1	0	0	1102.62	527	537
Ubiquitin-like modifier-activating enzyme 1	UBA1	UBA1_HUMAN	117.9	100.0%	5	5	8	0.01%	7.0%	LQTSSVLVSGLR	99.7%	71.9	25	61.7	1	0	0	1259.73	70	81
Ubiquitin-like modifier-activating enzyme 1	UBA1	UBA1_HUMAN	117.9	100.0%	5	5	8	0.01%	7.0%	SLVASLAEPDFVVTDFAK	99.7%	75.1	25	75.1	2	0	0	1909.00	305	322
Ubiquitin-protein ligase E3A	UBE3A	UBE3A_HUMAN	100.7	100.0%	2	2	3	0.00%	3.0%	EFVNLYSDYILNK	99.7%	85.4	25	79.5	1	0	0	1617.82	712	724
Ubiquitin-protein ligase E3A	UBE3A	UBE3A_HUMAN	100.7	100.0%	2	2	3	0.00%	3.0%	VFSSAEALVQSFR	99.7%	63	25	50.9	2	0	0	1440.75	156	168
Ubiquitin-protein ligase E3C	UBE3C	UBE3C_HUMAN	123.9	99.8%	2	2	2	0.00%	1.9%	LIWLYQNLIK	97.0%	29.7	25	29.7	1	0	0	1303.78	114	123
Ubiquitin-protein ligase E3C	UBE3C	UBE3C_HUMAN	123.9	99.8%	2	2	2	0.00%	1.9%	LPEFYDETLLR	99.7%	47.1	25	42.3	1	0	0	1395.72	1057	1067
UDP-glucose 6-dehydrogenase	UGDH	UGDH_HUMAN	55.0	100.0%	4	4	6	0.01%	10.3%	DVLNLVYLCEALNLPEVAR	99.0%	34.2	25	34	1	0	0	2201.16	280	298
UDP-glucose 6-dehydrogenase	UGDH	UGDH_HUMAN	55.0	100.0%	4	4	6	0.01%	10.3%	IAILGFAFK	99.7%	44.5	25	40	2	0	0	979.60	331	339
UDP-glucose 6-dehydrogenase	UGDH	UGDH_HUMAN	55.0	100.0%	4	4	6	0.01%	10.3%	VLIGGDETPEGQR	99.7%	42.4	25	42.4	1	0	0	1370.69	178	190
UDP-glucose 6-dehydrogenase	UGDH	UGDH_HUMAN	55.0	100.0%	4	4	6	0.01%	10.3%	VTVVDVNESR	99.7%	47.8	25	39.3	2	0	0	1117.58	32	41
UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	OGT	OGT1_HUMAN	116.9	100.0%	3	3	3	0.00%	2.9%	IIFSPVAPK	99.2%	35.3	25	25.9	1	0	0	971.59	900	908
UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	OGT	OGT1_HUMAN	116.9	100.0%	3	3	3	0.00%	2.9%	LVSIVADQLEK	99.7%	68.1	25	53.2	1	0	0	1214.70	489	499
UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	OGT	OGT1_HUMAN	116.9	100.0%	3	3	3	0.00%	2.9%	VPNSVLWLLR	99.5%	37.5	25	37.5	1	0	0	1196.72	868	877
Uncharacterized protein C11orf84	C11orf84	CK084_HUMAN	41.0	100.0%	4	4	7	0.01%	15.0%	DREVAEGGLPR	99.7%	44.7	25	32.5	2	0	0	1198.62	295	305
Uncharacterized protein C11orf84	C11orf84	CK084_HUMAN	41.0	100.0%	4	4	7	0.01%	15.0%	GTLDLQVIR	99.7%	40.3	25	28.5	2	0	0	1014.59	319	327
Uncharacterized protein C11orf84	C11orf84	CK084_HUMAN	41.0	100.0%	4	4	7	0.01%	15.0%	MPAEIVVLLDSEDNPSLPK	99.7%	46.1	25	44.7	1	0	0	2067.07	171	189
Uncharacterized protein C11orf84	C11orf84	CK084_HUMAN	41.0	100.0%	4	4	7	0.01%	15.0%	SNILEAWSEGVALLQDVR	99.7%	101	25	74.5	2	0	0	2000.04	126	143
Uncharacterized protein C19orf52	C19orf52	CS052_HUMAN	29.2	100.0%	3	4	6	0.01%	15.8%	AEAGDAVVAKPGVWAR	99.7%	50.5	25	50.5	1	1	0	1596.85	15	30
Uncharacterized protein C19orf52	C19orf52	CS052_HUMAN	29.2	100.0%	3	4	6	0.01%	15.8%	LALSQAHSLVQAEAPR	99.7%	71.5	25	71.5	0	2	0	1690.92	245	260
Uncharacterized protein C19orf52	C19orf52	CS052_HUMAN	29.2	100.0%	3	4	6	0.01%	15.8%	VLDVGFVGR	99.7%	51.9	25	51.9	2	0	0	961.55	163	171
Uncharacterized protein C2orf47, mitochondrial	C2orf47	CB047_HUMAN	32.5	100.0%	4	6	12	0.01%	16.8%	EFTQGVKPDWTIAR	99.7%	53	25	48.9	2	2	0	1647.85	270	283
Uncharacterized protein C2orf47, mitochondrial	C2orf47	CB047_HUMAN	32.5	100.0%	4	6	12	0.01%	16.8%	FDLLEELVAK	99.7%	58.4	25	54.1	2	0	0	1176.65	164	173
Uncharacterized protein C2orf47, mitochondrial	C2orf47	CB047_HUMAN	32.5	100.0%	4	6	12	0.01%	16.8%	MIVLGFSNPINWVR	99.7%	82.5	25	75.9	4	0	0	1645.89	110	123
Uncharacterized protein C2orf47, mitochondrial	C2orf47	CB047_HUMAN	32.5	100.0%	4	6	12	0.01%	16.8%	QLLSASYEFQR	99.7%	71	25	69.2	2	0	0	1341.68	259	269
Uncharacterized protein C7orf50	C7orf50	CG050_HUMAN	22.1	100.0%	4	4	6	0.01%	34.5%	ASAEGPLLGPEAAPSGEGAGSK	99.7%	72	25	72	2	0	0	1952.96	22	43
Uncharacterized protein C7orf50	C7orf50	CG050_HUMAN	22.1	100.0%	4	4	6	0.01%	34.5%	EAGLVAQHPPAR	99.7%	51.7	25	49.1	1	0	0	1245.67	84	95
Uncharacterized protein C7orf50	C7orf50	CG050_HUMAN	22.1	100.0%	4	4	6	0.01%	34.5%	GEAVLRPGLDAEPELSPEEQR	99.7%	55.4	25	55.4	0	2	0	2292.15	44	64
Uncharacterized protein C7orf50	C7orf50	CG050_HUMAN	22.1	100.0%	4	4	6	0.01%	34.5%	SGAELALDYLCR	99.7%	47.2	25	39.5	1	0	0	1367.66	97	108
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	13	13	21	0.02%	13.8%	EICELTGIDQSVLER	99.7%	69.9	25	53.8	1	0	0	1761.87	308	322
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	13	13	21	0.02%	13.8%	EQLLQSNPVLEAFGNAK	99.7%	85.9	25	85.9	2	0	0	1857.97	140	156
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	13	13	21	0.02%	13.8%	GDFLFSSDHLIEMATK	99.2%	35	25	34.8	1	0	0	1810.87	1061	1076
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	13	13	21	0.02%	13.8%	IFLLTNNNLLLADQK	99.7%	107	25	101	2	0	0	1729.98	1007	1021
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	13	13	21	0.02%	13.8%	IIIAEVVNK	99.7%	54	25	39.4	2	0	0	998.62	987	995
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	13	13	21	0.02%	13.8%	LEDLATLIQK	99.7%	49	25	38.7	1	0	0	1143.66	704	713
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	13	13	21	0.02%	13.8%	LGNIEFKPESR	99.7%	43.4	25	38.2	2	0	0	1289.68	281	291
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	13	13	21	0.02%	13.8%	SEVPLVDVTK	99.7%	44.8	25	37.6	2	0	0	1086.60	1027	1036
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	13	13	21	0.02%	13.8%	SLFPEGNPAK	98.7%	33.3	25	24.8	1	0	0	1059.55	552	561
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	13	13	21	0.02%	13.8%	SSALVIQSYIR	99.7%	76.3	25	62.4	2	0	0	1236.69	752	762
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	13	13	21	0.02%	13.8%	VSTTLNVAQAYYAR	99.7%	59.2	25	50	2	0	0	1556.81	336	349
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	13	13	21	0.02%	13.8%	YLGLLENVR	99.7%	47.3	25	33.5	2	0	0	1076.61	618	626
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	13	13	21	0.02%	13.8%	YNYLSLDSAK	99.7%	39.7	25	33.5	1	0	0	1173.58	232	241
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	13	13	20	0.02%	15.8%	DGTIDFTPGSELLITK	99.7%	70.4	25	70.4	2	0	0	1706.89	1032	1047
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	13	13	20	0.02%	15.8%	GDVVLQSDHVIETLTK	99.2%	29.1	25	29.1	0	1	0	1753.93	990	1005
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	13	13	20	0.02%	15.8%	GEELLSPLNLEQAAYAR	99.7%	97.4	25	87.5	2	0	0	1873.97	362	378
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	13	13	20	0.02%	15.8%	KYEAFLQR	99.6%	38.5	25	28.2	1	0	0	1054.57	667	674
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	13	13	20	0.02%	15.8%	LGTDEISPR	99.7%	77.1	25	60.3	2	0	0	987.51	901	909
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	13	13	20	0.02%	15.8%	LLQFYAETCPAPER	99.7%	83.4	25	64.9	1	0	0	1694.82	153	166
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	13	13	20	0.02%	15.8%	LLQSNPVLEAFGNAK	99.7%	76.4	25	75.9	2	0	0	1600.87	174	188
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	13	13	20	0.02%	15.8%	NPQSYLYLVK	98.1%	31.5	25	25.6	1	0	0	1224.66	260	269
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	13	13	20	0.02%	15.8%	QLLLTPNAVVIVEDAK	96.6%	29.2	25	21.5	1	0	0	1723.00	939	954

Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	13	13	20	0.02%	15.8%	TLFATEDALEVR	99.7%	69.6	25	65.8	1	0	0	1364.71	722	733
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	13	13	20	0.02%	15.8%	TSFLLNLR	99.7%	64	25	61.8	2	0	0	963.56	814	821
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	13	13	20	0.02%	15.8%	VLQALGSEPIQYAVPVVK	99.7%	73.1	25	73.1	2	0	0	1911.10	910	927
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	13	13	20	0.02%	15.8%	YLGLLENLR	99.7%	50.1	25	50.1	2	0	0	1090.63	648	656
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	6	6	8	0.01%	5.9%	IGELVGVLVNHFK	99.7%	56.9	25	54.2	2	0	0	1424.83	942	954
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	6	6	8	0.01%	5.9%	LFCWIVTR	98.5%	32.6	25	22.5	1	0	0	1094.58	351	358
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	6	6	8	0.01%	5.9%	SYIHEVAR	95.1%	27.7	25	22	1	0	0	974.51	738	745
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	6	6	8	0.01%	5.9%	TLFTLEELR	99.7%	55.4	25	46.5	2	0	0	1121.62	686	694
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	6	6	8	0.01%	5.9%	VIVQQPGER	96.3%	28.9	25	28.9	1	0	0	1025.57	191	199
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	6	6	8	0.01%	5.9%	VVSIIAELLSTK	99.7%	87.8	25	87.8	1	0	0	1272.78	296	307
Unconventional myosin-Ie	MYO1E	MYO1E_HUMAN	127.1	99.8%	2	2	2	0.00%	2.5%	DIILQSNPLLEAFGNAK	99.7%	56.1	25	56.1	1	0	0	1843.00	144	160
Unconventional myosin-Ie	MYO1E	MYO1E_HUMAN	127.1	99.8%	2	2	2	0.00%	2.5%	VFDFLVDSINK	99.7%	80.6	25	77.7	1	0	0	1296.68	363	373
Unconventional myosin-Vb	MYO5B	MYO5B_HUMAN	213.7	100.0%	8	8	11	0.01%	5.4%	AGQVAYLEK	96.2%	28.7	25	22.5	1	0	0	978.53	750	758
Unconventional myosin-Vb	MYO5B	MYO5B_HUMAN	213.7	100.0%	8	8	11	0.01%	5.4%	ELVHYQQSPGEDTSLR	98.1%	25.8	25	20.1	0	1	0	1858.89	965	980
Unconventional myosin-Vb	MYO5B	MYO5B_HUMAN	213.7	100.0%	8	8	11	0.01%	5.4%	ILNLYTPLNEFEER	99.7%	40.3	25	40.3	2	0	0	1750.90	1775	1788
Unconventional myosin-Vb	MYO5B	MYO5B_HUMAN	213.7	100.0%	8	8	11	0.01%	5.4%	LQEEVESLR	99.1%	34.6	25	28.5	1	0	0	1102.57	981	989
Unconventional myosin-Vb	MYO5B	MYO5B_HUMAN	213.7	100.0%	8	8	11	0.01%	5.4%	NDPQQLLLDAK	99.7%	41.2	25	36	1	0	0	1254.67	1805	1815
Unconventional myosin-Vb	MYO5B	MYO5B_HUMAN	213.7	100.0%	8	8	11	0.01%	5.4%	TIQAQLQER	99.6%	38.2	25	26.6	2	0	0	1086.59	1796	1804
Unconventional myosin-Vb	MYO5B	MYO5B_HUMAN	213.7	100.0%	8	8	11	0.01%	5.4%	VLASSPIMEAIGNAK	99.7%	64.4	25	52.2	2	0	0	1500.81	196	210
Unconventional myosin-Vb	MYO5B	MYO5B_HUMAN	213.7	100.0%	8	8	11	0.01%	5.4%	YFATVGGSASETNIEEK	99.7%	138	25	131	1	0	0	1802.84	179	195
Unhealthy ribosome biogenesis protein 2 homolog	URB2	URB2_HUMAN	170.5	100.0%	2	2	2	0.00%	1.7%	ADVQAVVSAVTLLR	99.7%	68.5	25	58	1	0	0	1441.84	1262	1275
Unhealthy ribosome biogenesis protein 2 homolog	URB2	URB2_HUMAN	170.5	100.0%	2	2	2	0.00%	1.7%	GEIAQNLLSLVK	99.5%	37.4	25	30.2	1	0	0	1284.75	868	879
UPF0488 protein C8orf33	C8orf33	CH033_HUMAN	25.0	99.8%	2	2	4	0.00%	10.9%	AAAYSAQVQPVDGATR	99.7%	99.2	25	95.9	2	0	0	1604.80	183	198
UPF0488 protein C8orf33	C8orf33	CH033_HUMAN	25.0	99.8%	2	2	4	0.00%	10.9%	LPGPVSSAR	99.7%	52.5	25	26.9	2	0	0	883.50	28	36
UPF0505 protein C16orf62	C16orf62	CP062_HUMAN	109.6	99.8%	2	2	3	0.00%	2.4%	FLPFLDMFQK	99.7%	41.8	25	37.8	1	0	0	1285.67	569	578
UPF0505 protein C16orf62	C16orf62	CP062_HUMAN	109.6	99.8%	2	2	3	0.00%	2.4%	FVLITDILDTFGK	99.7%	49.7	25	49.7	2	0	0	1481.83	231	243
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	13	0.01%	21.5%	AALGPLVTGLYDVQAFK	99.7%	60.4	25	60.4	2	0	0	1762.97	6	22
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	13	0.01%	21.5%	AAWEAYLSR	99.7%	48.7	25	24.4	1	0	0	1066.53	469	477
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	13	0.01%	21.5%	FGDFVLK	99.6%	38.1	25	28	2	0	0	825.45	23	29
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	13	0.01%	21.5%	IASWADLVNAHVVPGSGVVK	99.7%	33.2	25	33.2	0	1	0	2019.10	333	352
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	13	0.01%	21.5%	KFADIGNTVK	99.6%	38.5	25	34.5	1	0	0	1092.60	314	323
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	13	0.01%	21.5%	LHSVCTLSK	96.6%	29.1	25	22.9	1	0	0	1044.55	170	178
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	13	0.01%	21.5%	MLEILEQQK	99.7%	44.2	25	30.1	2	0	0	1131.61	179	187
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	13	0.01%	21.5%	SGLSSPIYIDLR	99.7%	57.6	25	46.3	2	0	0	1320.72	30	41
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	13	0.01%	21.5%	VTDAIVLLDR	99.7%	86.9	25	58.6	1	0	0	1114.65	146	155
Uridine-cytidine kinase 2	UCK2	UCK2_HUMAN	29.3	99.9%	2	2	3	0.00%	8.4%	TVQIPVYDFVSHSR	99.7%	51.4	25	51.3	1	0	0	1647.85	106	119
Uridine-cytidine kinase 2	UCK2	UCK2_HUMAN	29.3	99.9%	2	2	3	0.00%	8.4%	YADVIIPR	99.7%	40.4	25	40.4	2	0	0	946.54	203	210
Uridine-cytidine kinase-like 1	UCKL1	UCKL1_HUMAN	61.1	99.8%	2	2	2	0.00%	4.4%	EAFAIGLGGGSASGK	99.7%	92.3	25	84.7	1	0	0	1321.67	97	111
Uridine-cytidine kinase-like 1	UCKL1	UCKL1_HUMAN	61.1	99.8%	2	2	2	0.00%	4.4%	IITTAVDKR	98.0%	31.3	25	30.5	1	0	0	1016.61	503	511
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	6	7	12	0.01%	24.2%	EITGIGPSTTTETETIAK	99.7%	86.7	25	86.1	2	0	0	1848.94	215	232
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	6	7	12	0.01%	24.2%	ELALPGELTQSR	99.7%	68.4	25	63.8	2	0	0	1313.71	94	105
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	6	7	12	0.01%	24.2%	FESPESQASAEQPEM	99.7%	51.7	25	51.7	1	0	0	1682.69	313	327
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	6	7	12	0.01%	24.2%	HYLFYDGESVSGK	99.7%	61.5	25	60.3	2	0	0	1501.70	39	51
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	6	7	12	0.01%	24.2%	LFLAGYDPTPTMR	99.7%	79.8	25	78.6	4	0	0	1497.74	250	262
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	6	7	12	0.01%	24.2%	QQEIILWR	97.8%	30.9	25	20.2	1	0	0	1085.61	289	296
Vacuolar protein sorting-associated protein 29	VPS29	VPS29_HUMAN	20.5	99.8%	2	2	4	0.00%	12.6%	GDFDENLNYPEQK	99.6%	38.2	25	38.2	2	0	0	1568.69	61	73
Vacuolar protein sorting-associated protein 29	VPS29	VPS29_HUMAN	20.5	99.8%	2	2	4	0.00%	12.6%	TLAGDVHIVR	99.7%	54.3	25	44.2	2	0	0	1080.62	51	60
Vacuolar protein sorting-associated protein 33B	VPS33B	VP33B_HUMAN	70.6	99.8%	2	2	4	0.00%	3.4%	FIFLTTAVTNSAR	99.7%	68.5	25	62.2	2	0	0	1440.78	595	607
Vacuolar protein sorting-associated protein 33B	VPS33B	VP33B_HUMAN	70.6	99.8%	2	2	4	0.00%	3.4%	IIEQVLER	99.5%	37.6	25	21.1	2	0	0	999.58	524	531
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	12	21	0.02%	16.2%	AELAELPLR	99.7%	41.9	25	30.2	2	0	0	1011.58	574	582
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	12	21	0.02%	16.2%	ENDAVTIQVLNQLIQK	99.7%	78.6	25	70.1	2	0	0	1826.00	734	749

Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	12	21	0.02%	16.2%	ESPESEGPIYEGLIL	99.7%	41.9	25	41.9	1	0	0	1632.80	782	796
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	12	21	0.02%	16.2%	HASNMLGELR	99.7%	43.3	25	38.3	2	0	0	1127.56	45	54
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	12	21	0.02%	16.2%	ILVGTNLVR	99.7%	66	25	48.4	2	0	0	984.62	218	226
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	12	21	0.02%	16.2%	IPVDTYNNILTVLK	99.7%	87.5	25	84.3	4	0	0	1602.91	404	417
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	12	21	0.02%	16.2%	LFDIFSQQVATVIQSR	99.7%	93.1	25	76.9	2	0	0	1852.00	324	339
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	12	21	0.02%	16.2%	LNLEHIATSSAVSK	99.7%	67.7	25	65.8	1	1	0	1469.80	383	396
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	12	21	0.02%	16.2%	LSQLEGVNVER	99.7%	67.6	25	58.7	2	0	0	1243.66	227	237
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	12	21	0.02%	16.2%	SEDPDQQYLILNTAR	99.7%	75	25	66.8	2	0	0	1762.86	500	514
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	16	16	26	0.03%	14.5%	ADYNLTR	98.1%	31.6	25	12.1	1	0	0	852.42	1123	1129
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	16	16	26	0.03%	14.5%	ALSPLEEWLR	99.7%	41.2	25	34	2	0	0	1213.66	138	147
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	16	16	26	0.03%	14.5%	DINLDVNR	94.8%	27.5	25	2.25	1	0	0	958.50	935	942
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	16	16	26	0.03%	14.5%	DPGVITYDLPTPPGEK	99.7%	72.4	25	66.1	1	0	0	1698.86	274	289
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	16	16	26	0.03%	14.5%	EAFLQEVWK	99.5%	37.3	25	28.1	2	0	0	1149.59	410	418
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	16	16	26	0.03%	14.5%	EVYLHAIVR	99.2%	35.4	25	24	2	0	0	1099.63	848	856
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	16	16	26	0.03%	14.5%	IETMLGDVAVAVHPK	97.2%	24.5	25	24.5	0	1	0	1579.85	538	552
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	16	16	26	0.03%	14.5%	IQQQQPPPGEK	99.4%	36.8	25	28.4	2	0	0	1249.65	253	263
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	16	16	26	0.03%	14.5%	ITPAHDQNDYEVGQR	99.7%	34.7	25	32.1	0	1	0	1742.81	592	606
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	16	16	26	0.03%	14.5%	KVDEAIALFQK	99.7%	74	25	69.1	2	0	0	1261.72	1252	1262
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	16	16	26	0.03%	14.5%	LHEEGIIYR	99.2%	35.2	25	28.6	2	0	0	1129.60	462	470
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	16	16	26	0.03%	14.5%	LQQTEAELR	99.7%	63	25	52.9	2	0	0	1087.57	1243	1251
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	16	16	26	0.03%	14.5%	LSAAVTEAFVR	99.7%	111	25	106	2	0	0	1163.64	451	461
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	16	16	26	0.03%	14.5%	SSAQDPQAVLGALGR	99.7%	88.6	25	82.6	2	0	0	1469.77	123	137
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	16	16	26	0.03%	14.5%	VPLEVQEADEAK	99.7%	72.2	25	72.2	2	0	0	1327.67	1231	1242
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	16	16	26	0.03%	14.5%	YGEAGEGPGWGGAHPR	99.7%	43.5	25	43.5	0	1	0	1597.71	24	39
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	5	6	13	0.01%	11.3%	FSFTLPYPVK	99.7%	45	25	38.4	2	0	0	1198.65	310	319
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	5	6	13	0.01%	11.3%	LESEGSPETLTNLR	99.7%	117	25	110	3	0	0	1545.78	133	146
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	5	6	13	0.01%	11.3%	LRLESEGSPETLTNLR	99.7%	70.5	25	70.5	2	2	0	1814.96	131	146
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	5	6	13	0.01%	11.3%	QVNITVQK	99.7%	39.8	25	26.1	2	0	0	929.54	77	84
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	5	6	13	0.01%	11.3%	VSQWWER	99.6%	38.3	25	28.5	2	0	0	990.48	86	92
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	4	4	16	0.02%	12.3%	LLETLFVHR	99.7%	58.9	25	38.2	5	0	0	1127.66	142	150
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	4	4	16	0.02%	12.3%	LPVGTTATLYFR	99.7%	78.5	25	78.5	4	0	0	1338.74	68	79
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	4	4	16	0.02%	12.3%	SLKDEDVLQK	99.7%	48.6	25	38	4	0	0	1174.63	58	67
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	4	4	16	0.02%	12.3%	YDFTSSR	99.7%	40.1	25	30.8	3	0	0	875.39	117	123
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	21	23	41	0.04%	30.1%	AENSSLNLIGK	99.7%	83.7	25	66.4	2	0	0	1145.62	188	198
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	21	23	41	0.04%	30.1%	DFQSGQHVIVR	99.7%	55	25	49	2	0	0	1285.66	28	38
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	21	23	41	0.04%	30.1%	DIEAMDPSILK	99.7%	54.9	25	46.4	1	0	0	1231.62	151	161
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	21	23	41	0.04%	30.1%	GILLYGPPGCGK	99.7%	43.1	25	31.7	2	0	0	1231.65	255	266
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	21	23	41	0.04%	30.1%	GSMAGSTGVHDTVVNQLLSK	99.7%	51.8	25	47	0	2	0	2001.01	338	357
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	21	23	41	0.04%	30.1%	IAEESNFPFIK	99.5%	37.6	25	24	2	0	0	1294.67	556	566
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	21	23	41	0.04%	30.1%	KLLIIGTTSR	99.7%	51.6	25	43.2	2	0	0	1101.70	639	648
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	21	23	41	0.04%	30.1%	LFADAEEEQRR	99.4%	36.6	25	30.8	1	0	0	1363.66	305	315
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	21	23	41	0.04%	30.1%	LLDYVPIGPR	99.7%	54.3	25	48.2	2	0	0	1142.66	608	617
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	21	23	41	0.04%	30.1%	LLIIGTTSR	99.7%	63.7	25	56.5	2	0	0	973.60	640	648
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	21	23	41	0.04%	30.1%	LQILHIHTAR	98.1%	31.4	25	25.3	1	1	0	1201.72	404	413
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	21	23	41	0.04%	30.1%	MIGFSETAK	98.3%	32	25	28.2	1	0	0	983.49	573	581
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	21	23	41	0.04%	30.1%	NFSGAELEGLVR	99.7%	80.6	25	62	2	0	0	1291.66	435	446
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	21	23	41	0.04%	30.1%	QSIINPDWNFEK	99.7%	69	25	65.3	2	0	0	1490.73	206	217
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	21	23	41	0.04%	30.1%	SIDSNPYDTDK	98.2%	31.7	25	26.5	1	0	0	1254.55	106	116
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	21	23	41	0.04%	30.1%	SQLSCVVVDDIER	99.7%	113	25	113	2	0	0	1519.74	595	607
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	21	23	41	0.04%	30.1%	TPLVSVLLEGPPHSGK	99.7%	74.5	25	72.8	2	2	0	1630.92	534	549
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	21	23	41	0.04%	30.1%	VLDDGELLVQQTK	99.7%	94.9	25	94.9	3	0	0	1457.78	517	529

Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	21	23	41	0.04%	30.1%	VVNGPEILNK	99.7%	40	25	38.3	2	0	0	1082.62	284	293
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	21	23	41	0.04%	30.1%	YVGESEANIR	99.7%	44.9	25	35.4	2	0	0	1137.55	294	303
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	21	23	41	0.04%	30.1%	YVGESEANIRK	99.7%	50	25	44.2	2	0	0	1265.65	294	304
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	DGQVINETSQHHDDLE	99.7%	65.8	25	65.8	5	1	0	1836.80	451	466
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	DNLAEDIMR	99.7%	73.9	25	65.4	4	0	0	1076.50	176	184
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	EEAENTLQSFR	99.7%	72.3	25	64.8	2	0	0	1323.62	197	207
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	EEAENTLQSFRQDVDNASLAR	99.7%	47.9	25	47.9	0	2	0	2393.13	197	217
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	EKLQEEMLQR	99.7%	55.7	25	47.7	4	0	0	1319.66	187	196
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	EMEENFAVEAANYQDTIGR	99.7%	126	25	126	6	2	0	2186.97	346	364
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	ETNLDSLPLVDTHSK	99.7%	69.8	25	61.9	5	2	0	1668.84	425	439
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	ETNLDSLPLVDTHSKR	99.7%	58.6	25	56.6	2	3	0	1824.95	425	440
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	EYQDLLNVK	99.7%	52.6	25	46.8	7	0	0	1121.58	382	390
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	FADLSEAANR	99.7%	65.8	25	47.4	8	0	0	1093.53	295	304
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	FANYIDK	98.7%	33.2	25	25.1	2	0	0	870.44	114	120
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	FANYIDKVR	99.7%	72.8	25	64.9	4	0	0	1125.61	114	122
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	ILLAELEQLK	99.7%	70.5	25	59.8	8	0	0	1169.71	130	139
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	ILLAELEQLKGQGK	99.7%	73.7	25	73.7	4	4	0	1539.91	130	143
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	ISLPLPNFSSLNLR	99.7%	85	25	75.1	6	1	0	1570.90	411	424
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	KLLEGEESR	99.7%	53.5	25	34.8	3	0	0	1060.56	402	410
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	KVESLQEEIAFLK	99.7%	108	25	101	4	3	0	1533.85	223	235
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	LGDLYEEEMR	99.7%	63	25	56.6	2	0	0	1254.57	146	155
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	LGDLYEEEMRELR	99.7%	41.5	25	41.5	0	1	0	1668.79	146	158
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	LLEGEESR	99.6%	39	25	30.6	2	0	0	932.47	403	410
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	LLQDSVDFSLADAINTEFK	99.7%	130	25	123	15	4	0	2126.07	79	97
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	LQDEIQNMK	99.7%	39.7	25	33.2	3	0	0	1118.55	365	373
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	LQDEIQNMKEEMAR	99.7%	89.9	25	77.4	10	7	0	1734.82	365	378
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	LQEEMLQR	99.7%	50	25	37.7	5	0	0	1062.53	189	196
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	LQEEMLQREEAENTLQSFR	99.7%	58.9	25	58.9	2	2	0	2367.12	189	207
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	MALDIEIATYR	99.7%	74.9	25	48.5	4	0	0	1311.66	391	401
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	MALDIEIATYRK	99.7%	38.9	25	25.1	0	2	0	1423.76	391	402
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	MFGGPGTASRPSSSR	99.7%	38	25	35.4	2	3	0	1510.71	14	28
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	NLQEAEEWYK	99.7%	64.3	25	60.5	4	0	0	1309.61	283	292
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	QDVDNASLAR	99.7%	80.2	25	58.5	8	0	0	1088.53	208	217
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	QMREMEENFAVEAANYQDTIGR	99.7%	57.4	25	57.4	0	2	0	2634.16	343	364
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	QVDQLTNDKAR	99.7%	49.3	25	30.9	3	0	0	1287.67	160	170
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	QVQSLTCEVDALK	99.7%	81.1	25	72.4	4	0	0	1490.75	322	334
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	QVQSLTCEVDALKGTNESLER	99.7%	93.2	25	93.2	1	3	0	2377.17	322	342
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	SLYASSPGGVYATR	99.7%	104	25	104	14	0	0	1428.71	51	64
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	SRLGDLYEEEMR	99.1%	28.9	25	23.2	0	1	0	1497.70	144	155
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	SYVTTSTR	99.7%	40.9	25	39.5	2	0	0	914.46	29	36
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	TNEKVELQELNDR	99.7%	71.4	25	58.6	4	2	0	1587.80	101	113
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	TYSLGSALRPSTSR	99.7%	47.3	25	47.3	0	3	0	1495.79	37	50
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	VELQELNDR	99.7%	60.7	25	60.2	3	0	0	1115.57	105	113
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	VESLQEEIAFLK	99.7%	75.8	25	44.9	1	0	0	1405.76	224	235
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	42	68	224	0.23%	73.4%	VEVERDNLAEDIMR	99.7%	55.4	25	55.4	5	8	0	1704.82	171	184
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	5	7	13	0.01%	21.9%	GYGFGLIK	99.3%	35.7	25	27.5	1	0	0	854.48	21	28
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	5	7	13	0.01%	21.9%	KLETAVNLAWTAGNSNTR	99.7%	110	25	110	1	2	0	1946.01	201	218
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	5	7	13	0.01%	21.9%	LTFDSSFSPNTGK	99.7%	83.5	25	72.9	2	0	0	1400.67	97	109
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	5	7	13	0.01%	21.9%	LTFDSSFSPNTGKK	99.7%	69.7	25	69.7	2	1	0	1528.76	97	110
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	5	7	13	0.01%	21.9%	LTLSALLDGK	99.7%	88.2	25	0	12	0	0	1030.61	257	266
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	5	7	13	0.01%	21.9%	YQIDPDACFSAK	99.7%	62.9	25	61.5	4	0	0	1414.63	225	236

Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	9	10	42	0.04%	34.7%	GFGFGLVK	99.1%	34.5	25	25.9	2	0	0	824.47	32	39
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	9	10	42	0.04%	34.7%	LTFDTTFSPNTGK	99.7%	93.2	25	81.2	4	0	0	1428.70	108	120
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	9	10	42	0.04%	34.7%	LTFDTTFSPNTGKK	99.7%	75.5	25	75.5	5	0	0	1556.80	108	121
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	9	10	42	0.04%	34.7%	LTLSALVDGK	99.7%	88.3	25	79.3	6	0	0	1016.60	268	277
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	9	10	42	0.04%	34.7%	NNFAVGYR	99.7%	54.2	25	49	6	0	0	940.46	178	185
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	9	10	42	0.04%	34.7%	SCSGVEFSTSGSSNTDTGK	99.7%	119	25	119	5	0	0	1907.79	46	64
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	9	10	42	0.04%	34.7%	VNNSSLIGVGYTQTLRPGVK	99.7%	87.2	25	87.2	4	4	0	2103.16	248	267
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	9	10	42	0.04%	34.7%	WCEYGLTFTEK	99.7%	49.2	25	47.7	2	0	0	1433.64	75	85
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	9	10	42	0.04%	34.7%	YQLDPTASISAK	99.7%	68.2	25	59.5	4	0	0	1293.67	236	247
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	10	14	51	0.05%	39.6%	GYGFGMVK	99.7%	39.2	25	30.4	3	0	0	874.41	21	28
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	10	14	51	0.05%	39.6%	IETSINLAWTAGSNNTR	99.7%	127	25	127	3	0	0	1847.92	202	218
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	10	14	51	0.05%	39.6%	LSQNNFALGYK	99.7%	65.5	25	53	7	0	0	1254.65	164	174
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	10	14	51	0.05%	39.6%	LTLDTIFVPNTGK	99.7%	96.4	25	96.4	6	0	0	1418.79	97	109
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	10	14	51	0.05%	39.6%	LTLDTIFVPNTGKK	99.7%	45.1	25	45.1	2	2	0	1546.88	97	110
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	10	14	51	0.05%	39.6%	LTLSALIDGK	99.7%	88.2	25	0	12	0	0	1030.61	257	266
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	10	14	51	0.05%	39.6%	SCSGVEFSTSGHAYTDTGK	99.7%	88.5	25	88.5	4	2	0	1990.84	35	53
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	10	14	51	0.05%	39.6%	VCNYGLTFTQK	99.7%	72.9	25	63.9	4	0	0	1330.65	64	74
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	10	14	51	0.05%	39.6%	VNNASLIGLGYTQTLRPGVK	99.7%	101	25	101	2	2	0	2101.18	237	256
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	10	14	51	0.05%	39.6%	YKVCNYGLTFTQK	99.7%	76.5	25	70.7	2	0	0	1621.80	62	74
V-type proton ATPase 116 kDa subunit a isoform 1	ATP6V0A1	VPP1_HUMAN	96.4	99.8%	2	2	3	0.00%	2.8%	LGFVAGVINR	99.7%	56.2	25	47	2	0	0	1045.62	168	177
V-type proton ATPase 116 kDa subunit a isoform 1	ATP6V0A1	VPP1_HUMAN	96.4	99.8%	2	2	3	0.00%	2.8%	SVFIIFFQGDQLK	99.7%	61.1	25	42.8	1	0	0	1541.84	218	230
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	6	7	12	0.01%	12.2%	ALDEYYDKHFTEFVPLR	99.7%	47.2	25	47.2	0	2	0	2143.05	460	476
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	6	7	12	0.01%	12.2%	FTMVQVWPVR	99.7%	47.8	25	44.7	2	0	0	1262.67	203	212
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	6	7	12	0.01%	12.2%	GVNVSALSR	99.7%	75.8	25	59.1	2	0	0	902.51	121	129
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	6	7	12	0.01%	12.2%	LPANHPLLTGQR	99.7%	35.2	25	32	0	2	0	1316.74	221	232
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	6	7	12	0.01%	12.2%	TALVANTSNMPVAAR	99.7%	67.9	25	65.6	1	0	0	1515.79	309	323
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	6	7	12	0.01%	12.2%	VGHSELVGEIIR	99.7%	59.5	25	50.5	2	1	0	1308.73	45	56
V-type proton ATPase subunit d 1	ATP6V0D1	VA0D1_HUMAN	40.3	100.0%	3	3	6	0.01%	9.4%	LYPEGLAQLAR	99.7%	49.8	25	35.9	2	0	0	1230.68	247	257
V-type proton ATPase subunit d 1	ATP6V0D1	VA0D1_HUMAN	40.3	100.0%	3	3	6	0.01%	9.4%	NIVWIAECIAQR	99.7%	93.6	25	90.5	2	0	0	1472.77	328	339
V-type proton ATPase subunit d 1	ATP6V0D1	VA0D1_HUMAN	40.3	100.0%	3	3	6	0.01%	9.4%	NVADYYPEYK	99.7%	42.9	25	42.9	2	0	0	1261.57	266	275
V-type proton ATPase subunit H	ATP6V1H	VATH_HUMAN	55.9	100.0%	4	4	7	0.01%	12.6%	LLEVSDDPQVLAVAAHDVGEYVR	99.5%	31.4	25	30	0	1	0	2495.28	397	419
V-type proton ATPase subunit H	ATP6V1H	VATH_HUMAN	55.9	100.0%	4	4	7	0.01%	12.6%	QLQSEQPQTAAAR	99.7%	60.7	25	53.5	4	0	0	1427.72	470	482
V-type proton ATPase subunit H	ATP6V1H	VATH_HUMAN	55.9	100.0%	4	4	7	0.01%	12.6%	VSIFFDYAR	99.7%	53.6	25	47.7	1	0	0	1117.57	108	116
V-type proton ATPase subunit H	ATP6V1H	VATH_HUMAN	55.9	100.0%	4	4	7	0.01%	12.6%	YNIIPVLSDILQESVK	99.7%	66.6	25	62.2	1	0	0	1831.02	263	278
WASH complex subunit 7	KIAA1033	WASH7_HUMAN	136.4	100.0%	9	10	15	0.02%	8.4%	DLALFFSLNPIR	99.7%	61.8	25	56.4	2	0	0	1405.78	706	717
WASH complex subunit 7	KIAA1033	WASH7_HUMAN	136.4	100.0%	9	10	15	0.02%	8.4%	FLEEYTSQLR	99.7%	66.7	25	61.2	2	0	0	1285.64	34	43
WASH complex subunit 7	KIAA1033	WASH7_HUMAN	136.4	100.0%	9	10	15	0.02%	8.4%	KLDLISELR	99.7%	56.1	25	46.9	1	0	0	1086.65	586	594
WASH complex subunit 7	KIAA1033	WASH7_HUMAN	136.4	100.0%	9	10	15	0.02%	8.4%	LGEPSEIDQR	99.7%	67.9	25	58.3	1	0	0	1143.56	303	312
WASH complex subunit 7	KIAA1033	WASH7_HUMAN	136.4	100.0%	9	10	15	0.02%	8.4%	LLPYEQSSLLELIK	99.7%	41	25	40	2	0	0	1645.94	68	81
WASH complex subunit 7	KIAA1033	WASH7_HUMAN	136.4	100.0%	9	10	15	0.02%	8.4%	LLQTMNLTQK	99.7%	50.8	25	41.2	1	0	0	1205.66	1102	1111
WASH complex subunit 7	KIAA1033	WASH7_HUMAN	136.4	100.0%	9	10	15	0.02%	8.4%	MLVDVFAPEFR	99.7%	60.7	25	54	4	0	0	1323.68	993	1003
WASH complex subunit 7	KIAA1033	WASH7_HUMAN	136.4	100.0%	9	10	15	0.02%	8.4%	SIFANVEAK	95.1%	27.7	25	21.9	1	0	0	978.53	294	302
WASH complex subunit 7	KIAA1033	WASH7_HUMAN	136.4	100.0%	9	10	15	0.02%	8.4%	YLYNLNNQIFIER	99.7%	64.5	25	56.2	1	0	0	1699.88	796	808
WASH complex subunit strumpellin	KIAA0196	STRUM_HUMAN	134.3	99.8%	2	2	2	0.00%	2.4%	IVSCGNAIIAELLR	99.7%	52.7	25	47.4	1	0	0	1528.85	18	31
WASH complex subunit strumpellin	KIAA0196	STRUM_HUMAN	134.3	99.8%	2	2	2	0.00%	2.4%	VPINESFISMVIGR	99.7%	52.9	25	52.9	1	0	0	1561.84	215	228
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	9	10	20	0.02%	16.7%	DYSGQGVVK	99.5%	37.2	25	25.6	2	0	0	952.47	397	405
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	9	10	20	0.02%	16.7%	IAVVGEGR	99.7%	40.5	25	27.6	2	0	0	800.46	117	124
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	9	10	20	0.02%	16.7%	LATGSDDNCAAFFEGPPFK	99.7%	80.2	25	80.2	2	0	0	2043.91	162	180
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	9	10	20	0.02%	16.7%	LYSILGTTLKDEGK	99.7%	76.2	25	64	2	2	0	1537.85	471	484
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	9	10	20	0.02%	16.7%	SIQCLTVHK	99.3%	36.1	25	23	2	0	0	1085.58	322	330
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	9	10	20	0.02%	16.7%	VFASLPQVER	99.7%	43.8	25	40.4	2	0	0	1145.63	8	17

WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	9	10	20	0.02%	16.7%	YAPSGFYIASGDVSGK	99.7%	109	25	103	2	0	0	1618.77	66	81
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	9	10	20	0.02%	16.7%	YEYQPFAGK	99.7%	39.3	25	29.7	2	0	0	1102.52	96	104
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	9	10	20	0.02%	16.7%	YTSLMLR	99.7%	39.4	25	23.1	2	0	0	883.47	390	396
WD repeat-containing protein 5	WDR5	WDR5_HUMAN	36.6	100.0%	3	3	6	0.01%	12.0%	DGSLIVSSSYDGLCR	99.7%	96.1	25	96.1	2	0	0	1628.76	182	196
WD repeat-containing protein 5	WDR5	WDR5_HUMAN	36.6	100.0%	3	3	6	0.01%	12.0%	IWDTASGQCLK	99.7%	55.8	25	51.3	2	0	0	1278.61	197	207
WD repeat-containing protein 5	WDR5	WDR5_HUMAN	36.6	100.0%	3	3	6	0.01%	12.0%	TLIDDDNPPVSFVK	99.7%	70	25	68.6	2	0	0	1559.80	208	221
WD repeat-containing protein 6	WDR6	WDR6_HUMAN	121.7	100.0%	3	3	4	0.00%	3.4%	ATSELILLPVTGLECVGDR	99.7%	41.2	25	41.2	1	0	0	2043.08	12	30
WD repeat-containing protein 6	WDR6	WDR6_HUMAN	121.7	100.0%	3	3	4	0.00%	3.4%	GLGVSALCFK	98.6%	32.7	25	32.4	2	0	0	1051.56	334	343
WD repeat-containing protein 6	WDR6	WDR6_HUMAN	121.7	100.0%	3	3	4	0.00%	3.4%	LFLLQDSGR	98.4%	32.2	25	18.8	1	0	0	1048.58	890	898
WD repeat-containing protein 82	WDR82	WDR82_HUMAN	35.1	100.0%	2	3	6	0.01%	10.9%	VVALSMSPVDDTFISGSLDK	99.7%	107	25	107	4	0	0	2097.04	110	129
WD repeat-containing protein 82	WDR82	WDR82_HUMAN	35.1	100.0%	2	3	6	0.01%	10.9%	YTHAANTVVYSSNK	99.7%	56.9	25	56.9	2	0	0	1554.75	71	84
WD40 repeat-containing protein SMU1	SMU1	SMU1_HUMAN	57.5	99.8%	2	2	3	0.00%	3.9%	LMALLGQALK	99.7%	60.2	25	50.2	2	0	0	1057.64	161	170
WD40 repeat-containing protein SMU1	SMU1	SMU1_HUMAN	57.5	99.8%	2	2	3	0.00%	3.9%	NPEHFVVCNR	96.1%	28.6	25	28.6	1	0	0	1271.59	409	418
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	22	23	50	0.05%	31.6%	AFREEAIK	96.2%	28.8	25	5.34	2	0	0	963.53	641	648
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	22	23	50	0.05%	31.6%	ALQEKVEIK	99.6%	37.9	25	23.4	2	0	0	1057.63	661	669
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	22	23	50	0.05%	31.6%	ANPQVGVAFPHIK	99.7%	39.8	25	33.7	2	0	0	1377.76	401	413
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	22	23	50	0.05%	31.6%	CFSVLGFCK	99.7%	57.2	25	53	3	0	0	1117.52	339	347
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	22	23	50	0.05%	31.6%	EEASGSSVTAEEAK	99.7%	116	25	116	3	0	0	1394.63	689	702
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	22	23	50	0.05%	31.6%	EEASGSSVTAEEAKK	99.7%	94.2	25	79.3	4	0	0	1522.72	689	703
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	22	23	50	0.05%	31.6%	EPLPPIQQHIWNMLNPPAEVTTK	98.6%	27.1	25	27	0	1	0	2669.38	503	525
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	22	23	50	0.05%	31.6%	FFMGNQVLK	99.7%	42.8	25	34.3	2	0	0	1083.57	355	363
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	22	23	50	0.05%	31.6%	GITEQQKEGLEIVK	97.4%	24.6	25	24.6	0	1	0	1571.86	196	209
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	22	23	50	0.05%	31.6%	HIEIFTDLSSR	99.7%	53.7	25	43.7	2	0	0	1317.68	131	141
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	22	23	50	0.05%	31.6%	LFQCLLHR	99.4%	36.7	25	24.7	3	0	0	1086.59	490	497
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	22	23	50	0.05%	31.6%	LGGHGPSFPLK	99.7%	40.9	25	31.5	3	0	0	1109.61	185	195
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	22	23	50	0.05%	31.6%	LTIGSNLSIR	99.7%	62.4	25	51.6	2	0	0	1073.63	251	260
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	22	23	50	0.05%	31.6%	QYMFSSLK	96.1%	28.6	25	22.8	1	0	0	1003.49	432	439
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	22	23	50	0.05%	31.6%	RFFMGNQVLK	96.0%	28.5	25	9.77	1	0	0	1239.67	354	363
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	22	23	50	0.05%	31.6%	SQLDIIIHSLK	99.7%	65.8	25	59.7	2	0	0	1266.74	145	155
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	22	23	50	0.05%	31.6%	SQLDIIIHSLKK	98.5%	26.7	25	26.7	0	2	0	1394.84	145	156
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	22	23	50	0.05%	31.6%	TDTLEDLFPTTK	99.7%	60.3	25	56	2	0	0	1380.69	470	481
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	22	23	50	0.05%	31.6%	TEQGGAHFSVSSLAEGSVTSVGSVNPAENFR	99.7%	45	25	45	0	1	0	3121.48	569	599
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	22	23	50	0.05%	31.6%	TLFPLIEAK	99.7%	49.3	25	32.2	3	0	0	1031.61	535	543
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	22	23	50	0.05%	31.6%	VITMFVQR	99.7%	62.5	25	42.3	4	0	0	993.56	37	44
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	22	23	50	0.05%	31.6%	YGSDIVPFSK	99.7%	61.2	25	48.8	4	0	0	1112.56	316	325
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	16	19	37	0.04%	30.2%	DSLIFLVDASK	99.7%	96.3	25	85.8	6	0	0	1207.66	36	46
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	16	19	37	0.04%	30.2%	DTGIFLDLMHLK	99.7%	64.4	25	59.7	4	0	0	1402.74	195	206
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	16	19	37	0.04%	30.2%	FTVPMLK	97.4%	30.3	25	21.3	1	0	0	835.47	576	582
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	16	19	37	0.04%	30.2%	IISSDRDLLAVVFYGTEK	99.7%	41.3	25	28.6	0	2	0	2026.09	75	92
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	16	19	37	0.04%	30.2%	ILELDQFK	99.7%	39.4	25	11	2	0	0	1005.56	116	123
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	16	19	37	0.04%	30.2%	ILELDQFKGQQGQK	99.7%	82	25	67.6	2	0	0	1631.88	116	129
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	16	19	37	0.04%	30.2%	IMATPEQVGK	99.7%	53.5	25	41.2	4	0	0	1089.56	452	461
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	16	19	37	0.04%	30.2%	IMLFTNEDNPHGNDSAK	99.7%	41.7	25	40	0	3	0	1902.87	166	182
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	16	19	37	0.04%	30.2%	IQVTPPGFQLVFLPFADDK	99.5%	37	25	37	1	0	0	2132.14	425	443
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	16	19	37	0.04%	30.2%	KPGGFDISLFYR	99.7%	48.9	25	42.8	1	0	0	1399.74	207	218
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	16	19	37	0.04%	30.2%	KQELLEALTK	99.7%	49.3	25	38.7	2	0	0	1172.69	596	605
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	16	19	37	0.04%	30.2%	LGSLVDEFK	99.7%	39.8	25	29.5	2	0	0	1007.54	518	526
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	16	19	37	0.04%	30.2%	NIYVLQELDNPGAK	99.7%	135	25	125	3	0	0	1573.82	101	114
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	16	19	37	0.04%	30.2%	QELLEALTK	99.7%	42.5	25	25.9	1	0	0	1044.59	597	605
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	16	19	37	0.04%	30.2%	SDSFENPVLQQHFR	99.7%	51.1	25	45.8	0	1	0	1703.81	475	488
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	16	19	37	0.04%	30.2%	TFNTSTGGLLLPSDTKR	99.7%	93.3	25	92.9	2	0	0	1807.96	302	318

YEATS domain-containing protein 4	YEATS4	YETS4_HUMAN	26.5	100.0%	3	4	7	0.01%	16.7%	GVTIVKPIVYGNVAR	99.6%	39	25	39	2	2	0	1585.94	18	32
YEATS domain-containing protein 4	YEATS4	YETS4_HUMAN	26.5	100.0%	3	4	7	0.01%	16.7%	LFQSDTNAMLGK	99.1%	34.8	25	28.1	1	0	0	1324.66	120	131
YEATS domain-containing protein 4	YEATS4	YETS4_HUMAN	26.5	100.0%	3	4	7	0.01%	16.7%	MAEFGPDSGGR	99.7%	43.3	25	34.6	2	0	0	1139.48	5	15
YTH domain-containing family protein 2	YTHDF2	YTHD2_HUMAN	62.3	100.0%	3	3	7	0.01%	5.9%	LENNENKPVTNSR	99.7%	34.8	25	29.5	0	2	0	1514.76	515	527
YTH domain-containing family protein 2	YTHDF2	YTHD2_HUMAN	62.3	100.0%	3	3	7	0.01%	5.9%	LGSTEVASNVPK	99.7%	65.9	25	57.3	3	0	0	1201.64	194	205
YTH domain-containing family protein 2	YTHDF2	YTHD2_HUMAN	62.3	100.0%	3	3	7	0.01%	5.9%	SYSEDDIHR	99.7%	39.1	25	38.8	2	0	0	1121.49	417	425
Zinc finger CCCH domain-containing protein 18	ZC3H18	ZCH18_HUMAN	106.4	99.8%	2	2	2	0.00%	2.8%	GGQYENFR	99.5%	37.2	25	29.9	1	0	0	970.44	382	389
Zinc finger CCCH domain-containing protein 18	ZC3H18	ZCH18_HUMAN	106.4	99.8%	2	2	2	0.00%	2.8%	TLSGSGSGSGSSYSGSSSR	99.7%	53.8	25	53.8	1	0	0	1707.74	683	701
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	99.8%	2	2	3	0.00%	4.2%	DFVVGALILR	99.7%	59.8	25	55	2	0	0	1102.66	183	192
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	99.8%	2	2	3	0.00%	4.2%	TLFILFR	97.3%	30.1	25	27.2	1	0	0	909.56	255	261
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	99.8%	2	2	4	0.00%	8.8%	LADPAVTDFPAGK	99.7%	59.9	25	59.9	2	0	0	1301.67	225	237
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	99.8%	2	2	4	0.00%	8.8%	TVASSLGQIPMQR	96.7%	29.3	25	20	2	0	0	1403.73	270	282
Zinc finger protein 768	ZNF768	ZN768_HUMAN	60.2	100.0%	4	4	5	0.01%	8.0%	AFADSSYLLR	99.7%	45.6	25	40.7	1	0	0	1142.58	325	334
Zinc finger protein 768	ZNF768	ZN768_HUMAN	60.2	100.0%	4	4	5	0.01%	8.0%	AFSQSSDLIR	99.7%	52.2	25	30	2	0	0	1123.57	521	530
Zinc finger protein 768	ZNF768	ZN768_HUMAN	60.2	100.0%	4	4	5	0.01%	8.0%	FEPESPGFESR	99.4%	36.7	25	22.9	1	0	0	1281.57	79	89
Zinc finger protein 768	ZNF768	ZN768_HUMAN	60.2	100.0%	4	4	5	0.01%	8.0%	FGQSSVLAIHAR	99.7%	62.7	25	56.1	1	0	0	1285.70	438	449
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	3	3	3	0.00%	3.4%	LVSDSLSEHEK	99.7%	49.7	25	45.6	1	0	0	1243.62	757	767
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	3	3	3	0.00%	3.4%	STAPAVAYDSK	99.6%	38.3	25	28.2	1	0	0	1109.55	148	158
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	3	3	3	0.00%	3.4%	STPVTSAVQIPEVK	99.7%	40.2	25	38.8	1	0	0	1455.81	528	541

Table S-1-3. List of proteins identified in immunoprecipitation product of control vector (Replicate 3)

Protein name	Gene name	Accession number	M.W. (kDa)	Protein probability	No. of unique peptide	No. of unique spectra	No. of total spectra	Percentage of total spectra	Sequence coverage	Peptide sequence	Best peptide probability	Mascot			No. of spectra			Calculated +1H peptide mass (AMU)	Peptide index	
												ion score	identity score	delta ion score	+2H	+3H	+4H		start	stop
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	PDK1	PDK1_HUMAN	49.2	100.0%	3	3	4	0.00%	8.5%	AIYDFTDTVIR	99.7%	56.6	25	48.8	1	0	0	1313.67	134	144
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	PDK1	PDK1_HUMAN	49.2	100.0%	3	3	4	0.00%	8.5%	AVPLAGFGYGLPISR	99.7%	60.3	25	60.3	2	0	0	1517.85	349	363
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	PDK1	PDK1_HUMAN	49.2	100.0%	3	3	4	0.00%	8.5%	EISLLPDNLLR	98.4%	31.7	25	17.8	1	0	0	1282.74	93	103
10 kDa heat shock protein, mitochondrial	HSPE1	CH10_HUMAN	10.9	100.0%	4	4	7	0.01%	39.2%	GGEIQPVSVK	99.7%	39.3	25	28.6	2	0	0	1013.56	57	66
10 kDa heat shock protein, mitochondrial	HSPE1	CH10_HUMAN	10.9	100.0%	4	4	7	0.01%	39.2%	GKGGEIQPVSVK	94.8%	27	25	22.6	1	0	0	1198.68	55	66
10 kDa heat shock protein, mitochondrial	HSPE1	CH10_HUMAN	10.9	100.0%	4	4	7	0.01%	39.2%	VGDKVLLPEYGGTK	99.7%	47.7	25	47.7	2	0	0	1475.81	67	80
10 kDa heat shock protein, mitochondrial	HSPE1	CH10_HUMAN	10.9	100.0%	4	4	7	0.01%	39.2%	VLQATVVAVGSGSK	99.7%	107	25	107	2	0	0	1315.76	41	54
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	66	0.07%	28.7%	AFIPAIDSFGFETDLR	99.7%	54.5	25	54.5	3	0	0	1798.90	873	888
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	66	0.07%	28.7%	DSIVQGFQWGTR	99.7%	77	25	74.6	2	0	0	1393.69	764	775
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	66	0.07%	28.7%	EGPLCDELIR	99.7%	40.6	25	28.5	2	0	0	1201.59	776	785
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	66	0.07%	28.7%	FFDDPMLLELAK	99.7%	58.2	25	54.3	6	0	0	1454.72	952	963
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	66	0.07%	28.7%	GGGQIIPTAR	99.7%	42.3	25	39.4	5	0	0	969.55	804	813
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	66	0.07%	28.7%	GLSEDVSISK	99.7%	49.9	25	39.6	2	0	0	1034.54	942	951
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	66	0.07%	28.7%	GNEEAQIFRPLK	99.7%	55	25	44.3	3	0	0	1401.75	570	581
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	66	0.07%	28.7%	IAVEPVNPSELPK	99.7%	71.4	25	63.3	4	0	0	1392.77	590	602
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	66	0.07%	28.7%	ILAQVVGDVDTSLPR	99.7%	43.8	25	43.8	1	0	0	1582.88	380	394
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	66	0.07%	28.7%	ILDAVVAQEPLHR	99.7%	44.6	25	41.3	3	2	0	1460.82	791	803
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	66	0.07%	28.7%	ITMIAEPLEK	99.7%	48.8	25	42.8	4	0	0	1144.63	685	694
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	66	0.07%	28.7%	IYADTFGDINYQEFAK	99.7%	113	25	113	2	0	0	1894.89	326	341
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	66	0.07%	28.7%	KGLSEDVSISK	99.7%	47.3	25	41.7	2	0	0	1162.63	941	951
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	66	0.07%	28.7%	LGEFFQTK	99.7%	48.7	25	39.1	3	0	0	969.50	714	721
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	66	0.07%	28.7%	LNIRPLLR	97.4%	29.8	25	23.6	1	0	0	994.65	410	417
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	66	0.07%	28.7%	SFVEFILEPLYK	99.7%	49.2	25	38.7	3	0	0	1484.80	368	379
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	66	0.07%	28.7%	STPVTVVLPDTK	99.7%	74.9	25	70.5	4	0	0	1256.71	183	194
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	66	0.07%	28.7%	TLDELGIHLTK	99.7%	57.3	25	54.9	2	0	0	1239.69	395	405
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	66	0.07%	28.7%	VADPVVTFCETVVETSSLK	99.7%	65.3	25	59.8	2	0	0	2081.05	655	673
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	66	0.07%	28.7%	VLSGTIHAGQPVK	99.7%	90.6	25	84.4	3	0	0	1306.75	496	508
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	66	0.07%	28.7%	VPAGNWVLIEGVDQPIVK	99.7%	55.8	25	55.8	2	0	0	1934.07	544	561
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	66	0.07%	28.7%	VVYSAFLMATPR	97.9%	30.5	25	22.5	1	0	0	1354.72	815	826
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	66	0.07%	28.7%	YDWDLLAAR	99.7%	63	25	57.3	2	0	0	1122.56	722	730
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	24	27	66	0.07%	28.7%	YHIEVNR	97.1%	29.2	25	12.3	2	0	0	930.48	537	543
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	9	9	15	0.01%	35.3%	DSTLIMQLLR	99.7%	42.2	25	23	3	0	0	1205.66	216	225
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	9	9	15	0.01%	35.3%	EAAENSLVAYK	99.7%	60.5	25	56.9	2	0	0	1194.60	143	153
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	9	9	15	0.01%	35.3%	HLIPAANTGESK	97.0%	29.1	25	21.6	2	0	0	1237.65	107	118
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	9	9	15	0.01%	35.3%	IISSIEQKEENK	99.3%	35.5	25	31.4	1	0	0	1417.75	62	73
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	9	9	15	0.01%	35.3%	KEAAENSLVAYK	99.7%	51.3	25	51.3	1	0	0	1322.70	142	153
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	9	9	15	0.01%	35.3%	LICCDILDVLDK	99.7%	53.4	25	46.8	2	0	0	1476.74	95	106
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	9	9	15	0.01%	35.3%	QMVETELK	99.7%	46.6	25	31.7	1	0	0	977.50	87	94
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	9	9	15	0.01%	35.3%	VAGMDVELTVEER	99.7%	95.8	25	86.7	2	0	0	1463.70	30	42
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	9	9	15	0.01%	35.3%	YLAEFATGNDR	99.7%	40.2	25	36.9	2	0	0	1256.59	131	141
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	9	9	15	0.01%	35.3%	YLAEFATGNDRK	99.7%	49.5	25	43.3	2	0	0	1384.69	131	142
14-3-3 protein eta	YWHAH	1433F_HUMAN	28.2	100.0%	4	4	6	0.01%	22.8%	AVTELNEPLSNEDR	99.7%	49.4	25	48.9	1	0	0	1586.77	29	42
14-3-3 protein eta	YWHAH	1433F_HUMAN	28.2	100.0%	4	4	6	0.01%	22.8%	DSTLIMQLLR	99.7%	42.2	25	23	3	0	0	1205.66	218	227
14-3-3 protein eta	YWHAH	1433F_HUMAN	28.2	100.0%	4	4	6	0.01%	22.8%	NCNDFQYESK	96.2%	28.2	25	28.2	1	0	0	1304.52	111	120
14-3-3 protein eta	YWHAH	1433F_HUMAN	28.2	100.0%	4	4	6	0.01%	22.8%	NSVVEASEAAYK	99.7%	57.4	25	39.7	2	0	0	1267.62	144	155

14-3-3 protein eta	YWHAH	1433F_HUMAN	28.2	100.0%	4	4	6	0.01%	22.8%	YLAEVASGEK	99.7%	56.4	25	45	2	0	0	1066.54	133	142
14-3-3 protein gamma	YWHAG	1433G_HUMAN	28.3	99.8%	2	2	4	0.00%	13.8%	AYSEAHEISK	99.7%	45.5	25	36.1	2	0	0	1134.54	153	162
14-3-3 protein gamma	YWHAG	1433G_HUMAN	28.3	99.8%	2	2	4	0.00%	13.8%	DSTLIMQLLR	99.7%	42.2	25	23	3	0	0	1205.66	218	227
14-3-3 protein gamma	YWHAG	1433G_HUMAN	28.3	99.8%	2	2	4	0.00%	13.8%	NVTELNEPLSNEER	99.7%	92.6	25	92.6	2	0	0	1643.79	29	42
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	6	6	10	0.01%	26.5%	AVTEQGAELSNEER	99.7%	85.7	25	76.4	4	0	0	1532.72	28	41
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	6	6	10	0.01%	26.5%	DSTLIMQLLR	99.7%	42.2	25	23	3	0	0	1205.66	213	222
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	6	6	10	0.01%	26.5%	EKVESELR	99.4%	36.2	25	24.1	1	0	0	989.53	84	91
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	6	6	10	0.01%	26.5%	SICTTVLELLDK	98.1%	30.9	25	26.4	1	0	0	1391.75	92	103
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	6	6	10	0.01%	26.5%	YDDMATCMK	95.9%	27.9	25	27.9	1	0	0	1134.43	19	27
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	6	6	10	0.01%	26.5%	YLAEVACGDDR	94.9%	27	25	27	1	0	0	1268.56	128	138
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	6	6	10	0.01%	26.5%	YLAEVACGDDRK	99.7%	57.7	25	57.4	2	0	0	1396.65	128	139
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	5	5	15	0.01%	26.9%	DICNDVLSLLEK	99.7%	65.1	25	52.2	2	0	0	1418.72	92	103
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	5	5	15	0.01%	26.9%	DSTLIMQLLR	99.7%	42.2	25	23	3	0	0	1205.66	213	222
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	5	5	15	0.01%	26.9%	GIVDQSQQAYQEAFEISK	99.7%	77.2	25	77.2	2	0	0	2040.99	140	157
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	5	5	15	0.01%	26.9%	SVTEQGAELSNEER	99.7%	101	25	95.2	4	0	0	1548.71	28	41
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	5	5	15	0.01%	26.9%	YLAEVAAGDDKK	99.7%	58.8	25	47	4	0	0	1279.65	128	139
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	4	4	5	0.00%	10.0%	AGQVFLEELGNHK	99.7%	81.1	25	76.6	2	0	0	1441.74	205	217
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	4	4	5	0.00%	10.0%	GAFSEEYKR	99.7%	52.1	25	47	1	0	0	1086.52	94	102
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	4	4	5	0.00%	10.0%	GEEVGELSR	98.2%	31.2	25	11.3	1	0	0	975.47	361	369
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	4	4	5	0.00%	10.0%	RPPGVLHCTTK	94.8%	20.4	25	12.5	0	1	0	1265.68	245	255
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	46	0.05%	43.7%	ADHDFVVQEDFMK	99.7%	59.8	25	59.8	4	0	0	1596.70	357	369
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	46	0.05%	43.7%	ALQSVGQIVGEVLK	99.7%	91.9	25	90	7	0	0	1440.84	49	62
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	46	0.05%	43.7%	AVASQLDCNFLK	99.7%	80.8	25	69.4	4	0	0	1365.68	186	197
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	46	0.05%	43.7%	EVIELPLTNPELFQR	99.7%	44.7	25	44.7	5	0	0	1797.97	147	161
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	46	0.05%	43.7%	FSEGTSADR	99.7%	44.4	25	32.4	2	0	0	969.43	243	251
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	46	0.05%	43.7%	HGEIDYEAIVK	99.7%	97.2	25	89	4	0	0	1273.64	323	333
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	46	0.05%	43.7%	IHAGPITK	99.3%	35.4	25	19.6	1	0	0	836.50	315	322
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	46	0.05%	43.7%	IHIDLPNEQAR	99.2%	34.6	25	31	1	0	0	1305.69	299	309
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	46	0.05%	43.7%	LLEHKEIDGR	99.7%	50.2	25	50.2	2	0	0	1209.66	16	25
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	46	0.05%	43.7%	NVCTEAGMFAIR	99.7%	84.9	25	79.4	4	0	0	1384.63	345	356
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	46	0.05%	43.7%	QLTEEKFIVK	95.6%	27.6	25	17.2	1	0	0	1234.70	63	72
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	46	0.05%	43.7%	TLMELLNQMDGFDTLHR	97.5%	22.5	25	21.1	0	1	0	2065.97	256	272
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	46	0.05%	43.7%	VALDMTTLTIMR	99.7%	92.9	25	89.7	6	0	0	1364.73	98	109
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	46	0.05%	43.7%	VVSSSIVDKYIGESAR	99.7%	84.5	25	84.5	2	2	0	1709.91	198	213
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	19	36	0.04%	52.7%	AICTEAGLMALR	99.7%	77.7	25	65.7	3	0	0	1321.66	397	408
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	19	36	0.04%	52.7%	APQETYADIGGLDNQIQEIK	99.7%	83.9	25	82.4	1	0	0	2203.09	179	198
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	19	36	0.04%	52.7%	AVANQTSATFLR	99.7%	76.9	25	69.6	6	0	0	1278.68	238	249
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	19	36	0.04%	52.7%	DDLSGADIK	95.7%	27.7	25	16.9	1	0	0	933.45	388	396
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	19	36	0.04%	52.7%	GVILYGPPGTGK	99.7%	68.5	25	0	4	0	0	1158.65	221	232
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	19	36	0.04%	52.7%	IETLDPALIRPGR	99.7%	29.1	25	24.4	0	2	0	1450.84	334	346
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	19	36	0.04%	52.7%	IFQIHTSR	99.7%	47.1	25	31.7	2	0	0	1001.55	364	371
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	19	36	0.04%	52.7%	KIEFPLPDEK	99.7%	50.4	25	31.2	1	0	0	1215.66	350	359
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	19	36	0.04%	52.7%	KQEGTPEGLYL	99.7%	60.9	25	49.8	2	0	0	1234.63	430	440
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	19	36	0.04%	52.7%	KYEPPVPTR	99.0%	33.9	25	22.6	2	0	0	1086.59	24	32
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	19	36	0.04%	52.7%	LPLVTPHTQCR	99.7%	55.1	25	45.5	2	0	0	1321.70	49	59
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	19	36	0.04%	52.7%	MTLADDVTLDDLIMAK	99.7%	44.7	25	44.7	1	0	0	1780.87	372	387
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	19	36	0.04%	52.7%	NQEQMKPLEEKQEEER	97.8%	23	25	23	0	1	0	2060.96	81	96
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	19	36	0.04%	52.7%	TMLELLNQLDGFDSR	99.7%	93.9	25	87.8	4	0	0	1751.86	308	322
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	19	36	0.04%	52.7%	VAEEHAPSIVFIDEIDAIGTK	99.7%	72.9	25	72.9	0	2	0	2254.16	273	293
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	19	36	0.04%	52.7%	VAEEHAPSIVFIDEIDAIGTKR	99.7%	67.8	25	67.8	0	2	0	2410.26	273	294
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	19	36	0.04%	52.7%	VHAVIGVLMDDTDPLVTVMK	99.7%	34.9	25	34.9	0	2	0	2153.13	156	175

26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	19	36	0.04%	52.7%	VIMATNR	99.7%	40.6	25	36.2	1	0	0	804.44	327	333
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	17	19	36	0.04%	52.7%	VVGSELIQK	99.7%	62	25	47.9	2	0	0	972.57	250	258
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	48	0.05%	50.8%	AMEVDERPTEQYSDIGGLDK	99.7%	46.8	25	46.8	0	2	0	2269.03	174	193
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	48	0.05%	50.8%	APSIIFIDELDAIGTK	99.7%	78.9	25	74.2	2	0	0	1702.93	279	294
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	48	0.05%	50.8%	AVCVEAGMIALRR	98.4%	31.7	25	29.7	1	0	0	1445.77	398	410
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	48	0.05%	50.8%	DSYLILETLPTEYDSR	99.7%	81	25	73.5	2	0	0	1914.93	156	171
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	48	0.05%	50.8%	EKAPSIIFIDELDAIGTK	99.7%	29.4	25	29.4	0	1	0	1960.06	277	294
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	48	0.05%	50.8%	EKFENLGIQPPK	99.7%	51.8	25	44.7	2	0	0	1399.76	210	221
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	48	0.05%	50.8%	FENLGIQPPK	99.7%	39	25	25.3	2	0	0	1142.62	212	221
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	48	0.05%	50.8%	GVLMYGPPGTGK	99.7%	77.8	25	69.5	4	0	0	1192.60	222	233
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	48	0.05%	50.8%	IMQIHSR	99.6%	37.6	25	24.9	2	0	0	884.48	365	371
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	48	0.05%	50.8%	KMNVSPDVNYEELAR	99.7%	70.2	25	57	0	4	0	1780.85	372	386
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	48	0.05%	50.8%	LAGPQLVQMFIGDGAK	99.7%	87.3	25	87.3	4	0	0	1644.88	251	266
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	48	0.05%	50.8%	LLDSEIK	97.6%	30	25	12.4	1	0	0	817.47	47	53
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	48	0.05%	50.8%	MSTEEIIQR	99.7%	73.4	25	49.5	4	0	0	1106.55	36	44
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	48	0.05%	50.8%	QIQELVEAIVLPMNHK	99.7%	43.2	25	43.2	0	2	0	1862.02	194	209
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	48	0.05%	50.8%	QTYFLPVIGLVDAEK	99.7%	70.3	25	58.1	4	0	0	1692.92	130	144
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	48	0.05%	50.8%	TMLELLNQLDGFQPNTQVK	99.7%	81.3	25	81.3	3	0	0	2189.13	309	327
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	48	0.05%	50.8%	VDILDPALLR	99.7%	63.6	25	47.8	4	0	0	1124.67	335	344
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	48	0.05%	50.8%	VIAATNRVDILDPALLR	99.7%	70.1	25	70.1	1	2	0	1850.09	328	344
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	48	0.05%	50.8%	VTHELQAMKDK	99.7%	48.7	25	47.5	1	0	0	1299.67	62	72
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	16	22	39	0.04%	42.6%	ADTLDPALLRPGR	99.4%	36.1	25	34	2	0	0	1394.78	314	326
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	16	22	39	0.04%	42.6%	AVAHHTTAAFIR	99.7%	58.6	25	54.5	2	2	0	1294.70	218	229
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	16	22	39	0.04%	42.6%	EAVELPLTHFELYK	99.7%	48	25	46.5	2	0	0	1688.89	179	192
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	16	22	39	0.04%	42.6%	EFLHAQEEVKR	99.7%	59.5	25	41.7	2	0	0	1385.72	71	81
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	16	22	39	0.04%	42.6%	ELLKPNASVALHK	99.7%	41.3	25	40.1	0	2	0	1419.83	122	134
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	16	22	39	0.04%	42.6%	ENAPAIIFIDEIDAIATK	99.7%	77.3	25	77.3	2	1	0	1944.03	256	273
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	16	22	39	0.04%	42.6%	ENAPAIIFIDEIDAIATKR	99.7%	38	25	38	0	1	0	2100.13	256	274
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	16	22	39	0.04%	42.6%	FDAQTGADREVQR	99.7%	41.4	25	34.1	2	1	0	1492.71	275	287
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	16	22	39	0.04%	42.6%	GVLMYGPPGCGK	99.7%	60.3	25	60.3	4	0	0	1235.59	201	212
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	16	22	39	0.04%	42.6%	ILLELLNQMDGFDQNVNVK	99.7%	93.8	25	93.8	3	1	0	2219.14	288	306
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	16	22	39	0.04%	42.6%	LIFSTITSK	99.7%	47.2	25	43.4	2	0	0	1009.59	343	351
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	16	22	39	0.04%	42.6%	MNLSEEVDLEDYVARPDK	99.7%	57.2	25	57.2	1	0	0	2138.99	352	369
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	16	22	39	0.04%	42.6%	QIGIDPPR	99.5%	36.4	25	25.5	2	0	0	895.50	193	200
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	16	22	39	0.04%	42.6%	RFDAQTGADR	99.4%	35.7	25	21.5	2	0	0	1136.54	274	283
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	16	22	39	0.04%	42.6%	RLIFSTITSK	99.6%	38.2	25	38.2	2	0	0	1165.69	342	351
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	16	22	39	0.04%	42.6%	VIMATNR	99.7%	40.6	25	36.2	1	0	0	804.44	307	313
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	16	22	39	0.04%	42.6%	VVGSEFVQK	99.7%	76.4	25	61	3	0	0	992.54	230	238
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	28	57	0.06%	54.7%	ACLIFFDEIDAIGGAR	99.7%	56.2	25	56.2	1	0	0	1767.87	269	284
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	28	57	0.06%	54.7%	ALDEGDIALLK	99.7%	73.9	25	58.7	2	0	0	1157.64	24	34
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	28	57	0.06%	54.7%	DIRFELLAR	99.3%	35.5	25	32.5	2	0	0	1132.65	367	375
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	28	57	0.06%	54.7%	FDDGAGGDNEVQR	99.7%	86.6	25	86.6	3	0	0	1379.58	285	297
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	28	57	0.06%	54.7%	FVNLGIEPPK	99.7%	56.1	25	37.5	5	0	0	1113.63	201	210
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	28	57	0.06%	54.7%	FVNLGIEPPKGVLLFGPPGTGK	99.3%	26.8	25	26.8	0	1	0	2237.27	201	222
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	28	57	0.06%	54.7%	FVVDLSDQVAPTDIEEGMR	99.7%	71.1	25	62.7	4	0	0	2137.01	121	139
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	28	57	0.06%	54.7%	GVLLFGPPGTGK	99.7%	60.3	25	48.6	5	0	0	1142.66	211	222
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	28	57	0.06%	54.7%	IATEKDFLEAVNK	99.7%	69	25	61.4	2	2	0	1477.79	403	415
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	28	57	0.06%	54.7%	IEFSLPDLEGR	99.7%	41.6	25	32	2	0	0	1275.66	341	351
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	28	57	0.06%	54.7%	IINADSEDPK	99.6%	37.7	25	29.8	2	0	0	1101.54	101	110
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	28	57	0.06%	54.7%	IINADSEDPKYIINVK	99.7%	88.4	25	88.4	1	1	0	1831.98	101	116
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	28	57	0.06%	54.7%	KINELTGIK	99.7%	39.2	25	29.1	2	0	0	1015.61	58	66

26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	28	57	0.06%	54.7%	LCPNSTGAEIR	99.7%	53.7	25	35.3	2	0	0	1217.59	376	386
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	28	57	0.06%	54.7%	LREVVETPLLHPER	99.7%	49.6	25	40.9	1	2	0	1687.95	187	200
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	28	57	0.06%	54.7%	PDYLGADQRK	99.7%	42.2	25	32.4	2	0	0	1162.59	2	11
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	28	57	0.06%	54.7%	QVEDDIQQLLK	99.7%	77.5	25	68.8	2	0	0	1328.71	47	57
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	28	57	0.06%	54.7%	SVCTEAGMFAIR	99.7%	60.1	25	53.5	4	0	0	1341.63	387	398
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	28	57	0.06%	54.7%	TDACFIR	99.7%	44.7	25	38.2	1	0	0	882.41	233	239
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	28	57	0.06%	54.7%	TMLELINQLDGFDPR	99.7%	74.1	25	67.6	4	0	0	1777.88	298	312
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	28	57	0.06%	54.7%	TYGQSTYSR	99.4%	35.6	25	28	2	0	0	1062.49	35	43
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	22	28	57	0.06%	54.7%	VIGSELVQK	99.7%	56.4	25	41	2	0	0	972.57	240	248
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	23	51	0.05%	46.8%	AVAHHTDCTFIR	99.7%	56.1	25	45.6	2	2	0	1427.68	202	213
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	23	51	0.05%	46.8%	EHAPSIIFMDEIDSIGSSR	99.7%	43.5	25	43.5	0	2	0	2120.00	240	258
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	23	51	0.05%	46.8%	ELFVMAR	98.6%	32.4	25	18	2	0	0	865.46	233	239
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	23	51	0.05%	46.8%	FVVDVDKNIDINDVTPNCR	99.7%	32.4	25	32.4	0	2	0	2233.09	95	113
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	23	51	0.05%	46.8%	GVCTEAGMYALR	99.7%	65.9	25	61.7	4	0	0	1327.61	361	372
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	23	51	0.05%	46.8%	GVLLYGPPGTGK	99.7%	68.5	25	0	4	0	0	1158.65	185	196
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	23	51	0.05%	46.8%	IAELMPGASGAEVK	99.7%	62.2	25	47	4	0	0	1388.71	347	360
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	23	51	0.05%	46.8%	IDILDSALLRPGR	99.7%	62	25	60.1	2	2	0	1438.84	298	310
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	23	51	0.05%	46.8%	IEELQLIVNDK	99.7%	95.9	25	87.5	2	0	0	1313.73	28	38
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	23	51	0.05%	46.8%	LEGGSGGDSEVQR	99.7%	92.1	25	92.1	6	0	0	1290.59	259	271
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	23	51	0.05%	46.8%	NDSYTLHK	94.6%	26.9	25	24.4	1	0	0	977.47	118	125
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	23	51	0.05%	46.8%	TMLELLNQLDGFEATK	99.7%	116	25	114	5	0	0	1838.92	272	287
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	23	51	0.05%	46.8%	VALRNDSYTLHK	99.7%	37.1	25	23.4	0	2	0	1416.76	114	125
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	23	51	0.05%	46.8%	VIMATNR	99.7%	40.6	25	36.2	1	0	0	804.44	291	297
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	23	51	0.05%	46.8%	VPDSTYEMIGGLDK	99.7%	91.1	25	85.8	4	0	0	1540.72	143	156
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	16	23	51	0.05%	46.8%	VSGSELVQK	99.7%	78.4	25	45.8	4	0	0	946.52	214	222
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	19	24	47	0.05%	28.8%	AAVESLGFILFR	99.7%	82.9	25	82.9	7	0	0	1322.75	617	628
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	19	24	47	0.05%	28.8%	DTSEDIEELVEPVAAHGPK	99.7%	44.8	25	43.9	1	1	0	2035.98	916	934
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	19	24	47	0.05%	28.8%	EAINLLEPMTNDPVNYVR	99.7%	72.7	25	72.7	4	0	0	2088.04	667	684
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	19	24	47	0.05%	28.8%	EALQLMATYLPK	99.7%	60.6	25	50	4	0	0	1377.74	418	429
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	19	24	47	0.05%	28.8%	FTATASLGVIHK	99.7%	29.5	25	28.9	0	2	0	1244.70	402	413
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	19	24	47	0.05%	28.8%	GLAVGIALVMYGR	99.7%	74.6	25	74.6	2	0	0	1335.75	547	559
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	19	24	47	0.05%	28.8%	LLHVAVSDVNDDVRR	99.7%	49.5	25	45.7	0	2	0	1707.91	602	616
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	19	24	47	0.05%	28.8%	MEEADALIESLCR	99.7%	95.7	25	92.9	4	0	0	1536.70	560	572
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	19	24	47	0.05%	28.8%	NNNTDLMILK	99.7%	39.7	25	14.6	2	0	0	1191.60	345	354
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	19	24	47	0.05%	28.8%	QDVYDLLK	99.7%	40.8	25	16.8	2	0	0	993.53	491	498
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	19	24	47	0.05%	28.8%	QFAALVASK	99.7%	62.2	25	43.2	2	0	0	934.54	58	66
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	19	24	47	0.05%	28.8%	RLDVFEK	95.3%	27.4	25	10.9	1	0	0	906.50	159	165
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	19	24	47	0.05%	28.8%	SNCKPSTFAYPAPLEVPK	99.7%	29.1	25	15.5	0	2	0	2006.01	804	821
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	19	24	47	0.05%	28.8%	TILESNDVPGMLAYSLK	99.7%	90.1	25	88	2	0	0	1850.96	166	182
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	19	24	47	0.05%	28.8%	TPEASPEPK	99.7%	47.8	25	47.8	2	0	0	955.47	311	319
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	19	24	47	0.05%	28.8%	TPEQCPSVVSLLSESYNPHVR	99.7%	48.3	25	48.3	0	2	0	2399.17	629	649
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	19	24	47	0.05%	28.8%	TVGTPIASVPGSTNTGTVPGSEKDSDSMETEEK	99.7%	31.1	25	30.8	0	1	0	3324.53	270	302
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	19	24	47	0.05%	28.8%	VSTAVLSITAK	99.7%	93.8	25	90.4	2	0	0	1089.65	828	838
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	19	24	47	0.05%	28.8%	YGAAMALGICCAGTGNK	99.7%	93.4	25	84.8	2	0	0	1714.77	650	666
26S proteasome non-ATPase regulatory subunit 10	PSMD10	PSD10_HUMAN	24.4	100.0%	4	4	6	0.01%	28.8%	ASTNIQDTEGNTPLHLACDEERVEEAK	99.7%	58.7	25	57.9	0	2	0	3027.40	163	189
26S proteasome non-ATPase regulatory subunit 10	PSMD10	PSD10_HUMAN	24.4	100.0%	4	4	6	0.01%	28.8%	LEELKESILADK	99.7%	62.3	25	50.2	2	0	0	1387.77	19	30
26S proteasome non-ATPase regulatory subunit 10	PSMD10	PSD10_HUMAN	24.4	100.0%	4	4	6	0.01%	28.8%	LLVSQGASIYIENKEEK	99.6%	28.8	25	19.5	0	1	0	1921.03	190	206
26S proteasome non-ATPase regulatory subunit 10	PSMD10	PSD10_HUMAN	24.4	100.0%	4	4	6	0.01%	28.8%	MIHILLYYK	97.8%	30.4	25	20.2	1	0	0	1193.68	154	162
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	5	5	8	0.01%	14.0%	EQSILELGSLLAK	99.7%	42.3	25	42.3	2	0	0	1400.80	47	59
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	5	5	8	0.01%	14.0%	LYDNLLEQNLIR	99.7%	63.9	25	58.8	2	0	0	1503.82	326	337
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	5	5	8	0.01%	14.0%	TGQAAELGGLLK	99.7%	52.6	25	41.2	1	0	0	1157.65	60	71

26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	5	5	8	0.01%	14.0%	TTANAIYCPPK	99.7%	38.9	25	34.9	1	0	0	1235.61	195	205
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	5	5	8	0.01%	14.0%	VQIEHISSLIK	99.7%	45.2	25	45.2	2	0	0	1266.74	345	355
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	11	12	21	0.02%	32.7%	DLPVSEQQER	99.7%	46.3	25	45.2	2	0	0	1200.59	187	196
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	11	12	21	0.02%	32.7%	FLGCVDIKDLPVSEQQER	99.7%	41.4	25	41.4	0	1	0	2133.06	179	196
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	11	12	21	0.02%	32.7%	GSIDEVDKR	99.6%	37.8	25	27.2	2	0	0	1018.52	322	330
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	11	12	21	0.02%	32.7%	ITVNEVELLVMK	99.7%	65.2	25	65.2	2	0	0	1387.79	302	313
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	11	12	21	0.02%	32.7%	LNIGDLQVTK	99.7%	51.7	25	40.9	2	0	0	1100.63	123	132
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	11	12	21	0.02%	32.7%	LYENFISEFEHR	99.7%	53.6	25	53.6	1	0	0	1583.75	59	70
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	11	12	21	0.02%	32.7%	QLTFEEIAK	97.4%	29.6	25	26.5	1	0	0	1078.58	290	298
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	11	12	21	0.02%	32.7%	QMTDPNVALTFLEK	99.7%	50.9	25	45.9	4	0	0	1622.81	86	99
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	11	12	21	0.02%	32.7%	TAWGQQPDLAANEAQLLR	99.7%	73.7	25	73.7	2	0	0	1982.01	253	270
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	11	12	21	0.02%	32.7%	VLDLQQIK	99.7%	47.6	25	28	2	0	0	956.58	340	347
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	11	12	21	0.02%	32.7%	YYQTIGNHASYYK	99.7%	64.1	25	64.1	2	0	0	1607.75	162	174
26S proteasome non-ATPase regulatory subunit 14	PSMD14	PSDE_HUMAN	34.6	100.0%	2	3	6	0.01%	9.4%	AVAVVVDPIQSVK	99.7%	71.6	25	71.6	3	0	0	1324.78	140	152
26S proteasome non-ATPase regulatory subunit 14	PSMD14	PSDE_HUMAN	34.6	100.0%	2	3	6	0.01%	9.4%	AVEEEDKMTPEQLAIK	99.7%	41.5	25	41.5	3	0	0	1830.92	258	273
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	24	30	60	0.06%	31.6%	APVQPQQSPAAAPGGTDEKPSGK	99.7%	62.6	25	61.4	0	2	0	2218.11	9	31
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	24	30	60	0.06%	31.6%	AVPLALALISVSNPR	99.7%	68.2	25	68.2	2	2	0	1520.92	689	703
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	24	30	60	0.06%	31.6%	CALGVFR	99.4%	36	25	30.9	2	0	0	822.43	251	257
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	24	30	60	0.06%	31.6%	DIDENAYAK	99.6%	37.6	25	37.6	2	0	0	1038.47	220	228
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	24	30	60	0.06%	31.6%	DKAPVQPQQSPAAAPGGTDEKPSGK	99.7%	30.9	25	30.9	0	2	0	2461.23	7	31
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	24	30	60	0.06%	31.6%	DPNNLFMVR	98.7%	32.7	25	19.2	2	0	0	1105.55	755	763
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	24	30	60	0.06%	31.6%	DTSLYRPALEELRR	98.1%	23.4	25	22	0	1	0	1718.92	67	80
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	24	30	60	0.06%	31.6%	EDVLTLLLPVMGDSK	99.7%	92.4	25	85.3	4	0	0	1629.88	495	509
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	24	30	60	0.06%	31.6%	ELDIMEPK	99.7%	38.8	25	10.5	4	0	0	990.48	336	343
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	24	30	60	0.06%	31.6%	EPLLTLVK	98.5%	32	25	32	2	0	0	912.58	182	189
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	24	30	60	0.06%	31.6%	FAADIISVLAMTMSGER	99.7%	78.4	25	75.7	4	0	0	1843.89	121	137
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	24	30	60	0.06%	31.6%	FGGSGSQVDSAR	99.7%	109	25	91.6	4	0	0	1167.54	358	369
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	24	30	60	0.06%	31.6%	GTLTLCPYHSDR	99.7%	51.6	25	51.6	2	0	0	1419.67	774	785
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	24	30	60	0.06%	31.6%	LAQGLTHLGK	99.7%	71.6	25	69.3	2	0	0	1037.61	764	773
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	24	30	60	0.06%	31.6%	LGSIFGLGLAYAGSNR	99.7%	68.6	25	65.9	2	0	0	1595.85	479	494
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	24	30	60	0.06%	31.6%	LNILDTLSK	99.7%	50.7	25	30	2	0	0	1016.60	704	712
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	24	30	60	0.06%	31.6%	LVGSQEELASWGHEYVR	99.7%	29.6	25	27.7	0	2	0	1959.96	144	160
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	24	30	60	0.06%	31.6%	SETELKDTYAR	99.7%	38.9	25	38.9	1	2	0	1312.64	546	556
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	24	30	60	0.06%	31.6%	SFANTLVDVCAYAGSGNVLK	99.7%	113	25	109	2	0	0	2086.03	589	608
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	24	30	60	0.06%	31.6%	SSTTSMTSVPKPLK	99.7%	67.8	25	67.8	4	0	0	1463.78	84	97
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	24	30	60	0.06%	31.6%	VGQAVDVVGQAGKPK	99.7%	90.6	25	83.8	2	1	0	1452.82	846	860
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	24	30	60	0.06%	31.6%	VPDDIYK	97.9%	30.6	25	23.1	1	0	0	849.44	344	350
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	24	30	60	0.06%	31.6%	YGEPTLR	99.6%	38.4	25	30.1	2	0	0	835.43	681	687
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	24	30	60	0.06%	31.6%	YLYSSEDYIK	99.7%	52	25	45.5	2	0	0	1280.60	432	441
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	52	0.05%	46.4%	AIQLEYSEAR	99.7%	85.7	25	78.8	2	0	0	1179.60	297	306
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	52	0.05%	46.4%	AIRDGVIEASINHEK	98.5%	24.2	25	19.2	0	1	0	1651.88	441	455
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	52	0.05%	46.4%	ALDLVAAK	99.2%	34.8	25	18.9	1	0	0	800.49	202	209
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	52	0.05%	46.4%	APQHTAVGFK	99.7%	39.3	25	38.2	1	0	0	1055.56	316	325
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	52	0.05%	46.4%	AVQGFFTSNNATR	99.7%	93.9	25	93.9	2	0	0	1412.69	116	128
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	52	0.05%	46.4%	DGVIEASINHEK	99.7%	58.9	25	44	2	0	0	1311.65	444	455
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	52	0.05%	46.4%	DLESAEERR	99.2%	34.6	25	19.8	1	0	0	1104.53	504	512
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	52	0.05%	46.4%	ELDTVTLEDIKEHVK	99.7%	35.9	25	35.9	0	2	0	1768.93	66	80
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	52	0.05%	46.4%	EMIDIYSTR	99.7%	65.9	25	52	4	0	0	1127.54	462	470
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	52	0.05%	46.4%	EPQLAFHQR	99.7%	47.6	25	33.6	1	0	0	1125.58	471	479
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	52	0.05%	46.4%	EQQDLEFAK	99.7%	44.7	25	41.4	1	0	0	1107.53	515	523
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	52	0.05%	46.4%	EREQQDLEFAK	99.7%	42.2	25	32	1	0	0	1392.68	513	523

26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	52	0.05%	46.4%	FNQVLDQFGEK	99.7%	81.9	25	57.5	2	0	0	1324.65	375	385
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	52	0.05%	46.4%	HDADGQATLLNLLLR	99.7%	50.9	25	50.9	2	0	0	1649.90	242	256
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	52	0.05%	46.4%	ISDDLMQK	99.7%	49.1	25	16.4	3	0	0	949.47	187	194
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	52	0.05%	46.4%	ISFCLDIHNMSVK	99.7%	56.2	25	51	2	0	0	1563.77	480	492
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	52	0.05%	46.4%	ISLADIAQK	99.7%	64.2	25	17.1	3	0	0	958.56	417	425
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	52	0.05%	46.4%	LQLDSPEDAEFIVAK	99.7%	89.2	25	79.6	2	0	0	1674.86	426	440
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	52	0.05%	46.4%	MISLSYSR	99.7%	50.2	25	42	3	0	0	956.49	409	416
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	52	0.05%	46.4%	NYLHYSLYDQAEK	99.7%	80.5	25	70.8	2	2	0	1643.77	257	269
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	52	0.05%	46.4%	RALDLVAAK	95.1%	27.2	25	19.2	1	0	0	956.59	201	209
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	52	0.05%	46.4%	SLMPYFLLTQAVR	99.7%	88.9	25	71.7	4	0	0	1538.84	356	368
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	52	0.05%	46.4%	SVFPEQANNNEWAR	99.7%	72.3	25	69.7	2	0	0	1661.77	274	287
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	52	0.05%	46.4%	VYEFLDKLDVVR	99.7%	70.7	25	65	2	2	0	1495.82	217	228
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	52	0.05%	46.4%	YLYYTGR	97.8%	30.4	25	20.5	1	0	0	935.46	288	294
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	7	9	18	0.02%	25.2%	AAAASAAEAGIATTGTEDSDDALLK	99.7%	123	25	123	2	2	0	2320.12	238	262
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	7	9	18	0.02%	25.2%	IIAFVGSPVEDNEKDLVK	99.7%	72	25	70.3	2	2	0	1973.06	109	126
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	7	9	18	0.02%	25.2%	ITFCTGIR	99.7%	57.4	25	48.6	4	0	0	967.50	84	91
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	7	9	18	0.02%	25.2%	LQAQQDAVNIVCHSK	99.7%	36.5	25	26.7	0	2	0	1710.86	26	40
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	7	9	18	0.02%	25.2%	MTISQQEFGR	99.7%	44.2	25	37	1	0	0	1212.57	263	272
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	7	9	18	0.02%	25.2%	NAMGSLASQATK	98.7%	32.7	25	32.4	1	0	0	1194.58	354	365
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	7	9	18	0.02%	25.2%	VSMEEQR	99.7%	40.9	25	31.1	2	0	0	878.40	222	228
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	15	20	36	0.04%	41.1%	DNNMAPYYEALCK	99.7%	46.3	25	40	2	0	0	1604.67	47	59
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	15	20	36	0.04%	41.1%	FLLSLPEHR	99.7%	46.8	25	40	2	0	0	1111.63	24	32
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	15	20	36	0.04%	41.1%	GAEILEVLHSLPAVR	99.7%	79.9	25	74.8	2	0	0	1603.92	243	257
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	15	20	36	0.04%	41.1%	GDAAVRDELMAAVR	99.7%	47.2	25	38.7	3	3	0	1489.74	33	46
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	15	20	36	0.04%	41.1%	IDKVNEIVETNRPDSK	99.7%	38.4	25	38.4	0	2	0	1856.97	347	362
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	15	20	36	0.04%	41.1%	IGLFYMDNDLITR	99.7%	95.4	25	90.8	4	0	0	1570.79	147	159
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	15	20	36	0.04%	41.1%	IHAYSQLLESYR	99.7%	62.1	25	51.1	2	2	0	1479.76	301	312
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	15	20	36	0.04%	41.1%	KGDLLLNR	99.7%	53	25	40.1	2	0	0	928.56	372	379
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	15	20	36	0.04%	41.1%	LDIVFYLLR	99.7%	65.8	25	47.5	2	0	0	1151.68	138	146
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	15	20	36	0.04%	41.1%	PLENLEEEGLPK	99.7%	54.6	25	54.6	1	0	0	1367.71	2	13
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	15	20	36	0.04%	41.1%	PLENLEEEGLPKNPDLR	99.6%	28.9	25	28.7	0	2	0	1963.01	2	18
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	15	20	36	0.04%	41.1%	QYLFSLYECR	99.7%	48.8	25	41.6	2	0	0	1378.65	258	267
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	15	20	36	0.04%	41.1%	SLDWQIDVDLLNK	98.2%	31.2	25	29.9	1	0	0	1558.81	60	72
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	15	20	36	0.04%	41.1%	VNEIVETNRPDSK	99.7%	55.2	25	44.1	2	0	0	1500.77	350	362
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	15	20	36	0.04%	41.1%	VYQGLYCVAIR	99.7%	76.7	25	76.7	2	0	0	1341.70	182	192
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	4	4	9	0.01%	11.4%	DIQTNVYIK	99.7%	46.5	25	38.1	3	0	0	1093.59	219	227
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	4	4	9	0.01%	11.4%	ILFFNTPK	96.1%	28.1	25	19.5	1	0	0	979.56	290	297
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	4	4	9	0.01%	11.4%	ILFTEATR	99.5%	37.1	25	22.1	1	0	0	950.53	282	289
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	4	4	9	0.01%	11.4%	LVLLELNFLPTTGTK	99.7%	61.5	25	61.5	4	0	0	1658.97	121	135
28S ribosomal protein S10, mitochondrial	MRPS10	RT10_HUMAN	23.0	99.9%	2	2	3	0.00%	13.4%	AVLDSYEYFAVLAAK	98.0%	30.7	25	30.7	1	0	0	1659.86	86	100
28S ribosomal protein S10, mitochondrial	MRPS10	RT10_HUMAN	23.0	99.9%	2	2	3	0.00%	13.4%	NLPEGVAMEVTK	99.3%	35.4	25	31	2	0	0	1287.66	163	174
28S ribosomal protein S11, mitochondrial	MRPS11	RT11_HUMAN	20.6	100.0%	4	6	11	0.01%	22.2%	FSIYPPIPGEESSLR	96.7%	28.7	25	26.4	1	0	0	1691.86	60	74
28S ribosomal protein S11, mitochondrial	MRPS11	RT11_HUMAN	20.6	100.0%	4	6	11	0.01%	22.2%	GTGIAAQTAGIAAAAR	99.7%	80.6	25	75.7	2	0	0	1399.77	123	138
28S ribosomal protein S11, mitochondrial	MRPS11	RT11_HUMAN	20.6	100.0%	4	6	11	0.01%	22.2%	KFEEIPIAHIK	99.7%	41.4	25	41.4	2	2	0	1324.76	79	89
28S ribosomal protein S11, mitochondrial	MRPS11	RT11_HUMAN	20.6	100.0%	4	6	11	0.01%	22.2%	KGTGIAAQTAGIAAAAR	99.7%	105	25	96.1	2	2	0	1527.86	122	138
28S ribosomal protein S12, mitochondrial	MRPS12	RT12_HUMAN	15.2	99.9%	2	2	6	0.01%	14.5%	GVVLCTFTR	99.7%	44.8	25	33.6	4	0	0	1052.56	60	68
28S ribosomal protein S12, mitochondrial	MRPS12	RT12_HUMAN	15.2	99.9%	2	2	6	0.01%	14.5%	LGPTEGRPQLK	99.6%	37.7	25	28.9	2	0	0	1195.68	49	59
28S ribosomal protein S14, mitochondrial	MRPS14	RT14_HUMAN	15.1	100.0%	2	2	6	0.01%	21.9%	HLADHGQLSGIQR	99.7%	49.6	25	40.8	2	0	0	1431.75	113	125
28S ribosomal protein S14, mitochondrial	MRPS14	RT14_HUMAN	15.1	100.0%	2	2	6	0.01%	21.9%	ILQDVADEEIAALPR	99.7%	86.6	25	74.5	4	0	0	1652.89	66	80
28S ribosomal protein S15, mitochondrial	MRPS15	RT15_HUMAN	29.8	100.0%	5	5	10	0.01%	18.3%	IVANPEDTR	99.7%	41.6	25	35.9	3	0	0	1014.52	115	123
28S ribosomal protein S15, mitochondrial	MRPS15	RT15_HUMAN	29.8	100.0%	5	5	10	0.01%	18.3%	LDDDPPPSTLLK	99.7%	57.1	25	54.5	1	0	0	1310.68	63	74

28S ribosomal protein S15, mitochondrial	MRPS15	RT15_HUMAN	29.8	100.0%	5	5	10	0.01%	18.3%	NTNYDVFEK	99.7%	51.1	25	39.9	2	0	0	1129.52	172	180
28S ribosomal protein S15, mitochondrial	MRPS15	RT15_HUMAN	29.8	100.0%	5	5	10	0.01%	18.3%	SYEEHLEK	98.6%	32.2	25	26.2	1	0	0	1034.48	138	145
28S ribosomal protein S15, mitochondrial	MRPS15	RT15_HUMAN	29.8	100.0%	5	5	10	0.01%	18.3%	YLLMSIDQR	99.7%	77	25	68.5	3	0	0	1138.59	155	163
28S ribosomal protein S16, mitochondrial	MRPS16	RT16_HUMAN	15.3	100.0%	3	4	8	0.01%	26.3%	AREVLLASQK	99.7%	58.7	25	45.6	2	0	0	1114.66	115	124
28S ribosomal protein S16, mitochondrial	MRPS16	RT16_HUMAN	15.3	100.0%	3	4	8	0.01%	26.3%	FVEQLGSYDPLPNSHGEK	99.7%	48.1	25	48.1	2	2	0	2016.97	47	64
28S ribosomal protein S16, mitochondrial	MRPS16	RT16_HUMAN	15.3	100.0%	3	4	8	0.01%	26.3%	LVALNLDR	99.7%	61.3	25	46.6	2	0	0	913.55	65	72
28S ribosomal protein S17, mitochondrial	MRPS17	RT17_HUMAN	14.5	99.8%	2	2	3	0.00%	15.4%	HELAEIVFK	99.7%	48.1	25	48.1	2	0	0	1085.60	79	87
28S ribosomal protein S17, mitochondrial	MRPS17	RT17_HUMAN	14.5	99.8%	2	2	3	0.00%	15.4%	NLEELNISSAQ	99.7%	69.7	25	54.3	1	0	0	1217.60	120	130
28S ribosomal protein S18a, mitochondrial	MRPS18A	RT18A_HUMAN	22.2	100.0%	2	2	4	0.00%	12.8%	ESPNPPNPSGQCPICR	97.9%	30.6	25	30.6	2	0	0	1809.80	59	74
28S ribosomal protein S18a, mitochondrial	MRPS18A	RT18A_HUMAN	22.2	100.0%	2	2	4	0.00%	12.8%	MPVGSPLLR	97.3%	29.6	25	6.69	2	0	0	969.56	174	182
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	4	4	9	0.01%	21.7%	LYQGHLQEESGPPPESMPK	99.7%	46.6	25	41.2	0	2	0	2140.00	219	237
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	4	4	9	0.01%	21.7%	TPAEASSTGQTGPQSAL	99.7%	65	25	64.1	2	0	0	1602.76	242	258
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	4	4	9	0.01%	21.7%	VVGNPCPICR	99.7%	45	25	43.8	3	0	0	1171.57	100	109
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	4	4	9	0.01%	21.7%	YLESEEYQER	99.7%	72.3	25	71.2	2	0	0	1345.59	58	67
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	9	9	14	0.01%	27.4%	EPGDQGPAHPPGADMSHSL	99.2%	26	25	26	0	1	0	1915.82	278	296
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	9	9	14	0.01%	27.4%	FMEPYIFGSR	99.7%	43.3	25	39.9	2	0	0	1246.59	101	110
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	9	9	14	0.01%	27.4%	GIILFISR	99.7%	58.9	25	43.8	2	0	0	918.58	140	147
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	9	9	14	0.01%	27.4%	HSDFFNVK	99.7%	43.6	25	26.8	2	0	0	993.48	69	76
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	9	9	14	0.01%	27.4%	LFQTAITR	99.7%	59.6	25	43.8	2	0	0	949.55	252	259
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	9	9	14	0.01%	27.4%	LLFGPTVR	98.7%	32.5	25	10.5	1	0	0	902.55	181	188
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	9	9	14	0.01%	27.4%	QFSYLIENMAR	99.7%	46.1	25	36.6	1	0	0	1387.67	150	160
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	9	9	14	0.01%	27.4%	QQVEALYR	96.9%	29	25	22.6	2	0	0	1006.53	265	272
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	9	9	14	0.01%	27.4%	RQQVEALYR	97.4%	29.6	25	20.6	1	0	0	1162.63	264	272
28S ribosomal protein S21, mitochondrial	MRPS21	RT21_HUMAN	10.7	100.0%	3	5	11	0.01%	39.1%	ILTMDGLIEDIK	99.7%	47.1	25	37.1	3	0	0	1376.73	29	40
28S ribosomal protein S21, mitochondrial	MRPS21	RT21_HUMAN	10.7	100.0%	3	5	11	0.01%	39.1%	IYNMEMAR	98.0%	30.8	25	26.8	2	0	0	1059.46	63	70
28S ribosomal protein S21, mitochondrial	MRPS21	RT21_HUMAN	10.7	100.0%	3	5	11	0.01%	39.1%	TVMVQEGNVESAYR	99.7%	96.3	25	87.3	6	0	0	1598.75	11	24
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	12	15	25	0.02%	34.4%	DQAAEGINLIK	99.7%	67.5	25	53.7	2	0	0	1171.63	319	329
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	12	15	25	0.02%	34.4%	IDGLLIDQIQR	99.7%	58.8	25	38.9	2	0	0	1283.73	281	291
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	12	15	25	0.02%	34.4%	ILTPIIFKEENLR	99.7%	33.7	25	30.6	1	2	0	1585.93	204	216
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	12	15	25	0.02%	34.4%	KIDGLLIDQIQR	99.7%	82.4	25	74.4	2	2	0	1411.83	280	291
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	12	15	25	0.02%	34.4%	LMTQAQLEEATR	99.7%	90.1	25	83.6	4	0	0	1406.69	105	116
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	12	15	25	0.02%	34.4%	MIQVYFPK	99.7%	42.4	25	34.1	2	0	0	1025.55	192	199
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	12	15	25	0.02%	34.4%	MPPVLEER	99.3%	35	25	23.4	1	0	0	986.50	128	135
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	12	15	25	0.02%	34.4%	MTGLNLQK	97.2%	29.4	25	13	1	0	0	904.49	82	89
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	12	15	25	0.02%	34.4%	TFKPAIQELKPPTYK	99.1%	25.9	25	23	0	1	0	1760.99	90	104
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	12	15	25	0.02%	34.4%	VPINDVLAEDK	99.2%	34.4	25	28	1	0	0	1212.65	136	146
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	12	15	25	0.02%	34.4%	YFGGMVWYFVNNK	99.7%	65.3	25	65.3	2	0	0	1624.76	267	279
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	12	15	25	0.02%	34.4%	YVFTDISYSIPHR	99.7%	68.9	25	68.9	2	0	0	1597.80	156	168
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	4	5	9	0.01%	23.7%	AFDLFNPNFK	99.7%	68.1	25	68.1	2	0	0	1212.60	84	93
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	4	5	9	0.01%	23.7%	ALLAEGVILR	99.7%	71.3	25	44.2	2	0	0	1054.66	124	133
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	4	5	9	0.01%	23.7%	LETVGSIFSR	99.7%	80.9	25	68.1	2	0	0	1108.60	6	15
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	4	5	9	0.01%	23.7%	LGETDEEKLFVETGK	99.7%	61.3	25	57.7	2	1	0	1694.85	109	123
28S ribosomal protein S24, mitochondrial	MRPS24	RT24_HUMAN	19.0	100.0%	3	3	6	0.01%	10.8%	LHLQTVPSK	99.7%	46.8	25	35.9	2	0	0	1022.60	153	161
28S ribosomal protein S24, mitochondrial	MRPS24	RT24_HUMAN	19.0	100.0%	3	3	6	0.01%	10.8%	TVEDVFLR	99.7%	45	25	39.2	2	0	0	978.53	86	93
28S ribosomal protein S24, mitochondrial	MRPS24	RT24_HUMAN	19.0	100.0%	3	3	6	0.01%	10.8%	TVEDVFLRK	99.7%	39.2	25	33.7	2	0	0	1106.62	86	94
28S ribosomal protein S26, mitochondrial	MRPS26	RT26_HUMAN	24.2	100.0%	3	4	8	0.01%	14.6%	EVLQLQEEVK	99.7%	59.8	25	49.3	2	0	0	1214.66	156	165
28S ribosomal protein S26, mitochondrial	MRPS26	RT26_HUMAN	24.2	100.0%	3	4	8	0.01%	14.6%	KAEEVQAWAQR	99.7%	46.5	25	41.2	2	2	0	1315.68	142	152
28S ribosomal protein S26, mitochondrial	MRPS26	RT26_HUMAN	24.2	100.0%	3	4	8	0.01%	14.6%	MEFVSEVQR	99.7%	52.4	25	48.5	2	0	0	1124.54	72	80
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	8	8	21	0.02%	22.2%	EALDVLGAVLK	99.7%	81	25	73.6	4	0	0	1127.67	278	288
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	8	8	21	0.02%	22.2%	EEIDHAEYYLYK	99.6%	37.5	25	29.5	1	0	0	1572.72	83	94
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	8	8	21	0.02%	22.2%	IESEGLLSLTTQLVK	99.7%	67.4	25	67.4	4	0	0	1630.93	347	361

28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	8	8	21	0.02%	22.2%	KLPVSSLTISR	99.7%	64.9	25	58.8	2	0	0	1200.73	64	74
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	8	8	21	0.02%	22.2%	LIDNISSR	99.7%	39.1	25	0	3	0	0	917.51	75	82
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	8	8	21	0.02%	22.2%	LVEQLDIEETEQSK	99.7%	87.6	25	83.6	1	0	0	1660.83	313	326
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	8	8	21	0.02%	22.2%	NFGASLLLPGLK	99.7%	68.4	25	68.3	4	0	0	1229.73	203	214
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	8	8	21	0.02%	22.2%	VAASPEDIK	99.7%	41.6	25	37.3	2	0	0	929.49	266	274
28S ribosomal protein S28, mitochondrial	MRPS28	RT28_HUMAN	20.8	100.0%	3	3	6	0.01%	15.5%	AGGFASALER	99.7%	62.8	25	47.8	2	0	0	978.50	49	58
28S ribosomal protein S28, mitochondrial	MRPS28	RT28_HUMAN	20.8	100.0%	3	3	6	0.01%	15.5%	LLDLELTSR	99.7%	69.1	25	59.7	2	0	0	1059.60	144	152
28S ribosomal protein S28, mitochondrial	MRPS28	RT28_HUMAN	20.8	100.0%	3	3	6	0.01%	15.5%	NVESFASMLR	99.7%	55.5	25	48.2	2	0	0	1169.56	76	85
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	6	7	16	0.02%	18.1%	ELLFLSNANPSLLER	99.7%	100	25	96.4	2	0	0	1715.93	379	393
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	6	7	16	0.02%	18.1%	FDQPLEASTWLK	99.7%	77.1	25	63.4	2	0	0	1434.73	178	189
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	6	7	16	0.02%	18.1%	GSPLGEVVEQGITR	99.7%	90.2	25	83.5	4	0	0	1441.76	219	232
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	6	7	16	0.02%	18.1%	NATDAVGIVLK	99.7%	68.3	25	57.7	2	0	0	1100.63	235	245
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	6	7	16	0.02%	18.1%	NTSFAYPAIR	99.7%	59.7	25	52.9	2	0	0	1139.58	114	123
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	6	7	16	0.02%	18.1%	TFSEACLMVR	99.7%	47.2	25	44.1	4	0	0	1213.57	93	102
28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	5	7	14	0.01%	17.2%	EAPETDTSPSLWDVEFAK	99.7%	73.7	25	73.7	2	0	0	2021.93	267	284
28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	5	7	14	0.01%	17.2%	IQFDEGYDNYPGQEK	99.7%	75.8	25	75.4	2	0	0	1802.79	226	240
28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	5	7	14	0.01%	17.2%	ISFSNIISDMK	99.7%	75	25	67.3	4	0	0	1254.64	199	209
28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	5	7	14	0.01%	17.2%	SELLSQLQQHEEESR	99.7%	64.9	25	54.3	2	2	0	1812.87	175	189
28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	5	7	14	0.01%	17.2%	VELSTVNVR	99.7%	61.8	25	48.7	2	0	0	1016.57	108	116
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	4	5	10	0.01%	17.4%	AWGILTFK	99.1%	34.3	25	25.4	1	0	0	935.54	114	121
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	4	5	10	0.01%	17.4%	LLQLLGR	99.6%	37.8	25	12.1	2	0	0	812.54	64	70
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	4	5	10	0.01%	17.4%	LPLFGLGR	99.5%	36.4	25	31	3	0	0	872.54	71	78
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	4	5	10	0.01%	17.4%	NGDTSTEEPMLNVQR	99.7%	50.2	25	50.2	4	0	0	1706.77	181	195
28S ribosomal protein S35, mitochondrial	MRPS35	RT35_HUMAN	36.8	100.0%	3	3	5	0.00%	11.5%	EGNLELLK	95.6%	27.7	25	14.4	1	0	0	915.51	100	107
28S ribosomal protein S35, mitochondrial	MRPS35	RT35_HUMAN	36.8	100.0%	3	3	5	0.00%	11.5%	NILETLLQMK	99.7%	77.5	25	66.3	2	0	0	1202.68	261	270
28S ribosomal protein S35, mitochondrial	MRPS35	RT35_HUMAN	36.8	100.0%	3	3	5	0.00%	11.5%	SVVSLKNEEENENSISQYK	99.7%	39.8	25	39.8	0	2	0	2197.06	295	313
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	7	9	17	0.02%	18.4%	GAAGFSIGK	99.7%	39.8	25	20.5	2	0	0	807.44	252	260
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	7	9	17	0.02%	18.4%	LTADELWK	99.7%	47.7	25	40.8	2	0	0	975.51	93	100
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	7	9	17	0.02%	18.4%	NGAVQTIAQR	99.7%	64.4	25	54.8	2	0	0	1057.57	151	160
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	7	9	17	0.02%	18.4%	VLVAVGNGK	99.7%	39.8	25	39.8	1	0	0	856.53	243	251
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	7	9	17	0.02%	18.4%	VSGSINMLSLTQGLFR	99.7%	81.2	25	80.2	4	0	0	1722.92	336	351
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	7	9	17	0.02%	18.4%	YEDHTIFHDISLR	99.7%	30	25	30	0	2	0	1645.80	285	297
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	7	9	17	0.02%	18.4%	YGFLWPGLNVPLMK	99.7%	41.4	25	38	4	0	0	1634.88	137	150
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	5	6	11	0.01%	26.0%	LLEAFHNQGPVIK	99.7%	62.9	25	56.5	3	0	0	1465.82	209	221
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	5	6	11	0.01%	26.0%	NCEPMIGLVPILK	99.7%	39.6	25	30.3	3	0	0	1499.80	151	163
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	5	6	11	0.01%	26.0%	SLMIQTLEAVK	98.8%	33	25	20.1	1	0	0	1232.69	109	119
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	5	6	11	0.01%	26.0%	TSSVFEDPVISK	99.7%	54.1	25	49.3	3	0	0	1308.67	82	93
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	5	6	11	0.01%	26.0%	YHAASAEEQATIER	99.7%	41.7	25	34.6	1	0	0	1575.74	126	139
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	8	10	15	0.01%	24.5%	AIAYLFPSGLFEK	99.7%	47.1	25	44.8	2	0	0	1455.79	107	119
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	8	10	15	0.01%	24.5%	ALCSFVTEDEVEWMR	99.7%	52.1	25	52.1	2	0	0	1887.83	351	365
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	8	10	15	0.01%	24.5%	EQLMFPFHFVDR	99.5%	36.4	25	29	1	0	0	1565.76	311	322
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	8	10	15	0.01%	24.5%	ETYTEDFIKK	99.3%	35.4	25	25.5	2	0	0	1273.63	67	76
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	8	10	15	0.01%	24.5%	HDVTCTVSGGGR	99.7%	54.5	25	50.6	2	0	0	1245.56	326	337
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	8	10	15	0.01%	24.5%	HPEQIFPR	97.5%	29.9	25	25.1	1	0	0	1023.54	127	134
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	8	10	15	0.01%	24.5%	LLTSQCGAAEEEFVQR	99.7%	95.3	25	90.9	1	0	0	1837.88	228	243
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	8	10	15	0.01%	24.5%	LSDLDYMQFIR	99.7%	78.7	25	73.6	4	0	0	1400.69	213	223
2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	GCAT	KBL_HUMAN	45.3	100.0%	4	5	8	0.01%	14.6%	ALDLLMGSNTIVQSMAAK	99.7%	54.6	25	54.6	2	0	0	1862.97	309	326
2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	GCAT	KBL_HUMAN	45.3	100.0%	4	5	8	0.01%	14.6%	ALGGASGGYTTGPGPLVSLLR	99.7%	57.6	25	56.3	2	0	0	1944.06	266	286
2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	GCAT	KBL_HUMAN	45.3	100.0%	4	5	8	0.01%	14.6%	GIFVIGFSYPVVPK	99.7%	46.5	25	46.5	3	0	0	1522.87	370	383
2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	GCAT	KBL_HUMAN	45.3	100.0%	4	5	8	0.01%	14.6%	MADDMLKR	99.7%	41.2	25	26	1	0	0	979.47	362	369
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	COQ5	COQ5_HUMAN	37.1	100.0%	6	6	9	0.01%	23.2%	AQQNLSWEEIAK	99.7%	51.7	25	48.4	1	0	0	1416.71	142	153

2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	COQ5	COQ5_HUMAN	37.1	100.0%	6	6	9	0.01%	23.2%	EYQNEEDSLGGSR	99.7%	64.1	25	60.4	1	0	0	1483.63	154	166
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	COQ5	COQ5_HUMAN	37.1	100.0%	6	6	9	0.01%	23.2%	FLCLEFSQVNNPLISR	99.7%	57.5	25	56	2	0	0	1937.00	242	257
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	COQ5	COQ5_HUMAN	37.1	100.0%	6	6	9	0.01%	23.2%	FLNYVQSQHQR	99.7%	46.4	25	37.9	2	0	0	1419.71	124	134
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	COQ5	COQ5_HUMAN	37.1	100.0%	6	6	9	0.01%	23.2%	NVTHIDQALQEAHR	99.7%	39.3	25	39.3	0	1	0	1631.82	221	234
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	COQ5	COQ5_HUMAN	37.1	100.0%	6	6	9	0.01%	23.2%	VYQVFESVAK	99.7%	68.1	25	62.2	2	0	0	1169.62	68	77
39S ribosomal protein L10, mitochondrial	MRPL10	RM10_HUMAN	29.3	100.0%	3	3	5	0.00%	14.2%	EIAAVFQDNR	99.7%	73.3	25	65.1	2	0	0	1162.59	85	94
39S ribosomal protein L10, mitochondrial	MRPL10	RM10_HUMAN	29.3	100.0%	3	3	5	0.00%	14.2%	QGFINYSK	95.8%	27.8	25	20.3	1	0	0	956.48	189	196
39S ribosomal protein L10, mitochondrial	MRPL10	RM10_HUMAN	29.3	100.0%	3	3	5	0.00%	14.2%	TVPFLPLLGGCIDDTILSR	99.7%	82	25	80.2	2	0	0	2087.12	170	188
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	4	4	6	0.01%	23.4%	DLSSEELAAFQK	99.7%	55	25	47.7	1	0	0	1337.66	158	169
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	4	4	6	0.01%	23.4%	EADLAAQEEAAKK	97.3%	29.6	25	27.4	1	0	0	1373.69	180	192
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	4	4	6	0.01%	23.4%	GVSINQFCK	99.3%	35	25	28.8	2	0	0	1052.52	43	51
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	4	4	6	0.01%	23.4%	IGQPTVSYFLK	99.3%	35.3	25	35.3	2	0	0	1252.69	82	92
39S ribosomal protein L14, mitochondrial	MRPL14	RM14_HUMAN	15.9	100.0%	3	4	10	0.01%	22.8%	IKTPIPTSLR	95.0%	27.1	25	24.8	1	0	0	1125.70	119	128
39S ribosomal protein L14, mitochondrial	MRPL14	RM14_HUMAN	15.9	100.0%	3	4	10	0.01%	22.8%	VLAIAQNFV	99.2%	34.8	25	23.7	2	0	0	974.57	137	145
39S ribosomal protein L14, mitochondrial	MRPL14	RM14_HUMAN	15.9	100.0%	3	4	10	0.01%	22.8%	VVDNSALGNSPYHR	99.7%	69.2	25	60.5	4	3	0	1528.75	40	53
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	5	5	9	0.01%	22.0%	DYGVQLVEEGADTFTAK	99.7%	91.8	25	91.8	2	0	0	1842.88	135	151
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	5	5	9	0.01%	22.0%	GYLADPAKFPEAR	99.7%	50.2	25	46.7	1	0	0	1434.74	221	233
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	5	5	9	0.01%	22.0%	LGFEGGQTPFYIR	99.7%	51.1	25	50.1	2	0	0	1484.75	65	77
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	5	5	9	0.01%	22.0%	LQYLIDLGR	99.7%	40	25	40	2	0	0	1090.63	101	109
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	5	5	9	0.01%	22.0%	NGGVVTTAFYDPR	99.7%	45	25	41.4	2	0	0	1396.69	170	182
39S ribosomal protein L16, mitochondrial	MRPL16	RM16_HUMAN	28.5	100.0%	3	3	5	0.00%	12.4%	GAIDHYVTPVK	99.7%	67.1	25	47	2	0	0	1199.64	145	155
39S ribosomal protein L16, mitochondrial	MRPL16	RM16_HUMAN	28.5	100.0%	3	3	5	0.00%	12.4%	IATANMLGIR	94.9%	27	25	19	1	0	0	1059.60	218	227
39S ribosomal protein L16, mitochondrial	MRPL16	RM16_HUMAN	28.5	100.0%	3	3	5	0.00%	12.4%	VPAPFKPITR	99.7%	54.3	25	39.9	2	0	0	1125.68	124	133
39S ribosomal protein L17, mitochondrial	MRPL17	RM17_HUMAN	20.1	99.8%	2	2	3	0.00%	9.1%	LFQVLAPR	99.7%	48.1	25	35.3	2	0	0	943.57	89	96
39S ribosomal protein L17, mitochondrial	MRPL17	RM17_HUMAN	20.1	99.8%	2	2	3	0.00%	9.1%	MGLGPESR	97.5%	29.9	25	25.1	1	0	0	846.41	18	25
39S ribosomal protein L19, mitochondrial	MRPL19	RM19_HUMAN	33.5	100.0%	4	4	8	0.01%	13.7%	FLSPEFIPR	99.7%	45.6	25	39.8	2	0	0	1105.60	75	83
39S ribosomal protein L19, mitochondrial	MRPL19	RM19_HUMAN	33.5	100.0%	4	4	8	0.01%	13.7%	GLGATFILR	99.7%	64	25	52.9	2	0	0	947.57	144	152
39S ribosomal protein L19, mitochondrial	MRPL19	RM19_HUMAN	33.5	100.0%	4	4	8	0.01%	13.7%	ISQFLGICIQR	99.7%	50.5	25	48.6	2	0	0	1334.73	130	140
39S ribosomal protein L19, mitochondrial	MRPL19	RM19_HUMAN	33.5	100.0%	4	4	8	0.01%	13.7%	VTTADPYASGK	99.7%	52.7	25	42.5	2	0	0	1109.55	119	129
39S ribosomal protein L2, mitochondrial	MRPL2	RM02_HUMAN	33.3	99.8%	2	2	4	0.00%	7.2%	AAGTCGVLLR	99.7%	96.6	25	80.3	2	0	0	1017.55	209	218
39S ribosomal protein L2, mitochondrial	MRPL2	RM02_HUMAN	33.3	99.8%	2	2	4	0.00%	7.2%	SADIALVAGGSR	99.7%	63.2	25	46.1	2	0	0	1116.60	136	147
39S ribosomal protein L20, mitochondrial	MRPL20	RM20_HUMAN	17.4	100.0%	2	2	4	0.00%	14.8%	ITAASQEHGLK	99.7%	43	25	43	2	0	0	1154.62	72	82
39S ribosomal protein L20, mitochondrial	MRPL20	RM20_HUMAN	17.4	100.0%	2	2	4	0.00%	14.8%	VLADLAIYEPK	99.7%	92.7	25	79.8	2	0	0	1231.69	101	111
39S ribosomal protein L24, mitochondrial	MRPL24	RM24_HUMAN	24.9	100.0%	3	3	6	0.01%	13.9%	GTMIPSEAPLLHR	99.7%	30.5	25	30.5	0	2	0	1437.75	106	118
39S ribosomal protein L24, mitochondrial	MRPL24	RM24_HUMAN	24.9	100.0%	3	3	6	0.01%	13.9%	IIPKPEFPR	98.2%	31.1	25	24.1	2	0	0	1096.65	153	161
39S ribosomal protein L24, mitochondrial	MRPL24	RM24_HUMAN	24.9	100.0%	3	3	6	0.01%	13.9%	KPTEIEWR	98.9%	33.5	25.1	25.2	2	0	0	1058.56	129	136
39S ribosomal protein L27, mitochondrial	MRPL27	RM27_HUMAN	16.1	99.8%	2	2	5	0.00%	14.2%	CLYALEEGIVR	99.7%	61.6	25	49.7	2	0	0	1322.68	88	98
39S ribosomal protein L27, mitochondrial	MRPL27	RM27_HUMAN	16.1	99.8%	2	2	5	0.00%	14.2%	NTEAVDLITR	99.7%	58.5	25	43	3	0	0	1131.60	110	119
39S ribosomal protein L33, mitochondrial	MRPL33	RM33_HUMAN	7.6	99.8%	2	3	3	0.00%	38.5%	LTLLHYDPVVK	99.7%	38.6	25	30.6	1	0	0	1297.75	41	51
39S ribosomal protein L33, mitochondrial	MRPL33	RM33_HUMAN	7.6	99.8%	2	3	3	0.00%	38.5%	MVSEAGTGFCFNTK	99.7%	47.1	25	47.1	2	0	0	1548.68	20	33
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	5	5	12	0.01%	16.3%	ESLLLQVR	99.7%	54.2	25	37.3	3	0	0	957.57	216	223
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	5	5	12	0.01%	16.3%	ETYCPVIVDNLIQLCK	99.7%	45.6	25	45.6	1	0	0	1964.98	174	189
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	5	5	12	0.01%	16.3%	MILFAFGSALAQAR	99.7%	95.7	25	91.1	4	0	0	1495.81	313	326
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	5	5	12	0.01%	16.3%	VLEQPVVVQSVGTDGR	99.7%	64.1	25	64.1	1	0	0	1682.91	335	350
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	5	5	12	0.01%	16.3%	VYEIPGLEPITFAGK	99.7%	51	25	50.2	3	0	0	1633.88	49	63
39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	5	5	9	0.01%	14.2%	DLFHGATFVPR	99.7%	46	25	37.3	2	0	0	1259.65	160	170
39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	5	5	9	0.01%	14.2%	LAEYYGLYR	99.7%	63	25	53.4	2	0	0	1147.58	151	159
39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	5	5	9	0.01%	14.2%	LAFLLFK	99.7%	40.9	25	38.4	2	0	0	851.54	268	274
39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	5	5	9	0.01%	14.2%	TASVPLDAVR	96.2%	28.2	25	24.8	1	0	0	1028.57	127	136
39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	5	5	9	0.01%	14.2%	VAEGQVTCPYLPPFPAR	99.7%	53.4	25	49.3	2	0	0	1901.96	245	261
39S ribosomal protein L39, mitochondrial	MRPL39	RM39_HUMAN	38.7	100.0%	3	3	5	0.00%	11.2%	DLPFETLEVEAK	99.7%	53.8	25	41.3	2	0	0	1390.71	213	224

39S ribosomal protein L39, mitochondrial	MRPL39	RM39_HUMAN	38.7	100.0%	3	3	5	0.00%	11.2%	IGDFIDVSEGPLIPR	99.7%	39.8	25	39.4	2	0	0	1627.87	257	271
39S ribosomal protein L39, mitochondrial	MRPL39	RM39_HUMAN	38.7	100.0%	3	3	5	0.00%	11.2%	TDPGTVFVMNK	98.3%	31.3	25	25.3	1	0	0	1208.60	73	83
39S ribosomal protein L41, mitochondrial	MRPL41	RM41_HUMAN	15.4	100.0%	3	3	9	0.01%	19.7%	GIGFLTSGWR	99.7%	47.1	25	38.5	4	0	0	1093.58	40	49
39S ribosomal protein L41, mitochondrial	MRPL41	RM41_HUMAN	15.4	100.0%	3	3	9	0.01%	19.7%	LFQLYPR	98.9%	33.5	25	28.7	3	0	0	936.53	127	133
39S ribosomal protein L41, mitochondrial	MRPL41	RM41_HUMAN	15.4	100.0%	3	3	9	0.01%	19.7%	YGFEPTQEGK	98.9%	33.1	25	13.1	2	0	0	1155.53	117	126
39S ribosomal protein L43, mitochondrial	MRPL43	RM43_HUMAN	23.4	100.0%	2	2	4	0.00%	10.7%	FLASVLHNGLGR	99.7%	67.7	25	55.9	2	0	0	1283.72	10	21
39S ribosomal protein L43, mitochondrial	MRPL43	RM43_HUMAN	23.4	100.0%	2	2	4	0.00%	10.7%	SVEEISTLVQK	99.7%	57.9	25	45.8	2	0	0	1232.67	93	103
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	3	3	5	0.00%	12.0%	LIAEGPGETVLVAEEEAAR	99.6%	37.4	25	37.4	1	0	0	1954.01	280	298
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	3	3	5	0.00%	12.0%	LQENFSLDLLK	99.3%	35.5	25	26.9	2	0	0	1319.72	79	89
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	3	3	5	0.00%	12.0%	TAFVNSCYIK	99.3%	35.2	25	26.7	2	0	0	1202.59	90	99
39S ribosomal protein L46, mitochondrial	MRPL46	RM46_HUMAN	31.7	100.0%	3	3	7	0.01%	12.9%	ALLLTGDFSQAGNK	99.7%	87.3	25	87.3	3	0	0	1434.76	236	249
39S ribosomal protein L46, mitochondrial	MRPL46	RM46_HUMAN	31.7	100.0%	3	3	7	0.01%	12.9%	SLYSDHELR	99.4%	35.9	25	11.8	2	0	0	1119.54	82	90
39S ribosomal protein L46, mitochondrial	MRPL46	RM46_HUMAN	31.7	100.0%	3	3	7	0.01%	12.9%	TLATLSENNMEAK	99.7%	49.5	25	44.8	2	0	0	1437.69	191	203
39S ribosomal protein L47, mitochondrial	MRPL47	RM47_HUMAN	29.5	100.0%	3	3	6	0.01%	12.4%	LLQTGQER	98.5%	31.9	25	23.6	2	0	0	944.52	155	162
39S ribosomal protein L47, mitochondrial	MRPL47	RM47_HUMAN	29.5	100.0%	3	3	6	0.01%	12.4%	NMLLTLEQEAKR	99.7%	43.2	25	34.9	2	0	0	1461.77	110	121
39S ribosomal protein L47, mitochondrial	MRPL47	RM47_HUMAN	29.5	100.0%	3	3	6	0.01%	12.4%	SGAAWTCQQLR	99.7%	54	25	50.5	2	0	0	1277.61	81	91
39S ribosomal protein L53, mitochondrial	MRPL53	RM53_HUMAN	12.1	99.9%	2	2	4	0.00%	20.5%	STNLNCSVIADVR	99.7%	71.5	25	65.5	2	0	0	1448.72	44	56
39S ribosomal protein L53, mitochondrial	MRPL53	RM53_HUMAN	12.1	99.9%	2	2	4	0.00%	20.5%	TFLQTVSSEK	99.7%	42.9	25	36.4	2	0	0	1139.59	32	41
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	4	4	7	0.01%	15.4%	ENLELILTQSVENVGVR	99.7%	42.7	25	42.7	2	0	0	1913.03	92	108
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	4	4	7	0.01%	15.4%	LLPQGLAVYASPENK	99.6%	37.3	25	33.6	2	0	0	1599.87	123	137
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	4	4	7	0.01%	15.4%	LLPQGLAVYASPENKK	99.7%	53.6	25	53.6	1	0	0	1727.97	123	138
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	4	4	7	0.01%	15.4%	LPEEPITR	99.4%	35.9	25	29.5	2	0	0	954.53	208	215
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	6	10	15	0.01%	38.3%	GGIVGMTLPIAR	99.7%	62.7	25	54.2	3	0	0	1200.68	173	184
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	6	10	15	0.01%	38.3%	GLVAVITGGASGLGLATAER	99.7%	132	25	132	1	1	0	1813.02	10	29
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	6	10	15	0.01%	38.3%	GQTHTLEDFQR	99.7%	41.3	25	40.4	2	1	0	1331.63	106	116
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	6	10	15	0.01%	38.3%	GVIINTASVAAFEGQVGQAAYSASK	99.7%	118	25	118	1	2	0	2439.25	148	172
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	6	10	15	0.01%	38.3%	LVAGEMGQNEPDQGGQR	99.7%	98.7	25	98.7	2	0	0	1785.82	131	147
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	6	10	15	0.01%	38.3%	VDVAVNCAGIAVASK	99.7%	100	25	100	2	0	0	1473.77	85	99
3-ketoacyl-CoA thiolase, mitochondrial	ACAA2	THIM_HUMAN	41.9	99.9%	2	2	4	0.00%	5.5%	DFTATDLSEFAAK	99.7%	93.9	25	90.3	2	0	0	1415.67	26	38
3-ketoacyl-CoA thiolase, mitochondrial	ACAA2	THIM_HUMAN	41.9	99.9%	2	2	4	0.00%	5.5%	ETPALTINR	99.7%	47	25	47	2	0	0	1014.56	82	90
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	4	5	16	0.02%	20.6%	AEAGAGSATEFQFR	99.7%	82.6	25	74.5	2	0	0	1441.67	140	153
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	4	5	16	0.02%	20.6%	GYVKEQFAWR	99.7%	54.3	25	48.1	2	0	0	1283.65	56	65
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	4	5	16	0.02%	20.6%	IAIYELLFK	99.7%	65.6	25	65.6	8	0	0	1109.66	9	17
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	4	5	16	0.02%	20.6%	KAEAGAGSATEFQFR	99.7%	94.4	25	94.4	2	2	0	1569.77	139	153
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	9	11	31	0.03%	53.2%	CPFTGNVSIR	99.7%	73.2	25	58.3	6	0	0	1150.57	60	69
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	9	11	31	0.03%	53.2%	DVQIGDIVTVGECRPLSK	99.7%	84.9	25	84.1	3	3	0	1986.03	119	136
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	9	11	31	0.03%	53.2%	DYLHYIR	98.9%	33.4	25	20.5	2	0	0	979.50	91	97
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	9	11	31	0.03%	53.2%	EAIEGTYIDKK	99.7%	59.4	25	45.1	7	0	0	1266.66	49	59
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	9	11	31	0.03%	53.2%	ILSGVVTK	99.6%	38.3	25	15.4	3	0	0	816.52	72	79
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	9	11	31	0.03%	53.2%	NMSVHLSPCFR	99.7%	38.5	25	38.5	2	1	0	1347.63	108	118
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	9	11	31	0.03%	53.2%	QPTIFQNK	97.3%	29.5	25	19.4	1	0	0	975.53	13	20
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	9	11	31	0.03%	53.2%	RDYLHYIR	96.6%	28.6	25	9.75	1	0	0	1135.60	90	97
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	9	11	31	0.03%	53.2%	VLLGETGKEK	99.7%	42.1	25	20.6	2	0	0	1073.62	23	32
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	11	35	0.03%	57.6%	DVIEEYFK	98.9%	33.2	25	33.2	1	0	0	1042.51	122	129
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	11	35	0.03%	57.6%	ESQAKDVIEEYFK	99.7%	66.4	25	52.7	2	0	0	1585.77	117	129
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	11	35	0.03%	57.6%	KVVGCSCVVVK	99.7%	62.6	25	53.4	4	0	0	1234.66	102	112
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	11	35	0.03%	57.6%	LGEWVGLCK	99.7%	61.7	25	55.4	8	0	0	1061.55	85	93
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	11	35	0.03%	57.6%	LVEALCAEHQINLIK	99.7%	86.6	25	84.3	4	2	0	1750.95	64	78
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	11	35	0.03%	57.6%	QAHLCVLASNCDEPMYVK	99.7%	63.2	25	59.7	2	4	0	2150.97	46	63
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	11	35	0.03%	57.6%	TALIHDGLAR	99.7%	53.3	25	42	6	0	0	1066.60	24	33
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	11	35	0.03%	57.6%	VVGCSCVVVK	99.7%	67.6	25	55.1	2	0	0	1106.57	103	112

40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	10	11	31	0.03%	55.6%	FRLILIESR	98.7%	32.6	25	32.6	2	0	0	1146.70	113	121
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	10	11	31	0.03%	55.6%	FVTGNKILR	99.3%	35.4	25	30.7	1	0	0	1047.63	65	73
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	10	11	31	0.03%	55.6%	GLAPDLPEDLYHLIK	99.7%	40.9	25	40.6	3	0	0	1693.92	79	93
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	10	11	31	0.03%	55.6%	GLTPSQIGVILR	99.7%	69.5	25	55.5	4	0	0	1253.76	44	55
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	10	11	31	0.03%	55.6%	KGLTPSQIGVILR	99.7%	74.5	25	74.5	4	0	0	1381.85	43	55
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	10	11	31	0.03%	55.6%	LILIESR	99.7%	47.3	25	27.4	3	0	0	843.53	115	121
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	10	11	31	0.03%	55.6%	LTSDDVKEQIYK	99.7%	79	25	68.7	7	2	0	1438.74	28	39
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	10	11	31	0.03%	55.6%	RSVPTWLK	99.6%	37.5	25	24.9	2	0	0	986.58	20	27
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	10	11	31	0.03%	55.6%	VLPPNWKYESSTASALVA	99.7%	38.4	25	38.4	1	0	0	1933.01	134	151
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	10	11	31	0.03%	55.6%	YESSTASALVA	99.7%	43	25	43	2	0	0	1098.53	141	151
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	44	0.04%	41.7%	ADRDESSPYAAMLAAQDVAQR	99.7%	59.2	25	59.2	0	3	0	2281.05	64	84
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	44	0.04%	41.7%	CKELGITALHIK	99.7%	69.8	25	61.6	3	2	0	1382.78	85	96
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	44	0.04%	41.7%	DESSPYAAMLAAQDVAQR	99.7%	61.8	25	52	4	0	0	1938.89	67	84
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	44	0.04%	41.7%	ELGITALHIK	99.7%	46.8	25	38.5	3	0	0	1094.66	87	96
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	44	0.04%	41.7%	IEDVTPIPSDSTR	99.7%	67.1	25	56.8	3	0	0	1429.72	129	141
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	44	0.04%	41.7%	IEDVTPIPSDSTRR	99.7%	44.7	25	41.8	4	2	0	1585.82	129	142
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	44	0.04%	41.7%	IGRIEDVTPIPSDSTR	99.7%	65.1	25	64.2	3	2	0	1755.92	126	141
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	44	0.04%	41.7%	TKTPGPGAQSALR	99.7%	37.1	25	27	2	2	0	1283.71	105	117
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	44	0.04%	41.7%	TPGPGAQSALR	99.7%	72.2	25	63.7	11	0	0	1054.56	107	117
40S ribosomal protein S15	RPS15	RS15_HUMAN	17.0	100.0%	3	9	16	0.02%	22.1%	DMIILPEMVGSMVGVYNGK	99.7%	83.3	25	83.3	5	0	0	2101.00	82	100
40S ribosomal protein S15	RPS15	RS15_HUMAN	17.0	100.0%	3	9	16	0.02%	22.1%	EAPPMEKPEVVK	99.7%	53.8	25	44.9	3	1	0	1353.71	66	77
40S ribosomal protein S15	RPS15	RS15_HUMAN	17.0	100.0%	3	9	16	0.02%	22.1%	KEAPPMEKPEVVK	99.7%	39.2	25	37.7	3	4	0	1497.80	65	77
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	11	18	41	0.04%	75.4%	DLEKWQNNLLPSR	99.7%	48	25	20.7	2	0	0	1612.84	85	97
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	11	18	41	0.04%	75.4%	FDVQLKDLEK	99.7%	54.7	25	17.9	4	2	0	1234.67	79	88
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	11	18	41	0.04%	75.4%	FLTVMMK	99.7%	44.3	25	0	7	0	0	885.46	37	43
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	11	18	41	0.04%	75.4%	HGYIGEFEIIDDHR	99.7%	80.9	25	76.1	2	4	0	1700.80	44	57
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	11	18	41	0.04%	75.4%	IVVNLTGR	99.7%	51.9	25	42.6	2	0	0	871.54	61	68
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	11	18	41	0.04%	75.4%	LNKCGVISPR	99.3%	35.5	25	29.2	1	0	0	1143.63	69	78
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	11	18	41	0.04%	75.4%	MNVLADALK	99.7%	62.4	25	55.9	5	0	0	974.53	4	12
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	11	18	41	0.04%	75.4%	QFGFIVLTTSAGIMDHEEAR	99.7%	38.7	25	38.7	1	3	0	2238.09	98	117
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	11	18	41	0.04%	75.4%	QVLIRPCSK	96.6%	28.6	25	8.3	1	0	0	1100.62	24	32
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	11	18	41	0.04%	75.4%	VRMNVLADALK	99.7%	36.6	25	23.2	3	2	0	1245.70	2	12
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	11	18	41	0.04%	75.4%	WQNNLLPSR	99.5%	37	25	28.8	2	0	0	1127.60	89	97
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	13	18	75	0.07%	61.6%	ALVAYYQK	99.7%	50	25	47.1	6	0	0	955.52	91	98
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	13	18	75	0.07%	61.6%	EIKDILIQYDR	99.7%	74.2	25	60.8	7	7	0	1405.77	107	117
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	13	18	75	0.07%	61.6%	FAGVDIRVR	99.7%	42	25	33	3	0	0	1032.59	63	71
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	13	18	75	0.07%	61.6%	GGGHVAQIYAIR	99.7%	51	25	50.2	6	0	0	1241.68	74	85
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	13	18	75	0.07%	61.6%	GPLQSVQVFGR	99.7%	77.1	25	58.9	4	0	0	1187.65	5	15
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	13	18	75	0.07%	61.6%	GPLQSVQVFGRK	98.7%	32.4	25	32.4	2	0	0	1315.75	5	16
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	13	18	75	0.07%	61.6%	LLEPVLLLGK	99.7%	41.1	25	41.1	5	0	0	1094.72	51	60
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	13	18	75	0.07%	61.6%	LLEPVLLLGKER	99.7%	74.6	25	74.6	4	0	0	1379.86	51	62
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	13	18	75	0.07%	61.6%	PSKGPLQSVQVFGR	99.7%	74.2	25	74.2	4	4	0	1499.83	2	15
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	13	18	75	0.07%	61.6%	TLLVADPR	99.7%	41.5	25	20.5	3	0	0	884.52	118	125
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	13	18	75	0.07%	61.6%	TLLVADPRR	99.7%	49.7	25	40	4	0	0	1040.62	118	126
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	13	18	75	0.07%	61.6%	VKGGGHVAQIYAIR	99.7%	46.2	25	43.2	2	3	0	1468.84	72	85
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	13	18	75	0.07%	61.6%	VNGRPLEMIEPR	99.7%	40.5	25	33.7	3	8	0	1410.75	34	45
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	8	11	26	0.03%	46.7%	IAGYVTHLMK	99.7%	61.3	25	55.3	7	0	0	1132.62	50	59
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	8	11	26	0.03%	46.7%	LGNDFHTNK	99.7%	51.8	25	38.1	2	0	0	1045.51	24	32
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	8	11	26	0.03%	46.7%	LGNDFHTNKR	99.7%	64.2	25	49.2	2	2	0	1201.61	24	33
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	8	11	26	0.03%	46.7%	LLDFGSLSNLQVTQPTVGMNFK	99.7%	53	25	51	2	2	0	2425.24	108	129
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	8	11	26	0.03%	46.7%	RVCEEIAIIPSK	99.2%	34.6	25	24.3	1	0	0	1414.77	33	44

40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	8	11	26	0.03%	46.7%	VCEEIAIIPSK	99.7%	59.2	25	33.9	3	0	0	1258.67	34	44
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	8	11	26	0.03%	46.7%	VCEEIAIIPSKK	99.7%	58.3	25	49.5	3	0	0	1386.77	34	45
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	8	11	26	0.03%	46.7%	VIIEKYYTR	99.7%	62.7	25	55.2	2	0	0	1184.67	15	23
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	54	0.05%	57.2%	ADIDLTKR	99.7%	56.2	25	37.8	2	0	0	931.52	48	55
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	54	0.05%	57.2%	AGELTEDEVER	99.7%	81.8	25	78.3	4	0	0	1247.58	56	66
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	54	0.05%	57.2%	DGKYSQVLANGLDNK	99.7%	48.9	25	43.4	1	0	0	1621.82	92	106
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	54	0.05%	57.2%	HFWGLR	97.4%	29.7	25	17.5	1	0	0	815.43	125	130
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	54	0.05%	57.2%	IAFAITAIK	99.7%	72.5	25	61.6	2	0	0	947.59	26	34
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	54	0.05%	57.2%	IPDWFLNR	99.7%	47.2	25	36	11	0	0	1060.56	79	86
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	54	0.05%	57.2%	KADIDLTK	99.2%	34.8	25	27.7	2	0	0	903.51	47	54
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	54	0.05%	57.2%	KIAFAITAIK	99.7%	44.5	25	44.5	2	0	0	1075.69	25	34
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	54	0.05%	57.2%	LREDLER	95.7%	27.8	25	9.01	1	0	0	930.50	107	113
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	54	0.05%	57.2%	QYKIPDWFLNR	99.7%	32.5	25	25.7	1	1	0	1479.77	76	86
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	54	0.05%	57.2%	RAGELTEDEVER	99.7%	46.1	25	37.5	4	2	0	1403.68	55	66
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	54	0.05%	57.2%	VITIMQNPR	99.7%	66.6	25	58.2	9	0	0	1087.59	67	75
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	54	0.05%	57.2%	VLNTNIDGR	99.7%	46.5	25	34.5	7	0	0	1001.54	15	23
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	54	0.05%	57.2%	YSQVLANGLDNK	99.7%	86.4	25	79.7	2	0	0	1321.67	95	106
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	54	0.05%	57.2%	YSQVLANGLDNKLR	99.7%	54.8	25	43.6	2	0	0	1590.86	95	108
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	9	12	24	0.02%	49.0%	ALAAFLKK	98.7%	32.5	25	28.8	2	0	0	861.56	17	24
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	9	12	24	0.02%	49.0%	DLDRIAGQVAAANK	99.7%	50.6	25	45.9	2	2	0	1441.78	130	143
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	9	12	24	0.02%	49.0%	DVNQQEFVR	99.7%	63.9	25	51.7	2	0	0	1134.55	8	16
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	9	12	24	0.02%	49.0%	ELAPYDENWFYTR	99.7%	73.1	25	73.1	2	0	0	1703.77	44	56
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	9	12	24	0.02%	49.0%	IAGQVAAANK	99.7%	58.2	25	49.6	2	0	0	942.54	134	143
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	9	12	24	0.02%	49.0%	LKVPEWVDTVK	99.7%	49.9	25	43.3	2	2	0	1313.75	28	38
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	9	12	24	0.02%	49.0%	PGVTVKDVNQQEFVR	99.7%	87.4	25	83.3	2	2	0	1715.91	2	16
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	9	12	24	0.02%	49.0%	RVLQALEGLK	99.7%	40.1	25	23	2	0	0	1126.69	102	111
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	9	12	24	0.02%	49.0%	VLQALEGLK	99.7%	62.5	25	50.9	2	0	0	970.59	103	111
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	18	70	0.07%	43.7%	AEDKEWMPVTK	99.7%	44.1	25	33.4	8	3	0	1349.64	55	65
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	18	70	0.07%	43.7%	AFVAIGDYNGHVGLGVK	99.7%	57.2	25	49.3	2	0	0	1716.91	126	142
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	18	70	0.07%	43.7%	ATFDAISK	99.7%	44	25	33.3	4	0	0	852.45	239	246
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	18	70	0.07%	43.7%	GCTATLGNFAK	99.7%	62.3	25	54.8	6	0	0	1139.55	228	238
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	18	70	0.07%	43.7%	GTGIVSAPVPK	99.7%	50.8	25	50.8	9	0	0	1025.60	201	211
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	18	70	0.07%	43.7%	GTGIVSAPVPKK	95.7%	27.7	25	27.7	1	0	0	1153.69	201	212
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	18	70	0.07%	43.7%	IGKPHTVPCK	97.9%	30.6	25	19	1	0	0	1136.62	174	183
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	18	70	0.07%	43.7%	KLLMMAGIDDCYTSAR	99.7%	40.7	25	40.7	1	2	0	1876.86	212	227
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	18	70	0.07%	43.7%	LLMMAGIDDCYTSAR	99.7%	81.1	25	10.2	11	0	0	1732.77	213	227
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	18	70	0.07%	43.7%	LSIVPVRR	99.7%	45.1	25	24.5	4	0	0	939.61	160	167
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	18	70	0.07%	43.7%	SLEEIYLFSLPIK	99.7%	61.8	25	61.8	4	0	0	1551.87	77	89
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	18	70	0.07%	43.7%	SPYQEFTDHLVK	99.7%	63	25	62.3	6	4	0	1463.72	264	275
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	18	70	0.07%	43.7%	TYSYLTPDLWK	99.7%	62	25	61.4	4	0	0	1386.69	247	257
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	5	8	18	0.02%	29.4%	DTGKTPVEPEVAIHR	99.7%	52	25	49.2	2	2	0	1648.87	5	19
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	5	8	18	0.02%	29.4%	LIDLHSPSEIVK	99.7%	50.3	25	32.8	3	2	0	1350.76	88	99
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	5	8	18	0.02%	29.4%	RLIDLHSPSEIVK	99.7%	41.6	25	33.5	2	0	0	1506.86	87	99
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	5	8	18	0.02%	29.4%	TPVEPEVAIHR	99.7%	58.6	25	58.6	2	2	0	1247.67	9	19
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	5	8	18	0.02%	29.4%	VCADLIR	99.7%	44.7	25	31.9	3	0	0	846.45	35	41
40S ribosomal protein S21	RPS21	RS21_HUMAN	9.1	99.8%	2	2	4	0.00%	22.9%	MGESDDSILR	99.7%	42.2	25	38.9	2	0	0	1138.50	62	71
40S ribosomal protein S21	RPS21	RS21_HUMAN	9.1	99.8%	2	2	4	0.00%	22.9%	TYAICGAIR	98.9%	33.2	25	32	2	0	0	1024.52	52	60
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	4	5	14	0.01%	23.8%	ANPFGGASHAK	99.7%	42.9	25	38.7	5	0	0	1056.52	38	48
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	4	5	14	0.01%	23.8%	GHAVGDIPGVR	99.4%	36	25	27.8	2	0	0	1077.58	109	119
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	4	5	14	0.01%	23.8%	KGHAVGDIPGVR	99.7%	54.3	25	48.6	2	2	0	1205.68	108	119
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	4	5	14	0.01%	23.8%	VANVSLLALYK	99.7%	83.1	25	83.1	3	0	0	1190.71	125	135

40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	8	34	0.03%	30.1%	KQMVIDVLHPGK	99.7%	48.5	25	48.5	2	2	0	1380.77	21	32
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	8	34	0.03%	30.1%	QMVIDVLHPGK	99.7%	55.4	25	36.9	2	1	0	1236.68	22	32
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	8	34	0.03%	30.1%	TTGFGMIYDSLDYAK	99.7%	76.2	25	74.3	11	0	0	1681.78	69	83
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	8	34	0.03%	30.1%	TTGFGMIYDSLDYAKK	99.7%	44.1	25	44.1	2	0	0	1809.87	69	84
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	8	34	0.03%	30.1%	TTPDVIFVFGFR	99.7%	60.9	25	59.4	14	0	0	1398.74	50	61
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	6	6	23	0.02%	47.2%	AALQELLSK	99.7%	65.3	25	44.4	9	0	0	972.57	86	94
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	6	6	23	0.02%	47.2%	AQVIYTR	99.4%	36	25	28.5	2	0	0	850.48	105	111
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	6	6	23	0.02%	47.2%	ATYDKLCK	99.4%	35.7	25	28.7	2	0	0	998.50	53	60
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	6	6	23	0.02%	47.2%	DKLNNLVLFDK	99.7%	57.3	25	51.8	4	0	0	1318.74	42	52
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	6	6	23	0.02%	47.2%	LITPAVVSER	99.7%	65.3	25	52.8	5	0	0	1084.64	67	76
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	6	6	23	0.02%	47.2%	NTKGGDAPAAGEDA	99.7%	49.8	25	49.8	1	0	0	1273.57	112	125
40S ribosomal protein S26	RPS26	RS26_HUMAN	13.0	100.0%	3	4	17	0.02%	31.3%	DISEASVFDAYVLPK	99.7%	91.4	25	77.6	8	0	0	1653.84	52	66
40S ribosomal protein S26	RPS26	RS26_HUMAN	13.0	100.0%	3	4	17	0.02%	31.3%	LHYCVSCAIHSK	99.7%	56.9	25	56.9	2	1	0	1474.69	71	82
40S ribosomal protein S26	RPS26	RS26_HUMAN	13.0	100.0%	3	4	17	0.02%	31.3%	NIVEAAAVR	99.7%	81.9	25	69.8	6	0	0	942.54	43	51
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	5	8	28	0.03%	40.5%	DLLHPSPEEEK	99.4%	36	25	23.5	2	0	0	1293.63	6	16
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	5	8	28	0.03%	40.5%	DLLHPSPEEEKR	98.6%	32.1	25	26.7	2	2	0	1449.73	6	17
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	5	8	28	0.03%	40.5%	LTEGCSFR	99.3%	35.5	25	34.7	5	0	0	969.45	73	80
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	5	8	28	0.03%	40.5%	LVQSPNSYFMDVK	99.7%	56.8	25	51.5	14	0	0	1527.75	24	36
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	5	8	28	0.03%	40.5%	RLVQSPNSYFMDVK	99.3%	26.8	25	26.8	1	2	0	1699.85	23	36
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	27	101	0.10%	75.3%	ACYGVLR	99.7%	39.1	25	23.1	2	0	0	838.42	118	124
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	27	101	0.10%	75.3%	AELNEFLTR	99.7%	62.6	25	44.1	10	0	0	1092.57	19	27
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	27	101	0.10%	75.3%	DEILPTTPISEQK	99.7%	78.8	25	59.9	5	0	0	1470.77	215	227
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	27	101	0.10%	75.3%	ELAEDGYSGVEVR	99.7%	96	25	87.8	12	0	0	1423.67	28	40
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	27	101	0.10%	75.3%	ELTAVVQK	99.7%	60.7	25	41.5	2	0	0	887.52	68	75
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	27	101	0.10%	75.3%	ELTAVVQKR	99.7%	53.8	25	44.5	2	0	0	1043.62	68	76
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	27	101	0.10%	75.3%	FGFPEGSVELYAEK	99.7%	83.9	25	78.4	6	0	0	1572.76	77	90
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	27	101	0.10%	75.3%	FIMESGAK	99.7%	41.6	25	16.3	3	0	0	882.44	125	132
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	27	101	0.10%	75.3%	FVADGIFK	99.7%	39.2	25	35.7	2	0	0	896.49	11	18
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	27	101	0.10%	75.3%	FVDGLMIHSGDPVNYYVDTAVR	99.7%	49.8	25	43.5	3	4	0	2484.19	152	173
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	27	101	0.10%	75.3%	GCEVVVSGK	99.7%	47.7	25	45.3	1	0	0	934.47	133	141
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	27	101	0.10%	75.3%	GCEVVVSGKLR	99.7%	48	25	41.9	2	0	0	1203.65	133	143
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	27	101	0.10%	75.3%	GGKPEPPAMPQPVPTA	99.7%	47.9	25	46.1	6	0	0	1589.80	228	243
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	27	101	0.10%	75.3%	GLCAIAQAESLR	99.7%	79.6	25	63.8	8	0	0	1288.67	95	106
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	27	101	0.10%	75.3%	IMLPWDPTGK	99.7%	42.3	25	33.5	7	0	0	1157.60	188	197
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	27	101	0.10%	75.3%	IRELTAVVQK	99.7%	44.5	25	33.5	2	0	0	1156.70	66	75
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	27	101	0.10%	75.3%	KFVADGIFK	99.7%	48.2	25	38.6	5	0	0	1024.58	10	18
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	27	101	0.10%	75.3%	RACYGVLR	99.7%	40.3	25	24.8	2	0	0	994.53	117	124
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	27	101	0.10%	75.3%	TEIIILATR	99.7%	69.9	25	60	14	0	0	1029.63	46	54
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	27	101	0.10%	75.3%	TQNVLGEK	99.7%	52.6	25	38.4	2	0	0	888.48	55	62
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	27	101	0.10%	75.3%	YKLLGGLAVR	96.9%	29	25	19.9	1	0	0	1089.68	107	116
40S ribosomal protein S30	FAU	RS30_HUMAN	6.6	100.0%	3	3	4	0.00%	20.3%	FVNVVPTFGK	98.9%	33.4	25	26.1	2	0	0	1107.62	42	51
40S ribosomal protein S30	FAU	RS30_HUMAN	6.6	100.0%	3	3	4	0.00%	20.3%	FVNVVPTFGKK	99.6%	38.1	25	38.1	1	0	0	1235.71	42	52
40S ribosomal protein S30	FAU	RS30_HUMAN	6.6	100.0%	3	3	4	0.00%	20.3%	RFVNVVPTFGK	97.4%	29.6	25	29.6	1	0	0	1263.72	41	51
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	16	24	68	0.07%	56.1%	ACQSIYPLHDVFVR	99.7%	74.8	25	66.2	4	2	0	1704.85	200	213
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	16	24	68	0.07%	56.1%	ADGYEPPVQESV	99.7%	61.3	25	61.3	1	0	0	1290.58	253	264
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	16	24	68	0.07%	56.1%	APAMFNIR	99.7%	59.6	25	52.9	6	0	0	919.48	35	42
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	16	24	68	0.07%	56.1%	ATGDETGAKVER	99.7%	56.2	25	47.6	2	0	0	1233.61	241	252
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	16	24	68	0.07%	56.1%	EVQTNDLKEVVNK	99.7%	84.2	25	77.3	5	0	0	1515.80	175	187
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	16	24	68	0.07%	56.1%	FKLITEDVQGK	99.7%	62	25	33.7	2	0	0	1277.71	84	94
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	16	24	68	0.07%	56.1%	KDWYDVK	98.1%	30.9	25	18.6	1	0	0	953.47	28	34
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	16	24	68	0.07%	56.1%	LFCVGFTK	99.7%	49.4	25	36.1	6	0	0	971.50	137	144

40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	16	24	68	0.07%	56.1%	LIPDSIGKDIEK	99.7%	48.8	25	40.2	2	0	0	1327.75	188	199
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	16	24	68	0.07%	56.1%	LITEDVQGK	99.7%	56.4	25	25	6	0	0	1002.55	86	94
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	16	24	68	0.07%	56.1%	LMELHGEGSSSGK	99.7%	71.9	25	63.3	7	4	0	1331.63	228	240
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	16	24	68	0.07%	56.1%	MMEIMTR	99.7%	45	25	35	4	0	0	911.41	168	174
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	16	24	68	0.07%	56.1%	NCLTNFHGMDLTR	99.7%	77.6	25	68.9	4	1	0	1578.72	95	107
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	16	24	68	0.07%	56.1%	TSYAQHQQVR	99.7%	87.4	25	80.3	2	0	0	1217.60	153	162
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	16	24	68	0.07%	56.1%	TTDGYLLR	99.7%	62.2	25	42.4	8	0	0	938.49	129	136
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	16	24	68	0.07%	56.1%	VERADGYEPPVQESV	99.7%	44.3	25	43.3	1	0	0	1674.80	250	264
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	16	24	91	0.09%	57.8%	DANGNSFATR	99.7%	58.9	25	50.4	4	0	0	1052.48	212	221
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	16	24	91	0.09%	57.8%	ECLPLIIFLR	99.7%	57.5	25	50.9	4	0	0	1273.73	40	49
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	16	24	91	0.09%	57.8%	FDTGNLCMVTGGANLGR	99.7%	105	25	100	8	3	0	1798.82	175	191
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	16	24	91	0.09%	57.8%	GIPHLVTHDAR	99.7%	54.5	25	46.4	2	3	0	1215.66	135	145
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	16	24	91	0.09%	57.8%	GNKPWISLPR	99.7%	42.3	25	36.9	5	0	0	1167.66	231	240
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	16	24	91	0.09%	57.8%	HPGSFDVVHVK	99.7%	50	25	48.7	2	2	0	1221.64	201	211
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	16	24	91	0.09%	57.8%	LRECLPLIIFLR	99.7%	40.3	25	40.3	2	2	0	1542.92	38	49
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	16	24	91	0.09%	57.8%	LSNIFVIGK	99.7%	64.7	25	62.1	15	0	0	990.60	222	230
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	16	24	91	0.09%	57.8%	LTGVFAPRPSTGPHK	99.7%	48.6	25	43.3	2	0	0	1564.86	23	37
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	16	24	91	0.09%	57.8%	LTIAEER	99.7%	41.6	25	14.7	8	0	0	831.46	246	252
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	16	24	91	0.09%	57.8%	TDITYPAGFMDVISIDK	99.7%	76.3	25	76.3	10	0	0	1885.93	78	94
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	16	24	91	0.09%	57.8%	TIRYPDPLIK	99.7%	36.4	25	24.1	1	2	0	1215.71	146	155
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	16	24	91	0.09%	57.8%	VNDTIQIDLETGK	99.7%	106	25	106	5	0	0	1445.75	156	168
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	16	24	91	0.09%	57.8%	YALTGDEVK	99.7%	51.1	25	42.9	4	0	0	995.50	54	62
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	16	24	91	0.09%	57.8%	YALTGDEVKK	99.7%	65.5	25	53.1	6	0	0	1123.60	54	63
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	16	24	91	0.09%	57.8%	YPDPLIK	99.0%	33.8	25	11.8	1	0	0	845.48	149	155
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	6	7	17	0.02%	27.9%	KAQCPIVER	99.7%	40	25	36.3	2	0	0	1100.59	63	71
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	6	7	17	0.02%	27.9%	LTNSMMMHGR	99.7%	60.2	25	50.1	3	0	0	1177.53	72	81
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	6	7	17	0.02%	27.9%	QAVDVSPLR	99.7%	53	25	43.4	3	0	0	984.55	137	145
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	6	7	17	0.02%	27.9%	QAVDVSPLRR	98.0%	30.8	25	13.6	1	0	0	1140.65	137	146
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	6	7	17	0.02%	27.9%	TIAECLADELINAAK	99.7%	103	25	97.2	4	0	0	1631.83	168	182
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	6	7	17	0.02%	27.9%	VNQAIWLLCTGAR	99.7%	87.9	25	82.4	4	0	0	1501.79	147	159
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	11	13	41	0.04%	40.2%	DIPGLTDTTVPR	99.7%	69.6	25	63.1	6	0	0	1284.68	120	131
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	11	13	41	0.04%	40.2%	EDDVRQYVVR	99.7%	40.2	25	29.9	2	0	0	1278.64	150	159
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	11	13	41	0.04%	40.2%	GCIVDANLSVLNLVIVK	99.7%	51.7	25	51.7	5	0	0	1827.04	99	115
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	11	13	41	0.04%	40.2%	GEKDIPGLTDTTVPR	99.3%	26.6	25	26.6	0	1	0	1598.84	117	131
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	11	13	41	0.04%	40.2%	ISGGNDKQGFPMK	99.7%	67.9	25	61.6	4	0	0	1378.68	52	64
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	11	13	41	0.04%	40.2%	KLFNLSK	99.7%	41.5	25	24.4	2	0	0	849.52	143	149
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	11	13	41	0.04%	40.2%	LFNLSKEDDVR	99.7%	54.6	25	41	4	0	0	1335.69	144	154
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	11	13	41	0.04%	40.2%	LIEVDDER	99.7%	56.1	25	53.8	5	0	0	988.49	15	22
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	11	13	41	0.04%	40.2%	LIEVDDERK	99.7%	52.5	25	45.7	2	0	0	1116.59	15	23
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	11	13	41	0.04%	40.2%	MATEVAADALGEEWK	99.7%	100	25	98.5	8	0	0	1620.76	32	46
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	11	13	41	0.04%	40.2%	MKLNISFPATGCQK	99.7%	75.8	25	67.7	2	0	0	1610.80	1	14
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	11	12	27	0.03%	40.7%	AIIIFVPVPQLK	99.7%	65	25	65	6	0	0	1337.86	59	70
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	11	12	27	0.03%	40.7%	AQQNNVEHKVETFSGVYK	99.7%	41.9	25	40.8	2	2	0	2078.03	161	178
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	11	12	27	0.03%	40.7%	DVNFEFPEFQL	99.7%	59	25	58.8	3	0	0	1384.64	184	194
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	11	12	27	0.03%	40.7%	ELNITAAK	99.6%	38	25	25.5	1	0	0	859.49	42	49
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	11	12	27	0.03%	40.7%	ELNITAAKEIEVGGGR	99.7%	49	25	49	1	0	0	1656.89	42	57
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	11	12	27	0.03%	40.7%	HVVFIAQR	96.6%	28.7	25	28.7	4	0	0	969.56	91	98
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	11	12	27	0.03%	40.7%	KAIIIFVPVPQLK	99.7%	58.5	25	58.5	2	0	0	1465.95	58	70
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	11	12	27	0.03%	40.7%	LTGKDVNFEFPEFQL	99.7%	48.9	25	48.4	2	0	0	1783.89	180	194
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	11	12	27	0.03%	40.7%	RILPKPTR	98.0%	30.9	25	30.9	1	0	0	980.64	99	106
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	11	12	27	0.03%	40.7%	VETFSGVYK	99.7%	49.8	25	23.8	2	0	0	1029.53	170	178

40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	11	12	27	0.03%	40.7%	VETFSGVYKK	98.1%	31	25	27.1	1	0	0	1157.62	170	179
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	13	16	56	0.06%	58.7%	ADGYVLEGK	99.7%	64.6	25	55.5	2	0	0	951.48	185	193
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	13	16	56	0.06%	58.7%	ADGYVLEGKELEFYLR	97.9%	30.5	25	30.5	1	0	0	1901.96	185	200
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	13	16	56	0.06%	58.7%	ELEFYLR	99.7%	40.3	25	30.8	2	0	0	969.50	194	200
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	13	16	56	0.06%	58.7%	ELEFYLRK	96.2%	28.2	25	22.1	1	0	0	1097.60	194	201
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	13	16	56	0.06%	58.7%	IIDVVYNASNNELVR	99.7%	106	25	99.6	8	2	0	1718.91	78	92
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	13	16	56	0.06%	58.7%	ISSLLEEQFQQGK	99.7%	75.4	25	63	13	0	0	1506.78	158	170
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	13	16	56	0.06%	58.7%	KYELGRPAANTK	99.7%	43.9	25	37.2	2	1	0	1347.74	26	37
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	13	16	56	0.06%	58.7%	LDVGNFSWGSECCTR	99.7%	98.7	25	98.7	2	0	0	1787.75	60	74
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	13	16	56	0.06%	58.7%	LLACIASRPGQCGR	99.7%	49.9	25	47.4	2	2	0	1558.79	171	184
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	13	16	56	0.06%	58.7%	LTPEEEEILNK	99.7%	60.8	25	55.6	5	0	0	1314.68	129	139
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	13	16	56	0.06%	58.7%	NCIVLIDSTPYR	99.7%	83.8	25	69.8	9	0	0	1450.74	99	110
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	13	16	56	0.06%	58.7%	QWYESHYALPLGR	99.7%	41.3	25	31.6	2	0	0	1619.80	111	123
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	13	16	56	0.06%	58.7%	YELGRPAANTK	99.7%	49.4	25	41.5	2	0	0	1219.64	27	37
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	63	0.06%	55.2%	ELLTLDEKDPR	97.7%	30.2	25	24.7	1	0	0	1328.71	59	69
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	63	0.06%	55.2%	HIDFSLR	99.7%	45.3	25	25.8	2	0	0	887.47	156	162
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	63	0.06%	55.2%	IEDFLER	99.7%	51.3	25	43.4	1	0	0	921.47	102	108
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	63	0.06%	55.2%	IEDFLERR	99.0%	33.8	25	19.4	2	0	0	1077.57	102	109
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	63	0.06%	55.2%	IGVLDEGK	99.7%	55.3	25	31.9	7	0	0	830.46	84	91
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	63	0.06%	55.2%	IGVLDEGKMK	99.7%	44.4	25	33.7	3	0	0	1089.60	84	93
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	63	0.06%	55.2%	KQVVNIPSFIVR	99.7%	52.2	25	52.2	2	2	0	1399.84	139	150
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	63	0.06%	55.2%	LDYILGLK	99.7%	46.2	25	41.2	2	0	0	934.56	94	101
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	63	0.06%	55.2%	LFEGNALLR	99.7%	72.7	25	50.8	15	0	0	1032.58	71	79
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	63	0.06%	55.2%	LFEGNALLRR	99.7%	45.5	25	25	2	0	0	1188.68	71	80
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	63	0.06%	55.2%	LIGEYGLR	99.7%	61.5	25	47.5	2	0	0	920.52	31	38
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	63	0.06%	55.2%	LQTQVFK	99.7%	47.5	25	27	2	0	0	863.50	110	116
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	63	0.06%	55.2%	MKLDYILGLK	99.7%	50.5	25	24.1	4	0	0	1193.70	92	101
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	63	0.06%	55.2%	QVVNIPSFIVR	99.7%	45.3	25	31.8	6	0	0	1271.75	140	150
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	63	0.06%	55.2%	RLFEGNALLR	99.7%	62.4	25	46.1	2	0	0	1188.68	70	79
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	63	0.06%	55.2%	RLQTQVFK	99.1%	33.9	25	24.6	2	0	0	1019.60	109	116
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	63	0.06%	55.2%	SPYGGGRPGR	96.4%	28.4	25	21.3	1	0	0	1003.51	163	172
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	63	0.06%	55.2%	SRLDQELK	98.4%	31.7	25	4.82	3	0	0	988.54	23	30
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	63	0.06%	55.2%	VKFTLAK	97.5%	29.8	25	23	2	0	0	806.51	46	52
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	7	7	24	0.02%	25.4%	AIVAIENPADVSVISSR	99.7%	101	25	101	4	0	0	1740.95	64	80
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	7	7	24	0.02%	25.4%	FAAATGATPIAGR	99.7%	101	25	88.5	8	0	0	1203.65	90	102
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	7	7	24	0.02%	25.4%	FTPGTFTNQIQAAFR	99.7%	82.8	25	72.1	2	0	0	1698.86	103	117
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	7	7	24	0.02%	25.4%	KSDGIYIINLK	99.7%	46	25	20	2	0	0	1263.73	42	52
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	7	7	24	0.02%	25.4%	LLVVTDPR	99.7%	61.1	25	47.1	4	0	0	912.55	121	128
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	7	7	24	0.02%	25.4%	SDGIYIINLK	99.7%	53.2	25	40	2	0	0	1135.64	43	52
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	7	7	24	0.02%	25.4%	YVDIAIPCNNK	99.7%	48.7	25	42.4	2	0	0	1306.65	156	166
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	7	7	20	0.02%	14.3%	ADLLLSTQPGREEGSPLELER	99.7%	49.6	25	49.6	0	2	0	2310.19	593	613
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	7	7	20	0.02%	14.3%	FTGLSKEELLK	99.7%	42	25	35.1	2	0	0	1264.71	161	171
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	7	7	20	0.02%	14.3%	GLVLGPIHK	99.5%	36.9	25	33.1	2	0	0	933.59	258	266
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	7	7	20	0.02%	14.3%	GQSEDPGSLLSLFR	99.7%	64.4	25	59.7	5	0	0	1505.76	511	524
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	7	7	20	0.02%	14.3%	LLTSFLPAQLLR	99.7%	67.4	25	67.1	2	0	0	1371.84	440	451
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	7	7	20	0.02%	14.3%	VAEDEAEAAAAAK	99.7%	106	25	99.2	3	0	0	1245.60	148	160
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	7	7	20	0.02%	14.3%	VILDLTPNYR	99.7%	65.4	25	60.3	4	0	0	1203.67	304	313
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	3	3	9	0.01%	4.1%	ELTMASLPFTFDVER	99.7%	49.7	25	49.5	1	0	0	1755.86	316	330
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	3	3	9	0.01%	4.1%	NSLGGDVLFVGK	99.7%	61.4	25	56.1	4	0	0	1205.65	677	688
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	3	3	9	0.01%	4.1%	NSPGSQVASNPR	99.7%	66.1	25	59.8	4	0	0	1213.59	447	458
5'-AMP-activated protein kinase catalytic subunit alpha-1	PRKAA1	AAPK1_HUMAN	64.0	99.9%	2	2	3	0.00%	9.3%	IADFGLSNMMSDGEFLR	99.7%	42.9	25	42.9	1	0	0	1934.86	166	182

5'-AMP-activated protein kinase catalytic subunit alpha-1	PRKAA1	AAPK1_HUMAN	64.0	99.9%	2	2	3	0.00%	9.3%	TSCGSPNYAAPEVISGR	99.7%	47.2	25	47.2	1	0	0	1765.82	183	199
5'-AMP-activated protein kinase catalytic subunit alpha-1	PRKAA1	AAPK1_HUMAN	64.0	99.9%	2	2	3	0.00%	9.3%	VPFLVAETPR	99.7%	57.3	25	54.2	2	0	0	1128.64	375	384
5'-AMP-activated protein kinase catalytic subunit alpha-1	PRKAA1	AAPK1_HUMAN	64.0	99.9%	2	2	3	0.00%	9.3%	VVNPYYLR	97.9%	30.6	25	22.7	1	0	0	1023.56	437	444
5'-AMP-activated protein kinase catalytic subunit alpha-2	PRKAA2	AAPK2_HUMAN	62.3	100.0%	4	4	5	0.00%	9.4%	IADFGLSNMMSDGEFLR	99.7%	42.9	25	42.9	1	0	0	1934.86	155	171
5'-AMP-activated protein kinase catalytic subunit alpha-2	PRKAA2	AAPK2_HUMAN	62.3	100.0%	4	4	5	0.00%	9.4%	MPPLIADSPK	99.1%	34	25	30.5	2	0	0	1084.57	370	379
5'-AMP-activated protein kinase catalytic subunit alpha-2	PRKAA2	AAPK2_HUMAN	62.3	100.0%	4	4	5	0.00%	9.4%	TSCGSPNYAAPEVISGR	99.7%	47.2	25	47.2	1	0	0	1765.82	172	188
5'-AMP-activated protein kinase catalytic subunit alpha-2	PRKAA2	AAPK2_HUMAN	62.3	100.0%	4	4	5	0.00%	9.4%	VVNAYHLR	99.7%	43.2	25	31.5	1	0	0	971.54	432	439
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	6	6	10	0.01%	17.8%	AFFALVTNGVR	99.7%	79.2	25	72.8	1	0	0	1194.66	60	70
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	6	6	10	0.01%	17.8%	FDVINLAAEK	99.7%	60.4	25	49.3	2	0	0	1119.60	244	253
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	6	6	10	0.01%	17.8%	LVEAEVHR	99.7%	44.4	25	41.4	2	0	0	952.52	292	299
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	6	6	10	0.01%	17.8%	SHYFEGVLK	97.0%	29.2	25	21.3	1	0	0	1079.55	270	278
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	6	6	10	0.01%	17.8%	TYNNLDVSVTK	99.7%	56.8	25	52.1	2	0	0	1253.64	254	264
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	6	6	10	0.01%	17.8%	VSALPVVDEK	99.7%	59.9	25	44.2	2	0	0	1056.59	225	234
5-methylcytosine rRNA methyltransferase NSUN4	NSUN4	NSUN4_HUMAN	43.1	100.0%	2	2	4	0.00%	5.7%	NLAANDLSPSR	99.7%	51.3	25	43.5	2	0	0	1157.59	199	209
5-methylcytosine rRNA methyltransferase NSUN4	NSUN4	NSUN4_HUMAN	43.1	100.0%	2	2	4	0.00%	5.7%	TLALLQTGCCR	99.7%	48.2	25	41.8	2	0	0	1292.65	188	198
5'-nucleotidase domain-containing protein 2	NT5DC2	NT5D2_HUMAN	60.7	100.0%	3	3	4	0.00%	8.1%	QGNLFDFLR	99.7%	63	25	49.7	2	0	0	1109.57	336	344
5'-nucleotidase domain-containing protein 2	NT5DC2	NT5D2_HUMAN	60.7	100.0%	3	3	4	0.00%	8.1%	QLFLITNSPFSFVDK	99.7%	55.2	25	55.2	1	0	0	1755.93	263	277
5'-nucleotidase domain-containing protein 2	NT5DC2	NT5D2_HUMAN	60.7	100.0%	3	3	4	0.00%	8.1%	VLYFGDHLYSDLADLMLR	97.0%	22	25	22	0	1	0	2157.07	353	370
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	53	0.05%	40.3%	AAVEEGIVLGGGCALLR	99.7%	101	25	94	2	2	0	1684.91	430	446
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	53	0.05%	40.3%	ALMLQGVDLLADAVAVTMGPK	99.7%	37.5	25	37.5	0	3	0	2129.13	38	58
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	53	0.05%	40.3%	CEFQDAYVLLSEK	99.7%	80	25	70.2	2	0	0	1601.75	237	249
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	53	0.05%	40.3%	CIPALDSLTPANEDQK	99.7%	71.1	25	69.7	2	0	0	1771.85	447	462
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	53	0.05%	40.3%	GANPVEIR	99.7%	43.2	25	14.8	2	0	0	855.47	134	141
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	53	0.05%	40.3%	GANPVEIRR	99.7%	48.1	25	37.1	2	0	0	1011.57	134	142
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	53	0.05%	40.3%	GYISPYFINTSK	99.7%	69.6	25	61.2	2	0	0	1389.70	222	233
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	53	0.05%	40.3%	IGIEIIKR	99.7%	55.3	25	28.9	2	0	0	941.61	463	470
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	53	0.05%	40.3%	ISSIQSIVPALEIANAHR	99.7%	38.4	25	38.4	0	2	0	1919.07	251	268
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	53	0.05%	40.3%	LSDGVAVLK	99.7%	59	25	42.5	2	0	0	901.54	397	405
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	53	0.05%	40.3%	LVQDVANNTNEEAGDGTTTATVLAR	99.7%	153	25	153	2	2	0	2560.25	97	121
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	53	0.05%	40.3%	NAGVEGSLIVEK	99.7%	82.7	25	62.8	2	0	0	1215.66	482	493
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	53	0.05%	40.3%	TLNDELEIIEGMK	99.7%	91.1	25	91.1	2	0	0	1504.76	206	218
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	53	0.05%	40.3%	TVIIEQSWGSPK	99.7%	79.7	25	70.9	2	0	0	1344.72	61	72
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	53	0.05%	40.3%	VGEVIVTK	99.7%	74.5	25	52	2	0	0	844.51	345	352
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	53	0.05%	40.3%	VGEVIVTKDDAMLLK	99.7%	70.9	25	63.7	4	4	0	1630.91	345	359
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	53	0.05%	40.3%	VGGTSDVEVNEK	99.7%	78.9	25	72.7	3	0	0	1233.60	406	417
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	53	0.05%	40.3%	VGGTSDVEVNEKK	99.7%	69.5	25	52	2	1	0	1361.69	406	418
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	53	0.05%	40.3%	VGLQVVAVK	99.7%	80.7	25	73.3	2	0	0	912.59	293	301
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	53	0.05%	40.3%	VTDALNATR	99.7%	78.8	25	62.1	2	0	0	960.51	421	429
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	12	25	0.02%	20.4%	AIADWYNEK	99.7%	46.5	25	40.1	2	0	0	1109.53	151	159
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	12	25	0.02%	20.4%	ALDAAFYK	99.7%	38.7	25	36.1	2	0	0	898.47	352	359
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	12	25	0.02%	20.4%	ALLQEMPLTALLR	99.7%	90.5	25	79	5	0	0	1468.86	271	283
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	12	25	0.02%	20.4%	FLCFGSEGGTYYIK	99.7%	81.2	25	81.1	2	0	0	1641.76	36	49
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	12	25	0.02%	20.4%	GGMALALAVTK	99.7%	76.9	25	63.3	4	0	0	1031.59	160	170
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	12	25	0.02%	20.4%	LGLENAEALIR	99.7%	77.3	25	63.9	4	0	0	1198.68	53	63
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	12	25	0.02%	20.4%	LIEDGRGCEVIQEIK	98.6%	32.2	25	23.2	1	0	0	1758.91	64	78
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	12	25	0.02%	20.4%	MTANSVLEPGNSEVSLVCEK	99.7%	72.4	25	72.4	4	0	0	2180.02	288	307
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	12	25	0.02%	20.4%	WRPDEEILK	97.3%	29.6	25	14.1	1	0	0	1185.63	343	351
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	9	12	42	0.04%	43.2%	AFLADPSAFVAAAPVAAATTAAPAAAAAPAK	99.7%	42.5	25	42.5	2	2	0	2752.47	267	297
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	9	12	42	0.04%	43.2%	AGAIAPCEVTVPAQNTGLGPEK	99.7%	57.4	25	53.2	2	2	0	2180.10	113	134
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	9	12	42	0.04%	43.2%	CFIVGADNVGSK	99.5%	36.8	25	31.9	3	0	0	1266.61	27	38
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	9	12	42	0.04%	43.2%	GHLENNPALEK	99.7%	59.5	25	35	2	2	0	1221.62	67	77

60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	9	12	42	0.04%	43.2%	GNVGFVFTK	99.7%	61.4	25	48.5	7	0	0	968.52	84	92
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	9	12	42	0.04%	43.2%	GTIEILSDVQLIK	99.7%	52.6	25	44.4	6	0	0	1428.83	150	162
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	9	12	42	0.04%	43.2%	IIQLLDDYPK	99.7%	71.1	25	55.7	2	0	0	1217.68	17	26
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	9	12	42	0.04%	43.2%	TSFFQALGITTK	99.7%	74.6	25	74.6	10	0	0	1313.71	135	146
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	9	12	42	0.04%	43.2%	VLALSVETDYTFPLAEK	99.7%	69.2	25	68.9	2	0	0	1896.00	248	264
60S acidic ribosomal protein P2	RPLP2	RLA2_HUMAN	11.7	100.0%	5	6	11	0.01%	84.3%	ILDSVGIEADDDRLNK	99.7%	64.5	25	60.2	2	1	0	1772.90	26	41
60S acidic ribosomal protein P2	RPLP2	RLA2_HUMAN	11.7	100.0%	5	6	11	0.01%	84.3%	KEESEESDDDMGFGLFD	99.4%	36.2	25	36.2	2	0	0	1965.75	99	115
60S acidic ribosomal protein P2	RPLP2	RLA2_HUMAN	11.7	100.0%	5	6	11	0.01%	84.3%	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	99.7%	43.1	25	43.1	0	2	0	2774.43	62	94
60S acidic ribosomal protein P2	RPLP2	RLA2_HUMAN	11.7	100.0%	5	6	11	0.01%	84.3%	NIEDVIAQGIGK	99.7%	98	25	85.4	2	0	0	1256.68	50	61
60S acidic ribosomal protein P2	RPLP2	RLA2_HUMAN	11.7	100.0%	5	6	11	0.01%	84.3%	YVASYLLAALGGNSSPSAK	99.7%	68.6	25	68.6	2	0	0	1868.98	3	21
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	14	21	39	0.04%	56.1%	AKVDEFPLCGHMVSDEYEQLSSEALEAAR	99.7%	105	25	105	0	2	0	3281.51	41	69
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	14	21	39	0.04%	56.1%	EHVIEALR	99.2%	34.8	25	31.5	1	0	0	966.54	146	153
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	14	21	39	0.04%	56.1%	EHVIEALRR	99.7%	38.8	25	14.4	1	0	0	1122.64	146	154
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	14	21	39	0.04%	56.1%	FNADEFEDMVAEK	99.7%	75.3	25	69.6	2	0	0	1560.65	176	188
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	14	21	39	0.04%	56.1%	FNADEFEDMVAEKR	99.7%	66.4	25	57.4	2	3	0	1700.76	176	189
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	14	21	39	0.04%	56.1%	GAFGKPQGTVAR	99.7%	62	25	49.9	4	0	0	1188.65	117	128
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	14	21	39	0.04%	56.1%	GPLDKWR	95.1%	27.2	25	21.1	1	0	0	871.48	204	210
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	14	21	39	0.04%	56.1%	ICANKYMVK	95.3%	27.4	25	27.4	1	0	0	1142.57	70	78
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	14	21	39	0.04%	56.1%	IFDLGRK	98.8%	32.7	25	0	1	0	0	848.50	33	39
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	14	21	39	0.04%	56.1%	LQNKEHVIEALR	99.7%	38.2	25	38.2	0	2	0	1449.82	142	153
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	14	21	39	0.04%	56.1%	MLSCAGADR	99.7%	82.5	25	60.3	4	0	0	996.42	102	110
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	14	21	39	0.04%	56.1%	RLIPDGCGVK	99.6%	37.5	25	26.5	2	0	0	1114.60	189	198
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	14	21	39	0.04%	56.1%	VDEFPLCGHMVSDEYEQLSSEALEAAR	99.7%	63.8	25	63.1	0	4	0	3098.37	43	69
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	14	21	39	0.04%	56.1%	VHIGQVIMSIR	99.7%	52.2	25	51.6	5	4	0	1252.72	129	139
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	8	17	43	0.04%	39.2%	AVDIPHMDIEALK	99.7%	54.4	25	47	4	0	0	1467.75	79	91
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	8	17	43	0.04%	39.2%	AVDIPHMDIEALKK	99.7%	49.2	25	49.1	4	3	0	1579.85	79	92
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	8	17	43	0.04%	39.2%	DTLYEAVR	99.7%	67.3	25	45.3	4	0	0	966.49	8	15
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	8	17	43	0.04%	39.2%	FPSLLTHNENMVAK	99.7%	59.8	25	58.4	3	4	0	1600.82	134	147
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	8	17	43	0.04%	39.2%	FSVCVLGDQQHCDEAK	99.7%	81	25	81	2	2	0	1892.83	63	78
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	8	17	43	0.04%	39.2%	ILGPGLNK	99.7%	39.7	25	20.4	2	0	0	811.50	123	130
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	8	17	43	0.04%	39.2%	KYDAFLASESLIK	99.7%	76.4	25	76.4	4	2	0	1484.80	106	118
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	8	17	43	0.04%	39.2%	VLCLAVAVGHVK	99.7%	85.3	25	85.3	7	2	0	1265.74	162	173
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	7	8	25	0.02%	37.6%	IAVHCTVR	99.7%	46.2	25	38.3	2	0	0	955.51	68	75
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	7	8	25	0.02%	37.6%	ISKEEAMR	99.7%	48.4	25	28.2	2	0	0	963.49	157	164
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	7	8	25	0.02%	37.6%	LCLNICVGESGDRLTR	97.8%	23	25	22.4	0	1	0	1862.92	20	35
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	7	8	25	0.02%	37.6%	VLEQLTGQTPVFSK	99.7%	98.3	25	93.8	8	0	0	1546.85	39	52
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	7	8	25	0.02%	37.6%	VREYELR	99.3%	35.3	25	13.9	1	0	0	964.52	89	95
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	7	8	25	0.02%	37.6%	WFQQKYDGIILPGK	99.7%	39.2	25	30.8	2	2	0	1692.91	165	178
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	7	8	25	0.02%	37.6%	YDGIILPGK	99.7%	59.9	25	57.6	7	0	0	975.55	170	178
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	5	6	22	0.02%	43.0%	CTGGEVGATSALAPK	99.7%	96.5	25	79	4	0	0	1418.69	17	31
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	5	6	22	0.02%	43.0%	EILGTAQSVGCNVDGR	98.7%	32.5	25	32.5	1	0	0	1675.81	131	146
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	5	6	22	0.02%	43.0%	HSGNITFDEIVNIAR	99.7%	91.4	25	91.4	4	4	0	1685.86	100	114
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	5	6	22	0.02%	43.0%	IGPLGLSPK	99.7%	52.2	25	35.1	4	0	0	881.55	32	40
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	5	6	22	0.02%	43.0%	QAQIEVVPSASALIIK	99.7%	92.7	25	92.7	5	0	0	1666.97	68	83
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	69	0.07%	34.1%	GFSLEELR	99.7%	55.7	25	42.3	11	0	0	950.49	75	82
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	69	0.07%	34.1%	LATQLTGPVMPVR	99.7%	63.2	25	61.3	8	0	0	1382.78	146	158
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	69	0.07%	34.1%	NKSTESLQANVQR	99.7%	61.4	25	51.5	2	0	0	1474.76	104	116
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	69	0.07%	34.1%	RVATWFNQPAR	99.7%	46.5	25	44.6	2	2	0	1345.71	21	31
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	69	0.07%	34.1%	SKLILFPR	99.1%	34.2	25	34.2	3	0	0	973.62	122	129
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	69	0.07%	34.1%	STESLQANVQR	99.7%	88.7	25	78.4	16	0	0	1232.62	106	116
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	69	0.07%	34.1%	TIGISVDPR	99.7%	59.8	25	48.2	12	0	0	957.54	93	101

60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	69	0.07%	34.1%	VATWFNQPAR	99.7%	76.2	25	63.4	4	0	0	1189.61	22	31
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	69	0.07%	34.1%	VITEEEKNFK	99.7%	55.2	25	44.6	9	0	0	1236.65	168	177
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	6	6	16	0.02%	28.6%	CEGINISGNFYR	99.7%	61.7	25	53.2	3	0	0	1429.65	38	49
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	6	6	16	0.02%	28.6%	IDKYTEVLK	99.7%	44.1	25	30.3	1	0	0	1108.63	189	197
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	6	6	16	0.02%	28.6%	KFAYLGR	99.7%	39.4	25	27.1	2	0	0	854.49	134	140
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	6	6	16	0.02%	28.6%	LKYLAFLR	98.4%	31.8	25	26	1	0	0	1023.64	52	59
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	6	6	16	0.02%	28.6%	VFDGIPPPYDK	98.8%	32.9	25	28.3	2	0	0	1247.63	104	114
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	6	6	16	0.02%	28.6%	YQAVTATLEEK	99.7%	56.1	25	43.9	7	0	0	1252.64	149	159
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	8	82	0.08%	27.9%	ALVDGPCTQVR	99.7%	77.5	25	71.9	5	0	0	1215.62	36	46
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	8	82	0.08%	27.9%	CMQLTDFILK	99.7%	56.2	25	47.8	15	0	0	1268.64	54	63
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	8	82	0.08%	27.9%	LVAIVDVIDQNR	99.7%	90.3	25	90.3	38	0	0	1354.77	24	35
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	8	82	0.08%	27.9%	MTDFDRFK	99.7%	44.8	25	44.8	4	0	0	1059.49	104	111
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	8	82	0.08%	27.9%	RFVEVGR	96.7%	28.7	25	18.2	1	0	0	862.49	5	11
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	8	82	0.08%	27.9%	VAYVSFGPHAGK	99.7%	62.2	25	46.3	17	2	0	1232.64	12	23
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	8	10	17	0.02%	35.3%	FFEVILIDPFHK	99.7%	45.1	25	45.1	1	0	0	1504.82	129	140
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	8	10	17	0.02%	35.3%	GATYGKPVHHGVNQLK	99.7%	42	25	35.9	1	2	0	1705.91	78	93
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	8	10	17	0.02%	35.3%	NPDTQWITKPVHK	94.6%	20.3	25	19.3	0	1	0	1563.83	145	157
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	8	10	17	0.02%	35.3%	NTLQLHR	99.7%	43.8	25	29.7	3	0	0	881.50	196	202
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	8	10	17	0.02%	35.3%	QLSALHR	98.7%	32.5	25	3.3	1	0	0	824.47	32	38
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	8	10	17	0.02%	35.3%	RNPDTQWITKPVHK	99.7%	35.7	25	32.6	1	2	0	1719.93	144	157
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	8	10	17	0.02%	35.3%	SLQSVAEER	99.7%	40.5	25	31.8	4	0	0	1018.52	97	105
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	8	10	17	0.02%	35.3%	YIQELWR	99.7%	44.8	25	23.7	1	0	0	1007.53	6	12
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	12	34	0.03%	46.7%	EQIVPKPEEEVAQK	99.7%	54.2	25	44.8	2	0	0	1623.86	154	167
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	12	34	0.03%	46.7%	EQIVPKPEEEVAQKK	99.7%	33.4	25	30	0	1	0	1751.95	154	168
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	12	34	0.03%	46.7%	ETAQAIKGMHIR	96.5%	21.6	25	12.1	0	1	0	1370.72	31	42
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	12	34	0.03%	46.7%	GLDVDSLVIEHIQVNK	99.7%	84.1	25	71.9	5	0	0	1778.96	106	121
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	12	34	0.03%	46.7%	KSAEFLLHMLK	99.7%	58.6	25	53.4	0	2	0	1316.74	86	96
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	12	34	0.03%	46.7%	QWGWTQGR	98.1%	31	25	12.9	1	0	0	1018.49	75	82
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	12	34	0.03%	46.7%	QWGWTQGRWPK	99.3%	35.1	25	31.8	2	0	0	1429.71	75	85
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	12	34	0.03%	46.7%	SAEFLLHMLK	99.7%	58	25	50.1	6	0	0	1188.64	87	96
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	12	34	0.03%	46.7%	VRYSLDPENPTK	99.5%	36.8	25	34.8	1	0	0	1418.73	2	13
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	12	34	0.03%	46.7%	YLKDVTLQK	99.7%	47	25	39.6	5	0	0	1107.64	47	55
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	12	34	0.03%	46.7%	YSLDPENPTK	99.7%	56.4	25	56.4	8	0	0	1163.56	4	13
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	11	13	57	0.06%	45.2%	GCGTVLLSGPR	99.7%	87.3	25	75.1	12	0	0	1116.58	133	143
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	11	13	57	0.06%	45.2%	ILTFDQLALDSPK	99.7%	118	25	106	15	0	0	1460.80	120	132
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	11	13	57	0.06%	45.2%	LKVCALR	99.5%	36.6	25	22.4	2	0	0	859.52	98	104
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	11	13	57	0.06%	45.2%	RLFMSR	99.2%	34.5	25	17.8	2	0	0	809.45	50	55
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	11	13	57	0.06%	45.2%	RTNSTFNQVVLK	99.6%	38	25	3.1	2	1	0	1406.78	38	49
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	11	13	57	0.06%	45.2%	SQDIYLR	95.6%	27.6	25	12.2	1	0	0	894.47	20	26
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	11	13	57	0.06%	45.2%	TAVVVGTITDDVR	99.7%	109	25	98.3	9	0	0	1345.73	79	91
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	11	13	57	0.06%	45.2%	TAVVVGTITDDVRVQEVPK	99.7%	53.3	25	53.3	2	2	0	2026.12	79	97
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	11	13	57	0.06%	45.2%	TNRPPLSLSR	99.7%	39.5	25	33	4	0	0	1140.65	56	65
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	11	13	57	0.06%	45.2%	TNSTFNQVVLK	99.7%	64.5	25	46.5	2	0	0	1250.67	39	49
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	11	13	57	0.06%	45.2%	TNSTFNQVVLKR	99.7%	44.2	25	44.2	3	0	0	1406.78	39	50
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	9	11	32	0.03%	39.2%	AHSIQIMK	97.6%	30	25	25	1	0	0	943.50	121	128
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	9	11	32	0.03%	39.2%	DLTTAGAVTQCYR	99.7%	69.5	25	69.5	4	0	0	1455.69	99	111
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	9	11	32	0.03%	39.2%	EYRDLTTAGAVTQCYR	99.7%	45.3	25	41.1	1	4	0	1903.90	96	111
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	9	11	32	0.03%	39.2%	FWYFVSQLKK	99.7%	45	25	43.5	4	1	0	1345.73	44	53
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	9	11	32	0.03%	39.2%	IFAPNHVVAK	99.7%	49.7	25	41.3	6	0	0	1095.63	32	41
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	9	11	32	0.03%	39.2%	NFGIWLR	99.7%	40.4	25	24.6	4	0	0	905.50	77	83
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	9	11	32	0.03%	39.2%	SRFWYFVSQLK	99.7%	43.2	25	35	1	0	0	1460.77	42	52

60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	9	11	32	0.03%	39.2%	SSGEIVYCGQVFEK	99.7%	85.5	25	84	4	0	0	1602.75	57	70
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	9	11	32	0.03%	39.2%	VKNFGIWLR	99.6%	38.4	25	35.7	2	0	0	1132.66	75	83
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	7	8	19	0.02%	23.5%	HMYHSLYLK	98.0%	30.8	25	25.7	2	0	0	1191.60	118	126
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	7	8	19	0.02%	23.5%	ILMEHIHK	99.6%	37.6	25	30	3	0	0	1020.57	137	144
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	7	8	19	0.02%	23.5%	KLLADQAEAR	99.7%	51.6	25	49.9	2	0	0	1114.62	153	162
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	7	8	19	0.02%	23.5%	KVWLDPNETNEIANANSR	99.7%	45.6	25	45.6	0	2	0	2071.02	21	38
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	7	8	19	0.02%	23.5%	LLADQAEAR	99.7%	74.8	25	65.8	5	0	0	986.53	154	162
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	7	8	19	0.02%	23.5%	LLADQAEARR	97.2%	29.4	25	6.97	2	0	0	1142.63	154	163
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	7	8	19	0.02%	23.5%	VWLDPNETNEIANANSR	99.7%	124	25	124	3	0	0	1942.93	22	38
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	7	9	23	0.02%	41.9%	GDIVDIKGMGTVQK	99.7%	41.1	25	28.6	2	0	0	1476.77	37	50
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	7	9	23	0.02%	41.9%	GTWVQLK	98.0%	30.8	25	11.8	1	0	0	831.47	123	129
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	7	9	23	0.02%	41.9%	GTWVQLKR	99.7%	51.1	25	36.2	2	0	0	987.57	123	130
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	7	9	23	0.02%	41.9%	HGVVPLATYMR	99.7%	38.7	25	38.7	2	0	0	1243.66	22	32
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	7	9	23	0.02%	41.9%	KHGVVPLATYMR	99.7%	33.7	25	22.7	0	1	0	1371.76	21	32
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	7	9	23	0.02%	41.9%	TNGKEPELLEPIPYEFMA	99.7%	50.5	25	50.5	4	0	0	2094.01	143	160
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	7	9	23	0.02%	41.9%	VYNVTQHAVGIVVNK	99.7%	100	25	94.4	7	4	0	1640.91	64	78
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	33	0.03%	36.7%	AGNLGGGVVTIER	99.7%	92	25	80.7	6	0	0	1242.68	53	65
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	33	0.03%	36.7%	ITVTSEVPFSK	99.7%	76.8	25	69	6	0	0	1207.66	70	80
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	33	0.03%	36.7%	ITVTSEVPFSKR	99.7%	61.6	25	61.1	4	2	0	1363.76	70	81
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	33	0.03%	36.7%	NNLRDWLR	98.4%	31.6	25	18.1	4	0	0	1086.58	94	101
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	33	0.03%	36.7%	SKITVTSEVPFSK	99.7%	87.5	25	84.1	4	0	0	1422.78	68	80
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	33	0.03%	36.7%	VVANSKESYELR	99.7%	75.9	25	66.2	4	3	0	1394.73	102	113
60S ribosomal protein L22-like 1	RPL22L1	RL22L_HUMAN	14.6	99.8%	2	3	6	0.01%	26.2%	NNLRDWLR	98.4%	31.6	25	18.1	4	0	0	1086.58	88	95
60S ribosomal protein L22-like 1	RPL22L1	RL22L_HUMAN	14.6	99.8%	2	3	6	0.01%	26.2%	TGNLGNVVHIER	99.7%	61.2	25	53.3	2	0	0	1308.70	48	59
60S ribosomal protein L22-like 1	RPL22L1	RL22L_HUMAN	14.6	99.8%	2	3	6	0.01%	26.2%	VVASDKETYELR	99.7%	61	25	60.9	2	2	0	1409.73	96	107
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	7	15	69	0.07%	46.4%	ECADLWPR	99.7%	49.1	25	34.9	6	0	0	1046.47	124	131
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	7	15	69	0.07%	46.4%	GSAITGPVAK	99.7%	46.6	25	39.4	6	0	0	900.52	114	123
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	7	15	69	0.07%	46.4%	ISLGLPVGAVINCADNTGAK	99.7%	103	25	98.1	10	2	0	1970.04	16	35
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	7	15	69	0.07%	46.4%	LNRLPAAGVGDMVMATVK	99.7%	76.9	25	72.9	8	10	0	1842.99	49	66
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	7	15	69	0.07%	46.4%	LPAAGVGDMVMATVK	99.7%	92.7	25	14.6	15	0	0	1475.76	52	66
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	7	15	69	0.07%	46.4%	LPAAGVGDMVMATVKK	99.7%	87.4	25	82.1	5	3	0	1587.86	52	67
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	7	15	69	0.07%	46.4%	NLYIISVK	99.7%	45.6	25	41.1	4	0	0	949.57	36	43
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	10	12	49	0.05%	53.2%	EAPAPPKAEAK	99.7%	39.6	25	36.3	8	0	0	1108.60	8	18
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	10	12	49	0.05%	53.2%	FPLTTESAMK	98.8%	32.8	25	31.6	3	0	0	1124.57	79	88
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	10	12	49	0.05%	53.2%	KIEDNNTLVFIVDVK	99.7%	50.5	25	46.6	2	4	0	1746.96	89	103
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	10	12	49	0.05%	53.2%	LAPDYDALDVANK	99.7%	75.3	25	75.3	10	0	0	1404.70	140	152
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	10	12	49	0.05%	53.2%	LAPDYDALDVANKIGII	99.7%	43	25	43	2	0	0	1800.97	140	156
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	10	12	49	0.05%	53.2%	LDHYAIIK	99.2%	34.5	25	19.6	1	0	0	972.55	71	78
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	10	12	49	0.05%	53.2%	LYDIDVAK	99.7%	44.3	25	37.1	3	0	0	936.50	116	123
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	10	12	49	0.05%	53.2%	NKLDHYAIIK	99.7%	32.6	25	13.4	0	2	0	1214.69	69	78
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	10	12	49	0.05%	53.2%	VNTLIRPDGEK	99.7%	47.8	25	37.6	12	0	0	1241.69	124	134
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	10	12	49	0.05%	53.2%	VNTLIRPDGEKK	99.7%	39	25	35.4	2	0	0	1369.78	124	135
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	6	10	72	0.07%	34.4%	AITGASLADIMAK	99.7%	105	25	92.8	37	0	0	1261.68	81	93
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	6	10	72	0.07%	34.4%	CESAFLSK	99.7%	44	25	34.5	3	0	0	941.44	36	43
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	6	10	72	0.07%	34.4%	MKVELCSFSGYK	99.7%	47.7	25	47.7	6	2	0	1448.69	1	12
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	6	10	72	0.07%	34.4%	QINWTVLYR	99.7%	59.1	25	44.3	6	0	0	1192.65	48	56
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	6	10	72	0.07%	34.4%	TDGKVFQFLNAK	99.7%	58.3	25	55.1	2	2	0	1367.73	24	35
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	6	10	72	0.07%	34.4%	VFQFLNAK	99.7%	59.8	25	39.3	14	0	0	966.54	28	35
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	6	7	24	0.02%	24.1%	DDEVQVVR	99.7%	71.3	25	53.1	4	0	0	959.48	52	59
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	6	7	24	0.02%	24.1%	FNPFVTSDR	99.7%	50.5	25	38.8	2	0	0	1082.53	3	11
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	6	7	24	0.02%	24.1%	KDDEVQVVR	99.7%	67.9	25	50.1	4	0	0	1087.57	51	59

60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	6	7	24	0.02%	24.1%	MKFNPFVTSDR	99.7%	64.2	25	64.1	8	0	0	1357.66	1	11
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	6	7	24	0.02%	24.1%	YKEETIEK	99.4%	36.3	25	23.1	2	0	0	1039.53	135	142
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	6	7	24	0.02%	24.1%	YVIYIER	99.5%	36.6	25	27	4	0	0	955.52	78	84
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	6	10	26	0.03%	44.9%	NIDDGTSDRPYSHALVAGIDR	99.7%	52	25	52	0	2	0	2272.10	28	48
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	6	10	26	0.03%	44.9%	NKWFFQK	98.0%	30.8	25	9	1	0	0	997.53	127	133
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	6	10	26	0.03%	44.9%	VVLVLAGR	99.7%	48.3	25	44.8	4	0	0	826.55	10	17
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	6	10	26	0.03%	44.9%	VYNYNHLMPTR	99.7%	63.2	25	55.9	6	3	0	1407.68	74	84
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	6	10	26	0.03%	44.9%	YSVDIPLDK	99.7%	55.3	25	47.4	6	0	0	1049.55	85	93
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	6	10	26	0.03%	44.9%	YSVDIPLDKTVVNK	99.7%	63.8	25	61	2	2	0	1590.87	85	98
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	6	8	26	0.03%	38.5%	INFDKYHPGYFGK	99.7%	65.2	25	56.2	2	2	0	1585.78	43	55
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	6	8	26	0.03%	38.5%	LWTLVSEQTR	99.6%	37.3	25	27.7	2	0	0	1232.66	78	87
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	6	8	26	0.03%	38.5%	NKTGAAPIIDVVR	99.7%	47.2	25	39.7	2	2	0	1353.79	93	105
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	6	8	26	0.03%	38.5%	NQSFCPTVNLDK	99.7%	45.1	25	45.1	2	0	0	1422.67	66	77
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	6	8	26	0.03%	38.5%	SGYYKVLGK	97.7%	30.2	25	25	1	0	0	1014.56	106	114
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	6	8	26	0.03%	38.5%	TGAAPIIDVVR	99.7%	73.1	25	73.1	13	0	0	1111.65	95	105
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	30	0.03%	41.6%	GVVVVIKR	99.7%	48.7	25	43	2	0	0	869.59	59	66
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	30	0.03%	41.6%	KPATSYVR	99.7%	40.9	25	21.9	2	0	0	921.52	72	79
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	30	0.03%	41.6%	KTVGVEPAADGK	99.7%	76.2	25	65.8	2	0	0	1171.63	47	58
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	30	0.03%	41.6%	NCSSFLIK	99.7%	39.9	25	22.5	1	0	0	968.49	12	19
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	30	0.03%	41.6%	NCSSFLIKR	99.7%	54.8	25	48.2	2	0	0	1124.59	12	20
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	30	0.03%	41.6%	NKQTYSTEPNNLK	99.7%	73.1	25	65.8	4	2	0	1536.77	21	33
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	30	0.03%	41.6%	QTYSTEPNNLK	99.7%	64.4	25	55	3	0	0	1294.63	23	33
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	30	0.03%	41.6%	TVGVEPAADGK	99.7%	50.2	25	47.2	2	0	0	1043.54	48	58
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	30	0.03%	41.6%	TVGVEPAADGKGVVVVIK	99.7%	68	25	53	4	3	0	1738.01	48	65
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	30	0.03%	41.6%	YNGLIHR	99.7%	41.8	25	27.9	2	0	0	872.47	40	46
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	30	0.03%	41.6%	YNGLIHRK	99.4%	35.8	25	28.9	1	0	0	1000.57	40	47
60S ribosomal protein L29	RPL29	RL29_HUMAN	17.8	100.0%	4	4	18	0.02%	20.1%	AQAAAPASVPAQAPK	99.7%	86.4	25	84.1	14	0	0	1377.75	135	149
60S ribosomal protein L29	RPL29	RL29_HUMAN	17.8	100.0%	4	4	18	0.02%	20.1%	AQAAAPASVPAQAPKR	99.7%	30.2	25	30.2	0	1	0	1533.85	135	150
60S ribosomal protein L29	RPL29	RL29_HUMAN	17.8	100.0%	4	4	18	0.02%	20.1%	LAYIAHPK	98.6%	32.2	25	17.6	2	0	0	912.53	96	103
60S ribosomal protein L29	RPL29	RL29_HUMAN	17.8	100.0%	4	4	18	0.02%	20.1%	SQRYESLK	95.5%	27.5	25	8.55	1	0	0	1010.53	26	33
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	23	64	0.06%	44.7%	AFMGPLKK	98.9%	33.1	25	27.4	3	0	0	891.51	387	394
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	23	64	0.06%	44.7%	AGMTHIVR	99.7%	41.7	25	34	1	0	0	884.48	51	58
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	23	64	0.06%	44.7%	AHLMEIQVNGGTVAEK	98.5%	24.1	25	16.8	0	1	0	1696.87	178	193
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	23	64	0.06%	44.7%	DDPSKPVHLTAFLGYK	99.7%	51.1	25	51.1	2	2	0	1787.93	35	50
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	23	64	0.06%	44.7%	FQTMEEKK	99.7%	41.6	25	21.5	2	0	0	1040.51	379	386
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	23	64	0.06%	44.7%	HGSLGFLPR	99.7%	62.6	25	56.4	7	0	0	983.54	11	19
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	23	64	0.06%	44.7%	IGQGYLIK	99.7%	63.3	25	40.4	4	0	0	891.53	287	294
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	23	64	0.06%	44.7%	IGQGYLIKDGK	99.7%	68.5	25	62.3	4	0	0	1191.67	287	297
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	23	64	0.06%	44.7%	KSLLVQTK	97.9%	30.6	25	21.1	1	0	0	916.58	349	356
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	23	64	0.06%	44.7%	LEQQVPVNQVFGQDEMIDVIGVTK	99.7%	36.7	25	34.8	0	3	0	2686.38	201	224
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	23	64	0.06%	44.7%	NNASTDYDLSDK	99.7%	72.8	25	72.8	6	0	0	1342.58	301	312
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	23	64	0.06%	44.7%	SINPLGGFVHYGEVTNDFVMLK	99.7%	44.8	25	44.8	0	4	0	2453.22	313	334
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	23	64	0.06%	44.7%	TVFAEHISDECK	99.7%	83	25	83	6	0	0	1435.65	104	115
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	23	64	0.06%	44.7%	TVFAEHISDECKR	99.7%	53.8	25	53.8	2	4	0	1591.75	104	116
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	23	64	0.06%	44.7%	VACIGAWHPAR	99.7%	85.3	25	80.3	4	2	0	1237.63	251	261
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	23	64	0.06%	44.7%	VIAHTQMR	99.7%	44.3	25	37.8	4	0	0	955.51	162	169
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	17	23	64	0.06%	44.7%	YCQVIR	99.4%	35.8	25	25.5	2	0	0	838.42	156	161
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	13	32	0.03%	59.1%	KSEIEYYAMLAK	99.7%	79.2	25	79.2	2	4	0	1461.73	57	68
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	13	32	0.03%	59.1%	KSLESINSR	99.7%	51.9	25	41.8	2	0	0	1033.56	9	17
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	13	32	0.03%	59.1%	LVILANNCPALR	99.7%	73.6	25	50	6	0	0	1353.77	45	56
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	13	32	0.03%	59.1%	LVILANNCPALRK	99.7%	59.4	25	50.1	2	1	0	1481.86	45	57

60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	13	32	0.03%	59.1%	SEIEYYAMLAK	99.7%	90.3	25	77.8	4	0	0	1333.63	58	68
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	13	32	0.03%	59.1%	SLESINSR	99.7%	40	25	30.4	3	0	0	905.47	10	17
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	13	32	0.03%	59.1%	TGVHHYSGNNIELGTACGK	99.7%	65.4	25	61.4	2	2	0	2014.94	69	87
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	13	32	0.03%	59.1%	VCTLAIIDPGDSDIIR	99.7%	88.6	25	80.6	4	0	0	1757.91	91	106
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	9	37	0.04%	49.6%	EMGTPDVR	99.7%	39.8	25	33.3	2	0	0	904.42	56	63
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	9	37	0.04%	49.6%	EYTINIHK	98.7%	32.5	25	20.4	2	0	0	1017.54	24	31
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	9	37	0.04%	49.6%	EYTINIHKR	99.7%	56.5	25	42.2	4	0	0	1173.64	24	32
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	9	37	0.04%	49.6%	FAMKEMGTPDVR	99.7%	43	25	29.9	6	0	0	1397.66	52	63
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	9	37	0.04%	49.6%	IHGVGFKK	98.7%	32.7	25	25.8	2	0	0	885.53	33	40
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	9	37	0.04%	49.6%	LYTLVTYVPVTTFK	99.7%	92	25	92	4	0	0	1644.92	102	115
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	9	37	0.04%	49.6%	NLQTVNVDEN	99.7%	68.1	25	66.8	4	0	0	1145.54	116	125
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	9	37	0.04%	49.6%	SAINEVVTR	99.7%	83.1	25	64.7	13	0	0	988.54	15	23
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	5	10	26	0.03%	29.6%	ELEVLLMCNK	99.7%	51.8	25	46.9	4	0	0	1264.63	84	93
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	5	10	26	0.03%	29.6%	FKGQILMPNIGYGSNK	99.7%	49.5	25	49.5	2	2	0	1782.92	49	64
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	5	10	26	0.03%	29.6%	GQILMPNIGYGSNK	99.7%	48.5	25	42.8	4	0	0	1507.76	51	64
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	5	10	26	0.03%	29.6%	GQILMPNIGYGSNKK	99.7%	51.5	25	46.5	3	0	0	1635.85	51	65
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	5	10	26	0.03%	29.6%	SYCAEIAHNVSSK	99.7%	87.7	25	85.9	10	1	0	1465.67	94	106
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	10	25	0.02%	35.9%	AFLIEEQK	99.7%	51.3	25	30.4	6	0	0	977.53	94	101
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	10	25	0.02%	35.9%	AFLIEEQKIVVK	99.7%	65.2	25	61.8	3	2	0	1416.85	94	105
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	10	25	0.02%	35.9%	AYGGSMCAK	99.7%	49.2	25	49.2	2	0	0	944.40	77	85
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	10	25	0.02%	35.9%	IVYLYTK	99.7%	41.5	25	25.5	2	0	0	899.52	30	36
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	10	25	0.02%	35.9%	IVYLYTKK	99.7%	44.2	25	33.2	3	0	0	1027.62	30	37
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	10	25	0.02%	35.9%	LSYNTASNK	99.7%	44.8	25	28.5	2	0	0	997.49	11	19
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	10	25	0.02%	35.9%	LSYNTASNKTR	94.7%	26.9	25	23.1	1	0	0	1254.64	11	21
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	10	25	0.02%	35.9%	RAFLIEEQK	99.2%	34.7	25	23.1	2	0	0	1133.63	93	101
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	10	25	0.02%	35.9%	RLSYNTASNK	99.4%	35.6	25	29.7	2	0	0	1153.60	10	19
60S ribosomal protein L35	RPL35	RL35_HUMAN	14.6	100.0%	4	5	14	0.01%	29.3%	QLDDLKVELSQLR	99.7%	76.7	25	63.7	2	2	0	1556.86	20	32
60S ribosomal protein L35	RPL35	RL35_HUMAN	14.6	100.0%	4	5	14	0.01%	29.3%	VLTVINQTQK	99.7%	66.3	25	63.2	7	0	0	1143.67	57	66
60S ribosomal protein L35	RPL35	RL35_HUMAN	14.6	100.0%	4	5	14	0.01%	29.3%	VLTVINQTQKENLR	99.7%	96.2	25	96.2	2	0	0	1655.94	57	70
60S ribosomal protein L35	RPL35	RL35_HUMAN	14.6	100.0%	4	5	14	0.01%	29.3%	YKPLDLRPK	97.8%	30.3	25	30.3	1	0	0	1129.67	78	86
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	24	0.02%	39.1%	AIFAGYKR	99.7%	43.9	25	37.7	2	0	0	925.53	9	16
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	24	0.02%	39.1%	DETEFYLGK	99.7%	44.3	25	42.3	4	0	0	1101.51	37	45
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	24	0.02%	39.1%	DETEFYLGKR	99.7%	50.4	25	42.6	4	0	0	1257.61	37	46
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	24	0.02%	39.1%	IEGVYAR	99.2%	34.4	25	19.2	2	0	0	807.44	30	36
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	24	0.02%	39.1%	IEGVYARDETEFYLGK	99.7%	59.9	25	59.9	2	0	0	1889.93	30	45
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	24	0.02%	39.1%	NQREHTALLK	98.2%	31.2	25	20.9	1	0	0	1209.67	20	29
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	24	0.02%	39.1%	VMLYPSR	98.6%	32.2	25	19.6	2	0	0	881.46	103	109
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	24	0.02%	39.1%	VMLYPSRI	99.6%	37.7	25	37	7	0	0	994.54	103	110
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	6	11	28	0.03%	36.2%	ALRYPMAVGLNK	99.7%	51.3	25	47.6	2	2	0	1348.74	2	13
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	6	11	28	0.03%	36.2%	DMIREVCGFAPYER	99.7%	35	25	35	0	4	0	1742.80	42	55
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	6	11	28	0.03%	36.2%	EELSNVLAAMR	99.7%	98.6	25	94.9	6	0	0	1232.63	88	98
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	6	11	28	0.03%	36.2%	EVCGFAPYER	99.7%	47.2	25	47.2	6	0	0	1227.55	46	55
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	6	11	28	0.03%	36.2%	REELSNVLAAMR	99.7%	52.4	25	49.8	2	2	0	1388.73	87	98
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	6	11	28	0.03%	36.2%	YPMAVGLNK	99.7%	46.5	25	28.1	4	0	0	992.52	5	13
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	3	3	12	0.01%	21.7%	GKDSLYAQGR	99.7%	70.1	25	63.7	4	0	0	1094.56	29	38
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	3	3	12	0.01%	21.7%	IVLRLECVEPNCR	99.7%	35	25	35	0	4	0	1657.85	66	78
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	3	3	12	0.01%	21.7%	LECVEPNCR	99.7%	43.5	25	43.5	4	0	0	1176.51	70	78
60S ribosomal protein L37a	RPL37A	RL37A_HUMAN	10.3	100.0%	4	5	20	0.02%	51.1%	AVGIWHCGSCMK	99.7%	46.5	25	46.5	5	0	0	1421.61	51	62
60S ribosomal protein L37a	RPL37A	RL37A_HUMAN	10.3	100.0%	4	5	20	0.02%	51.1%	KIEISQHAK	99.7%	49.3	25	36	4	0	0	1053.61	28	36
60S ribosomal protein L37a	RPL37A	RL37A_HUMAN	10.3	100.0%	4	5	20	0.02%	51.1%	TVAGGAWTYNTTSAVTVK	99.7%	83.6	25	83.6	10	0	0	1826.93	63	80
60S ribosomal protein L37a	RPL37A	RL37A_HUMAN	10.3	100.0%	4	5	20	0.02%	51.1%	YTCSFCGK	96.7%	28.8	25	28.8	1	0	0	1022.41	37	44

60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	5	7	24	0.02%	51.4%	IEEIKDFLLTAR	99.7%	51.5	25	47.8	4	2	0	1447.82	5	16
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	5	7	24	0.02%	51.4%	LKQSLPPGLAVK	99.7%	38.7	25	38.7	3	0	0	1250.78	56	67
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	5	7	24	0.02%	51.4%	QSLPPGLAVK	99.7%	72.8	25	70.1	7	0	0	1009.60	58	67
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	5	7	24	0.02%	51.4%	YLYTLVITDK	99.7%	51.8	25	44	2	0	0	1228.68	41	50
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	5	7	24	0.02%	51.4%	YLYTLVITDKEK	99.7%	62.3	25	56.2	4	2	0	1485.82	41	52
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	22	32	119	0.12%	47.1%	AAAAAAAALQAK	99.7%	90.4	25	78.8	16	0	0	956.55	354	364
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	22	32	119	0.12%	47.1%	APIRPDIVNFVHTNLR	99.7%	52.3	25	52.3	1	2	0	1862.04	30	45
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	22	32	119	0.12%	47.1%	APIRPDIVNFVHTNLRK	99.0%	25.5	25	25.5	0	1	0	1990.13	30	46
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	22	32	119	0.12%	47.1%	AWNDIKK	99.7%	38.5	25	23.9	1	0	0	874.48	176	182
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	22	32	119	0.12%	47.1%	EAVLLLKK	99.7%	58.9	25	33.2	2	0	0	913.61	166	173
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	22	32	119	0.12%	47.1%	FCIWTESAFR	99.7%	61.5	25	53.1	12	0	0	1316.61	249	258
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	22	32	119	0.12%	47.1%	GPCIIYNEDNGIIK	99.7%	66.6	25	66.6	2	0	0	1605.79	206	219
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	22	32	119	0.12%	47.1%	IEEVPELPLVVEDK	99.7%	43.1	25	43.1	2	0	0	1608.87	144	157
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	22	32	119	0.12%	47.1%	IEEVPELPLVVEDKVEGYK	99.7%	62.8	25	62.8	1	0	0	2185.16	144	162
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	22	32	119	0.12%	47.1%	KLDELYGTWR	99.7%	68	25	61.5	6	1	0	1280.66	259	268
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	22	32	119	0.12%	47.1%	LAPGGHVGR	99.7%	47.5	25	40.3	2	0	0	863.48	240	248
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	22	32	119	0.12%	47.1%	LDELYGTWR	99.7%	57.4	25	53.2	1	0	0	1152.57	260	268
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	22	32	119	0.12%	47.1%	MINTDLSR	99.7%	60.9	25	49	11	0	0	949.48	284	291
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	22	32	119	0.12%	47.1%	NIPGITLLNVSK	99.7%	75.4	25	70.8	15	0	0	1268.76	223	234
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	22	32	119	0.12%	47.1%	NVTLPAVFK	99.6%	38	25	25.8	4	0	0	988.58	21	29
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	22	32	119	0.12%	47.1%	QPYAVSELAGHQTSAESWGTGR	99.7%	111	25	111	2	0	0	2332.10	50	71
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	22	32	119	0.12%	47.1%	RGPCIIYNEDNGIIK	99.7%	70.5	25	54.8	1	1	0	1761.90	205	219
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	22	32	119	0.12%	47.1%	SGQGAFGNMCR	99.7%	63.3	25	63.3	7	0	0	1184.49	87	97
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	22	32	119	0.12%	47.1%	SNYNLPMHK	99.7%	43.3	25	43.3	9	0	0	1119.53	275	283
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	22	32	119	0.12%	47.1%	TKEAVLLLK	99.7%	51.3	25	45.8	4	0	0	1014.66	164	172
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	22	32	119	0.12%	47.1%	VDKAAAAAAALQAK	99.7%	90.3	25	76.7	2	1	0	1298.74	351	364
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	22	32	119	0.12%	47.1%	YAICSALAASALPALVMSK	99.7%	66.8	25	66.8	7	5	0	1937.02	122	140
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	22	44	0.04%	44.4%	DIICQIAYAR	99.7%	61.1	25	45.3	2	0	0	1222.63	59	68
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	22	44	0.04%	44.4%	EFNAEVHR	99.7%	39.4	25	29.6	2	0	0	1001.48	189	196
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	22	44	0.04%	44.4%	EFNAEVHRK	97.8%	30.5	25	26.7	1	0	0	1129.57	189	197
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	22	44	0.04%	44.4%	FPGYDSESK	99.2%	34.5	25	34.5	2	0	0	1029.45	180	188
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	22	44	0.04%	44.4%	GAVDGGLSIPHSTK	99.7%	55.8	25	47.7	3	1	0	1338.70	165	178
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	22	44	0.04%	44.4%	GAVDGGLSIPHSTKR	98.8%	32.8	25	32.8	1	0	0	1494.80	165	179
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	22	44	0.04%	44.4%	HIMGQNVADYMR	99.7%	49.4	25	36.7	6	0	0	1434.66	198	209
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	22	44	0.04%	44.4%	IEGDMIVCAAYAHELPK	97.6%	22.7	25	15.5	0	2	0	1932.92	69	85
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	22	44	0.04%	44.4%	NSVTPDMMEEMYK	99.7%	56.5	25	56.5	1	0	0	1574.65	229	241
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	22	44	0.04%	44.4%	NSVTPDMMEEMYKK	99.7%	47	25	47	6	0	0	1702.75	229	242
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	22	44	0.04%	44.4%	RFPGYDSESK	99.7%	39	25	29.3	2	0	0	1185.55	179	188
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	22	44	0.04%	44.4%	TTTGNKVFGALK	98.9%	33.3	25	23.2	2	0	0	1236.69	153	164
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	22	44	0.04%	44.4%	VGLTNYAAAYCTGLLLAR	99.7%	58.5	25	58.5	2	0	0	1927.01	90	107
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	22	44	0.04%	44.4%	VTNRDIICQIAYAR	99.7%	40.8	25	31.6	2	2	0	1692.89	55	68
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	22	44	0.04%	44.4%	YLMEEDEDAYKK	99.7%	62.5	25	62.5	4	3	0	1549.67	210	221
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	10	12	41	0.04%	35.8%	AIPQLQGYLR	99.7%	58.8	25	47.5	4	0	0	1158.66	263	272
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	10	12	41	0.04%	35.8%	ASITPGTILIILTGR	99.7%	123	25	123	11	0	0	1525.93	142	156
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	10	12	41	0.04%	35.8%	AVDSQILPK	99.7%	58.5	25	31.6	3	0	0	970.56	252	260
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	10	12	41	0.04%	35.8%	FVIATSTK	99.1%	34	25	28.3	1	0	0	866.50	193	200
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	10	12	41	0.04%	35.8%	HLTDAYFK	98.8%	32.7	25	21.9	2	0	0	994.50	211	218
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	10	12	41	0.04%	35.8%	QLASGLLLVTGPLVLNR	99.7%	82.6	25	82.6	5	1	0	1764.07	167	183
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	10	12	41	0.04%	35.8%	SVFALTNGIYPHK	99.7%	53.7	25	53.7	4	0	0	1446.77	273	285
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	10	12	41	0.04%	35.8%	VLATVTKPVGGDK	99.7%	64	25	57.7	6	1	0	1284.75	88	100
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	10	12	41	0.04%	35.8%	YYPTEDVPR	99.7%	64.6	25	59	2	0	0	1139.54	115	123

60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	10	12	41	0.04%	35.8%	YYPTEDVPRK	99.2%	34.7	25	32.3	1	0	0	1267.63	115	124
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	23	50	0.05%	43.1%	AGNFYVPAEPK	99.7%	47.7	25	40.2	2	0	0	1192.60	78	88
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	23	50	0.05%	43.1%	ASINMLR	99.7%	60.8	25	46.4	6	0	0	804.44	128	134
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	23	50	0.05%	43.1%	EANNFLWPFK	99.7%	53.5	25	44.3	4	0	0	1265.63	203	212
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	23	50	0.05%	43.1%	EVPAVPETLK	97.7%	30.2	25	24.9	1	0	0	1082.61	10	19
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	23	50	0.05%	43.1%	EVPAVPETLKK	99.4%	36.3	25	35.9	1	1	0	1210.70	10	20
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	23	50	0.05%	43.1%	FKEANNFLWPFK	99.7%	57.9	25	48.4	3	1	0	1540.79	201	212
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	23	50	0.05%	43.1%	IALTDNALIAR	99.7%	75	25	61.8	4	0	0	1170.68	167	177
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	23	50	0.05%	43.1%	IVEPYIAWGYPNLK	99.7%	67.8	25	32.4	6	1	0	1662.89	135	148
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	23	50	0.05%	43.1%	KAGNFYVPAEPK	99.7%	58.5	25	56.9	2	2	0	1320.69	77	88
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	23	50	0.05%	43.1%	LRQIFNGTFVK	98.5%	24.2	25	24.2	0	1	0	1322.76	114	124
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	23	50	0.05%	43.1%	QIFNGTFVK	99.3%	35.3	25	31	2	0	0	1053.57	116	124
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	23	50	0.05%	43.1%	RIALTDNALIAR	99.7%	56.4	25	40.1	1	0	0	1326.79	166	177
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	23	50	0.05%	43.1%	SVNELIYK	99.7%	49.8	25	29.9	2	0	0	965.53	149	156
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	23	50	0.05%	43.1%	SVNELIYKR	99.7%	47.5	25	38.5	3	0	0	1121.63	149	157
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	23	50	0.05%	43.1%	TTHFVEGGDAGNR	99.7%	41.2	25	41.2	2	2	0	1360.62	224	236
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	23	50	0.05%	43.1%	TTHFVEGGDAGNREDQINR	99.7%	67	25	64.6	2	1	0	2115.98	224	242
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	65	0.06%	45.1%	AGVNTVTTLVENK	99.7%	97.1	25	92.1	8	0	0	1345.73	138	150
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	65	0.06%	45.1%	AGVNTVTTLVENKK	99.7%	77.7	25	77.7	5	3	0	1473.83	138	151
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	65	0.06%	45.1%	HWGGNVLGPK	99.7%	43.7	25	42.5	2	0	0	1064.56	236	245
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	65	0.06%	45.1%	KMGVPYCIIK	99.7%	41.6	25	39.4	3	4	0	1208.65	176	185
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	65	0.06%	45.1%	KVAPAPAVVK	99.6%	38.1	25	38.1	1	0	0	979.63	11	20
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	65	0.06%	45.1%	KVVNPLFEK	99.7%	38.8	25	25.3	2	0	0	1073.64	26	34
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	65	0.06%	45.1%	LKVPPAINQFTQALDR	99.7%	42.9	25	37.4	2	3	0	1811.02	74	89
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	65	0.06%	45.1%	MGVPYCIIK	99.7%	38.9	25	26.9	4	0	0	1080.56	177	185
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	65	0.06%	45.1%	NFGIGQDIQPK	99.7%	77.6	25	65.3	4	0	0	1216.63	38	48
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	65	0.06%	45.1%	QTATQLLK	99.7%	47.9	25	26	5	0	0	902.53	90	97
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	65	0.06%	45.1%	TCTTVAFTQVNSEDK	99.7%	93.8	25	86.7	2	0	0	1700.78	198	212
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	65	0.06%	45.1%	TCTTVAFTQVNSEDKGALAK	99.7%	108	25	108	2	3	0	2141.05	198	217
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	65	0.06%	45.1%	TNYNDRYDEIR	99.7%	49.2	25	41.8	1	2	0	1458.66	224	234
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	65	0.06%	45.1%	VAPAPAVVKK	98.7%	32.6	25	32.6	1	0	0	979.63	12	21
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	65	0.06%	45.1%	VPPAINQFTQALDR	99.7%	103	25	94.1	5	2	0	1569.84	76	89
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	65	0.06%	45.1%	VVNPLFEK	97.8%	30.3	25	30.3	1	0	0	945.54	27	34
60S ribosomal protein L7-like 1	RPL7L1	RL7L_HUMAN	28.7	100.0%	2	2	3	0.00%	9.8%	IDGVSLLVQR	99.7%	60.9	25	42.2	2	0	0	1099.65	96	105
60S ribosomal protein L7-like 1	RPL7L1	RL7L_HUMAN	28.7	100.0%	2	2	3	0.00%	9.8%	IVEPYVTWGFPNLK	96.8%	28.9	25	18.5	1	0	0	1662.89	133	146
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	8	9	29	0.03%	24.1%	ASGNYATVISHNPETK	99.7%	83.3	25	76.4	7	2	0	1688.82	129	144
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	8	9	29	0.03%	24.1%	ASGNYATVISHNPETKK	99.7%	56	25	49.6	2	0	0	1816.92	129	145
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	8	9	29	0.03%	24.1%	AVDFAER	99.7%	53.8	25	43.9	2	0	0	807.40	31	37
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	8	9	29	0.03%	24.1%	AVVGVVAGGGR	99.7%	86.4	25	71.1	8	0	0	941.55	164	174
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	8	9	29	0.03%	24.1%	DIIHDPGR	98.9%	33.1	25	24.3	2	0	0	922.47	47	54
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	8	9	29	0.03%	24.1%	GIVKDIIHDPGR	99.7%	35.5	25	35.5	0	2	0	1319.74	43	54
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	8	9	29	0.03%	24.1%	IDKPILK	98.2%	31.1	25	13.9	2	0	0	826.54	175	181
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	8	9	29	0.03%	24.1%	KVGLIAAR	99.4%	35.7	25	23.9	2	0	0	827.55	234	241
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	15	32	0.03%	39.6%	DFNHINVELSLLGK	99.7%	81.2	25	79.1	2	2	0	1598.85	37	50
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	15	32	0.03%	39.6%	DFNHINVELSLLGKK	99.7%	37.4	25	37.4	1	2	0	1726.95	37	51
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	15	32	0.03%	39.6%	FLDGIYVSEK	99.7%	70.2	25	61.7	7	0	0	1170.60	175	184
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	15	32	0.03%	39.6%	FLDGIYVSEKGTVQQADE	99.7%	78.9	25	76	2	0	0	1998.97	175	192
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	15	32	0.03%	39.6%	KFLDGIYVSEK	99.7%	65.7	25	57.4	2	0	0	1298.70	174	184
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	15	32	0.03%	39.6%	MRPGVACSVSQAQK	99.7%	46.4	25	35.4	0	4	0	1518.75	128	141
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	15	32	0.03%	39.6%	NFLGEKYIR	99.7%	40.2	25	20	2	0	0	1139.62	116	124
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	15	32	0.03%	39.6%	TICSHVQNMIK	99.7%	68.5	25	59.9	4	3	0	1330.66	72	82

60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	15	32	0.03%	39.6%	VDKWWGNR	99.6%	37.9	25	26	1	0	0	1060.53	57	64
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	PFKFB3	F263_HUMAN	59.6	100.0%	4	4	7	0.01%	7.5%	CLLAYFLDK	99.7%	47.6	25	42.1	2	0	0	1142.59	394	402
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	PFKFB3	F263_HUMAN	59.6	100.0%	4	4	7	0.01%	7.5%	IGGDSGLSSR	99.7%	42.9	25	39.3	2	0	0	948.47	265	274
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	PFKFB3	F263_HUMAN	59.6	100.0%	4	4	7	0.01%	7.5%	LEPVIMELER	99.7%	42	25	31.5	2	0	0	1228.66	370	379
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	PFKFB3	F263_HUMAN	59.6	100.0%	4	4	7	0.01%	7.5%	STIQTAEALR	99.7%	54.4	25	42.5	1	0	0	1089.59	303	312
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	8	8	12	0.01%	15.9%	AIGVLTSGGDAQGMNAAVR	99.7%	133	25	133	4	0	0	1787.91	26	44
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	8	8	12	0.01%	15.9%	EIGWTDVGGWTGQGGSILGTK	99.7%	49	25	49	1	0	0	2119.05	460	480
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	8	8	12	0.01%	15.9%	EWSGLLEELAR	99.7%	61.8	25	40.6	2	0	0	1302.67	140	150
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	8	8	12	0.01%	15.9%	GITNLCVIGGDGSLTGANLFR	99.7%	57.5	25	57.5	1	0	0	2135.09	118	138
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	8	8	12	0.01%	15.9%	NGQIDKEAVQK	99.7%	39.3	25	22.9	2	0	0	1229.65	151	161
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	8	8	12	0.01%	15.9%	NVIFQPVAELKK	99.0%	33.8	25	33.8	2	0	0	1385.82	726	737
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	8	8	12	0.01%	15.9%	SFAGNLNTYK	98.0%	30.7	25	20.9	1	0	0	1114.55	386	395
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	8	8	12	0.01%	15.9%	SFAGNLNTYKR	99.4%	36.1	25	32.1	1	0	0	1270.65	386	396
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	8	8	12	0.01%	15.9%	TFVLEVMGR	99.7%	68.7	25	61.2	2	0	0	1051.56	211	219
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	8	8	12	0.01%	15.9%	YLEEIATQMR	99.7%	67.6	25	60.3	2	0	0	1253.62	487	496
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	13	15	26	0.03%	22.3%	AIGVLTSGGDAQGMNAAVR	99.7%	133	25	133	4	0	0	1787.91	17	35
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	13	15	26	0.03%	22.3%	AMLWLSEK	98.9%	33.1	25	20.9	1	0	0	977.51	682	689
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	13	15	26	0.03%	22.3%	AVAFSPVTELKK	99.7%	43.7	25	43.7	2	0	0	1289.75	716	727
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	13	15	26	0.03%	22.3%	EQWWLSLR	99.7%	41.7	25	32.7	2	0	0	1117.58	738	745
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	13	15	26	0.03%	22.3%	GQLESIVENIR	99.7%	62.2	25	50.9	2	0	0	1257.68	475	485
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	13	15	26	0.03%	22.3%	IMEVIDAITTTAQSHQR	99.7%	51.7	25	11.5	0	3	0	1929.97	185	201
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	13	15	26	0.03%	22.3%	LPLMECVQMTK	99.7%	52.8	25	52.2	2	0	0	1349.66	346	356
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	13	15	26	0.03%	22.3%	SEWGSLLEELVAEGK	99.7%	53.9	25	39.9	1	0	0	1646.83	130	144
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	13	15	26	0.03%	22.3%	SNFSLAILNVGAPAAGMNAAVR	99.7%	59.7	25	59.7	1	0	0	2144.13	398	419
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	13	15	26	0.03%	22.3%	TFVLEVMGR	99.7%	68.7	25	61.2	2	0	0	1051.56	202	210
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	13	15	26	0.03%	22.3%	TNVLGHLQQGGAPTPFDR	99.7%	44	25	42.5	0	2	0	1907.97	655	672
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	13	15	26	0.03%	22.3%	VFANAPDSACVIGLK	99.7%	70.1	25	62.1	2	0	0	1561.80	699	713
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	13	15	26	0.03%	22.3%	VTVLGHVQR	99.7%	65.8	25	65.6	2	0	0	1008.59	293	301
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	9	9	14	0.01%	18.8%	AIAVLTSGGDAQGMNAAVR	99.7%	80.1	25	80.1	1	0	0	1817.92	17	35
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	9	9	14	0.01%	18.8%	DLQANVEHLVQK	99.7%	69.9	25	53.7	2	0	0	1393.74	604	615
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	9	9	14	0.01%	18.8%	GITNLCVIGGDGSLTGADTFR	99.7%	118	25	113	1	0	0	2124.04	109	129
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	9	9	14	0.01%	18.8%	IFANTPDSGCVLGMR	99.7%	56.8	25	56.8	2	0	0	1637.78	700	714
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	9	9	14	0.01%	18.8%	IGLIQGNR	99.7%	56.4	25	51	2	0	0	870.52	425	432
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	9	9	14	0.01%	18.8%	SEWSDLLSDLQK	99.7%	66.4	25	53.5	2	0	0	1420.70	130	141
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	9	9	14	0.01%	18.8%	SFEQISANITK	99.7%	65.7	25	52	2	0	0	1237.64	477	487
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	9	9	14	0.01%	18.8%	SGSHTVAVMNVGAPAAGMNAAVR	99.7%	35.6	25	35.6	0	1	0	2168.07	398	420
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	9	9	14	0.01%	18.8%	TFVLEVMGR	99.7%	68.7	25	61.2	2	0	0	1051.56	202	210
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	9	9	14	0.01%	18.8%	VGIFTGAR	99.2%	34.4	25	20.8	1	0	0	820.47	40	47
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	9	9	14	0.01%	18.8%	VTVLGHVQR	99.7%	65.8	25	65.6	2	0	0	1008.59	293	301
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	7	8	11	0.01%	18.2%	AGQAVDDFIEK	99.7%	40.5	25	26.1	1	0	0	1192.58	77	87
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	7	8	11	0.01%	18.2%	FQFDGDKK	99.3%	35.1	25	23.2	1	0	0	984.48	310	317
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	7	8	11	0.01%	18.2%	GILFVGSGVSGGEEGAR	99.7%	94.4	25	88.9	2	0	0	1591.81	120	136
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	7	8	11	0.01%	18.2%	IISYAQGFMLLR	99.7%	78.2	25	70.6	3	0	0	1411.78	332	343
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	7	8	11	0.01%	18.2%	LVPLLDTGDIIIDGGNSEYR	99.7%	64.7	25	64.7	1	0	0	2160.12	88	107
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	7	8	11	0.01%	18.2%	TIFQGIAAK	98.7%	32.7	25	26	2	0	0	948.55	155	163
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	7	8	11	0.01%	18.2%	YGPSLMPGGNK	95.9%	27.9	25	23.8	1	0	0	1120.55	137	147
6-phosphogluconolactonase	PGLS	6PGL_HUMAN	27.5	99.9%	2	2	4	0.00%	8.9%	TVIFVATGEGK	99.7%	75.2	25	68.8	2	0	0	1121.62	198	208
6-phosphogluconolactonase	PGLS	6PGL_HUMAN	27.5	99.9%	2	2	4	0.00%	8.9%	VTLTLPVLNAAR	99.7%	50.5	25	50.5	2	0	0	1267.77	186	197
6-pyruvoyl tetrahydrobiopterin synthase	PTS	PTPS_HUMAN	16.4	100.0%	4	4	7	0.01%	33.8%	FLSDEENLKLFGK	99.7%	56.3	25	56.3	2	0	0	1539.81	30	42
6-pyruvoyl tetrahydrobiopterin synthase	PTS	PTPS_HUMAN	16.4	100.0%	4	4	7	0.01%	33.8%	VLPVGVLYK	98.9%	33.4	25	33.4	2	0	0	987.62	121	129
6-pyruvoyl tetrahydrobiopterin synthase	PTS	PTPS_HUMAN	16.4	100.0%	4	4	7	0.01%	33.8%	VYETDNNIVVYKGE	99.7%	49.1	25	49.1	2	0	0	1642.80	132	145

6-pyruvoyl tetrahydrobiopterin synthase	PTS	PTPS_HUMAN	16.4	100.0%	4	4	7	0.01%	33.8%	YMEEAIMQPLDHK	98.7%	32.7	25	28.5	1	0	0	1620.74	79	91
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	18	31	0.03%	32.9%	DAGTIAGLNVMR	99.7%	88.1	25	80.1	3	0	0	1233.63	186	197
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	18	31	0.03%	32.9%	ELEEIVQPIISK	99.7%	57.3	25	44.4	2	0	0	1397.79	622	633
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	18	31	0.03%	32.9%	IINEPTAAAIAYGLDK	99.7%	112	25	112	2	0	0	1659.90	198	213
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	18	31	0.03%	32.9%	IINEPTAAAIAYGLDKR	99.7%	74.9	25	74.9	1	2	0	1816.00	198	214
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	18	31	0.03%	32.9%	ITPSYVAFTPEGER	99.7%	42.2	25	36.8	2	0	0	1566.78	61	74
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	18	31	0.03%	32.9%	LTPEEIER	97.4%	29.6	25	0	1	0	0	986.52	533	540
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	18	31	0.03%	32.9%	MKETAEAYLGK	99.7%	50.4	25	41.8	1	0	0	1240.62	153	163
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	18	31	0.03%	32.9%	NQLTSNPENTVFDAK	99.7%	99.8	25	86.5	2	0	0	1677.81	82	96
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	18	31	0.03%	32.9%	SDIDEIVLVGGSTR	99.7%	71.5	25	70.4	2	0	0	1460.76	354	367
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	18	31	0.03%	32.9%	SQIFSTASDNQPTVTIK	99.7%	126	25	112	2	0	0	1836.93	448	464
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	18	31	0.03%	32.9%	TFAPEEISAMVLTK	99.7%	80.4	25	74.5	2	0	0	1536.80	139	152
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	18	31	0.03%	32.9%	TKPYIQVDIGGGQTK	99.7%	65.1	25	60.2	2	0	0	1604.86	124	138
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	18	31	0.03%	32.9%	TWNDPSVQQDIK	99.7%	65.8	25	57.1	2	0	0	1430.69	102	113
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	18	31	0.03%	32.9%	VEIIANDQGNR	99.7%	70.8	25	0	2	0	0	1228.63	50	60
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	18	31	0.03%	32.9%	VLEDSDLKK	98.7%	32.4	25	13.7	1	0	0	1046.57	345	353
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	18	31	0.03%	32.9%	VMEHFIK	99.5%	36.7	25	24.2	2	0	0	903.48	262	268
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	18	31	0.03%	32.9%	VTHAVVTVPAYFNDAQR	99.7%	38.5	25	35.2	0	2	0	1887.97	165	181
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	18	31	0.03%	32.9%	VYEGERPLTK	99.7%	46.7	25	40.7	2	0	0	1191.64	465	474
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	6	7	25	0.02%	15.2%	FLPGYVGGIQEGAVTPAGVVNK	99.7%	89.7	25	89.7	4	1	0	2173.17	121	142
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	6	7	25	0.02%	15.2%	GYFFPTSAR	98.2%	31.1	25	22.8	2	0	0	1045.51	199	207
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	6	7	25	0.02%	15.2%	LLVSGFWGVAR	99.7%	84.2	25	74.5	6	0	0	1204.68	394	404
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	6	7	25	0.02%	15.2%	SLDGVTNDR	99.7%	49.6	25	35.9	4	0	0	976.47	14	22
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	6	7	25	0.02%	15.2%	VIECSYTSADGQR	99.7%	98.1	25	98.1	6	0	0	1485.66	377	389
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	6	7	25	0.02%	15.2%	YTAAVPYR	99.7%	45.7	25	38.1	2	0	0	940.49	462	469
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	18	23	43	0.04%	49.2%	AGIPKEEVK	99.7%	46.6	25	34.8	2	0	0	970.56	79	87
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	18	23	43	0.04%	49.2%	DGLTDVYNK	99.7%	50.8	25	40.7	2	0	0	1024.49	182	190
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	18	23	43	0.04%	49.2%	EAYMGNVLQGGEGQAPTR	99.7%	98.9	25	98.9	4	0	0	1877.88	88	105
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	18	23	43	0.04%	49.2%	EEVKEAYMGNVLQGGEGQAPTR	99.7%	47.3	25	43.2	0	4	0	2363.13	84	105
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	18	23	43	0.04%	49.2%	ENGTVTAANASTLNDGAAALVLMTADAAK	99.7%	46.1	25	43.5	0	1	0	2761.37	274	302
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	18	23	43	0.04%	49.2%	EVVIVSATR	99.7%	81.9	25	77.4	2	0	0	973.57	41	49
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	18	23	43	0.04%	49.2%	GSTPYGGVKLEDLIVK	99.7%	89	25	78.6	2	0	0	1675.93	166	181
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	18	23	43	0.04%	49.2%	IHMGSCAENTAK	99.7%	54.1	25	54.1	2	2	0	1318.59	191	202
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	18	23	43	0.04%	49.2%	IVGHLTHALK	99.7%	49.6	25	35.9	2	0	0	1088.66	394	403
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	18	23	43	0.04%	49.2%	LEDLIVK	99.1%	33.9	25	25.1	1	0	0	829.50	175	181
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	18	23	43	0.04%	49.2%	LGSIAIQGAIEK	99.7%	79.2	25	67.4	2	0	0	1199.70	67	78
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	18	23	43	0.04%	49.2%	LNVTPLAR	99.5%	37	25	32.3	2	0	0	883.54	304	311
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	18	23	43	0.04%	49.2%	MLEIDPQK	99.5%	36.9	25	25.2	2	0	0	989.50	366	373
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	18	23	43	0.04%	49.2%	NEQDAYAINSYTR	99.7%	90.9	25	90.7	2	0	0	1544.70	209	221
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	18	23	43	0.04%	49.2%	QAVLGAGLPISTPCTTINK	99.7%	103	25	101	2	0	0	1941.05	106	124
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	18	23	43	0.04%	49.2%	RLNVTPLAR	99.7%	42.6	25	41.6	2	0	0	1039.64	303	311
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	18	23	43	0.04%	49.2%	TPIGSFLGSLSLLPATK	99.7%	100	25	100	2	0	0	1701.98	50	66
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	18	23	43	0.04%	49.2%	VNINGGAVSLGHPIGMSGAR	99.7%	37	25	29.8	1	4	0	1922.99	374	393
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	6	6	10	0.01%	3.3%	AIGIGAYLVR	99.7%	61.2	25	50.4	2	0	0	1032.62	1824	1833
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	6	6	10	0.01%	3.3%	GVISDILDWK	99.7%	58	25	58	2	0	0	1145.62	2200	2209
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	6	6	10	0.01%	3.3%	IDTGWLDR	99.5%	36.7	25	25.1	1	0	0	975.49	608	615
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	6	6	10	0.01%	3.3%	IGSFGPQEDLLFLR	99.7%	62.6	25	62.6	2	0	0	1591.85	1688	1701
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	6	6	10	0.01%	3.3%	ITSENPDEGFKPSSGTVQELNFR	99.7%	44	25	44	0	2	0	2552.23	510	532
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	6	6	10	0.01%	3.3%	VQQAELHTGSLPR	99.7%	87.5	25	83.1	1	0	0	1435.77	826	838
Acidic fibroblast growth factor intracellular-binding protein	FIBP	FIBP_HUMAN	41.9	100.0%	4	4	5	0.00%	13.7%	DYAAIVFFANNR	99.7%	41.3	25	41.3	1	0	0	1400.70	172	183
Acidic fibroblast growth factor intracellular-binding protein	FIBP	FIBP_HUMAN	41.9	100.0%	4	4	5	0.00%	13.7%	LWLDGYSVTDAVALR	99.2%	34.7	25	34.7	1	0	0	1678.88	22	36

Acidic fibroblast growth factor intracellular-binding protein	FIBP	FIBP_HUMAN	41.9	100.0%	4	4	5	0.00%	13.7%	VLVADKDLLDLHK	97.1%	22.1	25	22.1	0	1	0	1478.86	246	258
Acidic fibroblast growth factor intracellular-binding protein	FIBP	FIBP_HUMAN	41.9	100.0%	4	4	5	0.00%	13.7%	YYAFDEAFVR	99.7%	53.8	25	53.8	2	0	0	1280.59	96	105
Acidic leucine-rich nuclear phosphoprotein 32 family member B	ANP32B	AN32B_HUMAN	28.8	100.0%	3	3	4	0.00%	13.9%	KLELSENR	99.7%	44.9	25	16.1	2	0	0	988.54	68	75
Acidic leucine-rich nuclear phosphoprotein 32 family member B	ANP32B	AN32B_HUMAN	28.8	100.0%	3	3	4	0.00%	13.9%	LKDISTLEPLK	99.4%	36.1	25	0	1	0	0	1256.75	100	110
Acidic leucine-rich nuclear phosphoprotein 32 family member B	ANP32B	AN32B_HUMAN	28.8	100.0%	3	3	4	0.00%	13.9%	SLDLFNCEVTNLNDYR	99.7%	52.1	25	52.1	1	0	0	1972.91	117	132
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	42	271	0.27%	70.7%	AGFAGDDAPR	99.7%	72.7	25	60.5	22	0	0	976.45	19	28
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	42	271	0.27%	70.7%	AVFPSIVGRPR	99.7%	57.7	25	57.7	5	0	0	1198.71	29	39
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	42	271	0.27%	70.7%	CDVDIRK	99.7%	41.4	25	21	4	0	0	905.45	285	291
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	42	271	0.27%	70.7%	CPEALFQPSFLGMESCGIHETTFNSIMK	97.7%	22.8	25	5.93	0	1	0	3247.46	257	284
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	42	271	0.27%	70.7%	DLTDYLMK	99.7%	57	25	44.4	8	0	0	1014.48	184	191
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	42	271	0.27%	70.7%	DLYANTVLSGGTTMYPGIADR	99.7%	126	25	126	22	6	0	2231.07	292	312
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	42	271	0.27%	70.7%	DSYVGDEAQSK	99.7%	70.9	25	67.7	11	0	0	1198.52	51	61
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	42	271	0.27%	70.7%	DSYVGDEAQSKR	99.7%	60.5	25	58.3	15	2	0	1354.62	51	62
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	42	271	0.27%	70.7%	EITALAPSTMK	99.7%	64.7	25	63.4	37	0	0	1161.62	316	326
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	42	271	0.27%	70.7%	GYSFTTTAER	99.7%	73.6	25	66.3	21	0	0	1132.53	197	206
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	42	271	0.27%	70.7%	GYSFTTTAEREIVR	98.7%	32.4	25	22.1	2	0	0	1629.82	197	210
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	42	271	0.27%	70.7%	HQGVMVGMGQK	99.7%	44.4	25	40.7	17	5	0	1203.56	40	50
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	42	271	0.27%	70.7%	IIAPPERK	99.7%	40.5	25	33.8	2	0	0	923.57	329	336
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	42	271	0.27%	70.7%	IWHHTFYNELR	99.7%	42.9	25	42.9	1	2	0	1515.75	85	95
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	42	271	0.27%	70.7%	KDLYANTVLSGGTTMYPGIADR	99.7%	66.3	25	66.3	0	3	0	2359.16	291	312
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	42	271	0.27%	70.7%	LCYVALDFEQEMATAASSSSLEK	99.7%	137	25	137	10	10	0	2566.17	216	238
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	42	271	0.27%	70.7%	LDLAGRDLTDYLMK	99.7%	39.2	25	34.6	7	4	0	1639.84	178	191
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	42	271	0.27%	70.7%	QEYDESGPSIVHR	99.7%	63.6	25	63.6	4	6	0	1516.70	360	372
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	42	271	0.27%	70.7%	QEYDESGPSIVHRK	99.7%	39.9	25	35.2	1	1	0	1644.80	360	373
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	42	271	0.27%	70.7%	RGILTLK	99.6%	37.7	25	18.5	2	0	0	800.54	62	68
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	42	271	0.27%	70.7%	SYELPDGQVITIGNER	99.7%	117	25	105	17	0	0	1790.89	239	254
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	42	271	0.27%	70.7%	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	99.7%	65.2	25	65.2	0	4	0	3183.61	148	177
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	42	271	0.27%	70.7%	VAPEEHPVLLTEAPLNPK	99.7%	94.8	25	57.7	9	10	0	1954.06	96	113
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	6	8	14	0.01%	16.5%	GYAFNHSADFETVR	99.7%	81.5	25	71	2	2	0	1613.73	201	214
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	6	8	14	0.01%	16.5%	ILLTEPPMNPTK	99.7%	49.7	25	41.3	4	0	0	1353.74	107	118
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	6	8	14	0.01%	16.5%	KVVVCDNGTGFVK	99.7%	42.3	25	42.3	1	0	0	1422.74	7	19
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	6	8	14	0.01%	16.5%	LCYVGYNIEQEQK	99.7%	81.9	25	80.2	2	0	0	1643.77	220	232
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	6	8	14	0.01%	16.5%	QLYLER	97.9%	30.6	25	7.97	1	0	0	821.45	323	328
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	6	8	14	0.01%	16.5%	RLDIAGR	98.8%	32.8	25	12.6	2	0	0	800.47	181	187
Actin-related protein 2/3 complex subunit 2	ARPC2	ARPC2_HUMAN	34.3	100.0%	2	2	4	0.00%	6.0%	IIEETLALK	98.9%	33.3	25	29.2	2	0	0	1029.62	10	18
Actin-related protein 2/3 complex subunit 2	ARPC2	ARPC2_HUMAN	34.3	100.0%	2	2	4	0.00%	6.0%	MILLEVNNR	99.7%	43.5	25	35.8	2	0	0	1101.61	1	9
Actin-related protein 2/3 complex subunit 4	ARPC4	ARPC4_HUMAN	19.7	100.0%	3	3	4	0.00%	13.1%	AENFFILR	99.7%	48.9	25	30.8	2	0	0	1009.55	98	105
Actin-related protein 2/3 complex subunit 4	ARPC4	ARPC4_HUMAN	19.7	100.0%	3	3	4	0.00%	13.1%	ELLLQPVTISR	98.9%	33.2	25	33.2	1	0	0	1268.76	45	55
Actin-related protein 2/3 complex subunit 4	ARPC4	ARPC4_HUMAN	19.7	100.0%	3	3	4	0.00%	13.1%	SSKELLLQPVTISR	99.1%	34.1	25	34.1	1	0	0	1570.92	42	55
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	6	7	10	0.01%	19.6%	AEPEDHYFLLTEPPLNTPENR	99.7%	29.7	25	29.7	0	2	0	2482.19	103	123
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	6	7	10	0.01%	19.6%	DITYFIQQLLR	99.7%	62.4	25	41.7	1	0	0	1409.78	199	209
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	6	7	10	0.01%	19.6%	EFSIDVGYER	99.7%	47.4	25	29.7	1	0	0	1214.57	266	275
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	6	7	10	0.01%	19.6%	FMEQVIFK	96.4%	28.4	25	25.4	1	0	0	1041.54	92	99
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	6	7	10	0.01%	19.6%	LGYAGNTEPQFIIPSCIAIK	99.7%	46.4	25	46.4	2	0	0	2192.14	19	38
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	6	7	10	0.01%	19.6%	NIVLSGGSTMFR	99.7%	72.1	25	66.3	3	0	0	1297.66	318	329
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	2	2	4	0.00%	0.9%	DLADWLNIK	99.7%	49.4	25	40.5	2	0	0	1087.58	1498	1506
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	2	2	4	0.00%	0.9%	TVAAELAIFR	99.7%	67.4	25	67.4	2	0	0	1090.63	1356	1365
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	7	8	14	0.01%	22.2%	ADATNVNNWHWTER	99.7%	32.9	25	30.9	0	2	0	1713.77	17	30
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	7	8	14	0.01%	22.2%	DASNWSTDKLK	99.7%	49.8	25	35.5	2	0	0	1264.62	31	41
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	7	8	14	0.01%	22.2%	EAMGIYISTLK	99.7%	40.2	25	33.5	3	0	0	1225.65	146	156
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	7	8	14	0.01%	22.2%	ETFLTSPEELYR	99.7%	40.2	25	35	2	0	0	1484.73	213	224

Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	7	8	14	0.01%	22.2%	GIPAPEEER	96.8%	28.8	25	24	1	0	0	997.50	306	314
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	7	8	14	0.01%	22.2%	LDGEASINNR	99.7%	92.3	25	69.5	2	0	0	1088.53	64	73
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	7	8	14	0.01%	22.2%	QTFGYGAR	99.2%	34.5	25	23.4	2	0	0	899.44	329	336
Acyl-CoA dehydrogenase family member 10	ACAD10	ACD10_HUMAN	118.8	99.9%	2	2	2	0.00%	2.5%	TSVPVDSFFSLLTSER	99.3%	35	25	34.8	1	0	0	1784.91	115	130
Acyl-CoA dehydrogenase family member 10	ACAD10	ACD10_HUMAN	118.8	99.9%	2	2	2	0.00%	2.5%	VAAILQGVYK	99.7%	39.2	25	25.7	1	0	0	1061.64	558	567
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	21	38	0.04%	34.3%	FFTEEVDSR	99.7%	70.8	25	58.4	2	0	0	1129.52	77	85
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	21	38	0.04%	34.3%	FSMGSVVAGLLK	99.7%	62.2	25	59.6	2	0	0	1208.67	305	316
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	21	38	0.04%	34.3%	GIILAGTEEQK	99.7%	57.3	25	45.7	2	0	0	1158.64	152	162
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	21	38	0.04%	34.3%	GSNTCEVHFENTK	99.7%	41.9	25	41.9	2	0	0	1522.66	267	279
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	21	38	0.04%	34.3%	ILLIFEGTNEILR	99.7%	102	25	91.4	2	0	0	1530.89	421	433
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	21	38	0.04%	34.3%	IPVENILGEVGDGFK	99.7%	90.4	25	90.4	2	0	0	1586.84	280	294
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	21	38	0.04%	34.3%	ITAFIVER	99.7%	52	25	39.2	2	0	0	948.55	242	249
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	21	38	0.04%	34.3%	LASGEHIAAFCLTEPASGSDAASIR	98.5%	24.2	25	20.6	0	1	0	2531.22	169	193
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	21	38	0.04%	34.3%	LIEMTAEYACTR	99.7%	83.9	25	83.9	4	0	0	1457.68	318	329
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	21	38	0.04%	34.3%	LSEFGLIQEK	99.7%	69.2	25	53.3	2	0	0	1163.63	336	345
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	21	38	0.04%	34.3%	MYIALTGLQHAGR	99.7%	68.4	25	61.9	1	0	0	1430.76	434	446
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	21	38	0.04%	34.3%	TEVVDSDGSVK	96.6%	28.6	25	28.6	1	0	0	1135.55	229	239
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	21	38	0.04%	34.3%	TEVVDSDGSVKDK	99.7%	59.6	25	51.6	2	0	0	1378.67	229	241
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	21	38	0.04%	34.3%	TIMEEQLVLKR	99.3%	35.4	25	31	2	0	0	1359.77	522	532
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	21	38	0.04%	34.3%	TVETLLLR	99.7%	55.4	25	33.8	2	0	0	944.58	511	518
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	21	38	0.04%	34.3%	VAMNILNSGR	99.7%	86.9	25	79	2	0	0	1090.57	295	304
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	21	38	0.04%	34.3%	VSQQILEK	99.7%	51.9	25	35	2	0	0	944.54	601	608
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	21	38	0.04%	34.3%	VSTVMDTVGR	99.7%	87.9	25	78.1	3	0	0	1064.54	460	469
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	21	38	0.04%	34.3%	YAPENLDEQIKK	99.7%	46.7	25	43.6	2	0	0	1447.74	589	600
Acyl-coenzyme A thioesterase 1	ACOT1	ACOT1_HUMAN	46.3	99.8%	2	2	3	0.00%	4.8%	GALFQAHAR	99.6%	37.5	25	25	1	0	0	970.52	43	51
Acyl-coenzyme A thioesterase 1	ACOT1	ACOT1_HUMAN	46.3	99.8%	2	2	3	0.00%	4.8%	GLAPEQPVTLR	99.7%	41	25	37.8	2	0	0	1180.67	25	35
Acyl-coenzyme A thioesterase 13	ACOT13	ACO13_HUMAN	15.0	100.0%	5	5	8	0.01%	40.7%	GAPGVSVDMNITYMSPAK	99.7%	41.9	25	41.9	1	0	0	1869.87	78	95
Acyl-coenzyme A thioesterase 13	ACOT13	ACO13_HUMAN	15.0	100.0%	5	5	8	0.01%	40.7%	ITLVSAAPGK	99.7%	45.1	25	33.4	2	0	0	956.58	28	37
Acyl-coenzyme A thioesterase 13	ACOT13	ACO13_HUMAN	15.0	100.0%	5	5	8	0.01%	40.7%	LGEDIVITAHVLK	99.7%	65.4	25	61.5	2	0	0	1407.82	96	108
Acyl-coenzyme A thioesterase 13	ACOT13	ACO13_HUMAN	15.0	100.0%	5	5	8	0.01%	40.7%	TLAFTSVDLTNK	99.7%	79.3	25	69	2	0	0	1309.70	112	123
Acyl-coenzyme A thioesterase 13	ACOT13	ACO13_HUMAN	15.0	100.0%	5	5	8	0.01%	40.7%	TLAFTSVDLTNKATGK	99.7%	41.5	25	40	1	0	0	1666.90	112	127
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	ACOT9_HUMAN	49.9	99.8%	2	2	4	0.00%	4.8%	SLEICHPQER	99.7%	45.6	25	42.1	2	0	0	1268.61	295	304
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	ACOT9_HUMAN	49.9	99.8%	2	2	4	0.00%	4.8%	VHSEVASLQEK	99.7%	43.5	25	39.7	2	0	0	1226.64	373	383
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	7	7	12	0.01%	21.3%	ATVFLNPAACK	99.7%	62.9	25	61.7	2	0	0	1191.62	63	73
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	7	7	12	0.01%	21.3%	EQPVFAMTGLR	97.5%	29.9	25	29.9	2	0	0	1248.64	200	210
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	7	7	12	0.01%	21.3%	GDFITIGSR	99.7%	68.4	25	57.5	2	0	0	965.51	343	351
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	7	7	12	0.01%	21.3%	GETVPLDVLQIK	99.7%	62.9	25	56	2	0	0	1311.75	185	196
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	7	7	12	0.01%	21.3%	IPIGFIPLGETSSLSHTLFAESGNK	99.7%	39	25	39	0	1	0	2615.37	147	171
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	7	7	12	0.01%	21.3%	RTDEATFSK	97.2%	29.4	25	22	1	0	0	1054.52	138	146
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	7	7	12	0.01%	21.3%	VQHITDATLAIVK	99.7%	48.8	25	48.8	2	0	0	1408.82	172	184
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	6	8	12	0.01%	46.7%	AELEIQKDALEPGQR	99.7%	69	25	69	2	2	0	1696.89	108	122
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	6	8	12	0.01%	46.7%	DISPVLKDPASFR	99.7%	49.5	25	49.5	2	1	0	1444.78	28	40
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	6	8	12	0.01%	46.7%	GFLFGPSLAQELGLGCVLIR	98.9%	25.2	25	25.2	0	1	0	2147.17	68	87
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	6	8	12	0.01%	46.7%	IDYIAGLDSR	99.7%	69.3	25	62.2	2	0	0	1122.58	58	67
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	6	8	12	0.01%	46.7%	LAPVPFFSLLQYE	99.7%	51.3	25	51.3	1	0	0	1523.81	168	180
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	6	8	12	0.01%	46.7%	SFPDFPTPGVVFR	99.0%	33.6	25	33.1	1	0	0	1465.75	15	27
Adenosylhomocysteinase	AHCY	SAHH_HUMAN	47.7	100.0%	5	5	8	0.01%	13.2%	GISEETTTGVHNLYK	99.7%	57.5	25	52.6	1	0	0	1648.82	152	166
Adenosylhomocysteinase	AHCY	SAHH_HUMAN	47.7	100.0%	5	5	8	0.01%	13.2%	IILLAEGR	99.7%	41.8	25	30.9	2	0	0	884.56	336	343
Adenosylhomocysteinase	AHCY	SAHH_HUMAN	47.7	100.0%	5	5	8	0.01%	13.2%	SKFDNLYGCR	99.7%	45.4	25	43.5	1	0	0	1259.58	187	196
Adenosylhomocysteinase	AHCY	SAHH_HUMAN	47.7	100.0%	5	5	8	0.01%	13.2%	VAVVAGYGDVGK	99.7%	65.5	25	57.8	2	0	0	1134.62	215	226
Adenosylhomocysteinase	AHCY	SAHH_HUMAN	47.7	100.0%	5	5	8	0.01%	13.2%	VPAINVNDSVTK	99.7%	70	25	68.5	2	0	0	1256.68	175	186

Adenylate kinase 2, mitochondrial	AK2	KAD2_HUMAN	26.5	99.8%	2	2	3	0.00%	8.8%	AVLLGPPGAGK	99.4%	36.1	25	36.1	1	0	0	979.59	18	28
Adenylate kinase 2, mitochondrial	AK2	KAD2_HUMAN	26.5	99.8%	2	2	3	0.00%	8.8%	NGFLLDGFPR	99.7%	50.5	25	50.5	2	0	0	1135.59	94	103
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	9	16	0.02%	34.5%	ASTEVGEMAK	98.9%	33.3	25	21.5	1	0	0	1022.48	46	55
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	9	16	0.02%	34.5%	AVILGPPGSGK	99.7%	42.7	25	32.5	2	0	0	995.59	8	18
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	9	16	0.02%	34.5%	DVAKPVIELYK	99.7%	48.9	25	45.6	2	0	0	1274.74	176	186
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	9	16	0.02%	34.5%	GVLHQFSGTETNK	99.7%	68.7	25	68.6	2	1	0	1417.71	189	201
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	9	16	0.02%	34.5%	IWPYVYTLFSNK	99.7%	47.6	25	40.3	2	0	0	1530.80	202	213
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	9	16	0.02%	34.5%	LMMSELENR	99.7%	61.1	25	51.5	4	0	0	1122.53	72	80
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	9	16	0.02%	34.5%	SLLVPDHVITR	99.6%	37.8	25	32.7	2	0	0	1249.73	61	71
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	8	8	13	0.01%	23.1%	AFIITGQTYTR	97.2%	29.3	25	29.1	1	0	0	1270.68	235	245
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	8	8	13	0.01%	23.1%	FLEEEVYPLLKPYESVMK	99.7%	32.7	25	32	0	2	0	2214.14	460	477
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	8	8	13	0.01%	23.1%	IQVDAYFSPIHSQLDHLLDPSSFTGR	99.7%	36.5	25	34.6	0	2	0	2943.46	427	452
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	8	8	13	0.01%	23.1%	NALDLLLPK	99.7%	50.2	25	25.4	2	0	0	996.61	126	134
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	8	8	13	0.01%	23.1%	QEGGDNDLIER	99.7%	55.3	25	39.5	1	0	0	1245.57	416	426
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	8	8	13	0.01%	23.1%	QELPFMATENIIMAMVK	99.5%	36.5	25	36.5	1	0	0	1965.98	375	391
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	8	8	13	0.01%	23.1%	SNLENIDFK	99.7%	49.2	25	39	2	0	0	1079.54	67	75
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	8	8	13	0.01%	23.1%	VLSQQAASVVK	99.7%	86.9	25	67.8	2	0	0	1129.66	405	415
Adenylosuccinate synthetase isozyme 2	ADSS	PURA2_HUMAN	50.1	99.8%	2	2	4	0.00%	5.5%	FIEDELQIPVK	99.7%	51	25	39.4	2	0	0	1330.73	431	441
Adenylosuccinate synthetase isozyme 2	ADSS	PURA2_HUMAN	50.1	99.8%	2	2	4	0.00%	5.5%	VVDLLAQDADIVCR	99.7%	77.3	25	77	2	0	0	1586.82	46	59
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	53.0%	AAYFGVYDTAK	99.7%	88.6	25	88.6	7	0	0	1205.58	189	199
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	53.0%	DFLAGGVAAAVSK	99.7%	90.7	25	87.4	5	0	0	1205.65	11	23
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	53.0%	EFHGLGDCIIK	99.7%	46.6	25	38.6	4	0	0	1288.64	153	163
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	53.0%	EQGFLSFWR	99.7%	40.9	25	40.9	6	0	0	1169.57	64	72
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	53.0%	GADIMYTGTVDCWR	99.7%	70.9	25	60.6	8	0	0	1660.71	246	259
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	53.0%	GAWSNVLR	99.7%	62.3	25	41.3	6	0	0	902.48	273	280
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	53.0%	GMGGAFVLVLYDEIK	99.7%	73.9	25	0	4	0	0	1627.84	281	295
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	53.0%	GMGGAFVLVLYDEIKK	98.7%	32.6	25	0	1	0	0	1739.94	281	296
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	53.0%	LLLQVQHASK	99.7%	46.5	25	37.2	25	0	0	1136.68	34	43
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	53.0%	MMMQSGR	97.9%	30.5	25	10.4	2	0	0	872.34	238	244
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	53.0%	QLFLGGVDR	99.7%	62.5	25	35.4	4	0	0	1004.55	97	105
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	53.0%	RMMMQSGR	99.7%	39.9	25	35.1	1	0	0	996.45	237	244
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	53.0%	TAVAPIER	99.7%	42.1	25	30.4	5	0	0	856.49	24	31
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	53.0%	YFAGNLASGGAAGATSLCFVYPLDFAR	99.7%	39	25	39	1	0	0	2796.35	112	138
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	53.0%	YFPTQALNFAFK	99.7%	90.6	25	74.2	39	0	0	1446.74	81	92
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	19	0.02%	53.0%	YFPTQALNFAFKDK	99.7%	84	25	84	5	0	0	1689.86	81	94
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	18	21	160	0.16%	44.0%	AAYFGIYDTAK	99.7%	71.5	25	56.5	5	0	0	1219.60	189	199
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	18	21	160	0.16%	44.0%	DFLAGGVAAAISK	99.7%	102	25	90.9	6	0	0	1219.67	11	23
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	18	21	160	0.16%	44.0%	EQGVLSFWR	99.7%	64.4	25	64.4	24	0	0	1121.57	64	72
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	18	21	160	0.16%	44.0%	GAWSNVLR	99.7%	62.3	25	41.3	6	0	0	902.48	273	280
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	18	21	160	0.16%	44.0%	GLGDCLVK	99.5%	36.8	25	18.7	4	0	0	861.45	156	163
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	18	21	160	0.16%	44.0%	GMGGAFVLVLYDEIK	99.7%	73.9	25	0	4	0	0	1627.84	281	295
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	18	21	160	0.16%	44.0%	GMGGAFVLVLYDEIKK	98.7%	32.6	25	0	1	0	0	1739.94	281	296
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	18	21	160	0.16%	44.0%	GTDIMYTGTLDCWR	99.7%	87.5	25	79.4	8	0	0	1704.74	246	259
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	18	21	160	0.16%	44.0%	GTDIMYTGTLDCWRK	98.5%	32	25	32	1	0	0	1816.84	246	260
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	18	21	160	0.16%	44.0%	KGTDIMYTGTLDCWR	99.7%	64.9	25	64.9	3	2	0	1832.83	245	259
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	18	21	160	0.16%	44.0%	LLLQVQHASK	99.7%	46.5	25	37.2	25	0	0	1136.68	34	43
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	18	21	160	0.16%	44.0%	MMMQSGR	97.9%	30.5	25	10.4	2	0	0	872.34	238	244
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	18	21	160	0.16%	44.0%	QIFLGGVDK	99.7%	47.9	25	32.5	8	0	0	976.55	97	105
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	18	21	160	0.16%	44.0%	QIFLGGVDKR	99.7%	58.1	25	44.3	11	0	0	1132.65	97	106
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	18	21	160	0.16%	44.0%	RMMMQSGR	99.7%	39.9	25	35.1	1	0	0	996.45	237	244
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	18	21	160	0.16%	44.0%	TAVAPIER	99.7%	42.1	25	30.4	5	0	0	856.49	24	31

ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	18	21	160	0.16%	44.0%	YFPTQALNFAFK	99.7%	90.6	25	74.2	39	0	0	1446.74	81	92
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	18	21	160	0.16%	44.0%	YFPTQALNFAFKDK	99.7%	84	25	84	5	0	0	1689.86	81	94
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	5	6	42	0.04%	56.0%	AAYFGVYDTAK	99.7%	88.6	25	88.6	7	0	0	1205.58	189	199
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	5	6	42	0.04%	56.0%	DFLAGGIAAAISK	99.7%	98.2	25	92	24	0	0	1233.68	11	23
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	5	6	42	0.04%	56.0%	EQGVLSFWR	99.7%	64.4	25	64.4	24	0	0	1121.57	64	72
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	5	6	42	0.04%	56.0%	GADIMYTGTVDCWR	99.7%	70.9	25	60.6	8	0	0	1660.71	246	259
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	5	6	42	0.04%	56.0%	GAWSNVLR	99.7%	62.3	25	41.3	6	0	0	902.48	273	280
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	5	6	42	0.04%	56.0%	GLGDCLVK	99.5%	36.8	25	18.7	4	0	0	861.45	156	163
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	5	6	42	0.04%	56.0%	GMGGAFVLVLYDELK	99.7%	73.9	25	0	4	0	0	1627.84	281	295
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	5	6	42	0.04%	56.0%	GMGGAFVLVLYDELKK	98.7%	32.6	25	0	1	0	0	1739.94	281	296
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	5	6	42	0.04%	56.0%	LAADVGKSGTER	97.4%	29.6	25	22.1	2	0	0	1203.63	141	152
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	5	6	42	0.04%	56.0%	LLLQVQHASK	99.7%	46.5	25	37.2	25	0	0	1136.68	34	43
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	5	6	42	0.04%	56.0%	MMMQSGR	97.9%	30.5	25	10.4	2	0	0	872.34	238	244
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	5	6	42	0.04%	56.0%	QIFLGGVDK	99.7%	47.9	25	32.5	8	0	0	976.55	97	105
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	5	6	42	0.04%	56.0%	RMMMQSGR	99.7%	39.9	25	35.1	1	0	0	996.45	237	244
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	5	6	42	0.04%	56.0%	TAVAPIER	99.7%	42.1	25	30.4	5	0	0	856.49	24	31
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	5	6	42	0.04%	56.0%	YFAGNLASGGAAGATSLCFVYPLDFAR	99.7%	39	25	39	1	0	0	2796.35	112	138
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	5	6	42	0.04%	56.0%	YFPTQALNFAFK	99.7%	90.6	25	74.2	39	0	0	1446.74	81	92
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	5	6	42	0.04%	56.0%	YFPTQALNFAFKDK	99.7%	84	25	84	5	0	0	1689.86	81	94
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN	20.7	99.8%	2	3	4	0.00%	24.9%	DAVLLVFANK	99.6%	37.3	25	31.5	1	0	0	1089.63	118	127
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN	20.7	99.8%	2	3	4	0.00%	24.9%	ILMVGLDAAGK	99.7%	76.6	25	58.6	6	0	0	1087.62	20	30
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN	20.7	99.8%	2	3	4	0.00%	24.9%	NISFTVWDVGGQDK	99.7%	88.2	25	86.6	2	0	0	1565.76	60	73
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN	20.7	99.8%	2	3	4	0.00%	24.9%	VNEAREELMR	99.7%	35.7	25	31.6	1	1	0	1262.62	100	109
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	99.8%	2	3	7	0.01%	11.7%	ILMVGLDAAGK	99.7%	76.6	25	58.6	6	0	0	1087.62	20	30
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	99.8%	2	3	7	0.01%	11.7%	IQEVADELQK	99.7%	49	25	33.7	1	0	0	1172.62	100	109
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	99.8%	2	2	2	0.00%	17.2%	DAVLLVFANK	99.6%	37.3	25	31.5	1	0	0	1089.63	118	127
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	99.8%	2	2	2	0.00%	17.2%	ILMVGLDAAGK	99.7%	76.6	25	58.6	6	0	0	1087.62	20	30
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	99.8%	2	2	2	0.00%	17.2%	VQESADELQK	99.2%	34.7	25	24.4	1	0	0	1146.56	100	109
ADP-ribosylation factor 6	ARF6	ARF6_HUMAN	20.1	100.0%	4	6	12	0.01%	30.3%	DAIILIFANK	99.7%	56.8	25	0	2	0	0	1117.66	114	123
ADP-ribosylation factor 6	ARF6	ARF6_HUMAN	20.1	100.0%	4	6	12	0.01%	30.3%	FNVWDVGGQDK	99.7%	73.8	25	61.9	2	0	0	1264.60	59	69
ADP-ribosylation factor 6	ARF6	ARF6_HUMAN	20.1	100.0%	4	6	12	0.01%	30.3%	ILMLGLDAAGK	99.7%	78.5	25	56.2	4	0	0	1117.63	16	26
ADP-ribosylation factor 6	ARF6	ARF6_HUMAN	20.1	100.0%	4	6	12	0.01%	30.3%	LGQSVTTIPTVGFNVETVTYK	99.7%	43.4	25	43.4	2	2	0	2254.20	35	55
ADP-ribosylation factor-like protein 1	ARL1	ARL1_HUMAN	20.4	100.0%	3	3	4	0.00%	21.5%	AILVVFANK	99.7%	65.2	25	65.2	2	0	0	974.60	119	127
ADP-ribosylation factor-like protein 1	ARL1	ARL1_HUMAN	20.4	100.0%	3	3	4	0.00%	21.5%	GTGLDEAMEWLVETLK	99.7%	54.1	25	52.4	1	0	0	1791.88	163	178
ADP-ribosylation factor-like protein 1	ARL1	ARL1_HUMAN	20.4	100.0%	3	3	4	0.00%	21.5%	SELVAMLEEEELRK	99.7%	48	25	43.3	1	0	0	1675.86	105	118
ADP-ribosylation factor-like protein 6	ARL6	ARL6_HUMAN	21.1	100.0%	2	2	3	0.00%	9.1%	IPILFFANK	99.1%	34	25	17.9	1	0	0	1062.63	123	131
ADP-ribosylation factor-like protein 6	ARL6	ARL6_HUMAN	21.1	100.0%	2	2	3	0.00%	9.1%	LSVLLGLK	99.7%	38.6	25	34.7	2	0	0	842.57	7	14
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	8	8	12	0.01%	10.4%	GLGYAQYLPK	98.3%	31.3	25	23.8	2	0	0	1109.60	602	611
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	8	8	12	0.01%	10.4%	ILINDAYKR	99.7%	53.5	25	42.8	1	0	0	1105.64	703	711
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	8	8	12	0.01%	10.4%	KTQVLQPEEK	99.7%	50.8	25	24.7	2	0	0	1199.66	559	568
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	8	8	12	0.01%	10.4%	QIFIGPPDIK	99.6%	37.5	25	21.3	1	0	0	1127.65	472	481
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	8	8	12	0.01%	10.4%	VALLLLEK	97.6%	30.1	25	30.1	1	0	0	898.60	726	733
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	8	8	12	0.01%	10.4%	VGQISFDLPR	99.7%	73.8	25	55	2	0	0	1131.62	670	679
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	8	8	12	0.01%	10.4%	VSEEIFFGR	99.7%	69.2	25	48	2	0	0	1083.55	633	641
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	8	8	12	0.01%	10.4%	VTQSAYAQIVQFGMNEK	99.7%	53.7	25	53.7	1	0	0	1913.94	653	669
A-kinase anchor protein 8-like	AKAP8L	AKP8L_HUMAN	71.6	99.8%	2	2	3	0.00%	3.4%	IQFVCSLCK	99.7%	42.9	25	23.9	1	0	0	1154.57	387	395
A-kinase anchor protein 8-like	AKAP8L	AKP8L_HUMAN	71.6	99.8%	2	2	3	0.00%	3.4%	QTADFLQEYVTNK	99.7%	88.7	25	82.9	2	0	0	1556.76	427	439
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	5	5	9	0.01%	12.1%	FAVALLDDSVR	99.7%	86.8	25	68.1	2	0	0	1205.65	166	176
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	5	5	9	0.01%	12.1%	GALLSVGWSTGR	99.7%	59.2	25	54.3	1	0	0	1203.65	467	478
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	5	5	9	0.01%	12.1%	GQWINLPVLQLTK	99.7%	50.5	25	41.1	3	0	0	1509.88	40	52
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	5	5	9	0.01%	12.1%	ILATTPSAVFR	99.7%	56.3	25	49.4	2	0	0	1175.68	302	312

Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	5	5	9	0.01%	12.1%	LLFTVLGEPLIYSLSFPER	99.7%	45	25	45	1	0	0	2194.22	343	361
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	15	16	24	0.02%	18.3%	AAFLNFFR	99.7%	41.1	25	30.1	2	0	0	985.53	44	51
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	15	16	24	0.02%	18.3%	AGLDPDLETR	99.7%	50.2	25	42.3	2	0	0	1086.54	178	187
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	15	16	24	0.02%	18.3%	AGQEDVLFPVAR	99.7%	45.8	25	41.9	1	0	0	1301.68	581	592
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	15	16	24	0.02%	18.3%	DIWLSLGVPASR	99.7%	43.5	25	32.1	2	0	0	1313.72	188	199
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	15	16	24	0.02%	18.3%	EADGSLQPLPQR	98.6%	32.2	25	19.4	1	0	0	1310.67	251	262
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	15	16	24	0.02%	18.3%	ELGQSLAQEVK	99.7%	51.3	25	39	1	0	0	1201.64	791	801
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	15	16	24	0.02%	18.3%	GPLIVDTVSAESLSVLVK	99.7%	66.4	25	66.4	2	0	0	1827.05	881	898
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	15	16	24	0.02%	18.3%	GVQLDSAGLER	99.7%	40.1	25	30.3	1	0	0	1144.60	461	471
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	15	16	24	0.02%	18.3%	HVDTGMGLER	99.7%	42.5	25	42.5	2	0	0	1114.53	263	272
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	15	16	24	0.02%	18.3%	LDVTTQTPLTPEQLR	99.7%	78.9	25	70.2	2	0	0	1711.92	664	678
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	15	16	24	0.02%	18.3%	LLAVTGEQAQQAR	99.7%	87.9	25	78.2	2	0	0	1384.75	778	790
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	15	16	24	0.02%	18.3%	LVPSASVRPR	99.5%	36.8	25	32.1	1	0	0	1081.65	58	67
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	15	16	24	0.02%	18.3%	SLDEVYPDPVR	99.7%	43.4	25	43.1	2	0	0	1289.64	712	722
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	15	16	24	0.02%	18.3%	TGAVGDLVIIGDR	99.7%	77.5	25	66.2	1	0	0	1285.71	757	769
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	15	16	24	0.02%	18.3%	TNFYAEQGGQASDR	99.7%	91.6	25	91.6	2	0	0	1543.68	562	575
Alcohol dehydrogenase class-3	ADH5	ADHX_HUMAN	39.7	100.0%	3	3	4	0.00%	9.6%	AFELMHSGK	99.4%	35.8	25	28.9	1	0	0	1019.50	358	366
Alcohol dehydrogenase class-3	ADH5	ADHX_HUMAN	39.7	100.0%	3	3	4	0.00%	9.6%	AGDTVIPLYIPQCGECK	99.7%	45.6	25	45.6	1	0	0	1920.92	85	101
Alcohol dehydrogenase class-3	ADH5	ADHX_HUMAN	39.7	100.0%	3	3	4	0.00%	9.6%	IIGVDINKDK	99.2%	34.7	25	10.4	2	0	0	1114.65	219	228
Aldehyde dehydrogenase family 16 member A1	ALDH16A1	A16A1_HUMAN	85.1	100.0%	5	5	5	0.00%	7.1%	AAEAEVELSAR	99.7%	59.6	25	50.7	1	0	0	1145.58	619	629
Aldehyde dehydrogenase family 16 member A1	ALDH16A1	A16A1_HUMAN	85.1	100.0%	5	5	5	0.00%	7.1%	GLDGAVDMGAR	99.7%	45.7	25	32.5	1	0	0	1061.50	335	345
Aldehyde dehydrogenase family 16 member A1	ALDH16A1	A16A1_HUMAN	85.1	100.0%	5	5	5	0.00%	7.1%	GWSAHPGVVR	99.7%	40.8	25	40.2	1	0	0	1065.56	92	101
Aldehyde dehydrogenase family 16 member A1	ALDH16A1	A16A1_HUMAN	85.1	100.0%	5	5	5	0.00%	7.1%	LLIQESVWDEAMR	99.7%	73.4	25	73	1	0	0	1589.80	309	321
Aldehyde dehydrogenase family 16 member A1	ALDH16A1	A16A1_HUMAN	85.1	100.0%	5	5	5	0.00%	7.1%	LLWTLESLVTGR	99.7%	63.8	25	54	1	0	0	1387.79	118	129
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	7	8	14	0.01%	18.6%	KIEEVVER	99.7%	63.5	25	46.2	2	0	0	1001.56	429	436
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	7	8	14	0.01%	18.6%	LAPALATGNTVVMK	99.7%	89.9	25	81.6	3	0	0	1385.78	196	209
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	7	8	14	0.01%	18.6%	LLNLLADLVER	99.7%	75.5	25	66.1	2	0	0	1268.76	104	114
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	7	8	14	0.01%	18.6%	TFVEESIYNEFLER	99.7%	73.5	25	61.5	2	0	0	1775.85	325	338
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	7	8	14	0.01%	18.6%	VAEQTPLSALYLASLIK	99.7%	119	25	119	2	0	0	1817.04	210	226
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	7	8	14	0.01%	18.6%	VGNPFELDTQQGPQVDKEQFER	99.7%	44.9	25	44.9	0	1	0	2561.23	348	369
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	7	8	14	0.01%	18.6%	VLGYIQLGQK	99.7%	63.9	25	55.1	2	0	0	1118.66	370	379
Aldehyde dehydrogenase, mitochondrial	ALDH2	ALDH2_HUMAN	56.4	100.0%	5	5	5	0.00%	11.8%	EEIFGPVMQILK	94.5%	26.8	25	17.7	1	0	0	1403.76	415	426
Aldehyde dehydrogenase, mitochondrial	ALDH2	ALDH2_HUMAN	56.4	100.0%	5	5	5	0.00%	11.8%	LLCGGGIAADR	99.7%	45.2	25	35.7	1	0	0	1102.57	384	394
Aldehyde dehydrogenase, mitochondrial	ALDH2	ALDH2_HUMAN	56.4	100.0%	5	5	5	0.00%	11.8%	TIEEVVGR	97.7%	30.2	25	15.9	1	0	0	902.49	429	436
Aldehyde dehydrogenase, mitochondrial	ALDH2	ALDH2_HUMAN	56.4	100.0%	5	5	5	0.00%	11.8%	VAEQTPLTALYVANLIK	98.6%	32.3	25	32.3	1	0	0	1844.05	210	226
Aldehyde dehydrogenase, mitochondrial	ALDH2	ALDH2_HUMAN	56.4	100.0%	5	5	5	0.00%	11.8%	VIQVAAGSSNLKR	99.7%	51.1	25	49.7	1	0	0	1342.78	269	281
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	6	6	8	0.01%	12.2%	ESISDVGFGMLK	99.7%	49.4	25	49.4	2	0	0	1282.63	629	640
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	6	6	8	0.01%	12.2%	GISDPLTVFEQTEAAAR	99.7%	81.2	25	71.7	2	0	0	1804.91	587	603
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	6	6	8	0.01%	12.2%	GVQFAPFSTCR	97.0%	29.1	25	24	1	0	0	1269.60	556	566
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	6	6	8	0.01%	12.2%	IRPVPEYQK	98.5%	31.9	25	22.4	1	0	0	1129.64	381	389
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	6	6	8	0.01%	12.2%	NIYGNIEDLVVHIK	99.7%	45.5	25	42.9	1	0	0	1626.89	324	337
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	6	6	8	0.01%	12.2%	YGSVAFPNFEQGVACLR	99.7%	42	25	42	1	0	0	1914.92	390	406
All-trans-retinol 13,14-reductase	RETSAT	RETST_HUMAN	66.8	100.0%	3	3	3	0.00%	6.2%	ATVQSVLLDSAGK	99.7%	76.1	25	68.6	1	0	0	1288.71	318	330
All-trans-retinol 13,14-reductase	RETSAT	RETST_HUMAN	66.8	100.0%	3	3	3	0.00%	6.2%	FLPLPVVQLLDR	95.7%	27.7	25	27.7	1	0	0	1409.85	213	224
All-trans-retinol 13,14-reductase	RETSAT	RETST_HUMAN	66.8	100.0%	3	3	3	0.00%	6.2%	VVSSGAPHAILLK	98.6%	32.3	25	24.7	1	0	0	1291.77	200	212
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	2	2	4	0.00%	5.8%	VGNPWDPNVLYGPLHTK	99.7%	41.3	25	41.2	0	2	0	1906.98	359	375
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	2	2	4	0.00%	5.8%	VNLLSFTGSTQVGK	99.7%	101	25	101	2	0	0	1450.79	267	280
Alpha-aminoadipic semialdehyde synthase, mitochondrial	AASS	AASS_HUMAN	102.1	99.9%	2	2	2	0.00%	2.9%	NSSQAVQAVR	99.6%	37.8	25	29.8	1	0	0	1059.55	190	199
Alpha-aminoadipic semialdehyde synthase, mitochondrial	AASS	AASS_HUMAN	102.1	99.9%	2	2	2	0.00%	2.9%	SIGPLTFVFTGTGNVSK	99.7%	66.6	25	66.6	1	0	0	1724.92	213	229
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	13	28	0.03%	37.0%	ACYLSINPQKDETLETEK	99.7%	65	25	54.4	2	2	0	2139.03	221	238
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	13	28	0.03%	37.0%	AGFAGDQIPK	99.7%	61.2	25	46.2	2	0	0	1003.52	23	32

Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	13	28	0.03%	37.0%	AQYYLPDGSTIEIGPSR	99.7%	112	25	112	2	0	0	1866.92	239	255
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	13	28	0.03%	37.0%	DQLQTFSEEHPVLLTEAPLNPR	99.7%	83.2	25	81.4	0	2	0	2534.29	97	118
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	13	28	0.03%	37.0%	EGYDFHSSSEFEIVK	99.7%	68	25	59	2	0	0	1773.80	201	215
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	13	28	0.03%	37.0%	IWQYVYSK	99.5%	36.6	25	17.2	2	0	0	1086.56	89	96
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	13	28	0.03%	37.0%	LLSEVKK	97.3%	29.5	25	7.63	2	0	0	816.52	314	320
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	13	28	0.03%	37.0%	TLFSNIVLSGGSTLFK	99.7%	131	25	131	5	1	0	1683.93	293	308
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	13	28	0.03%	37.0%	VMAGALEGDIFIGPK	99.7%	91.8	25	0	4	0	0	1517.80	47	61
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	10	13	28	0.03%	37.0%	YCFPNYVGRPK	99.7%	53.7	25	53.7	2	0	0	1400.68	33	43
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	12	26	0.03%	34.1%	AAVPSGASTGIYEALELR	99.7%	119	25	118	1	0	0	1804.94	33	50
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	12	26	0.03%	34.1%	DATNVGDEGGFAPNILENKEGLELLK	99.7%	63.2	25	63.2	0	2	0	2743.38	203	228
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	12	26	0.03%	34.1%	GNPTVEVDLFTSK	99.7%	90.7	25	36.9	2	0	0	1406.72	16	28
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	12	26	0.03%	34.1%	IGAEVYHNLK	99.7%	59.7	25	50.3	3	0	0	1143.62	184	193
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	12	26	0.03%	34.1%	KLNVTEQEK	99.4%	35.6	25	21.6	1	0	0	1088.59	81	89
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	12	26	0.03%	34.1%	LAMQEFMILPVGAANFR	99.7%	86.5	25	86.5	6	0	0	1939.98	163	179
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	12	26	0.03%	34.1%	SCNCLLLK	99.4%	35.7	25	29.2	2	0	0	1007.50	336	343
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	12	26	0.03%	34.1%	VNQIGSVTESLQACK	99.7%	120	25	0	3	0	0	1633.82	344	358
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	12	26	0.03%	34.1%	VVIGMDVAASEFFR	99.7%	76.7	25	76.7	2	0	0	1556.78	240	253
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	12	26	0.03%	34.1%	YISPDQLADLYK	99.7%	67.8	25	65	3	0	0	1425.73	270	281
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	12	26	0.03%	34.1%	YNQLLR	94.9%	27	25	11.2	1	0	0	806.45	407	412
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	13	14	25	0.02%	27.5%	ALEAELAALR	99.7%	70.4	25	57	2	0	0	1056.60	121	130
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	13	14	25	0.02%	27.5%	AQLEEASSAR	99.7%	61.6	25	50.8	3	0	0	1061.52	152	161
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	13	14	25	0.02%	27.5%	AQYESLAAK	97.8%	30.4	25	0	1	0	0	980.50	270	278
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	13	14	25	0.02%	27.5%	DVDGATLAR	99.7%	50.4	25	40.3	2	0	0	917.47	202	210
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	13	14	25	0.02%	27.5%	EYQDLLNVK	99.7%	54.4	25	47	8	0	0	1121.58	378	386
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	13	14	25	0.02%	27.5%	FANLNEQAAR	99.7%	81.2	25	33.8	2	0	0	1133.57	291	300
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	13	14	25	0.02%	27.5%	FAVFIEK	96.2%	28.2	25	24.1	1	0	0	853.48	105	111
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	13	14	25	0.02%	27.5%	HLREYQDLLNVK	99.7%	33.5	25	24.2	0	1	0	1527.83	375	386
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	13	14	25	0.02%	27.5%	LLEGEETR	94.6%	26.9	25	11.7	1	0	0	946.48	399	406
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	13	14	25	0.02%	27.5%	LSGAGGAGGFR	99.7%	78.5	25	61.9	2	0	0	949.49	29	39
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	13	14	25	0.02%	27.5%	NLQSAEEWYK	99.7%	46.7	25	31.6	2	0	0	1267.60	279	288
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	13	14	25	0.02%	27.5%	SNIEETTISSQKI	99.7%	66.5	25	66.5	2	0	0	1449.74	487	499
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	13	14	25	0.02%	27.5%	TIEIEGLR	99.7%	41.7	25	29.3	2	0	0	930.53	323	330
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	13	14	25	0.02%	27.5%	TNEKEQLQGLNDR	99.7%	72.6	25	66.7	2	1	0	1544.77	92	104
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	13	14	25	0.02%	27.5%	VGELFQR	99.7%	61.9	25	39.2	2	0	0	848.46	139	145
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	4	5	8	0.01%	14.1%	GAEADQIIEYLK	99.7%	66.4	25	60.4	2	0	0	1349.69	15	26
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	4	5	8	0.01%	14.1%	IGCIITAR	99.7%	71	25	60.3	2	0	0	903.51	159	166
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	4	5	8	0.01%	14.1%	QQSIAGSADSKPIDVSR	99.7%	62.1	25	58.6	1	2	0	1758.90	138	154
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	4	5	8	0.01%	14.1%	QQVSLLK	98.4%	31.7	25	10.8	1	0	0	815.50	27	33
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	5	6	18	0.02%	18.1%	FLFSLFGQK	99.7%	38.7	25	28.1	3	0	0	1086.60	216	224
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	5	6	18	0.02%	18.1%	FSIQTMCPIEGEGNIAR	99.7%	73.3	25	71.4	7	0	0	1938.91	199	215
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	5	6	18	0.02%	18.1%	LLCEHFR	99.4%	36.2	25	22.5	3	0	0	974.49	141	147
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	5	6	18	0.02%	18.1%	SCENLAPFNTALK	99.7%	61.7	25	51.3	2	0	0	1464.72	305	317
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	5	6	18	0.02%	18.1%	VLSTVHTHSSVK	99.7%	41	25	33.2	3	0	0	1294.71	148	159
Anaphase-promoting complex subunit 1	ANAPC1	APC1_HUMAN	216.5	100.0%	2	2	3	0.00%	1.1%	CLILWDDILPNSK	96.3%	28.3	25	19	2	0	0	1586.83	1412	1424
Anaphase-promoting complex subunit 1	ANAPC1	APC1_HUMAN	216.5	100.0%	2	2	3	0.00%	1.1%	LVLEFFSSR	99.7%	59.7	25	48.6	1	0	0	1097.60	1816	1824
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	16	17	29	0.03%	28.9%	AGQERPSVTSYK	99.7%	50.8	25	47.2	2	0	0	1322.67	182	193
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	16	17	29	0.03%	28.9%	AIQLNSNSVQALLLK	99.7%	91.9	25	80.8	2	0	0	1611.94	365	379
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	16	17	29	0.03%	28.9%	AISTICSLEK	98.3%	31.4	25	25.8	2	0	0	1121.59	254	263
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	16	17	29	0.03%	28.9%	ALTQRPDYIK	96.7%	28.7	25	12.1	1	0	0	1204.67	468	477
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	16	17	29	0.03%	28.9%	AYAFVHTGDNSR	99.7%	56.6	25	56.6	2	0	0	1337.62	242	253
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	16	17	29	0.03%	28.9%	DMAAAGLHSNVR	99.7%	56.3	25	50.8	4	0	0	1241.61	43	54

Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	16	17	29	0.03%	28.9%	DNVDLLGSLADLYFR	99.7%	64.7	25	64.7	2	0	0	1710.87	269	283
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	16	17	29	0.03%	28.9%	EAMVMANNVYK	98.9%	33.3	25	28.8	1	0	0	1269.60	425	435
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	16	17	29	0.03%	28.9%	EQKYEDGIALLR	98.9%	33.4	25	31.5	2	0	0	1434.76	489	500
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	16	17	29	0.03%	28.9%	FEQAQMLDPYLIK	99.7%	92.5	25	84.7	2	0	0	1595.81	294	306
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	16	17	29	0.03%	28.9%	GMDVYGYLLAR	99.7%	53.7	25	45.7	2	0	0	1257.63	307	317
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	16	17	29	0.03%	28.9%	LEDVENLGCR	99.7%	67.8	25	62.5	1	0	0	1204.56	321	330
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	16	17	29	0.03%	28.9%	NALANQSDCVLHR	99.7%	53.6	25	53.6	1	0	0	1497.72	501	513
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	16	17	29	0.03%	28.9%	VQEAIIHFR	99.5%	36.4	25	30.3	1	0	0	1112.62	389	397
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	16	17	29	0.03%	28.9%	YEDGIALLR	99.7%	52.1	25	40.3	2	0	0	1049.56	492	500
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	16	17	29	0.03%	28.9%	YTMALQQK	99.6%	37.7	25	26.9	2	0	0	982.50	100	107
Ancient ubiquitous protein 1	AUP1	AUP1_HUMAN	53.0	100.0%	3	3	4	0.00%	8.8%	GTQSLPTASASK	97.5%	29.9	25	22.7	1	0	0	1147.60	414	425
Ancient ubiquitous protein 1	AUP1	AUP1_HUMAN	53.0	100.0%	3	3	4	0.00%	8.8%	LPPTPLLLFPEEEATNGR	99.7%	42.5	25	42.5	1	0	0	1994.06	217	234
Ancient ubiquitous protein 1	AUP1	AUP1_HUMAN	53.0	100.0%	3	3	4	0.00%	8.8%	QLGEANEEFALR	99.7%	55.5	25	48.2	2	0	0	1376.68	298	309
Angio-associated migratory cell protein	AAMP	AAMP_HUMAN	46.7	99.8%	2	2	2	0.00%	5.5%	AVVGYEDGTIR	99.7%	56	25	51.1	1	0	0	1179.60	230	240
Angio-associated migratory cell protein	AAMP	AAMP_HUMAN	46.7	99.8%	2	2	2	0.00%	5.5%	DASLVVTTSGDHK	99.7%	54.2	25	44.9	1	0	0	1329.66	411	423
Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	ANFY1_HUMAN	128.4	100.0%	4	4	7	0.01%	3.5%	ESSSESFISR	99.7%	38.5	25	23.1	1	0	0	1128.52	44	53
Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	ANFY1_HUMAN	128.4	100.0%	4	4	7	0.01%	3.5%	FQLQLLR	99.3%	35.2	25	3.37	2	0	0	917.56	145	151
Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	ANFY1_HUMAN	128.4	100.0%	4	4	7	0.01%	3.5%	GDLFAATFLIK	99.7%	60.4	25	53.4	2	0	0	1195.67	300	310
Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	ANFY1_HUMAN	128.4	100.0%	4	4	7	0.01%	3.5%	TQDGETALQLAIR	99.7%	66	25	53.3	2	0	0	1415.75	652	664
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	16	17	29	0.03%	17.5%	AAMIWIVGEYAER	99.7%	77.6	25	77	2	0	0	1508.76	446	458
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	16	17	29	0.03%	17.5%	CVSTLLDLIQTK	99.7%	82.1	25	60.7	2	0	0	1390.76	391	402
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	16	17	29	0.03%	17.5%	DCEDPNPLIR	99.7%	47.4	25	38.4	2	0	0	1228.56	94	103
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	16	17	29	0.03%	17.5%	DCPLNAEAASSK	99.7%	51.6	25	37.2	2	0	0	1262.57	865	876
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	16	17	29	0.03%	17.5%	DLDYYGTLLK	99.7%	47.9	25	41.3	2	0	0	1200.61	273	282
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	16	17	29	0.03%	17.5%	DLDYYGTLLKK	98.8%	33.1	25	30.4	1	0	0	1328.71	273	283
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	16	17	29	0.03%	17.5%	GLEISGTFTR	99.7%	62.3	25	52.5	2	0	0	1080.57	731	740
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	16	17	29	0.03%	17.5%	ITEYLCEPLRK	99.7%	44.8	25	36.2	1	0	0	1421.75	118	128
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	16	17	29	0.03%	17.5%	KGEIFELK	99.7%	47.8	25	29	1	0	0	963.55	12	19
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	16	17	29	0.03%	17.5%	LASQANIAQVLAELK	99.7%	67.3	25	64.5	2	0	0	1568.90	345	359
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	16	17	29	0.03%	17.5%	LLSTDPVAAK	99.7%	40.9	25	22.1	2	0	0	1014.58	529	538
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	16	17	29	0.03%	17.5%	LQSSNIFTVAK	99.7%	60.2	25	44.6	2	0	0	1207.67	877	887
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	16	17	29	0.03%	17.5%	LSHANSAVVLSAVK	99.7%	65.3	25	65.2	2	1	0	1395.80	248	261
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	16	17	29	0.03%	17.5%	NINLIVQK	99.7%	38.7	25	30.8	2	0	0	941.58	305	312
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	16	17	29	0.03%	17.5%	VNYVVQEAIVVIK	99.7%	45.8	25	40.7	1	0	0	1473.87	403	415
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	16	17	29	0.03%	17.5%	YNDPIYVK	99.5%	37.1	25	28.8	2	0	0	1011.51	328	335
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	10	10	17	0.02%	12.4%	AALCAVHVIR	99.7%	72.7	25	67.6	2	0	0	1109.62	157	166
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	10	10	17	0.02%	12.4%	ADCASGIFLAAEK	99.7%	74.3	25	68.4	2	0	0	1352.65	398	410
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	10	10	17	0.02%	12.4%	DLDVSIKR	98.6%	32.3	25	18.6	1	0	0	945.54	356	363
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	10	10	17	0.02%	12.4%	ELLYFLDSCEPEFK	99.7%	62	25	60.9	2	0	0	1789.84	384	397
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	10	10	17	0.02%	12.4%	GYALTAIMK	99.1%	34.2	25	0	1	0	0	983.52	524	532
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	10	10	17	0.02%	12.4%	IEFTFER	98.9%	33.2	25	29	2	0	0	941.47	717	723
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	10	10	17	0.02%	12.4%	SSFREEDNTYR	95.5%	20.8	25	19.8	0	1	0	1403.62	36	46
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	10	10	17	0.02%	12.4%	TVQTDHNAVQR	99.7%	56	25	38.3	2	0	0	1268.63	335	345
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	10	10	17	0.02%	12.4%	VLAINILGR	99.7%	65.9	25	52.2	2	0	0	968.63	307	315
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	10	10	17	0.02%	12.4%	VLTTAGSYVR	99.7%	85.1	25	71.9	2	0	0	1066.59	425	434
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	10	11	16	0.02%	30.7%	FEIPYFTTSGIQVR	99.7%	114	25	111	2	0	0	1657.86	380	393
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	10	11	16	0.02%	30.7%	HNNLYLVATSK	99.7%	61.5	25	52	2	0	0	1259.67	62	72
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	10	11	16	0.02%	30.7%	ILQEYITQEGHK	99.7%	83.4	25	67.6	2	0	0	1458.76	130	141
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	10	11	16	0.02%	30.7%	LGLNDKVLFDNTGR	99.7%	76.9	25	69.5	1	0	0	1561.83	212	225
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	10	11	16	0.02%	30.7%	SEIVGSIK	97.0%	29.2	25	22.6	1	0	0	832.48	192	199
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	10	11	16	0.02%	30.7%	SGYQALPWVR	98.3%	31.5	25	27.6	1	0	0	1176.62	401	410

AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	10	11	16	0.02%	30.7%	STANNVEIHIPVPNDADSPK	99.7%	32.7	25	32.7	0	1	0	2118.05	305	324
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	10	11	16	0.02%	30.7%	SVELEDVKFHQCVR	96.5%	21.5	25	16.2	0	1	0	1745.86	230	243
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	10	11	16	0.02%	30.7%	TISFIPPDGEFELMSYR	96.3%	28.3	25	28.3	1	0	0	2017.96	252	268
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	10	11	16	0.02%	30.7%	VFLSGMPELR	99.7%	49.5	25	48	4	0	0	1148.61	202	211
AP-1 complex subunit sigma-1A	AP1S1	AP1S1_HUMAN	18.7	100.0%	4	4	8	0.01%	25.3%	AIEQADLLQEEDESPR	99.7%	105	25	105	2	0	0	1842.87	134	149
AP-1 complex subunit sigma-1A	AP1S1	AP1S1_HUMAN	18.7	100.0%	4	4	8	0.01%	25.3%	ELMQVVLAR	99.7%	69.3	25	59.9	2	0	0	1058.60	34	42
AP-1 complex subunit sigma-1A	AP1S1	AP1S1_HUMAN	18.7	100.0%	4	4	8	0.01%	25.3%	FMLLFSR	99.7%	39.5	25	28.6	2	0	0	913.50	4	10
AP-1 complex subunit sigma-1A	AP1S1	AP1S1_HUMAN	18.7	100.0%	4	4	8	0.01%	25.3%	MCSFLEWR	99.1%	34	25	34	2	0	0	1128.50	46	53
AP-1 complex subunit sigma-2	AP1S2	AP1S2_HUMAN	18.6	99.8%	2	2	5	0.00%	21.0%	AIEQADLLQEEAETPR	95.7%	27.8	25	27.8	1	0	0	1812.90	133	148
AP-1 complex subunit sigma-2	AP1S2	AP1S2_HUMAN	18.6	99.8%	2	2	5	0.00%	21.0%	ELVQTVLAR	99.7%	42.1	25	24.6	4	0	0	1028.61	33	41
AP-1 complex subunit sigma-2	AP1S2	AP1S2_HUMAN	18.6	99.8%	2	2	5	0.00%	21.0%	MCSFLEWR	99.1%	34	25	34	2	0	0	1128.50	45	52
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	11	12	19	0.02%	12.9%	ACNQLGQFLQHR	99.7%	38	25	30.8	0	2	0	1471.72	330	341
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	11	12	19	0.02%	12.9%	ALLLSTYIK	99.7%	52.9	25	52.9	2	0	0	1021.63	539	547
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	11	12	19	0.02%	12.9%	ALQVGCLLR	98.1%	30.9	25	22.6	1	0	0	1029.59	936	944
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	11	12	19	0.02%	12.9%	EMGEAFAADIPR	99.7%	46.8	25	46.4	1	0	0	1322.60	142	153
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	11	12	19	0.02%	12.9%	FFQPTEMAAQDFFQR	99.2%	34.5	25	34.5	1	0	0	1862.85	864	878
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	11	12	19	0.02%	12.9%	FINLFPETK	97.5%	29.9	25	22.1	2	0	0	1108.60	548	556
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	11	12	19	0.02%	12.9%	GLAVFISDIR	99.7%	84.5	25	71.9	2	0	0	1090.63	12	21
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	11	12	19	0.02%	12.9%	ILVAGDSMDSVK	99.7%	45.1	25	39.2	3	0	0	1234.63	154	165
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	11	12	19	0.02%	12.9%	TCVSLAVSR	99.7%	40.5	25	17.1	2	0	0	992.52	224	232
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	11	12	19	0.02%	12.9%	VGGYILGEFGNLIAGDPR	99.7%	67.2	25	67.2	2	0	0	1847.97	499	516
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	11	12	19	0.02%	12.9%	YGGAPQALTLK	94.5%	26.8	25	8.66	1	0	0	1118.62	846	856
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	8	8	13	0.01%	15.8%	ACNQLGQFLQHR	99.7%	38	25	30.8	0	2	0	1471.72	329	340
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	8	8	13	0.01%	15.8%	ALLLSTYIK	99.7%	52.9	25	52.9	2	0	0	1021.63	538	546
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	8	8	13	0.01%	15.8%	AVDLLYAMCDR	99.7%	58.7	25	56.5	1	0	0	1326.62	388	398
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	8	8	13	0.01%	15.8%	EMAEAFAGEIPK	99.7%	73.5	25	66.6	1	0	0	1292.62	142	153
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	8	8	13	0.01%	15.8%	FFQPTEMASQDFFQR	99.7%	69.5	25	23	2	0	0	1878.85	826	840
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	8	8	13	0.01%	15.8%	GLAVFISDIR	99.7%	84.5	25	71.9	2	0	0	1090.63	12	21
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	8	8	13	0.01%	15.8%	LTECLETILNK	99.7%	70.1	25	60.2	1	0	0	1333.70	279	289
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	8	8	13	0.01%	15.8%	THIETVINALK	99.7%	51.8	25	49.4	2	0	0	1238.71	367	377
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	8	8	13	0.01%	15.8%	TTQIGCLLR	99.7%	52.6	25	34.6	2	0	0	1061.58	898	906
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	8	8	13	0.01%	15.8%	VGGYILGEFGNLIAGDPR	99.7%	67.2	25	67.2	2	0	0	1847.97	498	515
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	8	8	13	0.01%	15.8%	VLVAGDTMDSVK	99.7%	54.2	25	53.9	2	0	0	1234.63	154	165
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	8	8	13	0.01%	15.8%	YGGTFQNVSVQLPITLNK	99.7%	93.9	25	93.9	2	0	0	1979.06	808	825
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	8	8	14	0.01%	20.0%	IPTPLNTSGVQVICMK	97.5%	29.8	25	29.8	1	0	0	1757.93	324	339
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	8	8	14	0.01%	20.0%	LNYSDHDVIK	99.7%	52.5	25	44.2	2	0	0	1203.60	411	420
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	8	8	14	0.01%	20.0%	MCDVMAAYFGK	99.7%	67.4	25	67.4	2	0	0	1292.55	85	95
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	8	8	14	0.01%	20.0%	SISFIPPDGEFELMR	99.7%	39.1	25	37.5	1	0	0	1737.85	262	276
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	8	8	14	0.01%	20.0%	SNFKPSLLAQK	99.7%	48.1	25	39.7	2	0	0	1232.70	309	319
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	8	8	14	0.01%	20.0%	SPVTNIAR	99.7%	39.6	25	26.8	2	0	0	857.48	45	52
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	8	8	14	0.01%	20.0%	TFITQQGIK	99.7%	43.9	25	36.3	2	0	0	1035.58	131	139
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	8	8	14	0.01%	20.0%	VNVIHAR	99.1%	34.2	25	31.6	2	0	0	808.48	34	40
AP-2 complex subunit sigma	AP2S1	AP2S1_HUMAN	17.0	100.0%	3	3	4	0.00%	22.5%	HTNFVEFR	97.4%	29.8	25	21.9	1	0	0	1049.52	46	53
AP-2 complex subunit sigma	AP2S1	AP2S1_HUMAN	17.0	100.0%	3	3	4	0.00%	22.5%	QLLMLQSLE	99.3%	35.1	25	28.4	2	0	0	1090.58	134	142
AP-2 complex subunit sigma	AP2S1	AP2S1_HUMAN	17.0	100.0%	3	3	4	0.00%	22.5%	VYTVVDEMFLAGEIR	99.7%	50.2	25	39.5	1	0	0	1741.88	110	124
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	24	0.02%	11.2%	ASILWLIGENCER	99.7%	67.7	25	67.7	2	0	0	1560.78	497	509
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	24	0.02%	11.2%	KIENIHIGEK	99.7%	45.7	25	38.1	1	0	0	1180.67	913	922
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	24	0.02%	11.2%	LLDSITVPVAR	99.7%	61.1	25	58.3	2	0	0	1183.70	486	496
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	24	0.02%	11.2%	LLTQYILNLGK	99.7%	74.2	25	69.7	6	0	0	1275.77	553	563
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	24	0.02%	11.2%	LQILNLGAK	99.7%	57.4	25	46.3	2	0	0	969.61	534	542
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	24	0.02%	11.2%	LYSLDPEQK	99.4%	36	25	28.1	1	0	0	1092.56	177	185

AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	24	0.02%	11.2%	NASELFPAVVK	99.7%	55.7	25	46.2	2	0	0	1174.65	75	85
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	24	0.02%	11.2%	NVEVIELAK	99.6%	37.6	25	36.5	1	0	0	1014.58	650	658
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	24	0.02%	11.2%	QFAAATIQTIGR	99.7%	92.9	25	87.7	2	0	0	1276.70	419	430
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	24	0.02%	11.2%	SFTSEDDLVK	97.8%	30.4	25	22.3	1	0	0	1140.54	524	533
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	24	0.02%	11.2%	TVIGSVLLR	99.7%	45.2	25	37.2	2	0	0	957.61	1077	1085
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	24	0.02%	11.2%	YDQNYDIR	99.7%	59.1	25	43.2	2	0	0	1086.49	564	571
AP-3 complex subunit sigma-1	AP3S1	AP3S1_HUMAN	21.7	100.0%	4	5	10	0.01%	23.3%	FYQPYSEDTQQQIIR	99.7%	81	25	72.8	2	0	0	1915.92	19	33
AP-3 complex subunit sigma-1	AP3S1	AP3S1_HUMAN	21.7	100.0%	4	5	10	0.01%	23.3%	NINIGDISIK	99.7%	41	25	25.7	2	0	0	1086.62	176	185
AP-3 complex subunit sigma-1	AP3S1	AP3S1_HUMAN	21.7	100.0%	4	5	10	0.01%	23.3%	NMNLPEIPR	99.2%	34.9	25	24.8	4	0	0	1099.56	167	175
AP-3 complex subunit sigma-1	AP3S1	AP3S1_HUMAN	21.7	100.0%	4	5	10	0.01%	23.3%	SEAGLAGAPAR	99.7%	62.4	25	48	2	0	0	999.52	150	160
Apolipoprotein O-like	APOOL	APOOL_HUMAN	29.2	100.0%	3	4	7	0.01%	16.0%	HSVPLPTELSSEAK	99.7%	41.8	25	41	2	0	0	1494.78	219	232
Apolipoprotein O-like	APOOL	APOOL_HUMAN	29.2	100.0%	3	4	7	0.01%	16.0%	MGVITVSGLAGLVSAR	99.7%	66.8	25	66.8	4	0	0	1530.87	115	130
Apolipoprotein O-like	APOOL	APOOL_HUMAN	29.2	100.0%	3	4	7	0.01%	16.0%	VYATSQQIFGAVK	99.7%	53.9	25	47.8	1	0	0	1411.76	168	180
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	42	0.04%	35.4%	AALSASEGEEVPQDK	99.7%	63.4	25	59.3	2	0	0	1530.73	113	127
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	42	0.04%	35.4%	ALGTEVIQLFPEK	99.7%	86.1	25	82.2	3	0	0	1444.80	325	337
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	42	0.04%	35.4%	CLIATGGTPR	99.7%	55.1	25	35.9	2	0	0	1045.55	256	265
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	42	0.04%	35.4%	DGEQHEDLNEVAK	99.7%	53.6	25	52.9	2	0	0	1483.67	594	606
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	42	0.04%	35.4%	ELWFSDDPNVTK	99.7%	44.2	25	40.6	2	0	0	1450.69	178	189
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	42	0.04%	35.4%	ILPEYLSNWTMEK	99.7%	79.8	25	79.8	4	0	0	1639.80	343	355
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	42	0.04%	35.4%	ISGLGLTPEQK	99.7%	58.5	25	45.7	3	0	0	1142.64	99	109
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	42	0.04%	35.4%	KVVQLDVR	98.2%	31.3	25	15.3	2	0	0	956.59	232	239
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	42	0.04%	35.4%	LFNIHED	98.0%	30.7	25	30.7	2	0	0	887.43	607	613
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	42	0.04%	35.4%	LNDGSQITYEK	99.7%	65.7	25	58.3	3	0	0	1267.62	245	255
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	42	0.04%	35.4%	SATEQSGTGIR	99.7%	65.7	25	41.7	2	0	0	1106.54	519	529
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	42	0.04%	35.4%	SNIWVAGDAACFYDIK	99.7%	94.9	25	94.9	2	0	0	1829.85	431	446
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	42	0.04%	35.4%	TGGLEIDSDFGGFR	99.7%	76.1	25	76.1	2	0	0	1470.69	409	422
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	42	0.04%	35.4%	VETDHIVAAVGLEPNVELAK	99.7%	38	25	38	0	1	0	2104.13	389	408
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	42	0.04%	35.4%	VLIVSEDPELPYMRPPLSK	99.7%	47.5	25	47.5	0	2	0	2183.18	159	177
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	42	0.04%	35.4%	VMPNAIVQSVGVSSGK	99.7%	114	25	103	4	0	0	1572.84	363	378
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	42	0.04%	35.4%	VNAELQAR	99.7%	48.2	25	37.3	2	0	0	900.49	423	430
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	20	42	0.04%	35.4%	VVQLDVR	99.5%	37.1	25	29.1	2	0	0	828.49	233	239
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	5	5	6	0.01%	4.3%	GLLVDRPSETK	98.8%	32.8	25	20.1	1	0	0	1214.67	1097	1107
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	5	5	6	0.01%	4.3%	GVPAGNSDTEGGQPGR	99.7%	50.7	25	50.7	2	0	0	1498.69	832	847
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	5	5	6	0.01%	4.3%	SQEQEVLER	99.6%	37.5	25	21.9	1	0	0	1117.55	328	336
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	5	5	6	0.01%	4.3%	TGTLVEEAFWIDK	99.7%	67	25	62.6	1	0	0	1508.76	1035	1047
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	5	5	6	0.01%	4.3%	VTLGDTLTR	99.7%	46.3	25	36.9	1	0	0	975.55	971	979
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	20	25	66	0.07%	34.1%	AAYPDLENPPLLVTPSQQAK	99.7%	70.2	25	70.2	4	0	0	2152.13	90	109
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	20	25	66	0.07%	34.1%	AYQCVVLLQGK	99.7%	75	25	47.4	4	0	0	1278.69	290	300
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	20	25	66	0.07%	34.1%	FPEILQK	99.7%	39.5	25	1.24	2	0	0	874.50	581	587
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	20	25	66	0.07%	34.1%	GESFYQDR	98.3%	31.4	25	31.4	2	0	0	1001.43	334	341
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	20	25	66	0.07%	34.1%	GFDILGIKPVQR	99.7%	40.6	25	29.7	2	1	0	1342.78	648	659
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	20	25	66	0.07%	34.1%	GFVQVDDGRK	99.7%	40.8	25	27.2	2	0	0	1120.57	353	362
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	20	25	66	0.07%	34.1%	GNTAAYLLYAFTR	99.7%	40.9	25	32.1	2	0	0	1460.75	528	540
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	20	25	66	0.07%	34.1%	IVFVPGCSIPLTIVK	99.7%	59.3	25	51.4	2	0	0	1642.96	363	377
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	20	25	66	0.07%	34.1%	LANIDEEMLQK	99.7%	69.1	25	58.2	4	0	0	1303.66	547	557
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	20	25	66	0.07%	34.1%	LFEFAGYDVLR	99.7%	87.7	25	76.4	2	0	0	1329.68	224	234
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	20	25	66	0.07%	34.1%	LLQQEEEIK	99.7%	51.5	25	34.6	2	0	0	1129.61	12	20
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	20	25	66	0.07%	34.1%	LMDLLGEGLKR	99.7%	47.1	25	40.6	2	1	0	1244.70	462	472
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	20	25	66	0.07%	34.1%	LNDYIFSFDK	99.7%	66	25	62.2	4	0	0	1261.61	513	522
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	20	25	66	0.07%	34.1%	MLLCEAVAAVMAK	99.7%	86.8	25	79.5	10	0	0	1422.72	635	647
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	20	25	66	0.07%	34.1%	NMINIISR	99.7%	47.7	25	34.7	2	0	0	960.53	72	79

Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	20	25	66	0.07%	34.1%	SDGGYTYDTSDLAAIK	99.7%	112	25	106	4	0	0	1676.77	378	393
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	20	25	66	0.07%	34.1%	SLTAEIDR	99.7%	43.7	25	28.6	2	0	0	904.47	21	28
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	20	25	66	0.07%	34.1%	STIIGESISR	99.7%	75.5	25	57.8	5	0	0	1062.58	214	223
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	20	25	66	0.07%	34.1%	VEIAGPGFINVHLR	99.7%	63.4	25	63.4	2	1	0	1521.85	154	167
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	20	25	66	0.07%	34.1%	YADLSHNR	99.7%	54.1	25	47.9	4	0	0	975.46	505	512
Argininosuccinate synthase	ASS1	ASSY_HUMAN	46.5	100.0%	4	4	6	0.01%	8.7%	FELSCYSLAPQIK	99.7%	41.5	25	30.5	2	0	0	1555.78	128	140
Argininosuccinate synthase	ASS1	ASSY_HUMAN	46.5	100.0%	4	4	6	0.01%	8.7%	GQVYILGR	99.7%	40.3	25	23	2	0	0	905.52	356	363
Argininosuccinate synthase	ASS1	ASSY_HUMAN	46.5	100.0%	4	4	6	0.01%	8.7%	MPEFYNR	97.2%	29.3	25	27.8	1	0	0	956.43	147	153
Argininosuccinate synthase	ASS1	ASSY_HUMAN	46.5	100.0%	4	4	6	0.01%	8.7%	VFIEDVSR	99.7%	46.7	25	35.5	1	0	0	964.51	59	66
Armadillo repeat-containing protein 6	ARMC6	ARMC6_HUMAN	54.1	100.0%	4	4	6	0.01%	10.2%	AIAGNDDVKDAIVR	99.7%	84.8	25	79	1	0	0	1456.78	353	366
Armadillo repeat-containing protein 6	ARMC6	ARMC6_HUMAN	54.1	100.0%	4	4	6	0.01%	10.2%	DQSGVQELVK	99.5%	37.2	25	23.1	1	0	0	1102.57	336	345
Armadillo repeat-containing protein 6	ARMC6	ARMC6_HUMAN	54.1	100.0%	4	4	6	0.01%	10.2%	GAYPIIFTAWK	99.7%	54	25	52.9	2	0	0	1266.69	135	145
Armadillo repeat-containing protein 6	ARMC6	ARMC6_HUMAN	54.1	100.0%	4	4	6	0.01%	10.2%	IIVEGGGAVAALQAMK	99.7%	85.5	25	83.6	2	0	0	1527.86	407	422
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	22	37	0.04%	37.8%	ADWLSHYWMPK	99.7%	39.6	25	37.9	2	0	0	1433.67	530	540
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	22	37	0.04%	37.8%	AMTEDGFLAVCSEAK	99.7%	101	25	101	4	0	0	1628.73	148	162
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	22	37	0.04%	37.8%	APSPEKAEEESER	99.7%	68.4	25	68.4	2	2	0	1458.67	380	392
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	22	37	0.04%	37.8%	ASVGMYLISK	99.4%	35.9	25	31.6	2	0	0	1084.57	341	350
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	22	37	0.04%	37.8%	DVPLHALYDNVEK	99.7%	82.4	25	82.4	2	0	0	1512.77	209	221
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	22	37	0.04%	37.8%	EAFSDGITSVK	99.7%	71.7	25	67.8	2	0	0	1153.57	468	478
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	22	37	0.04%	37.8%	ELYLFDVLR	99.7%	68.1	25	52.9	2	0	0	1167.64	396	404
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	22	37	0.04%	37.8%	ETFEDSNLIPK	99.7%	39	25	34.9	1	0	0	1292.64	450	460
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	22	37	0.04%	37.8%	FSSYYLSLPPEMR	99.7%	65.1	25	64.1	1	0	0	1589.77	425	437
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	22	37	0.04%	37.8%	HSATPFLK	98.4%	31.6	25	21.7	1	0	0	900.49	169	176
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	22	37	0.04%	37.8%	IGCLLSGGLDSSLVAATLLK	99.7%	85.4	25	85.4	2	0	0	1988.11	253	272
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	22	37	0.04%	37.8%	ILFNNAVK	97.9%	30.5	25	5.45	2	0	0	918.54	237	244
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	22	37	0.04%	37.8%	ILQEYVEHQVDDAMMANAAQK	99.7%	66.9	25	66.9	0	1	0	2436.12	484	504
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	22	37	0.04%	37.8%	LAVVDPLFGMQPIR	99.7%	63.8	25	60.9	4	0	0	1571.86	50	63
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	22	37	0.04%	37.8%	TTAAHGLELR	99.7%	59.8	25	43.8	1	0	0	1068.58	408	417
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	22	37	0.04%	37.8%	VASVEMVK	99.3%	35	25	20.3	3	0	0	878.47	196	203
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	22	37	0.04%	37.8%	VPFLDHR	99.2%	34.9	25	23.9	1	0	0	883.48	418	424
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	22	37	0.04%	37.8%	WINATDPSAR	99.6%	38.3	25	38.3	2	0	0	1130.56	541	550
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	8	8	13	0.01%	19.8%	ASAELALGENSEVLK	99.7%	57.8	25	52.1	1	0	0	1530.80	108	122
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	8	8	13	0.01%	19.8%	DAGMQLQGYR	99.7%	43.5	25	36.3	1	0	0	1154.53	171	180
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	8	8	13	0.01%	19.8%	FVTVQTISGTGALR	99.7%	104	25	98.9	2	0	0	1449.81	126	139
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	8	8	13	0.01%	19.8%	IAAAILNTPDLR	99.7%	63.2	25	45.7	2	0	0	1267.74	326	337
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	8	8	13	0.01%	19.8%	IAAAILNTPDLRK	99.7%	61.4	25	61.4	2	0	0	1395.83	326	338
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	8	8	13	0.01%	19.8%	TCGFDFTGAVEDISK	99.7%	74.7	25	68.3	1	0	0	1646.74	186	200
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	8	8	13	0.01%	19.8%	TQLVSNLKK	97.9%	30.6	25	26.5	2	0	0	1030.63	356	364
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	8	8	13	0.01%	19.8%	VGAFTMVCK	99.7%	47.9	25	45.5	2	0	0	1012.50	288	296
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	55	0.05%	52.7%	ADEVVWVR	99.7%	72.3	25	60.4	2	0	0	973.51	56	63
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	55	0.05%	52.7%	ALHHGIDLEK	97.0%	29.1	25	19.6	1	0	0	1132.61	442	451
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	55	0.05%	52.7%	ESIVDVEGVVR	99.7%	90.8	25	84.1	2	0	0	1201.64	111	121
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	55	0.05%	52.7%	FGAPPHAGGGIGLER	99.7%	44.8	25	28	0	2	0	1435.74	461	475
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	55	0.05%	52.7%	FLEPTLR	99.4%	36.3	25	21.8	2	0	0	875.50	339	345
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	55	0.05%	52.7%	GEEILSGAQR	99.7%	76.6	25	42.2	2	0	0	1059.54	422	431
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	55	0.05%	52.7%	GFVEIQTPK	99.7%	50.1	25	31.9	4	0	0	1018.56	214	222
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	55	0.05%	52.7%	IGSCTQQDVELHVQK	99.7%	81.8	25	81.8	1	2	0	1741.85	127	141
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	55	0.05%	52.7%	IHDPQLLTER	99.7%	32.2	25	20.4	0	2	0	1221.66	432	441
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	55	0.05%	52.7%	IYVISLAEPR	99.7%	42.7	25	37.5	2	0	0	1160.67	142	151
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	55	0.05%	52.7%	LEYCEALAMLR	99.7%	64.3	25	59	2	0	0	1368.67	346	356
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	55	0.05%	52.7%	LPLQLDDAVRPEAEGEEEGR	99.7%	54.3	25	53.3	2	2	0	2223.09	152	171

Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	55	0.05%	52.7%	LQSGICHLFR	99.7%	62.2	25	57.3	2	1	0	1230.64	198	207
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	55	0.05%	52.7%	NNAYLAQSPQLYK	99.7%	73.5	25	66.8	2	0	0	1509.77	242	254
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	55	0.05%	52.7%	QCFLVLR	99.7%	48.6	25	19.2	2	0	0	935.51	75	81
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	55	0.05%	52.7%	QMCICADFEK	99.7%	53.9	25	51.5	1	0	0	1301.53	255	264
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	55	0.05%	52.7%	QQQFNVQALVAVGDHASK	99.7%	44.6	25	44.6	0	2	0	1940.00	82	99
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	55	0.05%	52.7%	QSNSYDMFMR	99.7%	60.7	25	60.7	2	0	0	1278.52	412	421
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	55	0.05%	52.7%	QTSMFPR	99.2%	34.8	25	22.6	1	0	0	882.41	488	494
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	55	0.05%	52.7%	TSTSQAVFR	99.7%	78.9	25	63.4	2	0	0	996.51	189	197
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	55	0.05%	52.7%	VFSIGPVFR	99.7%	55.8	25	50.9	3	0	0	1021.58	265	273
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	55	0.05%	52.7%	VRDLTIQK	96.4%	28.4	25	15.1	1	0	0	972.58	48	55
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	55	0.05%	52.7%	VTMLFLGLHNVR	99.7%	64.8	25	63.7	4	2	0	1399.79	476	487
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	24	30	55	0.05%	52.7%	YGISSMIQSQEKPDR	99.7%	63.5	25	59.7	1	1	0	1754.84	29	43
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	10	11	18	0.02%	28.4%	AEGDISNVANGFK	99.7%	57.4	25	52.1	1	0	0	1321.64	359	371
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	10	11	18	0.02%	28.4%	ETTNIFSNCGCVR	99.7%	54.1	25	54.1	2	0	0	1557.68	346	358
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	10	11	18	0.02%	28.4%	ITSDEPLTKDDIPVFLR	99.7%	43.4	25	36	0	2	0	1959.04	254	270
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	10	11	18	0.02%	28.4%	LASEEPPDDEEALATIR	99.7%	78.6	25	75.1	1	0	0	1855.89	289	305
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	10	11	18	0.02%	28.4%	LIGNLCYK	99.7%	40.6	25	34	2	0	0	980.52	377	384
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	10	11	18	0.02%	28.4%	LSGVMVPAPIQDLEALR	99.2%	34.4	25	33.9	2	0	0	1824.99	11	27
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	10	11	18	0.02%	28.4%	NACIECSVNQNSIR	99.7%	75.3	25	70.4	2	0	0	1664.75	90	103
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	10	11	18	0.02%	28.4%	NLTEDNSQNQDLIAK	99.7%	70	25	70	1	0	0	1702.82	424	438
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	10	11	18	0.02%	28.4%	SPELVQAMFPK	99.7%	76.8	25	69.8	1	0	0	1262.65	227	237
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	10	11	18	0.02%	28.4%	VTLLDLMIAK	99.7%	62.1	25	51.6	4	0	0	1116.67	244	253
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	7	10	20	0.02%	39.1%	HVVQSISTQQEK	99.7%	59.8	25	53.7	1	0	0	1383.72	222	233
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	7	10	20	0.02%	39.1%	HYLFDVQR	99.6%	37.9	25	29.3	2	0	0	1077.55	164	171
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	7	10	20	0.02%	39.1%	NRLDYHISVQNMMR	99.7%	29.1	25	29.1	0	2	0	1776.86	195	208
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	7	10	20	0.02%	39.1%	QASIQHIQNAIDTEK	99.7%	68.8	25	65.2	2	2	0	1695.87	140	154
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	7	10	20	0.02%	39.1%	TGVTGPYVLGTGLILYALSK	99.7%	96.1	25	96.1	2	2	0	2023.15	71	90
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	7	10	20	0.02%	39.1%	YGLIPEEFFQFLYPK	99.7%	55.7	25	55.7	3	0	0	1890.97	56	70
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	7	10	20	0.02%	39.1%	YGPFVADFADKLNEQK	99.7%	45.9	25	43.2	2	2	0	1841.91	116	131
ATP synthase mitochondrial F1 complex assembly factor 2	ATPAF2	ATPF2_HUMAN	32.8	99.8%	2	2	3	0.00%	7.3%	LEEEYQIQK	99.7%	40.1	25	33.3	2	0	0	1179.59	239	247
ATP synthase mitochondrial F1 complex assembly factor 2	ATPAF2	ATPF2_HUMAN	32.8	99.8%	2	2	3	0.00%	7.3%	VEEPETLVELQR	99.7%	42.3	25	42.1	1	0	0	1441.75	144	155
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	AVDSLVPIGR	99.7%	70.2	25	70.2	11	0	0	1026.59	195	204
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	EAYPGDVFYLHSR	99.7%	82.3	25	73.3	8	2	0	1553.74	335	347
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	EIVTNFLAGFEA	99.7%	79.9	25	79.9	3	0	0	1310.66	542	553
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	ELIIGDR	99.0%	33.8	25	21.9	2	0	0	815.46	208	214
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	EPMQTGIK	99.7%	43.4	25	27.8	2	0	0	903.46	187	194
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	EVAAFAQFGSDLDAATQQLLSR	99.7%	123	25	123	6	7	0	2338.17	442	463
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	FENAFLSHVVSQHQALLGTIR	99.7%	71.3	25	71.3	0	2	0	2367.26	507	527
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	GIRPAINVGLSVSR	99.7%	55.3	25	55.3	1	2	0	1438.85	403	416
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	GMSLNLEPDNVGVVVFGNDK	99.7%	98.3	25	98	6	0	0	2104.04	104	123
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	GYLDKLEPSK	99.7%	48.4	25	39.2	5	0	0	1149.62	494	503
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	HALIIYDDLSK	99.7%	72	25	70.3	4	0	0	1287.69	306	316
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	ILGADTSVDLEETGR	99.7%	125	25	124	10	0	0	1575.79	59	73
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	ISVREPMQTGIK	99.7%	39.4	25	30	3	2	0	1358.75	183	194
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	LELAQYR	99.5%	37	25	21.4	2	0	0	892.49	435	441
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	LKEIVTNFLAGFEA	99.7%	102	25	102	5	0	0	1551.84	540	553
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	LTDADAMK	98.0%	30.8	25	21.1	1	0	0	880.41	263	270
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	LYCIYVAIGQK	99.7%	69.7	25	65.4	5	0	0	1327.71	242	252
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	NVQAEEMVEFSSGLK	99.7%	108	25	108	5	0	0	1667.79	89	103
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	QGQYSPMAIEEQVAVIYAGVR	99.7%	129	25	124	5	3	0	2309.16	473	493
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	QMSLLLR	98.8%	32.9	25	10.8	5	0	0	876.50	323	329

ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	QVAGTMKLELAQYR	99.7%	47.1	25	47.1	0	2	0	1623.85	428	441
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	RLTDADAMK	99.7%	46.5	25	26.3	2	0	0	1020.51	262	270
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	RSTVAQLVK	99.7%	38.9	25	23	1	0	0	1001.61	253	261
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	STVAQLVK	99.7%	71.2	25	45.7	4	0	0	845.51	254	261
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	TGAIVDVPVGEELLGR	99.7%	94.8	25	84.2	15	0	0	1624.89	134	149
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	TGTAEMSSILEER	99.7%	95.2	25	79.4	9	0	0	1423.67	46	58
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	TSIAIDTIINQK	99.7%	100	25	77.7	6	0	0	1316.74	219	230
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	TSIAIDTIINQKR	99.7%	66.6	25	63.3	2	1	0	1472.84	219	231
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	VLSIGDGIAR	99.7%	70.3	25	55.7	13	0	0	1000.58	74	83
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	VVDALGNAIDGK	99.7%	71.9	25	66.7	6	0	0	1171.63	150	161
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	31	44	180	0.18%	58.8%	VVDALGNAIDGKGPIGSK	99.7%	82.3	25	82.3	9	3	0	1710.94	150	167
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	46	207	0.21%	73.2%	AHGGYSVFAGVGER	99.7%	93.9	25	91.6	6	6	0	1406.68	226	239
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	46	207	0.21%	73.2%	AIAELGIYPAVDPLDSTSR	99.7%	87.3	25	85.3	11	0	0	1988.03	388	406
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	46	207	0.21%	73.2%	DQEGQDVLLFIDNIFR	99.7%	97	25	97	2	0	0	1921.97	295	310
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	46	207	0.21%	73.2%	EGNDLYHEMIESGVINLK	99.7%	74.2	25	65.2	2	2	0	2061.00	242	259
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	46	207	0.21%	73.2%	FLSQPFQVAEVFTGHMGK	99.7%	51.9	25	49.1	3	5	0	2023.01	463	480
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	46	207	0.21%	73.2%	FTQAGSEVSALLGR	99.7%	108	25	93.9	11	0	0	1435.75	311	324
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	46	207	0.21%	73.2%	GFQQILAGEYDHLPEQAFYMVGPIEEAVAK	99.7%	86.6	25	86.6	0	5	0	3366.64	490	519
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	46	207	0.21%	73.2%	GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	99.7%	48.3	25	48.3	0	1	0	3714.89	352	387
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	46	207	0.21%	73.2%	IGLFGGAGVGK	99.7%	52.4	25	43	8	0	0	975.56	202	212
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	46	207	0.21%	73.2%	IMDPNIVGSEHYDVAR	99.7%	89.8	25	87.6	9	6	0	1815.87	407	422
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	46	207	0.21%	73.2%	IMNVIGEPIDER	99.7%	67.5	25	58.6	8	0	0	1385.71	144	155
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	46	207	0.21%	73.2%	IMNVIGEPIDERGPIK	99.7%	47.3	25	31.8	5	3	0	1780.96	144	159
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	46	207	0.21%	73.2%	IPSAVGYQPTLATDMGTMQER	99.7%	91.3	25	91.3	5	4	0	2266.08	325	345
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	46	207	0.21%	73.2%	IPVGPETLGR	99.7%	59.7	25	53.4	2	0	0	1038.59	134	143
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	46	207	0.21%	73.2%	KGSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	99.7%	88.7	25	88.7	0	2	0	3842.98	351	387
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	46	207	0.21%	73.2%	LVLEVAQHLGESTVR	99.7%	106	25	106	6	4	0	1650.92	95	109
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	46	207	0.21%	73.2%	LVPLKETIK	98.6%	32.2	25	28.1	2	0	0	1040.67	481	489
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	46	207	0.21%	73.2%	QFAPIHAEAPEFMEMSVEQEILVTGIK	99.7%	38.3	25	32.8	0	2	0	3044.51	162	188
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	46	207	0.21%	73.2%	SLQDIIAILGMDELSEEDKLTVSR	99.7%	82.9	25	82.9	0	4	0	2691.38	433	456
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	46	207	0.21%	73.2%	TIAMDGTEGLVR	99.7%	73.2	25	58.3	14	0	0	1262.64	110	121
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	46	207	0.21%	73.2%	TVLIMELINNVAK	99.7%	94	25	78	21	0	0	1457.84	213	225
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	46	207	0.21%	73.2%	VALTGLTVAEYFR	99.7%	95	25	76.6	6	0	0	1439.79	282	294
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	46	207	0.21%	73.2%	VALVYGQMNEPPGAR	99.7%	111	25	100	17	0	0	1601.81	265	279
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	46	207	0.21%	73.2%	VLDSGAPIK	99.7%	64.1	25	51.4	6	0	0	899.52	125	133
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	46	207	0.21%	73.2%	VLDSGAPIKIPVGPETLGR	99.7%	83.4	25	82.1	6	6	0	1919.10	125	143
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	46	207	0.21%	73.2%	VVDLLAPYAK	99.7%	54.7	25	52.4	7	0	0	1088.64	189	198
ATP synthase subunit e, mitochondrial	ATP5I	ATP5I_HUMAN	7.9	100.0%	4	4	7	0.01%	60.9%	ELAEDDSILK	98.4%	31.7	25	20.4	1	0	0	1132.57	60	69
ATP synthase subunit e, mitochondrial	ATP5I	ATP5I_HUMAN	7.9	100.0%	4	4	7	0.01%	60.9%	VPPVQVSPLIK	99.5%	36.8	25	36.8	2	0	0	1176.74	2	12
ATP synthase subunit e, mitochondrial	ATP5I	ATP5I_HUMAN	7.9	100.0%	4	4	7	0.01%	60.9%	YNYLKPR	99.7%	42.2	25	31.8	2	0	0	953.52	30	36
ATP synthase subunit e, mitochondrial	ATP5I	ATP5I_HUMAN	7.9	100.0%	4	4	7	0.01%	60.9%	YSALFLGVAYGATR	99.7%	67.4	25	65.3	2	0	0	1488.78	16	29
ATP synthase subunit f, mitochondrial	ATP5J2	ATPK_HUMAN	10.9	100.0%	3	4	15	0.01%	35.1%	DFSPSGIFGAFQR	99.7%	57.2	25	54.4	6	0	0	1428.69	34	46
ATP synthase subunit f, mitochondrial	ATP5J2	ATPK_HUMAN	10.9	100.0%	3	4	15	0.01%	35.1%	LGELPSWILMR	99.7%	62.7	25	59.7	8	0	0	1330.72	23	33
ATP synthase subunit f, mitochondrial	ATP5J2	ATPK_HUMAN	10.9	100.0%	3	4	15	0.01%	35.1%	YYNKYINVK	99.7%	40.9	25	30.4	1	0	0	1204.64	51	59
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	28	0.03%	47.6%	IVNSAQTGSFK	99.7%	74.9	25	58.9	5	0	0	1151.61	56	66
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	28	0.03%	47.6%	KIVNSAQTGSFK	99.7%	51.1	25	50	2	0	0	1279.70	55	66
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	28	0.03%	47.6%	LATFWYYAK	99.7%	42.5	25	38	5	0	0	1162.59	27	35
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	28	0.03%	47.6%	TPALVNAAVTYSKPR	99.7%	56.4	25	56.4	6	5	0	1587.89	12	26
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	28	0.03%	47.6%	VELVPPTPAEIPR	99.7%	51.8	25	41.7	5	0	0	1417.81	36	48
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	36	0.04%	32.2%	ELIEIISGAAALD	99.7%	62.7	25	62.7	1	0	0	1314.72	286	298
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	36	0.04%	32.2%	EVMLVGIGDK	99.7%	41.9	25	33.3	3	0	0	1076.57	127	136

ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	36	0.04%	32.2%	EVMLVGIGDKIR	99.7%	80.7	25	65.8	4	0	0	1329.76	127	138
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	36	0.04%	32.2%	GLCGAIHSSIAK	99.7%	65	25	62.5	2	1	0	1213.64	101	112
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	36	0.04%	32.2%	HLLIGVSSDR	99.7%	64.6	25	55.3	4	0	0	1096.61	91	100
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	36	0.04%	32.2%	IYGLGSLALYEK	99.7%	88.8	25	82.5	6	0	0	1326.73	68	79
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	36	0.04%	32.2%	LTLTFNR	97.1%	29.3	25	14.4	1	0	0	864.49	271	277
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	36	0.04%	32.2%	NASEMIDKLTLTFNR	99.7%	86.7	25	86.1	3	2	0	1752.90	263	277
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	36	0.04%	32.2%	SEVATLTAAGK	99.7%	74.1	25	57.9	4	0	0	1047.57	116	126
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	36	0.04%	32.2%	THSDQFLVAFK	99.7%	76.7	25	65.1	3	2	0	1292.66	144	154
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	8	11	21	0.02%	45.1%	LSNTQGVVSAFSTMMSVHR	99.1%	34.2	25	31.7	1	1	0	2083.99	118	136
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	8	11	21	0.02%	45.1%	LVRPPVQVYGIEGR	99.2%	26	25	26	2	1	0	1582.91	27	40
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	8	11	21	0.02%	45.1%	SFLSQGQVLK	99.7%	67.1	25	57.7	2	0	0	1106.62	163	172
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	8	11	21	0.02%	45.1%	SLNDITAKER	99.7%	48.1	25	36.9	2	0	0	1146.61	91	100
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	8	11	21	0.02%	45.1%	TDPSILGGMIVR	99.7%	63.1	25	53.7	4	0	0	1274.68	177	188
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	8	11	21	0.02%	45.1%	VAASVLNPYVK	99.7%	71.1	25	64.3	2	0	0	1160.67	74	84
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	8	11	21	0.02%	45.1%	VAQILKEPK	99.7%	49.4	25	36.7	2	0	0	1025.64	65	73
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	8	11	21	0.02%	45.1%	YATALYSAASK	99.7%	96.1	25	85.6	4	0	0	1145.58	41	51
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	24	27	60	0.06%	42.6%	AEGPGRGDEPSPS	99.7%	51.7	25	51.2	2	0	0	1255.56	622	634
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	24	27	60	0.06%	42.6%	AERENADIIR	97.4%	29.6	25	12.2	1	0	0	1186.62	247	256
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	24	27	60	0.06%	42.6%	ATLNAFLYR	99.7%	71	25	60.2	2	0	0	1068.58	479	487
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	24	27	60	0.06%	42.6%	DALNLAQMQEQTLQLEQQSK	99.7%	105	25	99.8	3	1	0	2316.15	73	92
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	24	27	60	0.06%	42.6%	DKWSNFDPTGLER	99.6%	28.7	25	28.5	0	2	0	1564.74	45	57
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	24	27	60	0.06%	42.6%	GEGAGPPPPLPPAQPGAEGGGDR	99.7%	88.8	25	88.8	2	0	0	2081.01	13	35
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	24	27	60	0.06%	42.6%	GLGDRPAPK	99.7%	49.1	25	34.6	2	0	0	910.51	36	44
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	24	27	60	0.06%	42.6%	GLLLFVDEADAFLR	99.7%	79.4	25	68.3	2	0	0	1578.85	453	466
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	24	27	60	0.06%	42.6%	ITVLEALR	99.7%	54.2	25	37.4	4	0	0	914.57	339	346
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	24	27	60	0.06%	42.6%	LALHSGMDYAIMTGGDVAPMGR	99.5%	27.7	25	25.5	0	1	0	2311.05	413	434
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	24	27	60	0.06%	42.6%	LAQFDYGR	99.7%	45.3	25	17.7	4	0	0	969.48	554	561
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	24	27	60	0.06%	42.6%	LAQFDYGRK	99.7%	39.5	25	36.7	2	0	0	1097.57	554	562
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	24	27	60	0.06%	42.6%	LFDWANTSR	99.7%	59.2	25	47.8	3	0	0	1109.54	443	451
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	24	27	60	0.06%	42.6%	LGKPSLVR	99.7%	43.6	25	31	2	0	0	869.56	327	334
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	24	27	60	0.06%	42.6%	LLSRPQDALEGVVLSPSLEAR	99.7%	35.9	25	35.9	0	2	0	2250.25	355	375
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	24	27	60	0.06%	42.6%	LTEGMSGR	99.7%	52.1	25	47.2	1	0	0	850.41	569	576
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	24	27	60	0.06%	42.6%	MYFDKYVLKPATEGK	99.3%	26.4	25	26.4	0	1	0	1789.92	535	549
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	24	27	60	0.06%	42.6%	NILMYGPPGTGK	99.7%	69.2	25	61	4	0	0	1263.64	395	406
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	24	27	60	0.06%	42.6%	QQQLLNEENLR	99.7%	78.2	25	67.4	4	0	0	1384.72	195	205
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	24	27	60	0.06%	42.6%	QRYEDQLK	98.6%	32.2	25	22.4	1	0	0	1079.55	187	194
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	24	27	60	0.06%	42.6%	QTVLESIR	99.7%	59	25	37.7	3	0	0	945.54	268	275
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	24	27	60	0.06%	42.6%	TAGTLFGEGFR	99.7%	72.8	25	71.9	4	0	0	1155.58	276	286
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	24	27	60	0.06%	42.6%	VRDIAIATR	99.7%	41.4	25	34.6	4	0	0	1014.61	376	384
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	24	27	60	0.06%	42.6%	YVLKPATEGK	99.0%	33.8	25	27.1	3	0	0	1105.63	540	549
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	5	6	11	0.01%	36.9%	AERENADIIR	97.4%	29.6	25	12.2	1	0	0	1186.62	199	208
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	5	6	11	0.01%	36.9%	DKWSNFDPTGLER	99.6%	28.7	25	28.5	0	2	0	1564.74	45	57
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	5	6	11	0.01%	36.9%	EALNLAQMQEQTLQLEQQSK	99.7%	86.6	25	86.6	1	0	0	2330.17	73	92
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	5	6	11	0.01%	36.9%	GEGAGPPPPLPPAQPGAEGGGDR	99.7%	88.8	25	88.8	2	0	0	2081.01	13	35
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	5	6	11	0.01%	36.9%	GLGDRPAPK	99.7%	49.1	25	34.6	2	0	0	910.51	36	44
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	5	6	11	0.01%	36.9%	GLLLFMDEADAFLR	99.7%	73.9	25	72	1	0	0	1626.82	405	418
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	5	6	11	0.01%	36.9%	HILLYGPPGTGK	99.7%	38.6	25	29	2	0	0	1252.71	347	358
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	5	6	11	0.01%	36.9%	ITVLEALR	99.7%	54.2	25	37.4	4	0	0	914.57	291	298
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	5	6	11	0.01%	36.9%	LALHSGMDYAIMTGGDVAPMGR	99.5%	27.7	25	25.5	0	1	0	2311.05	365	386
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	5	6	11	0.01%	36.9%	LAQFDYGR	99.7%	45.3	25	17.7	4	0	0	969.48	506	513
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	5	6	11	0.01%	36.9%	LAQFDYGRK	99.7%	39.5	25	36.7	2	0	0	1097.57	506	514

ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	5	6	11	0.01%	36.9%	LFDWANTSR	99.7%	59.2	25	47.8	3	0	0	1109.54	395	403
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	5	6	11	0.01%	36.9%	LGKPSLVR	99.7%	43.6	25	31	2	0	0	869.56	279	286
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	5	6	11	0.01%	36.9%	LHFDNCVLKPATEGK	95.3%	20.7	25	19.8	0	1	0	1728.87	487	501
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	5	6	11	0.01%	36.9%	LKEYEAAVEQLK	99.7%	71.9	25	67.2	4	2	0	1420.77	93	104
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	5	6	11	0.01%	36.9%	LTEGMSGR	99.7%	52.1	25	47.2	1	0	0	850.41	521	528
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	5	6	11	0.01%	36.9%	QQQLLNEENLR	99.7%	78.2	25	67.4	4	0	0	1384.72	147	157
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	5	6	11	0.01%	36.9%	QRYEDQLK	98.6%	32.2	25	22.4	1	0	0	1079.55	139	146
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	5	6	11	0.01%	36.9%	QTVLESIR	99.7%	59	25	37.7	3	0	0	945.54	220	227
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	5	6	11	0.01%	36.9%	TAGTLFGEGFR	99.7%	72.8	25	71.9	4	0	0	1155.58	228	238
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	5	6	11	0.01%	36.9%	VRDIAIATR	99.7%	41.4	25	34.6	4	0	0	1014.61	328	336
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	6	6	10	0.01%	8.1%	LSSDTALLGR	99.7%	46	25	38.3	2	0	0	1032.57	275	284
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	6	6	10	0.01%	8.1%	QLNPVWLR	94.7%	26.9	25	17.2	1	0	0	1025.59	560	567
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	6	6	10	0.01%	8.1%	STVLSLLLR	99.7%	69.3	25	39.9	2	0	0	1001.64	534	542
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	6	6	10	0.01%	8.1%	TSLFSSILR	99.7%	42.9	25	33.5	2	0	0	1023.58	249	257
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	6	6	10	0.01%	8.1%	TVLVIAHR	99.7%	43.8	25	37.8	2	0	0	908.57	684	691
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	6	6	10	0.01%	8.1%	VTQDSLAQATQLAEER	99.7%	94.4	25	88.5	1	0	0	1759.88	342	357
ATP-binding cassette sub-family B member 7, mitochondrial	ABCB7	ABCB7_HUMAN	82.6	100.0%	3	3	8	0.01%	4.4%	AGAAFFNEVR	99.7%	45.9	25	37.3	2	0	0	1081.54	201	210
ATP-binding cassette sub-family B member 7, mitochondrial	ABCB7	ABCB7_HUMAN	82.6	100.0%	3	3	8	0.01%	4.4%	AMNIVVPFMFK	99.6%	38.2	25	38.2	2	0	0	1296.68	152	162
ATP-binding cassette sub-family B member 7, mitochondrial	ABCB7	ABCB7_HUMAN	82.6	100.0%	3	3	8	0.01%	4.4%	VAISLGFLGGAK	99.7%	78	25	62.7	4	0	0	1132.67	140	151
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	6	6	12	0.01%	10.6%	AVVDKVFFSR	99.7%	44.3	25	44.3	1	0	0	1167.65	57	66
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	6	6	12	0.01%	10.6%	DQVIYPDGREDQK	99.7%	39.5	25	28.5	1	0	0	1562.74	521	533
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	6	6	12	0.01%	10.6%	FSMGFIDSIIAK	99.1%	34.1	25	29	2	0	0	1328.69	311	322
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	6	6	12	0.01%	10.6%	IANPDQLLTQDVEK	99.7%	89.9	25	89.9	2	0	0	1583.83	182	195
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	6	6	12	0.01%	10.6%	ITELMQVLK	99.7%	39.8	25	23.1	2	0	0	1090.62	391	399
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	6	6	12	0.01%	10.6%	VLGELWPLFGGR	99.7%	73.9	25	63.1	4	0	0	1343.75	485	496
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	7	7	14	0.01%	13.7%	ADIFMFDEPSSYLDVK	99.7%	81.9	25	81.9	2	0	0	1876.87	235	250
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	7	7	14	0.01%	13.7%	AIIKPQYVDQIPK	96.3%	21.4	25	21.4	0	2	0	1512.88	166	178
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	7	7	14	0.01%	13.7%	GSELQNYFTK	99.7%	50.8	25	45.8	2	0	0	1186.57	149	158
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	7	7	14	0.01%	13.7%	GTVGSILDR	99.7%	57	25	44.2	1	0	0	917.51	182	190
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	7	7	14	0.01%	13.7%	NVEDLSGGELQR	99.7%	61.8	25	53.1	2	0	0	1316.64	213	224
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	7	7	14	0.01%	13.7%	VAETANEEEVKK	99.7%	52.1	25	47.8	3	0	0	1346.68	333	344
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	7	7	14	0.01%	13.7%	VIVFDGVPSK	99.6%	37.6	25	16.6	2	0	0	1060.60	532	541
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	9	9	17	0.02%	11.8%	ADDPYAHLSK	99.7%	49.9	25	36.7	1	0	0	1116.53	246	255
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	9	9	17	0.02%	11.8%	AVSEEQQPALK	99.7%	53.5	25	43.5	3	0	0	1199.63	164	174
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	9	9	17	0.02%	11.8%	GAVIVVSHDAR	99.7%	71	25	57	2	0	0	1123.62	790	800
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	9	9	17	0.02%	11.8%	GFNLPYQDAR	99.6%	37.6	25	23.5	2	0	0	1180.57	714	723
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	9	9	17	0.02%	11.8%	IGFFNQQYAEQLR	99.7%	70.2	25	51.1	1	0	0	1613.81	690	702
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	9	9	17	0.02%	11.8%	LQGQLEQGDDTAAER	99.7%	81.3	25	81.3	1	0	0	1630.77	397	411
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	9	9	17	0.02%	11.8%	STLLLLLTGK	99.7%	46.3	25	46.3	3	0	0	1058.68	665	674
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	9	9	17	0.02%	11.8%	TFFEELAVEDK	99.1%	34.2	25	31.3	1	0	0	1327.64	40	50
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	9	9	17	0.02%	11.8%	VVFAELACR	99.7%	63.8	25	59.2	3	0	0	1064.56	751	759
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	8	12	19	0.02%	15.4%	ILHGLGFTPAMQR	97.8%	23	25	17	0	1	0	1440.78	211	223
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	8	12	19	0.02%	15.4%	IPPPVIMVQNVSFK	99.7%	80.7	25	77	2	1	0	1568.89	391	404
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	8	12	19	0.02%	15.4%	LIQQVAQEIWVCEK	99.7%	71.3	25	65.5	2	2	0	1743.91	575	588
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	8	12	19	0.02%	15.4%	LLTGELLPTDGMIR	99.7%	68.5	25	63.9	4	0	0	1528.84	442	455
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	8	12	19	0.02%	15.4%	LVDEEPQLTK	99.7%	45.3	25	27.2	2	0	0	1171.62	609	618
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	8	12	19	0.02%	15.4%	MMASGLTER	99.7%	40.2	25	32	2	0	0	1027.45	366	374
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	8	12	19	0.02%	15.4%	VALVGPNGAGK	98.4%	31.8	25	31.8	1	0	0	982.57	426	436
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	8	12	19	0.02%	15.4%	YYTGNYDQYVK	99.7%	63.1	25	58.4	2	0	0	1413.63	305	315
ATP-binding cassette sub-family F member 3	ABCF3	ABCF3_HUMAN	79.7	99.8%	2	2	4	0.00%	3.2%	ASVILAGLGFTPK	99.7%	49.2	25	48.2	2	0	0	1273.75	307	319
ATP-binding cassette sub-family F member 3	ABCF3	ABCF3_HUMAN	79.7	99.8%	2	2	4	0.00%	3.2%	LLLGDLAPVR	99.7%	48.7	25	39.5	2	0	0	1066.66	537	546

ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	AFDSGIIPMEFVNK	99.7%	84.4	25	81.4	8	0	0	1583.78	949	962
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	AIVWGMQTR	99.7%	48.2	25	41.3	4	0	0	1061.56	499	507
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	AKPAMPQDSVPSPR	99.7%	42.6	25	41.1	3	0	0	1480.76	470	483
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	AVQGMLDFDYVCSR	99.7%	103	25	103	4	0	0	1660.75	508	521
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	DEPSVAAMVYPFTGDHK	99.7%	79.3	25	79.3	4	0	0	1879.85	522	538
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	DGVYVLDLAAK	99.7%	76.6	25	70.4	7	0	0	1163.63	210	220
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	DLVSSLTSGLLTIGDR	99.7%	92.7	25	87.4	5	0	0	1646.90	919	934
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	DYQGPLKEHEVTIFVR	99.7%	31.6	25	31.6	0	1	0	1931.00	363	378
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	EAYPEEAYIADLDAK	99.7%	78.3	25	78.3	2	0	0	1697.79	245	259
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	EGDYVLFHHEGGVDVGDVDAK	99.7%	46.3	25	46.3	0	2	0	2258.04	128	148
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	FGGALDAAAK	99.7%	71.5	25	51.8	2	0	0	920.48	935	944
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	FICTTSAIQNR	99.7%	68.7	25	65.4	2	0	0	1310.65	18	28
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	GGPNYQEGLR	99.7%	54.3	25	21.3	2	0	0	1090.53	380	389
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	GQELIYAGMPITEVFK	99.7%	49.8	25	49.8	3	0	0	1795.93	849	864
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	GVTIIGPATVGGIKPGCFK	99.7%	67.8	25	67.8	2	1	0	1872.04	617	635
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	IGNTGGMLDNILASK	99.7%	102	25	99.3	6	0	0	1503.78	636	650
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	ILIIGGSIANFTNVAATFK	99.7%	57.7	25	57.7	1	0	0	1950.11	337	355
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	KPASFMTSICDER	99.7%	68	25	55	4	2	0	1541.71	836	848
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	LGLVGVNLTLDGVK	99.7%	83.4	25	80.1	4	0	0	1397.84	69	82
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	LGQEATVGK	99.7%	61.3	25	44.8	4	0	0	902.49	89	97
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	LIMGIGHR	99.2%	34.8	25	22.5	2	0	0	912.51	969	976
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	LYRPGSVAYVSR	99.7%	37.3	25	29.9	2	4	0	1367.74	651	662
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	MIVVLGEIGGTEEYK	99.7%	116	25	116	5	0	0	1637.85	712	726
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	RGGPNYQEGLR	99.7%	45.4	25	36.9	2	0	0	1246.63	379	389
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	SAYDSTMETMNYAQIR	99.7%	99.2	25	99.2	6	0	0	1880.82	577	592
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	SGGMSNELNNIISR	99.7%	96.4	25	90.8	4	0	0	1491.72	663	676
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	SINNPDMR	97.8%	30.3	25	18.6	2	0	0	946.44	979	986
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	SMGFIGHYLDQK	99.7%	53.5	25	42.7	4	0	0	1395.67	1066	1077
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	STTLFSR	98.1%	31	25	12.8	1	0	0	811.43	489	495
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	TIAIIAEGIPEALTR	99.7%	106	25	98.8	11	0	0	1567.91	593	607
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	TILSLMTR	99.7%	45.3	25	41.5	5	0	0	950.53	322	329
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	TTDGVYEGVAIGGDR	99.7%	108	25	95.4	2	0	0	1509.72	677	691
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	VDATADYICK	99.7%	76.6	25	69.7	3	0	0	1155.54	221	230
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	VTPDTDWAR	99.7%	41.4	25	41.4	2	0	0	1060.51	34	42
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	WGDIEFPPPFGR	98.7%	32.5	25	32.5	1	0	0	1417.69	233	244
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	36	53	130	0.13%	41.1%	YQDTPGVK	97.8%	30.3	25	20.5	1	0	0	907.45	704	711
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	11	11	20	0.02%	21.2%	AAAAADLANR	99.7%	52	25	48.4	2	0	0	943.50	453	462
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	11	11	20	0.02%	21.2%	DLIEFGMIPEFVGR	99.6%	37.9	25	33.3	2	0	0	1638.82	486	499
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	11	11	20	0.02%	21.2%	DVGGEGVQQGLLK	99.7%	92.3	25	87.3	2	0	0	1299.69	374	386
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	11	11	20	0.02%	21.2%	LLEGTIVNVPEK	99.7%	53.2	25	50.4	2	0	0	1311.75	387	398
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	11	11	20	0.02%	21.2%	LLQDANYNVEK	99.7%	53.6	25	39.2	2	0	0	1306.66	339	349
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	11	11	20	0.02%	21.2%	SGESNTHQDIEEKDR	99.7%	39.5	25	39.5	0	2	0	1744.77	463	477
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	11	11	20	0.02%	21.2%	SIIKEPESAAEAVK	99.7%	39.1	25	24.5	1	0	0	1471.80	145	158
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	11	11	20	0.02%	21.2%	SNILLLGPTGSGK	99.7%	78.9	25	77.6	2	0	0	1256.72	287	299
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	11	11	20	0.02%	21.2%	TLLAQTLAK	99.7%	39.1	25	35.3	2	0	0	958.59	300	308
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	11	11	20	0.02%	21.2%	VLSVAVYNHYK	96.2%	28.2	25	28.2	1	0	0	1292.70	189	199
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	11	11	20	0.02%	21.2%	YLGFGTPSNLGK	99.7%	56.4	25	51	2	0	0	1253.65	438	449
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	AAECNIVVTQPR	99.7%	78.8	25	70.9	4	0	0	1357.69	435	446
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	AAMEALVVEVTK	99.7%	82.5	25	70.5	4	0	0	1276.68	1105	1116
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	AENNSEVGASGYGVPGPTWDR	99.7%	81.1	25	81.1	2	0	0	2162.97	121	141
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	DFVNYLVR	99.7%	52.7	25	39.9	6	0	0	1025.54	64	71

ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	DINTDFLLVVLR	99.7%	77.3	25	71.6	6	0	0	1417.81	517	528
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	DVVQAYPEVR	99.7%	63.1	25	50.5	4	0	0	1175.61	529	538
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	ELDALDANDELTPLGR	99.7%	101	25	91.2	5	0	0	1741.86	838	853
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	GANLKDYYSR	99.7%	54.5	25	48.3	4	0	0	1186.59	142	151
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	GISHVIVDEIHER	99.7%	46.3	25	42.3	0	2	0	1503.79	504	516
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	GMTLVTPLQLLLFASK	99.2%	34.9	25	34.9	2	0	0	1732.01	1058	1073
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	ISAVSVAER	99.7%	68.3	25	52.9	7	0	0	931.52	448	456
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	KMTPSYEIR	99.4%	36.1	25	23.4	2	0	0	1124.58	16	24
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	KVFDPVPVGVTK	99.7%	56.5	25	50.1	2	0	0	1285.75	697	708
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	LAAQSCALSLVR	99.7%	79.9	25	67.2	4	0	0	1288.70	237	248
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	LAQFEPSQR	99.7%	49.2	25	42.9	2	0	0	1075.55	315	323
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	LGGIGQFLAK	99.7%	76.9	25	68.3	9	0	0	1003.59	810	819
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	LNMATLR	99.7%	56.1	25	36.4	2	0	0	818.46	945	951
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	LNQYFQK	99.7%	45.1	25	33.1	3	0	0	940.49	185	191
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	LQISHEAAACITGLR	99.7%	36.2	25	36.2	0	2	0	1639.86	1090	1104
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	LSMSQLNEK	99.7%	47.3	25	39.7	4	0	0	1065.52	622	630
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	MGGEEAEIR	99.7%	75.4	25	61.1	6	0	0	991.45	930	938
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	MTPSYEIR	96.3%	28.3	25	21.4	2	0	0	996.48	17	24
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	NFLYAWCGK	99.6%	38.3	25	26.5	2	0	0	1158.54	6	14
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	QPAIISQLDPVNER	99.7%	77	25	76.1	3	0	0	1579.84	1117	1130
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	RISAVSVAER	99.7%	43	25	32.1	3	0	0	1087.62	447	456
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	RLNMATLR	99.4%	36	25	17.5	1	0	0	974.56	944	951
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	SFIAEMTIYIK	99.7%	60.8	25	53.5	2	0	0	1331.69	210	220
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	SSVNCPFSSQDMK	98.8%	33	25	33	2	0	0	1502.63	1025	1037
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	TPLHEIALSIK	99.7%	38.8	25	38.8	0	2	0	1221.72	796	806
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	TTQVPQFILDDFIQNDR	99.7%	46.3	25	45.1	3	0	0	2050.02	418	434
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	VFDPVPVGVTK	99.7%	51.6	25	50.6	4	0	0	1157.66	698	708
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	YGDGPRPPK	99.2%	34.9	25	34.9	3	0	0	986.51	1155	1163
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	YPSPFFVFGEK	99.7%	48.3	25	43.7	7	0	0	1317.65	1038	1048
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	YQILPLHSQIPR	99.7%	44.4	25	41.8	2	2	0	1464.83	681	692
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	35	40	123	0.12%	28.1%	YTQVGPDHNR	99.7%	41.4	25	28.6	3	0	0	1186.56	200	209
ATP-dependent RNA helicase DDX1	DDX1	DDX1_HUMAN	82.4	99.8%	2	2	4	0.00%	2.8%	ELLIIGGVAAR	99.7%	65.1	25	65.1	2	0	0	1111.68	320	330
ATP-dependent RNA helicase DDX1	DDX1	DDX1_HUMAN	82.4	99.8%	2	2	4	0.00%	2.8%	FLICTDVAAR	99.7%	56.3	25	49.4	2	0	0	1165.60	568	577
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	4	4	7	0.01%	6.1%	ELAMQTFGVLK	99.7%	78.8	25	70.2	2	0	0	1236.67	262	272
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	4	4	7	0.01%	6.1%	ISDIQSQLEK	99.7%	54.1	25	15.9	2	0	0	1160.62	558	567
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	4	4	7	0.01%	6.1%	QTMLFSATQTR	99.7%	72.1	25	58.5	2	0	0	1283.64	359	369
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	4	4	7	0.01%	6.1%	SIRPLLEGR	97.7%	30.2	25	22.6	1	0	0	1040.62	209	217
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	12	28	0.03%	29.3%	DPNSPLYSVK	99.7%	44	25	33.3	2	0	0	1119.57	82	91
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	12	28	0.03%	29.3%	GLAVNMVDSK	99.7%	57.5	25	51.6	2	0	0	1049.53	436	445
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	12	28	0.03%	29.3%	HSMNILNR	99.7%	42.1	25	31.8	2	0	0	984.50	446	453
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	12	28	0.03%	29.3%	IQEHFNK	99.6%	37.3	25	25	2	0	0	915.47	454	460
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	12	28	0.03%	29.3%	LDTDDLDEIEK	99.7%	62.5	25	54.6	2	0	0	1305.61	465	475
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	12	28	0.03%	29.3%	SMTNLQIKEEK	99.1%	34.3	25	10.8	1	0	0	1336.68	19	29
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	12	28	0.03%	29.3%	SNLVDNTNQVEVLQR	99.7%	104	25	89.9	4	0	0	1728.89	67	81
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	12	28	0.03%	29.3%	TAAFVLAMLSR	99.7%	73.9	25	69.1	6	0	0	1179.66	144	154
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	12	28	0.03%	29.3%	VEPSDRYPQCLCLSPTYELALQTGK	99.7%	45.7	25	45.7	0	1	0	2925.41	155	179
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	12	28	0.03%	29.3%	VFVLDEADVMIATQGHQDQSIR	99.7%	62	25	59.9	0	2	0	2472.22	237	258
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	12	28	0.03%	29.3%	VLVTTNVCAR	99.7%	63.5	25	63.5	4	0	0	1132.61	385	394
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	25	0.02%	28.3%	CMALAQLLVEQNFPAIAIHR	99.7%	82.7	25	82.7	0	4	0	2295.21	299	318
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	25	0.02%	28.3%	DFLLKPELLR	95.7%	27.7	25	19.4	1	0	0	1243.74	48	57
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	25	0.02%	28.3%	DVQEIFR	99.6%	37.9	25	20.1	2	0	0	906.47	209	215

ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	25	0.02%	28.3%	ELAFQISK	99.7%	42.7	25	33.2	2	0	0	935.52	123	130
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	25	0.02%	28.3%	GLAITFVSDENDAK	99.7%	66.1	25	66.1	2	0	0	1479.73	384	397
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	25	0.02%	28.3%	GSYVSIHSSGFR	99.7%	63.1	25	60.9	2	0	0	1296.63	36	47
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	25	0.02%	28.3%	ILNDVQDR	99.7%	41.9	25	30.7	2	0	0	972.51	398	405
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	25	0.02%	28.3%	ILVATNLFGR	99.7%	65.2	25	55.5	1	0	0	1103.66	339	348
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	25	0.02%	28.3%	NCPHVVVGTPGR	99.7%	78.9	25	66.5	2	2	0	1292.65	163	174
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	25	0.02%	28.3%	VSVFFGGLSIK	99.7%	55.1	25	50.4	3	0	0	1153.66	144	154
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	25	0.02%	28.3%	YQQFKDFQR	99.7%	53.2	25	52.5	2	0	0	1259.62	329	337
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	42	0.04%	31.0%	DKDAYSSFGSR	99.7%	60.8	25	60.8	2	0	0	1232.55	65	75
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	42	0.04%	31.0%	DLLDLLVEAK	99.7%	56.7	25	52	3	0	0	1128.65	555	564
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	42	0.04%	31.0%	DLMACAQTGSGK	99.7%	56.1	25	47	4	0	0	1238.55	219	230
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	42	0.04%	31.0%	DREEALHQFR	99.7%	45.5	25	29.9	2	1	0	1300.64	479	488
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	42	0.04%	31.0%	ELAVQIYEEAR	99.7%	68.6	25	53.7	2	0	0	1320.68	277	287
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	42	0.04%	31.0%	ELAVQIYEEARK	99.7%	60.2	25	50.6	2	0	0	1448.77	277	288
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	42	0.04%	31.0%	GCHLLVATPGR	99.7%	54.1	25	54.1	2	0	0	1180.63	316	326
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	42	0.04%	31.0%	GLDISNVK	99.6%	37.6	25	18.3	1	0	0	845.47	504	511
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	42	0.04%	31.0%	IGLDFCK	99.7%	40.3	25	34	2	0	0	852.43	336	342
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	42	0.04%	31.0%	IVEQDTMPPK	99.7%	39	25	39	2	0	0	1173.58	364	373
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	42	0.04%	31.0%	MLDMGFEPQIR	99.7%	72.6	25	66.2	5	0	0	1336.64	352	362
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	42	0.04%	31.0%	QSSGASSSSFSSSR	99.7%	78.3	25	66.4	2	0	0	1361.59	604	617
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	42	0.04%	31.0%	QYPISLVLAPTR	99.7%	50.3	25	42.6	2	0	0	1357.78	265	276
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	42	0.04%	31.0%	SDYDGIGSR	99.7%	41.9	25	41.9	2	0	0	969.43	102	110
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	42	0.04%	31.0%	SFLLDLLNATGK	99.7%	92.9	25	84.6	2	0	0	1291.73	429	440
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	42	0.04%	31.0%	SPILVATAVAAR	99.7%	97.6	25	88.6	3	0	0	1168.70	492	503
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	42	0.04%	31.0%	VGNLGLATSFFNER	99.7%	62.8	25	62.8	2	0	0	1524.78	535	548
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	42	0.04%	31.0%	VGSTSENITQK	99.7%	64.2	25	51.7	2	0	0	1163.59	408	418
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	42	0.04%	31.0%	VVWVEESDKR	99.2%	26.2	25	26.2	0	2	0	1246.64	419	428
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	19	21	42	0.04%	31.0%	YLVLDEADR	99.7%	57.5	25	39.6	2	0	0	1093.55	343	351
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	4	4	7	0.01%	9.5%	EGAFSNFPISEETIK	99.7%	67.2	25	64.2	8	0	0	1668.81	136	150
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	4	4	7	0.01%	9.5%	GVTYLFPIQVK	99.7%	63.7	25	42.8	2	0	0	1264.73	156	166
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	4	4	7	0.01%	9.5%	NGIDILVGTPGR	99.7%	80	25	70.8	2	0	0	1211.67	258	269
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	4	4	7	0.01%	9.5%	SRYEQVDLVGK	99.2%	34.8	25	10.2	1	0	0	1293.68	343	353
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	4	4	7	0.01%	9.5%	TFSFAIPLIER	99.7%	46.3	25	45.9	2	0	0	1293.72	188	198
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	4	4	7	0.01%	9.5%	VLVATNVAAR	99.7%	79.9	25	73.1	2	0	0	1013.61	441	450
ATP-dependent RNA helicase DDX54	DDX54	DDX54_HUMAN	98.6	100.0%	3	3	4	0.00%	3.4%	FEEEELQR	99.0%	33.5	25	26.5	1	0	0	1079.50	552	559
ATP-dependent RNA helicase DDX54	DDX54	DDX54_HUMAN	98.6	100.0%	3	3	4	0.00%	3.4%	TACFLLPMFER	94.7%	26.9	25	26.9	1	0	0	1384.68	147	157
ATP-dependent RNA helicase DDX54	DDX54	DDX54_HUMAN	98.6	100.0%	3	3	4	0.00%	3.4%	VADNAQQQYVR	99.7%	41.3	25	34.8	2	0	0	1291.64	511	521
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L1_HUMAN	86.5	100.0%	5	5	9	0.01%	8.0%	LAETQNIAPSFVK	99.7%	82.6	25	80.2	2	0	0	1417.77	225	237
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L1_HUMAN	86.5	100.0%	5	5	9	0.01%	8.0%	LGVMTYSDTGK	99.7%	43.7	25	43.7	2	0	0	1171.57	698	708
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L1_HUMAN	86.5	100.0%	5	5	9	0.01%	8.0%	LSPETQSAIEQEIR	99.7%	79.5	25	65.4	2	0	0	1600.82	709	722
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L1_HUMAN	86.5	100.0%	5	5	9	0.01%	8.0%	TGFAEGFLK	99.7%	53.7	25	53.7	2	0	0	969.50	270	278
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L1_HUMAN	86.5	100.0%	5	5	9	0.01%	8.0%	TTTGLDSAVDPVQMK	99.3%	35	25	35	1	0	0	1578.77	320	334
Basic leucine zipper and W2 domain-containing protein 1	BZW1	BZW1_HUMAN	48.0	99.8%	2	2	4	0.00%	4.8%	AEVLSEEPILK	99.7%	68.8	25	55.5	2	0	0	1227.68	369	379
Basic leucine zipper and W2 domain-containing protein 1	BZW1	BZW1_HUMAN	48.0	99.8%	2	2	4	0.00%	4.8%	LMELFPANK	99.7%	57.7	25	44.4	2	0	0	1062.57	215	223
Basic leucine zipper and W2 domain-containing protein 2	BZW2	BZW2_HUMAN	48.2	100.0%	3	3	5	0.00%	6.4%	EGIAASFAVK	99.7%	51.5	25	39.6	2	0	0	992.54	180	189
Basic leucine zipper and W2 domain-containing protein 2	BZW2	BZW2_HUMAN	48.2	100.0%	3	3	5	0.00%	6.4%	LLELFPVNR	99.7%	41.2	25	31.6	2	0	0	1100.65	216	224
Basic leucine zipper and W2 domain-containing protein 2	BZW2	BZW2_HUMAN	48.2	100.0%	3	3	5	0.00%	6.4%	NYAQVFNK	96.0%	28	25	16.4	1	0	0	983.49	110	117
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	3	3	4	0.00%	3.3%	LLASTLVHSVK	99.7%	51.1	25	42.6	2	0	0	1167.71	570	580
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	3	3	4	0.00%	3.3%	NTEEEGLKYK	99.6%	37.9	25	23.3	1	0	0	1210.60	430	439
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	3	3	4	0.00%	3.3%	TIAPQNAPR	97.9%	30.5	25	19.8	1	0	0	967.53	304	312
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	10	19	0.02%	16.4%	AGATLDLLVENMGR	99.7%	77.4	25	67.9	4	0	0	1459.76	469	482

Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	10	19	0.02%	16.4%	AYVAVDGIPQGVLER	99.7%	74.7	25	70	2	0	0	1586.85	443	457
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	10	19	0.02%	16.4%	MFEIDYSR	99.7%	42.2	25	42.2	2	0	0	1060.48	31	38
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	10	19	0.02%	16.4%	SLYPLTFIQVK	99.7%	61.5	25	61.3	2	0	0	1308.76	400	410
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	10	19	0.02%	16.4%	SSDPDYLAAVDK	99.7%	58.6	25	35.4	1	0	0	1280.60	149	160
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	10	19	0.02%	16.4%	TEAVASSLYDILAR	99.7%	96.4	25	82.2	2	0	0	1508.80	286	299
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	10	19	0.02%	16.4%	TVGAALDILCPSGPIK	99.7%	109	25	108	2	0	0	1611.88	384	399
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	10	19	0.02%	16.4%	VNYGAYINDFK	99.7%	64.4	25	53.3	2	0	0	1303.63	483	493
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	9	10	19	0.02%	16.4%	YISGSIHYSR	99.7%	64	25	63	2	0	0	1182.59	50	59
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	7	8	13	0.01%	17.7%	AVAQAGTVGTLLIVK	99.7%	70.1	25	60.6	2	0	0	1440.88	95	109
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	7	8	13	0.01%	17.7%	EGPPPASPAQLLSK	99.7%	64.9	25	62.9	2	0	0	1391.75	421	434
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	7	8	13	0.01%	17.7%	LEQPDPGAVAAAAILR	99.7%	63.6	25	62.5	2	1	0	1591.88	552	567
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	7	8	13	0.01%	17.7%	MALVLER	98.0%	30.8	25	17	1	0	0	831.48	374	380
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	7	8	13	0.01%	17.7%	SPGADLLQVLTK	99.7%	85.1	25	77.6	2	0	0	1241.71	511	522
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	7	8	13	0.01%	17.7%	VAGALAEAGVGLEEIAK	99.7%	95.3	25	81.8	2	0	0	1597.88	163	179
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	7	8	13	0.01%	17.7%	VAPAEPQEAPDSTAAGGSASK	99.7%	67.7	25	67.7	1	0	0	1940.92	352	372
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	AALLNQHYQVNFK	99.7%	61.9	25	60.4	2	0	0	1545.82	217	229
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	AYVDDTPAEQMK	99.7%	69.5	25	63	3	0	0	1367.61	289	300
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	DQDLEPGAPSMGAK	99.7%	56.7	25	56.7	3	0	0	1415.65	1464	1477
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	DQVDIAVQELLQLK	99.7%	62.6	25	44	1	0	0	1611.90	926	939
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	EYIPGQPPLSQSSDSSPTR	99.7%	63.9	25	61.1	2	0	0	2045.98	871	889
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	FAGGDYTTTIEAFISASGR	99.7%	47	25	47	1	0	0	1963.94	1216	1234
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	FVELPGAEMGK	99.7%	49.4	25	41.1	2	0	0	1177.59	187	197
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	GDIIQLQR	99.7%	67.2	25	31	2	0	0	942.54	667	674
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	GNAAWQEQLK	99.7%	47.8	25	31.4	2	0	0	1144.57	130	139
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	GSQFGQSCCLR	99.7%	51	25	51	2	0	0	1299.56	329	339
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	INEAVECLLSLK	99.7%	81.8	25	73.7	6	0	0	1388.75	850	861
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	KPYIWEYSR	99.7%	38.9	25	27.7	2	0	0	1241.63	417	425
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	KVIDPVAPR	99.7%	42.2	25	37	2	0	0	994.60	498	506
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	LGVENCYFPMFVSQSALEK	96.9%	29	25	29	1	0	0	2219.05	1071	1089
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	LLSVNIR	99.6%	37.9	25	23.9	2	0	0	814.51	1334	1340
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	LNLNNTVLSK	99.7%	64.4	25	47.7	4	0	0	1115.64	426	435
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	LNQWCNVVR	99.7%	49.6	25	37.1	2	0	0	1188.59	1144	1152
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	LTVAENEAETK	99.7%	77.3	25	76.3	9	0	0	1204.61	1390	1400
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	NPEVGLKPVWYSPK	99.7%	55.3	25	55.3	2	0	0	1613.87	536	549
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	NQGGGLSSSGAGEGQGPK	99.7%	88.2	25	88.2	5	0	0	1587.74	992	1009
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	NSEPAGLETPEAK	99.7%	65.1	25	48.3	4	0	0	1342.65	890	902
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	QFAYQNSWGLTTR	99.7%	65.3	25	56.9	2	0	0	1571.76	1266	1278
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	SCQFVAVR	99.7%	51.5	25	43.4	6	0	0	966.48	1376	1383
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	SLYDEVAAQGEVVR	99.7%	103	25	101	4	0	0	1535.77	825	838
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	SLYDEVAAQGEVVRK	99.7%	85.3	25	85.3	1	0	0	1663.87	825	839
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	TGQEYKPGNPPAEIGQNISSNSSASILESK	99.7%	57	25	57	0	2	0	3103.52	795	824
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	VASQGEVVR	99.7%	51.9	25	41.9	2	0	0	944.52	908	916
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	VAVQGDVVR	99.7%	59.3	25	44.4	4	0	0	942.54	757	765
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	VIDPVAPR	99.7%	46.5	25	46.5	4	0	0	866.51	499	506
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	32	85	0.08%	23.2%	VLFDKVASQGEVVR	99.7%	40.4	25	23.1	1	0	0	1546.86	903	916
Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	MTHFD2	MTDC_HUMAN	37.9	100.0%	3	3	5	0.00%	8.9%	EGAAVIDVGINR	99.7%	92.1	25	78	2	0	0	1213.65	267	278
Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	MTHFD2	MTDC_HUMAN	37.9	100.0%	3	3	5	0.00%	8.9%	LEEREVLK	98.0%	30.7	25	13.2	1	0	0	1015.58	334	341
Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	MTHFD2	MTDC_HUMAN	37.9	100.0%	3	3	5	0.00%	8.9%	LVGDVDFEGVR	99.7%	45	25	34.3	2	0	0	1205.62	289	299
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	16	0.02%	9.7%	ANSSVVSVNCK	99.7%	62.9	25	54.4	2	0	0	1164.57	587	597
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	16	0.02%	9.7%	EIPVESIEEVSK	99.7%	64	25	52.8	2	0	0	1358.71	258	269
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	16	0.02%	9.7%	ESQATLEER	99.7%	39.9	25	24.7	1	0	0	1062.51	5	13

Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	16	0.02%	9.7%	GGLAGEFQR	99.7%	53.2	25	45.6	1	0	0	934.47	683	691
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	16	0.02%	9.7%	LGCFEIAK	99.7%	41.8	25	38.3	2	0	0	937.48	894	901
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	16	0.02%	9.7%	LLPGIEVLWTGPK	99.7%	43.5	25	40.7	2	0	0	1422.84	241	253
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	16	0.02%	9.7%	SFVQWLGCR	99.7%	47.2	25	37.8	2	0	0	1152.56	656	664
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	16	0.02%	9.7%	SMMACLLSSLK	99.7%	50.8	25	40.4	2	0	0	1240.61	859	869
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	16	0.02%	9.7%	STELIPR	99.7%	44.6	25	27.2	2	0	0	815.46	300	306
Bifunctional purine biosynthesis protein PURH	ATIC	PUR9_HUMAN	64.6	100.0%	3	3	5	0.00%	6.9%	DVSELTGFPEMLGGR	97.0%	29.1	25	29.1	1	0	0	1607.77	50	64
Bifunctional purine biosynthesis protein PURH	ATIC	PUR9_HUMAN	64.6	100.0%	3	3	5	0.00%	6.9%	NLTALGLNLVASGGTAK	99.7%	99.4	25	99.4	2	0	0	1599.91	23	39
Bifunctional purine biosynthesis protein PURH	ATIC	PUR9_HUMAN	64.6	100.0%	3	3	5	0.00%	6.9%	SLFSNVVTK	99.0%	33.9	25	26.1	2	0	0	994.56	398	406
Bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase	GNE	GLCNE_HUMAN	79.3	99.8%	2	2	3	0.00%	3.6%	EVGAFGTPVINLGTR	99.7%	63.8	25	63.8	2	0	0	1530.83	307	321
Bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase	GNE	GLCNE_HUMAN	79.3	99.8%	2	2	3	0.00%	3.6%	ILGVGISTGGR	99.7%	82.3	25	70.2	1	0	0	1029.61	467	477
Bloom syndrome protein	BLM	BLM_HUMAN	159.0	100.0%	4	4	6	0.01%	3.0%	SDASLLGSLWR	99.7%	47.5	25	36.6	1	0	0	1204.63	419	429
Bloom syndrome protein	BLM	BLM_HUMAN	159.0	100.0%	4	4	6	0.01%	3.0%	SLIVDQVQK	96.7%	28.8	25	12.4	2	0	0	1029.59	718	726
Bloom syndrome protein	BLM	BLM_HUMAN	159.0	100.0%	4	4	6	0.01%	3.0%	SVEGYYQESGR	99.7%	65	25	61.7	2	0	0	1274.56	969	979
Bloom syndrome protein	BLM	BLM_HUMAN	159.0	100.0%	4	4	6	0.01%	3.0%	YGAEVISVLQK	99.7%	41.1	25	34.7	1	0	0	1206.67	1274	1284
BolA-like protein 2	BOLA2	BOLA2_HUMAN	10.1	100.0%	3	4	7	0.01%	39.5%	DLEAEHVEVEDTTLNR	99.7%	87.1	25	87.1	2	2	0	1869.88	15	30
BolA-like protein 2	BOLA2	BOLA2_HUMAN	10.1	100.0%	3	4	7	0.01%	39.5%	FEGKPLLQR	99.0%	33.7	25	28.3	2	0	0	1087.63	44	52
BolA-like protein 2	BOLA2	BOLA2_HUMAN	10.1	100.0%	3	4	7	0.01%	39.5%	TLTPDQWAR	98.9%	33.2	25	24.2	1	0	0	1087.55	74	82
BRCA2 and CDKN1A-interacting protein	BCCIP	BCCIP_HUMAN	36.0	99.8%	2	2	5	0.00%	7.3%	KGTQCVEQIQELVLR	99.7%	32.6	25	27.3	0	1	0	1800.96	137	151
BRCA2 and CDKN1A-interacting protein	BCCIP	BCCIP_HUMAN	36.0	99.8%	2	2	5	0.00%	7.3%	LLQQLFLK	99.7%	47.1	25	32.6	4	0	0	1002.63	77	84
Butyrophilin subfamily 1 member A1	BTN1A1	BT1A1_HUMAN	59.0	99.8%	2	2	3	0.00%	6.8%	ATLHAVDVTLDPDTAHPHLFLYEDSK	99.7%	54.9	25	54.9	0	1	0	2905.44	298	323
Butyrophilin subfamily 1 member A1	BTN1A1	BT1A1_HUMAN	59.0	99.8%	2	2	3	0.00%	6.8%	TPLPLAGPPR	99.7%	49.3	25	49.3	2	0	0	1018.60	411	420
Bystin	BYSL	BYST_HUMAN	49.6	100.0%	3	3	3	0.00%	6.9%	EALLELLR	98.7%	32.7	25	20.2	1	0	0	956.58	399	406
Bystin	BYSL	BYST_HUMAN	49.6	100.0%	3	3	3	0.00%	6.9%	FYNLVLLPR	99.7%	49.5	25	35.4	1	0	0	1134.67	249	257
Bystin	BYSL	BYST_HUMAN	49.6	100.0%	3	3	3	0.00%	6.9%	VLDALVFHFLGFR	99.7%	41.7	25	41.7	1	0	0	1533.86	356	368
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	AAEEIGIK	99.7%	56.4	25	37.5	2	0	0	830.46	59	66
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	AAQAPSSFQLLYDLK	99.7%	96.3	25	95.7	2	0	0	1651.87	805	819
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	APAEILNGK	99.7%	44.2	25	38	2	0	0	912.52	2	10
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	AYIQENLELVEK	99.7%	81.5	25	72.9	2	0	0	1448.76	722	733
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	DDSNLYINVK	99.7%	56.4	25	42.1	2	0	0	1180.58	47	56
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	EIGLLSEEVELYGETK	99.7%	102	25	102	2	0	0	1808.92	337	352
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	EQVPGFTPR	97.0%	29.2	25	21.9	1	0	0	1030.53	29	37
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	ETGVPIAGR	99.7%	48.2	25	37.9	2	0	0	899.49	158	166
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	FSDIQIR	99.7%	44.7	25	12.8	5	0	0	878.47	489	495
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	GALALAQAVQR	99.7%	84.9	25	82	4	0	0	1097.64	794	804
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	GDLNDCFIPCTPK	99.7%	54.1	25	54.1	2	0	0	1536.68	138	150
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	GVPTGFILPIR	99.7%	62.2	25	50.1	4	0	0	1169.70	879	889
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	IFHELTQTDK	99.7%	47.9	25	32.9	2	2	0	1231.63	464	473
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	ITIGQAPTEK	99.7%	45.6	25	40.1	2	0	0	1057.59	544	553
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	IYGADDIELLPEAQHK	99.7%	73.9	25	68.4	2	2	0	1811.92	833	848
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	KITIGQAPTEK	99.7%	50.3	25	24.3	2	0	0	1185.68	543	553
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	KVVGDVAYDEAK	99.7%	69.6	25	61.8	2	0	0	1293.67	251	262
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	LAILQVGNR	99.7%	78.7	25	59.6	2	0	0	983.60	38	46
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	LDIDPETITWQR	99.7%	73.1	25	67.4	2	0	0	1486.75	521	532
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	LVGPEGFVVTEAGFGADIGMEK	99.7%	65.9	25	55.3	3	2	0	2239.10	658	679
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	MFGIPVVVAVNAFK	99.7%	73.6	25	61	5	0	0	1491.84	747	760
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	MHGGGPTVTAGLPLPK	99.7%	43.7	25	42.7	2	2	0	1532.83	706	721
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	QGFGNLPICMAK	99.7%	42.2	25	31.5	2	0	0	1335.66	855	866
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	QPSQGPTFGIK	99.0%	33.6	25	25.9	2	0	0	1159.61	411	421
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	RFSDIQIR	97.5%	29.8	25	20.8	1	0	0	1034.57	488	495
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	TDPTTLTDEEINR	99.7%	81.7	25	65.3	2	0	0	1504.71	505	517

C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	TDTESELDLISR	99.7%	83.2	25	68.8	3	0	0	1378.67	761	772
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	THLSLSHNPEQK	99.7%	65.3	25	63.4	2	0	0	1390.71	867	878
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	TPVPSDIDISR	99.7%	59	25	59	2	0	0	1199.63	314	324
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	TTTESEVMK	95.3%	27.4	25	13.2	1	0	0	1025.48	75	83
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	VLLSALER	99.7%	61.6	25	43.6	5	0	0	900.55	355	362
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	VVGDVAYDEAK	99.7%	73.8	25	71.2	2	0	0	1165.57	252	262
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	VVGDVAYDEAKER	99.7%	68.9	25	62.5	2	0	0	1450.72	252	264
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	WMIQYNNLNLK	99.7%	55.1	25	39	2	0	0	1436.74	303	313
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	YSGLCPHVVVLVATVR	99.7%	54.5	25	53.9	0	1	0	1769.97	687	702
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	36	42	91	0.09%	41.3%	YVVVTGITPTPLGEGK	99.7%	94.6	25	92.1	2	0	0	1630.91	371	386
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	AAFALGGLGSGFASNR	99.7%	92.7	25	92.7	2	0	0	1495.77	556	571
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	AHWTPFEGQK	97.0%	29.1	25	29.1	2	0	0	1200.58	1769	1778
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	ASDPGLPAEEPK	99.6%	38.1	25	35.3	1	0	0	1210.60	1858	1869
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	ATGYPLAYVAAK	99.7%	50	25	50	2	0	0	1224.66	697	708
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	EATAGNPGGQTVR	99.7%	71.7	25	71.5	2	0	0	1257.62	359	371
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	ELSDLESAR	99.7%	50.9	25	42	2	0	0	1019.50	1067	1075
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	FLSSAAAVSK	99.7%	61	25	56.6	2	0	0	980.54	1110	1119
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	GEVRPELGSR	98.8%	32.9	25	29	2	0	0	1099.59	1658	1667
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	GHNQPCLLVGSGR	99.7%	40.9	25	40.9	1	0	0	1394.70	275	287
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	IIAHAQLLEQHR	99.7%	36.2	25	34.7	0	2	0	1428.81	843	854
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	ILALDCGLK	99.7%	45.5	25	24.9	2	0	0	1002.57	178	186
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	LALGIPLPELR	99.7%	60.2	25	60.2	2	0	0	1191.75	709	719
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	LFVEALGQIGPAPPLK	99.7%	93.9	25	93.9	2	0	0	1649.96	1435	1450
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	LGGAVLSFSEATSSVQK	99.7%	105	25	105	2	0	0	1680.88	1987	2003
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	LGYPVLVR	99.7%	51.4	25	43.2	2	0	0	916.56	548	555
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	LLDTIGISQPQWR	99.7%	90.8	25	90.8	2	0	0	1526.83	1054	1066
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	LYLNETFSELR	99.4%	36.1	25	28.5	2	0	0	1384.71	1557	1567
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	MAEIGEHVAPSEAANSLEQAQAAAER	99.7%	55.3	25	55.3	0	2	0	2680.26	522	547
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	MALLATVLGRF	99.7%	73.8	25	73.8	3	0	0	1207.69	2215	2225
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	NKSELLPTVR	98.9%	33.1	25	27.5	1	0	0	1156.67	1324	1333
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	NSVTGGTAAFEPSVDYCVVK	99.7%	110	25	110	2	0	0	2100.99	720	739
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	QELGICPAVK	99.2%	34.4	25	20	1	0	0	1114.59	892	901
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	SFEEAFQK	99.7%	44.9	25	33.9	2	0	0	985.46	771	778
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	SILEQLAEK	99.7%	53.4	25	41.3	2	0	0	1030.58	1379	1387
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	SVGEVMGIGR	99.7%	53.3	25	46.2	3	0	0	1020.51	761	770
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	SVHICHVAR	99.4%	36.3	25	30.6	1	0	0	1078.56	1609	1617
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	TLGVDLVALATR	99.7%	80.4	25	72.8	2	0	0	1228.73	1229	1240
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	TPHVLVLGSGVYR	99.7%	54	25	54	2	2	0	1397.79	932	944
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	TSSSFAAAMAR	99.7%	80.2	25	69	4	0	0	1099.52	1976	1986
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	VFNTGGAPR	99.7%	47	25	33.8	2	0	0	918.48	169	177
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	VHVDCMTSQK	99.0%	33.8	25	31.8	2	0	0	1204.55	1451	1460
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	VIMGEEVEPVGLMTGSGVVGVK	99.7%	70	25	55.7	2	0	0	2203.14	1241	1262
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	VLGTSPEAIDSAENR	99.7%	111	25	111	2	0	0	1558.77	1034	1048
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	VNEISVEVDSDPR	99.7%	89	25	79.6	2	0	0	1458.71	2188	2200
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	35	40	71	0.07%	19.2%	VPQFSFSR	99.7%	51.5	25	43	2	0	0	967.50	1263	1270
Calcium uniporter protein, mitochondrial	MCU	MCU_HUMAN	39.9	99.8%	2	2	3	0.00%	6.8%	DLLSHENAATLNDVK	99.7%	46.2	25	46.2	2	0	0	1639.83	166	180
Calcium uniporter protein, mitochondrial	MCU	MCU_HUMAN	39.9	99.8%	2	2	3	0.00%	6.8%	QEYVYPEAR	97.8%	30.3	25	28.3	1	0	0	1154.55	287	295
Calcium/calmodulin-dependent protein kinase type II subunit gamma	CAMK2G	KCC2G_HUMAN	62.6	99.9%	2	2	4	0.00%	4.7%	FTDDYQLFEELGK	99.7%	52.7	25	52.7	2	0	0	1604.75	10	22
Calcium/calmodulin-dependent protein kinase type II subunit gamma	CAMK2G	KCC2G_HUMAN	62.6	99.9%	2	2	4	0.00%	4.7%	NLINQMLTINPAK	99.7%	45.6	25	45.6	2	0	0	1469.81	247	259
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	AGQTTYSGVIDCFRK	99.7%	73.8	25	73.8	2	0	0	1702.82	552	566
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	DLGIFGLYK	98.8%	33	25	29.4	2	0	0	1025.57	474	482

Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	GLIPQLIGVAPEK	99.7%	48.9	25	0	3	0	0	1334.80	391	403
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	IVQLLAGVADQTK	99.7%	61	25	61	2	0	0	1355.79	56	68
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	KIYSTLAGTR	99.7%	59.6	25	48	2	0	0	1109.63	234	243
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	LATATFAGIENK	99.7%	85.2	25	71.4	2	0	0	1235.66	641	652
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	LQVAGEITTGPR	99.7%	69.4	25	55	2	0	0	1241.69	454	465
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	LTVNDFVR	99.7%	62.6	25	54.4	3	0	0	963.53	407	414
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	NIFLQYASTEVDGER	99.7%	93.4	25	93	1	0	0	1741.84	18	32
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	VSALNVLR	99.7%	65.7	25	42.6	2	0	0	871.54	466	473
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	YEGFFGLYR	99.7%	43.7	25	43.7	2	0	0	1151.55	382	390
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	43	0.04%	39.0%	AGQTTYSGVIDCFRK	99.7%	73.8	25	73.8	2	0	0	1702.82	554	568
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	43	0.04%	39.0%	ASGDSARPVLLQVAESAYR	99.7%	44.4	25	44.4	0	2	0	1990.04	313	331
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	43	0.04%	39.0%	DIPFSAIYFPCYAHVK	99.7%	46.2	25	17.2	2	0	0	1927.94	493	508
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	43	0.04%	39.0%	DLGFFGIYK	99.7%	46.6	25	44	2	0	0	1059.55	476	484
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	43	0.04%	39.0%	FGLGSVAGAVGATAVYPIDLVK	99.7%	85.9	25	85.9	2	0	0	2105.16	332	353
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	43	0.04%	39.0%	GLLPQLLGVAPEK	99.7%	48.9	25	0	3	0	0	1334.80	393	405
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	43	0.04%	39.0%	IAPLEEGTLPFNLAEAQR	99.7%	105	25	105	2	1	0	1969.04	293	310
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	43	0.04%	39.0%	INLPAPNPDHVGGYK	99.7%	62.3	25	56.7	2	0	0	1591.82	627	641
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	43	0.04%	39.0%	KIYSTLAGTR	99.7%	59.6	25	48	2	0	0	1109.63	235	244
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	43	0.04%	39.0%	LAVATFAGIENK	99.7%	92.4	25	88.7	2	0	0	1233.68	642	653
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	43	0.04%	39.0%	LQVAGEITTGPR	99.7%	69.4	25	55	2	0	0	1241.69	456	467
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	43	0.04%	39.0%	LTVNDFVR	99.7%	62.6	25	54.4	3	0	0	963.53	409	416
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	43	0.04%	39.0%	MTLADIER	99.7%	44.1	25	39.9	2	0	0	948.48	285	292
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	43	0.04%	39.0%	NGEFFMSPNDFVTR	99.7%	73.1	25	73.1	4	0	0	1676.74	30	43
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	43	0.04%	39.0%	SSPQFGVTLLTYELLQR	99.7%	103	25	102	1	0	0	1952.05	589	605
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	43	0.04%	39.0%	STGSFVGELMYK	99.7%	61	25	54.6	2	0	0	1318.63	361	372
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	43	0.04%	39.0%	TVELLSGVVDQTK	99.7%	104	25	93.3	2	0	0	1388.76	57	69
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	43	0.04%	39.0%	VSALSVVR	99.7%	49.7	25	43.6	2	0	0	830.51	468	475
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	43	0.04%	39.0%	YEGFFGLYR	99.7%	43.7	25	43.7	2	0	0	1151.55	384	392
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	43	0.04%	39.0%	YLNIFGESQPNPK	99.7%	72.2	25	72.2	1	0	0	1506.76	44	56
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	8	9	16	0.02%	22.9%	FISGSMAGATAQTFIYPMEVMK	99.7%	62.2	25	62.2	2	0	0	2380.14	292	313
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	8	9	16	0.02%	22.9%	HEGLGAFYK	99.7%	39.1	25	36.8	2	0	0	1021.51	337	345
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	8	9	16	0.02%	22.9%	MNIFGGFR	99.7%	46	25	36.9	2	0	0	941.47	232	239
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	8	9	16	0.02%	22.9%	NGDGVVDIGELQEGLR	99.7%	85.2	25	79.3	1	0	0	1670.83	34	49
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	8	9	16	0.02%	22.9%	NLGIPLGQDAEEK	99.7%	50.3	25	50.3	2	0	0	1383.71	50	62
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	8	9	16	0.02%	22.9%	QLLAGGIAGAVSR	99.7%	105	25	93.8	2	0	0	1212.71	197	209
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	8	9	16	0.02%	22.9%	TGQYSGIYDCAK	99.7%	72.3	25	72.3	2	0	0	1362.60	321	332
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	8	9	16	0.02%	22.9%	VLPAVGISYVVYENMK	99.7%	66.6	25	66.6	3	0	0	1781.95	454	469
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	4	4	8	0.01%	4.2%	APAEEEVGPR	99.7%	76.6	25	75.4	4	0	0	1054.52	964	973
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	4	4	8	0.01%	4.2%	ASPAAPADGAAPAQPSIR	99.1%	34.3	25	34.3	1	0	0	1647.85	192	209
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	4	4	8	0.01%	4.2%	AVASSPAATNSEVK	99.7%	40.4	25	38.2	2	0	0	1331.68	550	563
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	4	4	8	0.01%	4.2%	LSAALSSLQR	99.7%	40.8	25	27	1	0	0	1045.60	706	715
Calpain-2 catalytic subunit	CAPN2	CAN2_HUMAN	80.0	100.0%	3	3	5	0.00%	4.3%	NFFLTNR	95.7%	27.8	25	7	1	0	0	911.47	451	457
Calpain-2 catalytic subunit	CAPN2	CAN2_HUMAN	80.0	100.0%	3	3	5	0.00%	4.3%	NYPNTFWMNPQYLIK	99.5%	36.9	25	35.2	2	0	0	1928.94	376	390
Calpain-2 catalytic subunit	CAPN2	CAN2_HUMAN	80.0	100.0%	3	3	5	0.00%	4.3%	SDTFINLR	99.7%	54.7	25	25	2	0	0	965.51	462	469
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	6	6	8	0.01%	15.7%	AKEDFLK	97.1%	29.2	25	11.6	1	0	0	850.47	23	29
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	6	6	8	0.01%	15.7%	ATEQYYAMK	96.0%	28	25	27.2	1	0	0	1104.50	65	73
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	6	6	8	0.01%	15.7%	ILQAVNFPFLVR	99.7%	57.9	25	55.6	2	0	0	1416.84	95	106
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	6	6	8	0.01%	15.7%	KVEAPFIPK	99.7%	46.8	25	33.9	2	0	0	1028.61	310	318
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	6	6	8	0.01%	15.7%	NLLQVDLTK	98.5%	32	25	20.9	1	0	0	1043.61	272	280
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	6	6	8	0.01%	15.7%	TLGTGSFGR	99.7%	42.9	25	40.8	1	0	0	895.46	49	57
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	5	5	9	0.01%	30.0%	GKPLALVEEIR	99.7%	39.1	25	39.1	0	1	0	1224.73	149	159

Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	5	5	9	0.01%	30.0%	IGFDVVTLSGTR	99.7%	77.8	25	71.4	2	0	0	1264.69	48	59
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	5	5	9	0.01%	30.0%	QTLSTPGTIILGTIPVPK	99.7%	52.9	25	52.9	2	0	0	1836.08	131	148
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	5	5	9	0.01%	30.0%	RIGFDVVTLSGTR	99.7%	40.3	25	40.3	2	0	0	1420.79	47	59
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	5	5	9	0.01%	30.0%	SSGVPVDGFYTEEVR	99.7%	74.9	25	64.4	2	0	0	1641.78	28	42
Carbonic anhydrase 2	CA2	CAH2_HUMAN	29.2	100.0%	3	3	4	0.00%	13.5%	AVQQPDGLAVLGIFLK	99.1%	34.2	25	34.2	1	0	0	1668.97	133	148
Carbonic anhydrase 2	CA2	CAH2_HUMAN	29.2	100.0%	3	3	4	0.00%	13.5%	GGPLDGTYR	99.7%	43.9	25	41.5	1	0	0	935.46	81	89
Carbonic anhydrase 2	CA2	CAH2_HUMAN	29.2	100.0%	3	3	4	0.00%	13.5%	SADFTNFDPR	99.6%	37.6	25	32.1	2	0	0	1169.52	172	181
Carbonyl reductase [NADPH] 1	CBR1	CBR1_HUMAN	30.4	100.0%	3	3	8	0.01%	15.9%	EYGGLDVLVNNAGIAFK	99.7%	67.4	25	67.4	2	0	0	1779.93	80	96
Carbonyl reductase [NADPH] 1	CBR1	CBR1_HUMAN	30.4	100.0%	3	3	8	0.01%	15.9%	GQAAVQQLQAEGLSPR	99.7%	127	25	117	4	0	0	1652.87	43	58
Carbonyl reductase [NADPH] 1	CBR1	CBR1_HUMAN	30.4	100.0%	3	3	8	0.01%	15.9%	LFSGDVVLTAR	99.7%	81.9	25	72.4	2	0	0	1177.66	28	38
Carboxymethylenebutenolidase homolog	CMBL	CMBL_HUMAN	28.0	100.0%	2	2	3	0.00%	7.4%	AGVSVYGIVK	99.7%	51.6	25	45.3	2	0	0	992.58	150	159
Carboxymethylenebutenolidase homolog	CMBL	CMBL_HUMAN	28.0	100.0%	2	2	3	0.00%	7.4%	LEYGGLGR	94.6%	26.8	25	16.4	1	0	0	864.46	16	23
Cartilage-associated protein	CRTAP	CRTAP_HUMAN	46.6	100.0%	4	5	7	0.01%	12.7%	AFYECLAACEGSR	99.7%	94.6	25	89.8	2	0	0	1533.65	239	251
Cartilage-associated protein	CRTAP	CRTAP_HUMAN	46.6	100.0%	4	5	7	0.01%	12.7%	FLQFAYFK	99.7%	41.6	25	21.4	2	0	0	1063.56	150	157
Cartilage-associated protein	CRTAP	CRTAP_HUMAN	46.6	100.0%	4	5	7	0.01%	12.7%	SLPGAEDYIKDLETK	99.7%	50	25	50	1	0	0	1678.85	190	204
Cartilage-associated protein	CRTAP	CRTAP_HUMAN	46.6	100.0%	4	5	7	0.01%	12.7%	TSITDMELALPDFFK	99.7%	63.3	25	63.3	2	0	0	1727.86	224	238
Casein kinase II subunit alpha	CSNK2A1	CSK21_HUMAN	45.2	100.0%	3	3	5	0.00%	8.4%	GGPNIITLADIVK	99.7%	38.7	25	38.7	2	0	0	1310.77	90	102
Casein kinase II subunit alpha	CSNK2A1	CSK21_HUMAN	45.2	100.0%	3	3	5	0.00%	8.4%	GGPNIITLADIVKDPVSR	99.7%	47.7	25	47.7	2	0	0	1865.05	90	107
Casein kinase II subunit alpha	CSNK2A1	CSK21_HUMAN	45.2	100.0%	3	3	5	0.00%	8.4%	TPALVFEHVNNTDFK	99.7%	43	25	42.2	1	0	0	1731.87	108	122
Casein kinase II subunit alpha'	CSNK2A2	CSK22_HUMAN	41.2	99.8%	2	2	3	0.00%	6.0%	VLGTEELYGYLK	99.5%	36.7	25	31.6	1	0	0	1384.74	249	260
Casein kinase II subunit alpha'	CSNK2A2	CSK22_HUMAN	41.2	99.8%	2	2	3	0.00%	6.0%	VYAEVNSLR	99.7%	57.3	25	47.6	2	0	0	1050.56	12	20
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	10	13	25	0.02%	24.6%	ATHDGAPELGAGGTR	99.7%	52.5	25	39.5	2	2	0	1409.68	332	346
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	10	13	25	0.02%	24.6%	IEGVLLLGEPVR	99.7%	52.9	25	45.2	2	0	0	1294.77	189	200
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	10	13	25	0.02%	24.6%	LFSEYHEK	99.6%	37.4	25	25.5	2	0	0	1052.50	125	132
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	10	13	25	0.02%	24.6%	LFSEYHEKR	99.7%	56.9	25	39.6	2	0	0	1208.61	125	133
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	10	13	25	0.02%	24.6%	LVNSQGQLR	99.7%	57.3	25	46.9	2	0	0	1014.57	74	82
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	10	13	25	0.02%	24.6%	MAFPLLDMVDLER	99.7%	71	25	68.7	5	0	0	1549.78	162	174
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	10	13	25	0.02%	24.6%	MLVSGQGPVMENAQGLGFR	99.7%	88.3	25	88.3	3	0	0	1990.98	134	152
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	10	13	25	0.02%	24.6%	NVVTVDELR	99.7%	46.4	25	26.9	2	0	0	1044.57	153	161
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	10	13	25	0.02%	24.6%	RLVNSQGQLR	99.2%	34.8	25	26.9	1	0	0	1170.67	73	82
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	10	13	25	0.02%	24.6%	VPVVFVTNAGNILQHSK	99.7%	73.5	25	73.5	2	0	0	1823.02	83	99
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	8	8	17	0.02%	9.9%	AAALVLQTIWGYK	99.7%	58.5	25	58.5	2	0	0	1433.82	821	833
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	8	8	17	0.02%	9.9%	ALSAIADLLTNEHER	99.7%	68.1	25	68.1	2	0	0	1652.86	711	725
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	8	8	17	0.02%	9.9%	GIPVLVGLLDHPK	99.7%	51.3	25	51.3	2	0	0	1357.82	409	421
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	8	8	17	0.02%	9.9%	GYELLFQPEVVR	99.7%	60.7	25	44.4	4	0	0	1449.77	655	666
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	8	8	17	0.02%	9.9%	LVENCVCLLR	99.7%	59.8	25	46.2	2	0	0	1275.65	575	584
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	8	8	17	0.02%	9.9%	QDVYGPQPQVR	99.3%	35	25	26.9	1	0	0	1286.65	254	264
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	8	8	17	0.02%	9.9%	SLDNNYSTPNER	99.7%	49.9	25	41.9	2	0	0	1409.63	899	910
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	8	8	17	0.02%	9.9%	VGGSSVDLHR	99.7%	65.7	25	51.3	2	0	0	1026.53	265	274
CCAAT/enhancer-binding protein zeta	CEBPZ	CEBPZ_HUMAN	121.0	100.0%	3	3	4	0.00%	3.2%	ALLVQVVNK	99.7%	51.5	25	44.6	2	0	0	983.62	382	390
CCAAT/enhancer-binding protein zeta	CEBPZ	CEBPZ_HUMAN	121.0	100.0%	3	3	4	0.00%	3.2%	ELLITDLLPDNR	99.3%	35.4	25	33	1	0	0	1411.78	291	302
CCAAT/enhancer-binding protein zeta	CEBPZ	CEBPZ_HUMAN	121.0	100.0%	3	3	4	0.00%	3.2%	GKENTDSVVMQPK	94.5%	26.8	25	26.8	1	0	0	1448.71	769	781
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	21	0.02%	6.8%	AVEGLLDATSGADADLLLR	99.7%	76	25	67.7	1	0	0	1900.00	1665	1683
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	21	0.02%	6.8%	AVQELVHPVVDR	99.7%	41.9	25	37.3	1	0	0	1361.75	1400	1411
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	21	0.02%	6.8%	DAIAALGLLQK	99.7%	46.8	25	33.7	1	0	0	1112.67	1654	1664
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	21	0.02%	6.8%	EVTAAQVAR	99.7%	41.7	25	31.9	2	0	0	944.52	284	292
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	21	0.02%	6.8%	GAFGVGQEQIDAFLK	99.7%	73.6	25	68.6	1	0	0	1579.81	194	208
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	21	0.02%	6.8%	GQQELLYVVPFVAK	99.7%	75.2	25	75.2	2	0	0	1590.89	1228	1241
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	21	0.02%	6.8%	IVEPPENIQEK	99.6%	38.2	25	36.1	1	0	0	1295.68	1088	1098
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	21	0.02%	6.8%	NIIVQFGVR	99.6%	38.4	25	36.8	1	0	0	1045.62	275	283
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	21	0.02%	6.8%	NLDEQLSAPK	99.7%	42.7	25	27.9	1	0	0	1114.57	1311	1320

CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	21	0.02%	6.8%	NLILSAFPR	99.7%	41.5	25	27.2	2	0	0	1030.60	2130	2138
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	21	0.02%	6.8%	SLDLIESLLR	99.7%	73	25	57.9	2	0	0	1158.67	450	459
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	21	0.02%	6.8%	SLLEVVVLSR	99.7%	61.8	25	22.9	2	0	0	1114.68	1641	1650
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	21	0.02%	6.8%	SPVTFLSDLR	99.7%	64	25	49.2	2	0	0	1134.62	2188	2197
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	21	0.02%	6.8%	YLFLNAIANQLR	99.7%	41.4	25	41.4	2	0	0	1435.81	2264	2275
CCR4-NOT transcription complex subunit 2	CNOT2	CNOT2_HUMAN	59.7	99.8%	2	2	3	0.00%	5.6%	EGSGNPTPLINPLAGR	99.7%	57.9	25	57.9	2	0	0	1592.84	240	255
CCR4-NOT transcription complex subunit 2	CNOT2	CNOT2_HUMAN	59.7	99.8%	2	2	3	0.00%	5.6%	TNSMSSSGLGSPNR	99.7%	44.3	25	44.3	1	0	0	1410.63	155	168
CCR4-NOT transcription complex subunit 8	CNOT8	CNOT8_HUMAN	33.5	99.8%	2	2	4	0.00%	8.6%	GGLQEVADQLDLQR	99.7%	82.9	25	75.3	2	0	0	1541.79	207	220
CCR4-NOT transcription complex subunit 8	CNOT8	CNOT8_HUMAN	33.5	99.8%	2	2	4	0.00%	8.6%	LYGLGTGVAQK	99.7%	40.3	25	24.4	2	0	0	1106.62	259	269
CDGSH iron-sulfur domain-containing protein 1	CISD1	CISD1_HUMAN	12.2	99.8%	2	2	2	0.00%	22.2%	AMINLHIQK	96.3%	28.3	25	16.7	1	0	0	1083.60	43	51
CDGSH iron-sulfur domain-containing protein 1	CISD1	CISD1_HUMAN	12.2	99.8%	2	2	2	0.00%	22.2%	HNEETGDNVGPLIIK	97.1%	22.1	25	7.05	0	1	0	1635.83	90	104
CDP-diacylglycerol--inositol 3-phosphatidyltransferase	CDIPT	CDIPT_HUMAN	23.5	99.8%	2	2	3	0.00%	12.2%	MGLWVTAPIALLK	99.7%	41.2	25	32.3	1	0	0	1412.83	174	186
CDP-diacylglycerol--inositol 3-phosphatidyltransferase	CDIPT	CDIPT_HUMAN	23.5	99.8%	2	2	3	0.00%	12.2%	SLISVIHLITAAR	99.7%	64.6	25	64.6	2	0	0	1393.85	187	199
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	8	8	15	0.01%	9.5%	FAEFQYLQPGPPR	99.7%	52.5	25	44.9	1	0	0	1549.78	405	417
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	8	8	15	0.01%	9.5%	FSATEVTNK	99.7%	38.6	25	32.5	2	0	0	996.50	847	855
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	8	8	15	0.01%	9.5%	ILLTLGIR	99.7%	44	25	41.7	2	0	0	898.61	728	735
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	8	8	15	0.01%	9.5%	LAEAEETAR	99.7%	50.1	25	45.9	2	0	0	989.49	868	876
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	8	8	15	0.01%	9.5%	LTPLQLEIQR	94.9%	27.1	25	27.1	1	0	0	1210.72	896	905
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	8	8	15	0.01%	9.5%	SPAPPLLHVAALGQK	99.7%	63.7	25	62.1	2	0	0	1498.87	124	138
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	8	8	15	0.01%	9.5%	VLLLSSPGLEELYR	99.7%	60.6	25	60.6	3	0	0	1588.89	310	323
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	8	8	15	0.01%	9.5%	VVTQNICQYR	99.7%	54.7	25	54.2	2	0	0	1280.64	748	757
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	5	5	10	0.01%	18.4%	ENALLELSK	99.7%	41.2	25	35.4	2	0	0	1016.56	36	44
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	5	5	10	0.01%	18.4%	IYQWINELSSPETR	99.7%	80.3	25	73.1	2	0	0	1735.87	22	35
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	5	5	10	0.01%	18.4%	LTSLGVIGALVK	99.7%	74.4	25	66.2	2	0	0	1170.75	137	148
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	5	5	10	0.01%	18.4%	NLQEGQVTDPR	99.7%	54.2	25	49.3	2	0	0	1256.62	282	292
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	5	5	10	0.01%	18.4%	TVATFILQK	99.7%	63.6	25	48.5	2	0	0	1020.61	180	188
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	5	6	9	0.01%	10.6%	EFYEVVQSQR	99.7%	52.9	25	43.4	2	0	0	1284.62	9	18
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	5	6	9	0.01%	10.6%	LQEFLADMGLPLK	99.7%	54.9	25	52.3	3	0	0	1490.79	311	323
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	5	6	9	0.01%	10.6%	VLLFVASDVDALCACK	99.7%	64.5	25	64.5	1	0	0	1780.90	19	34
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	5	6	9	0.01%	10.6%	VQTFSIHFGFK	99.7%	43.2	25	39.1	1	0	0	1310.69	358	368
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	5	6	9	0.01%	10.6%	YVTDVGVLQR	99.7%	74.5	25	58.3	2	0	0	1149.63	238	247
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	6	6	11	0.01%	9.6%	ESDLPSAILQTSGVSEFTK	99.7%	89.1	25	89.1	2	0	0	2009.01	272	290
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	6	6	11	0.01%	9.6%	GVDYNAEIPFEK	99.7%	44.5	25	44.5	1	0	0	1381.66	207	218
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	6	6	11	0.01%	9.6%	ILLGGYQSR	99.5%	36.6	25	24.5	2	0	0	1006.57	719	727
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	6	6	11	0.01%	9.6%	LGLLGLPAPK	99.7%	69.3	25	69.3	2	0	0	978.63	478	487
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	6	6	11	0.01%	9.6%	LVLPAPQISDAELQEVVK	99.7%	71.2	25	69.9	2	0	0	1949.10	295	312
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	6	6	11	0.01%	9.6%	VGQASEIAR	99.7%	54.9	25	38	2	0	0	930.50	313	321
Cell division cycle protein 16 homolog	CDC16	CDC16_HUMAN	71.7	100.0%	4	4	4	0.00%	5.5%	IYDALDNR	99.7%	38.8	25	30.9	1	0	0	979.48	139	146
Cell division cycle protein 16 homolog	CDC16	CDC16_HUMAN	71.7	100.0%	4	4	4	0.00%	5.5%	LCNEEQELLR	99.4%	35.8	25	29.1	1	0	0	1303.63	193	202
Cell division cycle protein 16 homolog	CDC16	CDC16_HUMAN	71.7	100.0%	4	4	4	0.00%	5.5%	SSICLLR	98.3%	31.3	25	9.28	1	0	0	848.47	130	136
Cell division cycle protein 16 homolog	CDC16	CDC16_HUMAN	71.7	100.0%	4	4	4	0.00%	5.5%	YAEALDYHR	97.4%	29.7	25	21.8	1	0	0	1137.53	461	469
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	5	5	7	0.01%	10.2%	AWYGLGQTYEILK	99.7%	53	25	48.2	2	0	0	1541.80	401	413
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	5	5	7	0.01%	10.2%	AYAVGDVEK	99.7%	42.6	25	32.2	1	0	0	951.48	459	467
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	5	5	7	0.01%	10.2%	IENMDTFSNLLYVR	99.2%	34.7	25	27.2	2	0	0	1714.85	297	310
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	5	5	7	0.01%	10.2%	MLVALGECYEK	97.9%	30.5	25	30.5	1	0	0	1328.62	435	445
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	5	5	7	0.01%	10.2%	VETCCVIGNYYSLR	99.7%	43.5	25	43.5	1	0	0	1733.80	331	344
Cell division cycle protein 27 homolog	CDC27	CDC27_HUMAN	91.9	100.0%	3	3	3	0.00%	4.9%	ESLVYFLIGK	97.9%	30.6	25	30.6	1	0	0	1168.66	736	745
Cell division cycle protein 27 homolog	CDC27	CDC27_HUMAN	91.9	100.0%	3	3	3	0.00%	4.9%	ISTITPQIQAFNLQK	96.9%	29	25	22.2	1	0	0	1701.95	442	456
Cell division cycle protein 27 homolog	CDC27	CDC27_HUMAN	91.9	100.0%	3	3	3	0.00%	4.9%	LAEGEQILSGGVFNK	99.7%	76.5	25	68.5	1	0	0	1561.82	85	99
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	3	3	5	0.00%	7.4%	ELLEQISAFDNVPR	99.7%	71.9	25	71	2	0	0	1630.84	96	109
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	3	3	5	0.00%	7.4%	VKDAVEQQGEVK	99.7%	75.3	25	62.6	2	0	0	1329.70	174	185

Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	3	3	5	0.00%	7.4%	VRELLEQISAFDNVPR	99.7%	36.8	25	33.7	0	1	0	1886.01	94	109
Cellular tumor antigen p53	TP53	P53_HUMAN	43.7	100.0%	4	4	11	0.01%	11.5%	ALPNNTSSSPQPK	99.7%	54.7	25	46	4	0	0	1340.68	307	319
Cellular tumor antigen p53	TP53	P53_HUMAN	43.7	100.0%	4	4	11	0.01%	11.5%	SVTCTYSPALNK	99.7%	53.1	25	50.6	4	0	0	1340.65	121	132
Cellular tumor antigen p53	TP53	P53_HUMAN	43.7	100.0%	4	4	11	0.01%	11.5%	TYQGSYGFR	97.3%	29.6	25	29.5	2	0	0	1078.50	102	110
Cellular tumor antigen p53	TP53	P53_HUMAN	43.7	100.0%	4	4	11	0.01%	11.5%	VEYLDDRNTFR	96.0%	28	25	24.9	1	0	0	1427.69	203	213
Centlein	CNTLN	CNTLN_HUMAN	161.6	99.8%	2	2	3	0.00%	1.3%	SSHTAVPTR	96.6%	28.6	25	10.4	2	0	0	955.50	955	963
Centlein	CNTLN	CNTLN_HUMAN	161.6	99.8%	2	2	3	0.00%	1.3%	SSSNIILLR	99.6%	38.4	25	3.16	1	0	0	1002.59	977	985
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	5	7	10	0.01%	30.2%	LLLDTFEYQGLVK	99.7%	57.8	25	49.5	2	0	0	1538.85	135	147
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	5	7	10	0.01%	30.2%	SGASGASAAPAASAAAALAPSATR	99.7%	99.8	25	99.8	2	1	0	1985.00	18	41
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	5	7	10	0.01%	30.2%	SMVTEEFNGSDWEK	99.7%	39.7	25	39.7	2	0	0	1658.70	248	261
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	5	7	10	0.01%	30.2%	SNPGGFGIAPHCLDEGTVR	99.7%	39	25	39	0	2	0	1983.93	229	247
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	5	7	10	0.01%	30.2%	SQAVEKPPSEKPR	98.0%	23.2	25	23.2	0	1	0	1452.78	53	65
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	6	6	10	0.01%	9.2%	AMGTLLNTAISEVIGK	99.7%	65.8	25	65.8	2	0	0	1633.88	652	667
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	6	6	10	0.01%	9.2%	DSVVLSLLK	99.7%	50.8	25	36.3	1	0	0	973.59	102	110
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	6	6	10	0.01%	9.2%	LEKEDLGTR	99.7%	45.3	25	38.8	2	0	0	1060.56	15	23
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	6	6	10	0.01%	9.2%	NLMTSEIHNTVK	99.7%	56.1	25	56.1	1	0	0	1402.70	413	424
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	6	6	10	0.01%	9.2%	QLLDLPLDTDLENEK	99.7%	70.6	25	69.1	2	0	0	1755.90	306	320
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	6	6	10	0.01%	9.2%	YQEEVPVYVPK	99.7%	53.8	25	39	2	0	0	1350.69	709	719
Chitobiosyldiphosphodolichol beta-mannosyltransferase	ALG1	ALG1_HUMAN	52.5	99.8%	2	3	4	0.00%	5.6%	ETPLDLQHR	99.7%	41.7	25	32.2	1	0	0	1108.57	224	232
Chitobiosyldiphosphodolichol beta-mannosyltransferase	ALG1	ALG1_HUMAN	52.5	99.8%	2	3	4	0.00%	5.6%	IQIVGLTELQSLAVGPR	99.7%	60.1	25	60.1	2	1	0	1794.05	83	99
Chloride channel CLIC-like protein 1	CLCC1	CLCC1_HUMAN	62.0	100.0%	3	3	5	0.00%	6.2%	AFDVPDAEAR	99.6%	37.9	25	27.9	2	0	0	1090.52	444	453
Chloride channel CLIC-like protein 1	CLCC1	CLCC1_HUMAN	62.0	100.0%	3	3	5	0.00%	6.2%	ETGGILGEGTPK	99.0%	33.7	25	24.8	1	0	0	1158.60	473	484
Chloride channel CLIC-like protein 1	CLCC1	CLCC1_HUMAN	62.0	100.0%	3	3	5	0.00%	6.2%	LAFAQHQAEVAK	99.7%	54.9	25	48.7	2	0	0	1312.70	235	246
Chloride intracellular channel protein 1	CLIC1	CLIC1_HUMAN	26.9	100.0%	3	3	5	0.00%	15.8%	LAALNPESNTAGLDIFAK	99.7%	50.5	25	50.5	2	0	0	1844.98	96	113
Chloride intracellular channel protein 1	CLIC1	CLIC1_HUMAN	26.9	100.0%	3	3	5	0.00%	15.8%	NSNPALNDNLEK	99.7%	40	25	33	2	0	0	1328.64	120	131
Chloride intracellular channel protein 1	CLIC1	CLIC1_HUMAN	26.9	100.0%	3	3	5	0.00%	15.8%	YLSNAYAR	95.2%	27.3	25	14.3	1	0	0	957.48	209	216
Chromatin target of PRMT1 protein	CHTOP	CHTOP_HUMAN	26.4	100.0%	3	7	18	0.02%	16.9%	ASMQQQQQLASAR	99.7%	80.1	25	65.6	10	0	0	1462.71	39	51
Chromatin target of PRMT1 protein	CHTOP	CHTOP_HUMAN	26.4	100.0%	3	7	18	0.02%	16.9%	EQLDNQLDAYMSK	99.7%	92.1	25	92.1	2	0	0	1570.71	214	226
Chromatin target of PRMT1 protein	CHTOP	CHTOP_HUMAN	26.4	100.0%	3	7	18	0.02%	16.9%	LAQQMENRPSVQAALK	99.7%	53.1	25	27.2	3	3	0	1783.95	55	70
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	3	3	3	0.00%	3.2%	GIPTYIYYFPR	98.8%	32.9	25	32.2	1	0	0	1389.72	867	877
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	3	3	3	0.00%	3.2%	LLQPFLLR	99.7%	45.9	25	36.8	1	0	0	999.64	253	260
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	3	3	3	0.00%	3.2%	SFEQLVNLQK	99.7%	40.4	25	26.8	1	0	0	1205.65	591	600
Chromosome transmission fidelity protein 18 homolog	CHTF18	CTF18_HUMAN	107.4	100.0%	3	3	4	0.00%	3.6%	NLIQTLVSGIAPATR	99.7%	52.8	25	52.8	1	0	0	1553.90	735	749
Chromosome transmission fidelity protein 18 homolog	CHTF18	CTF18_HUMAN	107.4	100.0%	3	3	4	0.00%	3.6%	TTLAHVIAR	99.6%	38.2	25	34.1	1	0	0	981.58	381	389
Chromosome transmission fidelity protein 18 homolog	CHTF18	CTF18_HUMAN	107.4	100.0%	3	3	4	0.00%	3.6%	VVQGLFDNFLR	99.7%	47	25	42.5	2	0	0	1307.71	648	658
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	ALEHFTDLYDIKR	99.7%	55.6	25	52.4	0	2	0	1620.84	626	638
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	ENPYYDSR	99.5%	36.7	25	30.3	1	0	0	1043.44	896	903
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	ESYVETELIFALAK	99.7%	71.4	25	65.3	2	0	0	1612.85	1166	1179
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	EVCFACVDGK	99.7%	42.9	25	42.9	1	0	0	1184.51	1255	1264
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	GQCDLELINVCNENSLFK	99.7%	72.6	25	72.6	1	0	0	2153.00	924	941
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	HSSLAGCQIINYR	99.7%	52.6	25	52.6	1	0	0	1518.75	145	157
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	IAAYLFK	98.6%	32.2	25	18.9	1	0	0	825.49	1510	1516
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	IHEGCEEPATHNALAK	97.0%	22	25	22	0	1	0	1776.83	866	881
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	ISGETIFVTAPHEATAGIIGVNR	99.7%	56.5	25	56.5	0	2	0	2353.25	298	320
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	IVLDNSVFSEHR	99.7%	71.7	25	71.7	2	2	0	1415.73	1011	1022
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	IYIDSNNNPER	99.7%	65.2	25	54.3	3	0	0	1334.63	882	892
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	KFNALFAQGNYSEAAK	99.5%	27.5	25	26.4	0	1	0	1758.88	367	382
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	LASTLVHLGEYQAAVDGAR	99.7%	34.3	25	34.3	0	1	0	1971.03	1227	1245
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	LHIIEVGTPPTGNQPFPK	99.7%	30.8	25	30.8	0	2	0	1945.05	228	245
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	LLLPWLEAR	99.7%	38.8	25	22.1	1	0	0	1110.67	857	865
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	LLYNNVSNFGR	99.7%	54.3	25	51.5	2	0	0	1296.67	1216	1226

Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	LPVVIGGLLDVDCSEDVIK	99.7%	76.7	25	76.7	3	0	0	2041.09	812	830
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	NLQNLLILTAIK	99.7%	86.1	25	84.7	8	0	0	1353.85	1023	1034
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	NNLAGAEELFAR	99.7%	85.4	25	81.8	2	0	0	1304.66	355	366
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	NNRPSEGPLQTR	99.7%	31.5	25	26.9	0	1	0	1368.70	572	583
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	SVDPTLALSVYLR	99.7%	52.7	25	52.7	2	0	0	1433.80	469	481
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	TLQIFNIEMK	99.7%	57	25	47	2	0	0	1252.66	87	96
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	VANVELYYR	99.7%	75.3	25	71.1	2	0	0	1126.59	1398	1406
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	VGYTPDWIFLLR	99.7%	48.5	25	40.9	2	0	0	1479.80	508	519
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	VIQCFAETGQVQK	99.7%	93.2	25	82	2	0	0	1507.76	488	500
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	VVGAMQLYSVDR	99.7%	69.4	25	63.2	2	0	0	1337.69	177	188
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	27	28	54	0.05%	21.2%	WLLLTGISAQQNR	99.7%	77.3	25	71.3	2	0	0	1499.83	164	176
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	5	5	8	0.01%	3.6%	EVLLVALGSR	99.7%	81.3	25	66.6	2	0	0	1056.64	848	857
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	5	5	8	0.01%	3.6%	NVLDGELLNR	99.7%	60.9	25	45.6	2	0	0	1142.62	1397	1406
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	5	5	8	0.01%	3.6%	SSFLPSYIIDVR	99.7%	61.3	25	48.2	2	0	0	1396.75	183	194
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	5	5	8	0.01%	3.6%	YIVQVSPLGIR	99.7%	38.7	25	23.7	1	0	0	1244.74	617	627
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	5	5	8	0.01%	3.6%	YLYLSTMER	97.6%	30.1	25	24.5	1	0	0	1175.58	1407	1415
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	2	2	4	0.00%	11.9%	LFLVQLQEK	99.7%	63.3	25	51.2	2	0	0	1117.66	174	182
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	2	2	4	0.00%	11.9%	LPGGELNPGEDEVEGLKR	99.7%	74.3	25	74	0	2	0	1908.97	106	123
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	5	6	10	0.01%	11.1%	AISSSAISR	99.6%	37.8	25	25.7	1	0	0	891.49	423	431
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	5	6	10	0.01%	11.1%	GAAPNVVYTYTGK	99.7%	83.6	25	81.1	2	0	0	1340.68	67	79
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	5	6	10	0.01%	11.1%	GFALVGVGSEASSK	99.7%	103	25	91.8	2	0	0	1308.68	125	138
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	5	6	10	0.01%	11.1%	QFLSQFEMQSR	99.7%	57.2	25	57.1	1	0	0	1400.66	162	172
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	5	6	10	0.01%	11.1%	TPLSEAEFEEIMNR	99.7%	105	25	101	4	0	0	1665.78	407	420
CLIP-associating protein 2	CLASP2	CLAP2_HUMAN	141.1	99.8%	2	2	3	0.00%	2.6%	VLNTGSDVEEAVADALK	99.7%	70.8	25	69.8	1	0	0	1730.88	591	607
CLIP-associating protein 2	CLASP2	CLAP2_HUMAN	141.1	99.8%	2	2	3	0.00%	2.6%	VLTTTALSTVSSGVQR	99.7%	75	25	66.7	2	0	0	1619.90	467	482
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	47	0.05%	23.4%	ASNLENSTYDLYTIPK	99.7%	107	25	99.1	2	0	0	1828.90	383	398
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	47	0.05%	23.4%	CPLSGACYSPEFK	99.7%	45.9	25	45.9	2	0	0	1515.66	1185	1197
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	47	0.05%	23.4%	DADSQNPDAPEGKR	99.7%	41.5	25	41.5	1	0	0	1499.67	399	412
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	47	0.05%	23.4%	DVAVMQLR	99.7%	45.7	25	29.6	4	0	0	931.50	351	358
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	47	0.05%	23.4%	GFFEGTIASK	99.7%	58.9	25	58.9	3	0	0	1056.54	816	825
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	47	0.05%	23.4%	GITGVDLFGTTDAVVK	99.7%	94.3	25	90.7	2	0	0	1592.85	183	198
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	47	0.05%	23.4%	ISPLQFR	95.7%	27.7	25	20.1	1	0	0	860.50	1218	1224
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	47	0.05%	23.4%	KYDEVLHMVR	99.7%	31	25	27.9	0	2	0	1305.66	607	616
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	47	0.05%	23.4%	LLELGPKPEVAQQTR	99.7%	53.7	25	43.2	0	2	0	1678.95	1128	1142
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	47	0.05%	23.4%	LLHDQVGVIQFGPYK	95.1%	20.5	25	20.5	0	1	0	1713.93	942	956
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	47	0.05%	23.4%	LNDLIQR	99.7%	56.2	25	41.8	2	0	0	871.50	1003	1009
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	47	0.05%	23.4%	LSFLYLITGNLEK	99.7%	65.4	25	65.4	1	0	0	1510.85	703	715
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	47	0.05%	23.4%	LVGQSIIAYLQK	99.7%	91	25	91	2	0	0	1332.79	620	631
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	47	0.05%	23.4%	NLSPGAVESDVR	99.7%	58.5	25	46.5	2	0	0	1243.63	171	182
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	47	0.05%	23.4%	QELILSNSEDK	99.7%	39.3	25	29.2	1	0	0	1275.64	261	271
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	47	0.05%	23.4%	QLFLQTYAR	99.7%	52	25	37.2	2	0	0	1139.62	957	965
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	47	0.05%	23.4%	QQPLFVSGGDDYK	96.2%	28.2	25	28	1	0	0	1453.70	62	74
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	47	0.05%	23.4%	SILLSVPLLVVDNK	99.7%	69.9	25	69.9	3	0	0	1509.93	1031	1044
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	47	0.05%	23.4%	SSGLTAVWVAR	99.7%	75.1	25	46.5	2	0	0	1146.63	413	423
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	47	0.05%	23.4%	TALNLFFK	99.7%	55	25	43.6	1	0	0	953.55	1107	1114
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	47	0.05%	23.4%	TGVQTFR	98.1%	31	25	20.1	2	0	0	808.43	282	288
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	47	0.05%	23.4%	VLTIDPTEFK	99.6%	38.1	25	34.8	2	0	0	1162.64	589	598
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	47	0.05%	23.4%	VTTVTEIGKDVIGLR	99.7%	70.9	25	70.9	2	0	0	1600.93	1203	1217
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	47	0.05%	23.4%	VWDISGLR	99.7%	51.9	25	28.3	2	0	0	945.52	161	168
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	47	0.05%	23.4%	YAVTTGDHGIIR	99.7%	66.3	25	56.7	2	0	0	1302.68	551	562
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	26	31	62	0.06%	31.9%	AAAQCYIDLIIK	99.7%	69.7	25	59.3	2	0	0	1378.74	280	291

Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	26	31	62	0.06%	31.9%	ALSGYCGFMAANLYAR	99.7%	92.4	25	92.4	2	0	0	1764.82	883	898
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	26	31	62	0.06%	31.9%	CIYNLLQSSSPAVK	99.7%	99.9	25	96.1	2	0	0	1579.81	248	261
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	26	31	62	0.06%	31.9%	DLQHPNEFIR	99.7%	43.9	25	34.4	2	0	0	1268.64	108	117
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	26	31	62	0.06%	31.9%	EAELLEPLMPAIR	99.7%	41.7	25	29	2	0	0	1481.80	129	141
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	26	31	62	0.06%	31.9%	EAGELKPEEEITVGPVQK	99.7%	52.7	25	51.8	2	0	0	1953.02	496	513
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	26	31	62	0.06%	31.9%	GALWILGEYCSTK	99.7%	59.3	25	59.3	2	0	0	1497.74	457	469
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	26	31	62	0.06%	31.9%	KPITDDDVDR	99.7%	54	25	33.7	2	0	0	1173.57	603	612
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	26	31	62	0.06%	31.9%	LKEAELLEPLMPAIR	99.4%	27	25	21.6	0	1	0	1738.98	127	141
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	26	31	62	0.06%	31.9%	LLLVFWEIVPK	99.7%	38.6	25	38.6	2	0	0	1356.83	77	87
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	26	31	62	0.06%	31.9%	LPGLLMTIIR	99.7%	58.8	25	52.8	4	0	0	1126.70	55	64
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	26	31	62	0.06%	31.9%	LVTEMGTYATQSALSSSRPTK	99.7%	33.4	25	30.6	0	3	0	2244.12	514	534
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	26	31	62	0.06%	31.9%	MLEVFHAIK	99.7%	46.2	25	36.3	2	0	0	1087.60	442	450
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	26	31	62	0.06%	31.9%	NAVLAIYTIYR	99.7%	82.8	25	82.8	4	0	0	1296.73	154	164
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	26	31	62	0.06%	31.9%	NVEELVIVLK	99.7%	47.8	25	38.5	2	0	0	1155.70	352	361
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	26	31	62	0.06%	31.9%	NVEELVIVLKK	99.7%	47.1	25	43.1	2	0	0	1283.79	352	362
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	26	31	62	0.06%	31.9%	NVTVQPDDPISFMQLTAK	99.7%	76	25	74.4	4	0	0	2004.01	662	679
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	26	31	62	0.06%	31.9%	SLGEIPIVESEIKK	99.7%	56.9	25	56.9	2	0	0	1541.88	482	495
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	26	31	62	0.06%	31.9%	SQGMALSLGDK	99.7%	47.9	25	36	2	0	0	1106.55	933	943
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	26	31	62	0.06%	31.9%	TLQLALDLVSSR	99.7%	96.3	25	96.3	3	0	0	1315.76	340	351
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	26	31	62	0.06%	31.9%	TNNVSEHEDTDKYR	99.7%	45.4	25	45.4	0	1	0	1707.76	367	380
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	26	31	62	0.06%	31.9%	VIIMILNGEK	99.7%	44.7	25	37.6	2	0	0	1129.67	45	54
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	26	31	62	0.06%	31.9%	VLQDLVMDILR	99.7%	75.4	25	63.5	6	0	0	1314.75	317	327
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	26	31	62	0.06%	31.9%	VLSECSPLMNDIFNK	99.7%	84.3	25	84.3	3	0	0	1766.85	619	633
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	26	31	62	0.06%	31.9%	VLSTPDLEVR	95.8%	27.8	25	20	1	0	0	1128.63	328	337
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	26	31	62	0.06%	31.9%	YVALVQEK	99.7%	38.8	25	29.7	2	0	0	949.54	568	575
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	5	5	9	0.01%	6.4%	AAESLADPTEYENLFPGLK	99.7%	54.2	25	54.2	2	0	0	2065.01	784	802
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	5	5	9	0.01%	6.4%	HSEVQQANLK	99.7%	43.2	25	40.2	3	0	0	1153.60	319	328
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	5	5	9	0.01%	6.4%	TFEVCDLPVR	99.6%	38	25	32.9	1	0	0	1235.61	52	61
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	5	5	9	0.01%	6.4%	TMYLLGYIPK	99.7%	43.5	25	41.3	1	0	0	1198.65	560	569
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	5	5	9	0.01%	6.4%	VFNYNTLER	99.7%	41.7	25	34.3	2	0	0	1155.58	83	91
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	31	0.03%	34.6%	ENVNLAQIR	99.7%	78.7	25	66.4	2	0	0	1056.58	123	131
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	31	0.03%	34.6%	GVQLQTHPNVDKK	99.0%	33.7	25	33.7	1	0	0	1463.80	324	336
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	31	0.03%	34.6%	IEGLLAAFPK	99.7%	48.9	25	36	2	0	0	1058.62	29	38
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	31	0.03%	34.6%	KNYCNIQVTK	99.7%	42.6	25	41.6	2	0	0	1267.65	476	485
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	31	0.03%	34.6%	LFTAESLIGLK	99.7%	81	25	69	2	0	0	1191.70	337	347
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	31	0.03%	34.6%	LYMVLITTK	99.7%	62.1	25	62.1	2	0	0	1081.63	64	72
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	31	0.03%	34.6%	NSNILEDLETLR	99.7%	88.3	25	80.8	2	0	0	1416.73	73	84
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	31	0.03%	34.6%	NTLEWCLPVIDAK	99.7%	65.6	25	53.5	2	0	0	1558.79	436	448
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	31	0.03%	34.6%	NYCNIQVTK	99.7%	47.1	25	35.9	2	0	0	1139.55	477	485
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	31	0.03%	34.6%	QFVEMTR	99.6%	37.5	25	19.1	2	0	0	910.45	20	26
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	31	0.03%	34.6%	QHTFVETESVR	96.6%	28.6	25	26.1	1	0	0	1332.65	45	55
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	31	0.03%	34.6%	SEGETIMSSSMGK	99.7%	43.9	25	43	1	0	0	1343.58	244	256
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	31	0.03%	34.6%	SFPVNSDVGVLK	99.7%	54.8	25	51.7	2	0	0	1261.68	352	363
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	31	0.03%	34.6%	TFTEMDSHEEK	99.7%	44.5	25	40.4	2	0	0	1353.56	132	142
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	31	0.03%	34.6%	TRIEGLLAAFPK	99.7%	50.1	25	40.7	1	0	0	1315.77	27	38
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	31	0.03%	34.6%	VAPAPARPSGPSK	99.3%	35.3	25	20.2	1	0	0	1234.69	212	224
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	31	0.03%	34.6%	VLLAAAVCTK	99.7%	70.6	25	66.6	2	0	0	1045.61	2	11
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	31	0.03%	34.6%	VTQVDGNSPVR	99.7%	54.3	25	38.5	2	0	0	1171.61	486	496
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	5	5	8	0.01%	22.4%	APPAPGPASGGSGEVDELFDVK	99.7%	40.3	25	40.3	1	0	0	2097.01	2	23
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	5	5	8	0.01%	22.4%	DVERDVFLYR	98.8%	32.9	25	23.2	2	0	0	1311.67	49	58
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	5	5	8	0.01%	22.4%	ENDFDRLVLQYAPSA	97.6%	30	25	28.9	1	0	0	1737.84	294	308

Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	5	5	8	0.01%	22.4%	LDRLDLAR	98.3%	31.4	25	23.4	2	0	0	971.56	159	166
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	5	5	8	0.01%	22.4%	LQDAYYIFQEMADK	99.7%	54.9	25	51.4	2	0	0	1734.80	198	211
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	19	21	45	0.04%	30.0%	ALCQITDSTMLQAIER	99.7%	64.3	25	64.3	1	0	0	1849.91	127	142
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	19	21	45	0.04%	30.0%	ALQQYTLEPSEKPFDLK	99.7%	36.7	25	33	0	2	0	2007.04	561	577
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	19	21	45	0.04%	30.0%	ATFYLNVLEQK	99.7%	63.3	25	45.5	2	0	0	1325.71	528	538
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	19	21	45	0.04%	30.0%	ELAPAVSVLQLFCSSPK	99.7%	116	25	116	4	0	0	1845.98	284	300
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	19	21	45	0.04%	30.0%	EMSCIAEDVIIVTSSLTK	99.7%	86.4	25	79.5	2	0	0	1996.00	94	111
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	19	21	45	0.04%	30.0%	FGAQNEEMLPSILVLLK	99.7%	65.9	25	65.8	2	0	0	1902.04	498	514
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	19	21	45	0.04%	30.0%	ILHLLGQEGPK	99.7%	36.9	25	36.9	2	2	0	1204.71	455	465
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	19	21	45	0.04%	30.0%	LFQSNDPTLR	99.7%	45.5	25	36.9	1	0	0	1190.62	76	85
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	19	21	45	0.04%	30.0%	LLLLDTVTMQVTAR	99.7%	73.3	25	73.3	2	0	0	1589.89	846	859
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	19	21	45	0.04%	30.0%	QEIFQEQLAAVPEFR	99.7%	63.7	25	53.1	2	0	0	1804.92	610	624
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	19	21	45	0.04%	30.0%	SAVLQEAR	99.7%	40.2	25	12.6	2	0	0	873.48	25	32
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	19	21	45	0.04%	30.0%	SIATLAITTLLK	99.7%	97.7	25	97.7	7	0	0	1244.78	339	350
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	19	21	45	0.04%	30.0%	SLEELPVDIILASVG	97.8%	30.3	25	29.4	1	0	0	1554.86	860	874
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	19	21	45	0.04%	30.0%	SLPYNQPGTCYTLVALPK	99.7%	76.2	25	75.2	2	0	0	2022.04	697	714
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	19	21	45	0.04%	30.0%	SSPEPVALTESETEYVIR	99.7%	111	25	104	2	0	0	2006.99	632	649
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	19	21	45	0.04%	30.0%	SVPLATAPMAEQR	99.7%	45.6	25	44.2	2	0	0	1386.70	578	590
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	19	21	45	0.04%	30.0%	VFNETPINPR	99.4%	36.3	25	30.2	2	0	0	1186.62	33	42
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	19	21	45	0.04%	30.0%	VVLEHEEVR	99.7%	49.7	25	46.3	3	0	0	1109.59	480	488
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	19	21	45	0.04%	30.0%	VVVVQAISALCQK	99.7%	52.8	25	52.8	2	0	0	1414.81	377	389
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	8	8	17	0.02%	14.9%	AEITLVATKPEK	99.7%	44.3	25	44.3	1	0	0	1299.75	591	602
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	8	8	17	0.02%	14.9%	AIVDCIISIVEENPESK	99.7%	64.2	25	64.2	1	0	0	1915.97	416	432
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	8	8	17	0.02%	14.9%	ATFYLNVLQQR	99.7%	58.2	25	46.6	4	0	0	1352.73	528	538
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	8	8	17	0.02%	14.9%	EMATISEDVIIVTSSLTK	99.7%	62	25	62	1	0	0	1937.01	94	111
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	8	8	17	0.02%	14.9%	IFNETPINPR	99.7%	51.7	25	37.6	4	0	0	1200.64	33	42
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	8	8	17	0.02%	14.9%	ISYDVVKR	99.7%	40	25	18.8	1	0	0	979.56	169	176
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	8	8	17	0.02%	14.9%	ITDGTMLQAIER	99.7%	48.2	25	27.4	1	0	0	1347.69	131	142
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	8	8	17	0.02%	14.9%	SAVLQEAR	99.7%	40.2	25	12.6	2	0	0	873.48	25	32
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	8	8	17	0.02%	14.9%	SIATLAITTLLK	99.7%	97.7	25	97.7	7	0	0	1244.78	339	350
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	8	8	17	0.02%	14.9%	VVLENEAVR	99.7%	62.7	25	56.5	4	0	0	1028.57	480	488
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	8	8	17	0.02%	14.9%	VVVVQAISALCQK	99.7%	52.8	25	52.8	2	0	0	1414.81	377	389
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	4	4	10	0.01%	26.5%	AVLFCLSEDKK	99.7%	61.5	25	56.3	2	0	0	1309.68	35	45
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	4	4	10	0.01%	26.5%	LGGSAVISLEGKPL	99.7%	73.7	25	63	5	0	0	1340.78	153	166
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	4	4	10	0.01%	26.5%	VFNDMKVR	98.2%	31.2	25	21.5	1	0	0	1024.52	14	21
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	4	4	10	0.01%	26.5%	YALYDATYETK	99.7%	67.1	25	62.3	2	0	0	1337.63	82	92
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	7	7	10	0.01%	7.0%	FALTFGLDQLK	99.7%	51.1	25	0	2	0	0	1252.69	955	965
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	7	7	10	0.01%	7.0%	HTDTDVLEACSK	97.2%	29.4	25	22.3	1	0	0	1375.62	623	634
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	7	7	10	0.01%	7.0%	ITELFAVALPQLLAK	99.7%	39.1	25	39.1	1	0	0	1626.98	563	577
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	7	7	10	0.01%	7.0%	MYSDAFLNDSYLK	99.7%	59	25	59	1	0	0	1566.71	318	330
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	7	7	10	0.01%	7.0%	SQLIDELADKFNR	99.5%	37.1	25	31.6	1	0	0	1548.80	655	667
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	7	7	10	0.01%	7.0%	SSFCEFIGVLVR	99.7%	60.9	25	59.2	2	0	0	1413.72	173	184
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	7	7	10	0.01%	7.0%	YYNDYGDIIK	99.7%	53.8	25	51.8	2	0	0	1263.59	892	901
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	10	19	0.02%	24.4%	ARVEENFLK	99.7%	49	25	34.4	2	0	0	1105.60	411	419
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	10	19	0.02%	24.4%	ELLESNFTLVGDDGTNK	99.7%	92.4	25	92.4	2	0	0	1851.90	173	189
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	10	19	0.02%	24.4%	ELLESNFTLVGDDGTNKEATSTGK	99.7%	44.1	25	44.1	0	2	0	2526.22	173	196
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	10	19	0.02%	24.4%	EMQDLSEFCSDKPK	99.7%	68.6	25	65.4	2	0	0	1713.75	275	288
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	10	19	0.02%	24.4%	IMNEEDPEKQR	99.7%	51.5	25	51.5	2	0	0	1388.65	444	454
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	10	19	0.02%	24.4%	IMQEEGQPLK	99.6%	37.4	25	30.6	1	0	0	1172.60	342	351
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	10	19	0.02%	24.4%	MMRPVSDQVQIK	99.5%	27.5	25	23.9	0	2	0	1463.73	237	248
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	10	19	0.02%	24.4%	RQDLLNVLAR	99.7%	45.4	25	39	2	0	0	1197.71	227	236

Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	10	19	0.02%	24.4%	TLLFTFNVPGSGNTYPK	99.7%	55.2	25	54.8	2	0	0	1855.96	358	374
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	10	19	0.02%	24.4%	VCCEGMLIQLR	99.7%	64	25	58.1	2	0	0	1378.66	213	223
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	7	7	12	0.01%	25.6%	AAANEQLTR	99.7%	53.9	25	46.7	2	0	0	973.51	96	104
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	7	7	12	0.01%	25.6%	LSENVIDR	99.7%	54.5	25	45.7	2	0	0	945.50	28	35
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	7	7	12	0.01%	25.6%	RVAEELALEQAK	99.2%	34.7	25	24.1	1	0	0	1356.75	65	76
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	7	7	12	0.01%	25.6%	VAEELALEQAK	99.7%	83.9	25	74.7	2	0	0	1200.65	66	76
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	7	7	12	0.01%	25.6%	YESHPVCADLQAK	99.6%	37.4	25	37.3	1	0	0	1517.71	177	189
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	7	7	12	0.01%	25.6%	YSGAYGASVSDEELK	99.7%	103	25	103	2	0	0	1575.72	49	63
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	7	7	12	0.01%	25.6%	YSGAYGASVSDEELKR	99.7%	93.2	25	90.5	2	0	0	1731.82	49	64
COMM domain-containing protein 2	COMMD2	COMD2_HUMAN	22.7	99.8%	2	2	3	0.00%	7.5%	IAVEFLR	99.7%	44	25	26.8	2	0	0	847.50	30	36
COMM domain-containing protein 2	COMMD2	COMD2_HUMAN	22.7	99.8%	2	2	3	0.00%	7.5%	LDVQLASR	98.3%	31.4	25	23.6	1	0	0	901.51	131	138
Complement C3	C3	CO3_HUMAN	187.1	100.0%	3	3	3	0.00%	2.3%	EPGQDLVVLPLSITTDFIPSFR	99.7%	46.3	25	46.3	1	0	0	2444.31	509	530
Complement C3	C3	CO3_HUMAN	187.1	100.0%	3	3	3	0.00%	2.3%	LPYSVVR	99.7%	46.7	25	38.4	1	0	0	833.49	835	841
Complement C3	C3	CO3_HUMAN	187.1	100.0%	3	3	3	0.00%	2.3%	NTLIIYLDK	99.7%	45.6	25	45.1	1	0	0	1092.63	1442	1450
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	C1QBP_HUMAN	31.4	100.0%	4	6	12	0.01%	22.0%	AFVDFLSDEIKEER	99.7%	80.9	25	77.7	2	2	0	1697.84	81	94
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	C1QBP_HUMAN	31.4	100.0%	4	6	12	0.01%	22.0%	EVSFQSTGESEWK	99.7%	90.7	25	79.4	2	0	0	1513.68	208	220
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	C1QBP_HUMAN	31.4	100.0%	4	6	12	0.01%	22.0%	MSGGWELELNGTEAK	99.7%	87	25	84.7	4	0	0	1637.75	105	119
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	C1QBP_HUMAN	31.4	100.0%	4	6	12	0.01%	22.0%	VEEQEPELTSTPNFVVEVIK	99.7%	60.7	25	60.7	2	0	0	2287.17	155	174
Complex I assembly factor TIMMDC1, mitochondrial	TIMMDC1	TIDC1_HUMAN	32.2	99.8%	2	2	3	0.00%	8.8%	FDAVQSAHR	99.7%	55	25	45.5	2	0	0	1030.51	117	125
Complex I assembly factor TIMMDC1, mitochondrial	TIMMDC1	TIDC1_HUMAN	32.2	99.8%	2	2	3	0.00%	8.8%	LPYVPEPYYPESGWDR	99.0%	33.5	25	33.5	1	0	0	1967.92	42	57
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	8	8	15	0.01%	6.9%	DLAYCVSQLPLTER	99.7%	59	25	55	1	0	0	1664.83	1225	1238
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	8	8	15	0.01%	6.9%	EAITHLLGVALTR	99.7%	58.6	25	58.6	1	0	0	1393.82	221	233
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	8	8	15	0.01%	6.9%	EAVLNAYR	99.7%	52	25	27	3	0	0	935.49	691	698
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	8	8	15	0.01%	6.9%	GNAIYNLLPDIISR	99.7%	62.8	25	52.4	2	0	0	1558.86	1160	1173
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	8	8	15	0.01%	6.9%	LSDADLAGPLQK	99.7%	59	25	48.6	2	0	0	1227.66	441	452
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	8	8	15	0.01%	6.9%	QTLAAFVPLLLK	99.7%	42.5	25	41.6	3	0	0	1313.82	1009	1020
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	8	8	15	0.01%	6.9%	SGGVNQYVVQEVLSIK	99.7%	79.5	25	74.8	2	0	0	1719.93	20	35
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	8	8	15	0.01%	6.9%	SIVGEIVR	97.2%	29.4	25	16.1	1	0	0	872.52	273	280
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	7	7	14	0.01%	9.3%	APLQQCAEDR	99.7%	54	25	46.3	2	0	0	1187.55	304	313
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	7	7	14	0.01%	9.3%	EAALAEVADEK	99.7%	48.7	25	42	2	0	0	1145.57	675	685
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	7	7	14	0.01%	9.3%	IEIHYAK	98.5%	32	25	10	1	0	0	873.48	631	637
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	7	7	14	0.01%	9.3%	LLASPSSR	99.2%	34.8	25	25.7	3	0	0	830.47	84	91
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	7	7	14	0.01%	9.3%	VAAGTLDASTK	99.7%	63.1	25	62.7	1	0	0	1033.55	153	163
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	7	7	14	0.01%	9.3%	VDAVHADVYR	99.7%	44.2	25	31.1	3	0	0	1144.57	169	178
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	7	7	14	0.01%	9.3%	VFDLQFSTDSPR	99.7%	90	25	90	2	0	0	1411.69	72	83
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	8	8	20	0.02%	9.4%	APIVTVGVNNDPADVR	99.7%	103	25	102	3	0	0	1636.87	471	486
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	8	8	20	0.02%	9.4%	AVLSCIAPSAK	99.7%	40.5	25	29.5	1	0	0	1116.61	198	208
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	8	8	20	0.02%	9.4%	EFIGQQLILIIK	99.7%	48.4	25	39.6	2	0	0	1414.87	399	410
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	8	8	20	0.02%	9.4%	IQAVLALSR	99.7%	58.4	25	46.1	1	0	0	970.60	160	168
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	8	8	20	0.02%	9.4%	LLSDFLDSEVSELR	99.7%	95.2	25	89.3	4	0	0	1622.83	695	708
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	8	8	20	0.02%	9.4%	LMFSGLLVSSR	99.7%	74.5	25	69.9	4	0	0	1209.67	718	728
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	8	8	20	0.02%	9.4%	SLDTSEEGGR	99.7%	49.3	25	37.8	1	0	0	1050.47	411	420
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	8	8	20	0.02%	9.4%	TQIVTEIISEIR	99.7%	85	25	79.4	4	0	0	1401.79	459	470
Condensin-2 complex subunit D3	NCAPD3	CNDD3_HUMAN	168.9	100.0%	4	4	6	0.01%	3.3%	FLVQEIMFDR	99.7%	39.3	25	37.3	1	0	0	1297.66	443	452
Condensin-2 complex subunit D3	NCAPD3	CNDD3_HUMAN	168.9	100.0%	4	4	6	0.01%	3.3%	SALQVLVSILK	99.7%	56.2	25	50.5	2	0	0	1170.75	560	570
Condensin-2 complex subunit D3	NCAPD3	CNDD3_HUMAN	168.9	100.0%	4	4	6	0.01%	3.3%	TFAAQSLVQLLSK	99.7%	71.4	25	71.4	2	0	0	1405.81	372	384
Condensin-2 complex subunit D3	NCAPD3	CNDD3_HUMAN	168.9	100.0%	4	4	6	0.01%	3.3%	YIFTLGDIAQLCPAR	99.0%	33.8	25	33.8	1	0	0	1737.90	856	870
Condensin-2 complex subunit G2	NCAPG2	CNDG2_HUMAN	131.0	100.0%	3	3	4	0.00%	2.5%	GFSEAAAPR	99.6%	38.4	25	34.3	1	0	0	905.45	812	820
Condensin-2 complex subunit G2	NCAPG2	CNDG2_HUMAN	131.0	100.0%	3	3	4	0.00%	2.5%	LETDSRPVSR	98.1%	30.9	25	19	1	0	0	1159.61	507	516
Condensin-2 complex subunit G2	NCAPG2	CNDG2_HUMAN	131.0	100.0%	3	3	4	0.00%	2.5%	YSLHDNSEK	99.6%	37.4	25	33	2	0	0	1092.50	466	474
Conserved oligomeric Golgi complex subunit 1	COG1	COG1_HUMAN	109.0	100.0%	4	4	7	0.01%	5.0%	ALQLLYDLR	99.2%	34.7	25	25.7	2	0	0	1104.64	806	814

Conserved oligomeric Golgi complex subunit 1	COG1	COG1_HUMAN	109.0	100.0%	4	4	7	0.01%	5.0%	FGLLPLSMTSTR	99.2%	34.8	25	34.3	1	0	0	1322.71	911	922
Conserved oligomeric Golgi complex subunit 1	COG1	COG1_HUMAN	109.0	100.0%	4	4	7	0.01%	5.0%	QALTDFLLAR	98.4%	31.8	25	25.3	2	0	0	1147.65	225	234
Conserved oligomeric Golgi complex subunit 1	COG1	COG1_HUMAN	109.0	100.0%	4	4	7	0.01%	5.0%	TSVLFGLVTGTENQLAPR	99.7%	48.4	25	48.4	2	0	0	1903.03	872	889
Conserved oligomeric Golgi complex subunit 5	COG5	COG5_HUMAN	92.7	99.8%	2	2	2	0.00%	2.9%	IGALQGAVDR	99.7%	68.8	25	47.3	1	0	0	999.56	138	147
Conserved oligomeric Golgi complex subunit 5	COG5	COG5_HUMAN	92.7	99.8%	2	2	2	0.00%	2.9%	LFDPINLVFPPGGR	99.7%	49.7	25	38.6	1	0	0	1541.85	493	506
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	7	7	10	0.01%	8.1%	AEGSSTASSGSQLAEGK	99.7%	81.5	25	81.5	2	0	0	1566.72	503	519
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	7	7	10	0.01%	8.1%	EAALEAAVLNKEE	96.3%	28.3	25	15.7	1	0	0	1386.71	1106	1118
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	7	7	10	0.01%	8.1%	GVISTPVIR	99.7%	42.2	25	29.1	2	0	0	941.58	987	995
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	7	7	10	0.01%	8.1%	LYEPDQLQELK	99.7%	39.5	25	21.3	1	0	0	1375.71	748	758
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	7	7	10	0.01%	8.1%	NIQDTSDLDAIAK	99.7%	48.8	25	44.9	1	0	0	1403.70	292	304
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	7	7	10	0.01%	8.1%	SPQTPELVEALAFR	99.7%	50.4	25	49.9	1	0	0	1557.83	652	665
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	7	7	10	0.01%	8.1%	SQGGVQPIPSQGGK	99.7%	45.4	25	41.8	2	0	0	1339.70	933	946
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	6	6	12	0.01%	14.7%	AESTPEIAEQR	99.7%	44.3	25	35.2	2	0	0	1230.60	225	235
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	6	6	12	0.01%	14.7%	DSQTQAILTK	99.7%	45.5	25	33.5	2	0	0	1104.59	239	248
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	6	6	12	0.01%	14.7%	EGSQGELTPANSQSR	99.7%	67.5	25	61.4	4	0	0	1560.72	472	486
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	6	6	12	0.01%	14.7%	LQFIADHCPTLR	99.7%	31.8	25	24.5	0	1	0	1470.75	60	71
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	6	6	12	0.01%	14.7%	TLYTQIR	94.6%	26.8	25	26	1	0	0	894.50	364	370
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	6	6	12	0.01%	14.7%	VSVYLQNWSHVLSYVSK	99.5%	27.5	25	27.5	0	2	0	2009.05	208	224
COP9 signalosome complex subunit 4	COPS4	CSN4_HUMAN	46.3	100.0%	4	5	7	0.01%	11.8%	AIQLSGAEQLEALK	99.7%	73.7	25	55.4	1	0	0	1470.82	33	46
COP9 signalosome complex subunit 4	COPS4	CSN4_HUMAN	46.3	100.0%	4	5	7	0.01%	11.8%	ATTADGSSILDR	99.7%	75.2	25	65.1	1	0	0	1206.60	291	302
COP9 signalosome complex subunit 4	COPS4	CSN4_HUMAN	46.3	100.0%	4	5	7	0.01%	11.8%	AVIEHNLLSASK	99.7%	46.4	25	46.4	2	0	0	1281.72	303	314
COP9 signalosome complex subunit 4	COPS4	CSN4_HUMAN	46.3	100.0%	4	5	7	0.01%	11.8%	IASQMITEGR	99.7%	77.1	25	62.7	3	0	0	1105.57	338	347
COP9 signalosome complex subunit 7a	COPS7A	CSN7A_HUMAN	30.3	100.0%	2	2	4	0.00%	8.4%	LEVDYSIGR	99.7%	51.4	25	41.5	2	0	0	1051.54	152	160
COP9 signalosome complex subunit 7a	COPS7A	CSN7A_HUMAN	30.3	100.0%	2	2	4	0.00%	8.4%	VTGQNQEQFLLLAK	99.7%	60.3	25	48.6	2	0	0	1588.87	7	20
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	4	4	7	0.01%	12.3%	FCTGLTQIETLFK	99.7%	71	25	66.4	2	0	0	1557.80	253	265
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	4	4	7	0.01%	12.3%	FSEVLKR	99.7%	41.5	25	19.1	1	0	0	878.51	308	314
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	4	4	7	0.01%	12.3%	LAVEALSSLDGDLAGR	99.7%	99.2	25	99.2	2	0	0	1586.84	157	172
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	4	4	7	0.01%	12.3%	VLTPELYAELR	99.7%	45	25	36.9	2	0	0	1303.73	33	43
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	2	2	8	0.01%	6.1%	IGSGFDNIDIK	99.7%	54	25	40.2	4	0	0	1178.61	98	108
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	2	2	8	0.01%	6.1%	VGQAVALR	99.7%	57.6	25	38.8	4	0	0	813.49	185	192
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	2	2	8	0.01%	6.1%	VQSVEQIR	99.7%	46	25	24.8	4	0	0	958.53	156	163
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	6	6	11	0.01%	15.5%	EAAATEIRR	98.5%	31.8	25	19	1	0	0	1016.55	335	343
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	6	6	11	0.01%	15.5%	GAALDVHESEPFSFAQGPLK	99.7%	45.1	25	45.1	0	2	0	2100.04	292	311
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	6	6	11	0.01%	15.5%	GETLGLIGFGR	99.7%	43.3	25	39.8	1	0	0	1119.62	180	190
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	6	6	11	0.01%	15.5%	IGSGYDNVDIK	99.7%	51.6	25	38	2	0	0	1180.58	104	114
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	6	6	11	0.01%	15.5%	QGAFLVNAAR	99.7%	53.1	25	45.5	1	0	0	1046.57	263	272
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	6	6	11	0.01%	15.5%	VQSVEQIR	99.7%	46	25	24.8	4	0	0	958.53	162	169
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	41	0.04%	35.4%	ALEHSALAINHK	99.7%	39.7	25	39.7	2	2	0	1303.71	320	331
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	41	0.04%	35.4%	CSNPLDTSVK	99.7%	44.5	25	39.1	2	0	0	1120.53	218	227
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	41	0.04%	35.4%	ENFCNIHVSLVPQPSSTGEQK	97.5%	22.6	25	22.6	0	2	0	2371.13	173	193
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	41	0.04%	35.4%	FSDSYASVIK	99.7%	70.6	25	48.5	2	0	0	1116.56	310	319
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	41	0.04%	35.4%	FVGQDVEGER	99.7%	64.9	25	55.7	2	0	0	1135.54	499	508
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	41	0.04%	35.4%	GIIASSVGTILK	99.7%	68.1	25	65	2	0	0	1158.71	17	28
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	41	0.04%	35.4%	GLGLSPDLVVCR	99.7%	47.4	25	42.1	2	0	0	1285.69	206	217
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	41	0.04%	35.4%	IQAIAWAR	99.7%	61.7	25	43	2	0	0	928.54	382	389
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	41	0.04%	35.4%	IYQYVINK	99.7%	52	25	38.8	2	0	0	1040.58	93	100
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	41	0.04%	35.4%	KLYGDADYLEER	99.7%	77.3	25	66.9	2	2	0	1471.71	466	477
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	41	0.04%	35.4%	LCSAHGVLVPGGFGVR	99.7%	66.4	25	59.4	2	2	0	1625.86	361	376
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	41	0.04%	35.4%	LLETCSIALVGK	99.7%	95.4	25	87.9	1	0	0	1303.73	295	306
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	41	0.04%	35.4%	LYGDADYLEER	99.7%	85.2	25	72.6	2	0	0	1343.61	467	477
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	41	0.04%	35.4%	RLDLPIER	99.7%	42.7	25	25.5	2	0	0	1011.59	269	276

CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	41	0.04%	35.4%	SCGLHVTSIK	99.7%	46.3	25	39	2	0	0	1101.57	29	38
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	41	0.04%	35.4%	VPLLLEEQGVVDYFLR	99.7%	81.7	25	81.7	2	0	0	1890.04	253	268
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	41	0.04%	35.4%	YIDSADLEPITSQEEPVR	99.7%	87.3	25	78.9	2	0	0	2062.00	336	353
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	41	0.04%	35.4%	YILVTGGVISGIGK	99.7%	101	25	101	2	0	0	1376.82	3	16
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	5	5	8	0.01%	14.2%	ADGILVPGGFGIR	94.7%	26.9	25	9.3	1	0	0	1271.71	364	376
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	5	5	8	0.01%	14.2%	ALEHSALAINHK	99.7%	39.7	25	39.7	2	2	0	1303.71	320	331
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	5	5	8	0.01%	14.2%	GIIASSIGTILK	99.7%	55.5	25	30	2	0	0	1172.73	17	28
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	5	5	8	0.01%	14.2%	GLGLSPDLIVCR	98.9%	33.3	25	18.6	2	0	0	1299.71	206	217
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	5	5	8	0.01%	14.2%	LQAISWAR	99.7%	45.7	25	37	1	0	0	944.53	382	389
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	5	5	8	0.01%	14.2%	VPVLLEEQSIVK	99.7%	69.1	25	69.1	2	0	0	1353.80	253	264
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	5	5	8	0.01%	14.2%	YILVTGGVISGIGK	99.7%	101	25	101	2	0	0	1376.82	3	16
Cullin-1	CUL1	CUL1_HUMAN	89.7	100.0%	5	5	7	0.01%	6.2%	AGIQQVYTR	98.7%	32.6	25	19.2	1	0	0	1035.56	26	34
Cullin-1	CUL1	CUL1_HUMAN	89.7	100.0%	5	5	7	0.01%	6.2%	ESFESQFLADTER	99.7%	66.6	25	66.6	1	0	0	1558.70	230	242
Cullin-1	CUL1	CUL1_HUMAN	89.7	100.0%	5	5	7	0.01%	6.2%	FINNNAVTK	97.3%	29.6	25	20.9	1	0	0	1020.55	402	410
Cullin-1	CUL1	CUL1_HUMAN	89.7	100.0%	5	5	7	0.01%	6.2%	FTAFYASR	99.7%	45.1	25	43.5	2	0	0	962.47	566	573
Cullin-1	CUL1	CUL1_HUMAN	89.7	100.0%	5	5	7	0.01%	6.2%	LLIQAAIVR	99.7%	65.6	25	53.8	2	0	0	996.66	709	717
Cullin-4B	CUL4B	CUL4B_HUMAN	104.0	100.0%	3	3	5	0.00%	3.6%	ETVEEQASTTER	99.7%	69.5	25	69.5	1	0	0	1379.63	830	841
Cullin-4B	CUL4B	CUL4B_HUMAN	104.0	100.0%	3	3	5	0.00%	3.6%	QYQIDAAIVR	97.7%	30.2	25	27.2	1	0	0	1176.64	847	856
Cullin-4B	CUL4B	CUL4B_HUMAN	104.0	100.0%	3	3	5	0.00%	3.6%	TIDGILLLIER	99.7%	70.4	25	64.8	3	0	0	1255.76	346	356
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	AADIDQEVK	99.7%	45.6	25	33.6	2	0	0	988.49	578	586
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	AADIDQEVKER	99.7%	50.9	25	46.8	4	0	0	1273.64	578	588
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	ADVFHAYLSLLK	99.7%	34.2	25	32	0	2	0	1376.76	392	403
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	ALTLIAGSPLK	99.7%	88.4	25	80.6	6	0	0	1083.68	631	641
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	AVAALLTIPEAEK	99.7%	60.3	25	39.8	2	0	0	1325.77	1179	1191
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	CLGPLVSK	98.9%	33.1	25	19.2	1	0	0	873.49	71	78
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	DLLDTVLPHLYNETK	97.6%	29.9	25	24.1	1	0	0	1770.93	1043	1057
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	DSIKLDDDSER	96.8%	28.8	25	28.8	1	0	0	1292.60	37	47
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	EGPAVVGQFIQDVK	99.7%	61.3	25	58.8	4	0	0	1486.79	813	826
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	EYCIQAFESFVR	99.7%	76.7	25	76.7	2	0	0	1548.72	273	284
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	FMATNDLMTELQK	99.7%	90.5	25	84	7	0	0	1541.73	24	36
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	FTISDHPQPIDPLLK	99.7%	44.8	25	39.4	2	4	0	1720.93	991	1005
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	GYLISGSSYAR	99.7%	54.1	25	42	4	0	0	1173.59	972	982
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	HTVDDGLDIR	99.7%	47.1	25	39.9	2	0	0	1140.56	1073	1082
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	HTVDDGLDIRK	99.0%	33.7	25	29.1	2	0	0	1268.66	1073	1083
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	IGEYLEK	99.7%	40	25	30.5	2	0	0	851.45	249	255
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	ITSEALLVTQQLVK	99.7%	85.4	25	77.7	4	0	0	1542.91	535	548
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	LGTLSALDILIK	99.7%	76.4	25	65	5	0	0	1256.78	668	679
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	LLEDKNGEVQNLAVK	99.7%	42.2	25	25.6	0	1	0	1669.91	56	70
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	LSTLCPSAVLQR	99.7%	55.8	25	45	2	0	0	1344.73	1130	1141
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	LTLIDPETLLPR	99.7%	70.1	25	64.5	8	0	0	1380.81	958	969
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	MLTFLMLVR	99.7%	71.2	25	60.6	10	0	0	1123.64	1121	1129
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	MLTGPVYSQSTALTHK	99.7%	108	25	103	4	4	0	1733.89	778	793
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	NVVAECLGK	95.6%	27.6	25	26.1	1	0	0	989.51	949	957
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	QSYYSIAK	98.2%	31.3	25	14.4	2	0	0	959.48	794	801
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	SVILEAFSSPSEEVK	99.7%	81.2	25	73.1	6	0	0	1621.83	859	873
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	TLEDPDLNVR	99.7%	75.6	25	64.7	3	0	0	1171.60	1014	1023
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	TVIGELPPASSGSALAANVCK	99.7%	135	25	132	2	1	0	2042.06	112	132
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	TVSPALISR	99.7%	43.1	25	34.1	2	0	0	943.56	374	382
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	30	37	105	0.10%	27.4%	TYIQCIAAISR	99.7%	81.7	25	72.2	2	0	0	1295.68	233	243
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	16	22	58	0.06%	56.6%	ALGTPNNEVWPEVESLQDYK	99.7%	45	25	45	2	0	0	2289.10	219	238
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	16	22	58	0.06%	56.6%	DLKPQNLLIDDKGTIK	99.7%	44.5	25	44.2	2	4	0	1811.03	128	143

Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	16	22	58	0.06%	56.6%	IGEGTYGVVYK	99.7%	91.4	25	43.7	4	0	0	1185.62	10	20
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	16	22	58	0.06%	56.6%	IRLESEEEGVPSTAIR	99.7%	100	25	95.8	4	2	0	1785.93	35	50
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	16	22	58	0.06%	56.6%	LADFGLAR	99.7%	52.2	25	0	7	0	0	862.48	144	151
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	16	22	58	0.06%	56.6%	LESEEEGVPSTAIR	99.7%	77.4	25	68.7	2	0	0	1516.75	37	50
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	16	22	58	0.06%	56.6%	MALNHPYFNDLDNQIK	99.7%	66.2	25	66.2	4	3	0	1948.92	280	295
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	16	22	58	0.06%	56.6%	MLIYDPAK	99.7%	45	25	38.8	2	0	0	950.50	267	274
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	16	22	58	0.06%	56.6%	MLIYDPAKR	99.7%	42	25	23.6	4	0	0	1106.60	267	275
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	16	22	58	0.06%	56.6%	NLDENGLDLLSK	99.7%	74.6	25	57.6	2	0	0	1330.69	255	266
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	16	22	58	0.06%	56.6%	SPEVLLGSAR	99.7%	83.7	25	78.5	7	0	0	1028.57	171	180
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	16	22	58	0.06%	56.6%	TTGQVVAMK	99.7%	59.2	25	40.4	2	0	0	950.50	25	33
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	16	22	58	0.06%	56.6%	TTGQVVAMKK	98.1%	30.9	25	27	2	0	0	1062.60	25	34
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	16	22	58	0.06%	56.6%	VYTHEVVTLWYR	99.7%	52	25	52	2	0	0	1565.81	159	170
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	16	22	58	0.06%	56.6%	WKPGSLASHVK	99.3%	26.5	25	25.7	0	1	0	1209.67	244	254
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	16	22	58	0.06%	56.6%	YLDSIPPGQYMDSSLVK	98.9%	33.2	25	31.6	2	0	0	1928.93	90	106
Cyclin-dependent kinase 11B	CDK11B	CD11B_HUMAN	92.7	100.0%	5	5	7	0.01%	6.5%	APELLLGAK	99.7%	38.8	25	36	1	0	0	911.56	605	613
Cyclin-dependent kinase 11B	CDK11B	CD11B_HUMAN	92.7	100.0%	5	5	7	0.01%	6.5%	EGFPITSLR	96.7%	28.7	25	16.2	1	0	0	1019.55	476	484
Cyclin-dependent kinase 11B	CDK11B	CD11B_HUMAN	92.7	100.0%	5	5	7	0.01%	6.5%	FGALLSDQGFDLMNK	99.7%	61.9	25	59	1	0	0	1671.81	688	702
Cyclin-dependent kinase 11B	CDK11B	CD11B_HUMAN	92.7	100.0%	5	5	7	0.01%	6.5%	IEEGTYGVVYR	99.7%	77.6	25	75.9	2	0	0	1285.64	444	454
Cyclin-dependent kinase 11B	CDK11B	CD11B_HUMAN	92.7	100.0%	5	5	7	0.01%	6.5%	TLMIQLLR	99.7%	42.2	25	28	2	0	0	987.60	541	548
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	6	9	18	0.02%	33.6%	ALFPGDSEIDQLFR	99.7%	53.6	25	50.5	2	0	0	1607.81	201	214
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	6	9	18	0.02%	33.6%	APEILLGCK	99.7%	63.7	25	61.8	2	0	0	1000.55	170	178
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	6	9	18	0.02%	33.6%	DLKPQNLLINTEGAIK	99.7%	74.8	25	74.8	2	2	0	1767.00	127	142
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	6	9	18	0.02%	33.6%	FMDASALTGIPLPLIK	99.7%	64.6	25	62.9	4	0	0	1686.95	90	105
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	6	9	18	0.02%	33.6%	IGEGTYGVVYK	99.7%	91.4	25	43.7	4	0	0	1185.62	10	20
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	6	9	18	0.02%	33.6%	IRLDTETEGVPSTAIR	99.7%	63	25	61.2	2	2	0	1757.94	35	50
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	6	9	18	0.02%	33.6%	LADFGLAR	99.7%	52.2	25	0	7	0	0	862.48	143	150
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	6	9	18	0.02%	33.6%	LTGEVVALKK	99.7%	51.6	25	41	2	0	0	1057.66	25	34
Cyclin-dependent kinase 5	CDK5	CDK5_HUMAN	33.3	100.0%	3	3	4	0.00%	13.0%	DLKPQNLLINR	97.9%	30.6	25	26.9	1	0	0	1323.77	126	136
Cyclin-dependent kinase 5	CDK5	CDK5_HUMAN	33.3	100.0%	3	3	4	0.00%	13.0%	DLLQNLLK	99.7%	42.1	25	30.8	1	0	0	956.58	261	268
Cyclin-dependent kinase 5	CDK5	CDK5_HUMAN	33.3	100.0%	3	3	4	0.00%	13.0%	IGEGTYGTVFK	99.7%	70.9	25	64.5	2	0	0	1171.60	10	20
Cyclin-dependent kinase 5	CDK5	CDK5_HUMAN	33.3	100.0%	3	3	4	0.00%	13.0%	LADFGLAR	99.7%	52.2	25	0	7	0	0	862.48	142	149
Cyclin-dependent kinase 9	CDK9	CDK9_HUMAN	42.8	100.0%	3	3	6	0.01%	11.3%	GSQITQQSTNQSR	99.7%	70	25	61.1	2	0	0	1434.69	346	358
Cyclin-dependent kinase 9	CDK9	CDK9_HUMAN	42.8	100.0%	3	3	6	0.01%	11.3%	LADFGLAR	99.7%	52.2	25	0	7	0	0	862.48	165	172
Cyclin-dependent kinase 9	CDK9	CDK9_HUMAN	42.8	100.0%	3	3	6	0.01%	11.3%	LLVLDPAQR	99.7%	45.8	25	43.1	2	0	0	1024.62	295	303
Cyclin-dependent kinase 9	CDK9	CDK9_HUMAN	42.8	100.0%	3	3	6	0.01%	11.3%	NPATTNQTEFER	99.7%	67.7	25	67.7	2	0	0	1407.65	359	370
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	7	7	11	0.01%	14.5%	AAQELQEGQR	99.7%	62.7	25	51.1	2	0	0	1129.56	360	369
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	7	7	11	0.01%	14.5%	CVVILPDSVR	98.1%	31	25	24	1	0	0	1157.63	370	379
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	7	7	11	0.01%	14.5%	FDSPESHVGVAWR	99.7%	31.6	25	31.6	0	1	0	1486.71	197	209
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	7	7	11	0.01%	14.5%	GFLKEEDLTEK	99.7%	58.5	25	51.2	2	0	0	1308.67	395	405
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	7	7	11	0.01%	14.5%	IGDTPMVR	99.7%	40.3	25	27.4	2	0	0	904.46	84	91
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	7	7	11	0.01%	14.5%	PSETPQAEVGPTGCPHR	99.7%	55.8	25	49.5	0	1	0	1819.84	2	18
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	7	7	11	0.01%	14.5%	SNDEEAFTFAR	99.7%	75	25	75	2	0	0	1286.56	326	336
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	3	3	5	0.00%	7.0%	GVGAIYIR	99.3%	35.1	25	23.6	2	0	0	848.50	264	271
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	3	3	5	0.00%	7.0%	QPIAEIGR	99.1%	34.1	25	17.6	2	0	0	883.50	213	220
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	3	3	5	0.00%	7.0%	SLEAEGFQVTYLPVQK	99.7%	43	25	37.1	1	0	0	1808.94	165	180
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	8	9	13	0.01%	20.0%	ADLTEYLSTHYK	99.7%	70.9	25	70.9	2	0	0	1440.70	214	225
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	8	9	13	0.01%	20.0%	EHTAYYIK	99.7%	39	25	30.8	1	0	0	1024.51	127	134
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	8	9	13	0.01%	20.0%	FTGSEIR	99.7%	42.5	25	33.7	1	0	0	809.42	270	276
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	8	9	13	0.01%	20.0%	IAEVDASVVR	99.7%	83.8	25	54.9	2	0	0	1058.58	433	442
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	8	9	13	0.01%	20.0%	LCTSATESEVAR	99.7%	88.7	25	79.1	2	0	0	1323.62	379	390
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	8	9	13	0.01%	20.0%	MVLAAAGGVEHQQLLDLAQK	99.7%	51	25	51	0	3	0	2092.12	229	248

Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	8	9	13	0.01%	20.0%	NALVSHLDGTTPVCEDIGR	99.7%	33.2	25	33.2	0	1	0	2054.00	397	415
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	8	9	13	0.01%	20.0%	SGMFWLRF	99.6%	37.5	25	24.3	1	0	0	1043.51	473	480
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	ATAAPAGAPPQPQDLEFTK	99.7%	83.3	25	82.8	2	0	0	1909.97	24	42
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	AVAFQNPQTHVIENLHAAAYR	99.7%	49	25	49	0	2	0	2350.21	163	183
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	ENMAYTVECLR	99.7%	70.3	25	63.6	5	0	0	1401.61	117	127
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	GSNTTSHLHQAVAK	99.7%	64.4	25	56.9	2	1	0	1450.74	302	315
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	LPNGLVIASLENYSPVSR	99.7%	98.1	25	98.1	2	2	0	1929.04	43	60
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	MALIGLGVSHPVLK	99.7%	86.1	25	86.1	3	2	0	1450.85	218	231
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	NALANPLYCPDYR	99.7%	68.2	25	57.9	2	0	0	1566.74	184	196
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	QVAEQFLNMR	99.7%	77.5	25	69.8	4	0	0	1235.62	232	241
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	RWEVADLQPQLK	99.7%	62.1	25	57.9	2	1	0	1482.81	148	159
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	SMAASGNLGHTPFVDEL	99.7%	81.5	25	80.8	4	0	0	1761.81	437	453
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	TIAQGNLSNTDVQAAK	99.7%	109	25	102	4	0	0	1630.84	360	375
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	VTSEELHYFVQNHFTSAR	99.7%	39.5	25	39.5	0	2	0	2165.04	200	217
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	WEVADLQPQLK	99.7%	64.2	25	54.3	2	0	0	1326.71	149	159
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	YEDFSNLGTTHLLR	99.7%	80.3	25	80.3	2	0	0	1665.82	71	84
Cytochrome b-c1 complex subunit 8	UQCRQ	QCR8_HUMAN	9.9	100.0%	4	5	9	0.01%	47.6%	GREFGNLTR	96.6%	28.6	25	8.59	1	0	0	1049.55	2	10
Cytochrome b-c1 complex subunit 8	UQCRQ	QCR8_HUMAN	9.9	100.0%	4	5	9	0.01%	47.6%	HVISYSLSPFEQR	99.7%	68.5	25	68.5	4	1	0	1562.80	13	25
Cytochrome b-c1 complex subunit 8	UQCRQ	QCR8_HUMAN	9.9	100.0%	4	5	9	0.01%	47.6%	IRESFFR	99.6%	37.9	25	22.6	2	0	0	954.52	42	48
Cytochrome b-c1 complex subunit 8	UQCRQ	QCR8_HUMAN	9.9	100.0%	4	5	9	0.01%	47.6%	KNPAAYENDK	96.9%	29	25	21.3	1	0	0	1149.55	73	82
Cytochrome b-c1 complex subunit 9	UQCR10	QCR9_HUMAN	7.3	99.8%	2	2	4	0.00%	38.1%	AFDQGADAIYDHINEGK	99.7%	58.7	25	58.7	2	0	0	1863.85	35	51
Cytochrome b-c1 complex subunit 9	UQCR10	QCR9_HUMAN	7.3	99.8%	2	2	4	0.00%	38.1%	LYSLLFR	99.7%	43.4	25	32.1	2	0	0	911.53	10	16
Cytochrome b-c1 complex subunit Rieske, mitochondrial	UQCRFS1	UCRI_HUMAN	29.7	100.0%	3	3	5	0.00%	16.1%	EIEQEAAVELSQLR	99.7%	41.5	25	31.8	2	0	0	1614.83	183	196
Cytochrome b-c1 complex subunit Rieske, mitochondrial	UQCRFS1	UCRI_HUMAN	29.7	100.0%	3	3	5	0.00%	16.1%	NAVTQFVSSMSASADVLALAK	99.7%	87.9	25	85.4	1	0	0	2126.08	131	151
Cytochrome b-c1 complex subunit Rieske, mitochondrial	UQCRFS1	UCRI_HUMAN	29.7	100.0%	3	3	5	0.00%	16.1%	RLEVLDSTK	99.7%	45.8	25	38	2	0	0	1060.60	93	101
Cytochrome c	CYCS	CYC_HUMAN	11.7	99.8%	2	2	3	0.00%	23.8%	TGPNLHGLFGR	98.9%	33.2	25	33.2	1	0	0	1168.62	29	39
Cytochrome c	CYCS	CYC_HUMAN	11.7	99.8%	2	2	3	0.00%	23.8%	TGQAPGYSYTAANK	99.7%	50.4	25	43.6	2	0	0	1428.68	41	54
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	3	4	10	0.01%	14.5%	ILYMTDEVNDPSLTIK	99.7%	81.1	25	81.1	6	0	0	1851.94	83	98
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	3	4	10	0.01%	14.5%	LLDVDNRVVLPIEAPIR	99.7%	51.9	25	44.5	0	2	0	1932.13	135	151
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	3	4	10	0.01%	14.5%	VVLPIEAPIR	99.7%	47.7	25	47.7	2	0	0	1106.69	142	151
Cytochrome c oxidase subunit 7A2, mitochondrial	COX7A2	CX7A2_HUMAN	9.4	99.8%	2	2	3	0.00%	27.7%	GGVADALLYR	99.7%	66	25	47.1	1	0	0	1034.56	47	56
Cytochrome c oxidase subunit 7A2, mitochondrial	COX7A2	CX7A2_HUMAN	9.4	99.8%	2	2	3	0.00%	27.7%	LFQEDDEIPLYLK	99.7%	58.4	25	48.2	2	0	0	1622.83	34	46
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	5	5	10	0.01%	6.4%	FVEFFGPGVAQLSIADR	99.7%	85.6	25	84.9	2	0	0	1852.96	277	293
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	5	5	10	0.01%	6.4%	GPFLLGIK	99.7%	39.2	25	27.1	2	0	0	844.53	786	793
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	5	5	10	0.01%	6.4%	NIEVPFKPAR	98.6%	32.2	25	22.9	2	0	0	1170.66	73	82
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	5	5	10	0.01%	6.4%	VLLEAAIR	99.7%	52	25	44.3	2	0	0	884.56	41	48
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	5	5	10	0.01%	6.4%	YQQAGLPLIVLAGK	99.7%	67.1	25	67.1	2	0	0	1470.87	759	772
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	AATSPALFNR	99.7%	82.5	25	60.6	2	0	0	1047.56	3079	3088
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	ADLAAVEAK	99.7%	54	25	42.1	2	0	0	887.48	3463	3471
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	AERPDVDEKR	99.7%	36	25	28.3	1	2	0	1214.61	3719	3728
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	ALGEYLER	99.7%	52.7	25	47.7	2	0	0	950.49	1614	1621
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	ALGHQLGR	98.1%	30.9	25	21.5	2	0	0	851.48	1918	1925
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	ANEVEQMIR	99.7%	56.9	25	39.4	2	0	0	1089.54	3430	3438
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	ASLACGPMVK	99.7%	46.9	25	32.6	2	0	0	1033.52	3385	3394
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	ASVVTLPVYLNFTR	99.7%	55.1	25	53.3	3	0	0	1579.88	4602	4615
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	CYLTMTQALEAR	99.7%	72.3	25	71.1	2	0	0	1456.69	1888	1899
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	DAATIMQPYFTSNGLVTK	99.7%	75.3	25	72.5	2	0	0	1972.97	2418	2435
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	DLFQVAFNR	99.7%	54.2	25	48.3	5	0	0	1109.57	3862	3870
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	DLPPVSGSIIWAK	99.7%	49.6	25	46.5	2	0	0	1382.77	640	652
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	DSAIQQQVANLQMK	99.7%	96.1	25	83.1	2	0	0	1573.80	1229	1242
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	DYIPVDQEELRDYVK	99.7%	50.8	25	42.4	2	0	0	1881.92	2880	2894

Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	EAIVNSCVFVHQTLHQANAR	99.2%	26	25	19.3	0	2	0	2294.15	3141	3160
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	EALELTDTGLLSGSEER	99.7%	112	25	107	2	0	0	1819.89	1302	1318
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	EFGPVVIDYGK	99.7%	48	25	48	2	0	0	1223.63	1101	1111
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	EGLMLDSHEELYK	99.4%	36.2	25	31.9	1	0	0	1563.74	3040	3052
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	EHINSVSAMK	99.6%	37.5	25	31.3	2	0	0	1115.55	1499	1508
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	ESPEVLLTLDILK	99.7%	72.6	25	67.4	1	0	0	1469.85	293	305
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	EVWNTYELDLVNYQNK	99.7%	71	25	71	2	0	0	2027.97	1468	1483
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	EYQTQLIQR	99.7%	39.3	25	24.9	2	0	0	1178.62	603	611
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	FLSDPQVHTVLVER	99.7%	72.2	25	68	1	1	0	1639.88	68	81
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	FNALFVRPHIR	99.1%	25.6	25	21	0	1	0	1369.79	588	598
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	FNYGFEYLGVQDK	99.7%	100	25	100	2	0	0	1579.74	1866	1878
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	FQSISTEFLALMK	99.7%	77.1	25	72.3	3	0	0	1530.79	1568	1580
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	FTQDTQPHYIYSPR	99.7%	67.1	25	64.2	1	1	0	1752.83	2784	2797
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	FVAWMNGLSVYQIK	99.7%	64.7	25	64.7	2	0	0	1655.86	2949	2962
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	FYFVGDEDLLEIIGNSK	99.2%	34.5	25	28	1	0	0	1958.97	1629	1645
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	GTFDNAETKK	99.7%	50.6	25	42.4	2	0	0	1110.54	1091	1100
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	GTVGEPTYDAEFQHFLR	99.0%	25.6	25	24	0	1	0	1966.93	3894	3910
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	GWENHVEGQK	99.7%	41.4	25	31.9	1	0	0	1183.55	672	681
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	HLLPVETQR	97.9%	30.6	25	20.6	2	0	0	1092.62	1559	1567
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	IAFIMDESNVLDSGFLER	99.7%	92.1	25	91.6	3	0	0	2072.00	2990	3007
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	IFTIESTR	99.7%	62.9	25	49.1	2	0	0	966.53	717	724
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	IFVFEPPPGVK	99.6%	38.2	25	37.5	3	0	0	1229.69	4144	4154
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	IMFEVQDLK	99.7%	52.4	25	42.6	2	0	0	1138.58	2341	2349
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	INEWLTLVEK	99.7%	71.5	25	58.8	2	0	0	1244.69	1698	1707
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	INMLVIELK	99.7%	63.3	25	44.9	2	0	0	1088.64	1396	1404
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	IQFVGACNPPTDPGR	99.7%	106	25	99.3	2	0	0	1628.79	2706	2720
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	IQGLTVEQAEAVVR	99.7%	97.9	25	91.9	2	0	0	1512.84	3924	3937
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	ITNQVIYLNPPIEECR	99.7%	47.9	25	47.9	1	0	0	1959.00	964	979
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	IWAHEALR	99.0%	33.8	25	16.4	1	0	0	995.54	2824	2831
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	KIIDSVR	96.3%	28.3	25	3.55	2	0	0	830.51	2286	2292
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	KYEFGESDLR	99.7%	60.9	25	49.8	2	0	0	1243.60	4204	4213
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	LAETVFNFQEK	99.7%	55	25	46.6	2	0	0	1325.67	836	846
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	LCDEQLSSQSHYDFGLR	99.7%	30.4	25	28.1	0	2	0	2054.92	2075	2091
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	LFLTMEINPK	99.7%	53.7	25	37	3	0	0	1205.66	4124	4133
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	LGGSPFGPAGTGK	99.7%	59.4	25	55.9	2	0	0	1145.60	1900	1912
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	LKQDGDSFR	99.7%	44.5	25	44.5	2	0	0	1065.53	682	690
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	LLAESVTEVEIFGK	99.7%	68.2	25	68.2	1	0	0	1534.84	1716	1729
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	LLNTFLER	99.7%	51.7	25	39.4	4	0	0	1005.57	4264	4271
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	LNTQEIFDDWAR	99.7%	77.7	25	69.8	2	0	0	1507.72	693	704
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	LQGEFQLR	99.7%	52.5	25	40.1	2	0	0	990.54	3734	3741
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	LRDQLGTAK	99.7%	39.2	25	26.1	2	0	0	1001.57	568	576
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	LSCLPAFK	97.4%	29.7	25	20.3	1	0	0	935.50	3938	3945
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	LSCLPAFKDLIAK	99.7%	44	25	43.5	2	0	0	1475.83	3938	3950
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	LSLSNAISTALPLTQLR	99.7%	66.7	25	59.5	2	0	0	1798.04	4575	4591
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	LVQTPLTDR	99.7%	41.6	25	31.1	1	0	0	1042.59	1879	1887
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	MLSAVSQQVQCIQEALR	99.7%	104	25	98	2	0	0	1960.99	1967	1983
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	MVVLSLPR	99.7%	51	25	50	4	0	0	914.55	991	998
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	NTISLLVAGLK	99.1%	34.1	25	25.1	2	0	0	1128.70	799	809
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	NYMSNPSYNYEIVNR	99.7%	92.3	25	83.9	4	0	0	1863.83	3370	3384
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	QLIAQVMLYSQGFR	99.7%	41.5	25	41.5	1	0	0	1653.88	2047	2060
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	QLQNISLAAASGGAK	99.7%	93.4	25	82.1	2	0	0	1428.78	4488	4502

Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	QNLDALLNQLK	99.7%	79.7	25	64.5	2	0	0	1269.72	1361	1371
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	QPQGHLLLIGVSGAGK	99.7%	30.4	25	26	0	1	0	1574.90	2928	2943
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	QTDVLQQLSIQMANAK	99.7%	76.1	25	76.1	2	0	0	1787.93	1850	1865
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	QYASYEFVQR	99.7%	53.2	25	39.7	2	0	0	1290.61	1379	1388
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	SFEWLSQMR	99.7%	64.2	25	57.6	3	0	0	1183.56	1835	1843
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	SIPLDEGEDEAQR	99.7%	51.3	25	47.9	2	0	0	1458.67	2384	2396
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	SLETCMYDHK	99.7%	46	25	46	2	0	0	1283.54	863	872
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	SLLQALNEVK	99.7%	61.9	25	54.1	4	0	0	1114.65	3748	3757
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	SMANPPAAVK	99.7%	41.9	25	41	3	0	0	985.51	3309	3318
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	SNSLAFIK	99.7%	51	25	38.6	2	0	0	879.49	113	120
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	SPLVMDVLNIQGVQR	99.7%	90.9	25	84.6	4	0	0	1684.91	1585	1599
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	SSLQSQCLNEVLK	99.7%	79.8	25	71.6	2	0	0	1505.76	3706	3718
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	SVLVSAGNVK	99.7%	38.7	25	29.7	2	0	0	973.57	2095	2104
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	SVLVSAGNVKR	99.7%	50.9	25	41.5	2	0	0	1129.67	2095	2105
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	TEYLSNADER	99.7%	49.4	25	49.4	2	0	0	1197.54	3550	3559
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	TFDHYCEYRR	98.4%	23.9	25	23.9	0	1	0	1446.62	2634	2643
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	TFSEILNR	99.2%	34.7	25	19	2	0	0	979.52	873	880
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	TFSSIPVSR	99.7%	43.5	25	39.9	4	0	0	993.54	4160	4168
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	TLINELVK	98.2%	31.1	25	5.5	1	0	0	929.57	4450	4457
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	TLMAQSIYGGR	99.7%	68.5	25	63.2	2	0	0	1196.61	4245	4255
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	TMTLFSALR	99.7%	60.7	25	57.5	3	0	0	1055.56	2602	2610
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	TPNGVVLAPVQLGK	99.7%	39	25	39	1	0	0	1392.82	2644	2657
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	TPVIDADKPVSSQLR	99.7%	77.5	25	77.5	2	2	0	1625.89	122	136
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	TPVSITEHPK	99.7%	53.3	25	47.4	2	0	0	1108.60	1688	1697
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	TSAPITCELLNK	99.7%	56.4	25	46.2	2	0	0	1346.70	1993	2004
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	TSFLDDAFRK	99.7%	55.1	25	52.2	2	0	0	1199.61	3612	3621
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	TTDLLTDWEK	99.7%	53.6	25	49.8	2	0	0	1221.60	1254	1263
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	TVENIKDPLFR	99.0%	33.8	25	27.7	2	0	0	1331.73	4401	4411
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	VAAPDVVVPTLDTVR	99.7%	66.1	25	66.1	2	0	0	1551.87	2562	2576
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	VDNEFDQR	99.7%	56.6	25	47	2	0	0	1022.45	4256	4263
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	VEPLRNELQK	96.8%	28.9	25	12.8	1	0	0	1225.69	3409	3418
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	VLLTTQGVDMISK	99.7%	101	25	100	4	0	0	1404.78	4330	4342
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	VLRPQVTAVAQQNQGEVPEPQDMK	99.7%	52.8	25	46.4	0	3	0	2678.36	483	506
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	VMSQEIQEQLHK	99.7%	47.3	25	40.5	2	0	0	1469.74	3255	3266
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	VNFLPEIITLSK	99.7%	53	25	47.9	2	0	0	1373.80	737	748
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	VPLAIVNK	99.7%	49.7	25	49.7	2	0	0	853.55	760	767
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	VPQIEVETHK	99.7%	54.1	25	40.8	2	0	0	1179.64	2552	2561
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	VPVNLLR	99.1%	34	25	21.5	4	0	0	810.52	4134	4140
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	VQYPQSQACK	99.1%	34	25	23.5	2	0	0	1208.57	625	634
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	VTDFGDKVEDPTFLNQLQSGVNR	99.7%	62.1	25	58.8	0	2	0	2579.27	229	251
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	VTFVNFTVTR	99.7%	74.2	25	70.2	2	0	0	1183.65	3696	3705
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	107	123	228	0.23%	26.8%	YATLATVSR	99.7%	48	25	36.6	2	0	0	981.54	2350	2358
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	7	7	9	0.01%	20.1%	AGATSEGVLANFFNSLLSK	99.7%	104	25	104	2	0	0	1926.00	436	454
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	7	7	9	0.01%	20.1%	IPAVVVEK	97.8%	30.4	25	23.4	1	0	0	854.53	311	318
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	7	7	9	0.01%	20.1%	KPVTVSPTTPTSPTEGEAS	99.7%	74.5	25	74.5	1	0	0	1885.94	505	523
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	7	7	9	0.01%	20.1%	NVLLLGEDGAGK	99.7%	54.5	25	51.5	1	0	0	1185.65	69	80
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	7	7	9	0.01%	20.1%	QPPTAAGRPVDASPR	98.7%	24.6	25	24.6	0	1	0	1519.80	386	400
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	7	7	9	0.01%	20.1%	SGQKPVLDVHAELDR	99.7%	33.7	25	33.7	0	1	0	1663.88	487	501
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	7	7	9	0.01%	20.1%	SVSSNVASVSPIPAGSK	99.7%	91.7	25	79.2	2	0	0	1586.84	412	428
Cytoplasmic dynein 2 heavy chain 1	DYNC2H1	DYHC2_HUMAN	492.6	100.0%	4	4	6	0.01%	1.2%	IAEALLSDLPGFR	95.7%	27.7	25	25.2	1	0	0	1401.77	502	514
Cytoplasmic dynein 2 heavy chain 1	DYNC2H1	DYHC2_HUMAN	492.6	100.0%	4	4	6	0.01%	1.2%	NSLLTILDQLQR	99.7%	73	25	44.8	2	0	0	1413.81	1399	1410

Cytoplasmic dynein 2 heavy chain 1	DYNC2H1	DYHC2_HUMAN	492.6	100.0%	4	4	6	0.01%	1.2%	VLSFPGGSLLLAGR	99.7%	55	25	54.1	2	0	0	1386.81	2643	2656
Cytoplasmic dynein 2 heavy chain 1	DYNC2H1	DYHC2_HUMAN	492.6	100.0%	4	4	6	0.01%	1.2%	VTTLTTHAGIR	99.7%	48.5	25	37.4	1	0	0	1169.66	1388	1398
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	16	17	32	0.03%	15.1%	ALNLAYSSIYGSYR	99.7%	83.5	25	75.6	2	0	0	1577.80	893	906
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	16	17	32	0.03%	15.1%	AVGPSSTQLYMVR	99.7%	76.3	25	63.8	2	0	0	1424.72	551	563
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	16	17	32	0.03%	15.1%	DFVSEAYLITLGK	99.7%	65.8	25	0	4	0	0	1455.77	151	163
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	16	17	32	0.03%	15.1%	EANHNVSAPYGR	99.7%	49.5	25	48	2	0	0	1314.62	827	838
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	16	17	32	0.03%	15.1%	EFFLELTMGR	99.6%	37.8	25	37.8	1	0	0	1258.61	625	634
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	16	17	32	0.03%	15.1%	LGTPQQIAIAR	99.7%	68.5	25	54.8	2	0	0	1167.68	1066	1076
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	16	17	32	0.03%	15.1%	NAFVTGIAR	99.7%	49.7	25	35.4	2	0	0	948.53	50	58
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	16	17	32	0.03%	15.1%	NVIQSVLQAIR	99.7%	84.2	25	47.9	2	0	0	1240.74	505	515
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	16	17	32	0.03%	15.1%	SGDGEGTPVEHVR	98.7%	32.6	25	28.4	2	0	0	1339.62	1228	1240
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	16	17	32	0.03%	15.1%	SLLQGTILQYVK	99.7%	45.5	25	45.5	2	0	0	1362.80	939	950
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	16	17	32	0.03%	15.1%	SSLEGPTILDIEK	99.7%	63.9	25	53	2	0	0	1401.75	582	594
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	16	17	32	0.03%	15.1%	TVEVLEPEVTK	99.7%	55.5	25	44.6	2	0	0	1243.68	111	121
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	16	17	32	0.03%	15.1%	TVLPFSQEFQR	99.5%	36.7	25	32.2	1	0	0	1351.70	867	877
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	16	17	32	0.03%	15.1%	YAPLHLVPLIER	99.2%	34.5	25	34.5	2	0	0	1420.83	1054	1065
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	16	17	32	0.03%	15.1%	YLTLDGFDAMFR	99.7%	44.4	25	44.4	2	0	0	1464.68	815	826
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	16	17	32	0.03%	15.1%	YSNSEVVTGSGR	99.7%	107	25	99.7	2	0	0	1255.59	366	377
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	99.8%	2	2	2	0.00%	9.3%	DFVSEAYLLTLGK	99.7%	65.8	25	0	4	0	0	1455.77	151	163
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	99.8%	2	2	2	0.00%	9.3%	EANHNVSAPYGR	99.7%	49.5	25	48	2	0	0	1314.62	851	862
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	99.8%	2	2	2	0.00%	9.3%	EFFLELTMGR	99.6%	37.8	25	37.8	1	0	0	1258.61	649	658
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	99.8%	2	2	2	0.00%	9.3%	LGTPQQIAIAR	99.7%	68.5	25	54.8	2	0	0	1167.68	1090	1100
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	99.8%	2	2	2	0.00%	9.3%	NAFVTGIAR	99.7%	49.7	25	35.4	2	0	0	948.53	50	58
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	99.8%	2	2	2	0.00%	9.3%	SLLQGTILQYVK	99.7%	45.5	25	45.5	2	0	0	1362.80	963	974
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	99.8%	2	2	2	0.00%	9.3%	SVETDSSTVEHVR	99.7%	60.7	25	52.8	1	0	0	1445.69	1252	1264
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	99.8%	2	2	2	0.00%	9.3%	TVEVLEPEVTK	99.7%	55.5	25	44.6	2	0	0	1243.68	111	121
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	99.8%	2	2	2	0.00%	9.3%	YAPLHLVPLIER	99.2%	34.5	25	34.5	2	0	0	1420.83	1078	1089
Cytoplasmic FMR1-interacting protein 2	CYFIP2	CYFP2_HUMAN	148.4	99.8%	2	2	2	0.00%	9.3%	YSNSEVVTGSGLDSQK	99.7%	63.6	25	63.6	1	0	0	1670.79	366	381
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	3	3	4	0.00%	1.8%	EGLDEVAGIINDAK	99.7%	54.1	25	39.6	1	0	0	1443.73	879	892
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	3	3	4	0.00%	1.8%	HINDSAPEVR	98.5%	32.1	25	32.1	1	0	0	1137.56	447	456
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	3	3	4	0.00%	1.8%	TTGEVVSGVVSK	99.7%	59.2	25	49.1	2	0	0	1162.63	85	96
Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	NUBP2_HUMAN	28.8	99.8%	2	2	6	0.01%	10.0%	STISTELALALR	99.7%	55.2	25	46	2	0	0	1274.73	29	40
Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	NUBP2_HUMAN	28.8	99.8%	2	2	6	0.01%	10.0%	VGILDVDLCGPSIPR	99.7%	82.3	25	73.1	4	0	0	1610.86	46	60
Cytosolic non-specific dipeptidase	CNDP2	CNDP2_HUMAN	52.9	100.0%	3	3	5	0.00%	6.1%	TGQEIPVNVR	99.0%	33.8	25	29.1	2	0	0	1112.61	150	159
Cytosolic non-specific dipeptidase	CNDP2	CNDP2_HUMAN	52.9	100.0%	3	3	5	0.00%	6.1%	TVFGVEPDLTR	99.7%	43.1	25	32.3	1	0	0	1233.65	403	413
Cytosolic non-specific dipeptidase	CNDP2	CNDP2_HUMAN	52.9	100.0%	3	3	5	0.00%	6.1%	YNYIEGTK	99.7%	39.5	25	31	2	0	0	987.48	454	461
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	23	32	101	0.10%	53.7%	AGTGVDNVDLEAATR	99.7%	105	25	95	6	0	0	1488.73	76	90
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	23	32	101	0.10%	53.7%	AGTGVDNVDLEAATRK	99.7%	127	25	122	2	2	0	1616.82	76	91
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	23	32	101	0.10%	53.7%	ALQSGQCAGAALDVFTEEPPRDR	99.7%	101	25	101	0	2	0	2488.19	248	270
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	23	32	101	0.10%	53.7%	ALVDHENVISCPHLGASTK	99.7%	62	25	62	0	2	0	2048.02	271	289
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	23	32	101	0.10%	53.7%	CGEEIAVQFVDMVK	99.7%	102	25	97.7	7	0	0	1624.77	295	308
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	23	32	101	0.10%	53.7%	DLPLLLFR	99.7%	49.7	25	42.3	8	0	0	986.60	462	469
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	23	32	101	0.10%	53.7%	EELIAELQDCEGLIVR	99.2%	34.9	25	34.9	1	0	0	1886.95	39	54
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	23	32	101	0.10%	53.7%	FMGTELNGK	99.7%	51.2	25	46.4	3	0	0	996.48	138	146
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	23	32	101	0.10%	53.7%	GGIVDEGALLR	99.7%	84.1	25	48.5	6	0	0	1099.61	237	247
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	23	32	101	0.10%	53.7%	GTIQVITQGTSLK	99.7%	92	25	86.1	9	0	0	1345.77	352	364
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	23	32	101	0.10%	53.7%	ILQDGGLQVVEK	99.7%	72.3	25	61	2	0	0	1298.73	22	33
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	23	32	101	0.10%	53.7%	KVLISDSLDPCCR	99.7%	34.9	25	33.9	0	1	0	1562.77	8	20
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	23	32	101	0.10%	53.7%	LLSYQTSLVSDGETWHVMGISSLLPSLEAWK	99.7%	89.2	25	89.2	0	3	0	3447.75	492	522
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	23	32	101	0.10%	53.7%	MQSFGMK	99.2%	34.7	25	27	2	0	0	828.37	164	170
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	23	32	101	0.10%	53.7%	NAGNCLSPAVIVGLLK	99.7%	71.2	25	68.2	5	1	0	1625.90	365	380

D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	23	32	101	0.10%	53.7%	QADVNLVNAK	99.7%	60.8	25	51.4	2	0	0	1071.58	385	394
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	23	32	101	0.10%	53.7%	QHVTEAFQFHF	99.7%	68.2	25	64.3	2	0	0	1390.65	523	533
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	23	32	101	0.10%	53.7%	QIPQATASMK	99.7%	49.4	25	44.6	5	0	0	1090.56	120	129
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	23	32	101	0.10%	53.7%	QNLSKEELIAELQDCEGLIVR	99.7%	49.5	25	43.5	0	2	0	2457.27	34	54
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	23	32	101	0.10%	53.7%	TLGILGLGR	99.7%	70.3	25	58.3	7	0	0	899.57	147	155
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	23	32	101	0.10%	53.7%	TQTSDPAMLPTMIGLLAEAGVR	99.7%	129	25	126	8	4	0	2272.17	470	491
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	23	32	101	0.10%	53.7%	VLISDSLDPCCR	99.7%	79.9	25	79.9	2	0	0	1434.67	9	20
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	23	32	101	0.10%	53.7%	VTADVINAAEK	99.7%	107	25	84.9	7	0	0	1130.61	59	69
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	99.8%	2	2	3	0.00%	5.0%	ESVLTATSILNNPIVK	99.7%	107	25	97.7	2	0	0	1698.96	444	459
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	99.8%	2	2	3	0.00%	5.0%	NQGGSSWEAPYSR	95.7%	27.7	25	20	1	0	0	1438.63	126	138
DDB1- and CUL4-associated factor 7	DCAF7	DCAF7_HUMAN	38.9	100.0%	6	6	7	0.01%	22.2%	DMFASVGADGSVR	99.7%	49.9	25	49.9	1	0	0	1311.60	190	202
DDB1- and CUL4-associated factor 7	DCAF7	DCAF7_HUMAN	38.9	100.0%	6	6	7	0.01%	22.2%	GVYPDLLATSGDYLR	99.7%	88.3	25	83.4	2	0	0	1639.83	82	96
DDB1- and CUL4-associated factor 7	DCAF7	DCAF7_HUMAN	38.9	100.0%	6	6	7	0.01%	22.2%	LALGSFVEEYNNK	99.7%	47.8	25	47.8	1	0	0	1483.74	34	46
DDB1- and CUL4-associated factor 7	DCAF7	DCAF7_HUMAN	38.9	100.0%	6	6	7	0.01%	22.2%	NTFDHPYPTTK	97.1%	29.3	25	24.8	1	0	0	1320.62	63	73
DDB1- and CUL4-associated factor 7	DCAF7	DCAF7_HUMAN	38.9	100.0%	6	6	7	0.01%	22.2%	VPCTPVAR	98.3%	31.5	25	24	1	0	0	899.48	254	261
DDB1- and CUL4-associated factor 7	DCAF7	DCAF7_HUMAN	38.9	100.0%	6	6	7	0.01%	22.2%	VQLVGLDEESSEFICR	99.7%	59.8	25	58.7	1	0	0	1880.91	47	62
D-dopachrome decarboxylase	DDT	DOPD_HUMAN	12.7	99.8%	2	2	2	0.00%	16.1%	ELALGQDR	99.1%	34.1	25	23.3	1	0	0	901.47	88	95
D-dopachrome decarboxylase	DDT	DOPD_HUMAN	12.7	99.8%	2	2	2	0.00%	16.1%	FFPLESWQIGK	95.6%	27.6	25	25.3	1	0	0	1351.70	100	110
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	8	8	11	0.01%	5.3%	ESFCITSFLCSTK	99.7%	55	25	53	2	0	0	1579.71	565	577
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	8	8	11	0.01%	5.3%	ESGVSLIATVTR	99.7%	57.8	25	44.6	1	0	0	1232.68	1146	1157
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	8	8	11	0.01%	5.3%	HTTSVSPSPAGR	94.7%	26.9	25	21.6	1	0	0	1196.60	1803	1814
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	8	8	11	0.01%	5.3%	IGCTVSLLNFYK	99.7%	50.4	25	50.4	1	0	0	1414.74	1179	1190
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	8	8	11	0.01%	5.3%	LDWGNEQLGLDLVPR	99.7%	57.5	25	57.5	2	0	0	1724.90	150	164
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	8	8	11	0.01%	5.3%	NSAPASVSPDGTR	99.7%	44.5	25	44.5	1	0	0	1258.60	1613	1625
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	8	8	11	0.01%	5.3%	TSLYLVQSLPGISR	99.7%	42.8	25	42.8	2	0	0	1533.86	1441	1454
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	8	8	11	0.01%	5.3%	TVESQLYTNPDSR	99.7%	73.7	25	61.2	1	0	0	1509.72	815	827
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	7	11	25	0.02%	29.8%	GTIMDTTVDVDKR	99.6%	37.8	25	36.6	3	0	0	1466.72	149	161
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	7	11	25	0.02%	29.8%	NAVVVITGATSGLGK	99.7%	79.5	25	73.7	3	0	0	1386.80	52	66
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	7	11	25	0.02%	29.8%	QGHIVAISSIQGK	99.7%	73.6	25	63.6	1	0	0	1337.75	186	198
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	7	11	25	0.02%	29.8%	SPVEVAQDVLAAVGKK	99.7%	76.6	25	76.6	2	0	0	1610.91	268	283
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	7	11	25	0.02%	29.8%	TLAPGLFFSLMASR	99.7%	77.1	25	76.7	4	0	0	1510.81	302	315
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	7	11	25	0.02%	29.8%	VMETNYFGPVALTK	99.7%	96	25	74.9	7	0	0	1569.80	162	175
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	7	11	25	0.02%	29.8%	YGVMDTTTAQGR	99.7%	87.4	25	81.4	5	0	0	1299.60	256	267
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	5	5	9	0.01%	11.9%	NAAGNFYINDK	97.7%	30.2	25	30.2	1	0	0	1226.58	499	509
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	5	5	9	0.01%	11.9%	SADVESVVSGTLR	99.7%	90.5	25	80.3	2	0	0	1319.68	326	338
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	5	5	9	0.01%	11.9%	SSPSLTILAGGK	99.7%	53.7	25	45.4	2	0	0	1130.64	409	420
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	5	5	9	0.01%	11.9%	STGSIVGQQPFGGAR	99.7%	44.9	25	44.9	2	0	0	1461.74	510	524
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	5	5	9	0.01%	11.9%	VANEPVLAFTQGSPER	99.7%	86.2	25	82	2	0	0	1714.88	32	47
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	33	75	0.07%	35.7%	CEYPAACNALETLLIHR	98.6%	24.3	25	24.3	0	1	0	2030.98	606	622
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	33	75	0.07%	35.7%	DLEEAEGR	99.5%	36.4	25	20.8	2	0	0	918.42	410	417
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	33	75	0.07%	35.7%	EAVQLVNTR	99.7%	62	25	46.6	2	0	0	1029.57	531	539
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	33	75	0.07%	35.7%	EAVQLVNTREEVEDLCR	99.7%	53.9	25	51.5	0	2	0	2060.01	531	547
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	33	75	0.07%	35.7%	EMAIPVLEAR	99.7%	40	25	32	2	0	0	1144.60	150	159
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	33	75	0.07%	35.7%	EMMLVTSGAVAFGK	99.7%	74.7	25	71.9	5	0	0	1440.72	111	124
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	33	75	0.07%	35.7%	FASYLTFSPSEVK	99.7%	81.4	25	80.2	3	0	0	1475.74	650	662
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	33	75	0.07%	35.7%	GPVGLEGLLTTK	99.7%	71.8	25	71.8	2	0	0	1184.69	750	761
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	33	75	0.07%	35.7%	HEILLSQSVR	99.7%	57.8	25	49.8	2	0	0	1181.66	129	138
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	33	75	0.07%	35.7%	LAAPLLKR	99.2%	34.8	25	34.8	2	0	0	881.59	418	425
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	33	75	0.07%	35.7%	LASIVEQVSVLQNQGR	99.7%	98	25	81	5	0	0	1740.96	95	110
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	33	75	0.07%	35.7%	LGSAVVTR	99.7%	75.3	25	55.6	3	0	0	802.48	77	84
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	33	75	0.07%	35.7%	LIDIFYPGDQQSVTFGTK	99.7%	98.4	25	97.3	5	0	0	2029.03	283	300

Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	33	75	0.07%	35.7%	LNSLAIGLR	99.7%	88.3	25	70.5	4	0	0	956.59	433	441
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	33	75	0.07%	35.7%	MIDLIIPR	99.7%	57.9	25	46.3	6	0	0	970.58	551	558
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	33	75	0.07%	35.7%	MLATLEPEQR	99.7%	60.5	25	45.9	5	0	0	1203.60	376	385
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	33	75	0.07%	35.7%	NLNGTLHELLR	99.7%	55.2	25	46.9	2	0	0	1279.71	202	212
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	33	75	0.07%	35.7%	QIAASSQDSVGR	99.7%	59.2	25	52.8	2	0	0	1218.61	442	453
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	33	75	0.07%	35.7%	SWSNIPFITVPLSR	99.2%	34.5	25	26.1	2	0	0	1616.88	42	55
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	33	75	0.07%	35.7%	TPLFDQIIDMLR	99.7%	76.3	25	70.4	4	0	0	1477.77	627	638
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	33	75	0.07%	35.7%	VGMGGMEAK	99.7%	45.9	25	37.4	2	0	0	879.41	303	311
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	33	75	0.07%	35.7%	VGTFFSEVKPAGPTVEQQGEMAR	99.7%	90.3	25	90.3	0	4	0	2465.21	349	371
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	33	75	0.07%	35.7%	VSGHVITDIVEGK	99.7%	66.8	25	59	2	1	0	1353.74	335	347
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	33	75	0.07%	35.7%	VSGHVITDIVEGKK	99.7%	60.7	25	60.7	1	2	0	1481.83	335	348
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	33	75	0.07%	35.7%	YLHENLPIPQR	99.5%	37	25	33.1	2	0	0	1379.74	782	792
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	12	20	0.02%	22.5%	EWNDSTSVQNPTR	99.7%	50.1	25	16.9	2	0	0	1533.69	597	609
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	12	20	0.02%	22.5%	FIPLARPEVK	99.5%	37.2	25	25.6	2	0	0	1169.70	221	230
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	12	20	0.02%	22.5%	GGFEEPVLLK	99.7%	44.6	25	27.8	1	0	0	1088.60	57	66
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	12	20	0.02%	22.5%	IIDTPQFQR	99.7%	57.5	25	47.3	2	0	0	1117.60	135	143
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	12	20	0.02%	22.5%	ISTAIDDMEAYTK	99.7%	84.8	25	76.9	1	0	0	1457.68	409	421
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	12	20	0.02%	22.5%	LVQIHVDTMK	99.7%	57.4	25	49.9	2	0	0	1199.65	107	116
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	12	20	0.02%	22.5%	NQVSQLLPEK	99.6%	37.8	25	18.2	2	0	0	1155.64	535	544
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	12	20	0.02%	22.5%	QLGGGYYVFPGASHNR	99.7%	30.7	25	30.7	0	1	0	1722.83	149	164
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	12	20	0.02%	22.5%	SFLYEIVSNKR	99.5%	36.9	25	32.9	1	0	0	1355.73	295	305
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	12	20	0.02%	22.5%	TWGPEQVCSFLR	99.7%	51.5	25	41.8	2	0	0	1479.71	44	55
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	12	20	0.02%	22.5%	VGNIIDTMITDAFLK	99.7%	61.4	25	61.4	2	0	0	1650.88	378	392
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	12	20	0.02%	22.5%	YVGETQPTGQIK	99.7%	63.8	25	54.7	2	0	0	1320.68	456	467
Dephospho-CoA kinase domain-containing protein	DCAKD	DCAKD_HUMAN	26.6	100.0%	4	4	6	0.01%	19.9%	HVVQPGYPAHR	96.2%	28.2	25	28.1	1	0	0	1260.66	37	47
Dephospho-CoA kinase domain-containing protein	DCAKD	DCAKD_HUMAN	26.6	100.0%	4	4	6	0.01%	19.9%	INAQLPLTDK	99.7%	51.9	25	40.7	2	0	0	1112.63	159	168
Dephospho-CoA kinase domain-containing protein	DCAKD	DCAKD_HUMAN	26.6	100.0%	4	4	6	0.01%	19.9%	MFLVGLTGGIASGK	99.7%	111	25	111	2	0	0	1350.75	1	14
Dephospho-CoA kinase domain-containing protein	DCAKD	DCAKD_HUMAN	26.6	100.0%	4	4	6	0.01%	19.9%	QVILLHTELER	97.9%	30.5	25	28.5	1	0	0	1350.77	188	198
Derlin-1	DERL1	DERL1_HUMAN	28.8	99.8%	2	2	2	0.00%	10.0%	NFLSTPQFLYR	99.6%	37.6	25	26.2	1	0	0	1385.72	198	208
Derlin-1	DERL1	DERL1_HUMAN	28.8	99.8%	2	2	2	0.00%	10.0%	YWFAATVAVPLVGK	99.3%	35.2	25	35.2	1	0	0	1521.85	17	30
Dermcidin	DCD	DCD_HUMAN	11.3	100.0%	3	4	50	0.05%	22.7%	DAVEDLESVGK	99.7%	71.7	25	63.1	10	0	0	1161.56	86	96
Dermcidin	DCD	DCD_HUMAN	11.3	100.0%	3	4	50	0.05%	22.7%	ENAGEDPGLAR	99.7%	88.6	25	83.9	30	0	0	1128.53	43	53
Dermcidin	DCD	DCD_HUMAN	11.3	100.0%	3	4	50	0.05%	22.7%	LGKDAVEDLESVGK	99.7%	91.4	25	86.1	9	1	0	1459.76	83	96
Desmoglein-1	DSG1	DSG1_HUMAN	113.7	100.0%	10	12	25	0.02%	13.0%	DGSNVIVTER	99.7%	46.5	25	35.8	2	0	0	1089.55	888	897
Desmoglein-1	DSG1	DSG1_HUMAN	113.7	100.0%	10	12	25	0.02%	13.0%	ESSNVVVTER	99.7%	43.3	25	35.7	3	0	0	1119.56	916	925
Desmoglein-1	DSG1	DSG1_HUMAN	113.7	100.0%	10	12	25	0.02%	13.0%	EVTPFFIIYCR	98.6%	32.1	25	29.9	2	0	0	1444.73	118	128
Desmoglein-1	DSG1	DSG1_HUMAN	113.7	100.0%	10	12	25	0.02%	13.0%	ISGVGIDQPPYGIFVINQK	99.4%	35.7	25	35.7	3	0	0	2045.11	87	105
Desmoglein-1	DSG1	DSG1_HUMAN	113.7	100.0%	10	12	25	0.02%	13.0%	MTGFELTEGVK	99.4%	35.7	25	34.2	2	0	0	1211.60	651	661
Desmoglein-1	DSG1	DSG1_HUMAN	113.7	100.0%	10	12	25	0.02%	13.0%	QEPSDSPMFIINR	99.7%	41.7	25	41.1	4	0	0	1549.73	201	213
Desmoglein-1	DSG1	DSG1_HUMAN	113.7	100.0%	10	12	25	0.02%	13.0%	TYVVTGNMGSNDK	99.7%	45.8	25	45.8	2	0	0	1401.63	391	403
Desmoglein-1	DSG1	DSG1_HUMAN	113.7	100.0%	10	12	25	0.02%	13.0%	VGDFVATDLDTGRPSTTVR	99.7%	37.6	25	37.6	0	2	0	2007.01	404	422
Desmoglein-1	DSG1	DSG1_HUMAN	113.7	100.0%	10	12	25	0.02%	13.0%	YQGTILSIDDNLQR	99.7%	70.2	25	63	2	0	0	1635.83	460	473
Desmoglein-1	DSG1	DSG1_HUMAN	113.7	100.0%	10	12	25	0.02%	13.0%	YVMGNNPADLLAVDSR	99.7%	95.5	25	86.5	3	0	0	1734.85	423	438
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	AELIVQPELK	99.7%	56.1	25	42	4	0	0	1139.67	85	94
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	AITGFDDPFSGK	97.2%	29.4	25	26.4	1	0	0	1254.60	2092	2103
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	ALLQAILQTEDMLK	99.7%	95	25	92.6	4	0	0	1586.88	772	785
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	FGDSNTVMR	99.7%	64.3	25	54.9	2	0	0	1026.47	917	925
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	FLDQNLQK	97.9%	30.5	25	13.4	1	0	0	1005.54	1057	1064
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	GFFDPNTEENLTYLQLK	99.7%	54	25	54	1	0	0	2028.99	2414	2430
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	GIHNSIGDYR	95.0%	27.2	25	13.4	1	0	0	1131.55	223	232
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	IEVLEEELR	99.7%	51.9	25	39.8	3	0	0	1129.61	1034	1042

Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	IQSQFTDAQK	99.7%	47.2	25	37.9	3	0	0	1165.58	608	617
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	ITNLTQQLEQASIVK	99.7%	68.7	25	68.7	1	0	0	1685.94	1612	1626
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	LASLEELKR	99.7%	49.8	25	40.1	4	0	0	1058.62	1076	1084
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	LLEAQIATGGIIDPK	99.7%	73.6	25	66.9	4	0	0	1538.88	2367	2381
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	LLQLQEQMR	99.7%	54.6	25	37.8	3	0	0	1158.63	142	150
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	LNDSILQATEQR	99.7%	73.4	25	71.1	3	0	0	1387.72	1256	1267
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	LQSLTENLTK	99.7%	40	25	21	2	0	0	1146.64	1706	1715
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	LSSEVEALR	99.7%	67.5	25	45.1	2	0	0	1003.54	1657	1665
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	LTYEIEDEKR	99.7%	46.8	25	38	2	0	0	1295.65	1114	1123
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	NKYETEINITK	97.4%	29.7	25	26.1	1	0	0	1352.71	1208	1218
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	NQCTQVVQER	99.7%	41.7	25	28.2	1	0	0	1261.60	1803	1812
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	NTLTQTTENLR	99.7%	48.5	25	42.8	2	0	0	1290.66	1414	1424
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	QLLQEQESVK	99.7%	41.1	25	31.9	2	0	0	1201.64	1667	1676
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	QLQNIIQATSR	99.7%	75.7	25	74.1	6	0	0	1271.71	271	281
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	QQIQNDLNQWK	99.7%	43.9	25	42.9	2	0	0	1414.71	1858	1868
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	RVEEDIQQQK	99.7%	40.7	25	24.3	2	0	0	1272.65	1425	1434
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	SQLQISNNR	99.7%	48.5	25	38.8	2	0	0	1059.55	1754	1762
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	SVEEVASEIQPFLR	98.1%	30.9	25	18.9	1	0	0	1603.83	2000	2013
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	TLELQGLINDLQR	99.7%	77.1	25	71.1	1	0	0	1512.84	1763	1775
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	YEVTSGGGGTSR	99.7%	66.6	25	55.4	3	0	0	1170.54	28	39
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	YGDGIQLTR	99.7%	67.6	25	56.3	3	0	0	1022.53	95	103
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	30	31	71	0.07%	11.4%	YIELLTR	99.7%	42.9	25	35.1	4	0	0	907.52	1003	1009
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	5	6	10	0.01%	33.7%	INLVLSR	99.7%	49.3	25	32.1	2	0	0	814.51	72	78
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	5	6	10	0.01%	33.7%	LLPEYPGVLSDVQEEK	99.7%	75.5	25	71	2	0	0	1815.94	159	174
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	5	6	10	0.01%	33.7%	QNLVIMGK	98.5%	32	25	22	1	0	0	918.51	48	55
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	5	6	10	0.01%	33.7%	VDMVWIVGGSSVYK	99.7%	44.3	25	43.4	1	0	0	1539.79	110	123
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	5	6	10	0.01%	33.7%	VGSLNCIVAVSQNMGIGK	99.7%	72	25	72	2	2	0	1862.95	2	19
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	18	25	46	0.05%	48.9%	ADGGTQVIDTK	99.7%	59.8	25	47.6	2	0	0	1104.55	167	177
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	18	25	46	0.05%	48.9%	AEVITCDVLLVCIGR	99.7%	49.6	25	49.6	1	0	0	1717.90	301	315
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	18	25	46	0.05%	48.9%	ALLNNSHYYHMAHGK	99.6%	28.3	25	28.3	0	2	0	1755.84	90	104
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	18	25	46	0.05%	48.9%	ALTGGIAHLFK	99.7%	67.7	25	59.8	2	0	0	1127.66	133	143
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	18	25	46	0.05%	48.9%	EANLAASFGK	99.7%	73.2	25	67.5	2	0	0	1007.52	496	505
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	18	25	46	0.05%	48.9%	FPFAANSR	99.7%	39.8	25	25.3	2	0	0	909.46	421	428
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	18	25	46	0.05%	48.9%	GIEMSEVR	99.7%	51.3	25	43.3	2	0	0	936.45	110	117
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	18	25	46	0.05%	48.9%	GRIPVNTR	97.9%	30.6	25	21	2	0	0	912.54	335	342
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	18	25	46	0.05%	48.9%	IPNIYAIGDVVAGPMLAHK	99.7%	91.7	25	91.7	2	4	0	1979.08	347	365
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	18	25	46	0.05%	48.9%	MVVIGAGVIGVELGSVWQR	99.7%	67.6	25	67.6	3	1	0	1970.09	216	234
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	18	25	46	0.05%	48.9%	NETLGGTCLNVGCIPSK	99.7%	137	25	133	2	0	0	1819.87	73	89
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	18	25	46	0.05%	48.9%	NLGLEELGIELDPR	99.7%	82.3	25	69.4	4	0	0	1567.83	321	334
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	18	25	46	0.05%	48.9%	SDGKIDVSIEAASGGK	99.1%	25.7	25	25.7	0	1	0	1533.78	285	300
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	18	25	46	0.05%	48.9%	SEEQLKEEGIEYK	99.7%	70.4	25	70.4	2	2	0	1581.76	405	417
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	18	25	46	0.05%	48.9%	TNADTDGMVK	99.4%	35.9	25	30.1	1	0	0	1051.47	431	440
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	18	25	46	0.05%	48.9%	VCHAHPTLSEAFR	99.7%	38.4	25	32.5	1	2	0	1524.74	483	495
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	18	25	46	0.05%	48.9%	VLGAHILGPGAGEMVNEAALALEYGASCEDIAR	99.7%	79.9	25	75.3	0	4	0	3370.64	450	482
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	18	25	46	0.05%	48.9%	VVHVNGYGK	99.3%	35.2	25	26.9	2	0	0	972.53	147	155
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	8	9	15	0.01%	14.8%	DVPLGTPLCIIVEK	99.7%	43.6	25	43.6	1	0	0	1553.86	283	296
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	8	9	15	0.01%	14.8%	GVETIANDVVSLATK	99.7%	75	25	72.5	2	0	0	1516.82	533	547
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	8	9	15	0.01%	14.8%	ILVAEGTR	98.2%	31.2	25	23.1	2	0	0	858.50	148	155
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	8	9	15	0.01%	14.8%	ILVPEGTR	95.0%	27.1	25	19.5	1	0	0	884.52	275	282
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	8	9	15	0.01%	14.8%	ISVNDFIIK	98.3%	31.5	25	31.5	2	0	0	1048.60	474	482
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	8	9	15	0.01%	14.8%	VPLPSLSPTMQAGTIAR	99.7%	70.4	25	70.4	4	0	0	1738.95	94	110

Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	8	9	15	0.01%	14.8%	VVDGAVGAQWLAEFR	99.7%	77.4	25	77.4	2	0	0	1617.84	622	636
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	8	9	15	0.01%	14.8%	YLEKPITMLL	99.6%	37.7	25	31.7	1	0	0	1236.69	638	647
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	5	6	11	0.01%	10.8%	GMYDGPVYEVPATPK	99.7%	62	25	59.5	4	0	0	1623.77	497	511
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	5	6	11	0.01%	10.8%	IVFEDGNINVNK	99.7%	75	25	70.3	1	0	0	1361.71	452	463
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	5	6	11	0.01%	10.8%	MDENQFVAVTSTNAAK	99.7%	51.2	25	47.3	2	0	0	1725.81	375	390
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	5	6	11	0.01%	10.8%	SAADIIALAR	99.7%	86	25	73.1	2	0	0	1000.58	259	268
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	5	6	11	0.01%	10.8%	VFGLQGVSR	99.7%	59.1	25	45.9	2	0	0	962.54	488	496
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	6	6	10	0.01%	11.2%	GAPAVVISQGR	99.7%	62.7	25	58.5	2	0	0	1054.60	441	451
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	6	6	10	0.01%	11.2%	IFNFYPR	99.7%	42	25	13	1	0	0	956.50	391	397
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	6	6	10	0.01%	11.2%	LAEIHGVPR	99.7%	61.2	25	53.8	2	0	0	991.57	488	496
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	6	6	10	0.01%	11.2%	MFVTPGAGR	99.7%	45	25	40.2	2	0	0	935.48	459	467
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	6	6	10	0.01%	11.2%	QIGENLIVPGGIK	99.6%	37.6	25	37.6	2	0	0	1337.78	44	56
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	6	6	10	0.01%	11.2%	VAVGSDADLVIWNPK	99.7%	49.9	25	40	1	0	0	1583.84	401	415
Dihydropyrimidinase-related protein 5	DPYSL5	DPYL5_HUMAN	61.4	100.0%	3	3	5	0.00%	6.4%	FVAVTSSNAAK	99.7%	47.2	25	41.6	2	0	0	1094.58	373	383
Dihydropyrimidinase-related protein 5	DPYSL5	DPYL5_HUMAN	61.4	100.0%	3	3	5	0.00%	6.4%	IPHGVSGVQDR	95.6%	27.7	25	18.3	1	0	0	1164.61	344	354
Dihydropyrimidinase-related protein 5	DPYSL5	DPYL5_HUMAN	61.4	100.0%	3	3	5	0.00%	6.4%	VHAENGELVAEGAK	99.7%	58.2	25	52.4	2	0	0	1423.72	190	203
Dihydroxyacetone phosphate acyltransferase	GNPAT	GNPAT_HUMAN	77.2	99.7%	2	2	3	0.00%	3.7%	LYWAVFSEYVK	99.3%	35.2	25	35.2	2	0	0	1404.72	218	228
Dihydroxyacetone phosphate acyltransferase	GNPAT	GNPAT_HUMAN	77.2	99.7%	2	2	3	0.00%	3.7%	NGYAPVEFFLEGTR	94.8%	27	25	27	1	0	0	1599.78	233	246
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	6	7	10	0.01%	20.2%	FIPGLQMLSDAAPGK	99.2%	34.8	25	25.3	2	0	0	1544.81	90	104
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	6	7	10	0.01%	20.2%	LLELADIDPTLRPR	98.8%	32.8	25	32.8	2	0	0	1621.93	280	293
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	6	7	10	0.01%	20.2%	LSVMAQYLCNVR	99.7%	55.9	25	55.9	1	0	0	1453.73	196	207
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	6	7	10	0.01%	20.2%	QLSQNFLLDLR	99.7%	41.8	25	40.1	2	0	0	1346.74	32	42
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	6	7	10	0.01%	20.2%	TQMTLTFQK	97.1%	29.2	25	12.9	1	0	0	1113.56	170	178
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	6	7	10	0.01%	20.2%	VVQNVFQFR	99.7%	51.5	25	44.4	2	0	0	1136.62	248	256
Dimethyladenosine transferase 2, mitochondrial	TFB2M	TFB2M_HUMAN	45.4	100.0%	3	4	8	0.01%	8.6%	LYLIQMIPR	99.7%	56.7	25	37.4	4	0	0	1146.67	296	304
Dimethyladenosine transferase 2, mitochondrial	TFB2M	TFB2M_HUMAN	45.4	100.0%	3	4	8	0.01%	8.6%	NLGIEAVPWTADIPLK	99.5%	37	25	37	2	0	0	1736.96	175	190
Dimethyladenosine transferase 2, mitochondrial	TFB2M	TFB2M_HUMAN	45.4	100.0%	3	4	8	0.01%	8.6%	SATVIDHLR	99.7%	44.8	25	27.5	2	0	0	1011.56	332	340
DNA damage-binding protein 1	DDB1	DDB1_HUMAN	127.0	100.0%	2	2	2	0.00%	1.8%	EMLGGEIIPR	99.7%	46.8	25	29.5	1	0	0	1114.59	580	589
DNA damage-binding protein 1	DDB1	DDB1_HUMAN	127.0	100.0%	2	2	2	0.00%	1.8%	IVVFQYSDGK	99.7%	51.6	25	45.3	1	0	0	1155.60	848	857
DNA ligase 3	LIG3	DNLI3_HUMAN	112.9	100.0%	5	5	8	0.01%	5.6%	ALDLADMITR	99.7%	63.4	25	56.1	2	0	0	1118.59	639	648
DNA ligase 3	LIG3	DNLI3_HUMAN	112.9	100.0%	5	5	8	0.01%	5.6%	DLEQGDVSETIR	99.7%	67.9	25	67.9	2	0	0	1361.65	344	355
DNA ligase 3	LIG3	DNLI3_HUMAN	112.9	100.0%	5	5	8	0.01%	5.6%	SEAHTADGISIR	98.1%	31	25	21.6	1	0	0	1256.62	792	803
DNA ligase 3	LIG3	DNLI3_HUMAN	112.9	100.0%	5	5	8	0.01%	5.6%	VIQEGLEGLVLK	99.7%	80.5	25	76.4	1	0	0	1297.77	649	660
DNA ligase 3	LIG3	DNLI3_HUMAN	112.9	100.0%	5	5	8	0.01%	5.6%	VLLDIFTGVR	99.7%	75.7	25	75.7	2	0	0	1132.67	933	942
DNA methyltransferase 1-associated protein 1	DMAP1	DMAP1_HUMAN	53.0	100.0%	5	5	6	0.01%	12.4%	AAEEGKDYPFAR	99.7%	40.7	25	39.8	1	0	0	1353.64	117	128
DNA methyltransferase 1-associated protein 1	DMAP1	DMAP1_HUMAN	53.0	100.0%	5	5	6	0.01%	12.4%	AETDHLFDLSR	99.7%	50.5	25	48.7	1	0	0	1303.63	155	165
DNA methyltransferase 1-associated protein 1	DMAP1	DMAP1_HUMAN	53.0	100.0%	5	5	6	0.01%	12.4%	DAPPLLPSDTGQGYR	96.1%	28.1	25	27.9	1	0	0	1586.78	67	81
DNA methyltransferase 1-associated protein 1	DMAP1	DMAP1_HUMAN	53.0	100.0%	5	5	6	0.01%	12.4%	LITAADTTAEQR	99.7%	78.7	25	67.9	2	0	0	1289.67	271	282
DNA methyltransferase 1-associated protein 1	DMAP1	DMAP1_HUMAN	53.0	100.0%	5	5	6	0.01%	12.4%	SVEDLKER	94.9%	27	25	18.5	1	0	0	975.51	187	194
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	13.5%	DSLIIIDELGR	99.7%	72.9	25	61.9	2	0	0	1243.69	742	752
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	13.5%	LDSSAQFGYYFR	99.7%	64.9	25	61.3	2	0	0	1453.67	513	524
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	13.5%	LLLAVFVTPLTDLR	99.7%	77.2	25	77.2	3	0	0	1570.96	431	444
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	13.5%	LNLVEAFVEDAELR	99.7%	110	25	109	2	0	0	1617.85	360	373
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	13.5%	LTSLNEEYTK	99.7%	51.5	25	39.2	2	0	0	1197.60	556	565
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	13.5%	LYQGINQLPNVIQALEK	99.7%	71.7	25	71.7	2	0	0	1941.08	407	423
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	13.5%	MQSTLISAAR	99.7%	44	25	40	1	0	0	1093.57	492	501
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	13.5%	NFSTVDIQK	94.9%	27	25	16.6	1	0	0	1051.54	538	546
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	13.5%	NLQSVVLSK	99.7%	54.3	25	30.6	2	0	0	987.58	74	82
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	13.5%	NNSFVNEIISR	99.7%	62.9	25	44.1	2	0	0	1292.66	919	929
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	13.5%	QTLQEDLLR	99.7%	54.5	25	43.2	1	0	0	1115.61	374	382
DNA mismatch repair protein Msh3	MSH3	MSH3_HUMAN	127.4	100.0%	4	4	6	0.01%	4.3%	FFGEDAEIAAR	98.5%	31.8	25	31	1	0	0	1225.58	258	268

DNA mismatch repair protein Msh3	MSH3	MSH3_HUMAN	127.4	100.0%	4	4	6	0.01%	4.3%	KLPDIER	95.6%	27.6	25	0	1	0	0	870.50	617	623
DNA mismatch repair protein Msh3	MSH3	MSH3_HUMAN	127.4	100.0%	4	4	6	0.01%	4.3%	MGAADNIYK	96.5%	28.5	25	21.7	1	0	0	982.47	939	947
DNA mismatch repair protein Msh3	MSH3	MSH3_HUMAN	127.4	100.0%	4	4	6	0.01%	4.3%	STLIGEDVNPLIK	99.7%	48.3	25	39.2	2	0	0	1398.78	337	349
DNA mismatch repair protein Msh3	MSH3	MSH3_HUMAN	127.4	100.0%	4	4	6	0.01%	4.3%	VQTESLQER	99.6%	37.7	25	28.8	2	0	0	1089.55	151	159
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	11	12	20	0.02%	9.6%	AYGVCFVDTSLGK	99.7%	69.9	25	69.9	2	0	0	1416.68	555	567
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	11	12	20	0.02%	9.6%	GTATFDGTAIANAVVK	99.7%	88.4	25	76.2	2	0	0	1535.81	1218	1233
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	11	12	20	0.02%	9.6%	IIDFLSALEGFK	99.7%	73.2	25	63.2	3	0	0	1352.75	855	866
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	11	12	20	0.02%	9.6%	IIGIMEEVADGFK	99.7%	60.8	25	60.8	2	0	0	1421.73	871	883
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	11	12	20	0.02%	9.6%	KLPDLER	95.6%	27.6	25	0	1	0	0	870.50	814	820
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	11	12	20	0.02%	9.6%	LANLPEEVIQK	99.7%	47.4	25	33.3	2	0	0	1253.71	1305	1315
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	11	12	20	0.02%	9.6%	LSDGIGVMLPQVLK	99.7%	44	25	35.5	3	0	0	1485.83	647	660
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	11	12	20	0.02%	9.6%	STVDAEAVHK	98.7%	32.4	25	26.1	2	0	0	1056.53	1343	1352
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	11	12	20	0.02%	9.6%	TLLEEEYFREK	99.7%	44	25	36	1	0	0	1456.73	636	646
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	11	12	20	0.02%	9.6%	VHVQFFDDSPTR	99.7%	51.8	25	51.8	1	0	0	1447.70	129	140
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	11	12	20	0.02%	9.6%	YQLEIPENFTTR	99.4%	35.8	25	31.1	1	0	0	1510.75	977	988
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	18	36	0.04%	19.1%	DLEDQEQLLR	99.7%	65.1	25	48.2	2	0	0	1258.63	1088	1097
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	18	36	0.04%	19.1%	DNCPLVANLVTASLR	99.7%	60.5	25	56.5	2	0	0	1642.86	835	849
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	18	36	0.04%	19.1%	ELNLAISR	99.7%	45.6	25	20.8	2	0	0	915.53	167	174
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	18	36	0.04%	19.1%	ELTGPAVLAVELCSR	99.7%	85.6	25	79.2	2	0	0	1614.85	181	195
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	18	36	0.04%	19.1%	FGVSSVAEAMALGR	99.7%	98	25	98	2	0	0	1394.71	763	776
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	18	36	0.04%	19.1%	IDISQLVITK	99.7%	89.1	25	64	2	0	0	1129.68	876	885
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	18	36	0.04%	19.1%	IFEPILGEGR	99.7%	68.1	25	62.8	2	0	0	1130.62	969	978
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	18	36	0.04%	19.1%	LGLTEDQFIR	99.7%	79.5	25	68.1	2	0	0	1191.64	630	639
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	18	36	0.04%	19.1%	LLEQGIR	99.7%	44.4	25	0	1	0	0	828.49	226	232
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	18	36	0.04%	19.1%	LMVLVNAVEMAR	99.7%	62.3	25	62.3	3	0	0	1345.73	526	537
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	18	36	0.04%	19.1%	LPCLEISQSVTGFGR	99.7%	69.4	25	69.4	2	0	0	1663.85	711	725
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	18	36	0.04%	19.1%	SEGGEDYTGATVIEPLK	99.7%	86.6	25	86.6	2	0	0	1765.85	575	591
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	18	36	0.04%	19.1%	TPTGDEFVK	99.7%	39.4	25	28.3	2	0	0	993.49	640	648
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	18	36	0.04%	19.1%	VGGLLAFAK	99.0%	33.6	25	33.6	2	0	0	875.54	999	1007
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	18	36	0.04%	19.1%	VLSFDIECAGR	99.7%	84.6	25	80.7	2	0	0	1266.61	312	322
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	18	36	0.04%	19.1%	VQMDMLQVLLR	99.7%	69.2	25	55.8	3	0	0	1345.73	455	465
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	18	36	0.04%	19.1%	VSANSVYGFTGAQVGK	99.7%	75.5	25	70.6	2	0	0	1584.80	695	710
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	18	36	0.04%	19.1%	VTGVPLSYLLSR	99.7%	45.3	25	32.6	2	0	0	1304.76	538	549
DNA polymerase delta subunit 2	POLD2	DPOD2_HUMAN	51.3	99.8%	2	2	3	0.00%	6.0%	FLGTSGQNVSDIFR	99.7%	80.4	25	76.2	1	0	0	1540.78	341	354
DNA polymerase delta subunit 2	POLD2	DPOD2_HUMAN	51.3	99.8%	2	2	3	0.00%	6.0%	LVTGTVLAVFGSVR	99.7%	67.6	25	59.2	2	0	0	1418.84	153	166
DNA polymerase delta subunit 3	POLD3	DPOD3_HUMAN	51.4	100.0%	4	4	7	0.01%	11.2%	DSGPLFNTDYDILK	99.7%	44	25	31.5	2	0	0	1597.77	110	123
DNA polymerase delta subunit 3	POLD3	DPOD3_HUMAN	51.4	100.0%	4	4	7	0.01%	11.2%	FSAIQCAAAVPR	99.7%	43.2	25	33.2	2	0	0	1290.66	132	143
DNA polymerase delta subunit 3	POLD3	DPOD3_HUMAN	51.4	100.0%	4	4	7	0.01%	11.2%	IVEQPTVSVTEPK	99.7%	68.5	25	67.4	2	0	0	1426.78	262	274
DNA polymerase delta subunit 3	POLD3	DPOD3_HUMAN	51.4	100.0%	4	4	7	0.01%	11.2%	VNLDSEQAVKEEK	95.2%	27.3	25	16.3	1	0	0	1488.75	249	261
DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	4	4	5	0.00%	2.1%	AIPLAIFQAEPTVR	99.7%	53.1	25	53.1	1	0	0	1525.87	1093	1106
DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	4	4	5	0.00%	2.1%	IFQSSVFEAFLK	99.7%	59.9	25	45.1	2	0	0	1415.76	984	995
DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	4	4	5	0.00%	2.1%	IITIPAALQQVK	94.9%	27	25	25.8	1	0	0	1294.81	1144	1155
DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	4	4	5	0.00%	2.1%	SSSLQDFDIR	99.7%	48.3	25	22.5	1	0	0	1167.56	1116	1125
DNA primase large subunit	PRIM2	PRI2_HUMAN	58.8	100.0%	2	2	5	0.00%	4.9%	IPFADALDLFR	99.7%	61.9	25	60.2	3	0	0	1277.69	186	196
DNA primase large subunit	PRIM2	PRI2_HUMAN	58.8	100.0%	2	2	5	0.00%	4.9%	ISPGGISQILDLVK	99.7%	80.8	25	78.1	2	0	0	1439.85	403	416
DNA primase small subunit	PRIM1	PRI1_HUMAN	49.9	100.0%	4	4	6	0.01%	11.0%	ALKEDFGFK	95.0%	27.1	25	20.2	1	0	0	1054.56	145	153
DNA primase small subunit	PRIM1	PRI1_HUMAN	49.9	100.0%	4	4	6	0.01%	11.0%	LGAFQAQEK	99.7%	48.6	25	31.7	2	0	0	991.52	96	104
DNA primase small subunit	PRIM1	PRI1_HUMAN	49.9	100.0%	4	4	6	0.01%	11.0%	SGIVEYLSLVK	99.7%	46.9	25	44.2	2	0	0	1207.69	183	193
DNA primase small subunit	PRIM1	PRI1_HUMAN	49.9	100.0%	4	4	6	0.01%	11.0%	VDQFDPFTVPTISFICR	99.7%	43.9	25	43.9	1	0	0	2042.01	339	355
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	22	23	37	0.04%	16.5%	DVNGELIAVQR	99.7%	65.4	25	50.4	2	0	0	1213.65	88	98
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	22	23	37	0.04%	16.5%	EQVSPLETTLEK	99.7%	51.5	25	46.6	2	0	0	1373.72	910	921

DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	22	23	37	0.04%	16.5%	FDEIFSATR	99.7%	48.3	25	45.9	1	0	0	1085.53	176	184
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	22	23	37	0.04%	16.5%	GQDIEYIEIR	99.7%	72.4	25	65.7	2	0	0	1235.63	1157	1166
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	22	23	37	0.04%	16.5%	ILELDQELIK	99.7%	58.1	25	20.4	2	0	0	1213.70	474	483
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	22	23	37	0.04%	16.5%	KEEQLSSYEDK	98.1%	30.9	25	21.3	1	0	0	1355.63	618	628
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	22	23	37	0.04%	16.5%	LEENIDNIKR	99.7%	59.5	25	40.1	2	1	0	1243.66	1060	1069
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	22	23	37	0.04%	16.5%	LIQDQQEQIQHLK	99.7%	48.3	25	37.4	1	0	0	1620.87	852	864
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	22	23	37	0.04%	16.5%	LQGIDLDR	99.7%	55.6	25	45.4	2	0	0	929.51	816	823
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	22	23	37	0.04%	16.5%	MEVISLQNEK	99.7%	45.9	25	20.4	2	0	0	1190.61	502	511
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	22	23	37	0.04%	16.5%	NIDQCSEIVK	99.7%	48.3	25	41	2	0	0	1205.58	1292	1301
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	22	23	37	0.04%	16.5%	QKFDEIFSATR	98.5%	32.1	25	24	1	0	0	1341.68	174	184
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	22	23	37	0.04%	16.5%	QSIIDLK	99.1%	34	25	10.4	1	0	0	816.48	737	743
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	22	23	37	0.04%	16.5%	SELLVEQGR	99.7%	62.9	25	46.7	2	0	0	1030.55	344	352
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	22	23	37	0.04%	16.5%	SYENELDPLK	99.3%	35.1	25	35.1	2	0	0	1207.58	243	252
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	22	23	37	0.04%	16.5%	TANQLMNDFAEKETLK	98.4%	23.9	25	23.9	0	1	0	1852.91	410	425
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	22	23	37	0.04%	16.5%	TLDQAIMK	99.2%	34.8	25	25.4	1	0	0	935.49	1127	1134
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	22	23	37	0.04%	16.5%	VCLTDVTIMER	99.7%	65.7	25	58.7	2	0	0	1336.66	787	797
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	22	23	37	0.04%	16.5%	VIAQLSECEK	99.7%	47.4	25	47.4	2	0	0	1176.59	983	992
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	22	23	37	0.04%	16.5%	VKEYQMELK	98.8%	32.9	25	17.2	1	0	0	1167.61	203	211
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	22	23	37	0.04%	16.5%	VLASLIIR	99.7%	66.8	25	48.8	2	0	0	884.59	1207	1214
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	22	23	37	0.04%	16.5%	YELQQLEGSSDR	99.7%	71.2	25	62.5	2	0	0	1424.67	462	473
DNA replication licensing factor MCM2	MCM2	MCM2_HUMAN	101.9	99.8%	2	2	3	0.00%	2.4%	AGIVTSLQAR	99.5%	37.2	25	29	1	0	0	1015.59	614	623
DNA replication licensing factor MCM2	MCM2	MCM2_HUMAN	101.9	99.8%	2	2	3	0.00%	2.4%	GLALALFGGEPK	99.7%	67.1	25	56.8	2	0	0	1172.67	494	505
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	24	51	0.05%	28.7%	AILCLLLGGVER	99.7%	72.7	25	58.8	8	0	0	1313.76	316	327
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	24	51	0.05%	28.7%	ALKDFVASIDATYAK	99.7%	78	25	72.1	2	0	0	1612.86	79	93
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	24	51	0.05%	28.7%	APAGQLPR	99.7%	55.9	25	37.1	2	0	0	809.46	208	215
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	24	51	0.05%	28.7%	DAQPSFSAEDIAK	99.7%	52.1	25	50	2	0	0	1378.65	271	283
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	24	51	0.05%	28.7%	DFVASIDATYAK	99.7%	58.1	25	54.5	1	0	0	1300.64	82	93
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	24	51	0.05%	28.7%	DSEEPFSSVEIQAALSK	99.7%	106	25	90.6	2	0	0	1836.89	775	791
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	24	51	0.05%	28.7%	EAHAQSIGMNR	99.7%	50.8	25	47.5	2	0	0	1213.57	757	767
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	24	51	0.05%	28.7%	ELISDNQYR	99.7%	60.3	25	49.7	2	0	0	1137.55	38	46
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	24	51	0.05%	28.7%	GDINILLIGDPSVAK	99.7%	82.6	25	82.6	2	0	0	1524.86	337	351
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	24	51	0.05%	28.7%	GGYTSGTFR	99.7%	53.4	25	46.7	2	0	0	945.44	249	257
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	24	51	0.05%	28.7%	GSSGVGLTAAVTTDQETGER	99.7%	101	25	101	2	0	0	1935.93	372	391
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	24	51	0.05%	28.7%	LIVNVNDLR	99.7%	67.7	25	54.3	2	0	0	1055.62	47	55
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	24	51	0.05%	28.7%	LLNNAFEELVAFQR	99.7%	71.6	25	69.9	2	0	0	1663.88	65	78
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	24	51	0.05%	28.7%	SVDVILDDDLVDK	99.7%	61.8	25	55.5	2	0	0	1445.74	216	228
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	24	51	0.05%	28.7%	SVHYCPATK	97.9%	30.6	25	18.8	2	0	0	1062.50	144	152
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	24	51	0.05%	28.7%	TAIHEVMEQGR	99.7%	46	25	46	3	1	0	1270.62	420	430
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	24	51	0.05%	28.7%	TLETLIR	99.4%	35.8	25	15.2	2	0	0	845.51	617	623
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	24	51	0.05%	28.7%	TPMENIGLQDSLLSR	99.7%	74.9	25	74.9	4	0	0	1689.85	464	478
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	24	51	0.05%	28.7%	TVLIACNVK	98.9%	33.3	25	13.7	2	0	0	1017.58	258	266
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	24	51	0.05%	28.7%	VALLDVFR	99.7%	52.1	25	41.7	2	0	0	932.56	749	756
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	21	24	51	0.05%	28.7%	YVLCTAPR	99.7%	47.7	25	35.2	2	0	0	979.50	357	364
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	13	14	28	0.03%	19.4%	AEINILLCGDPGTSK	99.7%	59.5	25	59.5	2	0	0	1587.81	502	516
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	13	14	28	0.03%	19.4%	ALADDDFLTVTGK	99.7%	97.2	25	93.8	2	0	0	1365.69	846	858
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	13	14	28	0.03%	19.4%	GILLQLFGGTR	99.7%	79.3	25	79.3	5	0	0	1174.69	479	489
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	13	14	28	0.03%	19.4%	GMVSAYPR	99.1%	34	25	20.9	2	0	0	880.43	725	732
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	13	14	28	0.03%	19.4%	IAEPSVCGR	99.7%	46.7	25	32.9	2	0	0	988.49	322	330
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	13	14	28	0.03%	19.4%	LASALAPSIYEHEDIKK	99.6%	28.8	25	28.5	0	1	0	1885.01	462	478
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	13	14	28	0.03%	19.4%	LHGLDEEAEQK	99.4%	35.7	25	29.6	2	0	0	1268.61	429	439
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	13	14	28	0.03%	19.4%	LVIWGTDVNVAACK	99.7%	83.2	25	81.6	2	0	0	1545.81	150	163

DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	13	14	28	0.03%	19.4%	QRPDLGSAQK	99.7%	41.5	25	33.3	2	0	0	1099.59	114	123
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	13	14	28	0.03%	19.4%	TGIVDISILTTGMSATSR	99.7%	67.5	25	67.5	3	0	0	1822.96	778	795
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	13	14	28	0.03%	19.4%	TSVLAAANPIESQWNPK	97.6%	30	25	30	1	0	0	1825.94	611	627
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	13	14	28	0.03%	19.4%	TTIENIQLPHTLLSR	99.7%	71.7	25	59.7	2	0	0	1735.97	629	643
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	13	14	28	0.03%	19.4%	YQQLFEDIR	99.7%	58.1	25	36	2	0	0	1211.61	820	828
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	28	0.03%	21.0%	AGITTTLNSR	99.7%	75.8	25	55.9	2	0	0	1033.56	472	481
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	28	0.03%	21.0%	AIACLLFGGSR	99.7%	84.3	25	84.3	3	0	0	1164.62	352	362
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	28	0.03%	21.0%	CSVLAAANSVFGR	99.7%	63	25	63	2	0	0	1351.68	482	494
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	28	0.03%	21.0%	FAIGSQVSEHSIIK	99.7%	62.4	25	54.6	2	0	0	1515.82	683	696
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	28	0.03%	21.0%	GEDNIDFMPTILSR	99.7%	43.3	25	41.6	1	0	0	1607.77	500	513
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	28	0.03%	21.0%	HMQLYCDR	99.0%	33.7	25	26.1	2	0	0	1122.48	244	251
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	28	0.03%	21.0%	IPGIIIAASAVR	99.7%	99.4	25	99.4	2	0	0	1180.74	151	162
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	28	0.03%	21.0%	LAALPNVYEVISK	99.7%	63.2	25	63.2	2	0	0	1416.81	325	337
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	28	0.03%	21.0%	LQPFATEADVEEALR	99.7%	99.2	25	97.5	2	0	0	1688.85	628	642
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	28	0.03%	21.0%	SIAPSIFGGTDMK	99.7%	40.4	25	40.4	1	0	0	1323.66	338	350
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	28	0.03%	21.0%	SIAPSIFGGTDMKK	99.7%	38.6	25	34	3	0	0	1451.76	338	351
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	28	0.03%	21.0%	VLGIQVDTDGSGR	99.7%	89.9	25	89.9	2	0	0	1316.68	296	308
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	28	0.03%	21.0%	VLQLMLR	99.7%	42	25	7.21	2	0	0	872.54	711	717
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	14	15	28	0.03%	21.0%	VTIMGIYSIK	99.7%	60.1	25	42.2	2	0	0	1124.64	263	272
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	14	14	24	0.02%	20.3%	DFYVAFQDLPTR	99.7%	81.9	25	73.6	2	0	0	1471.72	109	120
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	14	14	24	0.02%	20.3%	EIESEIDSEEELINK	99.7%	92.1	25	77.3	1	0	0	1776.84	755	769
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	14	14	24	0.02%	20.3%	ELRDEEQTAESIK	99.7%	61.1	25	53	2	0	0	1547.75	314	326
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	14	14	24	0.02%	20.3%	GDINVCIVGDPSTAK	99.7%	41.5	25	29.8	2	0	0	1545.76	388	402
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	14	14	24	0.02%	20.3%	GVLLMLFGGVPK	99.7%	54.9	25	41.8	2	0	0	1230.73	367	378
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	14	14	24	0.02%	20.3%	HVEEFSPR	99.6%	37.4	25	37.4	1	0	0	1000.48	408	415
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	14	14	24	0.02%	20.3%	IQETQAELPR	99.7%	74.9	25	57.4	2	0	0	1184.63	208	217
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	14	14	24	0.02%	20.3%	LGFSEYCR	99.7%	49.3	25	49.3	2	0	0	1031.46	715	722
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	14	14	24	0.02%	20.3%	LVFLACCVAPTNPR	99.7%	84.2	25	83.2	2	0	0	1617.82	296	309
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	14	14	24	0.02%	20.3%	MHCCDEVQPK	99.7%	41.2	25	41.2	1	0	0	1303.52	634	643
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	14	14	24	0.02%	20.3%	TSILAAANPISGHYDR	99.7%	75.7	25	67.6	2	0	0	1685.86	497	512
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	14	14	24	0.02%	20.3%	VSGVDGYETEGIR	99.7%	79.9	25	73	2	0	0	1381.66	270	282
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	14	14	24	0.02%	20.3%	YLQLAEELIRPER	98.2%	31.3	25	31.3	1	0	0	1629.90	46	58
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	14	14	24	0.02%	20.3%	YTQPNICR	99.6%	38	25	29.9	2	0	0	1051.50	174	181
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	15	17	46	0.05%	25.2%	AGILTTLNAR	99.7%	61	25	48.1	4	0	0	1029.61	472	481
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	15	17	46	0.05%	25.2%	ALLLLLVGGVDQSPR	99.7%	85.4	25	85.4	5	0	0	1550.93	353	367
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	15	17	46	0.05%	25.2%	CSILAAANPAYGR	99.7%	53.3	25	52.3	1	0	0	1363.68	482	494
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	15	17	46	0.05%	25.2%	DSLLGDKGQTAR	99.7%	43.7	25	35.4	2	0	0	1260.65	642	653
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	15	17	46	0.05%	25.2%	GSSGVGLTAAVLR	99.7%	84.6	25	64.6	3	0	0	1187.67	408	420
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	15	17	46	0.05%	25.2%	IAQPGDHVSVTGIFLPILR	97.6%	22.7	25	22.7	0	1	0	2033.15	264	282
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	15	17	46	0.05%	25.2%	LFADAVQELLPQYK	99.7%	57	25	37.1	4	0	0	1634.88	76	89
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	15	17	46	0.05%	25.2%	QIAEEDFYEK	99.7%	39.4	25	37.2	2	0	0	1271.58	326	335
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	15	17	46	0.05%	25.2%	SITVLVEGENTR	99.7%	82.2	25	65	3	0	0	1317.70	252	263
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	15	17	46	0.05%	25.2%	SLEQNIQLPAALLSR	99.7%	87.1	25	87.1	4	0	0	1652.93	500	514
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	15	17	46	0.05%	25.2%	SPQNQYPAELMR	99.7%	48.8	25	48.8	4	0	0	1433.68	121	132
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	15	17	46	0.05%	25.2%	SQLLSYIDR	99.7%	66.5	25	35.9	4	0	0	1094.58	388	396
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	15	17	46	0.05%	25.2%	TLLAILR	98.9%	33.3	25	3.81	1	0	0	799.54	605	611
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	15	17	46	0.05%	25.2%	TQRPADVIFATVR	99.7%	46.7	25	44.8	2	2	0	1473.82	654	666
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	15	17	46	0.05%	25.2%	YGNQLVR	99.7%	43.6	25	31.5	4	0	0	849.46	33	39
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	12	31	0.03%	15.2%	AEEVATFFAK	99.7%	53.8	25	47.4	2	0	0	1112.56	253	262
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	12	31	0.03%	15.2%	AVAILCNHQR	99.7%	52.3	25	38	2	0	0	1181.62	625	634
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	12	31	0.03%	15.2%	ELTAPDENIPAK	99.7%	42.8	25	42.8	4	0	0	1297.66	604	615

DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	12	31	0.03%	15.2%	GPVFAPPYEPLPENVK	99.7%	63.4	25	60.9	4	0	0	1753.92	224	239
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	12	31	0.03%	15.2%	IEPPGLFR	94.7%	26.9	25	21.4	1	0	0	928.53	355	362
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	12	31	0.03%	15.2%	LEVQATDREENK	99.7%	59.9	25	55.2	4	0	0	1431.71	701	712
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	12	31	0.03%	15.2%	LNTGILNK	99.7%	40.1	25	22.8	4	0	0	872.52	568	575
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	12	31	0.03%	15.2%	MLDHEYTTK	99.7%	46.9	25	40.8	3	0	0	1137.52	263	271
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	12	31	0.03%	15.2%	TYNASITLQQQLK	99.7%	83	25	69.3	3	0	0	1507.81	591	603
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	12	31	0.03%	15.2%	VPSPPPGHK	98.8%	32.8	25	28.4	2	0	0	915.50	392	400
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	11	12	31	0.03%	15.2%	YIMLNPSSR	99.1%	34.2	25	27.3	2	0	0	1080.55	426	434
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	13	13	25	0.02%	9.7%	DKYGVFPLR	97.8%	30.4	25	27.5	1	0	0	1094.60	479	487
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	13	13	25	0.02%	9.7%	ELILFSNSDNER	99.7%	64.2	25	50.8	2	0	0	1436.70	702	713
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	13	13	25	0.02%	9.7%	EWLLGMLGAESAK	99.7%	39.8	25	39.8	1	0	0	1404.72	1035	1047
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	13	13	25	0.02%	9.7%	FLEEFITPIVK	99.7%	50.7	25	47.1	2	0	0	1335.76	569	579
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	13	13	25	0.02%	9.7%	FTVETASR	99.5%	36.9	25	29.5	1	0	0	910.46	177	184
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	13	13	25	0.02%	9.7%	GFQQISFVNSIATSK	99.7%	92.3	25	90.3	2	0	0	1626.85	307	321
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	13	13	25	0.02%	9.7%	HVDYVADQIVTK	99.7%	71.5	25	71.5	2	0	0	1387.72	325	336
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	13	13	25	0.02%	9.7%	IFDEILVNAADNK	99.7%	94.1	25	93.1	4	0	0	1461.76	84	96
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	13	13	25	0.02%	9.7%	LCNIFSTK	99.3%	35.1	25	25.7	3	0	0	982.50	169	176
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	13	13	25	0.02%	9.7%	QIMENAEINNIIK	99.7%	91	25	82.1	2	0	0	1529.80	500	512
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	13	13	25	0.02%	9.7%	SFGSTCQLSEK	99.7%	57.9	25	52.3	1	0	0	1243.56	387	397
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	13	13	25	0.02%	9.7%	TLAVSGLGVVGR	99.7%	85.4	25	74.6	3	0	0	1128.67	467	478
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	13	13	25	0.02%	9.7%	YIFTMLSSLAR	99.3%	35.2	25	30.4	1	0	0	1301.69	805	815
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	7	7	15	0.01%	8.2%	DLIQMLVQR	99.7%	53.7	25	42.4	3	0	0	1115.62	1093	1101
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	7	7	15	0.01%	8.2%	ELILFSNSDNER	99.7%	64.2	25	50.8	2	0	0	1436.70	723	734
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	7	7	15	0.01%	8.2%	EWLVGMLGAESTK	96.0%	28	25	27.9	1	0	0	1420.71	1056	1068
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	7	7	15	0.01%	8.2%	GFQQISFVNSIATTK	99.7%	62.8	25	50.2	1	0	0	1640.86	328	342
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	7	7	15	0.01%	8.2%	IFDEILVNAADNK	99.7%	94.1	25	93.1	4	0	0	1461.76	105	117
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	7	7	15	0.01%	8.2%	LAQAEAAGLHK	99.7%	45.6	25	31.5	2	0	0	1108.61	998	1008
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	7	7	15	0.01%	8.2%	LCNIFSTK	99.3%	35.1	25	25.7	3	0	0	982.50	190	197
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	7	7	15	0.01%	8.2%	LLFPAVDDNLLK	99.7%	47.4	25	38.9	4	0	0	1357.77	837	848
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	7	7	15	0.01%	8.2%	NTVEITELPVR	99.7%	52.2	25	45.7	3	0	0	1270.70	940	950
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	7	7	15	0.01%	8.2%	QIMENAEINNIIK	99.7%	91	25	82.1	2	0	0	1529.80	521	533
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	7	7	15	0.01%	8.2%	VSIDPESNIISIWNNGK	99.7%	38.8	25	38.8	1	0	0	1885.97	128	144
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	AALSALESFLK	99.7%	80	25	63.4	9	0	0	1149.65	311	321
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	AAYLSDPR	96.4%	28.4	25	15.2	2	0	0	892.45	3826	3833
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	AIRPQIDLKR	99.7%	40.6	25	24.4	2	1	0	1209.74	255	264
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	APPCEYKDWLTK	99.7%	58.2	25	58.2	2	0	0	1507.73	3834	3845
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	AQEPESGLSEETQVK	99.7%	83.4	25	71.4	2	0	0	1631.78	4091	4105
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	ATQMPEGGQGAPPMYQLYK	99.7%	57.1	25	51.7	2	0	0	2082.96	945	963
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	ATQQQHDFTLTQTADGR	99.7%	90.3	25	83.6	2	2	0	1917.91	2637	2653
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	AYVPALQMAFK	99.7%	39	25	20.5	3	0	0	1254.66	747	757
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	CFFLSK	97.4%	29.8	25	23.5	2	0	0	801.40	3187	3192
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	CFGTGAAGNR	99.7%	59.2	25	51.7	2	0	0	1010.45	1312	1321
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	CGAALAGHQLIR	99.7%	72	25	67	2	0	0	1266.67	25	36
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	DCLSIPYR	97.7%	30.3	25	21.1	1	0	0	1023.49	2247	2254
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	DFGLLVFVR	99.7%	66.3	25	54.6	4	0	0	1065.61	62	70
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	DFSAFINLVEFCR	99.7%	43.4	25	37.4	1	0	0	1617.77	619	631
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	DILETHLR	99.7%	43.5	25	28.6	2	0	0	996.55	1413	1420
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	DILPCLDGYLK	97.4%	29.8	25	15.2	2	0	0	1306.67	791	801
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	DLCNTHLMR	99.5%	36.9	25	35.2	1	0	0	1175.53	1362	1370
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	DLLLNTMSQEEK	99.5%	36.5	25	33.3	1	0	0	1436.69	3814	3825
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	DQNILLGTTYR	99.7%	97.8	25	90.7	4	0	0	1293.68	3325	3335

DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	DVDFMYVELIQR	99.7%	85.2	25	75.1	5	0	0	1543.75	380	391
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	EIFNFVLK	99.0%	33.5	25	15.9	2	0	0	1009.57	247	254
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	ELLNPVVEFVSHPSTTCR	99.7%	93.4	25	86.1	2	2	0	2085.04	2453	2470
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	ELSIAIR	95.7%	27.7	25	17	1	0	0	801.48	358	364
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	ETGLMYSIMVHALR	99.1%	34.1	25	34.1	2	0	0	1620.82	3976	3989
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	FMNAVFFLLPK	99.7%	86.6	25	71.8	4	0	0	1326.73	2378	2388
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	FVPLLPGNR	99.6%	37.4	25	35.4	2	0	0	1012.59	1194	1202
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	FYGELALK	98.6%	32.1	25	28.1	1	0	0	940.51	156	163
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	FYGELALKK	96.0%	28	25	23.1	1	0	0	1068.61	156	164
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	FYQGFLFSEKPEK	99.7%	46.8	25	46.5	2	0	0	1619.81	1961	1973
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	GGSWIQEINVAEK	99.7%	62.8	25	54.2	2	0	0	1430.73	4024	4036
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	GIAPGDER	97.7%	30.1	25	19	2	0	0	814.41	1490	1497
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	GIFTSEIGTK	99.7%	60	25	52.8	3	0	0	1052.56	2941	2950
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	GLSSLLCNFTK	99.7%	55.1	25	43.4	2	0	0	1239.64	226	236
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	GPESESEDHRASGEVR	94.6%	20.3	25	20.3	0	1	0	1741.77	500	515
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	GYGLFAGPCK	99.7%	39.2	25	30.7	2	0	0	1069.51	365	374
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	HGDLPDIQIK	99.7%	54.3	25	43	2	0	0	1135.61	2777	2786
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	HNLEIIK	99.7%	40.2	25	13.6	2	0	0	866.51	2233	2239
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	HSSLITPLQAVAQR	99.7%	59.9	25	55.1	2	2	0	1520.85	2787	2800
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	IAPYSVEIK	99.7%	41.8	25	31.5	2	0	0	1019.58	100	108
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	ICSKPVVLPK	99.7%	38.9	25	25.4	2	0	0	1140.68	490	499
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	IKYFEGVSPK	98.8%	32.9	25	19.9	2	0	0	1167.64	680	689
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	ILDVMYSR	99.7%	58.5	25	50.2	4	0	0	1012.51	1876	1883
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	ILELSGSSSEDSEK	99.7%	90.1	25	86.6	2	0	0	1480.70	3359	3372
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	ILELSGSSSEDSEKVIAGLYQR	99.7%	37.3	25	37.3	0	1	0	2381.22	3359	3380
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	IMEFTTTLLNTSPEGWK	99.7%	95.4	25	84.9	4	0	0	1983.97	1341	1357
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	INQVFHGSCITEGNELTK	99.7%	70	25	70	0	2	0	2046.99	1896	1913
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	IPALDLLIK	98.1%	31	25	26	2	0	0	995.65	125	133
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	KNILEESLCELVAK	99.7%	69.6	25	64.4	2	0	0	1645.88	2334	2347
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	KQNNFSLAMK	99.7%	67.4	25	59.3	4	0	0	1180.61	3248	3257
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LAAVVSACK	99.7%	56.3	25	45.3	2	0	0	918.51	1448	1456
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LACDVDQVTR	99.7%	77.7	25	59.3	2	0	0	1176.57	972	981
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LAGANPAVITCDELLLGHEK	99.7%	38	25	36.7	0	2	0	2121.10	4051	4070
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LATTILQHWK	99.7%	55.7	25	55.6	2	0	0	1210.69	1618	1627
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LCYDAFTENMAGENQLLER	99.7%	86.6	25	82.2	1	0	0	2274.02	1918	1936
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LGASLAFNNIYR	99.7%	70	25	32.4	3	0	0	1338.72	1076	1087
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LGLIEWLENTVTLK	99.7%	47.6	25	47.6	1	0	0	1628.93	3800	3813
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LGLPGDEVDNK	97.5%	29.9	25	28	1	0	0	1156.58	2705	2715
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LGLPGDEVDNKVK	99.7%	48.3	25	45.9	2	0	0	1383.75	2705	2717
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LGNPIVPLNIR	99.7%	39.7	25	39.7	2	0	0	1205.74	2133	2143
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LLEEALLR	99.7%	66.4	25	58.9	4	0	0	956.58	2892	2899
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LLLQGEADQSLLTFIDK	99.7%	103	25	103	4	0	0	1904.04	3051	3067
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LLNFLMK	98.6%	32.2	25	25.6	2	0	0	894.51	2215	2221
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LLNTWTNR	99.7%	40.1	25	38.2	3	0	0	1017.55	3160	3167
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LLNTWTNRYPDAK	99.0%	33.8	25	33.7	2	1	0	1591.82	3160	3172
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LLPAELPAKR	99.7%	40.2	25	40.2	2	0	0	1107.69	2900	2909
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LLQDFNR	99.0%	33.6	25	15.8	1	0	0	905.48	2836	2842
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LLQIIER	99.7%	48.1	25	32.7	3	0	0	884.56	3468	3474
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LLQIIERYPEETLSLMTK	99.7%	43.2	25	38.4	0	1	0	2193.18	3468	3485
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LLSITVR	99.2%	34.7	25	14.3	1	0	0	801.52	669	675
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LMDEFKIGELFSK	98.4%	31.7	25	31.7	1	0	0	1556.80	143	155

DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LNESTFDTQITK	99.7%	86.2	25	74.9	2	0	0	1396.70	1858	1869
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LNESTFDTQITKK	99.7%	75.6	25	69.7	2	0	0	1524.79	1858	1870
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LPKDDVHAK	99.7%	49.9	25	37.3	2	0	0	1022.56	1884	1892
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LPPDVLR	95.3%	27.4	25	27.4	1	0	0	809.49	2916	2922
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LPSNTLDR	99.7%	43.8	25	34.7	2	0	0	915.49	2531	2538
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LPVLAGCLK	99.7%	52.4	25	47.3	2	0	0	970.58	217	225
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LQETLSAADR	99.7%	82.7	25	62.2	3	0	0	1103.57	15	24
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LSDFNDITNMLLLK	99.7%	87.9	25	87.9	3	0	0	1636.86	3656	3669
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LSFAVPFR	99.7%	47.6	25	41.1	4	0	0	936.53	892	899
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LSLMYAR	99.7%	49.2	25	29	3	0	0	869.46	2739	2745
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LVINTEEVFRPYAK	99.7%	55.7	25	52.3	2	0	0	1678.92	2149	2162
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	LYSLALHPNAFK	96.8%	21.8	25	19.7	0	1	0	1373.76	1063	1074
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	MAVLALLAK	99.7%	58.9	25	48.7	4	0	0	929.59	1643	1651
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	MDPMNIWDDIITNR	99.7%	66.2	25	11.9	4	0	0	1749.79	3173	3186
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	MKQDAQVVLYR	99.7%	81.7	25	67.8	2	0	0	1350.72	2763	2773
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	MQLVCCR	98.7%	32.4	25	20.7	1	0	0	966.43	453	459
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	MSPYKDILETHLR	99.7%	40.5	25	40.5	0	2	0	1618.83	1408	1420
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	MSTSPEAFLALR	99.7%	77.8	25	64.1	10	0	0	1322.68	3890	3901
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	MYAALGDPK	99.6%	38.4	25	38.4	4	0	0	965.48	3613	3621
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	NCISTVVHQGLIR	99.7%	74.8	25	65.5	2	0	0	1496.80	477	489
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	NFWSHETR	98.9%	33.2	25	26.8	1	0	0	1076.49	2523	2530
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	NILEESLCELVAK	99.7%	82.7	25	82.7	2	0	0	1517.79	2335	2347
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	NLDLAVLELMQSSVDNTK	99.7%	116	25	116	3	0	0	2006.01	1574	1591
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	NLLIFENLIDLK	99.7%	97.2	25	81.3	3	0	0	1444.84	1974	1985
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	NLLIFENLIDLKR	99.7%	52.9	25	46.2	1	0	0	1600.94	1974	1986
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	NLLTVTSSDEMMK	99.7%	112	25	108	6	0	0	1500.69	869	881
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	NLSSNEAISLEEIR	99.7%	106	25	81.6	2	0	0	1574.80	839	852
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	NNWEVSALSR	99.7%	68.6	25	61.4	2	0	0	1175.58	811	820
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	NVDSNNKELSIAIR	99.7%	83.5	25	79.7	2	1	0	1572.83	351	364
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	QCLPSLDLSCK	99.7%	63.3	25	49.4	2	0	0	1320.63	1498	1508
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	QDAQVVLYR	99.7%	50.9	25	35.9	2	0	0	1091.58	2765	2773
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	QFINLMLPMK	99.7%	43.4	25	32	1	0	0	1266.66	3966	3975
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	QGNLSSQVPLKR	99.7%	44.4	25	41.5	2	1	0	1326.75	3148	3159
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	QITQSALLAEAR	99.7%	67.2	25	53.3	3	0	0	1300.72	2951	2962
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	QLFSSLFSGILK	99.7%	90.6	25	79.6	3	0	0	1339.76	2807	2818
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	QMFLTQTDTGDDR	99.7%	74.4	25	74.4	2	0	0	1527.67	394	406
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	RLSFAVPFR	99.6%	38.2	25	38.1	2	0	0	1092.63	891	899
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	RTFPVLLR	96.4%	28.4	25	5.2	1	0	0	1001.63	964	971
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	SDPGLLTNTMDVFVK	99.7%	88.5	25	84.2	5	0	0	1636.83	3993	4007
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	SIGEYDVLR	99.7%	48.5	25	44	2	0	0	1051.54	2932	2940
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	SKDFVQVMR	99.7%	54.6	25	40.8	2	0	0	1109.58	2417	2425
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	SLEYCSTASIDSENPPDLNK	99.7%	64.3	25	64.3	2	0	0	2240.00	3010	3029
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	SLGPPQGEEDSVPR	99.7%	79	25	77.6	2	0	0	1467.71	2107	2120
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	SLGTIQQCCDAIDHLCR	99.7%	46.6	25	46.6	0	2	0	2046.92	1120	1136
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	SLNSIEFR	99.5%	36.4	25	26.8	1	0	0	965.51	72	79
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	SMEEDPQTSR	99.6%	37.7	25	33.4	2	0	0	1179.49	237	246
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	SPNLWLK	99.7%	38.6	25	25.8	2	0	0	857.49	1203	1209
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	SQGCSEQVLTVLK	99.7%	82.5	25	73.6	5	0	0	1448.74	3290	3302
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	STVLTPMFVETQASQGTLQTR	99.7%	107	25	107	2	2	0	2295.17	2599	2619
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	SYVAWDREK	99.7%	38.9	25	38.9	1	0	0	1153.56	882	890
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	TETVTSFR	99.6%	38.2	25	27.4	3	0	0	940.47	3865	3872

DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	TFPVLLR	99.0%	33.8	25	25.3	1	0	0	845.52	965	971
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	TQMTSAVREPK	99.7%	50.8	25	44.2	1	0	0	1263.64	206	216
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	TSALSDETKNNWEVSALSR	99.7%	88.5	25	88.5	2	2	0	2108.03	802	820
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	TSPQEGERYNYSK	98.9%	33.4	25	29	1	0	0	1558.71	1322	1334
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	TVGALQVLGTEAQSSLLK	99.7%	116	25	111	4	0	0	1815.02	1275	1292
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	TVSLLDENNVSSYLSK	99.7%	107	25	103	5	0	0	1768.90	3303	3318
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	TYSVVPMTSR	99.3%	35	25	23.4	2	0	0	1140.57	3790	3799
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	VCLDIIYK	99.7%	39.2	25	19.6	2	0	0	1023.55	2434	2441
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	VEGMTELYFQLK	99.7%	80.3	25	75	1	0	0	1457.73	2405	2416
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	VFLALAAK	99.5%	37.1	25	23.4	2	0	0	832.53	464	471
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	VLEQLIVAHFPMQSR	99.7%	40	25	39.3	2	1	0	1767.96	1713	1727
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	VPADLLKR	99.6%	37.7	25	26.5	2	0	0	911.57	3878	3885
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	VPTYKDYVDLFR	95.1%	20.6	25	20.6	0	1	0	1515.78	521	532
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	VTELALTASDR	99.7%	111	25	97.2	4	0	0	1175.63	914	924
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	VTVMASLR	99.7%	51.5	25	31.1	2	0	0	876.50	3726	3733
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	VVQMLGSLGGQINK	99.7%	92.7	25	71.3	4	0	0	1459.79	855	868
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	YAVPSAGLR	98.3%	31.4	25	26.2	2	0	0	933.52	265	273
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	YNFPVEVEVPMER	99.7%	60.4	25	57.6	4	0	0	1608.77	1988	2000
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	140	165	341	0.34%	35.5%	YPEETLSLMTK	99.7%	67.8	25	63	2	0	0	1311.65	3475	3485
DNA-directed RNA polymerase II subunit RPB1	POLR2A	RPB1_HUMAN	217.2	99.8%	2	2	3	0.00%	1.2%	NSINQVVQLR	99.7%	49.6	25	38.3	1	0	0	1170.66	881	890
DNA-directed RNA polymerase II subunit RPB1	POLR2A	RPB1_HUMAN	217.2	99.8%	2	2	3	0.00%	1.2%	TPSLTVFLLGQSAR	99.7%	75.6	25	70.8	2	0	0	1489.84	1136	1149
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	6	6	9	0.01%	6.1%	EGEEQLQTQHQK	99.3%	35.1	25	33.2	1	0	0	1454.69	135	146
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	6	6	9	0.01%	6.1%	GEIGDATPFNDAVNVQK	99.7%	63.2	25	61	1	0	0	1774.86	994	1010
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	6	6	9	0.01%	6.1%	GPIQILNR	99.7%	56.6	25	46.9	2	0	0	910.55	1065	1072
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	6	6	9	0.01%	6.1%	NLTYSAPLYVDITK	99.7%	45.3	25	37.2	2	0	0	1597.85	117	130
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	6	6	9	0.01%	6.1%	QEVPIIIVFR	99.7%	64.2	25	54.7	2	0	0	1213.73	265	274
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	6	6	9	0.01%	6.1%	VSGDDVIIGK	99.7%	40.5	25	31.4	1	0	0	1002.55	860	869
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	7	7	8	0.01%	5.2%	GFSIGIGDVTPGQGLLK	97.0%	29.2	25	29.2	1	0	0	1658.91	695	711
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	7	7	8	0.01%	5.2%	IDEVAVPVHVAK	99.7%	64.2	25	49.5	1	0	0	1276.73	377	388
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	7	7	8	0.01%	5.2%	LAPVYLSNR	99.2%	34.6	25	30.6	1	0	0	1032.58	686	694
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	7	7	8	0.01%	5.2%	LEVNAETVR	99.7%	55.2	25	43.9	1	0	0	1030.55	1142	1150
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	7	7	8	0.01%	5.2%	LLVEGDNLR	98.9%	33.2	25	28.6	1	0	0	1028.57	1225	1233
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	7	7	8	0.01%	5.2%	NNIFYILLR	99.7%	48.5	25	28.9	2	0	0	1165.67	661	669
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	7	7	8	0.01%	5.2%	YGDIVER	96.6%	28.6	25	21.4	1	0	0	851.43	446	452
DNA-directed RNA polymerase III subunit RPC2	POLR3B	RPC2_HUMAN	127.8	100.0%	3	3	3	0.00%	3.4%	GAVGASVTSSTHEK	99.7%	61.6	25	61.6	1	0	0	1330.66	197	210
DNA-directed RNA polymerase III subunit RPC2	POLR3B	RPC2_HUMAN	127.8	100.0%	3	3	3	0.00%	3.4%	LNECPLDPGGYFIVK	99.7%	49.8	25	49.5	1	0	0	1721.86	158	172
DNA-directed RNA polymerase III subunit RPC2	POLR3B	RPC2_HUMAN	127.8	100.0%	3	3	3	0.00%	3.4%	VILIQEQLSK	99.7%	45.9	25	32.5	1	0	0	1170.71	177	186
DNA-directed RNA polymerase III subunit RPC3	POLR3C	RPC3_HUMAN	60.6	100.0%	3	3	3	0.00%	6.4%	ALASLATATLESVVQER	96.4%	28.4	25	28.4	1	0	0	1758.96	341	357
DNA-directed RNA polymerase III subunit RPC3	POLR3C	RPC3_HUMAN	60.6	100.0%	3	3	3	0.00%	6.4%	LADTHFVQR	97.1%	29.2	25	10.3	1	0	0	1086.57	151	159
DNA-directed RNA polymerase III subunit RPC3	POLR3C	RPC3_HUMAN	60.6	100.0%	3	3	3	0.00%	6.4%	SIANLIER	98.8%	32.9	25	22.1	1	0	0	915.53	442	449
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	9	9	14	0.01%	8.5%	ILEASQLK	98.5%	31.9	25	10.8	1	0	0	901.54	1198	1205
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	9	9	14	0.01%	8.5%	LLQEAPGK	98.4%	31.7	25	18.6	1	0	0	855.49	194	201
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	9	9	14	0.01%	8.5%	LSLAQHLR	99.7%	57.3	25	49	2	0	0	937.56	783	790
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	9	9	14	0.01%	8.5%	LSLDVEQAPSGQHSQAQLSGQQQR	99.7%	66.4	25	66.4	0	2	0	2592.28	202	225
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	9	9	14	0.01%	8.5%	QDQDAGTIER	99.7%	51.7	25	49.7	1	0	0	1132.52	309	318
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	9	9	14	0.01%	8.5%	QLQAESVSEVVVNR	99.7%	83.4	25	79.2	2	0	0	1557.82	72	85
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	9	9	14	0.01%	8.5%	SLQEMFSGTR	99.7%	56.8	25	41.9	1	0	0	1155.55	1039	1048
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	9	9	14	0.01%	8.5%	VAQVLEGFITR	99.7%	63.5	25	59.9	2	0	0	1232.70	977	987
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	9	9	14	0.01%	8.5%	VLDLVLQLFQAK	99.7%	81.8	25	65.2	2	0	0	1386.84	713	724
DNA-directed RNA polymerases I and III subunit RPAC1	POLR1C	RPAC1_HUMAN	39.2	100.0%	3	4	6	0.01%	10.4%	DSSDPNELYVNHK	99.1%	34.1	25	34.1	1	0	0	1517.69	155	167
DNA-directed RNA polymerases I and III subunit RPAC1	POLR1C	RPAC1_HUMAN	39.2	100.0%	3	4	6	0.01%	10.4%	FSPVATASYR	99.7%	70.9	25	57.3	2	0	0	1098.56	225	234

DNA-directed RNA polymerases I and III subunit RPAC1	POLR1C	RPAC1_HUMAN	39.2	100.0%	3	4	6	0.01%	10.4%	ILLAEVPTMAVEK	99.7%	76.2	25	76.2	3	0	0	1413.80	79	91
DNA-directed RNA polymerases I, II, and III subunit RPABC1	POLR2E	RPAB1_HUMAN	24.6	99.8%	2	2	2	0.00%	11.4%	ALIVVQQGMTPSAK	99.7%	60.7	25	57.2	1	0	0	1442.80	102	115
DNA-directed RNA polymerases I, II, and III subunit RPABC1	POLR2E	RPAB1_HUMAN	24.6	99.8%	2	2	2	0.00%	11.4%	IIRPSETAGR	99.7%	44	25	31.4	1	0	0	1099.62	193	202
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	4	5	10	0.01%	26.7%	ADQFEYVMYGK	99.7%	69.5	25	69.5	2	0	0	1350.60	85	95
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	4	5	10	0.01%	26.7%	IEGDETSTEAATR	99.7%	92.2	25	91.9	2	0	0	1379.63	99	111
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	4	5	10	0.01%	26.7%	LSAYVSYGGLLMR	99.7%	82.6	25	67.6	4	0	0	1445.75	112	124
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	4	5	10	0.01%	26.7%	VYRIEGDETSTEAATR	99.7%	53.4	25	53.4	2	0	0	1797.86	96	111
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	4	4	8	0.01%	10.8%	ELYDKGGEQAIK	99.7%	42.1	25	23.2	2	0	0	1350.69	62	73
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	4	4	8	0.01%	10.8%	ILEVHIDK	99.1%	34.2	25	12.4	2	0	0	966.56	207	214
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	4	4	8	0.01%	10.8%	NVICDKCEGR	99.6%	37.7	25	36.2	2	0	0	1250.56	131	140
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	4	4	8	0.01%	10.8%	TIVITSHPGQIVK	99.7%	60.9	25	60.9	2	0	0	1392.82	284	296
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	10	10	17	0.02%	24.0%	DGNDLHMTYK	99.7%	51.5	25	51.5	2	0	0	1193.53	263	272
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	10	10	17	0.02%	24.0%	EISFAYEVLSNPEK	99.7%	66.1	25	64.9	1	0	0	1625.81	49	62
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	10	10	17	0.02%	24.0%	EISFAYEVLSNPEKR	99.7%	68.8	25	67.2	2	0	0	1781.91	49	63
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	10	10	17	0.02%	24.0%	GEGMPQYR	96.1%	28.1	25	12.2	1	0	0	937.42	314	321
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	10	10	17	0.02%	24.0%	IGLVEALCGFQFTFK	99.7%	93.1	25	87.3	2	0	0	1729.90	273	287
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	10	10	17	0.02%	24.0%	ILEVHVDK	99.7%	47.2	25	25.4	2	0	0	952.55	216	223
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	10	10	17	0.02%	24.0%	LYDILGVPPGASENELKK	99.6%	28.3	25	27.5	0	2	0	1943.05	9	26
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	10	10	17	0.02%	24.0%	VIEPGCVR	99.1%	34.3	25	34.3	1	0	0	929.49	303	310
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	10	10	17	0.02%	24.0%	VSLEDLYNGK	99.7%	66.7	25	56.2	2	0	0	1137.58	122	131
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	10	10	17	0.02%	24.0%	YGEQGLR	99.7%	52.8	25	33	2	0	0	822.41	69	75
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	5	6	14	0.01%	14.2%	EAGEDEEGFLSK	99.7%	44.2	25	44.2	1	0	0	1310.57	462	473
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	5	6	14	0.01%	14.2%	FSQLAEAYEVLSDEVK	99.3%	35.1	25	35.1	2	0	0	1827.90	135	150
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	5	6	14	0.01%	14.2%	GGPTVDPEELFR	99.7%	61	25	58.7	3	0	0	1316.65	176	187
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	5	6	14	0.01%	14.2%	GSIIISPCVVCR	99.7%	56.8	25	31.7	3	0	0	1360.71	282	293
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	5	6	14	0.01%	14.2%	VMIPVPAGVEDGQTVR	99.7%	61.2	25	58.1	5	0	0	1667.88	304	319
DnaJ homolog subfamily B member 11	DNAJB11	DJB11_HUMAN	40.5	99.8%	2	2	4	0.00%	7.5%	FQDLGAAYEVLSDSEK	99.7%	134	25	128	2	0	0	1771.84	67	82
DnaJ homolog subfamily B member 11	DNAJB11	DJB11_HUMAN	40.5	99.8%	2	2	4	0.00%	7.5%	TLEVEIEPGVR	99.7%	66.2	25	48.9	2	0	0	1241.67	207	217
DnaJ homolog subfamily B member 12	DNAJB12	DJB12_HUMAN	41.8	100.0%	4	4	6	0.01%	9.6%	AIGTAYAVLSNPEK	99.7%	93.1	25	80	2	0	0	1433.76	153	166
DnaJ homolog subfamily B member 12	DNAJB12	DJB12_HUMAN	41.8	100.0%	4	4	6	0.01%	9.6%	AIGTAYAVLSNPEKR	97.4%	29.7	25	29.7	1	0	0	1589.86	153	167
DnaJ homolog subfamily B member 12	DNAJB12	DJB12_HUMAN	41.8	100.0%	4	4	6	0.01%	9.6%	DYYEILGVSR	97.6%	30	25	23.9	1	0	0	1214.61	110	119
DnaJ homolog subfamily B member 12	DNAJB12	DJB12_HUMAN	41.8	100.0%	4	4	6	0.01%	9.6%	NVEDDYIANLR	99.7%	68.8	25	68.8	2	0	0	1321.64	316	326
DnaJ homolog subfamily B member 6	DNAJB6	DNJB6_HUMAN	36.1	100.0%	4	4	8	0.01%	15.0%	APGPWDPLASAAGLK	99.7%	40.5	25	40.5	2	0	0	1450.77	288	302
DnaJ homolog subfamily B member 6	DNAJB6	DNJB6_HUMAN	36.1	100.0%	4	4	8	0.01%	15.0%	QVAEAYEVLSDAK	96.3%	28.3	25	25.5	1	0	0	1422.71	48	60
DnaJ homolog subfamily B member 6	DNAJB6	DNJB6_HUMAN	36.1	100.0%	4	4	8	0.01%	15.0%	VDYYEVLGVQR	99.7%	53	25	27.2	3	0	0	1340.68	2	12
DnaJ homolog subfamily B member 6	DNAJB6	DNJB6_HUMAN	36.1	100.0%	4	4	8	0.01%	15.0%	VEVEEDGQLK	99.7%	48.7	25	41.5	2	0	0	1145.57	216	225
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	10	10	31	0.03%	14.1%	AIAALISEK	99.7%	48.6	25	38.4	3	0	0	915.55	770	778
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	10	10	31	0.03%	14.1%	ASNLLYGQLK	99.7%	68	25	60.7	4	0	0	1106.62	493	502
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	10	10	31	0.03%	14.1%	GGDCLTSQTR	99.7%	65.5	25	49.9	2	0	0	1094.49	267	276
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	10	10	31	0.03%	14.1%	GVNSYPSLFIFR	99.7%	53.2	25	52.7	3	0	0	1399.74	197	208
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	10	10	31	0.03%	14.1%	IGAVNCGDDR	99.7%	59.4	25	47.8	2	0	0	1076.48	181	190
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	10	10	31	0.03%	14.1%	ILYDILAFAK	99.7%	53.2	25	51.3	5	0	0	1166.68	439	448
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	10	10	31	0.03%	14.1%	NFQEEQINTR	99.7%	73.5	25	55.4	4	0	0	1278.61	757	766
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	10	10	31	0.03%	14.1%	NSILFLNSLDAK	99.7%	85.6	25	82.7	3	0	0	1334.73	326	337
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	10	10	31	0.03%	14.1%	VDCQAYAQTCQK	99.7%	71.1	25	68.2	3	0	0	1471.63	726	737
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	10	10	31	0.03%	14.1%	YDFGIYDDDPEIITLER	99.7%	82	25	82	2	0	0	2073.97	120	136
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	6	6	11	0.01%	13.2%	AGFFGTVVEYGAER	99.7%	96.3	25	87.6	2	0	0	1502.73	328	341
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	6	6	11	0.01%	13.2%	AGLPGFYDPCVGEEK	99.7%	53.1	25	51.9	2	0	0	1638.75	509	523
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	6	6	11	0.01%	13.2%	GIRPGLTTVLAR	99.6%	37.5	25	22.4	2	0	0	1253.77	249	260
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	6	6	11	0.01%	13.2%	GLEMEGWEVVER	99.7%	72.7	25	61.3	1	0	0	1433.67	85	96
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	6	6	11	0.01%	13.2%	IIEAEESR	99.7%	45.9	25	25.6	2	0	0	946.48	452	459

DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	6	6	11	0.01%	13.2%	VIDVTVPLQCLVK	99.7%	54.1	25	52.2	2	0	0	1483.86	485	497
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	7	7	8	0.01%	3.9%	DQDNAIIRPLPK	99.7%	57.3	25	51.4	1	0	0	1379.76	1062	1073
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	7	7	8	0.01%	3.9%	DSLLASLLDGVR	99.7%	44.4	25	33.6	1	0	0	1258.70	312	323
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	7	7	8	0.01%	3.9%	ELIVGEIFVR	99.7%	55	25	52.6	1	0	0	1174.68	1685	1694
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	7	7	8	0.01%	3.9%	IFIAQPAWVLR	98.0%	30.7	25	23.6	1	0	0	1313.77	1987	1997
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	7	7	8	0.01%	3.9%	ITEMPSIIKDLCR	95.4%	20.7	25	17	0	1	0	1591.82	1494	1506
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	7	7	8	0.01%	3.9%	IVDGPDPENIILILK	99.7%	50.1	25	43.5	2	0	0	1648.95	1360	1374
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	7	7	8	0.01%	3.9%	QLVLETLYALTSSTK	99.7%	65	25	65	1	0	0	1666.93	1831	1845
DnaJ homolog subfamily C member 7	DNAJC7	DNJC7_HUMAN	56.4	99.8%	2	2	4	0.00%	4.3%	AVQFFVQALR	99.7%	56.3	25	45.7	2	0	0	1178.67	229	238
DnaJ homolog subfamily C member 7	DNAJC7	DNJC7_HUMAN	56.4	99.8%	2	2	4	0.00%	4.3%	EALGDAQQSVR	99.7%	58.5	25	49.4	2	0	0	1173.59	80	90
DnaJ homolog subfamily C member 9	DNAJC9	DNJC9_HUMAN	29.9	99.8%	2	2	2	0.00%	8.9%	ELGLDEGVDSLK	99.6%	38.2	25	38.2	1	0	0	1274.65	206	217
DnaJ homolog subfamily C member 9	DNAJC9	DNJC9_HUMAN	29.9	99.8%	2	2	2	0.00%	8.9%	ISLEDIQAFEK	99.4%	36.1	25	36.1	1	0	0	1292.67	108	118
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	7	8	19	0.02%	33.1%	ENLPLIVWLLVK	99.7%	45.9	25	45.9	1	0	0	1436.89	38	49
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	7	8	19	0.02%	33.1%	GYVFQMEMIVR	99.7%	49.8	25	49.8	4	0	0	1404.67	206	216
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	7	8	19	0.02%	33.1%	LGGNEIVSFLK	99.7%	72.2	25	68.4	2	0	0	1176.66	241	251
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	7	8	19	0.02%	33.1%	LGLGTAYIHGMK	99.7%	51.1	25	42.5	3	0	0	1260.68	96	107
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	7	8	19	0.02%	33.1%	QKEGNFDIVSGTR	97.1%	22.1	25	17	0	1	0	1450.73	135	147
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	7	8	19	0.02%	33.1%	QLNYTIGEVPISFVDR	99.7%	76.1	25	76.1	4	0	0	1850.96	219	234
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	7	8	19	0.02%	33.1%	YSVLLPTYNER	99.3%	35.2	25	34	4	0	0	1354.70	27	37
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	8	8	16	0.02%	20.4%	LPDVYGVFQFK	99.7%	49.2	25	36.4	2	0	0	1312.69	381	391
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	8	8	16	0.02%	20.4%	NTLLIAGLQAR	99.7%	101	25	77.9	2	0	0	1169.70	240	250
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	8	8	16	0.02%	20.4%	SSLNPILFR	99.7%	54.1	25	39.2	2	0	0	1046.60	190	198
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	8	8	16	0.02%	20.4%	TADDPSLSLIK	98.9%	33.2	25	21.5	2	0	0	1159.62	78	88
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	8	8	16	0.02%	20.4%	TLVLLDNLNVR	99.7%	73.7	25	59.2	2	0	0	1269.75	47	57
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	8	8	16	0.02%	20.4%	WVFKEEGVLR	99.7%	49.2	25	39.6	2	0	0	1262.69	298	307
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	8	8	16	0.02%	20.4%	WVPFDGDDIQLEFVR	99.7%	51.7	25	49	2	0	0	1835.90	345	359
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	8	8	16	0.02%	20.4%	YSQTGNYELAVALSR	99.7%	111	25	105	2	0	0	1671.83	283	297
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	30	0.03%	26.9%	ALTSEIALLQSR	99.7%	94.1	25	78.1	2	0	0	1301.74	525	536
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	30	0.03%	26.9%	ATSFLLALEPELEAR	99.7%	53.3	25	53	4	0	0	1659.90	66	80
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	30	0.03%	26.9%	DTYIENEKLISGK	99.7%	42.2	25	42.2	2	0	0	1509.78	580	592
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	30	0.03%	26.9%	DVPAYSQDTFK	99.7%	44.9	25	33.9	2	0	0	1270.60	205	215
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	30	0.03%	26.9%	FPLFGGWK	98.9%	33.2	25	20.1	1	0	0	951.51	320	327
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	30	0.03%	26.9%	FVDHVFDEQVIDSLTVK	99.7%	63.6	25	60.7	2	0	0	1991.01	355	371
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	30	0.03%	26.9%	HFDETVNR	95.8%	27.8	25	13.5	1	0	0	1017.47	495	502
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	30	0.03%	26.9%	IDHILDAL	99.3%	35	25	33.7	2	0	0	909.50	600	607
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	30	0.03%	26.9%	LKTEGSDLCDR	99.7%	47.6	25	34.7	2	0	0	1293.61	537	547
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	30	0.03%	26.9%	LPVALDPGAK	99.7%	38.9	25	38.9	2	0	0	980.58	117	126
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	30	0.03%	26.9%	NIEIDSPYEISR	99.7%	74.1	25	64	2	0	0	1435.71	380	391
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	30	0.03%	26.9%	QPDSGISSIR	99.7%	51.2	25	37	2	0	0	1059.54	269	278
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	30	0.03%	26.9%	SEDLLDYGPFR	99.7%	70.7	25	63.5	2	0	0	1311.62	194	204
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	30	0.03%	26.9%	VTAEVVLAHLGGGSTSR	99.7%	101	25	101	2	2	0	1653.89	49	65
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	8	9	16	0.02%	17.7%	FELDTSER	95.5%	27.6	25	19.5	1	0	0	996.46	461	468
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	8	9	16	0.02%	17.7%	ISTEVGITNVDLSTVDKDQSIAPK	99.7%	51.1	25	50.1	0	2	0	2530.33	369	392
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	8	9	16	0.02%	17.7%	LQVTNVLSQPLTQATVK	99.7%	110	25	100	4	0	0	1840.05	290	306
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	8	9	16	0.02%	17.7%	SIVEEIEDLVAR	99.7%	53.3	25	40.7	1	0	0	1372.73	179	190
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	8	9	16	0.02%	17.7%	TGQEVVFVAEPDNK	99.7%	73.3	25	66.6	2	0	0	1532.76	443	456
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	8	9	16	0.02%	17.7%	TGQEVVFVAEPDNKNVYK	99.7%	61.9	25	61.9	1	0	0	2037.03	443	460
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	8	9	16	0.02%	17.7%	TSFTPVGDVFELNFMNVK	99.7%	85.9	25	85.9	4	0	0	2045.00	323	340
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	8	9	16	0.02%	17.7%	YLAILGSVTFLAGNR	99.1%	34.1	25	34.1	1	0	0	1594.90	605	619
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	DAD1	DAD1_HUMAN	12.5	100.0%	3	3	10	0.01%	28.3%	ADFQGISPER	99.7%	40	25	30.5	4	0	0	1119.54	83	92
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	DAD1	DAD1_HUMAN	12.5	100.0%	3	3	10	0.01%	28.3%	FLEEYLSSTPQR	99.7%	59.7	25	53	4	0	0	1469.73	12	23

Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	DAD1	DAD1_HUMAN	12.5	100.0%	3	3	10	0.01%	28.3%	SASVVSVISR	99.7%	63.6	25	54.6	2	0	0	1004.57	2	11
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	5	5	9	0.01%	7.4%	ENDYYTPTGEFR	98.5%	32	25	31.7	1	0	0	1491.64	614	625
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	5	5	9	0.01%	7.4%	FGQVYTEAK	99.5%	36.5	25	32.5	1	0	0	1042.52	647	655
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	5	5	9	0.01%	7.4%	FLAEEGFYK	99.7%	42	25	25.3	3	0	0	1103.54	59	67
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	5	5	9	0.01%	7.4%	FYSLLDPSYAK	99.1%	34.1	25	30.1	2	0	0	1303.66	330	340
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	5	5	9	0.01%	7.4%	VGQAMASTEEK	99.7%	42	25	31.8	2	0	0	1150.54	555	565
Dolichyl-phosphate beta-glucosyltransferase	ALG5	ALG5_HUMAN	36.9	99.8%	2	2	3	0.00%	7.7%	ETLPSIWDSPTK	99.7%	45.8	25	37.2	1	0	0	1373.69	54	65
Dolichyl-phosphate beta-glucosyltransferase	ALG5	ALG5_HUMAN	36.9	99.8%	2	2	3	0.00%	7.7%	QLSVVVPSYNEEK	99.7%	44.1	25	36.4	2	0	0	1491.77	66	78
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	99.8%	2	2	2	0.00%	3.6%	LAQIQQAK	97.0%	29.1	25	19.5	1	0	0	899.53	291	298
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	99.8%	2	2	2	0.00%	3.6%	VSVGEFVGEGEGK	99.7%	62.6	25	55.8	1	0	0	1293.63	220	232
Double-stranded RNA-specific adenosine deaminase	ADAR	DSRAD_HUMAN	136.1	100.0%	3	3	7	0.01%	3.1%	DINAVLIDMER	99.7%	61.2	25	56.6	2	0	0	1288.66	329	339
Double-stranded RNA-specific adenosine deaminase	ADAR	DSRAD_HUMAN	136.1	100.0%	3	3	7	0.01%	3.1%	LVDQSGPPHEPK	99.7%	40.1	25	35.2	1	0	0	1303.66	746	757
Double-stranded RNA-specific adenosine deaminase	ADAR	DSRAD_HUMAN	136.1	100.0%	3	3	7	0.01%	3.1%	YLNTNPVGGLLEYAR	99.7%	69.7	25	65.5	4	0	0	1679.88	722	736
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	7	8	14	0.01%	18.3%	DVKPSNILVNSR	99.7%	57.5	25	48.2	2	0	0	1341.75	194	205
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	7	8	14	0.01%	18.3%	ISELGAGNGGVVTK	99.7%	78.7	25	73	2	0	0	1301.71	75	88
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	7	8	14	0.01%	18.3%	LNQPGTPTR	99.7%	59.2	25	47.2	2	0	0	983.53	389	397
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	7	8	14	0.01%	18.3%	RIPEEILGK	99.7%	40.2	25	26.1	2	0	0	1054.63	164	172
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	7	8	14	0.01%	18.3%	RLEAFLTQK	99.2%	34.8	25	27	2	0	0	1105.64	53	61
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	7	8	14	0.01%	18.3%	VGELKDDDFER	99.7%	43.4	25	36.4	2	1	0	1322.62	64	74
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	7	8	14	0.01%	18.3%	YPIPPPDAK	98.0%	30.8	25	16	1	0	0	997.54	265	273
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	7	9	13	0.01%	27.1%	DVKPSNVLINK	96.0%	28	25	23.9	1	0	0	1226.71	190	200
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	7	9	13	0.01%	27.1%	FPYESWGTPFQQLK	99.7%	41.5	25	41.5	2	0	0	1727.84	266	279
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	7	9	13	0.01%	27.1%	FSPEFVDFTAQCLR	99.7%	58	25	58	2	0	0	1716.81	294	307
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	7	9	13	0.01%	27.1%	ISCMSKPPAPNPTPPR	99.7%	31.4	25	27.6	0	3	0	1749.88	27	42
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	7	9	13	0.01%	27.1%	KTDIAAFVK	97.9%	30.5	25	16.7	1	0	0	992.58	332	340
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	7	9	13	0.01%	27.1%	MCDFGISGYLVDSVAK	99.7%	75.2	25	75	3	0	0	1761.82	206	221
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	7	9	13	0.01%	27.1%	QVVEEPSPQLPADR	99.7%	41.2	25	41.2	1	0	0	1564.80	280	293
Dual specificity protein phosphatase 9	DUSP9	DUS9_HUMAN	41.9	100.0%	2	2	4	0.00%	8.3%	ASFPVQILPNLYLGSAR	99.7%	51.4	25	49.8	2	0	0	1846.02	201	217
Dual specificity protein phosphatase 9	DUSP9	DUS9_HUMAN	41.9	100.0%	2	2	4	0.00%	8.3%	IGGALSVALPALLLR	99.7%	55.2	25	55.2	2	0	0	1463.93	38	52
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	53	0.05%	23.1%	AEITDAEGLGLK	99.7%	72.4	25	65.4	1	0	0	1216.64	933	944
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	53	0.05%	23.1%	AESLQQEVEALK	99.7%	50.6	25	44.3	1	0	0	1344.70	318	329
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	53	0.05%	23.1%	AFLQGGQEATDIALLLR	99.7%	65.2	25	50.5	2	0	0	1816.00	769	785
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	53	0.05%	23.1%	ASEQIYGTPSSSPYECLR	99.7%	68.7	25	58.8	1	0	0	2044.93	873	890
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	53	0.05%	23.1%	DLEEKLETLR	99.7%	50.7	25	37.7	2	0	0	1245.67	226	235
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	53	0.05%	23.1%	DLETSCSDIR	99.7%	71	25	55.8	2	0	0	1195.53	786	795
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	53	0.05%	23.1%	DSPLLLQQISAMR	99.7%	78.2	25	78.2	4	0	0	1471.79	1089	1101
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	53	0.05%	23.1%	ELTNQQEASVER	99.7%	76.9	25	69.9	2	0	0	1403.68	533	544
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	53	0.05%	23.1%	EQLDMAGAR	99.7%	57.1	25	51	2	0	0	990.47	487	495
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	53	0.05%	23.1%	FELSENCSERPGLR	97.7%	22.8	25	16.5	0	1	0	1693.80	630	643
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	53	0.05%	23.1%	FTQSALDCMSVEVGR	99.7%	71.2	25	71.2	2	0	0	1699.78	752	766
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	53	0.05%	23.1%	GSDGAASSYQLK	99.7%	65.4	25	51.8	2	0	0	1183.56	350	361
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	53	0.05%	23.1%	GTVAYVGATLFATGK	99.7%	70.2	25	70.2	2	0	0	1455.78	42	56
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	53	0.05%	23.1%	IKGEELSEANVR	99.7%	58.5	25	53.8	2	2	0	1344.71	961	972
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	53	0.05%	23.1%	IQLEQVQEWK	99.7%	61.1	25	53.3	2	0	0	1300.69	253	262
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	53	0.05%	23.1%	KNQELEVVR	99.7%	56.7	25	32.3	2	0	0	1114.62	398	406
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	53	0.05%	23.1%	LKDALVR	98.1%	30.9	25	12.9	1	0	0	814.51	370	376
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	53	0.05%	23.1%	LSHEGPGSELPAGALYR	99.7%	35.9	25	34.9	0	2	0	1753.89	1134	1150
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	53	0.05%	23.1%	MQEQQADLQR	99.7%	56.7	25	45.8	4	0	0	1246.58	265	274
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	53	0.05%	23.1%	NQELEVVR	99.7%	43.7	25	30.9	2	0	0	986.53	399	406
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	53	0.05%	23.1%	QLTAHLQDVNR	99.7%	61.1	25	49.5	2	0	0	1294.69	522	532
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	53	0.05%	23.1%	QSCNILISTMNK	99.7%	39.2	25	38.4	3	0	0	1408.69	891	902

Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	53	0.05%	23.1%	SPSAQLMEQVAQLK	99.7%	103	25	94.8	3	0	0	1529.80	1180	1193
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	53	0.05%	23.1%	VDELTTDLEILK	99.7%	94.3	25	69.9	2	0	0	1388.75	332	343
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	53	0.05%	23.1%	VTFSCAAGFGQR	99.7%	88.3	25	74.4	2	0	0	1300.61	1248	1259
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	5	5	10	0.01%	8.7%	FATEYCNTIEGTAK	99.7%	83.9	25	75	2	0	0	1604.73	340	353
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	5	5	10	0.01%	8.7%	GVSPEPIHLK	97.1%	29.3	25	15.1	2	0	0	1076.61	124	133
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	5	5	10	0.01%	8.7%	IFSPNVVNLTLVDLPGMTK	99.7%	44.7	25	44.4	2	0	0	2074.13	134	152
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	5	5	10	0.01%	8.7%	LGIIGVVNR	99.7%	70.4	25	54.5	2	0	0	940.59	239	247
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	5	5	10	0.01%	8.7%	YIETSELCGGAR	99.7%	69.4	25	54.7	2	0	0	1355.63	354	365
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	15	28	0.03%	18.6%	ALLQMVQQFGVDFEK	99.7%	68.6	25	68.6	4	0	0	1752.90	328	342
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	15	28	0.03%	18.6%	DMILQFISR	99.7%	57.2	25	34.8	2	0	0	1122.60	158	166
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	15	28	0.03%	18.6%	ESSLILAVTPANMDLANSDALK	99.7%	56.9	25	56.9	4	0	0	2273.17	167	188
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	15	28	0.03%	18.6%	FPFELVK	99.5%	37.2	25	0	2	0	0	879.50	370	376
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	15	28	0.03%	18.6%	GISPVPINLR	99.6%	37.7	25	37.4	2	0	0	1065.64	114	123
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	15	28	0.03%	18.6%	GYIGVVNR	99.7%	47.1	25	34.5	2	0	0	877.49	230	237
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	15	28	0.03%	18.6%	IEGSGDQVDTLELSGGAR	99.7%	79.6	25	79.6	1	0	0	1803.87	344	361
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	15	28	0.03%	18.6%	LQSQLLSLEK	99.7%	58	25	0	2	0	0	1158.67	300	309
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	15	28	0.03%	18.6%	NLVDSYVAIINK	99.7%	89.7	25	65.2	2	0	0	1348.75	658	669
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	15	28	0.03%	18.6%	SSVLENFVGR	99.7%	56.3	25	45.1	2	0	0	1107.58	45	54
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	15	28	0.03%	18.6%	TGLFTPDLAFEAIVK	99.7%	75.6	25	73.6	2	0	0	1621.88	400	414
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	15	28	0.03%	18.6%	TLNQQLTNHIR	99.7%	50.9	25	38.1	1	0	0	1337.73	280	290
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	13	15	28	0.03%	18.6%	VPVGDQPPDIEYQIK	99.7%	87.8	25	78.3	2	0	0	1697.87	143	157
Dynamin-like 120 kDa protein, mitochondrial	OPA1	OPA1_HUMAN	111.6	100.0%	4	4	6	0.01%	4.4%	ESVEQQADSFK	99.7%	58.5	25	50.4	2	0	0	1267.58	558	568
Dynamin-like 120 kDa protein, mitochondrial	OPA1	OPA1_HUMAN	111.6	100.0%	4	4	6	0.01%	4.4%	LDAFIEALHQEK	99.7%	55.9	25	51.3	2	0	0	1413.74	949	960
Dynamin-like 120 kDa protein, mitochondrial	OPA1	OPA1_HUMAN	111.6	100.0%	4	4	6	0.01%	4.4%	QQLTNTEVR	99.5%	36.9	25	22.4	1	0	0	1088.57	896	904
Dynamin-like 120 kDa protein, mitochondrial	OPA1	OPA1_HUMAN	111.6	100.0%	4	4	6	0.01%	4.4%	VIQHNALEDR	99.7%	40.1	25	33.2	1	0	0	1194.62	724	733
Dynein light chain 1, cytoplasmic	DYNLL1	DYL1_HUMAN	10.4	100.0%	3	4	10	0.01%	49.4%	NADMSEEMQQDSVECATQALEK	99.7%	48.2	25	48.2	1	2	0	2546.03	10	31
Dynein light chain 1, cytoplasmic	DYNLL1	DYL1_HUMAN	10.4	100.0%	3	4	10	0.01%	49.4%	NFGSYVTHETK	99.7%	50.7	25	43.6	3	0	0	1282.61	61	71
Dynein light chain 1, cytoplasmic	DYNLL1	DYL1_HUMAN	10.4	100.0%	3	4	10	0.01%	49.4%	YNPTWHCIVGR	99.7%	50.3	25	46.8	4	0	0	1402.67	50	60
Dynein light chain Tctex-type 1	DYNLT1	DYLT1_HUMAN	12.5	99.8%	2	3	5	0.00%	23.0%	EAIESAIGGNAYQHSK	99.7%	68	25	67.1	2	0	0	1674.81	23	38
Dynein light chain Tctex-type 1	DYNLT1	DYLT1_HUMAN	12.5	99.8%	2	3	5	0.00%	23.0%	YIVTCVIMQK	99.7%	47.7	25	41.2	3	0	0	1270.65	63	72
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	17	17	29	0.03%	7.0%	APGTNVAMASNQAVR	99.7%	72.1	25	70.8	1	0	0	1486.74	1307	1321
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	17	17	29	0.03%	7.0%	EGQWDCSVCLVR	99.7%	59.9	25	56.6	2	0	0	1508.66	1607	1618
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	17	17	29	0.03%	7.0%	EIVETFANK	97.7%	30.3	25	20.6	1	0	0	1050.55	371	379
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	17	17	29	0.03%	7.0%	ELLQSFDSALQSVK	99.7%	82.3	25	78.3	4	0	0	1564.82	257	270
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	17	17	29	0.03%	7.0%	ELVGPPLAETVFTPK	99.7%	73.3	25	69.4	2	0	0	1597.88	1384	1398
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	17	17	29	0.03%	7.0%	FGESTTGFNFSFK	99.7%	52.6	25	52.6	2	0	0	1468.67	2260	2272
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	17	17	29	0.03%	7.0%	FGISEPGNQEK	98.4%	31.8	25	24.3	2	0	0	1205.58	1900	1910
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	17	17	29	0.03%	7.0%	GVIFGQTSSTFTFADLAK	99.7%	67.6	25	67.6	2	0	0	1889.96	1935	1952
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	17	17	29	0.03%	7.0%	IAVAVLEETTR	99.7%	111	25	106	2	0	0	1201.68	2467	2477
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	17	17	29	0.03%	7.0%	LLVQHEINTLR	99.7%	43.7	25	34.6	2	0	0	1335.77	553	563
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	17	17	29	0.03%	7.0%	NLFASFPTEESSINYTFK	97.9%	30.5	25	29.8	1	0	0	2095.00	2595	2612
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	17	17	29	0.03%	7.0%	NSDIEQSSDSKVK	99.7%	39.9	25	38.9	1	0	0	1436.69	2582	2594
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	17	17	29	0.03%	7.0%	SGSSFVHQASFK	99.7%	53.3	25	46	1	0	0	1281.62	1447	1458
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	17	17	29	0.03%	7.0%	SLGGNDELSATFLEMK	99.7%	61.5	25	61.5	1	0	0	1711.82	271	286
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	17	17	29	0.03%	7.0%	TGSGLNSFYDQR	99.7%	78.2	25	72.4	1	0	0	1344.62	585	596
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	17	17	29	0.03%	7.0%	VWLWTACDFADGER	99.7%	48.5	25	48.5	2	0	0	1725.77	2401	2414
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	17	17	29	0.03%	7.0%	YIASVQGSTPSPR	99.7%	75	25	72.2	2	0	0	1362.70	11	23
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	23	23	38	0.04%	6.3%	ADGTATAPPPR	99.7%	43.6	25	37.4	2	0	0	1053.53	707	717
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	23	23	38	0.04%	6.3%	AIQDPAFSDGIR	99.7%	49.6	25	49.6	2	0	0	1289.65	518	529
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	23	23	38	0.04%	6.3%	ALAELFGLLVK	99.7%	89.6	25	76.2	2	0	0	1173.72	1062	1072
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	23	23	38	0.04%	6.3%	DSAVAISGADSR	99.7%	75.3	25	65.2	2	0	0	1148.55	2930	2941

E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	23	23	38	0.04%	6.3%	EMFNPMYALFR	99.7%	52.2	25	46.6	2	0	0	1418.66	4072	4082
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	23	23	38	0.04%	6.3%	FLGDEQDQITFVTR	99.7%	71	25	60.7	1	0	0	1668.82	418	431
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	23	23	38	0.04%	6.3%	FLQFVTGTSK	99.7%	59.7	25	52.7	2	0	0	1127.61	4296	4305
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	23	23	38	0.04%	6.3%	GLQSFVQCQPFER	99.7%	60.6	25	55.8	2	0	0	1595.76	617	629
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	23	23	38	0.04%	6.3%	HADHSSLTLGSGSSTTR	98.9%	25.3	25	25.3	0	1	0	1713.82	2522	2538
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	23	23	38	0.04%	6.3%	IVNQPSSLFGSK	99.5%	37.2	25	26	1	0	0	1276.69	2256	2267
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	23	23	38	0.04%	6.3%	LGSSGLGSASSIQAAVR	99.7%	101	25	93.2	2	0	0	1560.83	3750	3766
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	23	23	38	0.04%	6.3%	LLECYFTR	99.7%	41.1	25	24.4	1	0	0	1101.54	4123	4130
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	23	23	38	0.04%	6.3%	LLSLISIALPENK	99.7%	53.7	25	52.5	2	0	0	1410.86	3456	3468
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	23	23	38	0.04%	6.3%	LPGGVQNFPQFSALR	99.7%	62.9	25	62.9	2	0	0	1630.87	1226	1240
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	23	23	38	0.04%	6.3%	NLCYHAQTR	97.2%	29.4	25	19.5	1	0	0	1162.54	3211	3219
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	23	23	38	0.04%	6.3%	NPDIFTEVANCCIR	99.7%	69.9	25	68.3	2	0	0	1708.78	1881	1894
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	23	23	38	0.04%	6.3%	QIGTLLAELR	99.7%	51.5	25	47.7	2	0	0	1113.66	3637	3646
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	23	23	38	0.04%	6.3%	QVVNQVWEAADVLIK	99.7%	69.1	25	61.6	2	0	0	1711.94	1483	1497
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	23	23	38	0.04%	6.3%	SILTLSHEPK	99.2%	34.6	25	25.6	1	0	0	1124.63	830	839
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	23	23	38	0.04%	6.3%	SLLSILQR	99.7%	48.8	25	29.1	2	0	0	929.58	3225	3232
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	23	23	38	0.04%	6.3%	TPTEAPADCR	98.8%	33	25	33	1	0	0	1117.49	11	20
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	23	23	38	0.04%	6.3%	VSDGGSSSTDFK	99.7%	49.8	25	44.3	2	0	0	1186.52	3559	3570
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	23	23	38	0.04%	6.3%	YICQKPSIQK	95.6%	27.6	25	14.9	1	0	0	1264.67	697	706
E3 ubiquitin-protein ligase RING2	RNF2	RING2_HUMAN	37.7	99.9%	2	2	2	0.00%	6.9%	FCADCIITALR	99.7%	51.4	25	45.8	1	0	0	1339.65	71	81
E3 ubiquitin-protein ligase RING2	RNF2	RING2_HUMAN	37.7	99.9%	2	2	2	0.00%	6.9%	TSGNATVDHLSK	99.7%	49.2	25	45.1	1	0	0	1229.61	250	261
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	15	15	28	0.03%	28.8%	ALCWVCAQSR	99.7%	49.6	25	46.1	2	0	0	1250.58	109	118
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	15	15	28	0.03%	28.8%	DLDITSPELR	99.7%	61.2	25	50.4	2	0	0	1158.60	261	270
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	15	15	28	0.03%	28.8%	EAWDLGVCR	99.7%	47.7	25	46.7	2	0	0	1105.51	352	360
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	15	15	28	0.03%	28.8%	HYWEVDVTGK	99.7%	39.7	25	36.6	2	0	0	1233.59	342	351
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	15	15	28	0.03%	28.8%	IHAEFVQQK	99.7%	46.1	25	31.9	2	0	0	1099.59	178	186
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	15	15	28	0.03%	28.8%	LAQQSQALQELISELDRR	98.5%	24.1	25	24.1	0	1	0	2098.13	218	235
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	15	15	28	0.03%	28.8%	LGDTQQSIPGNEER	99.7%	78.9	25	74.2	2	0	0	1543.73	311	324
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	15	15	28	0.03%	28.8%	LQVALGELR	99.7%	60	25	29.2	2	0	0	998.60	139	147
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	15	15	28	0.03%	28.8%	LQVALGELRR	98.7%	32.6	25	27.2	2	0	0	1154.70	139	148
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	15	15	28	0.03%	28.8%	NFLVEEEQR	99.7%	52.6	25	28.6	2	0	0	1163.57	187	195
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	15	15	28	0.03%	28.8%	QLANMVNNLK	99.7%	43	25	41.8	2	0	0	1160.61	68	77
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	15	15	28	0.03%	28.8%	SESWNLKDLDITSPELR	99.7%	29.1	25	24.7	0	2	0	2003.01	254	270
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	15	15	28	0.03%	28.8%	SGFWTIWLWNK	99.7%	67.4	25	56.9	2	0	0	1437.73	375	385
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	15	15	28	0.03%	28.8%	SVCHVPGLK	96.6%	28.6	25	18.1	2	0	0	996.53	271	279
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	15	15	28	0.03%	28.8%	SVCHVPGLKK	96.8%	28.9	25	21.6	1	0	0	1124.62	271	280
E3 ubiquitin-protein ligase UBR4	UBR4	UBR4_HUMAN	573.8	99.9%	2	2	3	0.00%	0.4%	QLLQLLTTYIVR	99.7%	59.5	25	55.3	1	0	0	1460.88	1490	1501
E3 ubiquitin-protein ligase UBR4	UBR4	UBR4_HUMAN	573.8	99.9%	2	2	3	0.00%	0.4%	VCLNLPYFLR	98.0%	30.7	25	22.7	2	0	0	1294.70	259	268
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	14	14	23	0.02%	19.1%	AQFAEATQR	99.7%	43.5	25	35.1	2	0	0	1021.51	18	26
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	14	14	23	0.02%	19.1%	AVFVPDIYSR	97.5%	29.9	25	26.5	2	0	0	1166.62	242	251
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	14	14	23	0.02%	19.1%	CVPQIIAFLNSK	96.4%	28.4	25	28.4	1	0	0	1389.76	708	719
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	14	14	23	0.02%	19.1%	ELQELSSSIK	99.7%	44.3	25	39.2	1	0	0	1133.60	771	780
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	14	14	23	0.02%	19.1%	FFADDTQAALTK	99.7%	82.7	25	78.3	2	0	0	1327.65	560	571
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	14	14	23	0.02%	19.1%	FINDCTELFR	99.7%	45.5	25	41.1	2	0	0	1314.61	368	377
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	14	14	23	0.02%	19.1%	GVIFTEAFVAR	99.7%	95.7	25	88.3	2	0	0	1209.66	175	185
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	14	14	23	0.02%	19.1%	IISGHIDLDNR	99.3%	35	25	29.2	1	0	0	1252.66	164	174
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	14	14	23	0.02%	19.1%	LAADFQR	99.7%	40	25	29.9	2	0	0	820.43	11	17
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	14	14	23	0.02%	19.1%	LGIPDAVSYIK	99.7%	47.9	25	38.4	2	0	0	1175.67	275	285
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	14	14	23	0.02%	19.1%	NNPVHLITEEDLK	99.7%	62.1	25	54.4	1	0	0	1521.79	390	402
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	14	14	23	0.02%	19.1%	QISTLESVSTSK	99.7%	47.2	25	44.8	1	0	0	1279.67	403	414
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	14	14	23	0.02%	19.1%	TTQLLFLK	99.7%	43.7	25	35.4	2	0	0	963.59	290	297

E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	14	14	23	0.02%	19.1%	TYDLPGNFLTQALTQR	99.7%	81.6	25	54.9	2	0	0	1837.94	145	160
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	12	14	25	0.02%	24.7%	ADQIETQQLMR	99.7%	53.1	25	46.5	4	0	0	1332.66	221	231
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	12	14	25	0.02%	24.7%	EHQISPGDFPSLR	99.7%	39.6	25	32.5	0	2	0	1482.73	345	357
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	12	14	25	0.02%	24.7%	ELVNNLGEIYQK	99.7%	73	25	73	2	0	0	1419.75	330	341
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	12	14	25	0.02%	24.7%	IINTPEVVR	99.7%	41.3	25	31.9	2	0	0	1040.61	243	251
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	12	14	25	0.02%	24.7%	KLNDLIK	95.9%	27.9	25	8.72	2	0	0	843.53	293	299
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	12	14	25	0.02%	24.7%	LLDTVDDMLANDIAR	99.7%	113	25	113	2	0	0	1674.84	378	392
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	12	14	25	0.02%	24.7%	LLPLEEHYR	99.7%	39.7	25	32.6	2	0	0	1169.63	33	41
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	12	14	25	0.02%	24.7%	LNAFGNAFLNR	99.7%	50	25	42.7	1	0	0	1236.65	125	135
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	12	14	25	0.02%	24.7%	MQELLQTQDFSK	99.7%	73.2	25	63.1	2	0	0	1467.72	359	370
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	12	14	25	0.02%	24.7%	QEESLMPSQVVK	99.7%	40.2	25	32.7	2	0	0	1390.69	399	410
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	12	14	25	0.02%	24.7%	SKLPNTVLGK	99.4%	35.6	25	35.6	2	0	0	1056.64	474	483
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	12	14	25	0.02%	24.7%	VYGALMWSLGK	99.7%	40.7	25	33.9	2	0	0	1240.64	232	242
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	5	5	7	0.01%	13.3%	AGGADAVQTVTGGLR	99.7%	69.7	25	61.5	2	0	0	1372.72	15	29
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	5	5	7	0.01%	13.3%	EYQISAGDFPEVK	99.7%	64	25	59	2	0	0	1482.71	348	360
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	5	5	7	0.01%	13.3%	FGNAFLNR	99.7%	63.7	25	52	1	0	0	938.48	131	138
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	5	5	7	0.01%	13.3%	KLNDLIK	95.9%	27.9	25	8.72	2	0	0	843.53	296	302
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	5	5	7	0.01%	13.3%	LPEIYIQLQR	99.7%	48.6	25	37.4	1	0	0	1272.73	338	347
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	5	5	7	0.01%	13.3%	LPNSVLGK	95.1%	27.2	25	19.1	1	0	0	827.50	479	486
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	5	5	7	0.01%	13.3%	VYGALMWSLGK	99.7%	40.7	25	33.9	2	0	0	1240.64	235	245
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	6	6	14	0.01%	22.1%	AINTLNGLR	99.7%	45.4	25	33.6	2	0	0	971.56	77	85
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	6	6	14	0.01%	22.1%	FAANPNQNK	99.0%	33.6	25	25	2	0	0	1003.50	183	191
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	6	6	14	0.01%	22.1%	SLFSSIGEVESAK	99.7%	75	25	68.7	4	0	0	1353.69	38	50
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	6	6	14	0.01%	22.1%	TNLIVNYLPQNMTQDELR	99.7%	48.2	25	48.2	1	0	0	2178.09	20	37
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	6	6	14	0.01%	22.1%	VLVDQTTGLSR	99.7%	89.6	25	66.4	4	0	0	1188.66	137	147
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	6	6	14	0.01%	22.1%	VSYARPSSEVIK	99.7%	41.7	25	25.5	1	0	0	1335.73	93	104
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	13	17	40	0.04%	51.4%	AAVDAGFVPNDMQVGQTGK	99.7%	88.2	25	88.2	5	0	0	1920.91	250	268
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	13	17	40	0.04%	51.4%	ASSTSPVEISEWLDQK	99.7%	88.6	25	84.5	2	0	0	1776.87	188	203
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	13	17	40	0.04%	51.4%	CDKVAQDLCK	98.1%	30.9	25	23.5	1	0	0	1236.57	60	69
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	13	17	40	0.04%	51.4%	GLLPEELTPLILATQK	99.7%	91.6	25	91.2	2	2	0	1736.02	86	101
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	13	17	40	0.04%	51.4%	GTSFDAAATSGGSASSEK	99.7%	115	25	112	2	0	0	1630.72	170	187
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	13	17	40	0.04%	51.4%	LEVAPISDIIAIK	99.7%	94.6	25	77.9	6	0	0	1381.83	127	139
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	13	17	40	0.04%	51.4%	LGGEVSCLVAGTK	99.7%	90.8	25	84.8	3	0	0	1290.67	47	59
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	13	17	40	0.04%	51.4%	LLYDLADQLHAAVGASR	99.7%	95.8	25	90.8	3	2	0	1812.96	233	249
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	13	17	40	0.04%	51.4%	SDRPELTGAK	99.7%	42.9	25	31.5	2	0	0	1073.56	207	216
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	13	17	40	0.04%	51.4%	SPDTFVR	99.7%	50	25	28.5	2	0	0	821.42	140	146
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	13	17	40	0.04%	51.4%	TIYAGNALCTVK	99.7%	81.7	25	71.9	2	0	0	1310.68	147	158
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	13	17	40	0.04%	51.4%	VLVAQHDVYK	99.7%	62.3	25	46.4	3	0	0	1171.65	76	85
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	13	17	40	0.04%	51.4%	VVPEMTEILK	99.5%	36.9	25	26.5	3	0	0	1174.64	322	331
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	12	13	22	0.02%	49.4%	EIDGGLETLR	99.7%	76.3	25	67.2	2	0	0	1102.57	165	174
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	12	13	22	0.02%	49.4%	EKVDLVLLGK	99.7%	39.2	25	39.2	1	0	0	1113.69	115	124
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	12	13	22	0.02%	49.4%	EVIAVSCGPAQCQETIR	99.7%	99.7	25	99.7	2	0	0	1917.92	60	76
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	12	13	22	0.02%	49.4%	GIHVEVPPAEAER	99.7%	36.4	25	29.8	2	1	0	1403.73	86	98
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	12	13	22	0.02%	49.4%	IEVIKPGDLGVDLTSK	99.7%	60.1	25	60.1	2	0	0	1683.95	206	221
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	12	13	22	0.02%	49.4%	LGPLQVAR	99.7%	67.8	25	58.8	2	0	0	853.53	99	106
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	12	13	22	0.02%	49.4%	LKLPAVVTADLR	95.0%	27.1	25	27.1	1	0	0	1295.80	175	186
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	12	13	22	0.02%	49.4%	LPAVVTADLR	99.7%	39.5	25	31.6	2	0	0	1054.63	177	186
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	12	13	22	0.02%	49.4%	LSVISVEDPPQR	99.7%	65.3	25	59.8	2	0	0	1339.72	222	233
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	12	13	22	0.02%	49.4%	TALAMGADR	99.5%	36.6	25	23.5	1	0	0	905.45	77	85
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	12	13	22	0.02%	49.4%	TGVVTDGVK	98.1%	31	25	19	2	0	0	875.48	27	35
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	12	13	22	0.02%	49.4%	VETTEDLVAK	99.7%	52.3	25	41.7	2	0	0	1104.58	239	248

ELMO domain-containing protein 2	ELMOD2	ELMD2_HUMAN	35.0	100.0%	5	5	9	0.01%	16.7%	IENSLTYSK	99.7%	43.1	25	43.1	2	0	0	1054.54	47	55
ELMO domain-containing protein 2	ELMOD2	ELMD2_HUMAN	35.0	100.0%	5	5	9	0.01%	16.7%	IFDTYVGAQR	99.7%	84.1	25	74.2	2	0	0	1169.60	34	43
ELMO domain-containing protein 2	ELMOD2	ELMD2_HUMAN	35.0	100.0%	5	5	9	0.01%	16.7%	LWNLLMPTK	99.7%	46.9	25	39.4	1	0	0	1115.63	134	142
ELMO domain-containing protein 2	ELMOD2	ELMD2_HUMAN	35.0	100.0%	5	5	9	0.01%	16.7%	MCLLQITGYK	99.5%	36.4	25	36.4	2	0	0	1242.62	97	106
ELMO domain-containing protein 2	ELMOD2	ELMD2_HUMAN	35.0	100.0%	5	5	9	0.01%	16.7%	NINPEKDASFK	99.7%	40	25	26.4	2	0	0	1262.64	82	92
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	28	216	0.22%	48.9%	DGNASGTTLLEALDCILPPTRPTDKPLR	99.7%	74.1	25	74.1	0	2	0	3021.57	220	247
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	28	216	0.22%	48.9%	EHALLAYTLGVK	99.7%	72.5	25	65.1	22	4	0	1314.74	135	146
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	28	216	0.22%	48.9%	EVSTYIK	97.5%	29.8	25	13.8	1	0	0	839.45	173	179
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	28	216	0.22%	48.9%	EVSTYIKK	99.7%	51.9	25	40.5	3	0	0	967.55	173	180
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	28	216	0.22%	48.9%	FEKEAAEMGK	99.7%	55.5	25	44.3	4	0	0	1139.54	42	51
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	28	216	0.22%	48.9%	IGGIGTVPVGR	99.7%	89.5	25	83.9	29	0	0	1025.61	256	266
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	28	216	0.22%	48.9%	LPLQDVYK	99.7%	60	25	45.5	18	0	0	975.55	248	255
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	28	216	0.22%	48.9%	NMITGTSQADCAVLIVAAGVGEFEAGISK	99.7%	56	25	55.1	0	2	0	2909.44	101	129
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	28	216	0.22%	48.9%	QLIVGVNK	99.7%	38.8	25	18.6	12	0	0	870.54	147	154
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	28	216	0.22%	48.9%	QTVAVGVIK	99.7%	57.9	25	38.5	8	0	0	914.57	431	439
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	28	216	0.22%	48.9%	SGDAAIVDMVPGKPMCVESFSDYPPLGR	99.7%	62.5	25	62.5	0	6	0	3027.39	396	423
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	28	216	0.22%	48.9%	STTTGHLIYK	99.7%	52.5	25	37.8	30	0	0	1120.60	21	30
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	28	216	0.22%	48.9%	THINIVVIGHVDSGK	99.7%	116	25	116	12	16	0	1588.88	6	20
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	28	216	0.22%	48.9%	TIEKFEK	98.1%	30.9	25	17.7	3	0	0	894.49	38	44
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	28	216	0.22%	48.9%	VETGVLKPGMVVTFAPVNVTTEVK	99.7%	63	25	63	4	14	0	2531.38	267	290
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	28	216	0.22%	48.9%	YEEIVKEVSTYIK	99.7%	84.8	25	80.2	2	0	0	1600.85	167	179
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	28	216	0.22%	48.9%	YYVTIIDAPGHR	99.7%	62.2	25	60.6	14	6	0	1404.73	85	96
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	18	28	216	0.22%	48.9%	YYVTIIDAPGHRDFIK	99.7%	46.8	25	46.8	2	2	0	1908.00	85	100
Elongation factor 1-beta	EEF1B2	EF1B_HUMAN	24.8	100.0%	3	3	5	0.00%	15.1%	LEECVR	98.2%	31.3	25	14.3	1	0	0	805.39	158	163
Elongation factor 1-beta	EEF1B2	EF1B_HUMAN	24.8	100.0%	3	3	5	0.00%	15.1%	SIQADGLVWGSSK	99.7%	74.2	25	74.2	2	0	0	1347.69	164	176
Elongation factor 1-beta	EEF1B2	EF1B_HUMAN	24.8	100.0%	3	3	5	0.00%	15.1%	SPAGLQVLNDYLADK	99.7%	90.5	25	90.5	2	0	0	1603.83	8	22
Elongation factor 1-delta	EEF1D	EF1D_HUMAN	31.1	100.0%	4	4	6	0.01%	22.4%	ATAPQTQHVSPMR	99.7%	40.1	25	35.5	1	0	0	1439.71	124	136
Elongation factor 1-delta	EEF1D	EF1D_HUMAN	31.1	100.0%	4	4	6	0.01%	22.4%	FYEQMNGPVAGASR	99.7%	55.1	25	55.1	1	0	0	1526.71	25	38
Elongation factor 1-delta	EEF1D	EF1D_HUMAN	31.1	100.0%	4	4	6	0.01%	22.4%	IASLEVENQSLR	99.7%	79.6	25	62.5	2	0	0	1358.73	84	95
Elongation factor 1-delta	EEF1D	EF1D_HUMAN	31.1	100.0%	4	4	6	0.01%	22.4%	SLAGSSGPGASSGTSGDHGELVVR	99.7%	35.9	25	35.9	0	2	0	2185.05	60	83
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	15	32	0.03%	29.1%	AKDPFAHLPK	99.6%	37.4	25	26	2	0	0	1123.63	276	285
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	15	32	0.03%	29.1%	ALIAAQYSGAQVR	99.7%	92.6	25	92.6	4	0	0	1347.74	18	30
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	15	32	0.03%	29.1%	EYFSWEGAFQHVGK	99.7%	59.8	25	57.2	2	1	0	1684.78	415	428
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	15	32	0.03%	29.1%	FAETQPK	96.1%	28.1	25	19.1	1	0	0	820.42	221	227
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	15	32	0.03%	29.1%	ILGLLDAYLK	99.7%	59	25	51.7	6	0	0	1118.68	138	147
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	15	32	0.03%	29.1%	KLDPGSEETQTLVR	99.7%	71.6	25	69.2	2	2	0	1572.82	401	414
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	15	32	0.03%	29.1%	MAQFDAK	97.8%	30.4	25	24.5	1	0	0	810.38	213	219
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	15	32	0.03%	29.1%	QAFPNTNR	98.2%	31.2	25	23.7	1	0	0	947.47	182	189
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	15	32	0.03%	29.1%	STFVLDEFKR	99.7%	54.9	25	45.2	2	2	0	1241.65	286	295
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	15	32	0.03%	29.1%	TFLVGER	99.5%	36.4	25	28.1	2	0	0	821.45	150	156
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	15	32	0.03%	29.1%	VLSAPPHFHFGQTNR	99.7%	41.6	25	36.4	0	2	0	1707.87	31	45
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	15	32	0.03%	29.1%	WFLTCINQPQFR	99.7%	57.5	25	43.7	2	0	0	1609.79	190	201
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	21	24	47	0.05%	28.8%	ALLELQLEPEELYQTFQR	98.7%	32.5	25	32.5	1	0	0	2220.15	163	180
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	21	24	47	0.05%	28.8%	AYLPVNESFGFTADLR	99.7%	100	25	97.6	2	1	0	1799.90	786	801
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	21	24	47	0.05%	28.8%	CLYASVLTAQPR	99.7%	74.8	25	65.7	2	0	0	1378.71	728	739
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	21	24	47	0.05%	28.8%	EGALCEENMR	99.7%	68.2	25	53.4	3	0	0	1208.50	689	698
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	21	24	47	0.05%	28.8%	EGIPALDNFLDKL	99.7%	67.1	25	61.1	2	0	0	1444.77	846	858
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	21	24	47	0.05%	28.8%	ETVSEESNVLCLSK	99.7%	84.1	25	74.1	2	0	0	1594.76	581	594
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	21	24	47	0.05%	28.8%	FSVSPVVR	98.9%	33.2	25	22.4	2	0	0	890.51	499	506
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	21	24	47	0.05%	28.8%	GEGQLGPAER	99.6%	37.5	25	29.9	2	0	0	1013.50	240	249
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	21	24	47	0.05%	28.8%	GGGQIIPTAR	99.7%	42.3	25	39.4	5	0	0	969.55	717	726

Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	21	24	47	0.05%	28.8%	GHVFEESQVAGTPMFVVK	97.4%	22.4	25	22.4	0	1	0	1977.97	768	785
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	21	24	47	0.05%	28.8%	GPLMMYISK	99.7%	51.8	25	16.5	4	0	0	1055.53	392	400
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	21	24	47	0.05%	28.8%	IMGPNYTPGK	99.7%	51	25	45.2	4	0	0	1077.54	429	438
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	21	24	47	0.05%	28.8%	IMGPNYTPGKK	98.7%	32.5	25	24.8	1	0	0	1205.63	429	439
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	21	24	47	0.05%	28.8%	IWCFGPDGTGPNILTDITK	99.7%	39.1	25	16.1	1	0	0	2105.04	649	667
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	21	24	47	0.05%	28.8%	KEDLYLKPIQR	99.7%	33.2	25	33.2	0	2	0	1402.81	439	449
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	21	24	47	0.05%	28.8%	QFAEMYVAK	99.7%	58.5	25	55.1	2	0	0	1086.53	227	235
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	21	24	47	0.05%	28.8%	STLTDSLVCK	99.7%	62.9	25	57.6	2	0	0	1123.57	33	42
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	21	24	47	0.05%	28.8%	TFCQLILDPIFK	99.7%	52.3	25	46.3	3	0	0	1494.80	288	299
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	21	24	47	0.05%	28.8%	VFDAIMNFK	99.7%	48.4	25	44.2	2	0	0	1084.55	300	308
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	21	24	47	0.05%	28.8%	VFSGLVSTGLK	99.7%	85.2	25	73.6	4	0	0	1107.64	416	426
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	21	24	47	0.05%	28.8%	VNFTVDQIR	99.7%	76.6	25	58.8	2	0	0	1091.58	2	10
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	21	24	47	0.05%	28.8%	YEWDVAEAR	99.7%	59.6	25	53.4	2	0	0	1138.52	639	647
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	21	33	104	0.10%	50.0%	ADAVQDSEMVELVELEIR	99.7%	93.3	25	93.3	3	0	0	2062.00	183	200
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	21	33	104	0.10%	50.0%	AEAGDNLGALVR	99.7%	98.6	25	79.1	5	0	0	1185.62	316	327
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	21	33	104	0.10%	50.0%	DLEKPFLLPVEAVYSVPGR	99.7%	53.9	25	53.9	2	1	0	2129.16	253	271
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	21	33	104	0.10%	50.0%	EHLLLAR	99.5%	36.9	25	29.4	5	0	0	851.51	163	169
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	21	33	104	0.10%	50.0%	ELAMPGEDLK	99.4%	35.7	25	32.2	4	0	0	1102.55	396	405
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	21	33	104	0.10%	50.0%	ELAMPGEDLKFNLILR	97.7%	30.1	25	20.3	1	0	0	1875.00	396	411
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	21	33	104	0.10%	50.0%	GDECELLGHSK	99.7%	42.6	25	42.6	2	0	0	1244.56	287	297
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	21	33	104	0.10%	50.0%	GITINAAHVEYSTAAR	99.7%	97.4	25	87.6	5	5	0	1673.86	105	120
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	21	33	104	0.10%	50.0%	GTVVTGTLER	99.7%	65.3	25	46.6	8	0	0	1032.57	272	281
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	21	33	104	0.10%	50.0%	HYAHTDCPGHADYVK	99.7%	42	25	42	1	2	0	1770.77	121	135
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	21	33	104	0.10%	50.0%	IILPPEKELAMPGEDLK	99.7%	34	25	31.6	0	2	0	1909.04	389	405
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	21	33	104	0.10%	50.0%	KGDECELLGHSK	99.7%	62.1	25	60.9	2	2	0	1372.65	286	297
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	21	33	104	0.10%	50.0%	LLDAVDTYIPVPAR	99.7%	103	25	91.6	10	0	0	1542.85	239	252
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	21	33	104	0.10%	50.0%	QIGVEHVVVYVNK	99.7%	64.2	25	52	2	2	0	1483.83	170	182
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	21	33	104	0.10%	50.0%	TIGTGLVTNTLAMTEEEK	99.7%	111	25	106	9	0	0	1923.96	430	447
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	21	33	104	0.10%	50.0%	TIGTGLVTNTLAMTEEEKNIK	99.7%	31.6	25	30.6	0	2	0	2263.19	430	450
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	21	33	104	0.10%	50.0%	TTLTAAITK	99.7%	65.3	25	53.1	2	0	0	919.55	71	79
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	21	33	104	0.10%	50.0%	TVVTGIEMFHK	99.7%	66.1	25	42.1	9	2	0	1261.66	301	311
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	21	33	104	0.10%	50.0%	VEAQVYILSK	99.7%	75.8	25	63.4	10	0	0	1149.65	352	361
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	21	33	104	0.10%	50.0%	VEAQVYILSKEEGGR	99.7%	82.7	25	81.6	2	2	0	1677.88	352	366
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	21	33	104	0.10%	50.0%	YEEIDNAPEER	99.7%	77	25	69.5	2	0	0	1364.60	92	102
Elongator complex protein 1	IKBKAP	ELP1_HUMAN	150.3	100.0%	5	5	8	0.01%	4.1%	ALVLAQIR	99.7%	52.7	25	49	2	0	0	883.57	723	730
Elongator complex protein 1	IKBKAP	ELP1_HUMAN	150.3	100.0%	5	5	8	0.01%	4.1%	EYLPFLNTLK	99.0%	33.8	25	33	1	0	0	1237.68	916	925
Elongator complex protein 1	IKBKAP	ELP1_HUMAN	150.3	100.0%	5	5	8	0.01%	4.1%	IVSLMWDPVTPYR	98.2%	31.3	25	22.8	1	0	0	1576.82	346	358
Elongator complex protein 1	IKBKAP	ELP1_HUMAN	150.3	100.0%	5	5	8	0.01%	4.1%	SVVLQLADGQIFK	99.7%	68.9	25	68.2	2	0	0	1417.81	568	580
Elongator complex protein 1	IKBKAP	ELP1_HUMAN	150.3	100.0%	5	5	8	0.01%	4.1%	VFLGNVETFIK	99.7%	44.7	25	37.6	2	0	0	1266.71	762	772
Emerin	EMD	EMD_HUMAN	29.0	100.0%	6	6	11	0.01%	29.5%	APGAGLGQDR	99.7%	58.2	25	51.8	2	0	0	941.48	212	221
Emerin	EMD	EMD_HUMAN	29.0	100.0%	6	6	11	0.01%	29.5%	GDADMYDLPK	99.4%	35.7	25	35.7	2	0	0	1124.49	69	78
Emerin	EMD	EMD_HUMAN	29.0	100.0%	6	6	11	0.01%	29.5%	GYNDDYYEESYFTTR	99.7%	72.3	25	72.3	2	0	0	1922.77	89	103
Emerin	EMD	EMD_HUMAN	29.0	100.0%	6	6	11	0.01%	29.5%	KEDALLYQSK	99.7%	65.2	25	52.2	2	0	0	1194.64	79	88
Emerin	EMD	EMD_HUMAN	29.0	100.0%	6	6	11	0.01%	29.5%	KIFEYETQR	99.4%	36	25	26.3	2	0	0	1213.62	37	45
Emerin	EMD	EMD_HUMAN	29.0	100.0%	6	6	11	0.01%	29.5%	LSPPSSSAASSYSFSDLNSTR	99.7%	42.1	25	42.1	1	0	0	2161.00	48	68
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	5	5	8	0.01%	7.9%	DISTNYYASQK	99.7%	61.8	25	60.8	2	0	0	1289.60	672	682
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	5	5	8	0.01%	7.9%	ELISNASDALDK	99.7%	86.8	25	76	6	0	0	1275.64	103	114
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	5	5	8	0.01%	7.9%	ELISNASDALDKIR	99.7%	92.4	25	73.6	7	2	0	1544.83	103	116
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	5	5	8	0.01%	7.9%	FAFQAEVNR	99.7%	40.3	25	23.4	1	0	0	1081.54	76	84
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	5	5	8	0.01%	7.9%	GVVDSDDLPLNVSR	99.7%	79.6	25	75.7	2	0	0	1485.75	435	448
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	5	5	8	0.01%	7.9%	LIINSLYK	99.7%	39.2	25	24.6	2	0	0	963.59	88	95

Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	5	5	8	0.01%	7.9%	TFEINPR	99.3%	35.5	25	25.9	1	0	0	876.46	684	690
Enhancer of mRNA-decapping protein 3	EDC3	EDC3_HUMAN	56.1	100.0%	4	5	10	0.01%	9.1%	AAVAWANQNR	98.6%	32.4	25	12.6	2	0	0	1100.56	427	436
Enhancer of mRNA-decapping protein 3	EDC3	EDC3_HUMAN	56.1	100.0%	4	5	10	0.01%	9.1%	AGDITELK	99.5%	37.2	25	12.6	2	0	0	846.46	56	63
Enhancer of mRNA-decapping protein 3	EDC3	EDC3_HUMAN	56.1	100.0%	4	5	10	0.01%	9.1%	KPASSSSAPQNIPK	99.7%	66.4	25	57.6	2	0	0	1411.75	106	119
Enhancer of mRNA-decapping protein 3	EDC3	EDC3_HUMAN	56.1	100.0%	4	5	10	0.01%	9.1%	MLESITNELSLFSK	99.7%	53.4	25	53.4	4	0	0	1627.82	374	387
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	4	6	11	0.01%	41.3%	ADTQTYQPYNK	99.7%	41.6	25	39.6	2	0	0	1328.61	74	84
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	4	6	11	0.01%	41.3%	IYVLLRR	97.3%	29.6	25	12.1	2	0	0	932.60	91	97
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	4	6	11	0.01%	41.3%	MYEEHLKR	99.5%	36.4	25	30.9	3	0	0	1105.55	35	42
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	4	6	11	0.01%	41.3%	TYADYESVNECMEGVCK	99.7%	90.9	25	90.9	4	0	0	2070.81	18	34
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	9	11	23	0.02%	37.6%	AFAAGADIK	98.7%	32.5	25	16.8	2	0	0	863.46	93	101
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	9	11	23	0.02%	37.6%	ALNALCDGLIDELNQALK	99.7%	98.8	25	98.8	2	0	0	1971.02	57	74
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	9	11	23	0.02%	37.6%	AQFAQPEILIGTIPGAGGTQR	99.7%	92.2	25	92.2	2	1	0	2125.14	158	178
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	9	11	23	0.02%	37.6%	EGMTAFVEK	99.7%	45.1	25	37.1	1	0	0	1011.48	274	282
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	9	11	23	0.02%	37.6%	EGMTAFVEKR	99.0%	33.9	25	25.6	1	0	0	1167.58	274	283
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	9	11	23	0.02%	37.6%	EMQNLSFQDCYSSK	99.7%	65.5	25	65.5	2	0	0	1736.73	102	115
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	9	11	23	0.02%	37.6%	LFYSTFATDDRK	99.7%	70.5	25	64.2	2	0	0	1463.72	262	273
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	9	11	23	0.02%	37.6%	NNTVGLIQLNRPK	99.7%	78.5	25	78.5	2	0	0	1466.84	44	56
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	9	11	23	0.02%	37.6%	SLAMEMVLTGDR	99.7%	89.8	25	83.7	8	0	0	1354.63	186	197
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	3	3	7	0.01%	3.9%	FASLEFSPGSK	99.7%	45.5	25	45.5	2	0	0	1169.58	42	52
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	3	3	7	0.01%	3.9%	SLQTLALETEWELR	98.4%	31.7	25	31.7	2	0	0	1688.89	244	257
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	3	3	7	0.01%	3.9%	TFIGIFLIDGVTGR	99.7%	86.1	25	76.1	3	0	0	1508.85	755	768
ER membrane protein complex subunit 3	EMC3	EMC3_HUMAN	30.0	100.0%	3	3	5	0.00%	16.5%	AGPELLLDSNIR	99.7%	59.6	25	50.8	1	0	0	1297.71	2	13
ER membrane protein complex subunit 3	EMC3	EMC3_HUMAN	30.0	100.0%	3	3	5	0.00%	16.5%	LTQEQVSDSQVLIR	99.7%	105	25	81.2	2	0	0	1615.87	44	57
ER membrane protein complex subunit 3	EMC3	EMC3_HUMAN	30.0	100.0%	3	3	5	0.00%	16.5%	SIYSLILGQDNAADQSR	99.7%	104	25	102	2	0	0	1850.92	181	197
ER membrane protein complex subunit 6	EMC6	EMC6_HUMAN	12.0	99.8%	2	2	3	0.00%	20.0%	EGPPFISEAAVR	99.6%	37.8	25	34.8	1	0	0	1272.66	9	20
ER membrane protein complex subunit 6	EMC6	EMC6_HUMAN	12.0	99.8%	2	2	3	0.00%	20.0%	GNAAVLDYCR	99.7%	55.8	25	49.5	2	0	0	1138.53	21	30
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	8	10	17	0.02%	33.8%	ADAEYYAAHK	99.7%	58.1	25	52.1	2	0	0	1138.52	258	267
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	8	10	17	0.02%	33.8%	AKADAEYYAAHK	99.7%	43.7	25	38.7	1	0	0	1337.65	256	267
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	8	10	17	0.02%	33.8%	DLNLMAPGLTIQAVR	99.7%	84.2	25	73.4	4	0	0	1627.88	155	169
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	8	10	17	0.02%	33.8%	EALEPSGENVIQNK	99.7%	95	25	93.3	2	0	0	1527.77	329	342
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	8	10	17	0.02%	33.8%	ESSLPSKEALEPSGENVIQNK	99.7%	41.9	25	32	0	2	0	2256.14	322	342
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	8	10	17	0.02%	33.8%	IPEAIRR	96.7%	28.8	25	15.9	1	0	0	854.52	175	181
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	8	10	17	0.02%	33.8%	ISEIEDAAFLAR	99.7%	105	25	89.3	2	0	0	1334.70	242	253
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	8	10	17	0.02%	33.8%	IYFGSNIPNMFVDSSCALK	99.7%	41.4	25	41.4	3	0	0	2179.02	295	313
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	8	10	17	0.02%	33.8%	NFELMEAEK	97.2%	29.5	25	13.9	2	0	0	1110.51	182	190
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	8	10	17	0.02%	33.8%	SVQTTLQTDEVK	99.7%	81.9	25	66.6	4	0	0	1348.70	61	72
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	8	10	17	0.02%	33.8%	VVEKEAETER	97.6%	30.1	25	26	1	0	0	1189.61	202	211
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	13	15	31	0.03%	37.5%	ADAECYTAMK	99.7%	67.5	25	62.4	4	0	0	1159.48	258	267
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	13	15	31	0.03%	37.5%	AKADAECYTAMK	99.7%	52.5	25	52.5	2	0	0	1358.61	256	267
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	13	15	31	0.03%	37.5%	DIPNMFMDSAGSVSK	99.7%	96.6	25	86.9	5	0	0	1598.72	300	314
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	13	15	31	0.03%	37.5%	IEEGHIGVYYR	99.7%	47.7	25	39.4	1	0	0	1335.67	26	36
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	13	15	31	0.03%	37.5%	ISEIEDAAFLAR	99.7%	105	25	89.3	2	0	0	1334.70	242	253
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	13	15	31	0.03%	37.5%	KISEIEDAAFLAR	99.7%	89.8	25	89.8	2	0	0	1462.79	241	253
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	13	15	31	0.03%	37.5%	LALQQDLTSMAPGLVIQAVR	96.9%	21.9	25	21.9	0	1	0	2140.18	150	169
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	13	15	31	0.03%	37.5%	LTPEYLQLMK	99.7%	54	25	49.1	2	0	0	1251.67	276	285
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	13	15	31	0.03%	37.5%	SVQTTLQTDEVK	99.7%	81.9	25	66.6	4	0	0	1348.70	61	72
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	13	15	31	0.03%	37.5%	VAQVAEITYGQK	99.7%	96.6	25	94.8	4	0	0	1306.70	221	232
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	13	15	31	0.03%	37.5%	VTKPNIPEAIR	99.6%	37.7	25	37.3	1	0	0	1237.73	170	180
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	13	15	31	0.03%	37.5%	VTKPNIPEAIRR	99.6%	28.1	25	21.2	0	2	0	1393.83	170	181
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	13	15	31	0.03%	37.5%	VVEKEAETER	97.6%	30.1	25	26	1	0	0	1189.61	202	211
ERO1-like protein alpha	ERO1L	ERO1A_HUMAN	54.4	100.0%	3	3	4	0.00%	8.1%	FDGILTEGEGPR	99.7%	40	25	40	1	0	0	1290.63	288	299

ERO1-like protein alpha	ERO1L	ERO1A_HUMAN	54.4	100.0%	3	3	4	0.00%	8.1%	LGAVDESLSEETQK	99.7%	66	25	66	1	0	0	1505.73	137	150
ERO1-like protein alpha	ERO1L	ERO1A_HUMAN	54.4	100.0%	3	3	4	0.00%	8.1%	QEIVSLFNAFGR	99.7%	73.8	25	69.8	2	0	0	1380.73	438	449
Erythrocyte band 7 integral membrane protein	STOM	STOM_HUMAN	31.7	99.8%	2	2	4	0.00%	7.6%	AMAAEAEASR	98.4%	31.6	25	25.8	2	0	0	1006.46	206	215
Erythrocyte band 7 integral membrane protein	STOM	STOM_HUMAN	31.7	99.8%	2	2	4	0.00%	7.6%	VIAAEGEMNASR	99.7%	53.1	25	45.8	2	0	0	1263.60	221	232
Estradiol 17-beta-dehydrogenase 11	HSD17B11	DHB11_HUMAN	32.9	100.0%	3	3	4	0.00%	8.7%	FAAVGFHK	99.7%	47.4	25	11.1	2	0	0	876.47	190	197
Estradiol 17-beta-dehydrogenase 11	HSD17B11	DHB11_HUMAN	32.9	100.0%	3	3	4	0.00%	8.7%	FDAVIGYK	99.7%	40.8	25	33.9	1	0	0	912.48	289	296
Estradiol 17-beta-dehydrogenase 11	HSD17B11	DHB11_HUMAN	32.9	100.0%	3	3	4	0.00%	8.7%	LMHGILTEQK	98.4%	31.6	25	24	1	0	0	1169.63	246	255
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	11	31	0.03%	41.3%	GAILNISSGSGMLPVPLLTIYSATK	99.7%	34	25	34	0	1	0	2519.38	182	206
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	11	31	0.03%	41.3%	GVFVQSVLPYFVATK	99.7%	48.1	25	48.1	4	0	0	1654.92	224	238
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	11	31	0.03%	41.3%	ISYSLFTALR	99.7%	83.9	25	74.9	6	0	0	1170.65	26	35
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	11	31	0.03%	41.3%	KPTLDKPSPETFVK	99.6%	28.4	25	23.4	0	2	0	1586.88	244	257
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	11	31	0.03%	41.3%	LDQVSSEIKEK	99.7%	49.1	25	40.3	2	0	0	1275.68	87	97
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	11	31	0.03%	41.3%	MININILSVCK	99.7%	80.1	25	72.7	4	0	0	1304.71	157	167
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	11	31	0.03%	41.3%	MTQLVLPGMVER	99.7%	67.2	25	52.2	8	0	0	1389.72	168	179
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	11	31	0.03%	41.3%	TFVDFFSQCLHEEYR	99.7%	51.4	25	51.4	2	0	0	1977.88	207	221
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	11	31	0.03%	41.3%	TIAVDFASEDIYDKIK	99.7%	91.2	25	91.2	2	0	0	1827.94	104	119
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	8	8	24	0.02%	33.2%	DLLGTVWGGPANLEAIAK	99.7%	56.8	25	56.8	4	0	0	1824.99	284	301
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	8	8	24	0.02%	33.2%	ELYLEEALQNER	99.7%	72.9	25	66.7	3	0	0	1506.74	272	283
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	8	8	24	0.02%	33.2%	LVEIIGSR	99.7%	54	25	44.4	2	0	0	886.54	199	206
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	8	8	24	0.02%	33.2%	NALNIGMVEEVLQSSDETK	99.7%	78.4	25	78.4	1	0	0	2093.01	222	240
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	8	8	24	0.02%	33.2%	NTFSSGSDLNAVK	99.7%	62.7	25	56.5	4	0	0	1339.65	109	121
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	8	8	24	0.02%	33.2%	QFIQGPPEVIR	99.7%	55.8	25	39.1	4	0	0	1283.71	251	261
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	8	8	24	0.02%	33.2%	SLEEAQEWLK	99.7%	59.3	25	51	4	0	0	1232.62	241	250
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	8	8	24	0.02%	33.2%	VIELENWTEGK	99.7%	78.2	25	78.2	2	0	0	1317.67	90	100
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	42	0.04%	47.3%	ATQALVLAPTR	99.7%	68.8	25	58.6	2	0	0	1140.67	100	110
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	42	0.04%	47.3%	DFTVSAMHGDMDQKER	98.4%	24	25	18.1	0	2	0	1882.81	296	311
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	42	0.04%	47.3%	EELTLEGIR	99.7%	46.3	25	34.2	2	0	0	1059.57	239	247
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	42	0.04%	47.3%	ELAQQIQK	98.2%	31.3	25	21.2	1	0	0	957.54	111	118
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	42	0.04%	47.3%	GFKDQIYDIFQK	99.7%	67	25	60.2	2	1	0	1501.77	191	202
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	42	0.04%	47.3%	GIYAYGFEKPSAIQQR	99.7%	72	25	71.1	2	2	0	1827.94	46	61
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	42	0.04%	47.3%	GVAINMVTEEDKR	99.7%	66.6	25	66.6	2	0	0	1461.74	370	382
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	42	0.04%	47.3%	GYDVIAQAQSGTGK	99.7%	129	25	115	2	0	0	1394.69	69	82
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	42	0.04%	47.3%	KEELTLEGIR	99.7%	53.5	25	37.6	2	0	0	1187.66	238	247
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	42	0.04%	47.3%	KVDWLTEK	95.4%	27.5	25	14.2	1	0	0	1018.56	284	291
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	42	0.04%	47.3%	LNSNTQVVLLSATMPSDVLEVTK	99.7%	63.9	25	63.9	2	0	0	2459.31	203	225
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	42	0.04%	47.3%	LQMEAPHIIVGTPGR	99.7%	66.2	25	66.2	4	4	0	1618.87	147	161
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	42	0.04%	47.3%	MFVLDEADEMLSR	99.7%	110	25	103	7	0	0	1555.71	178	190
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	42	0.04%	47.3%	VLITTDLLAR	99.7%	75.1	25	71.7	2	0	0	1114.68	325	334
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	15	22	42	0.04%	47.3%	VVMALGDYMGASCHACIGGTNVR	99.7%	52.8	25	52.4	0	2	0	2471.09	119	141
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	10	12	21	0.02%	29.2%	ELAVQIQK	99.7%	49.1	25	35	2	0	0	928.55	117	124
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	10	12	21	0.02%	29.2%	ETQALILAPTR	99.7%	61.3	25	49.3	2	0	0	1212.69	106	116
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	10	12	21	0.02%	29.2%	GFKEQIYDVYR	99.7%	53.8	25	53.6	1	0	0	1417.71	196	206
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	10	12	21	0.02%	29.2%	GIYAYGFEKPSAIQQR	99.7%	72	25	71.1	2	2	0	1827.94	52	67
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	10	12	21	0.02%	29.2%	GRDVIAQSQSGTGK	99.7%	89.9	25	85.1	2	2	0	1403.72	75	88
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	10	12	21	0.02%	29.2%	KGVAINFVK	99.7%	47	25	30	2	0	0	975.60	374	382
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	10	12	21	0.02%	29.2%	KLDYGQHVVAGTPGR	99.7%	39.8	25	33.7	0	2	0	1597.84	152	166
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	10	12	21	0.02%	29.2%	KVDWLTEK	95.4%	27.5	25	14.2	1	0	0	1018.56	289	296
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	10	12	21	0.02%	29.2%	LDYGQHVVAGTPGR	99.7%	65.9	25	60.2	1	1	0	1469.75	153	166
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	10	12	21	0.02%	29.2%	QFFVAVER	99.7%	52.2	25	33.3	2	0	0	995.53	253	260
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	10	12	21	0.02%	29.2%	RDELTLEGIK	99.7%	41.3	25	23.5	2	0	0	1173.65	243	252
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	10	12	21	0.02%	29.2%	VLISTDVWAR	99.7%	62.7	25	53.9	2	0	0	1159.65	330	339

Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	5	6	11	0.01%	25.9%	AIVQQWLEYR	99.7%	49.9	25	45	2	0	0	1305.70	69	78
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	5	6	11	0.01%	25.9%	EYLLGSTAEEK	99.7%	58.2	25	51	2	0	0	1239.61	58	68
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	5	6	11	0.01%	25.9%	FIVDLTVQEKEK	99.2%	34.9	25	34.9	2	0	0	1448.80	127	138
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	5	6	11	0.01%	25.9%	NDIHTLLK	98.0%	30.7	25	19.3	2	0	0	953.54	89	96
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	5	6	11	0.01%	25.9%	QANKEYLLGSTAEEK	99.7%	69.3	25	63	2	1	0	1680.84	54	68
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	7	8	16	0.02%	24.8%	AGLNCSTENMPIK	99.7%	58.5	25	58.5	3	0	0	1434.67	214	226
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	7	8	16	0.02%	24.8%	GVFNVQMEPK	99.7%	45.9	25	33.8	2	0	0	1148.58	267	276
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	7	8	16	0.02%	24.8%	NECVVVIR	99.7%	38.8	25	23.9	2	0	0	988.52	68	75
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	7	8	16	0.02%	24.8%	TAWVFDDKYK	99.5%	36.7	25	34	2	0	0	1272.63	134	143
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	7	8	16	0.02%	24.8%	TEGLSVLSQAMAVIK	99.7%	66	25	65.2	2	0	0	1546.85	245	259
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	7	8	16	0.02%	24.8%	VVTDTDETELAR	99.7%	100	25	86.6	4	0	0	1348.66	277	288
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	7	8	16	0.02%	24.8%	YVMTTTTLER	99.1%	34	25	29.8	1	0	0	1230.60	235	244
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	IF2G_HUMAN	51.1	100.0%	2	2	2	0.00%	5.9%	IVLTNPVCTEVGEK	99.7%	59.1	25	59.1	1	0	0	1558.81	427	440
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	IF2G_HUMAN	51.1	100.0%	2	2	2	0.00%	5.9%	VGQEIEVRPGIVSK	99.7%	36.8	25	33.5	0	1	0	1510.86	290	303
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	ANEFLEVGK	99.7%	52.8	25	43.2	3	0	0	1006.52	15	23
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	ANEFLEVGKK	99.2%	34.9	25	14.3	2	0	0	1134.62	15	24
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	AREESWGPPR	99.7%	50.8	25	43.2	2	0	0	1184.58	1184	1193
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	AVEDIHGLFSLSK	99.7%	86.2	25	86.2	4	0	0	1415.75	252	264
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	EDAPIGPHLQSMPSEQIR	99.7%	40.7	25	40.7	0	6	0	2020.98	503	520
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	EEELREYQER	99.4%	36.2	25	25.7	2	0	0	1380.64	838	847
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	EESWGPPR	99.7%	44	25	38	1	0	0	957.44	1186	1193
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	ELEIEERER	99.7%	41.9	25	11.1	1	0	0	1202.60	862	870
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	FCLQYTR	99.7%	43.5	25	35.1	4	0	0	987.47	184	190
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	FLWESYR	99.7%	40	25	30.8	3	0	0	1000.49	152	158
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	FNVLQYVVPEVK	99.7%	77.4	25	62.6	6	0	0	1434.80	377	388
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	GLDEDRGSWR	99.3%	35.3	25	25.2	2	0	0	1190.56	1021	1030
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	IGLINDMVR	99.7%	57.6	25	41.8	9	0	0	1046.57	368	376
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	ILQEHEQIK	99.7%	50.8	25	44.1	5	0	0	1137.63	624	632
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	ITTMQLER	99.7%	59.8	25	40.7	4	0	0	991.52	733	740
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	KGPEADSEWR	99.7%	39.3	25	36.6	2	0	0	1174.55	901	910
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	KIDYFER	99.7%	39.6	25	26.4	4	0	0	970.50	694	700
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	KLCDNLR	97.7%	30.1	25	15.7	1	0	0	918.48	196	202
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	LATLLGLQAPPTR	99.7%	50	25	50	4	0	0	1350.81	355	367
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	LEEIPLIK	97.4%	29.6	25	16.2	2	0	0	954.59	704	711
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	LESLNIQR	99.7%	64.4	25	28.8	4	0	0	972.55	582	589
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	LGDSSLSR	99.7%	55.6	25	42.4	2	0	0	834.43	878	885
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	LKQFEER	99.0%	33.9	25	0	2	0	0	949.51	776	782
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	LLDMDGIIVEK	99.7%	82.2	25	77.7	10	0	0	1245.68	341	351
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	LLLTPWVK	99.7%	42.6	25	21.8	4	0	0	969.61	144	151
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	LLQQVSQIYQSIEFSR	99.7%	67	25	45.8	3	0	0	1939.03	439	454
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	LTSLVPFVDAFQLER	99.7%	79.9	25	79.7	5	0	0	1734.94	455	469
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	LYHDIAQQAFK	99.7%	49.5	25	34.5	3	0	0	1333.69	173	183
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	MHLSQIQR	99.1%	34.1	25	27.9	5	0	0	1028.53	203	210
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	MLEDRDLFVMR	99.7%	29.5	25	24.6	0	1	0	1440.70	753	763
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	NADDDRIPR	99.4%	35.7	25	11.5	2	0	0	1071.52	1122	1130
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	NICQQVNIK	99.7%	45.3	25	27.5	4	0	0	1116.58	76	84
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	NLTQDEMQR	99.4%	35.7	25	29.4	7	0	0	1150.52	309	317
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	NMDDDRLSR	99.7%	43.9	25	36.8	2	0	0	1121.50	1142	1150
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	NQLTAMSSVLAK	99.7%	93.2	25	80.1	9	0	0	1262.68	521	532
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	QCLDLLR	99.7%	42.9	25	4.64	4	0	0	917.49	159	165
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	QPALDVLYDVMK	98.0%	30.7	25	29.5	1	0	0	1407.72	25	36

Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	RGPAEESSSWR	99.7%	56.1	25	56.1	2	0	0	1261.59	1250	1260
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	RLGDSSLSR	99.2%	34.8	25	15	2	0	0	990.53	877	885
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	RVPPPALSR	98.3%	31.5	25	20	1	0	0	992.60	1329	1337
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	SGNALFHASTLHR	99.7%	51.1	25	50.6	1	5	0	1410.72	286	298
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	SLEDVVR	99.6%	37.6	25	10.6	2	0	0	817.44	85	91
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	TLSFGSDLNYATR	99.7%	86	25	79.9	6	0	0	1444.71	490	502
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	44	51	161	0.16%	30.0%	VLLATLSIPITPER	99.7%	69.8	25	69.8	7	0	0	1522.92	322	335
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	23	26	90	0.09%	32.3%	AQAVSEDAGGNEGR	99.7%	104	25	104	7	0	0	1360.61	121	134
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	23	26	90	0.09%	32.3%	DQYSVIFESGDR	99.7%	70.6	25	62.1	2	0	0	1415.64	304	315
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	23	26	90	0.09%	32.3%	ETIIAFAWEPNGSK	99.7%	71.9	25	62	3	0	0	1562.79	563	576
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	23	26	90	0.09%	32.3%	FAVLHGEAPR	99.7%	50.4	25	44.2	4	0	0	1096.59	577	586
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	23	26	90	0.09%	32.3%	FSHQGVQLIDFSPCER	99.7%	43.3	25	43.3	0	2	0	1919.91	371	386
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	23	26	90	0.09%	32.3%	GIALWGGEK	99.7%	42.3	25	34.4	4	0	0	930.50	356	364
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	23	26	90	0.09%	32.3%	GTQGVVTNFEIFR	99.7%	90.7	25	90.7	11	0	0	1467.76	536	548
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	23	26	90	0.09%	32.3%	GTYLATFHQR	99.7%	73.7	25	63.9	8	0	0	1193.61	346	355
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	23	26	90	0.09%	32.3%	GYIFLEYASPAHAVDAVK	99.7%	90.1	25	90.1	2	2	0	1951.00	231	248
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	23	26	90	0.09%	32.3%	ISVSFYHVK	98.6%	32.3	25	20.2	4	0	0	1079.59	587	595
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	23	26	90	0.09%	32.3%	ITNDFYPEEDGK	99.7%	66.2	25	66.2	2	0	0	1427.63	217	228
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	23	26	90	0.09%	32.3%	ITNDFYPEEDGKTK	99.7%	73.4	25	73.4	2	2	0	1656.78	217	230
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	23	26	90	0.09%	32.3%	MAQELYMEQK	99.7%	78.7	25	61.3	8	0	0	1270.58	763	772
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	23	26	90	0.09%	32.3%	MTLDTLSIYETPSMGLLDK	99.7%	53.2	25	48.5	2	0	0	2128.06	441	459
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	23	26	90	0.09%	32.3%	NADGYKLDK	99.3%	35.6	25	28.1	1	0	0	1023.51	249	257
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	23	26	90	0.09%	32.3%	NGDYLCVK	99.7%	54.9	25	45.1	2	0	0	968.45	522	529
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	23	26	90	0.09%	32.3%	NLFNVVDCK	99.7%	52.2	25	45.3	6	0	0	1108.55	508	516
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	23	26	90	0.09%	32.3%	QVPVDVVEMK	99.7%	52.2	25	39.1	3	0	0	1143.61	553	562
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	23	26	90	0.09%	32.3%	TMMEDFRK	98.9%	33.5	25	26.2	2	0	0	1057.48	752	759
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	23	26	90	0.09%	32.3%	TSIFWNDVKDPVSIEER	99.7%	43.9	25	43.9	0	2	0	2035.01	316	332
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	23	26	90	0.09%	32.3%	VDNAYWLWTFQGR	99.7%	75.1	25	74.1	2	0	0	1655.80	677	689
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	23	26	90	0.09%	32.3%	VTLMQLPTR	99.7%	65.9	25	50.3	6	0	0	1058.60	493	501
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	23	26	90	0.09%	32.3%	YVVTSVSWWSHK	98.9%	33.4	25	33.4	1	0	0	1478.74	665	676
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	15	16	27	0.03%	15.9%	CLEEFELLGK	99.7%	48.8	25	33.5	1	0	0	1237.61	79	88
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	15	16	27	0.03%	15.9%	DAHNALLDIQSSGR	99.7%	48.7	25	48.7	1	0	0	1496.75	628	641
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	15	16	27	0.03%	15.9%	DFESHITSYK	99.6%	37.3	25	24.3	2	0	0	1226.57	151	160
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	15	16	27	0.03%	15.9%	ELLGQGLLLR	99.7%	62.2	25	44.7	2	0	0	1111.68	644	653
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	15	16	27	0.03%	15.9%	FEELTNLIR	99.7%	61.3	25	39.6	2	0	0	1134.62	57	65
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	15	16	27	0.03%	15.9%	GCILTLVER	99.7%	67.7	25	51	2	0	0	1060.58	442	450
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	15	16	27	0.03%	15.9%	GTEITHAVVIK	99.7%	55.4	25	41.6	2	0	0	1167.67	321	331
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	15	16	27	0.03%	15.9%	KIQEESLR	99.7%	56.6	25	38	1	0	0	1002.56	782	789
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	15	16	27	0.03%	15.9%	KLNEILQAR	99.7%	49	25	27.2	2	0	0	1084.65	332	340
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	15	16	27	0.03%	15.9%	LGSLVENNER	99.7%	62.4	25	49.1	2	0	0	1130.58	863	872
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	15	16	27	0.03%	15.9%	LNEILQAR	99.7%	54.2	25	41.6	2	0	0	956.55	333	340
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	15	16	27	0.03%	15.9%	QGTYGGYFR	99.7%	41.5	25	33.4	1	0	0	1048.48	878	886
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	15	16	27	0.03%	15.9%	SIVDKEGVPR	99.4%	36.3	25	26	2	0	0	1099.61	95	104
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	15	16	27	0.03%	15.9%	TCHSFIINEK	99.4%	36.1	25	24.5	2	1	0	1248.60	751	760
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	15	16	27	0.03%	15.9%	TEPTAQQNLALQLAEK	99.7%	93.3	25	91.3	2	0	0	1754.93	847	862
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	9	9	23	0.02%	17.5%	GAVIATELK	99.6%	38.1	25	18.9	2	0	0	901.54	418	426
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	9	9	23	0.02%	17.5%	GAVIATELKNNSYK	99.7%	71.3	25	54.1	2	0	0	1507.81	418	431
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	9	9	23	0.02%	17.5%	IFHTVTTTDDPVIR	99.7%	64.1	25	56.2	2	0	0	1614.85	223	236
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	9	9	23	0.02%	17.5%	LGDDIDLIVR	99.7%	86.9	25	69	4	0	0	1128.63	365	374
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	9	9	23	0.02%	17.5%	NMLQFNLQILPK	99.7%	58.6	25	50.1	4	0	0	1458.81	113	124
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	9	9	23	0.02%	17.5%	SVYSWDIVVQR	99.7%	59.8	25	58.6	3	0	0	1351.70	261	271

Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	9	9	23	0.02%	17.5%	TLNEWDSR	97.5%	29.8	25	26.7	1	0	0	1020.47	395	402
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	9	9	23	0.02%	17.5%	VADWTGATYQDKR	99.7%	76.8	25	76.8	4	0	0	1510.73	42	54
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	9	9	23	0.02%	17.5%	WTCCALLAGSEYLK	99.7%	52.5	25	51.9	1	0	0	1671.79	435	448
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	53	0.05%	44.7%	EIYNEKELLQGK	99.7%	47.7	25	29	2	0	0	1463.77	30	41
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	53	0.05%	44.7%	ETIDNNSVSSPLQSLQQR	99.7%	100	25	92.7	1	0	0	2016.00	194	211
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	53	0.05%	44.7%	FQYECGNYSGAAEYLYFFR	99.7%	85.9	25	85.9	1	0	0	2385.03	137	155
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	53	0.05%	44.7%	IAHFLDR	99.7%	41.9	25	21.9	2	0	0	871.48	10	16
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	53	0.05%	44.7%	LFIFETFCR	99.7%	58.6	25	48.9	5	0	0	1232.61	338	346
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	53	0.05%	44.7%	LGHVVMGNNAVSPYQQVIEK	99.7%	62.4	25	62.1	0	2	0	2199.12	388	407
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	53	0.05%	44.7%	LKETIDNNSVSSPLQSLQQR	99.7%	102	25	102	1	2	0	2257.18	192	211
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	53	0.05%	44.7%	LNMTPEEAER	99.7%	39.7	25	33	1	0	0	1189.55	360	369
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	53	0.05%	44.7%	MFEDPETTR	99.7%	48.2	25	31.6	4	0	0	1141.48	94	102
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	53	0.05%	44.7%	MLFDYLADK	99.7%	58.2	25	41.2	4	0	0	1115.54	112	120
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	53	0.05%	44.7%	NLYSDDIPHALR	99.7%	61.2	25	53.5	3	2	0	1413.71	60	71
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	53	0.05%	44.7%	QLQAETEPIVK	99.7%	54.7	25	39.9	3	0	0	1255.69	83	93
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	53	0.05%	44.7%	RTTVVAQLK	99.7%	39.3	25	31.3	2	0	0	1015.63	74	82
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	53	0.05%	44.7%	SEAPNWATQDSGFY	99.7%	73.9	25	73.9	2	0	0	1572.66	432	445
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	53	0.05%	44.7%	SQMLAMNIEK	99.7%	58.5	25	43.5	4	0	0	1164.58	415	424
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	53	0.05%	44.7%	TTVVAQLK	99.5%	36.9	25	18.7	2	0	0	859.52	75	82
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	53	0.05%	44.7%	VLVPATDR	97.2%	29.4	25	23.9	1	0	0	870.50	156	163
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	53	0.05%	44.7%	WIVNLIR	99.7%	39.6	25	12.8	2	0	0	913.56	370	376
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	53	0.05%	44.7%	YLTTAVITNK	99.7%	68.6	25	66	5	0	0	1123.64	256	265
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	53	0.05%	44.7%	YLTTAVITNKDVR	99.7%	63.1	25	56.8	2	0	0	1493.83	256	268
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	9	17	0.02%	22.1%	AYVSTLMGVPGR	99.7%	48.3	25	44.7	4	0	0	1250.66	215	226
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	9	17	0.02%	22.1%	FLMSLVNQVPK	99.7%	71.8	25	51.8	2	0	0	1275.71	307	317
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	9	17	0.02%	22.1%	IGVDLIMK	99.2%	34.4	25	19	2	0	0	904.52	247	254
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	9	17	0.02%	22.1%	TMGVMFTPLTVK	99.7%	40.5	25	38.9	3	0	0	1324.70	227	238
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	9	17	0.02%	22.1%	VIGLSSDLQQVGGASAR	99.7%	133	25	133	2	0	0	1657.89	262	278
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	9	17	0.02%	22.1%	VIGTLLGTVDK	99.7%	52.2	25	49.1	2	0	0	1115.67	116	126
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	9	17	0.02%	22.1%	YAYYDTER	99.7%	46.4	25	46.4	2	0	0	1080.46	239	246
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	6	6	12	0.01%	19.7%	EKLPGELEPVQATQNK	99.7%	44.8	25	41.6	0	2	0	1780.94	194	209
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	6	6	12	0.01%	19.7%	ELAEQLGLSTGEK	99.7%	68.4	25	67.8	2	0	0	1374.71	181	193
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	6	6	12	0.01%	19.7%	ETDLQELFRPFGSISR	99.7%	35.1	25	35.1	0	2	0	1894.97	252	267
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	6	6	12	0.01%	19.7%	GFAFISFHR	99.7%	43	25	32.9	2	0	0	1081.56	281	289
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	6	6	12	0.01%	19.7%	LPGELEPVQATQNK	99.7%	62.9	25	60	2	0	0	1523.81	196	209
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	6	6	12	0.01%	19.7%	VTNLSEDTR	99.5%	37	25	19.5	2	0	0	1034.51	243	251
Eukaryotic translation initiation factor 3 subunit H	EIF3H	EIF3H_HUMAN	39.9	100.0%	3	3	6	0.01%	11.9%	EGTGSTATSSSSTAGAAGK	99.7%	85.6	25	76.7	2	0	0	1627.74	6	24
Eukaryotic translation initiation factor 3 subunit H	EIF3H	EIF3H_HUMAN	39.9	100.0%	3	3	6	0.01%	11.9%	LFMAQALQEYNN	99.7%	71	25	71	2	0	0	1441.68	341	352
Eukaryotic translation initiation factor 3 subunit H	EIF3H	EIF3H_HUMAN	39.9	100.0%	3	3	6	0.01%	11.9%	QVQIDGLVVLK	99.7%	53.8	25	47.8	2	0	0	1211.74	38	48
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	11	12	25	0.02%	32.9%	DMTMFVTASK	99.7%	63.3	25	57.8	4	0	0	1130.52	199	208
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	11	12	25	0.02%	32.9%	DPIVNVWYSVNGER	99.7%	45.5	25	45.5	2	0	0	1647.81	31	44
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	11	12	25	0.02%	32.9%	EGDLLFTVAK	99.7%	57.3	25	56.2	2	0	0	1092.59	21	30
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	11	12	25	0.02%	32.9%	HVLTGSADNSCR	99.7%	62.4	25	62	2	0	0	1316.60	66	77
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	11	12	25	0.02%	32.9%	IGKFEAR	99.3%	35.5	25	26.6	2	0	0	820.47	262	268
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	11	12	25	0.02%	32.9%	LFDSTTLEHQK	99.7%	63.2	25	48.7	2	0	0	1318.66	214	224
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	11	12	25	0.02%	32.9%	QINDIQLSR	99.7%	71.1	25	19.3	2	0	0	1086.59	190	198
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	11	12	25	0.02%	32.9%	SGEVLVNVK	99.7%	88.3	25	79.7	2	0	0	944.54	177	185
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	11	12	25	0.02%	32.9%	SGEVLVNVKEHSR	99.7%	34	25	34	0	2	0	1453.78	177	189
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	11	12	25	0.02%	32.9%	SITQIKYNR	99.4%	36	25	34.7	1	0	0	1122.63	12	20
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	11	12	25	0.02%	32.9%	SYSSGGEDGYVR	99.7%	51.3	25	51.3	4	0	0	1276.54	299	310
Eukaryotic translation initiation factor 3 subunit K	EIF3K	EIF3K_HUMAN	25.1	100.0%	5	6	12	0.01%	26.1%	ALTNLPHTDFTLCK	99.7%	50.8	25	41.8	2	0	0	1630.83	73	86

Eukaryotic translation initiation factor 3 subunit K	EIF3K	EIF3K_HUMAN	25.1	100.0%	5	6	12	0.01%	26.1%	CMIDQAHQEERPIR	99.0%	25.5	25	25.5	0	1	0	1798.83	87	100
Eukaryotic translation initiation factor 3 subunit K	EIF3K	EIF3K_HUMAN	25.1	100.0%	5	6	12	0.01%	26.1%	ENAYDLEANLAVLK	99.7%	95.7	25	82.4	2	0	0	1562.81	39	52
Eukaryotic translation initiation factor 3 subunit K	EIF3K	EIF3K_HUMAN	25.1	100.0%	5	6	12	0.01%	26.1%	GIDRYNPENLATLER	99.7%	78.2	25	78.2	3	2	0	1760.89	17	31
Eukaryotic translation initiation factor 3 subunit K	EIF3K	EIF3K_HUMAN	25.1	100.0%	5	6	12	0.01%	26.1%	YNPENLATLER	99.7%	58.3	25	46.7	2	0	0	1319.66	21	31
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	56	0.06%	40.6%	EPFLQQLK	98.9%	33.1	25	5.12	1	0	0	1002.56	438	445
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	56	0.06%	40.6%	IDESIHLQLR	99.7%	47.4	25	39.1	1	2	0	1223.67	382	391
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	56	0.06%	40.6%	KSEEEIDFLR	99.7%	60.8	25	57.4	2	0	0	1265.64	207	216
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	56	0.06%	40.6%	LAGFLDLTEQEFR	99.7%	96.6	25	91.1	5	0	0	1538.79	475	487
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	56	0.06%	40.6%	LHSLLGDYYQAIK	99.7%	63.3	25	59.2	2	2	0	1520.81	280	292
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	56	0.06%	40.6%	LYTTMPVAK	99.7%	48.8	25	35.8	2	0	0	1039.55	466	474
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	56	0.06%	40.6%	MLGYFSLVGLLR	99.7%	71.2	25	65.8	3	0	0	1384.77	268	279
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	56	0.06%	40.6%	NFIQYFHK	94.8%	27	25	9.78	1	0	0	1096.56	54	61
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	56	0.06%	40.6%	QDLAYER	98.3%	31.4	25	20.4	2	0	0	894.43	32	38
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	56	0.06%	40.6%	QLEVYTSGGDPESVAGEYGR	99.7%	115	25	115	2	0	0	2113.97	243	262
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	56	0.06%	40.6%	QYEQQTYQVIPEVIK	99.7%	64.2	25	61	2	0	0	1865.96	39	53
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	56	0.06%	40.6%	SEEEIDFLR	99.7%	51.6	25	43.8	2	0	0	1137.54	208	216
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	56	0.06%	40.6%	TTYKYEMINK	99.0%	33.7	25	26.6	2	0	0	1290.64	353	362
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	56	0.06%	40.6%	TVSDLIDQK	98.4%	31.8	25	21	1	0	0	1018.54	62	70
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	56	0.06%	40.6%	VFANILLYIQR	98.5%	32	25	32	1	0	0	1349.79	335	345
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	56	0.06%	40.6%	VFSDEVQQQAQLSTIR	99.7%	111	25	105	5	0	0	1848.95	446	461
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	56	0.06%	40.6%	VLENIELNKK	99.7%	62.7	25	45.8	2	2	0	1199.70	293	302
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	56	0.06%	40.6%	VSGGPSLEQR	99.7%	70	25	56.1	2	0	0	1029.53	144	153
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	56	0.06%	40.6%	VSSDVIDQK	99.7%	58.1	25	35.8	4	0	0	990.51	79	87
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	56	0.06%	40.6%	VYEIQDIYENSWTK	99.7%	98.3	25	98.3	2	0	0	1787.85	88	101
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	56	0.06%	40.6%	VYELQASR	99.7%	57.7	25	45.2	4	0	0	965.51	71	78
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	22	25	56	0.06%	40.6%	YGDFFIR	99.7%	51.8	25	33.6	2	0	0	917.45	539	545
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	15	0.01%	10.6%	FLLQDTVELR	99.7%	55.1	25	40.4	2	0	0	1233.68	296	305
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	15	0.01%	10.6%	GLSFLFPLLK	99.7%	63.8	25	54.6	2	0	0	1134.69	723	732
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	15	0.01%	10.6%	GVILLIVDK	99.7%	50.5	25	50.5	3	0	0	969.63	113	121
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	15	0.01%	10.6%	SDFFLEGPFMPPR	99.6%	38.4	25	33.4	2	0	0	1539.73	348	360
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	15	0.01%	10.6%	SYLAQFAAR	99.7%	52.5	25	38.9	2	0	0	1026.54	641	649
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	15	0.01%	10.6%	TAGNSEFLGK	98.3%	31.3	25	30.9	1	0	0	1023.51	32	41
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	15	0.01%	10.6%	TNPPLIQEKPAK	98.8%	33	25	29.9	1	0	0	1335.76	521	532
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	15	0.01%	10.6%	TQTPPLGQTPQLGLK	99.1%	34	25	34	1	0	0	1578.89	506	520
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	15	0.01%	10.6%	VIILSLDR	99.7%	41.5	25	34.2	1	0	0	928.58	585	592
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	11	14	53	0.05%	20.5%	AASIFGGAKPVDTAAR	99.7%	59.8	25	53.8	7	7	0	1531.82	357	372
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	11	14	53	0.05%	20.5%	ARPATDSFDDYPPR	99.5%	37.2	25	25.5	2	0	0	1607.75	201	214
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	11	14	53	0.05%	20.5%	DENKVDGMNAPK	98.8%	33	25	25.1	1	0	0	1317.61	526	537
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	11	14	53	0.05%	20.5%	GDDSFGDKYR	99.3%	35.1	25	28.5	1	0	0	1159.50	216	225
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	11	14	53	0.05%	20.5%	GLNISAVR	99.7%	60.2	25	35.9	6	0	0	829.49	118	125
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	11	14	53	0.05%	20.5%	QLDEPKLER	98.1%	31	25	18	1	0	0	1127.61	390	398
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	11	14	53	0.05%	20.5%	SILPTAPR	99.7%	39.1	25	29.5	2	0	0	854.51	71	78
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	11	14	53	0.05%	20.5%	SQSSDTEQQSPTSGGGK	99.7%	106	25	106	4	0	0	1680.73	495	511
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	11	14	53	0.05%	20.5%	STPKEDDSSASTSQSTR	99.7%	74.4	25	74.4	4	2	0	1783.79	340	356
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	11	14	53	0.05%	20.5%	VAPAQPSEEGPGR	99.7%	61.2	25	52.2	13	0	0	1294.64	512	524
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	11	14	53	0.05%	20.5%	VAPAQPSEEGPGRK	99.7%	41.5	25	32.8	2	1	0	1422.73	512	525
Eukaryotic translation initiation factor 6	EIF6	IF6_HUMAN	26.6	99.8%	2	2	3	0.00%	9.8%	LNEAQPSTIATSMR	99.7%	59.5	25	59.5	2	0	0	1534.75	224	237
Eukaryotic translation initiation factor 6	EIF6	IF6_HUMAN	26.6	99.8%	2	2	3	0.00%	9.8%	NSLPDTVQIR	96.1%	28.1	25	21.2	1	0	0	1142.62	86	95
Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	ECSIT	ECSIT_HUMAN	49.1	100.0%	3	3	5	0.00%	10.7%	ALVPFEDLFGQAPGGER	99.7%	58.9	25	57.5	2	0	0	1802.91	68	84
Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	ECSIT	ECSIT_HUMAN	49.1	100.0%	3	3	5	0.00%	10.7%	DLAVYNQLLNIFPK	99.7%	43.1	25	43.1	1	0	0	1647.91	125	138
Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	ECSIT	ECSIT_HUMAN	49.1	100.0%	3	3	5	0.00%	10.7%	DLPQDPVELAMFGLR	99.7%	62.1	25	59.4	2	0	0	1700.87	218	232

Exocyst complex component 2	EXOC2	EXOC2_HUMAN	104.1	100.0%	5	5	7	0.01%	5.8%	ASNTADTLFQEVLGR	99.7%	92	25	81.7	2	0	0	1621.82	249	263
Exocyst complex component 2	EXOC2	EXOC2_HUMAN	104.1	100.0%	5	5	7	0.01%	5.8%	FLFNLPLNIER	97.5%	29.9	25	23.9	1	0	0	1375.77	282	292
Exocyst complex component 2	EXOC2	EXOC2_HUMAN	104.1	100.0%	5	5	7	0.01%	5.8%	GALLPLSIR	98.6%	32.1	25	32.1	1	0	0	939.60	519	527
Exocyst complex component 2	EXOC2	EXOC2_HUMAN	104.1	100.0%	5	5	7	0.01%	5.8%	VIEAVSEELSR	99.7%	63.2	25	43.1	2	0	0	1231.65	828	838
Exocyst complex component 2	EXOC2	EXOC2_HUMAN	104.1	100.0%	5	5	7	0.01%	5.8%	YYAEVETR	96.3%	28.3	25	24.7	1	0	0	1030.48	324	331
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	5	5	8	0.01%	7.5%	DASVPLIDVTNLPTPR	99.7%	80.9	25	71.6	2	0	0	1707.93	224	239
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	5	5	8	0.01%	7.5%	ESEVLIGNLGDK	99.7%	59.8	25	51.7	2	0	0	1273.66	682	693
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	5	5	8	0.01%	7.5%	SGELQGGPDDNLIEGGGTK	99.7%	47.1	25	47.1	1	0	0	1843.87	468	486
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	5	5	8	0.01%	7.5%	SQTGVGELTTQNTR	99.7%	69.5	25	64.1	1	0	0	1491.74	935	948
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	5	5	8	0.01%	7.5%	STTQVADSGYQR	99.7%	69.5	25	69.5	2	0	0	1312.61	314	325
Exocyst complex component 5	EXOC5	EXOC5_HUMAN	81.9	99.7%	2	2	2	0.00%	3.0%	LIQNVFEIK	94.6%	26.8	25	15.3	1	0	0	1103.65	275	283
Exocyst complex component 5	EXOC5	EXOC5_HUMAN	81.9	99.7%	2	2	2	0.00%	3.0%	NVDTVLMELGVR	99.0%	33.5	25	25.3	1	0	0	1345.71	598	609
Exocyst complex component 6	EXOC6	EXOC6_HUMAN	93.7	100.0%	3	3	3	0.00%	4.1%	HAAEGEIYTK	97.2%	29.3	25	29.3	1	0	0	1118.55	595	604
Exocyst complex component 6	EXOC6	EXOC6_HUMAN	93.7	100.0%	3	3	3	0.00%	4.1%	TLSSCLLNLIR	98.8%	32.8	25	17.6	1	0	0	1289.72	528	538
Exocyst complex component 6	EXOC6	EXOC6_HUMAN	93.7	100.0%	3	3	3	0.00%	4.1%	VNPNTALTLLEK	99.7%	40	25	40	1	0	0	1312.75	750	761
Exocyst complex component 8	EXOC8	EXOC8_HUMAN	81.8	100.0%	2	2	2	0.00%	3.0%	QLSQQSDGDR	95.7%	27.7	25	11.6	1	0	0	1133.52	30	39
Exocyst complex component 8	EXOC8	EXOC8_HUMAN	81.8	100.0%	2	2	2	0.00%	3.0%	SAMGMFVDAFSK	99.2%	34.7	25	34.7	1	0	0	1290.59	495	506
Exosome complex component CSL4	EXOSC1	EXOS1_HUMAN	21.5	100.0%	3	3	3	0.00%	21.0%	LCNLEEGSPGSGTYTR	99.7%	81.6	25	81.6	1	0	0	1740.79	14	29
Exosome complex component CSL4	EXOSC1	EXOS1_HUMAN	21.5	100.0%	3	3	3	0.00%	21.0%	SFRPGDIVLAK	99.7%	38.8	25	23.2	1	0	0	1202.69	121	131
Exosome complex component CSL4	EXOSC1	EXOS1_HUMAN	21.5	100.0%	3	3	3	0.00%	21.0%	SSENGALPVVSVVR	99.7%	47	25	46	1	0	0	1413.77	44	57
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	6	6	12	0.01%	25.7%	ELALALQEALEPAVR	99.7%	49.8	25	48.3	2	0	0	1622.91	121	135
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	6	6	12	0.01%	25.7%	GGGPAGAGGEAPAALR	99.7%	67.3	25	65	2	0	0	1308.67	78	93
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	6	6	12	0.01%	25.7%	GSAYLEAGGTK	99.7%	46.9	25	41.4	2	0	0	1053.52	51	61
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	6	6	12	0.01%	25.7%	LGLEGCQR	99.7%	42.2	25	33.6	2	0	0	932.46	243	250
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	6	6	12	0.01%	25.7%	LYPVLQQSLVR	99.7%	56.2	25	48.9	2	0	0	1315.77	251	261
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	6	6	12	0.01%	25.7%	VLCAVSGPR	99.7%	64.1	25	54	2	0	0	958.51	62	70
Exosome complex component RRP4	EXOSC2	EXOS2_HUMAN	32.8	100.0%	4	4	9	0.01%	16.4%	LGQGVLVQVSPSLVK	99.7%	43	25	37.1	3	0	0	1523.92	166	180
Exosome complex component RRP4	EXOSC2	EXOS2_HUMAN	32.8	100.0%	4	4	9	0.01%	16.4%	LIASVAGSVER	99.7%	46	25	34.6	2	0	0	1101.63	52	62
Exosome complex component RRP4	EXOSC2	EXOS2_HUMAN	32.8	100.0%	4	4	9	0.01%	16.4%	NCIISLVTQR	99.7%	47.5	25	37.1	3	0	0	1203.65	239	248
Exosome complex component RRP4	EXOSC2	EXOS2_HUMAN	32.8	100.0%	4	4	9	0.01%	16.4%	YIGEVGDIVVGR	99.7%	50	25	38.6	1	0	0	1276.69	76	87
Exosome complex component RRP41	EXOSC4	EXOS4_HUMAN	26.4	100.0%	3	3	5	0.00%	12.7%	ALAVVYGPHEIR	99.7%	42.5	25	39	2	0	0	1324.74	48	59
Exosome complex component RRP41	EXOSC4	EXOS4_HUMAN	26.4	100.0%	3	3	5	0.00%	12.7%	SCEMGLQLR	99.7%	60.4	25	55	1	0	0	1093.51	96	104
Exosome complex component RRP41	EXOSC4	EXOS4_HUMAN	26.4	100.0%	3	3	5	0.00%	12.7%	VLEAAAQAAR	99.7%	93	25	77.8	2	0	0	999.56	213	222
Exosome complex component RRP43	EXOSC8	EXOS8_HUMAN	30.0	99.8%	2	2	4	0.00%	10.9%	LGNTTVICGVK	99.7%	65.6	25	55.9	2	0	0	1161.63	53	63
Exosome complex component RRP43	EXOSC8	EXOS8_HUMAN	30.0	99.8%	2	2	4	0.00%	10.9%	TTTVNIGSISTADGSALVK	99.7%	89.7	25	88.7	2	0	0	1834.98	34	52
Exosome complex component RRP46	EXOSC5	EXOS5_HUMAN	25.2	100.0%	4	4	7	0.01%	19.1%	ATLEVILRPK	99.6%	38.2	25	38.2	2	0	0	1139.71	74	83
Exosome complex component RRP46	EXOSC5	EXOS5_HUMAN	25.2	100.0%	4	4	7	0.01%	19.1%	AVLTFALDSVER	99.7%	88.4	25	58	2	0	0	1320.72	179	190
Exosome complex component RRP46	EXOSC5	EXOS5_HUMAN	25.2	100.0%	4	4	7	0.01%	19.1%	IGLPGVAEK	97.1%	29.2	25	17.9	1	0	0	883.52	84	92
Exosome complex component RRP46	EXOSC5	EXOS5_HUMAN	25.2	100.0%	4	4	7	0.01%	19.1%	NTCEAVVLGTLHPR	99.7%	67.6	25	67.6	2	0	0	1566.81	100	113
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	25	0.02%	17.7%	AIEEGIPAFTCEEYVK	98.8%	33	25	30	2	0	0	1855.88	184	199
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	25	0.02%	17.7%	AVHEDIVAVELLPK	99.7%	53.9	25	48.8	2	0	0	1532.87	286	299
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	25	0.02%	17.7%	IDSANMNDDITTSLR	99.7%	73	25	71	1	0	0	1665.78	597	611
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	25	0.02%	17.7%	IEDTVFHVFDK	99.7%	59.9	25	55.2	2	0	0	1349.67	896	906
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	25	0.02%	17.7%	IIFSEHLPLSK	99.7%	54	25	46.8	2	0	0	1283.74	226	236
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	25	0.02%	17.7%	IIVAIDGWPR	99.7%	67.5	25	59.9	2	0	0	1139.66	398	407
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	25	0.02%	17.7%	IMLDSSNLQHQK	97.9%	30.5	25	24.6	1	0	0	1429.71	911	922
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	25	0.02%	17.7%	LLAVAIGADCTYPELTDK	99.7%	51.8	25	49.9	1	0	0	1949.99	790	807
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	25	0.02%	17.7%	NAIVVLIPK	99.7%	38.4	25	38.4	2	0	0	966.63	858	866
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	25	0.02%	17.7%	NVIVLQTVLQEVR	99.7%	69.6	25	69.4	3	0	0	1510.90	87	99
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	25	0.02%	17.7%	RGTTVYLCEK	98.0%	30.8	25	22.5	2	0	0	1226.62	526	535
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	25	0.02%	17.7%	SLTANPELIDR	99.5%	37	25	22.4	2	0	0	1228.65	200	210

Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	25	0.02%	17.7%	YADVIVHR	99.7%	48.8	25	37.1	2	0	0	972.53	782	789
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	25	0.02%	17.7%	YGLEGTVFFEEK	99.7%	75.1	25	75.1	1	0	0	1418.68	867	878
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	6	6	11	0.01%	7.9%	AAAEQAISVR	99.7%	61.3	25	37.3	2	0	0	1015.55	759	768
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	6	6	11	0.01%	7.9%	ASGGLPQFGDEYDFYR	95.0%	27.1	25	27.1	1	0	0	1821.81	49	64
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	6	6	11	0.01%	7.9%	FALGSVVAVTK	99.7%	81.3	25	74.8	2	0	0	1091.65	38	48
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	6	6	11	0.01%	7.9%	LAQVQVQK	99.5%	36.6	25	14.3	2	0	0	913.55	726	733
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	6	6	11	0.01%	7.9%	TEDFIIDTLELR	99.7%	79.1	25	63.7	2	0	0	1464.76	335	346
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	6	6	11	0.01%	7.9%	VGILLDEASGVNK	99.7%	79.7	25	76.2	2	0	0	1314.73	124	136
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	26	36	78	0.08%	27.9%	AIIASNIMYIVGQYPR	99.7%	74.8	25	74.5	4	2	0	1808.97	538	553
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	26	36	78	0.08%	27.9%	AVGHPFVIQLGR	99.7%	62	25	60.5	2	2	0	1293.74	701	712
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	26	36	78	0.08%	27.9%	EFAGEDTSDLFLEER	99.7%	93.5	25	85.7	2	0	0	1757.79	1024	1038
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	26	36	78	0.08%	27.9%	EFMKDTDSINLYK	99.7%	48.1	25	43.8	2	0	0	1619.76	443	455
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	26	36	78	0.08%	27.9%	EPEVLSTMAIIVNK	99.7%	84.6	25	81.7	4	0	0	1543.84	797	810
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	26	36	78	0.08%	27.9%	ETLVYLTHLDYVDTER	99.7%	104	25	97.1	2	2	0	1966.98	459	474
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	26	36	78	0.08%	27.9%	FLNVPMFR	99.7%	40.3	25	33.1	2	0	0	1023.54	254	261
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	26	36	78	0.08%	27.9%	IYLDMLNVYK	99.7%	62.3	25	59.6	4	0	0	1271.67	713	722
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	26	36	78	0.08%	27.9%	LISGWVSR	99.7%	49.7	25	32.5	2	0	0	917.52	758	765
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	26	36	78	0.08%	27.9%	LISTLIYK	99.7%	53.4	25	47.9	2	0	0	950.59	246	253
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	26	36	78	0.08%	27.9%	LLSEEVFDFSSGQITQVK	99.7%	96.3	25	96.3	4	0	0	2027.03	173	190
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	26	36	78	0.08%	27.9%	LNMILVQILK	99.7%	54.5	25	34.8	2	0	0	1200.74	130	139
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	26	36	78	0.08%	27.9%	LVLDSIIWAFK	99.7%	82.9	25	82.9	7	0	0	1304.76	873	883
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	26	36	78	0.08%	27.9%	MAKPEEVLVVENDQGEVVR	99.7%	54.3	25	46.5	0	2	0	2157.09	424	442
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	26	36	78	0.08%	27.9%	MAQEVLTHLK	99.7%	62.7	25	46.3	4	0	0	1169.63	45	54
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	26	36	78	0.08%	27.9%	NVDILKDPETVK	99.7%	56.9	25	49.3	2	1	0	1370.75	675	686
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	26	36	78	0.08%	27.9%	QLLDFSQK	97.2%	29.4	25	15	1	0	0	978.53	15	22
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	26	36	78	0.08%	27.9%	QLYLPMLFK	97.0%	29.1	25	19.6	1	0	0	1168.64	407	415
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	26	36	78	0.08%	27.9%	QMLPLNTNIR	99.7%	54.8	25	42.7	2	0	0	1199.66	296	305
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	26	36	78	0.08%	27.9%	SAFPHLQDAQVK	99.7%	56.8	25	46.4	2	0	0	1340.70	984	995
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	26	36	78	0.08%	27.9%	TSESLCQNNMVILK	99.7%	99.2	25	88.7	4	0	0	1636.80	159	172
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	26	36	78	0.08%	27.9%	TSSDPTCVEK	99.7%	52.2	25	33.9	2	0	0	1123.49	113	122
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	26	36	78	0.08%	27.9%	TSSDPTCVEKEK	99.7%	46.2	25	38	2	0	0	1380.63	113	124
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	26	36	78	0.08%	27.9%	VDTILEFSQNMNTK	99.7%	110	25	109	4	0	0	1655.79	63	76
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	26	36	78	0.08%	27.9%	YVVGLIIK	99.7%	43.9	25	32.6	2	0	0	904.59	105	112
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	26	36	78	0.08%	27.9%	YYGLQILENVIK	99.7%	106	25	106	4	0	0	1452.81	77	88
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	AACDLVR	99.7%	40.3	25	27.5	3	0	0	804.40	385	391
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	AADEEAFEDNSEEYIR	99.7%	119	25	119	2	0	0	1887.79	356	371
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	AADEEAFEDNSEEYIRR	99.7%	41.5	25	41.5	1	2	0	2043.89	356	372
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	ALTLPGSSENEYIMK	99.7%	85.6	25	77.3	4	0	0	1652.82	560	574
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	ANIVHLMLSSPEQIQK	99.7%	69.9	25	69.9	3	2	0	1823.97	94	109
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	ATIELCSTHANDASALR	99.7%	107	25	107	2	2	0	1829.88	190	206
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	DAAIYLVTSLASK	99.7%	98.4	25	95.7	2	0	0	1351.75	428	440
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	DLEGSDIDTR	99.7%	49.7	25	37.2	2	0	0	1120.51	373	382
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	DLEGSDIDTRR	99.7%	38.9	25	24.1	2	0	0	1276.61	373	383
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	EHDPVGQMVNNPK	99.7%	70.1	25	68.3	2	2	0	1480.69	913	925
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	FQSGDFHVINGVLR	99.7%	33.6	25	33.6	0	1	0	1588.82	138	151
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	GSNTIASAAADK	99.7%	61.5	25	52.7	2	0	0	1105.55	715	726
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	GSNTIASAAADKIPGLLGVFQK	99.7%	44.2	25	42	0	1	0	2158.19	715	736
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	ICAVGITK	98.9%	33.2	25	20.9	1	0	0	861.49	841	848
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	IHLAQSLHK	99.7%	39.8	25	34.8	2	0	0	1046.61	926	934
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	IIIPEIQK	98.1%	31	25	0	4	0	0	953.60	825	832
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	ILFSSLILISK	99.7%	87.1	25	87.1	2	0	0	1233.78	207	217

Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	IVEDEPNKICEADR	99.7%	102	25	102	2	2	0	1687.80	76	89
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	KICAVGITK	99.7%	42.1	25	30.6	2	0	0	989.58	840	848
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	LLQAFLER	99.7%	57.8	25	35.9	7	0	0	989.58	707	714
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	LLQTDDEEEAGLLELLK	99.7%	118	25	111	2	0	0	1929.01	252	268
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	LLTECPPMMDTEYTK	99.7%	58.8	25	58.8	4	0	0	1860.81	849	863
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	LSTACPGR	94.9%	27	25	20.1	1	0	0	861.42	935	942
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	LVLDAFALPLTNLFK	99.7%	58.2	25	57.2	2	0	0	1674.98	175	189
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	MFGMVLEK	95.4%	27.5	25	19.1	1	0	0	970.47	817	824
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	NLFEDQNTLTSICEK	99.7%	101	25	101	2	0	0	1811.85	332	346
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	QIFILLFQR	99.7%	63.5	25	63.5	6	0	0	1177.71	769	777
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	QLSDAISIIGR	99.7%	90.3	25	65.7	2	0	0	1172.66	110	120
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	SANVNEFPVLK	99.7%	53.4	25	36.2	2	0	0	1217.65	471	481
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	SNELWTEIK	99.7%	50.9	25	39.4	1	0	0	1119.57	166	174
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	SQICDNAALYAQK	99.7%	82.9	25	72.1	2	0	0	1481.71	269	281
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	TGNIPALVR	99.7%	55.7	25	41.8	4	0	0	940.56	698	706
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	TLDPDPAIR	97.4%	29.6	25	27.8	2	0	0	997.53	18	26
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	VIVPNMEFR	99.7%	50.7	25	48.8	2	0	0	1104.59	347	355
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	YDEEFQR	99.7%	43.4	25	43.4	2	0	0	986.42	282	288
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	36	44	95	0.09%	39.6%	YGALALQEIFDGIQPK	99.7%	97.7	25	97.7	3	0	0	1762.94	801	816
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	24	25	47	0.05%	23.2%	AGGFVVGYTSSGNPIFR	99.7%	105	25	105	2	0	0	1728.87	746	762
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	24	25	47	0.05%	23.2%	ALDMLDAEK	99.7%	43.5	25	37.7	2	0	0	1021.49	802	810
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	24	25	47	0.05%	23.2%	ASMTNLVK	94.7%	26.9	25	12.8	1	0	0	863.47	400	407
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	24	25	47	0.05%	23.2%	AVMEQIPEIQK	99.7%	58.1	25	51.2	2	0	0	1285.68	1113	1123
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	24	25	47	0.05%	23.2%	AVTVMMDPNSTQR	99.7%	63.2	25	63.2	2	0	0	1481.67	16	28
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	24	25	47	0.05%	23.2%	DIQQTLTQNMER	99.7%	53.8	25	45.1	3	0	0	1476.71	177	188
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	24	25	47	0.05%	23.2%	DPLLLAIIPK	99.7%	49.3	25	49.3	5	0	0	1092.70	387	396
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	24	25	47	0.05%	23.2%	EVMDLITVCCVSK	99.7%	62.5	25	57.9	2	0	0	1553.74	968	980
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	24	25	47	0.05%	23.2%	FCEEFKEK	99.6%	38.2	25	22.3	2	0	0	1116.50	36	43
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	24	25	47	0.05%	23.2%	IFSFLLNTLQENVNK	99.7%	83.4	25	67.3	2	0	0	1779.96	189	203
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	24	25	47	0.05%	23.2%	IVVEMIKR	98.8%	32.8	25	21.1	2	0	0	987.60	119	126
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	24	25	47	0.05%	23.2%	LFSSVTFETVEESK	99.7%	113	25	111	2	0	0	1602.79	577	590
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	24	25	47	0.05%	23.2%	LIAGCIGKPLGEQFR	99.7%	31.1	25	27.6	0	1	0	1658.91	1153	1167
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	24	25	47	0.05%	23.2%	LLDNLLALIR	99.7%	69.9	25	54.9	3	0	0	1153.73	772	781
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	24	25	47	0.05%	23.2%	LLNPSLQK	99.3%	35.4	25	15.1	2	0	0	912.55	1133	1140
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	24	25	47	0.05%	23.2%	NPCTEQILK	99.7%	44.1	25	34.4	2	0	0	1102.56	763	771
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	24	25	47	0.05%	23.2%	QLLSNELLLTQMEK	99.7%	79.1	25	65.2	2	0	0	1659.90	632	645
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	24	25	47	0.05%	23.2%	SSTQMTWGALFR	99.7%	48.9	25	48.9	1	0	0	1384.67	369	380
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	24	25	47	0.05%	23.2%	TCWPTDLEEAK	96.9%	29	25	29	1	0	0	1349.60	735	745
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	24	25	47	0.05%	23.2%	TDSPSCEYSR	99.7%	41.3	25	41.3	2	0	0	1201.48	414	423
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	24	25	47	0.05%	23.2%	THNTLYAPEMLAK	98.8%	33	25	33	1	0	0	1504.75	782	794
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	24	25	47	0.05%	23.2%	TSFQMAGEWLK	99.7%	56.4	25	50.5	1	0	0	1297.62	457	467
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	24	25	47	0.05%	23.2%	TTSQLCWPLLK	99.7%	45.5	25	44.7	2	0	0	1346.71	1047	1057
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	24	25	47	0.05%	23.2%	VLSDVDAFIAYVGTDQK	99.7%	79.2	25	79.2	2	0	0	1840.93	688	704
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	7	7	10	0.01%	6.5%	AELFELLFR	99.7%	63.9	25	63.9	2	0	0	1137.63	936	944
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	7	7	10	0.01%	6.5%	FCLYFLSSTR	99.5%	36.4	25	32.2	2	0	0	1293.63	47	56
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	7	7	10	0.01%	6.5%	FNDALTVVER	99.7%	59.1	25	51.8	1	0	0	1163.61	580	589
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	7	7	10	0.01%	6.5%	LAEYFIGDVFAAR	99.7%	49.3	25	43.9	2	0	0	1471.76	567	579
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	7	7	10	0.01%	6.5%	MFQQTFYLLQK	99.7%	53.5	25	48.9	1	0	0	1446.75	336	346
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	7	7	10	0.01%	6.5%	NLKPSAVAPQR	99.5%	37.2	25	30.6	1	0	0	1180.68	764	774
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	7	7	10	0.01%	6.5%	STVLASVQR	99.7%	42.6	25	25.6	1	0	0	960.55	956	964
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	20	20	33	0.03%	21.6%	AALSGSYVNFGVFR	99.7%	97.9	25	94.1	2	0	0	1487.76	841	854

Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	20	20	33	0.03%	21.6%	ALVEFTNSPDCLSK	99.7%	55.8	25	47.5	2	0	0	1580.76	33	46
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	20	20	33	0.03%	21.6%	DSSLFDIFTLSCNLLK	99.7%	54.4	25	54.4	1	0	0	1872.94	183	198
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	20	20	33	0.03%	21.6%	GIAFAFNAK	99.7%	41.7	25	29.4	2	0	0	938.51	728	736
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	20	20	33	0.03%	21.6%	GSSSYSQLLAATCLTK	99.7%	108	25	103	2	0	0	1686.84	54	69
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	20	20	33	0.03%	21.6%	IYIGDQVQK	99.7%	41.3	25	29.9	2	0	0	1063.58	560	568
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	20	20	33	0.03%	21.6%	LAASVPYVK	98.3%	31.4	25	31.4	2	0	0	947.56	387	395
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	20	20	33	0.03%	21.6%	LESVHIILR	99.7%	51.3	25	51.3	2	0	0	1079.66	418	426
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	20	20	33	0.03%	21.6%	LMAELVHNR	99.7%	48.4	25	42.6	1	0	0	1082.58	774	782
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	20	20	33	0.03%	21.6%	LQFDVSSPNGILLFR	99.7%	64.9	25	62	2	0	0	1705.93	786	800
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	20	20	33	0.03%	21.6%	LYGDDALDNALQTFIK	99.7%	78.7	25	76.4	2	0	0	1796.91	855	870
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	20	20	33	0.03%	21.6%	NSIVNSQPPEK	99.5%	36.7	25	30.3	1	0	0	1212.62	1021	1031
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	20	20	33	0.03%	21.6%	NYVLNYLATRPK	99.7%	57.1	25	57.1	2	0	0	1451.80	88	99
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	20	20	33	0.03%	21.6%	QLYETTDTTTR	99.7%	42	25	37.6	1	0	0	1328.63	17	27
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	20	20	33	0.03%	21.6%	SNYQLGELVK	99.7%	43.3	25	35.5	2	0	0	1150.61	339	348
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	20	20	33	0.03%	21.6%	TLQLLNDLSIGYSSVR	98.9%	33.2	25	33.2	1	0	0	1778.96	613	628
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	20	20	33	0.03%	21.6%	TNNPLPLEQR	99.7%	48.5	25	34.8	2	0	0	1181.63	74	83
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	20	20	33	0.03%	21.6%	TTFYTALGR	99.7%	54	25	44.8	1	0	0	1029.54	666	674
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	20	20	33	0.03%	21.6%	VENYPEVIR	99.7%	40.9	25	34.8	2	0	0	1118.58	349	357
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	20	20	33	0.03%	21.6%	VLQLMNLTDSR	99.7%	74.2	25	65.5	1	0	0	1289.69	527	537
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	16	19	37	0.04%	20.1%	ALAYFEQLK	99.7%	65.8	25	61.3	2	0	0	1082.59	21	29
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	16	19	37	0.04%	20.1%	ANVEAIMLAVMK	99.7%	84.1	25	78.4	2	0	0	1289.70	370	381
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	16	19	37	0.04%	20.1%	ASALQDMMR	99.7%	58.5	25	54.5	4	0	0	1022.48	475	483
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	16	19	37	0.04%	20.1%	DGPVGFADFVYK	99.7%	63.4	25	63.4	2	0	0	1314.64	860	871
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	16	19	37	0.04%	20.1%	DLQEFIPLINQITAK	99.7%	64.4	25	59.6	2	0	0	1742.97	738	752
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	16	19	37	0.04%	20.1%	FMEVEVAIR	99.7%	58.9	25	50.1	4	0	0	1093.57	443	451
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	16	19	37	0.04%	20.1%	LAQVSPELLLASVR	99.7%	72	25	72	6	0	0	1495.88	415	428
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	16	19	37	0.04%	20.1%	LMLAQDEER	98.5%	31.9	25	11.5	1	0	0	1104.54	635	643
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	16	19	37	0.04%	20.1%	NAQEALQAIETK	99.7%	75.6	25	68.3	2	0	0	1315.69	317	328
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	16	19	37	0.04%	20.1%	QASLADCLNHAVGFASR	99.7%	29	25	29	0	1	0	1816.88	644	660
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	16	19	37	0.04%	20.1%	QLTVLSDQQK	99.1%	34.4	25	24.2	1	0	0	1159.63	360	369
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	16	19	37	0.04%	20.1%	QMNPFIEDILNR	99.7%	38.9	25	38.8	1	0	0	1489.75	558	569
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	16	19	37	0.04%	20.1%	TCFIILSK	99.7%	45.8	25	37	2	0	0	981.54	844	851
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	16	19	37	0.04%	20.1%	VFSSTLQNWQTTR	99.7%	65.8	25	64.3	1	0	0	1567.79	430	442
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	16	19	37	0.04%	20.1%	VLVTVIQGAVEYPDPIAQK	99.7%	104	25	103	2	2	0	2040.14	825	843
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	16	19	37	0.04%	20.1%	YSELTTVQQQLIR	99.7%	86.4	25	78.7	2	0	0	1578.85	68	80
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	6	6	8	0.01%	7.7%	ALALLEDEER	99.7%	51.3	25	45.2	1	0	0	1158.60	163	172
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	6	6	8	0.01%	7.7%	ITVPLVSEVQIAQLR	99.7%	83.2	25	83.2	2	0	0	1665.99	365	379
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	6	6	8	0.01%	7.7%	LLDEWFTLDEVPK	99.7%	54.3	25	52.2	2	0	0	1604.82	484	496
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	6	6	8	0.01%	7.7%	SSSSLLASPGHISVK	99.0%	33.6	25	27.6	1	0	0	1469.80	736	750
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	6	6	8	0.01%	7.7%	VDVGQQPLR	99.7%	43.9	25	36.3	1	0	0	1011.56	240	248
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	6	6	8	0.01%	7.7%	VYTENVDKR	99.0%	33.8	25	20.5	1	0	0	1123.57	254	262
FACT complex subunit SSRP1	SSRP1	SSRP1_HUMAN	81.1	99.8%	2	2	3	0.00%	3.7%	ADVIQATGDAICIFR	99.7%	49.4	25	45.2	1	0	0	1649.83	189	203
FACT complex subunit SSRP1	SSRP1	SSRP1_HUMAN	81.1	99.8%	2	2	3	0.00%	3.7%	FDEISFVNFAR	99.7%	66.5	25	62.3	2	0	0	1344.66	371	381
F-actin-capping protein subunit alpha-1	CAPZA1	CAZA1_HUMAN	32.9	99.8%	2	2	4	0.00%	8.7%	FTITPPTAQVVGVLK	98.8%	32.9	25	32.9	2	0	0	1570.92	179	193
F-actin-capping protein subunit alpha-1	CAPZA1	CAZA1_HUMAN	32.9	99.8%	2	2	4	0.00%	8.7%	LLLNNDNLLR	99.7%	63.1	25	42.3	2	0	0	1197.70	38	47
F-actin-capping protein subunit beta	CAPZB	CAPZB_HUMAN	31.4	99.8%	2	2	3	0.00%	8.3%	RLPPQQIEK	99.4%	36	25	13.3	1	0	0	1108.65	15	23
F-actin-capping protein subunit beta	CAPZB	CAPZB_HUMAN	31.4	99.8%	2	2	3	0.00%	8.3%	SGSGTMNLGGSLTR	99.7%	81.3	25	71.2	2	0	0	1353.64	182	195
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	15	15	21	0.02%	13.8%	DVPLTAEEVEFVVEK	99.7%	68	25	62.9	2	0	0	1703.87	183	197
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	15	15	21	0.02%	13.8%	EGDLTNLLQNQAVK	99.7%	75.8	25	66.5	2	0	0	1542.81	26	39
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	15	15	21	0.02%	13.8%	ETGHVSGPDGQNPEK	99.7%	41.2	25	39.7	2	0	0	1551.70	855	869
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	15	15	21	0.02%	13.8%	FVSSLLTALFR	99.4%	36.3	25	36.3	1	0	0	1253.73	809	819

Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	15	15	21	0.02%	13.8%	GSPCSEEAGTLR	99.7%	49.8	25	49.8	1	0	0	1263.56	53	64
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	15	15	21	0.02%	13.8%	IFQNLCDITR	99.7%	52.9	25	37.9	2	0	0	1279.65	870	879
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	15	15	21	0.02%	13.8%	LSDILNEK	94.8%	27	25	15.3	1	0	0	931.51	781	788
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	15	15	21	0.02%	13.8%	QLINTLCSGR	95.5%	27.6	25	25.9	1	0	0	1161.60	159	168
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	15	15	21	0.02%	13.8%	SADFSQSTSIGIK	99.7%	42.1	25	39.1	1	0	0	1340.67	726	738
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	15	15	21	0.02%	13.8%	SAVAGFLLLLK	99.7%	67.7	25	67.7	2	0	0	1131.71	535	545
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	15	15	21	0.02%	13.8%	SISLLCLEGLQK	99.7%	52.4	25	38.5	1	0	0	1360.75	903	914
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	15	15	21	0.02%	13.8%	SLLNLLSSQEEDFNSK	99.7%	57.2	25	53.4	2	0	0	1823.90	965	980
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	15	15	21	0.02%	13.8%	TAAPTVCLLVLSQAEK	94.9%	27.1	25	23.3	1	0	0	1700.93	1079	1094
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	15	15	21	0.02%	13.8%	VLEEVDWLITK	99.7%	58.6	25	52.4	1	0	0	1344.74	1095	1105
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	15	15	21	0.02%	13.8%	YAVNVALQK	99.7%	46.7	25	40.6	1	0	0	1005.57	841	849
Far upstream element-binding protein 2	KHSRP	FUBP2_HUMAN	73.1	100.0%	4	4	7	0.01%	6.6%	AINQQTGAFVEISR	99.7%	57.3	25	48.2	1	0	0	1533.80	449	462
Far upstream element-binding protein 2	KHSRP	FUBP2_HUMAN	73.1	100.0%	4	4	7	0.01%	6.6%	DAFADAVQR	99.7%	48.1	25	38.1	2	0	0	992.48	72	80
Far upstream element-binding protein 2	KHSRP	FUBP2_HUMAN	73.1	100.0%	4	4	7	0.01%	6.6%	IGGGIDVPVPR	99.7%	78.1	25	65.2	2	0	0	1079.62	321	331
Far upstream element-binding protein 2	KHSRP	FUBP2_HUMAN	73.1	100.0%	4	4	7	0.01%	6.6%	SVSLTGAPESVQK	99.3%	35.4	25	28.4	2	0	0	1302.69	191	203
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	4	4	7	0.01%	7.3%	AAQVMGPPDR	99.7%	47.4	25	47.4	2	0	0	1057.51	300	309
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	4	4	7	0.01%	7.3%	AEGFVDALHR	99.7%	41.2	25	33.5	2	0	0	1114.56	16	25
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	4	4	7	0.01%	7.3%	LLGQIVDR	99.7%	43.3	25	33.2	2	0	0	913.55	140	147
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	4	4	7	0.01%	7.3%	SINQQSGAHVELQR	99.5%	37	25	30.7	1	0	0	1566.80	379	392
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	7	11	20	0.02%	19.6%	ATPEQYQILK	99.2%	34.7	25	19.9	2	0	0	1190.64	344	353
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	7	11	20	0.02%	19.6%	CSWLVVQCLQR	99.7%	68.8	25	62.6	2	0	0	1448.71	333	343
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	7	11	20	0.02%	19.6%	GLTVVVAFR	99.7%	68.7	25	59.2	2	0	0	961.58	127	135
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	7	11	20	0.02%	19.6%	IGTDIQDNK	99.7%	40.7	25	30.5	2	0	0	1003.51	324	332
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	7	11	20	0.02%	19.6%	LKEVLEYNAIGGK	99.7%	74.9	25	68.4	2	2	0	1433.80	111	123
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	7	11	20	0.02%	19.6%	QDFVQHFSQIVR	99.7%	35.3	25	31	1	1	0	1503.77	81	92
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	7	11	20	0.02%	19.6%	VLTEDEMGHPEIGDAIAR	99.7%	70.5	25	66.5	2	4	0	1952.94	93	110
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	7	9	16	0.02%	22.2%	AHPVFYQGTYSQALNDAKR	99.7%	29.2	25	29.2	0	1	0	2166.07	150	168
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	7	9	16	0.02%	22.2%	DLTQEQTEK	99.4%	35.7	25	24.4	1	0	0	1091.52	8	16
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	7	9	16	0.02%	22.2%	ENTYPFLAMIMLK	99.7%	53	25	52.7	2	0	0	1570.80	227	239
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	7	9	16	0.02%	22.2%	FTYYTILDIFR	99.7%	84	25	77.5	3	0	0	1451.76	105	115
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	7	9	16	0.02%	22.2%	HTLEQHNWNIEAAVQDR	99.7%	38.2	25	38.2	0	1	0	2060.99	34	50
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	7	9	16	0.02%	22.2%	IYSYVVSRPQPR	99.6%	28.5	25	28	2	2	0	1464.80	78	89
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	7	9	16	0.02%	22.2%	VTDPVGDIVSFMHSFEEK	99.7%	77.8	25	77.1	2	2	0	2036.96	129	146
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	11	12	16	0.02%	19.9%	DAPIALKR	99.7%	48.9	25	15.6	1	0	0	883.54	320	327
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	11	12	16	0.02%	19.9%	DIISELLTSDDMK	99.7%	67.7	25	58.4	4	0	0	1479.73	523	535
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	11	12	16	0.02%	19.9%	ILVDQQVWK	98.9%	33.3	25	30.6	1	0	0	1128.64	295	303
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	11	12	16	0.02%	19.9%	IVEDPESLNMK	99.7%	40	25	34.7	1	0	0	1274.63	444	454
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	11	12	16	0.02%	19.9%	IYSVEALPVAAVNVQSTQ	99.7%	66.2	25	64	1	0	0	1889.00	693	710
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	11	12	16	0.02%	19.9%	LGIPQNTILVQTLLR	98.7%	32.7	25	25.9	1	0	0	1679.02	242	256
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	11	12	16	0.02%	19.9%	NQVLPLSDVDTTSATDIQR	99.7%	122	25	113	2	0	0	2073.05	615	633
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	11	12	16	0.02%	19.9%	SAYCLGSSHPR	99.7%	53.1	25	52.2	1	0	0	1234.56	642	652
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	11	12	16	0.02%	19.9%	SLILLDECSK	99.4%	36.2	25	32.3	1	0	0	1177.61	359	368
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	11	12	16	0.02%	19.9%	VNLNHEVSNEDVLTK	99.7%	30.1	25	30.1	0	1	0	1710.87	133	147
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	11	12	16	0.02%	19.9%	VVLDNIHGCPLR	99.7%	59.6	25	46.7	2	0	0	1392.74	369	380
FAST kinase domain-containing protein 3	FASTKD3	FAKD3_HUMAN	75.7	99.8%	2	2	2	0.00%	2.7%	ELVEYLQR	99.7%	46.9	25	38.5	1	0	0	1049.56	642	649
FAST kinase domain-containing protein 3	FASTKD3	FAKD3_HUMAN	75.7	99.8%	2	2	2	0.00%	2.7%	IGLTNLLGAR	99.7%	59.9	25	37.3	1	0	0	1027.63	542	551
FAST kinase domain-containing protein 5	FASTKD5	FAKD5_HUMAN	86.6	99.8%	2	2	3	0.00%	3.3%	AAVPLGGFLCNVADK	99.7%	49.4	25	42.2	2	0	0	1531.79	661	675
FAST kinase domain-containing protein 5	FASTKD5	FAKD5_HUMAN	86.6	99.8%	2	2	3	0.00%	3.3%	EATPAENVAK	95.1%	27.2	25	27.2	1	0	0	1029.52	606	615
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	24	25	49	0.05%	11.0%	AALQEELQLCK	99.7%	47.2	25	20.2	2	0	0	1302.67	1132	1142
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	24	25	49	0.05%	11.0%	AGLYGLPR	99.7%	46.3	25	38.4	2	0	0	846.48	42	49
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	24	25	49	0.05%	11.0%	AINCATSGVVGLVNCLR	99.7%	77.8	25	77.3	2	2	0	1803.92	1445	1461

Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	24	25	49	0.05%	11.0%	AQVADVVVSR	99.7%	61	25	48.2	2	0	0	1043.58	1073	1082
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	24	25	49	0.05%	11.0%	DGAWGAFR	99.3%	35.4	25	19.2	1	0	0	879.41	1508	1515
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	24	25	49	0.05%	11.0%	DNLEFFLAGIGR	99.7%	66.3	25	48.2	4	0	0	1351.70	791	802
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	24	25	49	0.05%	11.0%	EDGLAQQQTQLNLR	99.7%	82	25	74.5	2	0	0	1613.82	2207	2220
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	24	25	49	0.05%	11.0%	FDASFFGVHPK	99.7%	54.9	25	45	2	0	0	1251.62	60	70
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	24	25	49	0.05%	11.0%	GLVQALQTK	99.7%	53.7	25	34.2	2	0	0	957.57	1143	1151
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	24	25	49	0.05%	11.0%	GMGLSLMR	99.5%	36.6	25	26.7	2	0	0	864.44	505	512
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	24	25	49	0.05%	11.0%	GVDLVLNSLAEEK	99.7%	52.7	25	42.7	2	0	0	1386.75	1740	1752
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	24	25	49	0.05%	11.0%	HGLYLPTR	99.4%	35.8	25	33.2	2	0	0	956.53	1044	1051
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	24	25	49	0.05%	11.0%	LLEQGLR	99.7%	44.4	25	0	1	0	0	828.49	437	443
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	24	25	49	0.05%	11.0%	LPEDPLLSGLLDSPALK	99.7%	87.5	25	87.5	3	0	0	1778.00	1209	1225
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	24	25	49	0.05%	11.0%	LQVVDQPLPVR	99.7%	57.2	25	54.7	2	0	0	1263.74	374	384
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	24	25	49	0.05%	11.0%	SDEAVKPFGLK	99.7%	60.1	25	53.3	1	0	0	1190.64	523	533
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	24	25	49	0.05%	11.0%	SEGVVAVLLTK	99.7%	64.3	25	56.9	2	0	0	1115.67	225	235
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	24	25	49	0.05%	11.0%	SFYGSTLFLCR	99.7%	61.5	25	46.7	2	0	0	1350.65	1394	1404
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	24	25	49	0.05%	11.0%	TGTVSLEVR	99.7%	68.1	25	54.9	3	0	0	961.53	928	936
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	24	25	49	0.05%	11.0%	TLLEGSGLESIISIIHSSLAEPR	99.7%	55.4	25	55.4	0	1	0	2422.32	2483	2505
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	24	25	49	0.05%	11.0%	VAAAVDLIIK	99.7%	40.8	25	32.9	1	0	0	1012.64	2397	2406
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	24	25	49	0.05%	11.0%	VVEVLAGHGHLYSR	97.9%	23.1	25	20.2	0	1	0	1536.83	1242	1255
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	24	25	49	0.05%	11.0%	VVVQVLAEEPEAVLK	99.7%	92.9	25	75.4	4	0	0	1622.94	1852	1866
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	24	25	49	0.05%	11.0%	YSGTLNLDR	95.0%	27.1	25	22.5	1	0	0	1038.52	1996	2004
FH1/FH2 domain-containing protein 1	FHOD1	FHOD1_HUMAN	126.6	99.8%	2	2	4	0.00%	2.2%	AALLNFDEFAVSK	99.7%	63.3	25	63.3	2	0	0	1424.74	718	730
FH1/FH2 domain-containing protein 1	FHOD1	FHOD1_HUMAN	126.6	99.8%	2	2	4	0.00%	2.2%	FLENVAAAETEK	99.7%	51.3	25	44.7	2	0	0	1321.66	443	454
Filaggrin-2	FLG2	FILA2_HUMAN	248.1	99.8%	2	2	12	0.01%	1.0%	FSNSSSSNEFSK	99.7%	63.7	25	63.5	6	0	0	1320.57	404	415
Filaggrin-2	FLG2	FILA2_HUMAN	248.1	99.8%	2	2	12	0.01%	1.0%	SVVTVIDVFYK	99.7%	65.6	25	57.6	6	0	0	1269.71	7	17
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	32	0.03%	9.0%	AGVAPLQVK	98.9%	33.3	25	23.4	2	0	0	882.54	1478	1486
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	32	0.03%	9.0%	AHVVPCFDASK	97.9%	30.5	25	30.5	2	0	0	1230.59	1152	1162
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	32	0.03%	9.0%	ALTQTGGPHVK	97.5%	29.8	25	20.7	2	0	0	1108.61	1284	1294
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	32	0.03%	9.0%	ANLPQSFQVDTSK	98.1%	31	25	24.1	1	0	0	1434.72	1465	1477
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	32	0.03%	9.0%	AWGPGLEGGVVGK	99.7%	62.7	25	60.7	2	0	0	1226.65	581	593
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	32	0.03%	9.0%	EGPYSISVLYGDEEVPR	99.7%	75.4	25	75.4	2	0	0	1909.92	1516	1532
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	32	0.03%	9.0%	LIALLEVLSQK	99.7%	47.2	25	43.4	1	0	0	1226.77	77	87
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	32	0.03%	9.0%	LLGWIQNK	99.7%	45.1	25	36.8	2	0	0	971.57	172	179
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	32	0.03%	9.0%	LYSVSYLLK	98.7%	32.7	25	17.1	1	0	0	1085.62	2613	2621
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	32	0.03%	9.0%	SPFSVAVSPSLDLSK	99.7%	61.7	25	53.3	2	0	0	1533.82	959	973
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	32	0.03%	9.0%	TGVAVNKPAEFTVDAK	99.3%	26.6	25	26.6	0	2	0	1646.87	685	700
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	32	0.03%	9.0%	TGVELGKPTHFTVNAK	99.5%	27.5	25	27.5	0	1	0	1698.92	885	900
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	32	0.03%	9.0%	TPCEEILVK	96.9%	29	25	16.5	1	0	0	1088.57	2599	2607
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	32	0.03%	9.0%	VANPSGNLTETYVQDR	99.7%	89.5	25	87.4	1	0	0	1763.86	1297	1312
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	32	0.03%	9.0%	VNVGAGSHPNK	99.7%	43.2	25	42	2	0	0	1079.56	761	771
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	32	0.03%	9.0%	VPVHDVTDASK	99.7%	51.1	25	43.5	2	0	0	1167.60	1440	1450
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	32	0.03%	9.0%	VTAQGPGLEPSGNIANK	99.7%	86.8	25	86.8	2	0	0	1652.86	384	400
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	32	0.03%	9.0%	VTVLFAGQHIAK	99.7%	38.7	25	38.7	2	0	0	1283.75	356	367
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	32	0.03%	9.0%	YGGDEIPFSPYR	99.7%	46.4	25	24.3	2	0	0	1400.65	1622	1633
Flap endonuclease 1	FEN1	FEN1_HUMAN	42.6	100.0%	4	4	7	0.01%	12.1%	KLPIQEFHLSR	99.7%	36.2	25	34.5	0	2	0	1367.78	201	211
Flap endonuclease 1	FEN1	FEN1_HUMAN	42.6	100.0%	4	4	7	0.01%	12.1%	LIADVAPSAIR	99.7%	59.9	25	47.6	2	0	0	1125.66	9	19
Flap endonuclease 1	FEN1	FEN1_HUMAN	42.6	100.0%	4	4	7	0.01%	12.1%	QLQQAQAAGAEQEVEK	99.7%	88.2	25	86.1	2	0	0	1727.86	110	125
Flap endonuclease 1	FEN1	FEN1_HUMAN	42.6	100.0%	4	4	7	0.01%	12.1%	RAVDLIQK	95.6%	27.6	25	20.5	1	0	0	942.57	245	252
Formin-like protein 2	FMNL2	FMNL2_HUMAN	123.3	100.0%	2	2	3	0.00%	2.3%	AAAVSLENVLLDVK	99.7%	40.2	25	36.3	2	0	0	1441.83	891	904
Formin-like protein 2	FMNL2	FMNL2_HUMAN	123.3	100.0%	2	2	3	0.00%	2.3%	LQSLDLLLDTK	99.6%	38	25	31.7	1	0	0	1258.73	845	855
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	4	4	7	0.01%	7.0%	AGYSTDESSSSSLHATR	99.7%	67.1	25	64.9	1	0	0	1755.78	407	423

Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	4	4	7	0.01%	7.0%	IYGETPEACR	99.7%	39.6	25	31.9	2	0	0	1195.54	274	283
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	4	4	7	0.01%	7.0%	LQIDEQLR	99.7%	54.7	25	45.5	3	0	0	1014.56	379	386
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	4	4	7	0.01%	7.0%	LRPVNPNPLATK	99.4%	36.1	25	36.1	1	0	0	1319.78	122	133
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	7	7	14	0.01%	23.6%	AAQEEYVKR	99.7%	56	25	45.4	2	0	0	1093.56	323	331
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	7	7	14	0.01%	23.6%	ADDGRPFPQVIK	99.6%	37.6	25	28.5	2	0	0	1342.71	88	99
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	7	7	14	0.01%	23.6%	ALANSLACQGK	99.7%	62.7	25	46.8	2	0	0	1132.58	332	342
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	7	7	14	0.01%	23.6%	ELSDIAHR	99.7%	46.2	25	22.8	2	0	0	940.48	15	22
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	7	7	14	0.01%	23.6%	GGVVGIKVDK	99.7%	40	25	31.9	2	0	0	971.59	102	111
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	7	7	14	0.01%	23.6%	GILAADESTGSIAK	99.7%	93.4	25	92.7	2	0	0	1332.70	29	42
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	7	7	14	0.01%	23.6%	YTPSGQAGAAASESLFVSNHAY	99.7%	83.4	25	83.4	2	0	0	2228.03	343	364
Fucose-1-phosphate guanylyltransferase	FPGT	FPGT_HUMAN	66.6	99.8%	2	2	4	0.00%	4.9%	IFPVCSSLSDSVITSLK	99.7%	44.3	25	40.5	2	0	0	1852.97	527	543
Fucose-1-phosphate guanylyltransferase	FPGT	FPGT_HUMAN	66.6	99.8%	2	2	4	0.00%	4.9%	TSCIIQSILDSR	99.7%	43.1	25	36.3	2	0	0	1392.72	399	410
Fumarylacetoacetate hydrolase domain-containing protein 2A	FAHD2A	FAH2A_HUMAN	34.6	99.9%	2	2	6	0.01%	8.3%	ALAAQLPVLPR	99.7%	41.9	25	35.8	2	0	0	1148.72	83	93
Fumarylacetoacetate hydrolase domain-containing protein 2A	FAHD2A	FAH2A_HUMAN	34.6	99.9%	2	2	6	0.01%	8.3%	TFDTFCPLGPALVTK	99.7%	54.7	25	44.2	4	0	0	1666.85	210	224
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	9	9	15	0.01%	28.1%	AFREEFGAEPELAVSAPGR	99.7%	34	25	34	0	1	0	2033.01	19	37
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	9	9	15	0.01%	28.1%	EVQLEELEAAR	99.7%	77.1	25	70.2	2	0	0	1286.66	257	267
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	9	9	15	0.01%	28.1%	GHALLIDCR	99.7%	45.7	25	44.1	2	0	0	1054.55	196	204
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	9	9	15	0.01%	28.1%	HSLASSEYPVR	99.7%	54.5	25	37.2	2	0	0	1245.62	229	239
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	9	9	15	0.01%	28.1%	KDGLVSLLTTSEGADEPQR	99.7%	48.7	25	38.5	0	1	0	2016.02	69	87
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	9	9	15	0.01%	28.1%	LMVESHR	96.1%	28.1	25	12.9	1	0	0	871.45	306	312
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	9	9	15	0.01%	28.1%	QPQVAELLAEAR	99.7%	62.2	25	54.3	2	0	0	1324.72	6	17
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	9	9	15	0.01%	28.1%	SLETSLVPLSDPK	99.7%	69.2	25	63	2	0	0	1385.75	205	217
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	9	9	15	0.01%	28.1%	TAQAAAALR	99.7%	52.5	25	41.2	2	0	0	872.49	288	296
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	4	4	8	0.01%	5.3%	NLDPLVYLLSK	99.7%	41	25	40.4	2	0	0	1274.74	77	87
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	4	4	8	0.01%	5.3%	TFLVDPNLDLSIR	99.7%	53.7	25	43.8	2	0	0	1502.82	245	257
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	4	4	8	0.01%	5.3%	VLLDFLMEEK	99.7%	56.1	25	45.7	2	0	0	1236.65	498	507
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	4	4	8	0.01%	5.3%	YTIVQQQIPSFLQK	99.7%	61.9	25	61.9	2	0	0	1692.93	432	445
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	9	10	16	0.02%	23.9%	EMVHADVELMR	99.4%	35.6	25	34.1	1	0	0	1329.63	357	367
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	9	10	16	0.02%	23.9%	ETTPFYPR	99.4%	35.9	25	29.8	2	0	0	1010.49	169	176
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	9	10	16	0.02%	23.9%	FYQASTSELYGK	99.7%	76.4	25	67.6	2	0	0	1393.66	150	161
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	9	10	16	0.02%	23.9%	GYEVHGIVR	99.7%	40.6	25	39	2	0	0	1029.55	47	55
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	9	10	16	0.02%	23.9%	LHYGDLTDSTCLVK	99.7%	58.9	25	58.9	2	0	0	1621.79	82	95
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	9	10	16	0.02%	23.9%	NPQAHIEGNMK	99.3%	35	25	32.9	2	0	0	1238.59	71	81
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	9	10	16	0.02%	23.9%	SFLHIGK	98.2%	31.3	25	23.4	1	0	0	801.46	288	294
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	9	10	16	0.02%	23.9%	TCGLINSVK	99.7%	49.6	25	19.7	2	0	0	991.52	141	149
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	9	10	16	0.02%	23.9%	VHVTVDLK	99.2%	34.4	25	27.8	2	0	0	910.54	315	322
Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	5	5	6	0.01%	6.0%	ALEDITASIAMAVIQQK	99.6%	38.2	25	33.6	1	0	0	1817.97	398	414
Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	5	5	6	0.01%	6.0%	LLETVIDVSTADR	99.7%	91.3	25	91.3	2	0	0	1431.77	457	469
Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	5	5	6	0.01%	6.0%	LVIVHPEVTVK	98.0%	30.7	25	24	1	0	0	1233.76	552	562
Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	5	5	6	0.01%	6.0%	SIAEGIGPEER	99.7%	62.1	25	51.3	1	0	0	1157.58	1037	1047
Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	5	5	6	0.01%	6.0%	TNPSVSSLLQR	99.1%	34.4	25	27.7	1	0	0	1201.65	1018	1028
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	5	5	11	0.01%	3.7%	GVLQTAAER	99.7%	51.5	25	25.2	4	0	0	944.52	934	942
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	5	5	11	0.01%	3.7%	LSGEAFDINK	99.7%	50.8	25	43.8	1	0	0	1093.55	515	524
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	5	5	11	0.01%	3.7%	SLEAFFLYGR	99.7%	58.8	25	57.2	4	0	0	1202.62	1275	1284
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	5	5	11	0.01%	3.7%	SLLPLSTSLDHR	95.9%	27.9	25	27.9	1	0	0	1338.74	847	858
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	5	5	11	0.01%	3.7%	TVAEVQETLAEMIR	99.7%	54.7	25	54.7	1	0	0	1589.82	1373	1386
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	3	3	4	0.00%	1.6%	IASNVLNTK	99.7%	44.2	25	30	1	0	0	959.55	1278	1286
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	3	3	4	0.00%	1.6%	LCYMGLLQFGPTEK	99.7%	40.5	25	35.2	1	0	0	1656.81	972	985
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	3	3	4	0.00%	1.6%	LIESLFTIQK	99.7%	69.8	25	60.3	2	0	0	1191.70	630	639
General transcription factor 3C polypeptide 2	GTF3C2	TF3C2_HUMAN	100.7	100.0%	3	3	4	0.00%	3.1%	EGLPEDGTLYR	95.4%	27.4	25	23.6	1	0	0	1249.61	363	373
General transcription factor 3C polypeptide 2	GTF3C2	TF3C2_HUMAN	100.7	100.0%	3	3	4	0.00%	3.1%	GLASPLGHR	99.7%	44.7	25	35.4	1	0	0	907.51	868	876

General transcription factor 3C polypeptide 2	GTF3C2	TF3C2_HUMAN	100.7	100.0%	3	3	4	0.00%	3.1%	SPLFSVQR	99.7%	41.2	25	29.4	2	0	0	933.52	355	362
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	8	8	13	0.01%	9.9%	AIFAVLTSVLTK	99.7%	93.4	25	93.4	2	0	0	1262.77	611	622
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	8	8	13	0.01%	9.9%	ELEYFGLSAAILDK	99.7%	70.2	25	65	2	0	0	1568.82	667	680
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	8	8	13	0.01%	9.9%	GLMGEANIR	97.6%	30	25	16.5	1	0	0	976.49	151	159
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	8	8	13	0.01%	9.9%	ISFEEFER	99.0%	33.8	25	24.7	1	0	0	1056.50	16	23
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	8	8	13	0.01%	9.9%	ISLSTLQQQLGQPEK	99.7%	57	25	52.4	2	0	0	1669.91	494	508
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	8	8	13	0.01%	9.9%	LAEMSLEQDNIK	99.7%	47.3	25	10	1	0	0	1390.69	223	234
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	8	8	13	0.01%	9.9%	STLLFSQGK	99.7%	75.1	25	75.1	2	0	0	980.54	540	548
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	8	8	13	0.01%	9.9%	YNLAVVWLR	99.7%	56.1	25	44.8	2	0	0	1133.65	453	461
General transcription factor 3C polypeptide 4	GTF3C4	TF3C4_HUMAN	92.0	100.0%	4	4	4	0.00%	5.5%	LSDVFGSVR	99.7%	44.1	25	27.7	1	0	0	979.52	468	476
General transcription factor 3C polypeptide 4	GTF3C4	TF3C4_HUMAN	92.0	100.0%	4	4	4	0.00%	5.5%	MSGLIVGSAFGPIK	99.5%	36.4	25	33.2	1	0	0	1376.76	328	341
General transcription factor 3C polypeptide 4	GTF3C4	TF3C4_HUMAN	92.0	100.0%	4	4	4	0.00%	5.5%	NYQVQFVTLK	99.7%	44	25	44	1	0	0	1239.67	507	516
General transcription factor 3C polypeptide 4	GTF3C4	TF3C4_HUMAN	92.0	100.0%	4	4	4	0.00%	5.5%	QLIPIFTDVALK	99.4%	36.2	25	22.7	1	0	0	1357.81	449	460
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	10	11	20	0.02%	22.0%	DPYCHPVCANR	96.3%	28.3	25	27.6	1	0	0	1388.58	68	78
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	10	11	20	0.02%	22.0%	EGYNNPPISGENLIGLSR	99.7%	93.7	25	93.7	2	0	0	1929.97	192	209
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	10	11	20	0.02%	22.0%	FSTSSLLLR	99.7%	55.2	25	39.6	2	0	0	1023.58	79	87
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	10	11	20	0.02%	22.0%	HGYAPSDLPVK	99.7%	43.4	25	43.4	2	0	0	1183.61	329	339
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	10	11	20	0.02%	22.0%	IYQVLDFR	99.7%	62.3	25	54.2	2	0	0	1053.57	315	322
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	10	11	20	0.02%	22.0%	LKDSVYIFR	99.2%	34.6	25	27.5	2	0	0	1140.64	388	396
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	10	11	20	0.02%	22.0%	MLPTLGGEEGVSR	99.7%	63.4	25	57.6	4	0	0	1345.68	39	51
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	10	11	20	0.02%	22.0%	MVCVEYPGVVR	99.7%	45.2	25	44.2	2	0	0	1308.64	24	34
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	10	11	20	0.02%	22.0%	QGLGPSGTSGAR	99.6%	37.4	25	35.7	1	0	0	1087.55	368	379
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	10	11	20	0.02%	22.0%	STYNYSLPITVK	99.7%	44.9	25	44.9	2	0	0	1385.73	343	354
General transcription factor II-I	GTF2I	GTF2I_HUMAN	112.4	100.0%	6	6	8	0.01%	6.1%	APSYLEISSMR	95.3%	27.4	25	27.4	1	0	0	1253.62	917	927
General transcription factor II-I	GTF2I	GTF2I_HUMAN	112.4	100.0%	6	6	8	0.01%	6.1%	EQVNDLFSR	99.7%	48.6	25	36.4	2	0	0	1107.54	870	878
General transcription factor II-I	GTF2I	GTF2I_HUMAN	112.4	100.0%	6	6	8	0.01%	6.1%	FAEALGSTEAK	99.7%	72.9	25	61.8	1	0	0	1123.56	478	488
General transcription factor II-I	GTF2I	GTF2I_HUMAN	112.4	100.0%	6	6	8	0.01%	6.1%	FAQALGLTEAVK	99.7%	69.6	25	51.1	2	0	0	1247.70	583	594
General transcription factor II-I	GTF2I	GTF2I_HUMAN	112.4	100.0%	6	6	8	0.01%	6.1%	RPSTFGIPR	99.4%	36.1	25	18.2	1	0	0	1030.58	782	790
General transcription factor II-I	GTF2I	GTF2I_HUMAN	112.4	100.0%	6	6	8	0.01%	6.1%	SPTWFGIPR	99.6%	37.3	25	24.2	1	0	0	1060.56	620	628
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	12	13	25	0.02%	16.2%	EQDDLLVLLADQDQK	99.7%	101	25	78.5	2	0	0	1742.88	905	919
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	12	13	25	0.02%	16.2%	EQDLQLEELR	99.7%	42.2	25	37.1	2	0	0	1272.64	661	670
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	12	13	25	0.02%	16.2%	GVMGGQSAGPQHTEAETIQK	99.7%	40	25	40	0	2	0	2041.96	6	25
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	12	13	25	0.02%	16.2%	IVAFENAFER	99.7%	72.9	25	72.6	2	0	0	1195.61	203	212
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	12	13	25	0.02%	16.2%	LMDLLADSR	99.7%	62.3	25	46.9	2	0	0	1049.53	171	179
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	12	13	25	0.02%	16.2%	LSALLQETK	99.7%	58.7	25	51.8	2	0	0	1002.58	850	858
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	12	13	25	0.02%	16.2%	NDGVLLLQALTR	99.7%	105	25	93.7	2	0	0	1312.76	184	195
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	12	13	25	0.02%	16.2%	QSEDLGSQFTEIFIK	99.7%	77.9	25	76.6	2	0	0	1741.86	105	119
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	12	13	25	0.02%	16.2%	SQLNSQSVEITK	99.7%	87.4	25	82.1	2	0	0	1333.70	799	810
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	12	13	25	0.02%	16.2%	SSQTSGTNEQSSAIVSAR	99.7%	124	25	111	2	0	0	1809.86	765	782
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	12	13	25	0.02%	16.2%	SVEVQGETETIIATK	99.7%	101	25	82.9	2	0	0	1604.84	828	842
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	12	13	25	0.02%	16.2%	VASSTLLDDRR	99.4%	27.2	25	21.4	2	1	0	1232.66	30	40
Glomulin	GLMN	GLMN_HUMAN	68.2	100.0%	5	6	10	0.01%	9.3%	GLELLENSLLR	99.7%	41.7	25	23.9	2	0	0	1256.72	335	345
Glomulin	GLMN	GLMN_HUMAN	68.2	100.0%	5	6	10	0.01%	9.3%	IEDNSLLYQYLEIK	99.7%	41.3	25	41.3	2	0	0	1740.91	346	359
Glomulin	GLMN	GLMN_HUMAN	68.2	100.0%	5	6	10	0.01%	9.3%	IMASLNLLR	99.7%	42	25	34.9	3	0	0	1030.61	471	479
Glomulin	GLMN	GLMN_HUMAN	68.2	100.0%	5	6	10	0.01%	9.3%	SLAMLQLYINK	99.7%	38.9	25	24.7	2	0	0	1293.72	384	394
Glomulin	GLMN	GLMN_HUMAN	68.2	100.0%	5	6	10	0.01%	9.3%	STSEENIGIK	97.7%	30.2	25	22.9	1	0	0	1077.54	585	594
Glucose-6-phosphate isomerase	GPI	G6PI_HUMAN	63.1	100.0%	3	4	5	0.00%	8.4%	ILLANFLAQTEALMR	99.7%	87.7	25	78.7	3	0	0	1703.95	424	438
Glucose-6-phosphate isomerase	GPI	G6PI_HUMAN	63.1	100.0%	3	4	5	0.00%	8.4%	TLAQLNPESSLFIIASK	99.7%	44.9	25	44.9	1	0	0	1832.02	195	211
Glucose-6-phosphate isomerase	GPI	G6PI_HUMAN	63.1	100.0%	3	4	5	0.00%	8.4%	VFEGNRPTNSIVFTK	99.7%	39.3	25	29.5	1	0	0	1708.90	467	481
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	7	7	13	0.01%	24.7%	AQTGAPCLSFDIVR	99.7%	59.2	25	58.7	2	0	0	1534.77	60	73
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	7	7	13	0.01%	24.7%	DPEAGDVEADPGLADLPQQLLFVHQGETELK	99.7%	66.3	25	66.3	0	2	0	3331.63	388	418

Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	7	7	13	0.01%	24.7%	GQVEVFALR	99.7%	63.4	25	51.4	2	0	0	1018.57	173	181
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	7	7	13	0.01%	24.7%	LLQVVEEPQALAAFLR	99.7%	88.2	25	82.7	1	0	0	1797.03	183	198
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	7	7	13	0.01%	24.7%	REPFLLSGGDDGALK	99.7%	51.6	25	51.6	0	2	0	1574.82	319	333
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	7	7	13	0.01%	24.7%	SGSPVATFK	99.7%	41.1	25	35.5	2	0	0	893.47	342	350
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	7	7	13	0.01%	24.7%	VSWLGEEPVAGVWSEK	99.7%	79.3	25	79.3	2	0	0	1772.89	157	172
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	7	7	11	0.01%	11.7%	EIFEQPESVVNTMR	99.7%	53.2	25	29.6	1	0	0	1678.81	346	359
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	7	7	11	0.01%	11.7%	EILETLIK	99.3%	35	25	24.9	1	0	0	958.58	18	25
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	7	7	11	0.01%	11.7%	EVLSMDDEIQK	99.7%	44.4	25	44.4	1	0	0	1322.61	537	547
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	7	7	11	0.01%	11.7%	GSPLLIGVR	99.6%	37.3	25	19.9	2	0	0	911.57	204	212
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	7	7	11	0.01%	11.7%	GYDFESETDTETIAK	99.7%	81.3	25	81.3	2	0	0	1705.74	140	154
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	7	7	11	0.01%	11.7%	LATELYHQK	99.6%	38.2	25	28.4	2	0	0	1102.59	548	556
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	7	7	11	0.01%	11.7%	VIFLEDDDVAAVVDGR	99.7%	63.3	25	60.2	2	0	0	1732.88	291	306
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	26	0.03%	21.0%	AINFNFGYAK	99.7%	48.2	25	35.2	2	0	0	1144.58	283	292
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	26	0.03%	21.0%	AMAVLESLR	99.7%	67.7	25	36.2	1	0	0	989.54	568	576
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	26	0.03%	21.0%	DVLNDTAPR	99.7%	47.4	25	41.4	2	0	0	1000.51	559	567
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	26	0.03%	21.0%	EAATQAQQTLGSTIDK	99.7%	89.3	25	85.9	2	0	0	1661.83	35	50
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	26	0.03%	21.0%	FDDTNPEKEEAK	99.7%	57.1	25	48.9	2	0	0	1422.64	302	313
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	26	0.03%	21.0%	FSEGEATLR	99.7%	54	25	44.9	2	0	0	1009.49	395	403
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	26	0.03%	21.0%	GLAYVCHQR	99.7%	39.3	25	25	2	0	0	1103.54	353	361
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	26	0.03%	21.0%	GPSGCVESLEVTCR	99.7%	87.2	25	87.2	2	0	0	1550.69	653	666
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	26	0.03%	21.0%	ILQLVATGAVR	99.7%	99.9	25	93.6	2	0	0	1140.71	499	509
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	26	0.03%	21.0%	LEADLEKK	98.5%	32	25	24.2	1	0	0	945.53	181	188
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	26	0.03%	21.0%	LFTLTALR	99.7%	57.7	25	41.3	2	0	0	934.57	516	523
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	26	0.03%	21.0%	LGYFSVDPDSHQGK	99.0%	33.5	25	33.5	1	0	0	1549.73	746	759
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	26	0.03%	21.0%	LSFLVSYIASK	99.7%	71.2	25	70	2	0	0	1227.70	69	79
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	26	0.03%	21.0%	NSALSAQLR	99.7%	67.6	25	55.8	2	0	0	959.53	26	34
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	26	0.03%	21.0%	SHPLDPIDTVDFER	99.2%	34.6	25	34.6	1	0	0	1640.79	96	109
Glutaminyl-peptide cyclotransferase	QPCT	QPCT_HUMAN	40.9	99.8%	2	2	4	0.00%	6.9%	SFSNIISTLNPTAK	99.7%	44.9	25	39	3	0	0	1492.80	119	132
Glutaminyl-peptide cyclotransferase	QPCT	QPCT_HUMAN	40.9	99.8%	2	2	4	0.00%	6.9%	YPGSPGSYAAR	98.2%	31.1	25	8.98	1	0	0	1125.53	78	88
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	9	11	26	0.03%	20.9%	ELRVPLIGSLPEAR	99.7%	38.2	25	38.2	2	2	0	1549.91	67	80
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	9	11	26	0.03%	20.9%	FLEATLR	99.7%	42.8	25	28.1	2	0	0	849.48	118	124
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	9	11	26	0.03%	20.9%	GLMEPLLPPK	99.7%	43.5	25	43.5	6	0	0	1094.63	17	26
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	9	11	26	0.03%	20.9%	HLAQLMESIPHSPGPTR	99.7%	46.2	25	46.2	0	2	0	1886.95	242	258
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	9	11	26	0.03%	20.9%	HLTLACHYDSK	99.7%	50.7	25	44.6	2	0	0	1344.64	162	172
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	9	11	26	0.03%	20.9%	KFLEATLR	99.7%	38.7	25	17.1	2	0	0	977.58	117	124
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	9	11	26	0.03%	20.9%	TPGSPGNLQVR	99.7%	65.4	25	55.3	3	0	0	1125.60	106	116
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	9	11	26	0.03%	20.9%	VPLIGSLPEAR	99.7%	57	25	52.7	3	0	0	1151.68	70	80
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	9	11	26	0.03%	20.9%	VVGQLDPQR	99.7%	52	25	52	2	0	0	1011.56	84	92
Glutaryl-CoA dehydrogenase, mitochondrial	GCDH	GCDH_HUMAN	48.1	99.8%	2	2	2	0.00%	7.8%	EIISEMGELGVLGPTIK	99.7%	46.4	25	46.4	1	0	0	1785.97	95	111
Glutaryl-CoA dehydrogenase, mitochondrial	GCDH	GCDH_HUMAN	48.1	99.8%	2	2	2	0.00%	7.8%	GYGCAGVSSVAYGLLAR	99.7%	63.5	25	63.5	1	0	0	1700.84	112	128
Glutathione S-transferase kappa 1	GSTK1	GSTK1_HUMAN	25.5	100.0%	4	4	5	0.00%	23.9%	AGMSAEQAQGLLEK	99.7%	82.7	25	69.7	2	0	0	1432.71	145	158
Glutathione S-transferase kappa 1	GSTK1	GSTK1_HUMAN	25.5	100.0%	4	4	5	0.00%	23.9%	DFLSVMLEK	97.5%	29.8	25	16.3	1	0	0	1097.55	86	94
Glutathione S-transferase kappa 1	GSTK1	GSTK1_HUMAN	25.5	100.0%	4	4	5	0.00%	23.9%	FLTAVNLEHPEMLEK	98.8%	33	25	33	1	0	0	1770.91	102	116
Glutathione S-transferase kappa 1	GSTK1	GSTK1_HUMAN	25.5	100.0%	4	4	5	0.00%	23.9%	NEDITEPQSILAAAEK	99.7%	53	25	50.6	1	0	0	1728.87	129	144
Glutathione S-transferase Mu 3	GSTM3	GSTM3_HUMAN	26.6	100.0%	3	3	3	0.00%	12.9%	FSWFAGEK	95.5%	27.6	25	10.1	1	0	0	971.46	149	156
Glutathione S-transferase Mu 3	GSTM3	GSTM3_HUMAN	26.6	100.0%	3	3	3	0.00%	12.9%	IAAYLQSDQFCK	95.9%	27.9	25	27.9	1	0	0	1443.69	198	209
Glutathione S-transferase Mu 3	GSTM3	GSTM3_HUMAN	26.6	100.0%	3	3	3	0.00%	12.9%	ITQSNAILR	99.2%	34.9	25	26.9	1	0	0	1015.59	74	82
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	5	6	21	0.02%	21.5%	GALQNIIPASTGAAK	99.7%	68.8	25	66.2	6	0	0	1411.79	201	215
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	5	6	21	0.02%	21.5%	IISNASCTTNCLAPLAK	99.7%	120	25	114	5	0	0	1833.92	146	162
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	5	6	21	0.02%	21.5%	LISWYDNEFGYSNR	99.7%	82.8	25	82.8	2	0	0	1763.80	310	323
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	5	6	21	0.02%	21.5%	VPTANVSVVDLTCR	99.7%	80	25	79	2	0	0	1530.79	235	248

Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	5	6	21	0.02%	21.5%	VVDLMAHMASKE	99.7%	77.7	25	68.9	6	0	0	1330.65	324	335
Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	GPD1L_HUMAN	38.4	100.0%	3	3	5	0.00%	8.6%	GIDEGPEGLK	96.6%	28.6	25	25.1	1	0	0	1014.51	123	132
Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	GPD1L_HUMAN	38.4	100.0%	3	3	5	0.00%	8.6%	ICDEITGR	99.7%	50.1	25	36	2	0	0	963.46	103	110
Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	GPD1L_HUMAN	38.4	100.0%	3	3	5	0.00%	8.6%	LQGPQTSAEVYR	99.5%	36.5	25	35.4	2	0	0	1348.69	299	310
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	7	7	11	0.01%	12.6%	IYLYLTK	96.8%	28.9	25	7.54	1	0	0	913.54	413	419
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	7	7	11	0.01%	12.6%	LPFAAAQIGNSFR	99.7%	71.4	25	58.4	2	0	0	1391.74	319	331
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	7	7	11	0.01%	12.6%	SCYDLSCHAR	99.2%	34.5	25	34.5	1	0	0	1268.51	465	474
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	7	7	11	0.01%	12.6%	SPITGNDLSPPVSFNLMFK	99.2%	34.7	25	34.7	2	0	0	2064.05	265	283
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	7	7	11	0.01%	12.6%	TFFSFPAVVAPFK	99.5%	36.3	25	31	2	0	0	1457.78	603	615
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	7	7	11	0.01%	12.6%	TLYVEEVVPNVIEPSFGLGR	99.4%	35.7	25	35.7	1	0	0	2218.18	564	583
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	7	7	11	0.01%	12.6%	TVNVVQFEPSK	99.7%	57.7	25	49.3	2	0	0	1247.66	491	501
Glycogen [starch] synthase, muscle	GYS1	GYS1_HUMAN	83.8	99.8%	2	2	3	0.00%	3.0%	GADVFLEALAR	99.7%	71.5	25	60.9	2	0	0	1161.63	338	348
Glycogen [starch] synthase, muscle	GYS1	GYS1_HUMAN	83.8	99.8%	2	2	3	0.00%	3.0%	VGGIYTVLQTK	99.7%	60.4	25	0	1	0	0	1178.68	40	50
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	18.1%	DYFFALAHTVR	99.7%	59	25	51.9	2	0	0	1339.68	51	61
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	18.1%	GLAGLGDVAEVR	99.7%	89.2	25	76.3	2	0	0	1156.63	18	29
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	18.1%	IGEEFLTDLSQLK	99.7%	57.6	25	54.4	1	0	0	1492.79	508	520
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	18.1%	LLPLVSDEVFIR	99.7%	50.7	25	50.7	2	0	0	1400.81	522	533
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	18.1%	LVTSIGDVVNHDPVVGDR	99.7%	47.7	25	47.7	0	2	0	1891.99	623	640
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	18.1%	NLAENISR	99.7%	53	25	28.2	2	0	0	916.48	271	278
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	18.1%	VEDVEALDR	99.7%	47.5	25	40.2	2	0	0	1045.52	716	724
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	18.1%	VIFLENYR	99.7%	57.4	25	48	4	0	0	1053.57	643	650
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	18.1%	VIPAADLSQQISTAGTEASGTGNMK	99.3%	26.4	25	26.4	0	1	0	2463.20	657	681
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	18.1%	VLYPNDNFFEGK	99.7%	69.4	25	67.9	3	0	0	1442.70	279	290
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	18.1%	WLLLCNPGLADTIVEK	99.0%	33.6	25	33.6	2	0	0	1841.98	492	507
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	18.1%	YEFGIFNQK	99.7%	41.6	25	40.1	2	0	0	1145.56	162	170
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	APNDFNLR	99.7%	55	25	42.8	2	0	0	946.47	249	256
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	DFNVGDYIQAVLDR	99.7%	68.6	25	64.1	1	0	0	1624.80	257	270
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	DYYFALAHTVR	99.7%	62.7	25	50	2	0	0	1355.67	51	61
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	EYAQNIWNVEPSDLK	99.7%	52.1	25	52.1	1	0	0	1805.87	820	834
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	EYYEALPELK	99.7%	46.2	25	41.1	2	0	0	1254.63	731	740
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	FSQFLETEYK	99.7%	68.8	25	62.3	2	0	0	1291.62	546	555
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	GIVGVENVAELK	99.7%	46.1	25	36.7	1	0	0	1227.69	18	29
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	GIVGVENVAELKK	99.7%	68.7	25	65.4	2	0	0	1355.79	18	30
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	HLEIIYEINQK	99.7%	54.8	25	43.4	2	0	0	1399.76	400	410
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	IDDVAALDK	99.6%	38.2	25	33.1	1	0	0	959.50	716	724
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	IDDVAALDKK	99.7%	50.5	25	35	2	0	0	1087.60	716	725
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	IGEDYVK	99.6%	37.9	25	21.8	1	0	0	823.42	508	514
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	IGEDYVKDLSQLTK	99.7%	47.3	25	26	2	0	0	1608.85	508	521
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	INPSSMFDVQVK	99.7%	80.1	25	63.8	2	0	0	1364.69	558	569
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	LHSFLGDDVFLR	99.7%	67.2	25	57.4	2	2	0	1418.74	522	533
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	LITSVADVVNNDPMVGSK	99.7%	117	25	113	4	0	0	1874.95	623	640
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	LVIDQIDNGFFSPK	99.7%	81.2	25	79.6	3	0	0	1592.83	741	754
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	MSLIEEEGSKR	99.7%	72.9	25	58	2	0	0	1278.64	429	439
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	NLAENISR	99.7%	53	25	28.2	2	0	0	916.48	271	278
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	TFAYTNHTVLPEALER	99.7%	48.5	25	46.5	0	2	0	1861.94	372	387
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	VFADYEAYVK	99.7%	56.3	25	53.8	2	0	0	1204.59	774	783
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	VIFLENYR	99.7%	57.4	25	48	4	0	0	1053.57	643	650
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	VIPATDLSEQISTAGTEASGTGNMK	99.7%	40.1	25	40.1	0	4	0	2478.20	657	681
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	VLYPNDNFFEGK	99.7%	69.4	25	67.9	3	0	0	1442.70	279	290
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	VSQLYMNPK	99.7%	57.5	25	54	4	0	0	1095.55	788	796
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	WPVDLVEK	96.1%	28.1	25	27.7	2	0	0	985.54	388	395

Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	27	31	61	0.06%	34.0%	YEYGIFNQK	99.3%	35.3	25	35.1	2	0	0	1161.56	162	170
GMP synthase [glutamine-hydrolyzing]	GMPS	GUAA_HUMAN	76.7	100.0%	2	2	3	0.00%	4.3%	EPPTDVTPTFLTTGVLSTLR	99.4%	36	25	36	1	0	0	2145.14	570	589
GMP synthase [glutamine-hydrolyzing]	GMPS	GUAA_HUMAN	76.7	100.0%	2	2	3	0.00%	4.3%	VVYIFGPPVK	98.5%	31.9	25	31.9	2	0	0	1118.66	560	569
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	5	5	6	0.01%	3.6%	AASSSSPGSPVASSPSR	99.7%	50.8	25	50.8	1	0	0	1531.73	1776	1792
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	5	5	6	0.01%	3.6%	FLQLESLQELMK	99.7%	80.2	25	75.6	1	0	0	1478.79	1125	1136
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	5	5	6	0.01%	3.6%	GATPEGIFLR	99.7%	48.3	25	29.9	2	0	0	1060.58	907	916
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	5	5	6	0.01%	3.6%	SEDTTGPITGLALTSVNK	99.7%	61.8	25	61.8	1	0	0	1803.93	74	91
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	5	5	6	0.01%	3.6%	SLEETIIQK	99.7%	42	25	32.1	1	0	0	1060.59	945	953
GPI transamidase component PIG-T	PIGT	PIGT_HUMAN	65.7	100.0%	3	3	4	0.00%	4.5%	LYVHTLTITSK	99.7%	38.5	25	38.5	2	0	0	1275.73	395	405
GPI transamidase component PIG-T	PIGT	PIGT_HUMAN	65.7	100.0%	3	3	4	0.00%	4.5%	TFHIEEPR	97.7%	30.1	25	19.9	1	0	0	1028.52	550	557
GPI transamidase component PIG-T	PIGT	PIGT_HUMAN	65.7	100.0%	3	3	4	0.00%	4.5%	VSIQFER	96.5%	28.5	25	7.68	1	0	0	878.47	442	448
GPI-anchor transamidase	PIGK	GPI8_HUMAN	45.3	100.0%	3	3	5	0.00%	7.6%	HVANTLSVYR	99.7%	52.2	25	52.2	2	0	0	1159.62	61	70
GPI-anchor transamidase	PIGK	GPI8_HUMAN	45.3	100.0%	3	3	5	0.00%	7.6%	KVEITTETIK	99.7%	39.7	25	24.9	2	0	0	1161.67	309	318
GPI-anchor transamidase	PIGK	GPI8_HUMAN	45.3	100.0%	3	3	5	0.00%	7.6%	SLCVSTPGHR	99.7%	41.7	25	33.8	1	0	0	1113.55	278	287
GrpE protein homolog 1, mitochondrial	GRPEL1	GRPE1_HUMAN	24.3	100.0%	3	3	5	0.00%	16.1%	ALADTENLR	99.7%	39.7	25	24.3	2	0	0	1002.52	81	89
GrpE protein homolog 1, mitochondrial	GRPEL1	GRPE1_HUMAN	24.3	100.0%	3	3	5	0.00%	16.1%	NLYEGLVMTEVQIQK	99.1%	34.3	25	24.4	1	0	0	1764.92	139	153
GrpE protein homolog 1, mitochondrial	GRPEL1	GRPE1_HUMAN	24.3	100.0%	3	3	5	0.00%	16.1%	TLRPALVGVVK	99.6%	38.2	25	38.2	2	0	0	1152.75	205	215
GTP:AMP phosphotransferase AK3, mitochondrial	AK3	KAD3_HUMAN	25.6	100.0%	3	3	4	0.00%	14.1%	LALHELK	97.8%	30.4	25	13.8	1	0	0	823.50	74	80
GTP:AMP phosphotransferase AK3, mitochondrial	AK3	KAD3_HUMAN	25.6	100.0%	3	3	4	0.00%	14.1%	TLPQAEALDR	99.7%	39.1	25	28	1	0	0	1113.59	95	104
GTP:AMP phosphotransferase AK3, mitochondrial	AK3	KAD3_HUMAN	25.6	100.0%	3	3	4	0.00%	14.1%	TVGIDDLTGEPLIQR	99.7%	44.5	25	36.4	2	0	0	1626.87	147	161
GTPase Era, mitochondrial	ERAL1	ERAL1_HUMAN	48.3	100.0%	6	6	11	0.01%	18.8%	DPNTQSVGNPQR	99.7%	46	25	40.8	2	0	0	1312.62	285	296
GTPase Era, mitochondrial	ERAL1	ERAL1_HUMAN	48.3	100.0%	6	6	11	0.01%	18.8%	EIFMLSALSQEDVK	99.7%	55.6	25	55.6	2	0	0	1609.81	304	317
GTPase Era, mitochondrial	ERAL1	ERAL1_HUMAN	48.3	100.0%	6	6	11	0.01%	18.8%	ETQVILLDTPGIISPGK	99.7%	83.4	25	83.4	2	0	0	1781.01	160	176
GTPase Era, mitochondrial	ERAL1	ERAL1_HUMAN	48.3	100.0%	6	6	11	0.01%	18.8%	STLSNQLLGR	99.7%	68.4	25	18.1	2	0	0	1088.61	127	136
GTPase Era, mitochondrial	ERAL1	ERAL1_HUMAN	48.3	100.0%	6	6	11	0.01%	18.8%	TAVWEEGPGGELVIQQK	99.7%	76.1	25	66.6	2	0	0	1840.94	372	388
GTPase Era, mitochondrial	ERAL1	ERAL1_HUMAN	48.3	100.0%	6	6	11	0.01%	18.8%	YSQIPSVLVMNK	99.4%	35.6	25	35.6	1	0	0	1378.74	226	237
GTPase-activating protein and VPS9 domain-containing protein 1	GAPVD1	GAPD1_HUMAN	165.0	100.0%	3	3	4	0.00%	2.7%	AVETPPLSSVNLLEGLSR	99.7%	54.2	25	53.9	2	0	0	1882.03	387	404
GTPase-activating protein and VPS9 domain-containing protein 1	GAPVD1	GAPD1_HUMAN	165.0	100.0%	3	3	4	0.00%	2.7%	LIASSLVAGEK	99.7%	48	25	37.5	1	0	0	1087.64	109	119
GTPase-activating protein and VPS9 domain-containing protein 1	GAPVD1	GAPD1_HUMAN	165.0	100.0%	3	3	4	0.00%	2.7%	VQEMVESNEAK	97.1%	29.3	25	22.4	1	0	0	1279.58	247	257
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	31	0.03%	50.5%	DGYYIQAQCAIIMFDVTSR	99.7%	88.1	25	88.1	2	0	0	2251.05	77	95
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	31	0.03%	50.5%	GPIKFNVWDTAGQEK	99.7%	84.2	25	80.5	2	2	0	1689.86	57	71
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	31	0.03%	50.5%	HLTGEFEK	99.0%	33.5	25	27.6	2	0	0	960.48	30	37
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	31	0.03%	50.5%	HLTGEFEKK	95.6%	27.6	25	19.3	1	0	0	1088.57	30	38
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	31	0.03%	50.5%	KYVATLGVEVHPLVFHTNR	99.7%	57	25	50.2	0	1	0	2180.20	38	56
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	31	0.03%	50.5%	LVLVGDGGTGK	99.7%	78.6	25	19.2	3	0	0	1015.58	13	23
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	31	0.03%	50.5%	NLQYYDISAK	99.7%	45.1	25	38.7	8	0	0	1214.61	143	152
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	31	0.03%	50.5%	SNYNFEKPFLWLAR	99.7%	41.2	25	41.2	2	4	0	1784.91	153	166
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	31	0.03%	50.5%	VCENIPIVLCGNK	99.7%	52.6	25	51.5	2	0	0	1515.77	111	123
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	31	0.03%	50.5%	YVATLGVEVHPLVFHTNR	99.7%	44.8	25	41.1	0	2	0	2052.10	39	56
GTP-binding protein 10	GTPBP10	GTPBA_HUMAN	42.9	100.0%	4	4	6	0.01%	11.6%	FVAGVGANSK	95.4%	27.5	25	21	1	0	0	949.51	67	76
GTP-binding protein 10	GTPBP10	GTPBA_HUMAN	42.9	100.0%	4	4	6	0.01%	11.6%	GGDVWVVAQNR	97.8%	30.3	25	29.9	1	0	0	1200.61	42	52
GTP-binding protein 10	GTPBP10	GTPBA_HUMAN	42.9	100.0%	4	4	6	0.01%	11.6%	LIADVGLVGFPNAGK	99.7%	66.4	25	66.4	2	0	0	1470.83	147	161
GTP-binding protein 10	GTPBP10	GTPBA_HUMAN	42.9	100.0%	4	4	6	0.01%	11.6%	LLTNFLPLK	99.7%	45.6	25	36.6	2	0	0	1058.66	127	135
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	6	8	13	0.01%	33.7%	ALAESWNAAFLESSAK	99.7%	89	25	89	2	0	0	1694.84	136	151
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	6	8	13	0.01%	33.7%	ENQTAVDVFR	99.7%	65.6	25	54.3	2	0	0	1178.58	152	161
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	6	8	13	0.01%	33.7%	IAILGYR	97.5%	29.8	25	23.9	1	0	0	805.49	9	15
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	6	8	13	0.01%	33.7%	IILEAEKMDGAASQGK	99.7%	67.4	25	67.4	4	2	0	1660.86	163	178
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	6	8	13	0.01%	33.7%	KIAILGYR	94.6%	26.9	25	12.2	1	0	0	933.59	8	15
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	6	8	13	0.01%	33.7%	VQIPIMLVGNKK	97.8%	30.3	25	22.5	1	0	0	1355.81	110	121
GTP-binding protein SAR1a	SAR1A	SAR1A_HUMAN	22.4	99.8%	2	2	3	0.00%	9.6%	LVFLGLDNAGK	99.7%	58.4	25	58.4	1	0	0	1146.65	28	38
GTP-binding protein SAR1a	SAR1A	SAR1A_HUMAN	22.4	99.8%	2	2	3	0.00%	9.6%	QGYGEGFR	96.9%	29	25	20.3	2	0	0	913.42	184	191

Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	GBB2_HUMAN	37.3	100.0%	3	3	4	0.00%	12.4%	ACGDSTLTQITAGLDPVGR	99.7%	52.3	25	52.3	1	0	0	1931.95	24	42
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	GBB2_HUMAN	37.3	100.0%	3	3	4	0.00%	12.4%	LIIWDSYTTNK	99.7%	53.2	25	44.9	1	0	0	1353.71	79	89
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	GBB2_HUMAN	37.3	100.0%	3	3	4	0.00%	12.4%	TFVSGACDASIK	99.7%	70	25	64.1	2	0	0	1255.60	198	209
Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	GNAS	GNAS1_HUMAN	45.7	100.0%	4	4	9	0.01%	5.7%	LLLLGAGESGK	99.7%	70.5	25	0	5	0	0	1057.63	43	53
Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	GNAS	GNAS1_HUMAN	45.7	100.0%	4	4	9	0.01%	5.7%	SKIEDYFPEFAR	99.7%	70.5	25	70.5	1	0	0	1501.73	306	317
Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	GNAS	GNAS1_HUMAN	45.7	100.0%	4	4	9	0.01%	5.7%	TISVILFLNK	99.7%	39.6	25	38.2	2	0	0	1147.71	284	293
Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	GNAS	GNAS1_HUMAN	45.7	100.0%	4	4	9	0.01%	5.7%	VLTSGIFETK	99.7%	55.7	25	48.6	4	0	0	1094.61	202	211
Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	GNAS	GNAS1_HUMAN	45.7	100.0%	4	4	9	0.01%	5.7%	YTTPEDATPEPGEDPR	99.7%	50.8	25	50.8	2	0	0	1774.78	318	333
Guanine nucleotide-binding protein subunit alpha-11	GNA11	GNA11_HUMAN	42.1	100.0%	2	2	4	0.00%	7.2%	IATLGYLPTQQDVLR	99.7%	62.3	25	62.3	2	0	0	1687.94	167	181
Guanine nucleotide-binding protein subunit alpha-11	GNA11	GNA11_HUMAN	42.1	100.0%	2	2	4	0.00%	7.2%	LLLLGTGESGK	99.7%	59.3	25	35.2	2	0	0	1087.64	42	52
Guanine nucleotide-binding protein subunit alpha-13	GNA13	GNA13_HUMAN	44.1	100.0%	5	6	14	0.01%	14.3%	ALWADSGIQNAYDR	99.7%	70.1	25	67	1	0	0	1579.75	151	164
Guanine nucleotide-binding protein subunit alpha-13	GNA13	GNA13_HUMAN	44.1	100.0%	5	6	14	0.01%	14.3%	APMAAQGMVETR	99.7%	70.6	25	65.2	6	0	0	1261.60	129	140
Guanine nucleotide-binding protein subunit alpha-13	GNA13	GNA13_HUMAN	44.1	100.0%	5	6	14	0.01%	14.3%	FLVECFR	99.2%	34.8	25	25.2	1	0	0	970.48	325	331
Guanine nucleotide-binding protein subunit alpha-13	GNA13	GNA13_HUMAN	44.1	100.0%	5	6	14	0.01%	14.3%	GIHEYDFEIK	97.5%	29.9	25	23.7	1	0	0	1250.61	205	214
Guanine nucleotide-binding protein subunit alpha-13	GNA13	GNA13_HUMAN	44.1	100.0%	5	6	14	0.01%	14.3%	ILLLGAGESGK	99.7%	70.5	25	0	5	0	0	1057.63	51	61
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	75	0.07%	45.4%	DETNYGIPQR	99.7%	67.8	25	58.6	4	0	0	1192.56	48	57
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	75	0.07%	45.4%	DGQAMLWDLNEGK	99.7%	102	25	102	8	0	0	1476.68	213	225
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	75	0.07%	45.4%	DKTIIMWK	99.7%	42.7	25	30.4	4	0	0	1034.57	37	44
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	75	0.07%	45.4%	DVLSVAFSSDNR	99.7%	79.7	25	72	9	0	0	1309.64	107	118
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	75	0.07%	45.4%	FSPNSSNPIIVSCGWDK	99.7%	71.7	25	59.3	4	0	0	1907.90	156	172
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	75	0.07%	45.4%	IIVDELK	96.7%	28.7	25	6.72	1	0	0	829.50	265	271
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	75	0.07%	45.4%	IIVDELKQEVISTSSK	99.7%	90.5	25	90.5	5	2	0	1789.00	265	280
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	75	0.07%	45.4%	LTRDETNYGIPQR	99.7%	51.7	25	51.3	4	2	0	1562.79	45	57
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	75	0.07%	45.4%	LWDLTTGTTTR	99.7%	82.7	25	82.2	4	0	0	1264.65	89	99
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	75	0.07%	45.4%	LWNTLGVCK	99.7%	60.2	25	50.3	7	0	0	1090.57	131	139
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	75	0.07%	45.4%	QEVISTSSK	96.1%	28	25	23.2	1	0	0	978.51	272	280
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	75	0.07%	45.4%	VWNLANCK	99.7%	45.3	25	42.3	3	0	0	1004.50	176	183
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	75	0.07%	45.4%	VWQVTIGTR	99.7%	71.1	25	63	6	0	0	1059.59	309	317
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	75	0.07%	45.4%	YTVQDESHSEWVSCVR	99.7%	91.9	25	91.9	4	5	0	1981.87	140	155
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	75	0.07%	45.4%	YWLCAATGPSIK	99.7%	73.6	25	66.4	2	0	0	1366.68	246	257
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	8	8	13	0.01%	16.8%	CPQVEEAIVQSGQK	99.7%	38.9	25	36.8	1	0	0	1572.77	158	171
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	8	8	13	0.01%	16.8%	ELPTVVFR	96.3%	28.3	25	22.9	2	0	0	960.55	198	205
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	8	8	13	0.01%	16.8%	GGIPNVEGAAK	98.2%	31.3	25	26.2	1	0	0	1012.54	378	388
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	8	8	13	0.01%	16.8%	KDPGVPNSAPFK	99.7%	39.1	25	33.5	2	0	0	1256.66	46	57
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	8	8	13	0.01%	16.8%	LLGGFQETCSK	99.7%	57.9	25	55.7	2	0	0	1239.60	243	253
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	8	8	13	0.01%	16.8%	SGFNLEELEK	99.7%	45.9	25	40.2	1	0	0	1165.57	425	434
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	8	8	13	0.01%	16.8%	VGVIGFPNVGK	99.7%	46.5	25	36.5	2	0	0	1086.63	257	267
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	8	8	13	0.01%	16.8%	VIEASDVVLEVLDAR	99.7%	50.6	25	39.3	2	0	0	1627.89	137	151
H/ACA ribonucleoprotein complex subunit 1	GAR1	GAR1_HUMAN	22.3	100.0%	2	2	4	0.00%	7.4%	FYIDPYK	99.7%	39.7	25	34.3	2	0	0	945.47	144	150
H/ACA ribonucleoprotein complex subunit 1	GAR1	GAR1_HUMAN	22.3	100.0%	2	2	4	0.00%	7.4%	VDEIFGQLR	99.7%	60.8	25	50	2	0	0	1076.57	113	121
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	5	5	9	0.01%	11.3%	APQVVAEAAK	99.7%	39	25	36.3	2	0	0	983.55	434	443
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	5	5	9	0.01%	11.3%	DSAVNAICYGAK	99.7%	48.8	25	41.4	2	0	0	1268.59	303	314
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	5	5	9	0.01%	11.3%	EVVAEVVK	99.7%	46.6	25	32.5	2	0	0	872.51	426	433
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	5	5	9	0.01%	11.3%	LGIFWVSCEAGTYIR	99.6%	38	25	38	1	0	0	1771.88	213	227
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	5	5	9	0.01%	11.3%	LHNAIEGGTQLSR	99.7%	74.8	25	73.7	2	0	0	1395.73	159	171
HCLS1-associated protein X-1	HAX1	HAX1_HUMAN	31.6	99.8%	2	2	3	0.00%	7.2%	GFFGFPGPR	96.5%	28.5	25	26.7	1	0	0	981.49	9	17
HCLS1-associated protein X-1	HAX1	HAX1_HUMAN	31.6	99.8%	2	2	3	0.00%	7.2%	IFGGVLESDAR	99.7%	75.7	25	61.1	2	0	0	1163.61	140	150
HEAT repeat-containing protein 1	HEATR1	HEAT1_HUMAN	242.4	100.0%	2	2	3	0.00%	1.1%	LVPDLLAIVQR	99.7%	59	25	47.8	2	0	0	1236.77	1644	1654
HEAT repeat-containing protein 1	HEATR1	HEAT1_HUMAN	242.4	100.0%	2	2	3	0.00%	1.1%	VSLLNEQFLPLIR	99.7%	58.2	25	51.3	1	0	0	1541.91	418	430
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	20	0.02%	17.3%	AIQDAILEVLK	99.7%	73.3	25	65.3	2	0	0	1212.72	804	814
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	20	0.02%	17.3%	ATDTINSQGQFPSYLETVTK	99.7%	83.2	25	83.2	2	0	0	2200.08	636	655

HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	20	0.02%	17.3%	CSLLDPFAAVR	97.8%	30.4	25	16.5	1	0	0	1248.64	173	183
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	20	0.02%	17.3%	EGSGLFPDLLVR	99.7%	58.5	25	53.1	2	0	0	1302.71	815	826
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	20	0.02%	17.3%	LFDDVPQVR	99.7%	56.7	25	48.1	2	0	0	1088.57	254	262
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	20	0.02%	17.3%	LIPLLLSSLNDEVPEVR	99.7%	85.4	25	84	2	0	0	1907.09	286	302
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	20	0.02%	17.3%	LLPGLEADSKPGR	99.7%	53	25	49.1	2	0	0	1352.75	34	46
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	20	0.02%	17.3%	SAELVGTFVSPEVFLK	99.7%	63.7	25	60.4	2	0	0	1722.93	423	438
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	20	0.02%	17.3%	SVDDVLSHFAQR	99.7%	54.8	25	50.2	2	0	0	1373.68	242	253
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	20	0.02%	17.3%	SYYQSSVQYLYR	99.7%	64.3	25	61.5	1	0	0	1556.74	781	792
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	20	0.02%	17.3%	TPSASGLLVLASAMR	99.7%	90.9	25	90.9	2	0	0	1473.81	447	461
HEAT repeat-containing protein 3	HEATR3	HEAT3_HUMAN	74.6	99.8%	2	2	2	0.00%	3.2%	DIMTPLVALLK	96.0%	28	25	27.7	1	0	0	1213.72	122	132
HEAT repeat-containing protein 3	HEATR3	HEAT3_HUMAN	74.6	99.8%	2	2	2	0.00%	3.2%	SQAEIINALLK	99.4%	35.8	25	9.12	1	0	0	1199.70	268	278
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	30	66	0.07%	39.5%	AFYPEEISSMVLTK	99.7%	91.4	25	91.3	6	0	0	1630.80	113	126
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	30	66	0.07%	39.5%	AQIHDLVLVGGSTR	99.7%	93.6	25	88.8	2	2	0	1465.81	329	342
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	30	66	0.07%	39.5%	ARFEELCSDLFR	99.7%	51.5	25	47.6	2	2	0	1542.74	300	311
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	30	66	0.07%	39.5%	ATAGDTHLGGEDFDNR	99.7%	51.3	25	51	3	2	0	1675.73	221	236
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	30	66	0.07%	39.5%	DAGVIAGLNVLR	99.7%	99	25	87.1	4	0	0	1197.70	160	171
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	30	66	0.07%	39.5%	DNNLLGR	99.7%	42.5	25	27.9	2	0	0	801.42	452	458
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	30	66	0.07%	39.5%	FEELCSDLFR	99.7%	44.3	25	44.3	2	0	0	1315.60	302	311
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	30	66	0.07%	39.5%	FGDPVVQSDMK	99.7%	39.6	25	39.6	2	0	0	1222.58	78	88
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	30	66	0.07%	39.5%	GGSGSGPTIEEVD	99.7%	43.8	25	43.8	2	0	0	1204.53	629	641
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	30	66	0.07%	39.5%	HWPFQVINDGDKPK	99.7%	53.7	25	53.7	0	1	0	1680.85	89	102
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	30	66	0.07%	39.5%	IINEPTAAAIAYGLDR	99.7%	133	25	124	4	3	0	1687.90	172	187
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	30	66	0.07%	39.5%	ITITNDKGR	99.7%	51.2	25	43.4	2	0	0	1017.57	501	509
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	30	66	0.07%	39.5%	KFGDPVVQSDMK	99.7%	38.9	25	38.3	2	0	0	1350.67	77	88
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	30	66	0.07%	39.5%	LLQDFFNGR	99.7%	60.3	25	45.5	2	0	0	1109.57	349	357
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	30	66	0.07%	39.5%	LSKEEIER	99.7%	59.6	25	33.8	3	0	0	1003.54	510	517
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	30	66	0.07%	39.5%	LVNHFVEEFK	99.3%	35.3	25	32.7	2	0	0	1261.66	237	246
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	30	66	0.07%	39.5%	LVNHFVEEFKR	99.7%	37.7	25	37.2	0	2	0	1417.76	237	247
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	30	66	0.07%	39.5%	MVQEAEKYK	99.6%	38	25	32	2	0	0	1125.56	518	526
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	30	66	0.07%	39.5%	NALESYAFNMK	99.7%	71.3	25	71.3	5	0	0	1287.60	540	550
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	30	66	0.07%	39.5%	NQVALNPQNTVFDAK	99.7%	105	25	97.7	2	0	0	1658.85	57	71
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	30	66	0.07%	39.5%	NQVALNPQNTVFDAKR	99.7%	61	25	61	1	2	0	1814.95	57	72
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	30	66	0.07%	39.5%	SAVEDEGLK	99.7%	39.2	25	33.7	2	0	0	947.47	551	559
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	30	66	0.07%	39.5%	TTPSYVAFTDTER	99.7%	88.4	25	83.6	3	0	0	1487.70	37	49
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	30	66	0.07%	39.5%	VEIIANDQGNR	99.7%	70.8	25	0	2	0	0	1228.63	26	36
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	30	66	0.07%	39.5%	VQVSYKGETK	99.7%	43.7	25	38.8	2	0	0	1138.61	103	112
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	22	30	66	0.07%	39.5%	YKAEDEVQR	99.7%	49.3	25	40.3	2	0	0	1137.55	525	533
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	9	9	15	0.01%	16.1%	AFSDPFVEAEK	99.7%	52.6	25	43.9	2	0	0	1239.59	74	84
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	9	9	15	0.01%	16.1%	AGGIETIANEYSDR	99.7%	66.4	25	63.8	2	0	0	1495.70	20	33
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	9	9	15	0.01%	16.1%	EDIYAVEIVGGATR	99.7%	87.5	25	80.3	1	0	0	1492.76	333	346
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	9	9	15	0.01%	16.1%	ELSTTLNADEAVTR	99.7%	54.2	25	51.3	2	0	0	1519.76	361	374
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	9	9	15	0.01%	16.1%	FLEMCNDLLAR	99.7%	49.9	25	41.8	1	0	0	1381.66	306	316
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	9	9	15	0.01%	16.1%	FQESEERPK	98.9%	33.1	25	18.2	2	0	0	1149.55	689	697
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	9	9	15	0.01%	16.1%	GCALQCAILSPAFK	99.7%	89.3	25	74.6	2	0	0	1535.77	375	388
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	9	9	15	0.01%	16.1%	MIMQDKLEK	98.1%	30.9	25	23.2	3	0	0	1135.59	604	612
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	9	9	15	0.01%	16.1%	NAVEEYVYEMR	99.7%	55.9	25	55.2	2	0	0	1402.63	619	629
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	9	9	15	0.01%	16.1%	SVMDATQIAGLNCLR	99.7%	59.3	25	44	1	0	0	1648.81	155	169
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	9	9	15	0.01%	16.1%	VLATAFDTTLGGR	99.7%	102	25	95.3	2	0	0	1321.71	222	234
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	36	71	0.07%	37.6%	ARFEELNADLFR	99.7%	63.5	25	53.5	2	2	0	1480.75	300	311
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	36	71	0.07%	37.6%	DAGTIAGLNVLR	99.7%	87.8	25	70.8	4	0	0	1199.67	160	171
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	36	71	0.07%	37.6%	EIAEAYLGK	99.7%	59.3	25	46.9	2	0	0	993.53	129	137

Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	36	71	0.07%	37.6%	FEELNADLFR	99.7%	63.1	25	55.6	2	0	0	1253.62	302	311
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	36	71	0.07%	37.6%	IINEPTAAAIAYGLDK	99.7%	112	25	112	2	0	0	1659.90	172	187
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	36	71	0.07%	37.6%	IINEPTAAAIAYGLDKK	99.7%	92	25	92	2	2	0	1787.99	172	188
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	36	71	0.07%	37.6%	ITITNDKGR	99.7%	51.2	25	43.4	2	0	0	1017.57	501	509
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	36	71	0.07%	37.6%	LDKSQIHDIVLVGGSTR	99.7%	35.5	25	35.5	0	1	0	1838.01	326	342
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	36	71	0.07%	37.6%	LLQDFFNGK	99.7%	46.2	25	28.8	2	0	0	1081.57	349	357
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	36	71	0.07%	37.6%	LSKEDIER	99.7%	59.8	25	16	2	0	0	989.53	510	517
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	36	71	0.07%	37.6%	MKEIAEAYLGK	99.7%	68.1	25	56.8	4	0	0	1268.66	127	137
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	36	71	0.07%	37.6%	MVNHFIAEFK	99.7%	49.2	25	35.9	4	1	0	1235.62	237	246
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	36	71	0.07%	37.6%	MVQEAEKYK	99.6%	38	25	32	2	0	0	1125.56	518	526
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	36	71	0.07%	37.6%	NQVAMNPTNTVFDAK	99.7%	107	25	104	4	0	0	1649.80	57	71
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	36	71	0.07%	37.6%	NQVAMNPTNTVFDAKR	99.7%	32.1	25	31.8	0	2	0	1805.90	57	72
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	36	71	0.07%	37.6%	NSLESYAFNMK	99.7%	84.8	25	83.2	2	0	0	1319.59	540	550
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	36	71	0.07%	37.6%	RFDDAVVQSDMK	99.7%	61.7	25	58.8	3	0	0	1410.67	77	88
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	36	71	0.07%	37.6%	SFYPEEVSSMVLTK	99.7%	83.3	25	83.3	4	0	0	1616.79	113	126
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	36	71	0.07%	37.6%	SQIHDIVLVGGSTR	99.7%	79.3	25	74.4	2	2	0	1481.81	329	342
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	36	71	0.07%	37.6%	STAGDTHLGGEDFDNR	99.7%	73.6	25	73.6	2	1	0	1691.73	221	236
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	36	71	0.07%	37.6%	TTPSYVAFTDTER	99.7%	88.4	25	83.6	3	0	0	1487.70	37	49
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	36	71	0.07%	37.6%	TVTNAVVTVPAYFNDSQR	99.7%	69.5	25	68.1	2	2	0	1982.00	138	155
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	36	71	0.07%	37.6%	VCNPIITK	99.5%	36.5	25	14	2	0	0	944.52	602	609
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	36	71	0.07%	37.6%	VEIIANDQGNR	99.7%	70.8	25	0	2	0	0	1228.63	26	36
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	36	71	0.07%	37.6%	VQVEYKGETK	99.7%	51.3	25	45.3	2	0	0	1180.62	103	112
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	16	44	0.04%	19.7%	AGGIETIANEFSDR	99.7%	68.7	25	68.7	4	0	0	1479.71	20	33
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	16	44	0.04%	19.7%	CTPSVISFGSK	96.7%	28.8	25	22.2	1	0	0	1182.58	34	44
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	16	44	0.04%	19.7%	DISTTLNADEAVAR	99.7%	98.9	25	87.8	4	0	0	1475.73	361	374
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	16	44	0.04%	19.7%	DKLCGPYEK	98.0%	30.8	25	23	1	0	0	1109.53	647	655
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	16	44	0.04%	19.7%	FQEAEERPK	99.5%	37.2	25	19.6	4	0	0	1133.56	706	714
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	16	44	0.04%	19.7%	FVVQNVSAQK	99.7%	57.7	25	53.7	4	0	0	1119.62	462	471
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	16	44	0.04%	19.7%	GCALQCAILSPAFK	99.7%	89.3	25	74.6	2	0	0	1535.77	375	388
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	16	44	0.04%	19.7%	LKETAENSLK	99.7%	51.1	25	14.3	2	0	0	1132.62	125	134
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	16	44	0.04%	19.7%	MFEELGQR	99.0%	33.6	25	32.1	2	0	0	1009.48	715	722
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	16	44	0.04%	19.7%	MIMQDKLEK	98.1%	30.9	25	23.2	3	0	0	1135.59	621	629
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	16	44	0.04%	19.7%	NAVEEYVYEFR	99.7%	61.3	25	60.5	2	0	0	1418.66	636	646
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	16	44	0.04%	19.7%	SLDQDPVVR	99.5%	36.9	25	28.7	3	0	0	1028.54	773	781
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	16	44	0.04%	19.7%	SQFEELCAELLQK	99.7%	80.2	25	71.5	2	0	0	1594.78	304	316
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	16	44	0.04%	19.7%	SVLDAAQIVGLNCLR	99.7%	79.8	25	71	4	0	0	1628.88	155	169
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	16	44	0.04%	19.7%	VLGTAFDPFLGGK	99.7%	83.2	25	66.6	6	0	0	1321.72	222	234
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	29	0.03%	26.4%	AFLDALQNQAEASSK	99.7%	110	25	106	2	0	0	1592.79	182	196
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	29	0.03%	26.4%	AQLLQPTLEINPR	99.7%	78.9	25	78.2	2	0	0	1492.85	635	647
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	29	0.03%	26.4%	EGIVTATEQEVKEDIAK	99.7%	68.2	25	68.1	2	0	0	1859.96	450	466
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	29	0.03%	26.4%	ELGSSVALYSR	99.7%	62.1	25	58.9	2	0	0	1181.62	358	368
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	29	0.03%	26.4%	ELISNASDALEK	99.7%	92.5	25	80.8	3	0	0	1289.66	115	126
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	29	0.03%	26.4%	ELLQESALIR	99.7%	75.9	25	61.7	2	0	0	1171.67	403	412
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	29	0.03%	26.4%	FFEDYGLFMR	99.7%	65.3	25	65.3	2	0	0	1324.60	440	449
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	29	0.03%	26.4%	GVVDSEDIPLNLSR	99.7%	107	25	0	17	0	0	1513.79	389	402
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	29	0.03%	26.4%	LRDVLQQR	99.2%	34.6	25	25.5	1	0	0	1027.60	414	421
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	29	0.03%	26.4%	MNTLQAIWMMDPK	99.7%	43.1	25	43.1	2	0	0	1578.75	292	304
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	29	0.03%	26.4%	NIYYLCAPNR	99.7%	39.4	25	33.8	2	0	0	1283.62	496	505
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	29	0.03%	26.4%	SDCKEFSSEAR	99.7%	54.7	25	54.7	2	1	0	1315.56	259	269
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	29	0.03%	26.4%	TDAPLNIR	99.7%	41.5	25	33	2	0	0	899.49	333	340
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	29	0.03%	26.4%	YESSALPSGQLTSLSEYASR	99.7%	101	25	90.1	2	0	0	2146.03	470	489

Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	14	15	29	0.03%	26.4%	YSNFVSFPLYLNGR	99.6%	38.1	25	38.1	2	0	0	1676.84	277	290
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	ADLINNLGTIAK	99.7%	71.3	25	64.2	20	0	0	1242.71	101	112
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	ALLFVPR	99.7%	39.5	25	0	3	0	0	815.51	339	345
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	APFDLFENR	99.7%	65.1	25	65.1	2	0	0	1108.54	347	355
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	DNSTMGYMAAK	99.7%	58.4	25	53.3	4	0	0	1188.50	621	631
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	DQVANSAFVER	99.7%	78.6	25	71.6	6	0	0	1235.60	500	510
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	EDQTEYLEER	99.7%	66.2	25	62.7	4	0	0	1311.57	192	201
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	EDQTEYLEERR	97.1%	22.1	25	19.7	0	1	0	1467.67	192	202
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	EGLELPEDEEEKK	99.7%	51.4	25	49.8	2	0	0	1544.73	547	559
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	EKYIDQEELNK	99.7%	55.8	25	43.6	2	0	0	1408.70	282	292
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	ELHINLIPNK	98.9%	33.4	25	28	2	0	0	1190.69	75	84
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	ELHINLIPNKQDR	99.7%	46.1	25	46.1	2	0	0	1589.88	75	87
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	ELISNSSDALDK	99.7%	75.2	25	65.2	1	0	0	1291.64	47	58
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	ELISNSSDALDKIR	99.7%	96.4	25	86.6	2	0	0	1560.82	47	60
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	FENLCK	97.6%	30	25	13.4	2	0	0	810.38	568	573
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	FYEQFSK	99.7%	52.8	25	30.9	2	0	0	948.45	437	443
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	GVVDSEDLPLNISR	99.7%	107	25	0	17	0	0	1513.79	387	400
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	HFSVEGQLEFR	99.7%	73.1	25	70.8	11	3	0	1348.66	328	338
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	HIYYITGETK	99.7%	47.4	25	44.9	2	0	0	1224.63	490	499
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	HLEINPDHSIIETLR	99.7%	35	25	35	0	2	0	1786.94	633	647
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	HNDDEQYAWESSAGGSFTVR	99.7%	56.9	25	56.9	0	2	0	2255.96	154	173
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	HSQFIGYPITLFVEK	99.7%	44.9	25	44.9	1	0	0	1778.95	210	224
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	IMKDILEK	99.7%	47.2	25	4.89	2	0	0	989.57	574	581
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	IRYESLTDPSK	99.7%	40.9	25	37.7	2	1	0	1308.68	59	69
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	LGIHEDSQNR	99.7%	50.5	25	44.1	5	0	0	1168.57	447	456
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	LVTSPCCIVTSTYGWTANMER	99.7%	77.7	25	77.7	3	0	0	2446.12	592	612
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	NPDDITNEEYGEFYK	99.7%	80.2	25	75.7	2	0	0	1833.78	300	314
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	RAPFDLFENR	99.7%	42.6	25	37.2	2	0	0	1264.64	346	355
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	SLTNDWEDHLAVK	99.7%	85.5	25	79.6	7	3	0	1527.74	315	327
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	TLTIVDTGIGMTK	99.7%	111	25	0	22	0	0	1349.73	88	100
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	VILHLKEDQTEYLEER	99.7%	59.7	25	59.7	0	2	0	2015.04	186	201
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	YESLTDPSK	99.7%	66.2	25	59.5	3	0	0	1039.49	61	69
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	YESLTDPSKLDSGK	99.7%	74.5	25	56.8	4	1	0	1539.75	61	74
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	YIDQEELNK	99.7%	60.5	25	39.5	16	0	0	1151.56	284	292
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	YYTSASGDEMVSLK	99.7%	71.9	25	71.9	4	0	0	1566.70	465	478
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	22	49	0.05%	45.1%	YYTSASGDEMVSLKDYCTR	99.7%	41.8	25	41.4	0	2	0	2245.97	465	483
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	ADLINNLGTIAK	99.7%	71.3	25	64.2	20	0	0	1242.71	96	107
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	AKFENLCK	99.4%	35.6	25	27	1	0	0	1009.51	558	565
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	ALLFIPR	99.5%	37.2	25	14.3	10	0	0	829.53	331	337
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	APFDLFENK	99.7%	42.8	25	38.8	3	0	0	1080.54	339	347
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	APFDLFENKK	99.7%	49.3	25	44.5	2	0	0	1208.63	339	348
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	DNSTMGYMMAK	99.7%	70.4	25	20.5	12	0	0	1264.50	613	623
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	EDQTEYLEER	99.7%	66.2	25	62.7	4	0	0	1311.57	187	196
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	EDQTEYLEERR	97.1%	22.1	25	19.7	0	1	0	1467.67	187	197
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	EGLELPEDEEEKK	99.7%	51.4	25	49.8	2	0	0	1544.73	539	551
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	EKYIDQEELNK	99.7%	55.8	25	43.6	2	0	0	1408.70	274	284
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	ELISNASDALDK	99.7%	86.8	25	76	6	0	0	1275.64	42	53
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	ELISNASDALDKIR	99.7%	92.4	25	73.6	7	2	0	1544.83	42	55
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	ELKIDIIPNPQER	99.7%	47.2	25	43.8	4	0	0	1564.87	70	82
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	EQVANSAFVER	99.7%	74.9	25	65.9	13	0	0	1249.62	492	502
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	FENLCK	97.6%	30	25	13.4	2	0	0	810.38	560	565

Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	FYEAFSK	99.4%	35.6	25	28.1	3	0	0	891.42	429	435
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	GFEVVYMTEPIDEYCVQQLK	99.7%	90.4	25	50.8	5	2	0	2464.14	507	526
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	GVVDSEDLPLNISR	99.7%	107	25	0	17	0	0	1513.79	379	392
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	HFSVEGQLEFR	99.7%	73.1	25	70.8	11	3	0	1348.66	320	330
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	HLEINPDHPIVETLR	99.7%	72	25	65.9	2	2	0	1782.95	625	639
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	HNDDEQYAWESSAGGSFTVR	99.7%	56.9	25	56.9	0	2	0	2255.96	149	168
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	HSQFIGYPITLYLEK	99.7%	35.3	25	0	0	2	0	1808.96	205	219
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	IDIIPNPQER	99.7%	48.8	25	38.3	4	0	0	1194.65	73	82
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	IRYESLTDPSK	99.7%	40.9	25	37.7	2	1	0	1308.68	54	64
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	KFYEAFSK	97.1%	29.3	25	19.1	2	0	0	1019.52	428	435
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	LGIHEDSTNR	99.7%	64.7	25	63.4	6	0	0	1141.56	439	448
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	LGIHEDSTNRR	99.7%	50.9	25	42.7	1	2	0	1297.66	439	449
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	LVSSPCCIVTSTYGWTANMER	99.7%	99.3	25	99.3	4	4	0	2432.10	584	604
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	NPDDITQEEYGEFYK	99.7%	98.9	25	98.9	9	0	0	1847.80	292	306
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	RAPFDLFENK	99.7%	60.1	25	47.5	7	0	0	1236.64	338	347
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	RLSELLR	99.7%	40.6	25	13.6	3	0	0	886.55	450	456
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	SIYYITGESK	99.7%	68.8	25	66.6	11	0	0	1160.58	482	491
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	SLTNDWEDHLAVK	99.7%	85.5	25	79.6	7	3	0	1527.74	307	319
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	TLTLVDTGIGMTK	99.7%	111	25	0	22	0	0	1349.73	83	95
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	VILHLKEDQTEYLEER	99.7%	59.7	25	59.7	0	2	0	2015.04	181	196
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	YESLTDPSK	99.7%	66.2	25	59.5	3	0	0	1039.49	56	64
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	YESLTDPSKLDSGK	99.7%	74.5	25	56.8	4	1	0	1539.75	56	69
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	YHTSQSGDEMTSLSEYVSR	99.7%	107	25	107	4	8	0	2176.95	457	475
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	39	56	266	0.26%	48.9%	YIDQEELNK	99.7%	60.5	25	39.5	16	0	0	1151.56	276	284
Helicase SKI2W	SKIV2L	SKIV2_HUMAN	137.8	100.0%	3	3	5	0.00%	2.8%	LVGEPVLGAK	95.9%	27.9	25	27.9	1	0	0	982.59	1216	1225
Helicase SKI2W	SKIV2L	SKIV2_HUMAN	137.8	100.0%	3	3	5	0.00%	2.8%	TQGELFLLLDSR	99.6%	37.4	25	35.6	2	0	0	1391.75	499	510
Helicase SKI2W	SKIV2L	SKIV2_HUMAN	137.8	100.0%	3	3	5	0.00%	2.8%	TVVAEYAIALAQK	99.7%	67.2	25	67.2	2	0	0	1376.78	339	351
Helicase-like transcription factor	HLTF	HLTF_HUMAN	113.9	100.0%	3	3	5	0.00%	2.8%	ASGFVFTR	99.7%	57.1	25	47.2	2	0	0	884.46	873	880
Helicase-like transcription factor	HLTF	HLTF_HUMAN	113.9	100.0%	3	3	5	0.00%	2.8%	MSELSSSRPK	99.7%	39.2	25	36.2	1	0	0	1121.56	377	386
Helicase-like transcription factor	HLTF	HLTF_HUMAN	113.9	100.0%	3	3	5	0.00%	2.8%	VILDEGHAIR	99.7%	40.3	25	33.7	2	0	0	1122.63	554	563
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	3	3	8	0.01%	6.7%	LEDVLPLAFTR	99.7%	51.1	25	32.6	5	0	0	1273.72	259	269
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	3	3	8	0.01%	6.7%	SSAVDPEPQVK	99.7%	49.7	25	36.1	1	0	0	1156.58	248	258
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	3	3	8	0.01%	6.7%	TIPSWATLSASQLAR	99.7%	56.8	25	56.8	2	0	0	1601.86	132	146
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	5	6	12	0.01%	15.7%	DLKDYFTK	99.0%	33.8	25	16.6	2	0	0	1029.53	84	91
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	5	6	12	0.01%	15.7%	EVYQQQQYGSGGR	99.7%	86	25	74.1	2	0	0	1499.69	233	245
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	5	6	12	0.01%	15.7%	FGEVVDCTIK	99.7%	66.5	25	0	7	0	0	1167.57	92	101
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	5	6	12	0.01%	15.7%	GFGFILFK	99.7%	45.2	25	35.5	2	0	0	928.53	111	118
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	5	6	12	0.01%	15.7%	MFVGGLSWDTSK	99.7%	46.5	25	46.5	2	0	0	1343.63	71	82
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	5	6	12	0.01%	15.7%	MFVGGLSWDTSKK	99.7%	68	25	60.8	4	0	0	1455.73	71	83
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	4	4	8	0.01%	14.4%	AEIIADKQSGK	99.7%	54.3	25	42.9	2	0	0	1159.63	127	137
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	4	4	8	0.01%	14.4%	AVPKEDIYSGGGGGGSR	99.7%	93	25	89.1	2	0	0	1606.78	173	189
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	4	4	8	0.01%	14.4%	EDIYSGGGGGGSR	99.7%	62.8	25	62.8	2	0	0	1211.53	177	189
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	4	4	8	0.01%	14.4%	LFIGGLNVQTSESGLR	99.7%	109	25	105	2	0	0	1690.91	9	24
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	6	8	22	0.02%	22.6%	EDSQRPGAHLTVK	98.9%	33.2	25	23.2	2	0	0	1437.74	93	105
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	6	8	22	0.02%	22.6%	IEVIEIMTDR	99.7%	58.9	25	54.2	2	0	0	1234.64	131	140
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	6	8	22	0.02%	22.6%	LFIGGLSFETTDESLR	99.7%	70.5	25	65.6	3	0	0	1784.91	16	31
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	6	8	22	0.02%	22.6%	NQGGYGGSSSSSSYGSGR	99.7%	123	25	123	4	0	0	1694.70	353	370
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	6	8	22	0.02%	22.6%	SESPKEPEQLR	99.5%	27.6	25	21.2	2	2	0	1299.65	4	14
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	6	8	22	0.02%	22.6%	SSGPYGGGGQYFAKPR	99.7%	100	25	93.7	5	2	0	1628.78	337	352
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	4	5	9	0.01%	16.1%	EDSVKPGAHLTVK	99.7%	44.1	25	40.3	2	0	0	1380.75	114	126
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	4	5	9	0.01%	16.1%	IETIEVMEDR	99.7%	77.2	25	69.3	4	0	0	1234.60	152	161

Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	4	5	9	0.01%	16.1%	IFVGGIKEDTEEYNLR	99.7%	31.4	25	31.3	0	1	0	1882.95	128	143
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	4	5	9	0.01%	16.1%	SSGSPYGGGYGSGGGSGGYGSR	99.7%	130	25	130	2	0	0	1910.79	355	376
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	6	6	24	0.02%	18.3%	DLKDYFSK	99.2%	34.9	25	26.8	2	0	0	1015.51	112	119
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	6	6	24	0.02%	18.3%	FGEVVDCTLK	99.7%	66.5	25	0	7	0	0	1167.57	120	129
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	6	6	24	0.02%	18.3%	FGEVVDCTLKLDPITGR	99.7%	42.8	25	35.8	0	4	0	1919.99	120	136
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	6	6	24	0.02%	18.3%	GFGFVLFK	99.7%	44.3	25	40.3	4	0	0	914.51	139	146
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	6	6	24	0.02%	18.3%	IDASKNEEDEGHSNSSPR	99.7%	37.2	25	37.2	0	2	0	1971.86	68	85
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	6	6	24	0.02%	18.3%	IFVGGLSPDTPEEK	99.7%	72.2	25	65.4	5	0	0	1488.76	184	197
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	5	7	13	0.01%	23.6%	ATENDIYNFFSPLNPVR	99.7%	83.6	25	81	9	2	0	1996.98	300	316
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	5	7	13	0.01%	23.6%	DLSYCLSGMYDHR	99.7%	38.5	25	38.5	1	0	0	1632.68	263	275
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	5	7	13	0.01%	23.6%	HSGPNSADSANDGFVR	99.7%	90.9	25	87.6	2	2	0	1630.72	99	114
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	5	7	13	0.01%	23.6%	QSGEAFVELGSEDDVK	99.7%	111	25	110	2	0	0	1709.79	53	68
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	5	7	13	0.01%	23.6%	RYIGIVK	99.5%	37	25	24.1	2	0	0	848.54	218	224
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	5	7	13	0.01%	23.6%	VHIEIGPDGR	99.7%	57.3	25	50.5	5	0	0	1092.58	317	326
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	5	7	13	0.01%	23.6%	YGDSEFTVQSTTGHCVHMR	99.7%	64.4	25	64.4	0	4	0	2227.95	276	294
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	13	17	82	0.08%	42.5%	ATENDIYNFFSPLNPVR	99.7%	83.6	25	81	9	2	0	1996.98	300	316
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	13	17	82	0.08%	42.5%	DLNYCFSGMSDHR	99.7%	67.1	25	67.1	8	0	0	1601.65	263	275
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	13	17	82	0.08%	42.5%	EGRPSGEAFVELESEDEVK	99.7%	60.1	25	52.3	0	4	0	2106.98	50	68
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	13	17	82	0.08%	42.5%	FFSDCK	97.4%	29.7	25	25.5	1	0	0	803.34	30	35
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	13	17	82	0.08%	42.5%	GLPWSCSADEVQR	99.7%	76.2	25	73.6	8	0	0	1504.69	17	29
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	13	17	82	0.08%	42.5%	HTGPNSPDTANDGFVR	99.7%	72.4	25	68.4	6	10	0	1684.77	99	114
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	13	17	82	0.08%	42.5%	IQNGAQGIR	99.7%	55	25	38.1	4	0	0	956.53	36	44
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	13	17	82	0.08%	42.5%	SNNVEMDWVLK	99.7%	67.6	25	63	4	0	0	1334.64	88	98
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	13	17	82	0.08%	42.5%	STGEAFVQFASQEIAEK	99.7%	107	25	102	10	0	0	1841.89	151	167
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	13	17	82	0.08%	42.5%	VHIEIGPDGR	99.7%	57.3	25	50.5	5	0	0	1092.58	317	326
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	13	17	82	0.08%	42.5%	VTGEADVEFATHEDAVAAMSK	99.7%	31.8	25	29.4	0	1	0	2194.00	327	347
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	13	17	82	0.08%	42.5%	YGDGGSTFQSTTGHCVHMR	99.7%	60.9	25	60.9	0	8	0	2113.88	276	294
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	13	17	82	0.08%	42.5%	YVELFLNSTAGASGGAYEHR	98.5%	24.1	25	19.5	0	2	0	2142.03	356	375
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	4	6	10	0.01%	28.5%	ATENDIYNFFSPLNPMR	99.7%	83.1	25	83.1	4	0	0	2028.95	300	316
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	4	6	10	0.01%	28.5%	DLNYCFSGMSDHR	99.7%	67.1	25	67.1	8	0	0	1601.65	263	275
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	4	6	10	0.01%	28.5%	EGRPSGEAFVELESEEEVK	98.8%	24.8	25	24.8	0	1	0	2121.00	50	68
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	4	6	10	0.01%	28.5%	FFSDCK	97.4%	29.7	25	25.5	1	0	0	803.34	30	35
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	4	6	10	0.01%	28.5%	HTGPNSPDTANDGFVR	99.7%	72.4	25	68.4	6	10	0	1684.77	99	114
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	4	6	10	0.01%	28.5%	SNSVEMDWVLK	99.7%	45.9	25	35.5	2	0	0	1307.63	88	98
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	4	6	10	0.01%	28.5%	STGEAFVQFASQEIAEK	99.7%	107	25	102	10	0	0	1841.89	151	167
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	4	6	10	0.01%	28.5%	VHIEIGPDGR	99.7%	57.3	25	50.5	5	0	0	1092.58	317	326
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	4	6	10	0.01%	28.5%	YGDGGSSFQSTTGHCVHMR	99.7%	58.7	25	58.7	0	3	0	2083.87	276	294
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	4	4	8	0.01%	13.9%	ATENDIANFFSPLNPIR	99.7%	43.3	25	41.4	2	0	0	1918.97	206	222
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	4	4	8	0.01%	13.9%	EIAENALGK	98.4%	31.7	25	22.1	2	0	0	944.50	68	76
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	4	4	8	0.01%	13.9%	STGEAFVQFASK	99.7%	71.1	25	67.4	2	0	0	1271.63	56	67
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	4	4	8	0.01%	13.9%	VHIDIGADGR	99.7%	43.5	25	32.5	2	0	0	1052.55	223	232
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	23	56	0.06%	44.7%	DLAGSIIGK	99.7%	44.7	25	28.6	2	0	0	873.50	397	405
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	23	56	0.06%	44.7%	DYDDMSPR	99.7%	43.3	25	43.3	2	0	0	998.39	279	286
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	23	56	0.06%	44.7%	GGDLMAYDR	99.7%	51.8	25	49.2	4	0	0	1013.44	317	325
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	23	56	0.06%	44.7%	GGDLMAYDRR	99.4%	36.3	25	20.9	2	0	0	1153.54	317	326
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	23	56	0.06%	44.7%	GSDFDCELR	99.7%	50.8	25	46.2	2	0	0	1098.45	140	148
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	23	56	0.06%	44.7%	GSYGDLGGPIITTQVTIPK	99.7%	97.9	25	97.9	5	0	0	1917.03	378	396
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	23	56	0.06%	44.7%	IDEPLEGSEDR	99.7%	75.6	25	66	2	0	0	1259.58	423	433
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	23	56	0.06%	44.7%	IILDLISESPIK	99.7%	83.6	25	78.2	7	0	0	1340.80	208	219
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	23	56	0.06%	44.7%	IITITGTQDQIQNAQYLLQNSVK	99.7%	51	25	51	0	2	0	2589.39	434	456
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	23	56	0.06%	44.7%	ILSISADIETIGEILK	99.7%	58.9	25	58.9	1	0	0	1714.98	87	102

Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	23	56	0.06%	44.7%	LFQECCPHSTDR	99.7%	80.9	25	80.9	2	2	0	1549.65	180	191
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	23	56	0.06%	44.7%	LLIHQSLAGGIIGVK	99.7%	71.4	25	71.4	2	2	0	1518.94	149	163
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	23	56	0.06%	44.7%	NLPLPPPPPPR	99.1%	34.2	25	18.1	2	0	0	1194.70	306	316
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	23	56	0.06%	44.7%	NTDEMVELR	99.7%	78.8	25	60.7	4	0	0	1106.51	38	46
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	23	56	0.06%	44.7%	RPAEDMEEEQAFKR	99.7%	87.1	25	87.1	0	2	0	1735.81	22	35
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	23	56	0.06%	44.7%	SRNTDEMVELR	99.7%	35.2	25	14.1	2	2	0	1349.65	36	46
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	23	56	0.06%	44.7%	TDYNASVSVPDSSGPER	99.7%	107	25	105	2	0	0	1780.80	70	86
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	18	23	56	0.06%	44.7%	VVLIGGKPDR	99.7%	63.4	25	40	5	0	0	1053.64	192	201
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	9	10	23	0.02%	20.0%	AITHLNNNFMFGQK	99.7%	71.6	25	66.4	2	1	0	1634.81	435	448
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	9	10	23	0.02%	20.0%	ASLNGADIYSGCCTLK	99.7%	65.8	25	60.3	2	0	0	1729.79	249	264
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	9	10	23	0.02%	20.0%	IEYAKPTR	99.7%	46.6	25	37.8	4	0	0	977.54	265	272
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	9	10	23	0.02%	20.0%	ISRPGDSDDSR	97.6%	30.1	25	21.2	1	0	0	1204.56	179	189
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	9	10	23	0.02%	20.0%	LCFSTAQHAS	99.7%	54.3	25	54.3	4	0	0	1121.50	580	589
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	9	10	23	0.02%	20.0%	MGPPVGGHR	97.1%	29.2	25	15.9	1	0	0	907.46	345	353
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	9	10	23	0.02%	20.0%	NDQDTWDYTNPNLSGQGDPGSNPNKR	99.7%	78.4	25	78.4	0	1	0	2890.26	278	303
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	9	10	23	0.02%	20.0%	NPNGPYPYTLK	99.5%	36.6	25	30.9	2	0	0	1263.64	569	579
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	9	10	23	0.02%	20.0%	VFNVFCLYGNVEK	99.7%	92.8	25	83.5	5	0	0	1588.78	399	411
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	ACQIFVR	99.7%	44.5	25	32.8	1	0	0	893.47	652	658
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	ADILEDKDGK	99.7%	40	25	24.2	4	0	0	1103.56	233	242
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	AFITNIPFDVK	99.7%	79.4	25	64.3	4	0	0	1264.69	73	83
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	EVFSMAGVVVR	99.7%	63.8	25	56.4	1	0	0	1193.63	222	232
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	FEPYANPTKR	98.0%	30.8	25	17.5	1	0	0	1222.62	61	70
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	FESPEVAER	99.7%	55.1	25	43.8	4	0	0	1063.51	699	707
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	FGSGMNMGR	99.7%	58.5	25	12.2	7	0	0	972.40	363	371
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	GCAVVEFK	99.7%	45.2	25	29.5	2	0	0	909.45	113	120
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	GCGVVKFESPEVAER	95.6%	20.9	25	20.9	0	1	0	1663.81	693	707
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	GGNRFEPYANPTK	99.7%	39.1	25	27.9	2	1	0	1450.71	57	69
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	GIGMGNIGPAGMGMEGIGFGINK	99.7%	90	25	90	7	1	0	2226.04	323	345
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	GNFGGSFAGSFGGAGGHAPGVAR	99.7%	71.8	25	71.8	2	2	0	2034.95	628	650
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	INEILSNALK	99.7%	71	25	56.2	9	0	0	1114.65	372	381
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	INEILSNALKR	99.7%	46.9	25	39.2	2	0	0	1270.75	372	382
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	KACQIFVR	99.7%	58	25	43.8	2	0	0	1021.56	651	658
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	LGGAGMER	96.5%	28.5	25	28.5	1	0	0	806.38	411	418
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	LGSTVFVANLDYK	99.7%	92.8	25	83.9	4	0	0	1426.76	202	214
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	LKEVFSMAGVVVR	99.7%	66.2	25	61	3	3	0	1450.81	220	232
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	MGAGLGHGMDR	99.7%	68.5	25	64.2	7	0	0	1101.49	419	429
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	MGAGMGFGLER	99.7%	87.2	25	85.3	15	0	0	1125.52	486	496
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	MGANNLER	99.7%	71	25	59.3	4	0	0	904.43	558	565
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	MGANSLER	99.7%	70.4	25	62	6	0	0	877.42	571	578
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	MGGMEGPFGGGMENMGR	99.7%	63.1	25	63.1	5	0	0	1778.66	346	362
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	MGLAMGGGGGASFDR	99.7%	92.4	25	44.8	10	0	0	1399.61	607	621
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	MGLSMER	99.7%	56.8	25	47.3	4	0	0	823.38	525	531
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	MGLVMDR	99.7%	43.6	25	41.9	2	0	0	821.40	437	443
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	MGPAMGPALGAGIER	99.7%	76.6	25	63.9	8	0	0	1427.71	592	606
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	MGPLGLDHMASSIER	99.7%	81.6	25	81.6	7	4	0	1613.78	457	471
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	MGPVMDR	99.6%	38.4	25	22.2	2	0	0	805.37	544	550
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	MVPAGMGAGLER	99.7%	61	25	50.9	5	0	0	1188.59	532	543
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	NLPFDFTWK	98.8%	32.8	25	23.2	1	0	0	1167.58	659	667
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	QGGGGGGGSVPGIER	99.7%	80.6	25	80	6	0	0	1284.63	389	403
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	VGEVTYVELLMDAEGK	99.7%	76.5	25	66.3	4	0	0	1768.87	95	110
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	34	54	155	0.15%	47.4%	VGQTIER	99.7%	54.3	25.2	35.5	1	0	0	802.44	504	510

Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	10	11	28	0.03%	15.7%	DLFEDELVPLFEK	99.7%	69.5	25	62.6	3	0	0	1593.80	172	184
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	10	11	28	0.03%	15.7%	EQILEEFSK	96.4%	28.4	25	13.8	1	0	0	1122.57	257	265
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	10	11	28	0.03%	15.7%	GFCFLEYEDHK	99.7%	50.3	25	50.3	2	0	0	1444.62	287	297
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	10	11	28	0.03%	15.7%	GYAFVTFCTK	99.7%	63.2	25	63.2	2	0	0	1193.57	204	213
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	10	11	28	0.03%	15.7%	LMMDPLTGLNR	99.7%	55	25	46.5	5	0	0	1260.64	193	203
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	10	11	28	0.03%	15.7%	LYNNHEIR	99.1%	33.9	25	15.4	2	0	0	1058.54	222	229
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	10	11	28	0.03%	15.7%	NLANTVTEEILEK	99.7%	107	25	99.4	2	0	0	1473.78	344	356
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	10	11	28	0.03%	15.7%	SAFLCGVMK	98.8%	32.9	25	28.2	2	0	0	1012.50	92	100
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	10	11	28	0.03%	15.7%	TGYTLDVTTGQR	99.7%	70.5	25	68.6	7	0	0	1311.65	131	142
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	10	11	28	0.03%	15.7%	TKEQILEEFSK	99.7%	59.2	25	57.1	2	0	0	1351.71	255	265
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	8	8	22	0.02%	22.1%	DLYEDELVPLFEK	99.7%	66	25	59.4	4	0	0	1609.80	175	187
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	8	8	22	0.02%	22.1%	GFCFLEYEDHK	99.7%	50.3	25	50.3	2	0	0	1444.62	290	300
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	8	8	22	0.02%	22.1%	GYAFITFCGK	99.7%	61.3	25	57.8	2	0	0	1163.56	207	216
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	8	8	22	0.02%	22.1%	LCDSYEIRPGK	99.7%	58.9	25	44.3	2	0	0	1337.65	225	235
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	8	8	22	0.02%	22.1%	LMMDPLSGQNR	99.7%	47.4	25	28.8	2	0	0	1261.60	196	206
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	8	8	22	0.02%	22.1%	NLATTVTEEILEK	99.7%	122	25	112	7	0	0	1460.78	347	359
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	8	8	22	0.02%	22.1%	SAFLCGVMK	98.8%	32.9	25	28.2	2	0	0	1012.50	95	103
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	8	8	22	0.02%	22.1%	STAYEDYYYHPPPR	96.6%	21.7	25	21.7	0	1	0	1758.78	428	441
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	8	8	22	0.02%	22.1%	TGYTLDVTTGQR	99.7%	70.5	25	68.6	7	0	0	1311.65	134	145
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	8	8	22	0.02%	22.1%	TKENILEEFSK	99.7%	58	25	44.2	3	0	0	1337.69	258	268
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	8	8	22	0.02%	22.1%	YGGPPPDSVYSGVQPGIGTEVFVGK	97.0%	22	25	22	0	1	0	2507.25	147	171
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	AEGGGGGGRPGAPAAGDGK	99.7%	64.2	25	63.9	2	0	0	1538.73	216	234
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	AEGGGGGGRPGAPAAGDGKTEQK	99.7%	37.4	25	37.4	0	1	0	2024.97	216	238
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	AVVVCPKDEDYK	99.7%	40.8	25	40.8	2	0	0	1422.69	603	614
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	DCEVVMMIGLPGAGK	99.7%	96.2	25	85.4	4	0	0	1576.75	496	510
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	DIDIHEVR	99.7%	49.3	25	40.7	10	0	0	996.51	353	360
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	DLPEHAVLK	99.7%	43	25	31.4	5	0	0	1021.57	627	635
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	FIEIAAR	99.7%	48.3	25	33.1	7	0	0	819.47	566	572
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	GKVCFEMK	98.5%	32	25	22	2	0	0	998.48	332	339
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	GYFEYIEENK	99.7%	59.5	25	51.9	4	0	0	1291.58	256	265
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	GYFEYIEENKYSR	99.7%	72.1	25	72.1	7	2	0	1697.78	256	268
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	KAEGGGGGGRPGAPAAGDGK	99.4%	26.9	25	26.9	0	1	0	1666.83	215	234
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	KDCEVVMMIGLPGAGK	99.7%	92.4	25	92.4	6	3	0	1704.85	495	510
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	KMCLFAGFQR	99.7%	49.7	25	46.5	4	0	0	1257.62	592	601
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	LLEQYKEESK	99.7%	60.8	25	55.5	7	0	0	1266.66	665	674
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	LQAALDDEEAGGRPAMEPGNGSLDLGGDSAGR	99.7%	85.1	25	85.1	0	3	0	3142.43	38	69
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	LSASSLTMESFAFLWAGGR	99.7%	41.2	25	41.2	1	0	0	2047.00	306	324
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	MCLFAGFQR	99.7%	63.7	25	59.1	10	0	0	1145.52	593	601
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	MMVAGFK	95.3%	27.4	25	2.75	1	0	0	799.38	537	543
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	MMVAGFKK	98.1%	30.9	25	20.5	2	0	0	911.48	537	544
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	NFILDQTNVSAAAQR	99.7%	135	25	123	12	1	0	1647.84	576	590
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	NGQDLGVAFK	99.7%	62	25	57.5	8	0	0	1048.54	424	433
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	SSGPTSLFAVTVAPPGAR	99.7%	45.2	25	42.9	8	1	0	1714.91	187	204
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	TCNCETEDYGEK	99.7%	44.7	25	44.7	2	0	0	1505.55	388	399
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	VCFEMK	97.4%	29.7	25	19.9	1	0	0	813.36	334	339
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	VSELKEELK	99.7%	47.6	25	25.6	2	0	0	1074.60	13	21
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	VTEKIPVR	99.7%	52.9	25	39.3	7	0	0	941.58	340	347
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	27	37	142	0.14%	31.5%	YNILGTNTIMDK	99.7%	77.9	25	64.2	16	0	0	1382.70	525	536
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	7	7	13	0.01%	12.0%	EALGGQALYPHVLVK	99.7%	67.2	25	60.6	2	0	0	1594.90	361	375
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	7	7	13	0.01%	12.0%	HLPSTEPDPHVVR	99.4%	27.2	25	27.2	0	1	0	1483.77	271	283
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	7	7	13	0.01%	12.0%	NCAVEFNFGQR	99.7%	55.7	25	55.7	3	0	0	1341.60	376	386

Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	7	7	13	0.01%	12.0%	NPPGASTYNK	96.1%	28.1	25	28.1	1	0	0	1048.51	722	731
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	7	7	13	0.01%	12.0%	NYILDQTNVYGSAQR	99.7%	118	25	113	3	0	0	1741.85	501	515
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	7	7	13	0.01%	12.0%	QGAPTSFLPPEASQLKPDR	99.7%	35.9	25	35.9	0	1	0	2039.06	147	165
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	7	7	13	0.01%	12.0%	VCFEMK	97.4%	29.7	25	19.9	1	0	0	813.36	257	262
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	7	7	13	0.01%	12.0%	WDVLIQQATQCLNR	99.7%	78.9	25	73.7	2	0	0	1744.88	477	490
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	7	8	12	0.01%	11.4%	DLLVQQASQCLSK	99.7%	92.3	25	87.9	2	0	0	1489.77	509	521
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	7	8	12	0.01%	11.4%	EGCTEVSLLR	99.7%	50.5	25	34.7	2	0	0	1163.57	306	315
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	7	8	12	0.01%	11.4%	NCVVELNFGQK	99.7%	67.4	25	56	1	0	0	1307.64	407	417
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	7	8	12	0.01%	11.4%	NFILDQCNVYNSGQR	99.7%	64.9	25	62.2	2	0	0	1827.84	532	546
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	7	8	12	0.01%	11.4%	SGDETPGSEVPGDK	98.5%	32	25	32	1	0	0	1374.60	161	174
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	7	8	12	0.01%	11.4%	VTQNLPMK	94.5%	26.8	25	9.01	1	0	0	930.51	298	305
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	7	8	12	0.01%	11.4%	YNVLGAETVLNQMR	99.7%	91.4	25	85.4	3	0	0	1623.82	481	494
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	8	9	22	0.02%	28.6%	GGGGNFGPGPGSNFR	99.7%	57.8	25	52.8	6	0	0	1377.63	214	228
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	8	9	22	0.02%	28.6%	GGNFGFGDSR	99.7%	49.2	25	40.5	4	0	0	1013.44	204	213
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	8	9	22	0.02%	28.6%	IDTIEIITDR	99.7%	71.9	25	66.4	1	0	0	1188.65	138	147
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	8	9	22	0.02%	28.6%	LFIGGLSFETTEESLR	99.7%	86	25	86	2	0	0	1798.92	23	38
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	8	9	22	0.02%	28.6%	LTDCVVMR	99.7%	38.8	25	34.5	1	0	0	993.49	47	54
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	8	9	22	0.02%	28.6%	NMGGPYGGGNYGPGGSGGSGGYGGR	99.7%	101	25	101	3	0	0	2205.90	326	350
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	8	9	22	0.02%	28.6%	NYYEQWGK	99.4%	35.9	25	35.9	2	0	0	1087.48	39	46
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	8	9	22	0.02%	28.6%	TLETVPLER	99.7%	50.7	25	50.7	3	0	0	1057.59	4	12
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	10	12	27	0.03%	28.4%	GFAFVQYVNER	99.7%	89.2	25	88.9	2	0	0	1329.66	51	61
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	10	12	27	0.03%	28.4%	KSDVEAIFSK	99.7%	59.5	25	42.5	2	0	0	1123.60	30	39
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	10	12	27	0.03%	28.4%	LKGDDLQAIK	99.4%	35.7	25	27.9	2	0	0	1100.63	188	197
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	10	12	27	0.03%	28.4%	MIAGQVLDINLAAEPK	99.7%	128	25	128	7	0	0	1682.91	74	89
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	10	12	27	0.03%	28.4%	MYSYPAR	98.6%	32.4	25	27.9	1	0	0	903.40	136	142
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	10	12	27	0.03%	28.4%	QKVDSLLENLEK	99.7%	47.1	25	40	2	2	0	1415.77	205	216
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	10	12	27	0.03%	28.4%	SDVEAIFSK	99.7%	52	25	48.5	2	0	0	995.50	31	39
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	10	12	27	0.03%	28.4%	VFIGNLNTLVVK	99.7%	70.5	25	68.6	4	0	0	1316.79	18	29
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	10	12	27	0.03%	28.4%	VFIGNLNTLVVKK	99.2%	34.9	25	34.9	2	0	0	1444.89	18	30
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	10	12	27	0.03%	28.4%	VPPPPPIAR	94.9%	27	25	23.9	1	0	0	943.57	143	151
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	13	14	26	0.03%	16.0%	ASGVEGADVVK	99.7%	43.7	25	24	2	0	0	1031.54	177	187
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	13	14	26	0.03%	16.0%	ATDCVGHDVVTLLR	99.7%	48.1	25	48.1	2	0	0	1555.79	625	638
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	13	14	26	0.03%	16.0%	FLLSESGSGK	99.7%	41.4	25	22.8	2	0	0	1024.53	442	451
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	13	14	26	0.03%	16.0%	FLSQIESDR	99.7%	56.6	25	42.9	2	0	0	1094.55	786	794
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	13	14	26	0.03%	16.0%	GAALITAVGVR	99.7%	80.9	25	69.4	2	0	0	1027.63	900	910
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	13	14	26	0.03%	16.0%	GAAMVTAVAYR	99.7%	99.5	25	84.9	3	0	0	1125.57	452	462
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	13	14	26	0.03%	16.0%	GDFIALDLGGSSFR	99.7%	86.3	25	86.3	2	0	0	1454.73	78	91
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	13	14	26	0.03%	16.0%	IDEAILITWTK	99.7%	57.2	25	53.1	2	0	0	1302.73	163	173
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	13	14	26	0.03%	16.0%	LALLQVR	99.7%	41.3	25	18.4	2	0	0	812.54	795	801
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	13	14	26	0.03%	16.0%	LSDETLIDIMTR	99.7%	68.9	25	62	2	0	0	1406.72	31	42
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	13	14	26	0.03%	16.0%	LVDEYSLNAGK	99.7%	62	25	61.3	2	0	0	1208.62	728	738
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	13	14	26	0.03%	16.0%	SANLVAATLGAILNR	99.7%	80.6	25	78.9	2	0	0	1483.86	382	396
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	13	14	26	0.03%	16.0%	TTVGVDGSLYK	98.8%	33	25	28.8	1	0	0	1139.59	408	418
HHIP-like protein 2	HHIPL2	HIPL2_HUMAN	80.8	100.0%	3	3	6	0.01%	3.6%	LEQPFLDLK	99.5%	37	25	19.6	2	0	0	1102.61	251	259
HHIP-like protein 2	HHIPL2	HIPL2_HUMAN	80.8	100.0%	3	3	6	0.01%	3.6%	LMALQEDR	99.7%	45.1	25	35.5	2	0	0	991.49	528	535
HHIP-like protein 2	HHIPL2	HIPL2_HUMAN	80.8	100.0%	3	3	6	0.01%	3.6%	SVTGGYVYR	99.7%	48	25	27	2	0	0	1001.51	499	507
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	15	0.01%	16.2%	ISICSSDKR	99.5%	37.1	25	30.8	2	0	0	1065.54	405	413
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	15	0.01%	16.2%	LGCFNLTIK	99.7%	53.6	25	36.8	2	0	0	1065.58	271	279
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	15	0.01%	16.2%	LHISPSNMTNQNTNEYLEK	99.7%	34.7	25	34.7	0	2	0	2249.05	343	361
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	15	0.01%	16.2%	SIRPDNMSEYSK	99.6%	38.1	25	26.3	3	0	0	1426.66	78	89
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	15	0.01%	16.2%	VMTVSFHK	99.7%	51	25	38.1	2	0	0	948.50	193	200

Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	15	0.01%	16.2%	YGEYFPGTGDLR	99.7%	66.1	25	65.2	3	0	0	1374.63	201	212
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	15	0.01%	16.2%	YYAVNYPLR	99.7%	47.5	25	37.6	1	0	0	1158.59	221	229
Histone deacetylase 8	HDAC8	HDAC8_HUMAN	41.8	99.8%	2	2	3	0.00%	7.4%	FSPGFFPGTGDVSDVGLGK	99.7%	45.3	25	45.3	1	0	0	1883.92	203	221
Histone deacetylase 8	HDAC8	HDAC8_HUMAN	41.8	99.8%	2	2	3	0.00%	7.4%	IQQILNYIK	99.7%	42.9	25	35.8	2	0	0	1132.67	362	370
Histone deacetylase complex subunit SAP18	SAP18	SAP18_HUMAN	17.6	99.9%	2	2	3	0.00%	15.7%	KGTDDSMTLQSQK	99.1%	33.9	25	33.5	1	0	0	1438.68	114	126
Histone deacetylase complex subunit SAP18	SAP18	SAP18_HUMAN	17.6	99.9%	2	2	3	0.00%	15.7%	VKEIGSTMSGR	99.7%	46.7	25	42.1	2	0	0	1164.60	103	113
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	8	10	137	0.14%	24.7%	ALAAAGYDVEK	99.7%	79.5	25	65.9	27	0	0	1107.57	65	75
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	8	10	137	0.14%	24.7%	ALAAAGYDVEKNNSR	99.7%	97.3	25	97.3	14	3	0	1578.79	65	79
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	8	10	137	0.14%	24.7%	ASGPPVSELITK	99.7%	70.3	25	65.4	30	0	0	1198.67	35	46
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	8	10	137	0.14%	24.7%	KALAAAGYDVEK	99.7%	66.1	25	56.9	3	0	0	1235.66	64	75
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	8	10	137	0.14%	24.7%	KASGPPVSELITK	99.7%	82.3	25	76.2	22	2	0	1326.76	34	46
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	8	10	137	0.14%	24.7%	SETAPAAPAAPAPAEK	98.2%	31.2	25	0.97	1	0	0	1478.75	2	17
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	8	10	137	0.14%	24.7%	SGVSLAALK	99.7%	64.7	25	39.3	2	0	0	845.51	55	63
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	8	10	137	0.14%	24.7%	SGVSLAALKK	99.7%	76.3	25	74.2	33	0	0	973.60	55	64
Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	3	3	17	0.02%	17.4%	ALVQNDTLLQVK	99.7%	76.9	25	67.5	5	0	0	1341.77	95	106
Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	3	3	17	0.02%	17.4%	GAPAAATAPAPTAHK	99.7%	69.7	25	69	7	0	0	1331.71	129	143
Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	3	3	17	0.02%	17.4%	YSQLVVETIR	99.7%	91	25	78.9	5	0	0	1207.67	48	57
Histone H2A type 1-B/E	HIST1H2AB	H2A1B_HUMAN	14.1	100.0%	4	5	21	0.02%	32.3%	AGLQFPVGR	99.7%	66.3	25	55.2	13	0	0	944.53	22	30
Histone H2A type 1-B/E	HIST1H2AB	H2A1B_HUMAN	14.1	100.0%	4	5	21	0.02%	32.3%	HLQLAIR	99.3%	35.3	25	24	2	0	0	850.53	83	89
Histone H2A type 1-B/E	HIST1H2AB	H2A1B_HUMAN	14.1	100.0%	4	5	21	0.02%	32.3%	HLQLAIRNDEELNK	97.9%	23.1	25	19	0	1	0	1692.90	83	96
Histone H2A type 1-B/E	HIST1H2AB	H2A1B_HUMAN	14.1	100.0%	4	5	21	0.02%	32.3%	VTIAQGGVLPNIQAVLLPK	99.7%	64.3	25	64.3	3	2	0	1931.17	101	119
Histone H2B type 1-B	HIST1H2BB	H2B1B_HUMAN	14.0	99.8%	2	2	4	0.00%	35.7%	AMGIMNSFVNDIFER	99.7%	107	25	107	11	0	0	1743.82	59	73
Histone H2B type 1-B	HIST1H2BB	H2B1B_HUMAN	14.0	99.8%	2	2	4	0.00%	35.7%	ESYSIYVYK	99.5%	36.9	25	36.7	2	0	0	1151.56	36	44
Histone H2B type 1-B	HIST1H2BB	H2B1B_HUMAN	14.0	99.8%	2	2	4	0.00%	35.7%	KESYSIYVYK	99.7%	53.4	25	48.1	2	0	0	1279.66	35	44
Histone H2B type 1-B	HIST1H2BB	H2B1B_HUMAN	14.0	99.8%	2	2	4	0.00%	35.7%	LLLPGELAK	99.7%	38.9	25	8.03	9	0	0	953.60	101	109
Histone H2B type 1-B	HIST1H2BB	H2B1B_HUMAN	14.0	99.8%	2	2	4	0.00%	35.7%	QVHPDTGISSK	95.0%	27.1	25	22.2	1	0	0	1168.60	48	58
Histone H2B type 1-C/E/F/G/I	HIST1H2BC	H2B1C_HUMAN	13.9	100.0%	5	6	24	0.02%	35.7%	AMGIMNSFVNDIFER	99.7%	107	25	107	11	0	0	1743.82	59	73
Histone H2B type 1-C/E/F/G/I	HIST1H2BC	H2B1C_HUMAN	13.9	100.0%	5	6	24	0.02%	35.7%	ESYSVYVYK	97.4%	29.6	25	25.7	1	0	0	1137.55	36	44
Histone H2B type 1-C/E/F/G/I	HIST1H2BC	H2B1C_HUMAN	13.9	100.0%	5	6	24	0.02%	35.7%	KESYSVYVYK	99.7%	60.4	25	52.4	2	0	0	1265.64	35	44
Histone H2B type 1-C/E/F/G/I	HIST1H2BC	H2B1C_HUMAN	13.9	100.0%	5	6	24	0.02%	35.7%	LLLPGELAK	99.7%	38.9	25	8.03	9	0	0	953.60	101	109
Histone H2B type 1-C/E/F/G/I	HIST1H2BC	H2B1C_HUMAN	13.9	100.0%	5	6	24	0.02%	35.7%	QVHPDTGISSK	95.0%	27.1	25	22.2	1	0	0	1168.60	48	58
Histone H3.1t	HIST3H3	H31T_HUMAN	15.5	100.0%	2	2	6	0.01%	13.2%	EIAQDFKTDLR	99.7%	40.5	25	23.1	2	0	0	1335.69	74	84
Histone H3.1t	HIST3H3	H31T_HUMAN	15.5	100.0%	2	2	6	0.01%	13.2%	STELLIR	99.7%	39	25	27	4	0	0	831.49	58	64
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	8	26	0.03%	51.5%	DAVTYTEHAK	99.7%	45.3	25	43	4	0	0	1134.54	69	78
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	8	26	0.03%	51.5%	DNIQGITKPAIR	99.7%	62.3	25	45.3	6	2	0	1325.75	25	36
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	8	26	0.03%	51.5%	ISGLIYEETR	99.7%	60.2	25	53.5	4	0	0	1180.62	47	56
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	8	26	0.03%	51.5%	TVTAMDVVYALK	99.7%	50.6	25	44.6	3	0	0	1326.70	81	92
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	8	26	0.03%	51.5%	TVTAMDVVYALKR	98.9%	33.3	25	33	2	0	0	1466.80	81	93
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	8	26	0.03%	51.5%	VFLENVIR	99.7%	48.3	25	34	5	0	0	989.58	61	68
HLA class I histocompatibility antigen, Cw-4 alpha chain	HLA-C	1C04_HUMAN	40.9	99.8%	2	2	3	0.00%	6.3%	FDSDAASPR	99.7%	41.8	25	32	2	0	0	965.43	60	68
HLA class I histocompatibility antigen, Cw-4 alpha chain	HLA-C	1C04_HUMAN	40.9	99.8%	2	2	3	0.00%	6.3%	FIAVGYVDDTQFVR	96.8%	28.8	25	24.9	1	0	0	1629.83	46	59
Hornerin	HRNR	HORN_HUMAN	282.4	100.0%	6	8	24	0.02%	4.0%	GPYESGSGHSSGLGHQESR	99.7%	46.1	25	46.1	0	2	0	1928.85	572	590
Hornerin	HRNR	HORN_HUMAN	282.4	100.0%	6	8	24	0.02%	4.0%	GPYESGSGHSSGLGHR	99.7%	110	25	110	6	8	0	1584.72	1038	1053
Hornerin	HRNR	HORN_HUMAN	282.4	100.0%	6	8	24	0.02%	4.0%	GSGSGQSPSSGQHGTGFGR	99.7%	67.5	25	67.2	2	1	0	1747.77	430	448
Hornerin	HRNR	HORN_HUMAN	282.4	100.0%	6	8	24	0.02%	4.0%	HGSGSGQSSSYGPYR	99.7%	39.7	25	36.8	2	0	0	1526.66	1014	1028
Hornerin	HRNR	HORN_HUMAN	282.4	100.0%	6	8	24	0.02%	4.0%	HGSGSGQSSSYSPYGSGSGWSSSR	99.7%	37.1	25	37.1	0	1	0	2348.98	1484	1507
Hornerin	HRNR	HORN_HUMAN	282.4	100.0%	6	8	24	0.02%	4.0%	QSLGHGQHGSGSGQSPSPSR	96.6%	21.6	25	21.1	0	2	0	1947.90	992	1011
Hsp70-binding protein 1	HSPBP1	HPBP1_HUMAN	39.5	99.8%	2	2	4	0.00%	5.5%	ALFAISCLVR	99.7%	54	25	46.4	2	0	0	1149.64	211	220
Hsp70-binding protein 1	HSPBP1	HPBP1_HUMAN	39.5	99.8%	2	2	4	0.00%	5.5%	YLEAGAAGLR	99.4%	36.2	25	25.6	2	0	0	1020.55	156	165
Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	HMGCL_HUMAN	34.4	100.0%	4	4	8	0.01%	16.0%	AAQSANISVR	99.7%	47.3	25	42.5	2	0	0	1016.55	156	165
Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	HMGCL_HUMAN	34.4	100.0%	4	4	8	0.01%	16.0%	EVVIFGAASELFTK	99.7%	67.9	25	67.2	2	0	0	1510.82	123	136

Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	HMGCL_HUMAN	34.4	100.0%	4	4	8	0.01%	16.0%	FPGINYPVLTPNLK	99.7%	49	25	45	2	0	0	1572.88	98	111
Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	HMGCL_HUMAN	34.4	100.0%	4	4	8	0.01%	16.0%	LLEAGNFICQALNR	99.7%	82	25	78.2	2	0	0	1618.84	299	312
Hydroxysteroid dehydrogenase-like protein 2	HSDL2	HSDL2_HUMAN	45.4	100.0%	4	4	7	0.01%	11.5%	LAGCTVFITGASR	99.7%	98.5	25	79.2	2	0	0	1352.70	8	20
Hydroxysteroid dehydrogenase-like protein 2	HSDL2	HSDL2_HUMAN	45.4	100.0%	4	4	7	0.01%	11.5%	LLGTIYTAAEEIEAVGGK	99.7%	83.8	25	82.1	2	0	0	1834.98	50	67
Hydroxysteroid dehydrogenase-like protein 2	HSDL2	HSDL2_HUMAN	45.4	100.0%	4	4	7	0.01%	11.5%	LQLQPKPR	95.2%	27.3	25	27.3	1	0	0	979.60	299	306
Hydroxysteroid dehydrogenase-like protein 2	HSDL2	HSDL2_HUMAN	45.4	100.0%	4	4	7	0.01%	11.5%	SGAVEETFR	99.7%	51.3	25	45.6	2	0	0	995.48	307	315
Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	HPRT_HUMAN	24.6	100.0%	3	4	6	0.01%	15.6%	SIPMTVDFIR	99.5%	37.2	25	25	1	0	0	1178.62	92	101
Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	HPRT_HUMAN	24.6	100.0%	3	4	6	0.01%	15.6%	VFIPHGLIMDR	99.7%	51.2	25	48.4	0	3	0	1297.71	35	45
Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	HPRT_HUMAN	24.6	100.0%	3	4	6	0.01%	15.6%	VIGGDDLSTLTGK	99.7%	77.4	25	64.3	2	0	0	1275.68	116	128
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	17	19	34	0.03%	21.2%	AANSLEAFIFETQDK	99.7%	91.8	25	81.1	2	0	0	1683.82	739	753
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	17	19	34	0.03%	21.2%	AEAGPEGVAPAPEGEK	99.7%	80.1	25	72.4	2	0	0	1508.72	670	685
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	17	19	34	0.03%	21.2%	AEAGPEGVAPAPEGEKK	99.7%	51	25	51	2	2	0	1636.82	670	686
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	17	19	34	0.03%	21.2%	DAVITVPVFFNQAER	99.7%	39.3	25	38.4	2	0	0	1705.89	171	185
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	17	19	34	0.03%	21.2%	DAVVYPILVEFTR	99.7%	81.5	25	81.5	2	0	0	1521.83	439	451
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	17	19	34	0.03%	21.2%	EAGMQPQLQIR	99.2%	34.7	25	33.4	2	0	0	1270.66	252	262
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	17	19	34	0.03%	21.2%	EVQYLLNK	96.1%	28.1	25	9.85	1	0	0	1006.56	901	908
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	17	19	34	0.03%	21.2%	FFGDSAASMAIK	99.7%	73.7	25	64.7	2	0	0	1244.60	80	91
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	17	19	34	0.03%	21.2%	KVITFNR	96.0%	28	25	12.5	1	0	0	877.53	480	486
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	17	19	34	0.03%	21.2%	LAGLFNEQR	99.7%	58.4	25	48	2	0	0	1047.56	283	291
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	17	19	34	0.03%	21.2%	LGNTISSLFGGGTTPDAK	99.7%	112	25	112	2	0	0	1735.89	577	594
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	17	19	34	0.03%	21.2%	LYQPEYQEVSTEEQREEISGK	99.7%	34	25	34	0	1	0	2542.19	754	774
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	17	19	34	0.03%	21.2%	TLGGLEMELR	99.7%	81	25	72.1	4	0	0	1118.59	269	278
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	17	19	34	0.03%	21.2%	VAIVKPGVPMEIVLNK	96.1%	21.2	25	21.2	0	1	0	1723.02	47	62
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	17	19	34	0.03%	21.2%	VEFEELCADLFER	99.7%	70	25	64.8	2	0	0	1656.76	346	358
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	17	19	34	0.03%	21.2%	VLQLINDNTATALSYGVFR	99.7%	75.4	25	75.4	2	0	0	2095.12	199	217
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	17	19	34	0.03%	21.2%	YFQHLLGK	96.7%	28.7	25	22.1	2	0	0	1005.55	99	106
Ig kappa chain V-I region Lay	IGKV1-13	KV113_HUMAN	11.8	99.8%	2	2	6	0.01%	25.0%	DIQMTQSPSSLSVSVGDR	99.7%	52.3	25	47.7	3	0	0	1922.91	1	18
Ig kappa chain V-I region Lay	IGKV1-13	KV113_HUMAN	11.8	99.8%	2	2	6	0.01%	25.0%	LLIYGASTR	99.7%	71.2	25	17.6	3	0	0	993.57	46	54
Ig kappa chain V-II region RPMI 6410	IGKV2-30	KV206_HUMAN	14.7	99.8%	2	3	334	0.33%	12.0%	FSGSGSGTDFTLK	99.7%	103	25	0	309	0	0	1303.62	87	99
Ig kappa chain V-II region RPMI 6410	IGKV2-30	KV206_HUMAN	14.7	99.8%	2	3	334	0.33%	12.0%	FSGSGSGTDFTLKISR	99.7%	95.2	25	0	10	15	0	1659.83	87	102
Ig kappa chain V-IV region (Fragment)	IGKV4-1	KV401_HUMAN	13.4	99.8%	2	2	20	0.02%	19.8%	LLIYWASTR	99.7%	64	25	60.4	19	0	0	1122.63	72	80
Ig kappa chain V-IV region (Fragment)	IGKV4-1	KV401_HUMAN	13.4	99.8%	2	2	20	0.02%	19.8%	NYLAWYQQKPGQPPK	99.7%	39.2	25	38.7	1	0	0	1817.93	57	71
Immunoglobulin-binding protein 1	IGBP1	IGBP1_HUMAN	39.2	99.8%	2	2	3	0.00%	5.9%	LPELFETGR	99.7%	49.7	25	45	1	0	0	1061.56	12	20
Immunoglobulin-binding protein 1	IGBP1	IGBP1_HUMAN	39.2	99.8%	2	2	3	0.00%	5.9%	YGALPDQGIAK	98.0%	30.7	25	26.3	2	0	0	1132.60	277	287
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	8	8	15	0.01%	22.3%	ASLSLIEK	99.7%	48.6	25	37.5	2	0	0	860.51	487	494
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	8	8	15	0.01%	22.3%	EATWTMSNITAGR	98.9%	33.4	25	33.4	1	0	0	1453.67	354	366
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	8	8	15	0.01%	22.3%	EKQPPIDNIIR	96.9%	29	25	29	1	0	0	1322.74	107	117
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	8	8	15	0.01%	22.3%	GINSSNVENQLQATQAAR	99.7%	88.4	25	79.7	1	0	0	1900.95	84	101
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	8	8	15	0.01%	22.3%	LLGASELPIVTPALR	99.7%	63.3	25	63.3	4	0	0	1549.93	301	315
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	8	8	15	0.01%	22.3%	NKNPAPPIDAVEQILPTLVR	99.7%	76.9	25	76.9	1	0	0	2185.23	239	258
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	8	8	15	0.01%	22.3%	NLTWTLSNLCR	99.7%	69.8	25	0	2	0	0	1377.69	228	238
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	8	8	15	0.01%	22.3%	QDQIQQVVNHGLVPFLVSVLSK	99.7%	89.5	25	88.7	0	3	0	2448.36	367	388
Importin subunit alpha-5	KPNA1	IMA5_HUMAN	60.2	100.0%	4	4	6	0.01%	10.8%	EAAWAITNATSGGSAEQIK	99.7%	72.7	25	70.3	1	0	0	1904.93	399	417
Importin subunit alpha-5	KPNA1	IMA5_HUMAN	60.2	100.0%	4	4	6	0.01%	10.8%	EACWTISNITAGNR	99.7%	70.7	25	69.8	2	0	0	1592.75	357	370
Importin subunit alpha-5	KPNA1	IMA5_HUMAN	60.2	100.0%	4	4	6	0.01%	10.8%	IVQVALNGLENILR	98.7%	32.4	25	32.4	1	0	0	1551.92	439	452
Importin subunit alpha-5	KPNA1	IMA5_HUMAN	60.2	100.0%	4	4	6	0.01%	10.8%	NAVWALSNLCR	99.7%	55.5	25	48.3	2	0	0	1303.66	231	241
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	19	42	0.04%	25.9%	AAVENLPTFLVELSR	99.7%	111	25	108	6	0	0	1658.91	28	42
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	19	42	0.04%	25.9%	ESCLEAYTGIVQGLK	99.7%	90.7	25	84.1	2	0	0	1667.83	763	777
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	19	42	0.04%	25.9%	GALQYLVPILTQTLTK	99.7%	40	25	40	1	0	0	1759.04	317	332
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	19	42	0.04%	25.9%	GDQENVHPDVMLVQPR	99.7%	51.5	25	51.5	0	2	0	1849.89	778	793
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	19	42	0.04%	25.9%	LAATNALLNSLEFTK	99.7%	114	25	108	4	0	0	1605.88	192	206

Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	19	42	0.04%	25.9%	LLETTDRPDGHQNNLR	99.7%	38.6	25	36.5	0	2	0	1878.94	510	525
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	19	42	0.04%	25.9%	LQQVLQMESHIQSTSDR	99.1%	25.7	25	22.8	0	2	0	2015.98	558	574
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	19	42	0.04%	25.9%	SDYDMVDYLNELR	99.7%	86.5	25	86.5	2	0	0	1632.72	750	762
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	19	42	0.04%	25.9%	SNEILTAIIQGMR	99.7%	92.6	25	85.8	2	0	0	1445.78	170	182
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	19	42	0.04%	25.9%	SSAYESLMEIVK	99.7%	82.7	25	73.6	4	0	0	1356.67	526	537
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	19	42	0.04%	25.9%	TTLVIMER	99.7%	50.2	25	43.3	3	0	0	962.53	550	557
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	19	42	0.04%	25.9%	TVSPDRLELEAAQK	99.7%	53	25	43.4	2	0	0	1556.83	10	23
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	19	42	0.04%	25.9%	VAAGLQIK	99.7%	42.4	25	28.2	2	0	0	799.50	55	62
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	19	42	0.04%	25.9%	VAALQNLVK	99.7%	45.7	25	38.2	2	0	0	955.59	235	243
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	19	42	0.04%	25.9%	VLANPGNSQVAR	99.7%	63.7	25	57.5	2	0	0	1225.66	43	54
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	19	42	0.04%	25.9%	WLAIDANAR	99.7%	48.8	25	45.5	2	0	0	1029.55	80	88
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	19	42	0.04%	25.9%	YLEVVLNTLQQASQAQVDK	99.7%	87	25	85.3	2	0	0	2147.13	731	749
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	8	9	15	0.01%	9.6%	ALLTFYHVTK	99.7%	45.8	25	41.6	2	0	0	1192.67	147	156
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	8	9	15	0.01%	9.6%	FIVQCMNLIK	99.7%	47.3	25	39.6	2	0	0	1265.67	316	325
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	8	9	15	0.01%	9.6%	IFQNMSPLLELSSENLR	99.7%	59	25	59	1	0	0	2007.02	688	704
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	8	9	15	0.01%	9.6%	LTVDDFEFR	99.7%	69.4	25	68.4	2	0	0	1141.55	541	549
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	8	9	15	0.01%	9.6%	MAFFTYPTLTEICR	99.7%	46.9	25	43.1	3	0	0	1765.83	354	367
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	8	9	15	0.01%	9.6%	NFEDSSPETLEAHK	99.7%	51	25	42.2	2	0	0	1603.72	338	351
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	8	9	15	0.01%	9.6%	SIGTDNVCR	99.7%	51.2	25	42.2	2	0	0	1021.47	255	263
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	8	9	15	0.01%	9.6%	VAPHALSEEEK	98.0%	30.8	25	25	1	0	0	1209.61	77	87
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	18	23	46	0.05%	18.0%	ACYALENFVENLGPK	99.7%	82.1	25	79.2	2	0	0	1724.83	458	472
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	18	23	46	0.05%	18.0%	AQELQAVLGLS	99.7%	43.5	25	43.3	2	0	0	1128.63	1071	1081
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	18	23	46	0.05%	18.0%	ATEQLQIVLR	99.7%	57.8	25	38.4	2	0	0	1170.68	24	33
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	18	23	46	0.05%	18.0%	DNICGALAR	99.7%	41.9	25	32.6	2	0	0	989.48	959	967
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	18	23	46	0.05%	18.0%	EVMPLLLAYLK	99.7%	69.5	25	56.6	6	0	0	1289.75	435	445
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	18	23	46	0.05%	18.0%	GLEDPSQVVR	99.7%	49	25	31.7	2	0	0	1099.57	402	411
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	18	23	46	0.05%	18.0%	ILCCLTFLVK	99.7%	46.8	25	41.6	2	0	0	1266.70	267	276
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	18	23	46	0.05%	18.0%	LAELCGVLK	99.7%	54.9	25	44.4	4	0	0	1002.57	793	801
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	18	23	46	0.05%	18.0%	LIMAMQTLIPIDEAK	99.7%	66.5	25	60.4	4	0	0	1686.92	206	220
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	18	23	46	0.05%	18.0%	LLECPHLNVR	99.7%	41	25	36.7	2	0	0	1250.67	705	714
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	18	23	46	0.05%	18.0%	LLMASPTR	97.1%	29.2	25	22.7	1	0	0	904.49	968	975
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	18	23	46	0.05%	18.0%	LLPVLLSTAQEADPEVR	99.7%	74.3	25	67.3	3	1	0	1851.02	900	916
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	18	23	46	0.05%	18.0%	QFAAVLTR	99.7%	41.3	25	20.2	1	0	0	905.52	55	62
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	18	23	46	0.05%	18.0%	SCGTLTLKPPGR	99.7%	40.3	25	35.9	1	0	0	1286.69	781	792
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	18	23	46	0.05%	18.0%	SLILTALQR	99.7%	58.8	25	42.7	2	0	0	1014.63	82	90
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	18	23	46	0.05%	18.0%	TLTTMAPYLSTEDVPLAR	99.7%	79.5	25	77.8	4	0	0	1979.02	183	200
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	18	23	46	0.05%	18.0%	VRDNICGALAR	99.7%	42.8	25	33.9	2	0	0	1244.65	957	967
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	18	23	46	0.05%	18.0%	VVPSYMQAVNR	99.7%	57.3	25	53.7	3	0	0	1263.65	751	761
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	23	92	0.09%	23.3%	EFQQYLPVVMGPLMK	99.7%	38.9	25	35.1	1	0	0	1779.92	618	632
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	23	92	0.09%	23.3%	EGFVEYTEQVVK	99.7%	45.4	25	38.9	2	0	0	1427.71	694	705
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	23	92	0.09%	23.3%	FLFDSVSSQNVGLR	99.7%	105	25	102	9	0	0	1568.81	135	148
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	23	92	0.09%	23.3%	FMQDASDVMQLLLK	99.7%	98	25	88.5	8	0	0	1638.82	573	586
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	23	92	0.09%	23.3%	FVPYYDLFMPSLK	99.7%	67.1	25	0	11	0	0	1635.81	527	539
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	23	92	0.09%	23.3%	HIVENAVQK	98.5%	32.1	25	32.1	3	0	0	1037.57	540	548
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	23	92	0.09%	23.3%	LMVPLLK	96.3%	28.3	25	7.04	1	0	0	829.52	706	712
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	23	92	0.09%	23.3%	LQELIQK	99.7%	39.3	25	7.94	1	0	0	871.52	497	503
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	23	92	0.09%	23.3%	LVLEQVVTSIASVADTAEEK	99.2%	26.3	25	26.3	0	1	0	2102.12	507	526
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	23	92	0.09%	23.3%	QAEETYENIPGQSK	99.7%	64.9	25	60.9	1	0	0	1593.74	28	41
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	23	92	0.09%	23.3%	QMAAVLLR	99.6%	38.3	25	20.1	5	0	0	901.53	60	67
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	23	92	0.09%	23.3%	SLLIPYLDNLVK	99.6%	37.9	25	24.3	4	0	0	1387.82	476	487
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	23	92	0.09%	23.3%	SLVEIADTVPK	99.7%	84.5	25	75.4	9	0	0	1171.66	239	249

Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	23	92	0.09%	23.3%	STACQMLVCYAK	99.7%	68	25	68	5	0	0	1431.64	679	690
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	23	92	0.09%	23.3%	TIECISLIGLAVGK	99.7%	97.7	25	92.8	7	0	0	1473.83	557	570
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	23	92	0.09%	23.3%	VAAAESMPLLLECAR	99.7%	83.4	25	75	5	0	0	1630.83	721	735
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	23	92	0.09%	23.3%	VCDIAAELAR	99.7%	67	25	40.9	7	0	0	1117.57	109	118
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	23	92	0.09%	23.3%	VIAALLQTMEDQGNQR	99.7%	109	25	109	6	0	0	1786.91	442	457
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	23	92	0.09%	23.3%	VSDILHSIFSSYK	99.7%	61.5	25	52.5	4	0	0	1495.78	842	854
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	23	92	0.09%	23.3%	YAACNAVGQMATDFAPGFQK	99.7%	45.1	25	38.7	2	0	0	2146.97	417	436
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	15	17	52	0.05%	18.7%	AFAVGVQQVLLK	99.7%	96.2	25	81.3	8	0	0	1272.77	295	306
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	15	17	52	0.05%	18.7%	AIFQTIQNR	99.7%	56.5	25	47.4	5	0	0	1090.60	964	972
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	15	17	52	0.05%	18.7%	ENIVEAIIHSPELIR	99.7%	73.5	25	61.9	2	0	0	1732.96	93	107
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	15	17	52	0.05%	18.7%	ETENDDLTNVIQK	99.7%	71.1	25	66.1	2	0	0	1518.73	552	564
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	15	17	52	0.05%	18.7%	EYNEFAEVFLK	99.7%	70.8	25	67.6	4	0	0	1388.67	284	294
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	15	17	52	0.05%	18.7%	FIQLLSDQSDQSVLIQK	99.7%	102	25	102	4	0	0	1962.05	185	201
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	15	17	52	0.05%	18.7%	GIDQCIPLFVEAALER	99.6%	37.9	25	34.1	1	0	0	1830.94	753	768
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	15	17	52	0.05%	18.7%	GTMDPALR	99.7%	48.7	25	30.3	4	0	0	876.42	12	19
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	15	17	52	0.05%	18.7%	LLEVIILQCK	99.7%	68.6	25	68.6	6	0	0	1228.73	741	750
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	15	17	52	0.05%	18.7%	QLQDIATLADQR	99.7%	55.2	25	42.6	2	0	0	1371.72	991	1002
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	15	17	52	0.05%	18.7%	SDQNLQTALELTR	99.7%	78.2	25	55.2	2	0	0	1488.77	490	502
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	15	17	52	0.05%	18.7%	SPLVAAMQHFLPVLK	99.0%	25.5	25	25.5	0	1	0	1666.94	168	182
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	15	17	52	0.05%	18.7%	TMGFCYQILTEPNADPR	99.7%	50.8	25	50.8	3	0	0	2012.92	411	427
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	15	17	52	0.05%	18.7%	VLTGVAGEDAECHAAK	99.7%	107	25	107	4	2	0	1627.77	725	740
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	15	17	52	0.05%	18.7%	YLEMIYSMCK	99.7%	58.2	25	53.2	2	0	0	1337.59	714	723
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	4	4	8	0.01%	5.0%	DNIVEGIIR	99.7%	54.2	25	36.2	1	0	0	1028.57	94	102
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	4	4	8	0.01%	5.0%	EYFEFSEFFLK	99.7%	45.8	25	39.5	2	0	0	1485.69	285	295
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	4	4	8	0.01%	5.0%	IAAENELNQSYK	99.7%	58.7	25	58.7	1	0	0	1379.68	20	31
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	4	4	8	0.01%	5.0%	IINFAPSLLR	99.7%	48.8	25	42.7	4	0	0	1143.69	32	41
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	4	4	8	0.01%	5.0%	LLEVIILQCK	99.7%	68.6	25	68.6	6	0	0	1228.73	741	750
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	15	24	0.02%	15.6%	AIWGYCDQLK	99.7%	47	25	46.9	2	0	0	1253.60	540	549
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	15	24	0.02%	15.6%	ELSQIEACQGPMQMR	99.7%	61.1	25	61.1	1	0	0	1777.80	632	646
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	15	24	0.02%	15.6%	EVTDTQMPLVAPVILPEMYK	98.1%	30.9	25	21.1	1	0	0	2290.17	176	195
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	15	24	0.02%	15.6%	FRPPETTER	97.2%	29.4	25	11.4	1	0	0	1132.57	96	104
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	15	24	0.02%	15.6%	IFTMAEVYGIR	99.7%	73.9	25	65.1	4	0	0	1299.68	196	206
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	15	24	0.02%	15.6%	IHEACMLALGSVK	99.7%	46.1	25	43.2	1	0	0	1428.73	446	458
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	15	24	0.02%	15.6%	LIINELSNVMEANAAR	99.7%	108	25	99.7	4	0	0	1757.92	920	935
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	15	24	0.02%	15.6%	LIPTLVSIMQAPADK	99.7%	52.5	25	50.1	1	0	0	1612.90	647	661
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	15	24	0.02%	15.6%	LLQHGINADDKR	98.9%	33.4	25	25	1	0	0	1379.74	866	877
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	15	24	0.02%	15.6%	NSGTEHWWK	95.3%	27.4	25	27.4	1	0	0	1144.52	437	445
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	15	24	0.02%	15.6%	QLASVILK	99.7%	49.1	25	16.1	2	0	0	871.56	75	82
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	15	24	0.02%	15.6%	VSSVALCK	94.8%	27	25	3.09	1	0	0	863.47	858	865
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	13	15	24	0.02%	15.6%	YSNDPVVASLAQDIFK	99.7%	68.4	25	63.8	4	0	0	1766.90	616	631
Inactive hydroxysteroid dehydrogenase-like protein 1	HSDL1	HSDL1_HUMAN	37.0	100.0%	5	5	7	0.01%	14.8%	AYAEELASR	99.7%	63.3	25	60.7	2	0	0	1009.49	82	90
Inactive hydroxysteroid dehydrogenase-like protein 1	HSDL1	HSDL1_HUMAN	37.0	100.0%	5	5	7	0.01%	14.8%	AYLDHFSR	96.0%	28	25	22.9	1	0	0	1008.49	223	230
Inactive hydroxysteroid dehydrogenase-like protein 1	HSDL1	HSDL1_HUMAN	37.0	100.0%	5	5	7	0.01%	14.8%	GLNIILISR	99.7%	47.7	25	47.7	2	0	0	998.64	91	99
Inactive hydroxysteroid dehydrogenase-like protein 1	HSDL1	HSDL1_HUMAN	37.0	100.0%	5	5	7	0.01%	14.8%	NEEKLQVVAK	99.1%	33.9	25	26.8	1	0	0	1157.65	100	109
Inactive hydroxysteroid dehydrogenase-like protein 1	HSDL1	HSDL1_HUMAN	37.0	100.0%	5	5	7	0.01%	14.8%	SITVICDFYSLIR	98.9%	33.3	25	26.4	1	0	0	1586.82	37	49
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	4	4	7	0.01%	24.2%	IDLPEYQGEPDEISIQK	99.7%	60.4	25	57.8	2	0	0	1973.97	40	56
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	4	4	7	0.01%	24.2%	IVFVTGNAK	99.7%	41	25	30.5	2	0	0	948.55	10	18
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	4	4	7	0.01%	24.2%	KIVFVTGNAK	98.9%	33.4	25	33.4	1	0	0	1076.65	9	18
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	4	4	7	0.01%	24.2%	SAYALCTFALSTGDPSQPVR	99.7%	55.8	25	55.8	2	0	0	2141.03	111	130
Inosine-5'-monophosphate dehydrogenase 2	IMPDH2	IMDH2_HUMAN	55.8	100.0%	4	4	8	0.01%	10.5%	EANEILQR	99.7%	42.4	25	25.2	2	0	0	972.51	196	203
Inosine-5'-monophosphate dehydrogenase 2	IMPDH2	IMDH2_HUMAN	55.8	100.0%	4	4	8	0.01%	10.5%	LPIVNEDDELVAIIAR	99.7%	82.8	25	77.6	2	0	0	1779.99	209	224

Inosine-5'-monophosphate dehydrogenase 2	IMPDH2	IMDH2_HUMAN	55.8	100.0%	4	4	8	0.01%	10.5%	TSSAQVEGGVHSLHSYEK	99.7%	34.3	25	34.3	0	2	0	1915.91	494	511
Inosine-5'-monophosphate dehydrogenase 2	IMPDH2	IMDH2_HUMAN	55.8	100.0%	4	4	8	0.01%	10.5%	VAQGVSGAVQDK	99.7%	72.1	25	59.3	2	0	0	1158.61	439	450
Insulin receptor substrate 4	IRS4	IRS4_HUMAN	133.8	99.9%	2	2	3	0.00%	1.8%	AAVSAFPTDSLER	99.7%	39	25	30.4	1	0	0	1363.69	1098	1110
Insulin receptor substrate 4	IRS4	IRS4_HUMAN	133.8	99.9%	2	2	3	0.00%	1.8%	LAPSPARPR	99.7%	42.1	25	42.1	2	0	0	964.57	436	444
Insulin-degrading enzyme	IDE	IDE_HUMAN	118.0	99.8%	2	2	2	0.00%	2.8%	NEFIPTNFEILPLEK	97.9%	30.6	25	27.7	1	0	0	1803.95	528	542
Insulin-degrading enzyme	IDE	IDE_HUMAN	118.0	99.8%	2	2	2	0.00%	2.8%	NLYVTFPIPDLQK	99.7%	40.3	25	40.3	1	0	0	1547.85	312	324
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	19	26	65	0.06%	38.6%	AIETFSGK	99.7%	44.8	25	44.8	2	0	0	852.45	53	60
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	19	26	65	0.06%	38.6%	AISVHSTPEGCSSACK	99.7%	61.9	25	61.9	2	3	0	1690.75	243	258
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	19	26	65	0.06%	38.6%	DQTPDENDQVIVK	99.7%	69.6	25	63.6	4	0	0	1500.72	526	538
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	19	26	65	0.06%	38.6%	EEVKLETHIR	99.7%	44.7	25	40.1	1	0	0	1253.68	484	493
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	19	26	65	0.06%	38.6%	IIGHFYASQMAQR	99.7%	58.2	25	54.1	4	3	0	1521.76	539	551
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	19	26	65	0.06%	38.6%	ILAHNNFVGR	99.7%	50.6	25	39.5	4	0	0	1140.63	281	290
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	19	26	65	0.06%	38.6%	IRDILAQVK	99.7%	43.8	25	23.5	1	0	0	1055.66	553	561
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	19	26	65	0.06%	38.6%	ISYSGQFLVK	99.7%	68.2	25	60.4	2	0	0	1141.63	27	36
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	19	26	65	0.06%	38.6%	ITISSLQDLTLYNPER	99.7%	79.8	25	74	3	0	0	1862.99	310	325
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	19	26	65	0.06%	38.6%	LKEENFFGPK	99.7%	56.5	25	51.7	2	0	0	1208.63	474	483
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	19	26	65	0.06%	38.6%	LLVPTQYVGAIIGK	99.7%	81.6	25	81.6	4	0	0	1471.89	200	213
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	19	26	65	0.06%	38.6%	LYIGNLNESVTPADLEK	99.7%	101	25	94.2	2	0	0	1875.97	4	20
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	19	26	65	0.06%	38.6%	MILEIMHK	99.7%	39.8	25	24.7	2	0	0	1014.55	259	266
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	19	26	65	0.06%	38.6%	MVIITGPPEAQFK	99.7%	84.1	25	74.2	8	0	0	1430.77	453	465
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	19	26	65	0.06%	38.6%	QGSPVAAGAPAK	99.7%	56.1	25	47.8	4	0	0	1053.57	179	190
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	19	26	65	0.06%	38.6%	QQQVDIPLR	99.7%	48.5	25	35.2	4	0	0	1096.61	191	199
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	19	26	65	0.06%	38.6%	RLEIEHSVPK	99.5%	28	25	28	2	2	0	1207.68	67	76
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	19	26	65	0.06%	38.6%	TADEVPLK	99.7%	46.8	25	35.2	2	0	0	872.47	273	280
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	19	26	65	0.06%	38.6%	TVNELQNLTAAEVVVPR	99.7%	101	25	81.1	2	2	0	1853.01	509	525
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	11	11	22	0.02%	28.2%	ALQSGPPQSR	99.5%	36.5	25	25.3	2	0	0	1040.55	568	577
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	11	11	22	0.02%	28.2%	DQTPDENDQVVVK	99.7%	65.4	25	61.4	2	0	0	1486.70	526	538
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	11	11	22	0.02%	28.2%	IAPAEAPDAK	99.0%	33.7	25	33.7	2	0	0	982.52	441	450
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	11	11	22	0.02%	28.2%	IKEENFVSPK	98.5%	31.8	25	14.4	2	0	0	1190.64	474	483
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	11	11	22	0.02%	28.2%	ILAHNNFVGR	99.7%	50.6	25	39.5	4	0	0	1140.63	281	290
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	11	11	22	0.02%	28.2%	IPVSGPFLVK	99.5%	37.2	25	37.2	2	0	0	1056.65	27	36
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	11	11	22	0.02%	28.2%	ITISPLQELTLYNPER	99.7%	62.3	25	62.3	2	0	0	1887.02	310	325
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	11	11	22	0.02%	28.2%	LLVPTQFVGAIIGK	99.7%	66.3	25	0	4	0	0	1455.89	200	213
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	11	11	22	0.02%	28.2%	MVIITGPPEAQFK	99.7%	84.1	25	74.2	8	0	0	1430.77	453	465
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	11	11	22	0.02%	28.2%	SITILSTPEGTSAACK	99.7%	68.5	25	63.9	2	0	0	1635.83	243	258
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	11	11	22	0.02%	28.2%	TGYAFVDCPDESWALK	99.7%	55.5	25	55.5	1	0	0	1858.83	37	52
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	11	11	22	0.02%	28.2%	TVNELQNLSSAEVVVPR	99.7%	38.8	25	33.3	2	0	0	1854.99	509	525
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	11	11	22	0.02%	28.2%	VPSFAAGR	99.7%	38.8	25	38.1	1	0	0	804.44	494	501
Integrator complex subunit 11	CPSF3L	INT11_HUMAN	67.7	100.0%	3	3	5	0.00%	5.7%	VLIPVFALGR	98.9%	33.2	25	33.2	1	0	0	1084.69	235	244
Integrator complex subunit 11	CPSF3L	INT11_HUMAN	67.7	100.0%	3	3	5	0.00%	5.7%	VPIYFSTGLTEK	99.7%	45.1	25	45.1	2	0	0	1354.73	263	274
Integrator complex subunit 11	CPSF3L	INT11_HUMAN	67.7	100.0%	3	3	5	0.00%	5.7%	VTPLGAGQDVGR	99.7%	83.3	25	78.3	2	0	0	1169.63	6	17
Interferon-induced protein with tetratricopeptide repeats 5	IFIT5	IFIT5_HUMAN	55.8	100.0%	2	2	4	0.00%	5.6%	IDPENAEFLTALCELR	99.7%	47.8	25	47.8	2	0	0	1890.93	464	479
Interferon-induced protein with tetratricopeptide repeats 5	IFIT5	IFIT5_HUMAN	55.8	100.0%	2	2	4	0.00%	5.6%	LALYNLLAYVK	99.7%	62.8	25	62.8	2	0	0	1280.76	51	61
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	100.0%	3	3	4	0.00%	6.7%	IGDFGLVTSLK	99.7%	72.7	25	66.8	2	0	0	1149.65	430	440
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	100.0%	3	3	4	0.00%	6.7%	LAYLQILSEETSVK	99.7%	73.4	25	73.4	1	0	0	1593.87	160	173
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	100.0%	3	3	4	0.00%	6.7%	VLALELFEQITK	98.6%	32.3	25	32.3	1	0	0	1403.81	389	400
Interferon-related developmental regulator 1	IFRD1	IFRD1_HUMAN	50.3	99.8%	2	2	2	0.00%	8.7%	GSSAGGGGSGAAAATAATAGGQHR	99.7%	59.4	25	59.4	0	1	0	1927.90	13	36
Interferon-related developmental regulator 1	IFRD1	IFRD1_HUMAN	50.3	99.8%	2	2	2	0.00%	8.7%	IAAGESLALLFELAR	99.7%	91.9	25	85.8	1	0	0	1573.89	284	298
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	11	17	35	0.03%	33.1%	GTMTTGHNVADLVVILK	99.7%	56.1	25	56.1	3	4	0	1784.96	111	127
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	11	17	35	0.03%	33.1%	ILITTVPPNLR	99.7%	45.4	25	43.1	2	0	0	1236.77	175	185
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	11	17	35	0.03%	33.1%	ILPTLEAVAALGNK	99.7%	80	25	75.3	4	0	0	1409.84	128	141

Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	11	17	35	0.03%	33.1%	ILSHGGFR	99.3%	35.5	25	24.3	2	0	0	886.49	320	327
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	11	17	35	0.03%	33.1%	KLDPELHLDIK	99.7%	47.8	25	24.4	2	2	0	1320.75	186	196
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	11	17	35	0.03%	33.1%	LDPELHLDIK	99.7%	44.4	25	36.5	2	0	0	1192.66	187	196
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	11	17	35	0.03%	33.1%	NQDLAPNSAEQASILSLVTK	99.7%	120	25	120	2	2	0	2099.10	61	80
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	11	17	35	0.03%	33.1%	QPLALNVAYR	99.7%	56.9	25	53.1	2	0	0	1144.65	260	269
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	11	17	35	0.03%	33.1%	VKPAPDETSFSEALLK	99.7%	63	25	61.7	2	2	0	1731.92	44	59
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	11	17	35	0.03%	33.1%	VLQSALAAIR	99.7%	90.5	25	82.2	2	0	0	1041.64	197	206
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	11	17	35	0.03%	33.1%	WFEENASQSTVK	99.7%	68.4	25	68.4	2	0	0	1425.66	210	221
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	20	25	53	0.05%	25.2%	AEPPQAMNALMR	99.1%	34.3	25	34.3	1	0	0	1360.63	397	408
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	20	25	53	0.05%	25.2%	AYAALAALEK	99.7%	77.4	25	63.6	4	0	0	1020.57	578	587
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	20	25	53	0.05%	25.2%	CLAALASLR	99.7%	45.3	25	35.2	2	0	0	974.55	203	211
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	20	25	53	0.05%	25.2%	EATDAIGHLDR	99.7%	74.6	25	56	2	0	0	1197.59	298	308
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	20	25	53	0.05%	25.2%	EDITQSAQHALR	99.7%	67.8	25	55.2	2	2	0	1368.69	312	323
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	20	25	53	0.05%	25.2%	EPPLSLTIHLTSPVVR	99.7%	67.5	25	65.8	1	2	0	1759.01	162	177
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	20	25	53	0.05%	25.2%	FVMEVEVDGQK	99.7%	62.1	25	47.5	3	0	0	1280.62	555	565
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	20	25	53	0.05%	25.2%	GDLDLELVLLCK	99.7%	59.5	25	55.9	2	0	0	1387.75	106	117
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	20	25	53	0.05%	25.2%	GWPLELLCEK	99.7%	43	25	0	2	0	0	1244.63	248	257
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	20	25	53	0.05%	25.2%	IFVNDDR	99.3%	35.4	25	17.4	2	0	0	878.44	6	12
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	20	25	53	0.05%	25.2%	LAAFGQLHK	99.7%	47.7	25	44.1	4	0	0	984.56	324	332
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	20	25	53	0.05%	25.2%	LFPDTPLALDANK	99.7%	68.3	25	60.9	3	0	0	1414.76	588	600
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	20	25	53	0.05%	25.2%	LFPDTPLALDANKK	99.7%	51.3	25	40.1	2	0	0	1542.85	588	601
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	20	25	53	0.05%	25.2%	LNQLKPGLQYK	99.7%	43.2	25	34	3	1	0	1301.76	409	419
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	20	25	53	0.05%	25.2%	NPVMELNEK	99.7%	44.3	25	33	2	0	0	1089.52	527	535
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	20	25	53	0.05%	25.2%	SIGTANRPMGAGEALR	97.9%	30.5	25	25.5	1	0	0	1600.82	258	273
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	20	25	53	0.05%	25.2%	VLAGETLSVNDPPDVLDR	99.7%	91.4	25	90.9	2	0	0	1909.99	183	200
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	20	25	53	0.05%	25.2%	VLGMDPLPSK	99.7%	44	25	39	3	0	0	1056.58	333	342
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	20	25	53	0.05%	25.2%	VLQDMGLPTGAEGR	99.7%	80.9	25	74.3	5	0	0	1443.73	461	474
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	20	25	53	0.05%	25.2%	YELISETGGSHDKR	99.7%	41.9	25	41.9	0	2	0	1591.77	541	554
Iron-sulfur protein NUBPL	NUBPL	NUBPL_HUMAN	34.1	99.8%	2	2	6	0.01%	10.7%	AIGLLDVDVYGPSVPK	99.7%	67.8	25	67.8	4	0	0	1642.91	100	115
Iron-sulfur protein NUBPL	NUBPL	NUBPL_HUMAN	34.1	99.8%	2	2	6	0.01%	10.7%	STTAVNLALALAANDSSK	99.7%	50.7	25	50.7	2	0	0	1746.92	82	99
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	11	14	25	0.02%	29.0%	APIQWEER	99.7%	66.3	25	55.5	2	0	0	1028.52	59	66
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	11	14	25	0.02%	29.0%	CSDFTEEICR	99.7%	67.9	25	61.3	2	0	0	1316.52	351	360
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	11	14	25	0.02%	29.0%	EVAESCKDIK	95.3%	27.4	25	12.6	1	0	0	1178.57	217	226
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	11	14	25	0.02%	29.0%	IAEFAFEYAR	99.7%	76.6	25	70	2	0	0	1216.60	179	188
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	11	14	25	0.02%	29.0%	IEAACFATIK	99.7%	63.7	25	53.3	2	0	0	1123.58	327	336
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	11	14	25	0.02%	29.0%	IEAACFATIKDGK	99.6%	37.8	25	36.3	1	0	0	1423.73	327	339
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	11	14	25	0.02%	29.0%	MGLKGPLK	99.0%	33.8	25	17.8	1	0	0	843.51	93	100
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	11	14	25	0.02%	29.0%	MSDGLFLQK	99.7%	55.4	25	32.3	4	0	0	1054.52	206	214
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	11	14	25	0.02%	29.0%	NVTAIQGPGGK	99.7%	57.5	25	54.1	2	0	0	1041.57	67	77
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	11	14	25	0.02%	29.0%	TPIAAGHPSMNLLLR	99.7%	78.7	25	74.9	4	2	0	1590.88	101	115
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	11	14	25	0.02%	29.0%	TPYTDVNIVTIR	99.7%	74.4	25	66.1	2	0	0	1391.75	135	146
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	11	14	29	0.03%	29.4%	DMGGYSTTTDFIK	99.7%	78.3	25	72.7	4	0	0	1435.64	362	374
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	11	14	29	0.03%	29.4%	EQTEGEYSSLEHESAR	99.7%	79.3	25	76	2	2	0	1851.80	165	180
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	11	14	29	0.03%	29.4%	FAFDYATK	99.2%	34.9	25	32.4	2	0	0	962.46	200	207
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	11	14	29	0.03%	29.4%	FAFDYATKK	99.7%	43.6	25	41.7	2	0	0	1090.56	200	208
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	11	14	29	0.03%	29.4%	GELASYDMR	96.8%	28.9	25	27	1	0	0	1041.47	123	131
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	11	14	29	0.03%	29.4%	HNNLDLVIIR	99.7%	68.4	25	55.2	2	0	0	1206.70	155	164
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	11	14	29	0.03%	29.4%	HPFAQAVGR	99.0%	33.7	25	27.7	1	0	0	982.52	309	317
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	11	14	29	0.03%	29.4%	LGDGLFLQCCEEVAELYPK	99.7%	70.7	25	70.7	2	0	0	2241.06	224	242
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	11	14	29	0.03%	29.4%	NIANPTAMLLSASNMLR	99.7%	125	25	110	8	0	0	1816.94	318	334
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	11	14	29	0.03%	29.4%	SVIGHLQTK	99.7%	44.1	25	43.1	2	0	0	982.57	375	383

Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	11	14	29	0.03%	29.4%	TRDMGGYSTTTDFIK	99.2%	34.9	25	34.9	1	0	0	1708.79	360	374
Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G	IDH3G_HUMAN	42.8	100.0%	4	4	7	0.01%	10.4%	LGDGLFLQCCR	99.7%	79.3	25	79.3	2	0	0	1338.63	227	237
Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G	IDH3G_HUMAN	42.8	100.0%	4	4	7	0.01%	10.4%	LHSYATSIR	97.7%	30.1	25	20.7	2	0	0	1047.56	341	349
Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G	IDH3G_HUMAN	42.8	100.0%	4	4	7	0.01%	10.4%	SLPGVVTR	99.4%	35.9	25	24	1	0	0	828.49	150	157
Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G	IDH3G_HUMAN	42.8	100.0%	4	4	7	0.01%	10.4%	TSLDLYANVIHCK	99.7%	60.5	25	55.9	2	0	0	1533.77	137	149
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	15	19	40	0.04%	35.8%	ATDFVADR	99.7%	43.3	25	40	2	0	0	894.43	181	188
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	15	19	40	0.04%	35.8%	CATITPDEAR	99.7%	40.7	25	38.8	2	0	0	1133.53	113	122
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	15	19	40	0.04%	35.8%	DQTDDQVTIDSALATQK	99.7%	122	25	122	1	0	0	1848.88	90	106
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	15	19	40	0.04%	35.8%	FKDIFQEIFDK	99.7%	60	25	56.6	2	0	0	1429.74	262	272
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	15	19	40	0.04%	35.8%	GKLDGNQDLIR	99.7%	62.1	25	42.8	2	0	0	1228.66	383	393
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	15	19	40	0.04%	35.8%	IIWQFIK	98.5%	31.9	25	23.1	2	0	0	947.57	61	67
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	15	19	40	0.04%	35.8%	LIDDMVAQVLK	99.7%	92.2	25	73.4	4	0	0	1244.69	289	299
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	15	19	40	0.04%	35.8%	LILPHVDIQLK	99.7%	50.3	25	34	2	2	0	1288.80	70	80
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	15	19	40	0.04%	35.8%	LNEHFLNTTDFLDTIK	99.7%	66.2	25	63.2	2	2	0	1920.97	427	442
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	15	19	40	0.04%	35.8%	NILGGTVFR	99.7%	55.2	25	50.1	4	0	0	976.56	141	149
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	15	19	40	0.04%	35.8%	NILGGTVFREPIICK	99.7%	58.9	25	58.9	2	0	0	1716.95	141	155
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	15	19	40	0.04%	35.8%	SSGGFVWACK	99.7%	62.3	25	54.7	2	0	0	1098.50	300	309
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	15	19	40	0.04%	35.8%	TIEAEAAHGTVTR	99.7%	107	25	101	4	0	0	1355.69	341	353
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	15	19	40	0.04%	35.8%	VCVETVESGAMTK	99.7%	137	25	130	3	0	0	1426.66	401	413
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	15	19	40	0.04%	35.8%	YFDLGLPNR	99.7%	53.5	25	40.4	2	0	0	1094.56	81	89
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	24	29	65	0.06%	21.6%	APLKPYPVSPSDK	99.7%	55.2	25	52.5	2	2	0	1398.76	1039	1051
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	24	29	65	0.06%	21.6%	AVPSWFVR	99.4%	36.3	25	27.4	2	0	0	961.53	411	418
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	24	29	65	0.06%	21.6%	CNLVPTDEITVYYK	99.7%	40	25	40	2	0	0	1714.84	1001	1014
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	24	29	65	0.06%	21.6%	DVLLPWYNAYR	99.5%	36.5	25	36.5	2	0	0	1409.72	651	661
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	24	29	65	0.06%	21.6%	EIVVIHQDPEALK	99.7%	70.2	25	56.4	2	0	0	1490.82	849	861
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	24	29	65	0.06%	21.6%	ESVDHLTIPSR	99.7%	46	25	25.8	2	0	0	1253.65	501	511
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	24	29	65	0.06%	21.6%	FLIQNVLR	99.7%	44.1	25	29.1	4	0	0	1002.61	662	669
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	24	29	65	0.06%	21.6%	FVDILTNWYVR	99.7%	73.3	25	72.6	7	0	0	1425.75	726	736
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	24	29	65	0.06%	21.6%	GSELEITLTR	99.7%	57.5	25	29.6	2	0	0	1118.61	1062	1071
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	24	29	65	0.06%	21.6%	LESDYEILER	99.7%	69.5	25	55.3	2	0	0	1266.62	269	278
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	24	29	65	0.06%	21.6%	LFLNETQTQEITEDIPVK	99.7%	88.1	25	83.7	2	0	0	2118.10	1227	1244
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	24	29	65	0.06%	21.6%	LLILMEAR	99.7%	65.9	25	47.8	4	0	0	974.57	255	262
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	24	29	65	0.06%	21.6%	LYLINSPVVR	99.7%	54.6	25	46.2	6	0	0	1173.70	625	634
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	24	29	65	0.06%	21.6%	MGITEYNNQCR	99.7%	61.9	25	61.9	4	0	0	1401.59	111	121
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	24	29	65	0.06%	21.6%	NNDLCYWVPELVR	99.7%	43.7	25	33.3	2	0	0	1677.81	429	441
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	24	29	65	0.06%	21.6%	NVIVNGLVLASDGQK	99.7%	105	25	105	2	0	0	1526.85	586	600
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	24	29	65	0.06%	21.6%	QLSSEELEQFQK	99.7%	75.8	25	65.6	2	0	0	1465.72	918	929
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	24	29	65	0.06%	21.6%	TESAVSQMQSVIELGR	99.7%	108	25	102	4	0	0	1734.87	818	833
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	24	29	65	0.06%	21.6%	TVYVSVLPTTADF	99.7%	52.8	25	50.7	1	0	0	1412.73	1250	1262
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	24	29	65	0.06%	21.6%	VCMDFNIIR	99.5%	36.8	25	27.9	1	0	0	1183.56	335	343
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	24	29	65	0.06%	21.6%	VENMVDQLLR	99.7%	74.1	25	56	3	0	0	1216.64	419	428
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	24	29	65	0.06%	21.6%	VLIDPVSVQDK	96.6%	28.6	25	23.3	1	0	0	1212.68	786	796
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	24	29	65	0.06%	21.6%	VREELIDK	98.8%	32.8	25	16.5	2	0	0	1001.56	809	816
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	24	29	65	0.06%	21.6%	YIIEELNVR	99.7%	61.4	25	11.5	2	0	0	1148.63	869	877
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	27	49	0.05%	23.7%	ASPLLPANHVTMAK	99.7%	48.4	25	40.5	3	0	0	1465.78	373	386
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	27	49	0.05%	23.7%	AVLEEGTDVVIK	99.7%	88.3	25	82.5	4	0	0	1272.70	434	445
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	27	49	0.05%	23.7%	DQLGGWFQSSLLTSVAAR	99.7%	78.3	25	78.3	2	0	0	1935.99	626	643
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	27	49	0.05%	23.7%	DSFLGSIPGK	99.7%	55.6	25	43.2	2	0	0	1020.54	887	896
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	27	49	0.05%	23.7%	EAQNLSAMEIR	99.7%	64.3	25	54.8	4	0	0	1261.62	171	181
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	27	49	0.05%	23.7%	ELSNFYFSIIK	99.7%	81.6	25	69.3	2	0	0	1360.71	793	803
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	27	49	0.05%	23.7%	EMTADVIELK	99.7%	58.2	25	34.2	4	0	0	1148.59	948	957

Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	27	49	0.05%	23.7%	EPPYGADVLR	99.7%	43.7	25	37	2	0	0	1116.57	688	697
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	27	49	0.05%	23.7%	FLINLEGGDIR	99.7%	59.1	25	43.1	2	0	0	1246.68	960	970
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	27	49	0.05%	23.7%	FLINLEGGDIREESSYK	99.7%	36	25	30.4	1	2	0	1969.99	960	976
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	27	49	0.05%	23.7%	FPLLKPSPK	99.7%	53.6	25	49.6	2	0	0	1026.63	273	281
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	27	49	0.05%	23.7%	LVHSYPYDWR	96.4%	28.4	25	23.2	1	0	0	1335.65	459	468
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	27	49	0.05%	23.7%	QQPDTELEIQQK	99.7%	56.2	25	54.6	2	0	0	1456.73	79	90
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	27	49	0.05%	23.7%	SCQTALVEILDVIVR	99.7%	113	25	105	2	1	0	1715.94	818	832
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	27	49	0.05%	23.7%	SGDLYVLAADK	99.7%	80.3	25	70.8	2	0	0	1151.59	326	336
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	27	49	0.05%	23.7%	SYKPVFWSPSSR	97.8%	30.4	25	29.1	1	0	0	1440.73	239	250
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	27	49	0.05%	23.7%	TALAEAELEYNPEHVSR	99.7%	60.3	25	60.3	1	2	0	1928.93	251	267
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	27	49	0.05%	23.7%	TKDEYLINSQTTEHIVK	99.7%	43.7	25	43.7	0	2	0	2019.04	539	555
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	27	49	0.05%	23.7%	TVIVHGFTLGEK	99.7%	66	25	53.8	1	2	0	1300.73	650	661
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	27	49	0.05%	23.7%	YTAESSDTLCPR	99.7%	86	25	81	2	0	0	1399.62	993	1004
Isovaleryl-CoA dehydrogenase, mitochondrial	IVD	IVD_HUMAN	46.3	99.8%	2	2	3	0.00%	4.5%	FLQEHLAPK	98.0%	30.8	25	20	1	0	0	1082.60	56	64
Isovaleryl-CoA dehydrogenase, mitochondrial	IVD	IVD_HUMAN	46.3	99.8%	2	2	3	0.00%	4.5%	TDLAAVPASR	99.7%	46.8	25	38.8	2	0	0	1000.54	211	220
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	6	6	11	0.01%	8.7%	ISEDKNPDYR	98.5%	32.1	25	31.7	2	0	0	1236.59	652	661
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	6	6	11	0.01%	8.7%	LAEPSQLLK	99.3%	35.5	25	12.2	1	0	0	998.59	116	124
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	6	6	11	0.01%	8.7%	LLNDEDPVVVTK	99.7%	69.9	25	62.9	2	0	0	1341.73	150	161
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	6	6	11	0.01%	8.7%	LLNQPNQWPLVK	97.7%	30.2	25	28.1	1	0	0	1449.82	488	499
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	6	6	11	0.01%	8.7%	LNYGIPAIVK	99.7%	43	25	33.4	4	0	0	1087.65	478	487
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	6	6	11	0.01%	8.7%	TMQNTSDLDTAR	99.7%	44.8	25	44.8	1	0	0	1352.61	192	203
Katanin p60 ATPase-containing subunit A1	KATNA1	KTNA1_HUMAN	56.0	100.0%	6	6	10	0.01%	15.7%	DIISQNPNVR	99.7%	50.3	25	40.6	3	0	0	1155.61	198	207
Katanin p60 ATPase-containing subunit A1	KATNA1	KTNA1_HUMAN	56.0	100.0%	6	6	10	0.01%	15.7%	EAVVLPMWMPEFFK	99.7%	54.2	25	50.9	1	0	0	1723.86	223	236
Katanin p60 ATPase-containing subunit A1	KATNA1	KTNA1_HUMAN	56.0	100.0%	6	6	10	0.01%	15.7%	FYSPATIFIDEIDSICSR	99.7%	90.9	25	90.9	2	0	0	2134.02	299	316
Katanin p60 ATPase-containing subunit A1	KATNA1	KTNA1_HUMAN	56.0	100.0%	6	6	10	0.01%	15.7%	GVLMVGPPGTGK	98.0%	30.7	25	20.4	1	0	0	1112.61	244	255
Katanin p60 ATPase-containing subunit A1	KATNA1	KTNA1_HUMAN	56.0	100.0%	6	6	10	0.01%	15.7%	SVSAADIER	99.7%	53.2	25	29.7	2	0	0	947.48	472	480
Katanin p60 ATPase-containing subunit A1	KATNA1	KTNA1_HUMAN	56.0	100.0%	6	6	10	0.01%	15.7%	TTFFNVSSSTLTSK	99.7%	50.9	25	50.9	1	0	0	1519.76	268	281
Katanin p80 WD40 repeat-containing subunit B1	KATNB1	KTNB1_HUMAN	72.3	99.9%	2	2	2	0.00%	4.3%	ELHLLMASLD	98.1%	30.9	25	27.5	1	0	0	1141.59	646	655
Katanin p80 WD40 repeat-containing subunit B1	KATNB1	KTNB1_HUMAN	72.3	99.9%	2	2	2	0.00%	4.3%	LNTPEELIVAGSQSGSIR	99.7%	77.3	25	75.6	1	0	0	1870.99	71	88
KATNB1-like protein 1	KATNBL1	KTBL1_HUMAN	34.8	100.0%	3	3	4	0.00%	13.8%	LNVALTFWR	99.7%	46.6	25	40.5	2	0	0	1119.63	165	173
KATNB1-like protein 1	KATNBL1	KTBL1_HUMAN	34.8	100.0%	3	3	4	0.00%	13.8%	TEIINDGNIQILK	99.7%	59.3	25	47.8	1	0	0	1470.82	257	269
KATNB1-like protein 1	KATNBL1	KTBL1_HUMAN	34.8	100.0%	3	3	4	0.00%	13.8%	TYLVNSSDSGSSQTESPSSK	99.7%	82.5	25	82.5	1	0	0	2060.93	120	139
Keratinocyte proline-rich protein	KPRP	KPRP_HUMAN	64.1	99.8%	2	2	3	0.00%	3.5%	GRPAVCQPQGR	98.3%	31.3	25	28.8	1	0	0	1225.62	167	177
Keratinocyte proline-rich protein	KPRP	KPRP_HUMAN	64.1	99.8%	2	2	3	0.00%	3.5%	RSEPIYNSR	99.1%	34	25	19.6	2	0	0	1121.57	300	308
Kidney mitochondrial carrier protein 1	SLC25A30	KMCP1_HUMAN	32.5	99.8%	2	2	3	0.00%	9.6%	AAIVVGVELPVYDITK	99.7%	42.9	25	42.9	1	0	0	1686.97	172	187
Kidney mitochondrial carrier protein 1	SLC25A30	KMCP1_HUMAN	32.5	99.8%	2	2	3	0.00%	9.6%	ALYSGIAPAMLR	99.4%	35.9	25	35.9	2	0	0	1278.69	67	78
Kinase D-interacting substrate of 220 kDa	KIDINS220	KDIS_HUMAN	196.5	99.8%	2	2	2	0.00%	1.2%	NIEVVELLLDK	99.7%	66.1	25	60	1	0	0	1284.74	347	357
Kinase D-interacting substrate of 220 kDa	KIDINS220	KDIS_HUMAN	196.5	99.8%	2	2	2	0.00%	1.2%	SILTQIFGAR	99.5%	37.1	25	31.9	1	0	0	1105.64	417	426
Kinesin-like protein KIF11	KIF11	KIF11_HUMAN	119.2	100.0%	3	3	5	0.00%	3.4%	ETTIDGEELVK	98.0%	30.7	25	28.9	1	0	0	1233.62	247	257
Kinesin-like protein KIF11	KIF11	KIF11_HUMAN	119.2	100.0%	3	3	5	0.00%	3.4%	LNLVDLAGSENIGR	99.7%	74.9	25	73.2	2	0	0	1470.79	261	274
Kinesin-like protein KIF11	KIF11	KIF11_HUMAN	119.2	100.0%	3	3	5	0.00%	3.4%	TVLQELINVLK	99.6%	38.2	25	31.9	2	0	0	1269.78	619	629
Kinesin-like protein KIF22	KIF22	KIF22_HUMAN	73.3	99.8%	2	2	7	0.01%	3.8%	ALMDLLQLTR	99.7%	53.1	25	39.8	4	0	0	1173.67	150	159
Kinesin-like protein KIF22	KIF22	KIF22_HUMAN	73.3	99.8%	2	2	7	0.01%	3.8%	VLDLLDPASGDLVIR	99.1%	34.1	25	34.1	3	0	0	1595.90	184	198
Kinetochore-associated protein 1	KNTC1	KNTC1_HUMAN	250.8	100.0%	4	4	6	0.01%	2.2%	LGISFQPVFR	99.7%	44.3	25	42.4	2	0	0	1163.66	1414	1423
Kinetochore-associated protein 1	KNTC1	KNTC1_HUMAN	250.8	100.0%	4	4	6	0.01%	2.2%	LSEDSVSVLVLR	99.7%	73.8	25	65.4	1	0	0	1316.74	378	389
Kinetochore-associated protein 1	KNTC1	KNTC1_HUMAN	250.8	100.0%	4	4	6	0.01%	2.2%	TSVDILKILCDIQK	96.2%	28.2	25	17.6	1	0	0	1645.92	958	971
Kinetochore-associated protein 1	KNTC1	KNTC1_HUMAN	250.8	100.0%	4	4	6	0.01%	2.2%	VLAPELIPSILEK	99.7%	48.8	25	48.8	2	0	0	1421.86	727	739
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	6	6	9	0.01%	17.1%	GLLEESSFATLFPK	99.7%	76.8	25	73.3	2	0	0	1538.81	53	66
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	6	6	9	0.01%	17.1%	ILQDDVACDIIK	99.7%	65.2	25	51.3	1	0	0	1402.73	135	146
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	6	6	9	0.01%	17.1%	LGALTAEEIALK	99.7%	74.7	25	52.8	1	0	0	1228.71	358	369
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	6	6	9	0.01%	17.1%	NIHPIYNIK	98.1%	31	25	23.6	1	0	0	1111.63	212	220

KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	6	6	9	0.01%	17.1%	SVSFEQAVR	99.6%	38.2	25	27.8	2	0	0	1022.53	126	134
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	6	6	9	0.01%	17.1%	TFDPYIIIR	99.7%	38.5	25	31.2	2	0	0	1137.63	107	115
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	4	4	8	0.01%	9.5%	FIPEITISDILR	99.7%	65	25	58.1	2	0	0	1416.81	388	399
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	4	4	8	0.01%	9.5%	ISELSGCTPDPR	99.7%	55.2	25	46	2	0	0	1331.63	266	277
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	4	4	8	0.01%	9.5%	LIQQEDIK	98.9%	33.4	25	17.1	2	0	0	986.55	166	173
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	4	4	8	0.01%	9.5%	LIVAVEQEEIPR	99.7%	69	25	44.6	2	0	0	1395.78	137	148
Lactoperoxidase	LPO	PERL_HUMAN	80.3	99.8%	2	2	6	0.01%	2.7%	DGGIDPLVR	99.7%	49	25	39.3	2	0	0	941.51	506	514
Lactoperoxidase	LPO	PERL_HUMAN	80.3	99.8%	2	2	6	0.01%	2.7%	ISNVFTFAFR	99.7%	65	25	51	4	0	0	1201.64	456	465
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	5	5	8	0.01%	22.8%	DFLLQQTMLR	98.4%	31.6	25	18.8	1	0	0	1264.67	29	38
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	5	5	8	0.01%	22.8%	IAWALSR	99.2%	34.6	25	22.1	2	0	0	816.47	89	95
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	5	5	8	0.01%	22.8%	KSLDFYTR	98.8%	33	25	17.1	1	0	0	1029.54	44	51
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	5	5	8	0.01%	22.8%	RFEELGVK	99.7%	46.6	25	21.1	2	0	0	977.54	141	148
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	5	5	8	0.01%	22.8%	VLGMTLIQK	99.7%	46	25	41.4	2	0	0	1002.60	52	60
Lamina-associated polypeptide 2, isoform alpha	TMPO	LAP2A_HUMAN	75.5	100.0%	3	3	6	0.01%	5.6%	EATQILSVPK	97.5%	29.8	25	23.3	1	0	0	1085.62	526	535
Lamina-associated polypeptide 2, isoform alpha	TMPO	LAP2A_HUMAN	75.5	100.0%	3	3	6	0.01%	5.6%	SSTPLPTISSSAENTR	99.7%	53.7	25	47.8	2	0	0	1647.82	158	173
Lamina-associated polypeptide 2, isoform alpha	TMPO	LAP2A_HUMAN	75.5	100.0%	3	3	6	0.01%	5.6%	YGVNPGPIVGTTR	99.7%	44.8	25	44.8	3	0	0	1330.71	127	139
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	21	0.02%	13.7%	KFADGEVVR	98.4%	31.7	25	24.7	1	0	0	1020.55	5	13
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	21	0.02%	13.7%	LTPLILKPFGNSISR	99.7%	39.7	25	39.7	2	2	0	1655.98	117	131
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	21	0.02%	13.7%	NDLSPASSGNAVYDFFIGR	99.7%	104	25	104	6	0	0	2029.96	354	372
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	21	0.02%	13.7%	NLLVSGWWGFVR	99.7%	77.7	25	75.1	3	0	0	1433.77	533	544
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	21	0.02%	13.7%	TFEVTPIR	99.4%	35.7	25	30.6	3	0	0	962.53	196	203
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	21	0.02%	13.7%	VVEGTPLIDGR	99.7%	72.4	25	57.7	2	0	0	1155.64	280	290
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	21	0.02%	13.7%	YNGEPEHIER	99.7%	57.9	25	44.7	2	0	0	1243.57	132	141
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	AEHDQLLLNYAK	99.0%	25.4	25	25.4	0	1	0	1414.73	112	123
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	AGGPTTPLSPTR	99.7%	57.6	25	57.6	4	0	0	1154.62	15	26
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	AKLQIELGK	99.7%	58.6	25	38.7	2	0	0	999.62	101	109
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	ALYETELADAR	99.7%	73.3	25	55.4	4	0	0	1251.62	80	90
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	ALYETELADARR	98.0%	30.8	25	28.4	2	0	0	1407.72	80	91
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	CQSLTEDLEFR	99.7%	61.9	25	50.2	1	0	0	1397.64	198	208
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	CQSLTEDLEFRK	99.7%	57.6	25	48.9	2	2	0	1525.73	198	209
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	DAALATALGDKK	99.7%	78.5	25	55.9	6	0	0	1173.65	146	157
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	IESLSSQLSNLQK	99.7%	99.6	25	86.5	3	0	0	1446.78	300	312
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	IGDTSVSYK	99.7%	68.1	25	65.4	2	0	0	969.49	475	483
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	IQELEDLLAK	99.7%	70.5	25	39.6	2	0	0	1171.66	321	330
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	KESDLNGAQIK	99.0%	33.6	25	23.4	2	0	0	1202.64	124	134
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	KLLEGEEER	99.5%	36.8	25	19.7	2	0	0	1102.57	379	387
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	KQLADETLLK	98.9%	33.5	25	26.2	1	0	0	1158.67	182	191
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	LALDMEISAYR	99.7%	60.7	25	56.7	2	0	0	1297.65	368	378
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	LALDMEISAYRK	99.7%	44.2	25	43.4	2	2	0	1425.74	368	379
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	LAQALHEMR	99.7%	57.3	25	50.7	2	0	0	1084.56	242	250
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	LAVYIDK	95.7%	27.7	25	27.7	1	0	0	821.48	43	49
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	LAVYIDKVR	99.7%	44.9	25	38.6	2	0	0	1076.65	43	51
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	LLEGEEER	99.4%	36.2	25	30.2	4	0	0	974.48	380	387
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	LLEGEEERLK	99.7%	52.5	25	36.9	2	0	0	1215.66	380	389
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	LQEKEELR	99.7%	50.2	25	22.9	4	0	0	1044.57	30	37
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	LQIELGK	99.2%	34.6	25	0	2	0	0	800.49	103	109
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	LREYEAALNSK	99.7%	60.2	25	42.2	4	1	0	1293.68	135	145
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	LSSEMNTSTVNSAR	99.7%	104	25	93.8	4	0	0	1496.70	277	290
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	LVEVDSGR	98.8%	33	25	22	2	0	0	874.46	227	234
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	LYKEELEQTYHAK	99.7%	69.4	25	64.1	2	4	0	1651.83	259	271
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	MRIESLSSQLSNLQK	99.7%	40.9	25	33.2	1	3	0	1749.92	298	312

Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	NQNSWGTGEDVK	99.7%	63.9	25	63.9	2	0	0	1334.60	517	528
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	QIEYEYK	99.7%	42.2	25	39.5	2	0	0	972.47	235	241
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	QLADETLLK	99.7%	51.7	25	42.6	2	0	0	1030.58	183	191
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	SLETENSALQLQVTEREEVR	99.7%	58.4	25	58.4	0	3	0	2331.18	52	71
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	33	40	91	0.09%	45.7%	SMYEEEINETR	99.7%	72.4	25	72.4	2	0	0	1416.59	210	220
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	17	17	43	0.04%	35.7%	AGGPATPLSPTR	99.7%	57	25	42.6	3	0	0	1124.61	9	20
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	17	17	43	0.04%	35.7%	ALELENDRLLLK	99.7%	44.2	25	29.6	2	0	0	1426.83	46	57
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	17	17	43	0.04%	35.7%	ALYESELADAR	99.7%	71.9	25	64.2	2	0	0	1237.61	74	84
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	17	17	43	0.04%	35.7%	ATSSSSGSLSATGR	99.7%	92.2	25	92.2	4	0	0	1268.61	397	410
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	17	17	43	0.04%	35.7%	EGELTVAQGR	99.7%	65.5	25	36.1	3	0	0	1059.54	119	128
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	17	17	43	0.04%	35.7%	GLESDVAELR	99.7%	84.1	25	62.8	4	0	0	1088.56	152	161
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	17	17	43	0.04%	35.7%	ISEKEEVTTR	99.7%	70.5	25	46.6	2	0	0	1191.62	58	67
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	17	17	43	0.04%	35.7%	KLLEGEEER	99.5%	36.8	25	19.7	2	0	0	1102.57	373	381
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	17	17	43	0.04%	35.7%	LLEGEEER	99.4%	36.2	25	30.2	4	0	0	974.48	374	381
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	17	17	43	0.04%	35.7%	LLEGEEERLK	99.7%	52.5	25	36.9	2	0	0	1215.66	374	383
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	17	17	43	0.04%	35.7%	LQEKEELR	99.7%	50.2	25	22.9	4	0	0	1044.57	24	31
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	17	17	43	0.04%	35.7%	LQIEIGK	99.2%	34.6	25	0	2	0	0	800.49	97	103
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	17	17	43	0.04%	35.7%	LRAELDEVNK	98.9%	33.3	25	15.4	1	0	0	1186.64	104	113
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	17	17	43	0.04%	35.7%	LSSDQNDKAASAAR	99.7%	63.4	25	61	4	0	0	1433.70	271	284
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	17	17	43	0.04%	35.7%	LYKLELEQTYQAK	99.7%	57.8	25	50.4	2	0	0	1626.87	253	265
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	17	17	43	0.04%	35.7%	QQEYDFK	96.5%	28.5	25	25	1	0	0	957.43	229	235
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	17	17	43	0.04%	35.7%	QVLEGEEIAYK	99.7%	76.1	25	64.6	2	0	0	1278.66	486	496
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	17	17	43	0.04%	35.7%	RLVEVDSSR	99.7%	51.2	25	35.9	4	0	0	1060.57	220	228
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	17	17	43	0.04%	35.7%	SEVELAAALSDKR	99.7%	76.8	25	68.8	2	0	0	1388.74	139	151
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	17	17	43	0.04%	35.7%	SVFEEEVR	96.4%	28.4	25	17.7	1	0	0	994.48	204	211
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	17	17	43	0.04%	35.7%	TVLVNADGEEVAMR	99.7%	78.9	25	77.8	2	0	0	1519.74	542	555
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	17	17	43	0.04%	35.7%	VKDLESLFHR	99.7%	50.9	25	40	0	4	0	1243.68	129	138
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	5	5	7	0.01%	4.1%	ETESAPGSPR	95.5%	27.6	25	26.4	1	0	0	1030.48	514	523
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	5	5	7	0.01%	4.1%	FWSFFLR	99.7%	50.1	25	47.1	2	0	0	1002.52	918	924
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	5	5	7	0.01%	4.1%	LQEYLGK	96.7%	28.7	25	10.8	1	0	0	850.47	1011	1017
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	5	5	7	0.01%	4.1%	SLPTTVPESPNYR	98.8%	32.9	25	31.3	1	0	0	1460.74	766	778
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	5	5	7	0.01%	4.1%	YGLECLFR	99.7%	55	25	46	2	0	0	1057.51	949	956
La-related protein 7	LARP7	LARP7_HUMAN	66.9	100.0%	4	4	7	0.01%	8.9%	AIEFLNNPPEEAPR	99.7%	81	25	78.2	2	0	0	1596.80	182	195
La-related protein 7	LARP7	LARP7_HUMAN	66.9	100.0%	4	4	7	0.01%	8.9%	LEILSGDHEQR	99.7%	46.9	25	36.7	1	0	0	1296.65	521	531
La-related protein 7	LARP7	LARP7_HUMAN	66.9	100.0%	4	4	7	0.01%	8.9%	SSSEDAESLAPR	99.7%	49	25	39.2	2	0	0	1248.57	298	309
La-related protein 7	LARP7	LARP7_HUMAN	66.9	100.0%	4	4	7	0.01%	8.9%	VNATGPQFVSGVIVK	99.7%	57.5	25	53.9	2	0	0	1515.85	444	458
Large neutral amino acids transporter small subunit 1	SLC7A5	LAT1_HUMAN	55.0	100.0%	2	3	5	0.00%	6.3%	ALAAPAAEEKEEAR	99.7%	83.9	25	83.9	2	1	0	1455.74	10	23
Large neutral amino acids transporter small subunit 1	SLC7A5	LAT1_HUMAN	55.0	100.0%	2	3	5	0.00%	6.3%	SADGSAPAGEGEGVTLQR	99.7%	101	25	101	2	0	0	1701.80	31	48
Lethal(2) giant larvae protein homolog 1	LLGL1	L2GL1_HUMAN	115.4	99.8%	2	2	3	0.00%	2.4%	APVVAIAVLDGR	99.7%	88.7	25	82.8	2	0	0	1180.70	788	799
Lethal(2) giant larvae protein homolog 1	LLGL1	L2GL1_HUMAN	115.4	99.8%	2	2	3	0.00%	2.4%	TGPLPWPAGFQPR	99.7%	39.3	25	31.7	1	0	0	1423.75	578	590
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	AFAETHIK	99.3%	35.1	25	32.2	1	0	0	916.49	1091	1098
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	AGDMENAENILTVMR	99.7%	67.5	25	67.5	6	0	0	1695.77	245	259
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	AGYPQYVSEILEK	99.7%	74.8	25	69.2	2	0	0	1496.76	315	327
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	ALYEHLTAK	99.7%	40	25	24.1	2	0	0	1045.57	1339	1347
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	CVANNQVETLEK	99.7%	71.8	25	61.7	2	0	0	1404.68	930	941
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	DAHLLVESK	99.7%	47.7	25	38.4	2	0	0	1011.55	641	649
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	DLPVTEAVFSALVTGHAR	99.7%	50.8	25	50.8	1	0	0	1883.00	227	244
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	EKDIQEESTFSSR	99.7%	73.2	25	65.1	2	0	0	1555.72	65	77
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	EQNIVFNAETYSNLIK	99.7%	80.2	25	80.2	2	0	0	1882.95	1060	1075
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	FSPTDFLAK	95.1%	27.2	25	17.7	1	0	0	1025.53	179	187
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	GAYDIFLNAK	99.7%	64	25	58	2	0	0	1111.58	1050	1059

Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	GDLSTALEVAIDCYEK	99.7%	47.5	25	47.5	1	0	0	1783.84	836	851
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	GDVENIEVVQK	99.7%	68.6	25	56.4	2	0	0	1229.64	1153	1163
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	GFTLNDAANSR	99.7%	69.3	25	52.4	2	0	0	1165.56	1099	1109
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	IPENIYR	98.8%	32.8	25	20.6	1	0	0	904.49	618	624
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	IQEENVIPR	99.7%	58.9	25	48.8	1	0	0	1097.60	981	989
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	KIIETPGIR	99.7%	52.2	25	45.4	2	0	0	1026.63	909	917
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	LDDLFLKR	99.7%	59.1	25	44.6	2	0	0	1019.59	1351	1358
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	LDSSAVLDTGK	99.7%	73.2	25	64.7	2	0	0	1105.57	740	750
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	LGAVYDVSHYNALLK	99.7%	80.8	25	68.2	2	1	0	1662.89	156	170
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	LIASYCNVGDIEGASK	99.7%	118	25	116	2	0	0	1696.82	203	218
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	LLMSEDYFTQAMEVK	99.7%	85.4	25	78.1	5	0	0	1804.85	1076	1090
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	LQDAINILK	99.7%	51.7	25	37.2	2	0	0	1027.61	764	772
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	LVEKGETDLIQK	99.7%	53.2	25	44.2	2	0	0	1372.77	865	876
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	MEEANIQPNR	99.7%	62.7	25	49.3	2	0	0	1201.56	188	197
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	MLNGLEDSIGLSK	99.7%	78.9	25	75.2	3	0	0	1376.71	1164	1176
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	MVFINNIALAQIK	99.7%	94.2	25	88.2	4	0	0	1474.85	1177	1189
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	NVQGIIEILK	99.7%	68.2	25	59.5	2	0	0	1126.68	454	463
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	SCGSLLPELK	99.7%	48.4	25	39.1	2	0	0	1103.58	129	138
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	SGGLGGSHALLLLR	99.7%	47.4	25	41.9	2	2	0	1350.79	115	128
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	SNTLPISLQSIR	99.7%	98.8	25	69.1	2	0	0	1328.75	530	541
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	SYVSEKDVTSAK	99.7%	59.9	25	59.3	2	0	0	1313.66	1327	1338
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	TVLDQQQTPSR	99.7%	62.8	25	52.7	2	0	0	1272.65	1129	1139
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	TVQLTSSELESTLETLK	99.7%	89.5	25	85.6	2	0	0	1878.99	656	672
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	VIEPQYFGLAYLFR	99.7%	72.8	25	69.7	2	0	0	1715.92	1210	1223
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	36	42	79	0.08%	30.5%	VYLQNEYK	99.6%	37.5	25	28.4	2	0	0	1056.54	171	178
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	9	9	16	0.02%	14.5%	GTAAILEYLR	99.7%	65.9	25	42.4	2	0	0	1106.62	588	597
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	9	9	16	0.02%	14.5%	LNLSSNELK	99.6%	37.7	25	0.49	1	0	0	1017.56	202	210
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	9	9	16	0.02%	14.5%	LQTINLSFNR	99.7%	54.6	25	47.2	2	0	0	1205.66	497	506
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	9	9	16	0.02%	14.5%	LTFLDLR	99.7%	41.2	25	32.5	2	0	0	877.51	474	480
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	9	9	16	0.02%	14.5%	NLSEVPQCVWR	99.7%	53.4	25	49.2	2	0	0	1387.68	47	57
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	9	9	16	0.02%	14.5%	SGQLNLSGR	99.7%	44.9	25	23.3	1	0	0	931.50	38	46
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	9	9	16	0.02%	14.5%	SNIVTSINFSK	99.7%	51.8	25	49.5	2	0	0	1209.65	424	434
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	9	9	16	0.02%	14.5%	SVPDEIILLR	99.7%	51.8	25	32.8	2	0	0	1154.68	303	312
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	9	9	16	0.02%	14.5%	TLLLDGNPFR	99.7%	57.1	25	50.8	2	0	0	1145.63	569	578
Leucine-rich repeat-containing protein 47	LRRC47	LRC47_HUMAN	63.5	100.0%	4	4	7	0.01%	9.1%	DGPSLLVVEQVR	99.7%	46.6	25	40.5	1	0	0	1311.73	543	554
Leucine-rich repeat-containing protein 47	LRRC47	LRC47_HUMAN	63.5	100.0%	4	4	7	0.01%	9.1%	ELLLTGPGLEER	99.7%	61.9	25	54.8	2	0	0	1326.73	23	34
Leucine-rich repeat-containing protein 47	LRRC47	LRC47_HUMAN	63.5	100.0%	4	4	7	0.01%	9.1%	NALGPGLSPELGPLPALR	99.7%	55.7	25	55.7	2	0	0	1772.01	85	102
Leucine-rich repeat-containing protein 47	LRRC47	LRC47_HUMAN	63.5	100.0%	4	4	7	0.01%	9.1%	TAATLATHELR	99.7%	67.5	25	57.6	2	0	0	1183.64	371	381
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	20	21	40	0.04%	21.3%	CEFAVGYQR	99.7%	46.2	25	44.6	2	0	0	1129.51	70	78
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	20	21	40	0.04%	21.3%	ELMGEEILGASLSAPLTSYK	99.7%	48.3	25	48.3	2	0	0	2109.08	351	370
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	20	21	40	0.04%	21.3%	EVWDYVFFK	97.9%	30.5	25	30.5	2	0	0	1232.60	633	641
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	20	21	40	0.04%	21.3%	FASEAEDKIR	99.7%	47.3	25	38	1	0	0	1165.58	1040	1049
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	20	21	40	0.04%	21.3%	FDDPLLGPR	99.7%	55.1	25	40	2	0	0	1029.54	1118	1126
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	20	21	40	0.04%	21.3%	GFYEGIMLVDGFK	99.7%	74.1	25	58.2	4	0	0	1475.72	471	483
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	20	21	40	0.04%	21.3%	GTGVVTSVPSDSPDDIAALR	99.7%	75.1	25	75.1	2	0	0	1956.99	385	404
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	20	21	40	0.04%	21.3%	MIDAGDALIYMEPEK	99.7%	72.7	25	72.7	2	0	0	1695.80	498	512
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	20	21	40	0.04%	21.3%	QGDNCDSIIR	99.6%	37.6	25	34.2	1	0	0	1177.53	1089	1098
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	20	21	40	0.04%	21.3%	QTGEGVGPQEYTLLK	99.7%	53.4	25	44.3	2	0	0	1619.83	254	268
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	20	21	40	0.04%	21.3%	SFITTDVNPYYDSFVR	99.7%	90.8	25	90.8	2	0	0	1923.91	204	219
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	20	21	40	0.04%	21.3%	SGPASTFNDR	98.4%	31.8	25	27.9	2	0	0	1051.48	786	795
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	20	21	40	0.04%	21.3%	SLGLSDEEIVK	99.7%	53.4	25	44.9	2	0	0	1189.63	163	173

Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	20	21	40	0.04%	21.3%	STGNFLTLTQAIDK	99.7%	83.7	25	73.2	2	0	0	1508.80	720	733
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	20	21	40	0.04%	21.3%	TGFFEFQAAK	99.7%	55	25	48.1	2	0	0	1145.56	823	832
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	20	21	40	0.04%	21.3%	VDIGDTIIYLVH	99.7%	68.3	25	65.3	2	0	0	1357.74	1165	1176
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	20	21	40	0.04%	21.3%	VFASELNAGIIK	99.7%	95.6	25	84.9	2	0	0	1261.72	796	807
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	20	21	40	0.04%	21.3%	VFEVNASNLEK	99.7%	66.6	25	58.8	2	0	0	1249.64	29	39
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	20	21	40	0.04%	21.3%	VIASELGSMPELK	99.7%	65.4	25	55.2	2	0	0	1389.73	971	983
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	20	21	40	0.04%	21.3%	VIYVLPMLTIK	99.7%	54.1	25	54.1	2	0	0	1289.79	371	381
LINE-1 retrotransposable element ORF1 protein	L1RE1	LORF1_HUMAN	40.1	99.8%	2	2	2	0.00%	6.8%	DFVTTRPALK	99.4%	36	25	33.5	1	0	0	1147.65	305	314
LINE-1 retrotransposable element ORF1 protein	L1RE1	LORF1_HUMAN	40.1	99.8%	2	2	2	0.00%	6.8%	LTADLSAETLQAR	99.7%	57.9	25	47.9	1	0	0	1388.74	249	261
Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	DBT	ODB2_HUMAN	53.5	99.8%	2	2	3	0.00%	4.8%	LSFMPFFLK	99.4%	36	25	21.2	2	0	0	1129.61	305	313
Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	DBT	ODB2_HUMAN	53.5	99.8%	2	2	3	0.00%	4.8%	SYLENPAFMLLDLK	99.7%	73.1	25	70.2	1	0	0	1653.86	469	482
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	5	5	8	0.01%	2.1%	EIFVDFAPFLSR	99.7%	75.2	25	72.4	3	0	0	1440.75	1813	1824
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	5	5	8	0.01%	2.1%	IQNPQILK	96.7%	28.7	25	24.8	1	0	0	953.58	813	820
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	5	5	8	0.01%	2.1%	NAGLAFIELVNEGR	99.4%	36.2	25	34.1	1	0	0	1502.80	1869	1882
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	5	5	8	0.01%	2.1%	VGVGTSFGLPQTR	98.4%	31.6	25	31.2	1	0	0	1318.71	2183	2195
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	5	5	8	0.01%	2.1%	YGPDAFFNFPGK	99.7%	68.4	25	68.4	2	0	0	1359.64	201	212
Lipoprotein lipase	LPL	LIPL_HUMAN	53.2	100.0%	5	6	12	0.01%	12.8%	EPDSNVIVVDWLSR	99.7%	75	25	75	2	0	0	1628.83	103	116
Lipoprotein lipase	LPL	LIPL_HUMAN	53.2	100.0%	5	6	12	0.01%	12.8%	GLGDVDQLVK	99.7%	53.9	25	35.4	2	0	0	1043.57	256	265
Lipoprotein lipase	LPL	LIPL_HUMAN	53.2	100.0%	5	6	12	0.01%	12.8%	ITGLDPAGPNFEYAEAPSR	99.7%	96.1	25	83	2	0	0	2004.97	179	197
Lipoprotein lipase	LPL	LIPL_HUMAN	53.2	100.0%	5	6	12	0.01%	12.8%	LSPDDADFVDVLHTFTR	99.7%	105	25	97.9	2	2	0	1947.94	198	214
Lipoprotein lipase	LPL	LIPL_HUMAN	53.2	100.0%	5	6	12	0.01%	12.8%	REPDSNVIVVDWLSR	99.7%	43.7	25	40.8	0	2	0	1784.93	102	116
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	15	17	113	0.11%	44.9%	DLADELALVDVIEDK	97.8%	30.3	25	22.8	1	0	0	1657.85	43	57
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	15	17	113	0.11%	44.9%	DQLIYNLLK	99.7%	61.7	25	42.7	3	0	0	1119.64	6	14
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	15	17	113	0.11%	44.9%	DQLIYNLLKEEQTPQNK	99.7%	32	25	32	2	2	0	2074.08	6	22
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	15	17	113	0.11%	44.9%	DYNVTANSK	99.7%	58.4	25	52.5	5	0	0	1011.47	82	90
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	15	17	113	0.11%	44.9%	FIIPNVVK	98.7%	32.6	25	17.4	3	0	0	929.58	119	126
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	15	17	113	0.11%	44.9%	GEMMDLQHGSLFLR	98.7%	32.6	25	0.03	2	0	0	1649.78	60	73
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	15	17	113	0.11%	44.9%	IVSGKDYNVTANSK	99.7%	90.8	25	90.8	5	2	0	1495.78	77	90
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	15	17	113	0.11%	44.9%	LLIVSNPVDILTYVAWK	99.7%	102	25	0	2	0	0	1944.12	133	149
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	15	17	113	0.11%	44.9%	LVIITAGAR	99.7%	75.9	25	54.7	22	0	0	913.58	91	99
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	15	17	113	0.11%	44.9%	QVVESAYEVIK	99.7%	71.8	25	63.1	12	0	0	1264.68	233	243
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	15	17	113	0.11%	44.9%	SADTLWGIQK	99.7%	65.9	25	55.5	6	0	0	1118.58	319	328
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	15	17	113	0.11%	44.9%	TLHPDLGTDK	99.7%	42.6	25	42.6	2	0	0	1096.56	213	222
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	15	17	113	0.11%	44.9%	VIGSGCNLDSAR	99.7%	84.7	25	76.5	20	0	0	1248.60	158	169
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	15	17	113	0.11%	44.9%	VTLTSEEEAR	99.7%	68.4	25	63.5	22	0	0	1134.56	306	315
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	15	17	113	0.11%	44.9%	VTLTSEEEARLK	99.5%	36.4	25	31.8	2	0	0	1375.74	306	317
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	19	94	0.09%	49.7%	EKLIAPVAEEEATVPNNK	99.7%	82.7	25	81.1	2	0	0	1952.03	6	23
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	19	94	0.09%	49.7%	FIIPQIVK	99.7%	42.8	25	40.3	4	0	0	957.61	120	127
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	19	94	0.09%	49.7%	GEMMDLQHGSLFLQTPK	99.7%	36.8	25	36.8	0	2	0	1963.93	61	77
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	19	94	0.09%	49.7%	GLTSVINQK	99.7%	57.5	25	35.6	10	0	0	959.55	300	308
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	19	94	0.09%	49.7%	IHPVSTMVK	97.5%	29.9	25	19.8	1	0	0	1011.57	271	279
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	19	94	0.09%	49.7%	ITVVGVGQVGMACAISILGK	99.7%	79.3	25	79.3	2	2	0	1989.09	24	43
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	19	94	0.09%	49.7%	IVADKDYSVTANSK	99.7%	97.8	25	92.4	13	3	0	1510.77	78	91
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	19	94	0.09%	49.7%	IVVVTAGVR	99.7%	78.7	25	61.3	8	0	0	913.58	92	100
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	19	94	0.09%	49.7%	KSADTLWDIQK	99.7%	50.4	25	47.1	2	0	0	1304.68	319	329
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	19	94	0.09%	49.7%	LIAPVAEEEATVPNNK	99.7%	96.2	25	92.9	7	2	0	1694.90	8	23
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	19	94	0.09%	49.7%	LKDDEVAQLK	99.7%	60.6	25	35.9	2	0	0	1158.64	309	318
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	19	94	0.09%	49.7%	MVVESAYEVIK	99.7%	92.9	25	87.2	21	0	0	1267.66	234	244
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	19	94	0.09%	49.7%	SADTLWDIQK	99.7%	80.9	25	70.4	10	0	0	1176.59	320	329
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	19	94	0.09%	49.7%	SADTLWDIQKDLK	98.8%	33	25	28	1	0	0	1532.80	320	332
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	19	94	0.09%	49.7%	SLADELALVDVLEDK	99.7%	42.5	25	42.5	2	0	0	1629.86	44	58

L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	19	94	0.09%	49.7%	VIGSGCNLDSAR	99.7%	84.7	25	76.5	20	0	0	1248.60	159	170
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	9	9	16	0.02%	10.9%	DIIALNPLYR	99.7%	60.4	25	52.4	2	0	0	1187.68	302	311
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	9	9	16	0.02%	10.9%	EAEDELSAR	96.7%	28.8	25	23	2	0	0	1019.46	245	253
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	9	9	16	0.02%	10.9%	FSVGGMTDVAEIK	99.7%	59.6	25	52.9	1	0	0	1353.67	547	559
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	9	9	16	0.02%	10.9%	ILCFYGPPGVGK	99.7%	61.2	25	56.2	1	0	0	1307.68	518	529
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	9	9	16	0.02%	10.9%	ILEFIAVSQLR	99.7%	69.7	25	62.7	2	0	0	1288.76	501	511
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	9	9	16	0.02%	10.9%	LAQPYVGVFLK	99.7%	43.2	25	42.7	2	0	0	1234.72	159	169
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	9	9	16	0.02%	10.9%	LGLLDNHSSEFNVTR	96.5%	21.6	25	20.2	0	1	0	1701.86	445	459
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	9	9	16	0.02%	10.9%	LSSDVLTLLIK	99.7%	81.7	25	57.8	3	0	0	1201.74	691	701
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	9	9	16	0.02%	10.9%	TENPLILIDEVDK	99.7%	49.4	25	47	2	0	0	1498.80	582	594
Long-chain fatty acid transport protein 4	SLC27A4	S27A4_HUMAN	72.1	99.8%	2	2	5	0.00%	3.1%	ILSFVYPIR	99.3%	35.2	25	23.9	1	0	0	1107.66	409	417
Long-chain fatty acid transport protein 4	SLC27A4	S27A4_HUMAN	72.1	99.8%	2	2	5	0.00%	3.1%	TVPILFASTVR	99.7%	52.8	25	52.5	4	0	0	1203.71	75	85
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	8	8	15	0.01%	13.6%	IGYSSPQTLADQSSK	99.7%	78.2	25	78.1	2	0	0	1581.78	349	363
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	8	8	15	0.01%	13.6%	LKDIVSLVPR	99.7%	51.1	25	45.3	2	0	0	1139.71	221	230
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	8	8	15	0.01%	13.6%	LLLCGGAPLSATTQR	99.7%	87.4	25	79.1	2	0	0	1557.84	447	461
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	8	8	15	0.01%	13.6%	LQAGEYVSLGK	99.7%	38.5	25	38.5	2	0	0	1164.63	586	596
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	8	8	15	0.01%	13.6%	LSPEPWTPETGLVTDAFK	99.7%	73.8	25	73.3	2	0	0	1988.00	682	699
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	8	8	15	0.01%	13.6%	NTPLCDSFVFR	99.6%	37.3	25	34.3	2	0	0	1355.64	425	435
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	8	8	15	0.01%	13.6%	THYQADIER	97.2%	29.4	25	29.4	2	0	0	1132.54	707	715
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	8	8	15	0.01%	13.6%	VSEMSSFQR	99.3%	35.2	25	31.2	1	0	0	1086.49	398	406
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	8	8	16	0.02%	19.4%	FVETPGQK	95.8%	27.8	25	20.6	1	0	0	905.47	167	174
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	8	8	16	0.02%	19.4%	GSIFVVFDSIESAK	99.7%	80.8	25	76.7	2	0	0	1498.78	152	165
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	8	8	16	0.02%	19.4%	GSIFVVFDSIESAKK	99.7%	77.9	25	73.5	2	0	0	1626.87	152	166
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	8	8	16	0.02%	19.4%	IIEDQQESLNK	99.7%	91.5	25	79.2	3	0	0	1316.67	318	328
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	8	8	16	0.02%	19.4%	KFVETPGQK	97.8%	30.4	25	23	2	0	0	1033.57	166	174
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	8	8	16	0.02%	19.4%	LDEGWVPLEIMIK	99.7%	51.2	25	38.6	1	0	0	1542.82	42	54
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	8	8	16	0.02%	19.4%	LTTDFNVIVEALSK	99.7%	101	25	96.4	3	0	0	1549.85	61	74
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	8	8	16	0.02%	19.4%	SPSKPLPEVTDEYKNDVK	99.0%	25.4	25	24.1	0	2	0	2046.04	92	109
Lys-63-specific deubiquitinase BRCC36	BRCC3	BRCC3_HUMAN	36.1	99.8%	2	2	4	0.00%	7.6%	VCLESAVELPK	99.7%	51.1	25	40	2	0	0	1244.66	227	237
Lys-63-specific deubiquitinase BRCC36	BRCC3	BRCC3_HUMAN	36.1	99.8%	2	2	4	0.00%	7.6%	VLYTCFQSIQAQK	99.7%	68.2	25	62.3	2	0	0	1585.80	168	180
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	14	0.01%	15.6%	IAPELYHK	97.0%	29.1	25	11.9	2	0	0	970.54	298	305
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	14	0.01%	15.6%	ILDDICVAK	95.5%	27.6	25	2.53	1	0	0	1046.56	422	430
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	14	0.01%	15.6%	INMVEELEK	96.7%	28.8	25	21.6	1	0	0	1104.56	394	402
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	14	0.01%	15.6%	LPETNLFETEETRK	97.9%	23.1	25	18.7	0	2	0	1706.86	408	421
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	14	0.01%	15.6%	LQVMANSR	94.9%	27.1	25	15.9	1	0	0	934.48	154	161
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	14	0.01%	15.6%	MLVVGGIDR	99.7%	58	25	49.8	2	0	0	959.53	306	314
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	14	0.01%	15.6%	RGDIIGVQGNPGK	99.7%	62.3	25	60.4	2	0	0	1310.72	178	190
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	14	0.01%	15.6%	SEEEFIHINNK	99.7%	47.4	25	46	1	0	0	1359.65	165	175
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	14	0.01%	15.6%	VAMFLTDSNNIK	99.7%	55.1	25	49	2	0	0	1352.69	554	565
Lysophosphatidylcholine acyltransferase 1	LPCAT1	PCAT1_HUMAN	59.2	100.0%	4	4	6	0.01%	10.1%	ITFADFHR	99.4%	35.7	25	26.3	2	0	0	1006.51	471	478
Lysophosphatidylcholine acyltransferase 1	LPCAT1	PCAT1_HUMAN	59.2	100.0%	4	4	6	0.01%	10.1%	NPFVHELR	99.7%	45.3	25	35	2	0	0	1011.54	30	37
Lysophosphatidylcholine acyltransferase 1	LPCAT1	PCAT1_HUMAN	59.2	100.0%	4	4	6	0.01%	10.1%	TALGVAELTVTDLFR	99.7%	78.9	25	77.2	1	0	0	1605.88	447	461
Lysophosphatidylcholine acyltransferase 1	LPCAT1	PCAT1_HUMAN	59.2	100.0%	4	4	6	0.01%	10.1%	TCLITFKPGAFIPGAPVQPVVLR	98.9%	25.1	25	25.1	0	1	0	2481.41	215	237
Macrophage migration inhibitory factor	MIF	MIF_HUMAN	12.5	99.8%	2	3	6	0.01%	17.4%	LLCGLLAER	99.7%	72.7	25	51.9	2	0	0	1044.59	79	87
Macrophage migration inhibitory factor	MIF	MIF_HUMAN	12.5	99.8%	2	3	6	0.01%	17.4%	PMFIVNTNVPR	99.7%	73.7	25	64.8	4	0	0	1287.69	2	12
Magnesium transporter protein 1	MAGT1	MAGT1_HUMAN	38.0	100.0%	3	3	6	0.01%	8.1%	GFSAEQIAR	99.7%	41.3	25	32.7	2	0	0	978.50	160	168
Magnesium transporter protein 1	MAGT1	MAGT1_HUMAN	38.0	100.0%	3	3	6	0.01%	8.1%	RGDTYELQVR	99.7%	42.3	25	35.7	2	0	0	1236.63	150	159
Magnesium transporter protein 1	MAGT1	MAGT1_HUMAN	38.0	100.0%	3	3	6	0.01%	8.1%	YSSAFTNR	99.7%	59.4	25	50.5	2	0	0	945.44	106	113
Malate dehydrogenase, cytoplasmic	MDH1	MDHC_HUMAN	36.4	99.8%	2	2	3	0.00%	7.8%	LGVTANDVK	99.7%	41.8	25	27.9	2	0	0	916.51	171	179
Malate dehydrogenase, cytoplasmic	MDH1	MDHC_HUMAN	36.4	99.8%	2	2	3	0.00%	7.8%	VIVVGNPANTNCLTASK	99.7%	64.5	25	57.4	1	0	0	1757.92	126	142
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	6	6	10	0.01%	25.4%	AGAGSATLSMAYAGAR	99.7%	45.9	25	45.9	1	0	0	1454.71	242	257

Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	6	6	10	0.01%	25.4%	ANTFVAELK	99.7%	47.4	25	33.8	2	0	0	992.54	177	185
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	6	6	10	0.01%	25.4%	IFGVTTLDIVR	97.4%	29.7	25	25.3	2	0	0	1233.72	166	176
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	6	6	10	0.01%	25.4%	SQETECTYFSTPLLLGK	99.7%	44.8	25	44.8	2	0	0	1973.95	280	296
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	6	6	10	0.01%	25.4%	VAVLGASGGIGQPLSLLLK	99.7%	57	25	57	1	0	0	1793.09	27	45
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	6	6	10	0.01%	25.4%	VDFPQDQLTALTGR	99.6%	38.2	25	32.8	2	0	0	1560.80	216	229
Malectin	MLEC	MLEC_HUMAN	32.2	100.0%	4	4	9	0.01%	18.5%	FAEVYFAQSQQK	99.7%	94.5	25	91.4	2	0	0	1445.71	127	138
Malectin	MLEC	MLEC_HUMAN	32.2	100.0%	4	4	9	0.01%	18.5%	LSVQGEVSTFTGK	99.7%	68.6	25	64.5	3	0	0	1352.71	178	190
Malectin	MLEC	MLEC_HUMAN	32.2	100.0%	4	4	9	0.01%	18.5%	SNPEDQILYQTER	99.7%	77.8	25	70.9	2	0	0	1592.76	91	103
Malectin	MLEC	MLEC_HUMAN	32.2	100.0%	4	4	9	0.01%	18.5%	VCALYIMAGTVDDVPK	99.7%	90.8	25	76.8	2	0	0	1751.87	205	220
Malonyl-CoA-acyl carrier protein transacylase, mitochondrial	MCAT	FABD_HUMAN	43.0	100.0%	3	3	4	0.00%	6.7%	FNFACLEAR	99.0%	33.6	25	23.9	1	0	0	1127.53	204	212
Malonyl-CoA-acyl carrier protein transacylase, mitochondrial	MCAT	FABD_HUMAN	43.0	100.0%	3	3	4	0.00%	6.7%	GLLNYPR	94.7%	26.9	25	12.6	1	0	0	832.47	80	86
Malonyl-CoA-acyl carrier protein transacylase, mitochondrial	MCAT	FABD_HUMAN	43.0	100.0%	3	3	4	0.00%	6.7%	VISGHQEALR	99.7%	59.8	25	52.3	2	0	0	1109.61	237	246
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	6	6	10	0.01%	16.4%	AVILIGGPQK	99.7%	51.2	25	48.2	2	0	0	995.63	4	13
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	6	6	10	0.01%	16.4%	GVTVGEGVR	99.5%	36.5	25	26.7	1	0	0	873.48	310	318
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	6	6	10	0.01%	16.4%	LLPAITILGCR	97.5%	29.8	25	29.8	1	0	0	1226.73	380	390
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	6	6	10	0.01%	16.4%	SAGSALYASR	99.7%	51.9	25	46.3	2	0	0	982.50	250	259
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	6	6	10	0.01%	16.4%	VAPSAVLGPNVSIGK	99.7%	62.6	25	61.4	2	0	0	1408.82	295	309
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	6	6	10	0.01%	16.4%	VEGTPSDPNPNDPR	98.5%	31.9	25	20	2	0	0	1494.68	353	366
Mannose-1-phosphate guanyltransferase beta	GMPPB	GMPPB_HUMAN	39.8	100.0%	5	5	9	0.01%	20.3%	ALILVGGYGTR	99.7%	67.6	25	67.6	2	0	0	1119.65	3	13
Mannose-1-phosphate guanyltransferase beta	GMPPB	GMPPB_HUMAN	39.8	100.0%	5	5	9	0.01%	20.3%	FVEKPQVFVSNK	99.7%	55.2	25	53.4	2	0	0	1421.78	159	170
Mannose-1-phosphate guanyltransferase beta	GMPPB	GMPPB_HUMAN	39.8	100.0%	5	5	9	0.01%	20.3%	ISMSHEEEPLGTAGPLALAR	98.7%	24.5	25	24.5	0	1	0	2095.05	75	94
Mannose-1-phosphate guanyltransferase beta	GMPPB	GMPPB_HUMAN	39.8	100.0%	5	5	9	0.01%	20.3%	LCSGPGIVGNVLVDPSAR	99.7%	66.6	25	66.6	2	0	0	1810.95	244	261
Mannose-1-phosphate guanyltransferase beta	GMPPB	GMPPB_HUMAN	39.8	100.0%	5	5	9	0.01%	20.3%	YGVVVCEADTGR	99.7%	67.7	25	63.3	2	0	0	1325.62	144	155
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	15	17	38	0.04%	20.4%	GDADQASNILASFGLSAR	99.7%	79.9	25	79.9	3	0	0	1792.88	103	120
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	15	17	38	0.04%	20.4%	GNLGAGNGNLQGPR	99.7%	55.5	25	55.5	2	0	0	1324.67	374	387
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	15	17	38	0.04%	20.4%	GPGPLQER	99.5%	37.2	25	28.9	2	0	0	853.45	256	263
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	15	17	38	0.04%	20.4%	GPLPLSSQHR	99.7%	40	25	37.6	2	0	0	1091.60	93	102
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	15	17	38	0.04%	20.4%	GPSLNPVLDYDHGSR	99.7%	42.4	25	38.1	0	1	0	1626.79	193	207
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	15	17	38	0.04%	20.4%	IGPYQPNVPVGIDYVIPK	99.7%	72	25	72	4	0	0	1969.08	781	798
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	15	17	38	0.04%	20.4%	ITPENLPQILLQLK	99.7%	60.8	25	58.2	2	0	0	1619.97	133	146
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	15	17	38	0.04%	20.4%	LCSLFYTNEEVAK	99.7%	70.9	25	64.4	3	0	0	1573.76	805	817
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	15	17	38	0.04%	20.4%	MDYEDDRLR	99.7%	47.5	25	37.6	2	0	0	1212.53	217	225
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	15	17	38	0.04%	20.4%	NYILMR	98.4%	31.7	25	14.3	2	0	0	825.43	525	530
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	15	17	38	0.04%	20.4%	SFQQSSLSR	99.7%	60.5	25	43	2	0	0	1039.52	4	12
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	15	17	38	0.04%	20.4%	SQAFIEMETR	99.7%	68.7	25	62.2	4	0	0	1227.57	533	542
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	15	17	38	0.04%	20.4%	SQESGYYDR	99.7%	44.3	25	44.3	2	0	0	1104.46	208	216
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	15	17	38	0.04%	20.4%	TEEGPTLSYGR	99.7%	72.4	25	64.6	3	0	0	1209.57	150	160
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	15	17	38	0.04%	20.4%	VVHIMDFQR	99.7%	38.5	25	30.8	4	0	0	1144.59	399	407
MAX gene-associated protein	MGA	MGAP_HUMAN	331.8	100.0%	3	3	4	0.00%	1.4%	ISNPSAFSIVPR	99.7%	61.5	25	47.1	2	0	0	1287.71	2208	2219
MAX gene-associated protein	MGA	MGAP_HUMAN	331.8	100.0%	3	3	4	0.00%	1.4%	VGSFIIELASQR	99.7%	83.7	25	71.9	1	0	0	1319.73	1369	1380
MAX gene-associated protein	MGA	MGAP_HUMAN	331.8	100.0%	3	3	4	0.00%	1.4%	VLQSEGEAVDPEANVIK	99.7%	73.7	25	73.7	1	0	0	1797.92	1954	1970
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	4	4	6	0.01%	3.4%	EVGNALLNVVLK	99.7%	41.7	25	26.6	2	0	0	1268.76	1121	1132
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	4	4	6	0.01%	3.4%	FLTEVLLPIVK	99.7%	52.9	25	52.9	2	0	0	1271.80	1230	1240
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	4	4	6	0.01%	3.4%	LFDLLYPEK	99.6%	38.2	25	37.1	1	0	0	1137.62	398	406
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	4	4	6	0.01%	3.4%	SSVALAPALVETYSR	99.7%	49.9	25	49.2	1	0	0	1563.84	555	569
Mediator of RNA polymerase II transcription subunit 24	MED24	MED24_HUMAN	110.3	99.8%	2	2	3	0.00%	2.8%	SLDLLLAAAAATGK	96.3%	28.3	25	28.3	1	0	0	1314.76	447	460
Mediator of RNA polymerase II transcription subunit 24	MED24	MED24_HUMAN	110.3	99.8%	2	2	3	0.00%	2.8%	VVLAITDLSLPLGR	99.7%	45.1	25	45.1	2	0	0	1466.89	966	979
Melanoma-associated antigen D2	MAGED2	MAGD2_HUMAN	65.0	100.0%	2	2	3	0.00%	4.0%	LQSSQEPEAPPPR	99.7%	45.9	25	45.9	1	0	0	1435.72	262	274
Melanoma-associated antigen D2	MAGED2	MAGD2_HUMAN	65.0	100.0%	2	2	3	0.00%	4.0%	SSEAVIWEVLR	99.7%	72.8	25	42.9	2	0	0	1288.69	386	396
Membrane magnesium transporter 1	MMGT1	MMGT1_HUMAN	14.7	99.8%	2	2	2	0.00%	26.7%	NHPSFYVFNHR	99.7%	30.2	25	27.7	0	1	0	1417.68	86	96
Membrane magnesium transporter 1	MMGT1	MMGT1_HUMAN	14.7	99.8%	2	2	2	0.00%	26.7%	VLFRPSDTANSSNQDALSSNTSLK	99.7%	54	25	54	0	1	0	2552.26	99	122

Metaxin-1	MTX1	MTX1_HUMAN	51.5	100.0%	3	3	6	0.01%	8.4%	ECLTLLSQR	99.4%	36.2	25	14.6	2	0	0	1119.58	325	333
Metaxin-1	MTX1	MTX1_HUMAN	51.5	100.0%	3	3	6	0.01%	8.4%	ISNPWQSPSGTLPALR	99.7%	46.1	25	46.1	2	0	0	1723.91	191	206
Metaxin-1	MTX1	MTX1_HUMAN	51.5	100.0%	3	3	6	0.01%	8.4%	QTPAGPETEEEPYR	99.7%	44.5	25	43.5	2	0	0	1603.72	403	416
Metaxin-2	MTX2	MTX2_HUMAN	29.8	100.0%	3	3	5	0.00%	16.0%	LGTQPYFFNK	99.7%	43.8	25	36.5	1	0	0	1214.62	197	206
Metaxin-2	MTX2	MTX2_HUMAN	29.8	100.0%	3	3	5	0.00%	16.0%	NYSNLLAFCR	99.7%	62.2	25	62.2	2	0	0	1257.60	238	247
Metaxin-2	MTX2	MTX2_HUMAN	29.8	100.0%	3	3	5	0.00%	16.0%	VPFIHVGNQVVSELGPIVQFVK	99.7%	64.6	25	64.6	0	2	0	2406.35	72	93
Methionine adenosyltransferase 2 subunit beta	MAT2B	MAT2B_HUMAN	37.6	99.8%	2	2	2	0.00%	7.5%	AVLENNLGAAVLR	99.2%	34.4	25	34.2	1	0	0	1339.77	169	181
Methionine adenosyltransferase 2 subunit beta	MAT2B	MAT2B_HUMAN	37.6	99.8%	2	2	2	0.00%	7.5%	VLVTGATGLLGR	99.7%	69.5	25	51.6	1	0	0	1156.71	31	42
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	21	25	49	0.05%	33.9%	ADKNEVAAEVAK	99.7%	60.6	25	35.3	2	0	0	1244.65	864	875
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	21	25	49	0.05%	33.9%	AEVLISTVGPEDCVVPFLTRPK	99.7%	39.2	25	39.2	0	2	0	2427.30	26	47
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	21	25	49	0.05%	33.9%	ALTHIDHSLSR	99.7%	46.3	25	44.8	2	1	0	1249.66	120	130
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	21	25	49	0.05%	33.9%	FFGGYVPEMVLTPDDQR	99.7%	59.9	25	59.9	3	0	0	1970.93	664	680
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	21	25	49	0.05%	33.9%	FVEGVCPFCGYEEAR	99.7%	70	25	70	2	0	0	1819.78	400	414
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	21	25	49	0.05%	33.9%	GFVLQDTVEQLR	99.7%	95	25	77.9	3	0	0	1404.75	377	388
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	21	25	49	0.05%	33.9%	GLESLPPLRPQQNPVLPVAGER	99.7%	47.8	25	45.3	0	2	0	2367.31	243	264
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	21	25	49	0.05%	33.9%	GVGVFGDMAQDTGIPADIWR	96.0%	28	25	26.3	1	0	0	2105.01	599	618
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	21	25	49	0.05%	33.9%	ITQDIFQQLLK	99.7%	81.2	25	68.4	4	0	0	1346.77	365	375
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	21	25	49	0.05%	33.9%	KGEDVLGSVR	99.7%	59.9	25	49.8	2	0	0	1059.58	109	118
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	21	25	49	0.05%	33.9%	LENDQIESLR	99.7%	87	25	69.6	2	0	0	1216.62	805	814
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	21	25	49	0.05%	33.9%	LFVSDGVPGCLPVLAAAGR	99.7%	52.1	25	51.3	2	0	0	1899.02	3	21
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	21	25	49	0.05%	33.9%	LINAVELK	99.7%	61.6	25	49	2	0	0	899.56	424	431
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	21	25	49	0.05%	33.9%	NNSELLNNLGNFINR	99.7%	103	25	96.8	2	0	0	1731.88	642	656
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	21	25	49	0.05%	33.9%	NPEQVDLYQFMAK	99.7%	79.2	25	79.2	4	0	0	1582.76	542	554
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	21	25	49	0.05%	33.9%	QLAVAEGKPPEAPK	99.7%	57	25	54.2	2	0	0	1434.80	882	895
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	21	25	49	0.05%	33.9%	QQGVLALRPYLQK	99.7%	61.3	25	52.1	2	0	0	1513.89	192	204
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	21	25	49	0.05%	33.9%	RLEEWLGR	99.7%	39.4	25	25	2	0	0	1058.57	460	467
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	21	25	49	0.05%	33.9%	SCPVVQSSQHLFLDLPK	99.7%	75.3	25	73.3	2	1	0	1955.01	440	456
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	21	25	49	0.05%	33.9%	TLPGSDWTPNAQFITR	99.7%	81	25	78.1	2	0	0	1803.90	468	483
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	21	25	49	0.05%	33.9%	VPVLQLDSGNYLFSTSAICR	99.7%	145	25	142	2	0	0	2240.14	48	67
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	12	19	197	0.20%	37.7%	AHAAQVTCVAASPHK	99.7%	101	25	98.1	9	15	0	1547.77	165	179
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	12	19	197	0.20%	37.7%	CWAGSLWLFK	99.5%	36.7	25	29.7	8	0	0	1267.63	53	62
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	12	19	197	0.20%	37.7%	DSVFLSCSEDNR	99.7%	72.3	25	65.3	15	0	0	1428.61	180	191
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	12	19	197	0.20%	37.7%	ETPPPLVPPAAR	99.7%	41.9	25	29.2	5	0	0	1244.70	4	15
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	12	19	197	0.20%	37.7%	EWNLPPNAPACMER	99.7%	86.3	25	86.3	20	0	0	1684.76	16	29
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	12	19	197	0.20%	37.7%	FCKYEHDDIVSTVSVLSSGTQAVSGSK	99.7%	103	25	102	0	2	0	2901.39	119	145
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	12	19	197	0.20%	37.7%	ILLWDTR	99.7%	53.3	25	48.2	23	0	0	916.53	192	198
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	12	19	197	0.20%	37.7%	KETPPPLVPPAAR	99.7%	56	25	50.6	2	1	0	1372.79	3	15
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	12	19	197	0.20%	37.7%	SDGALLLGASSLSGR	99.7%	126	25	121	33	1	0	1403.75	38	52
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	12	19	197	0.20%	37.7%	VWDLAQQVVLSSYR	99.7%	115	25	111	20	3	0	1663.88	151	164
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	12	19	197	0.20%	37.7%	YEHDDIVSTVSVLSSGTQAVSGSK	99.7%	120	25	120	10	12	0	2466.20	122	145
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	12	19	197	0.20%	37.7%	YRSDGALLLGASSLSGR	99.7%	113	25	110	8	10	0	1722.91	36	52
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	4	6	31	0.03%	24.1%	GLGTGTLYIAESR	99.7%	105	25	91.5	7	0	0	1337.71	31	43
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	4	6	31	0.03%	24.1%	LEGMLSQSVSSQYNMAGVR	99.7%	108	25	105	12	4	0	2056.98	188	206
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	4	6	31	0.03%	24.1%	QQPDTEAVLNGK	99.7%	74.1	25	71.9	4	0	0	1299.65	19	30
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	4	6	31	0.03%	24.1%	SFPPPGPAEGLLR	99.7%	44	25	40.8	4	0	0	1337.72	6	18
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	8	8	15	0.01%	27.1%	DLADVAAR	99.7%	38.9	25	14.6	2	0	0	830.44	102	109
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	8	8	15	0.01%	27.1%	EAEREGATEEAVR	99.7%	57.7	25	48.6	2	0	0	1446.68	110	122
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	8	8	15	0.01%	27.1%	EIIIEERPGQELTDVNGVR	99.4%	27.2	25	21.1	0	1	0	2167.14	294	312
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	8	8	15	0.01%	27.1%	GSLQILDQLLLPK	99.7%	71.5	25	49.6	2	0	0	1437.87	11	23
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	8	8	15	0.01%	27.1%	GVSAVVVGADR	99.7%	75.6	25	63	2	0	0	1029.57	239	249
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	8	8	15	0.01%	27.1%	TALTTTISSR	99.7%	78.8	25	69.3	2	0	0	1050.58	351	360

Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	8	8	15	0.01%	27.1%	VGTYQLAIVAK	99.7%	85	25	79.1	2	0	0	1162.68	260	270
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	8	8	15	0.01%	27.1%	YEAVGSVHQAWEAIR	99.7%	46.5	25	44.3	0	2	0	1715.85	27	41
Methyltransferase-like protein 13	METTL13	MET13_HUMAN	78.8	99.8%	2	2	4	0.00%	3.3%	LAEAVQER	99.7%	52.3	25	26.8	2	0	0	915.49	242	249
Methyltransferase-like protein 13	METTL13	MET13_HUMAN	78.8	99.8%	2	2	4	0.00%	3.3%	LATPELLETAQALER	99.7%	74.8	25	61.5	2	0	0	1654.90	660	674
Microsomal glutathione S-transferase 1	MGST1	MGST1_HUMAN	17.6	100.0%	3	6	17	0.02%	27.1%	IYHTIAYLTPLPQPNR	99.7%	86.8	25	83.1	2	2	0	1897.03	115	130
Microsomal glutathione S-transferase 1	MGST1	MGST1_HUMAN	17.6	100.0%	3	6	17	0.02%	27.1%	KVFANPEDCVAFGK	99.7%	48.1	25	48.1	2	2	0	1581.77	42	55
Microsomal glutathione S-transferase 1	MGST1	MGST1_HUMAN	17.6	100.0%	3	6	17	0.02%	27.1%	MMLMSTATAFYR	99.7%	72.7	25	72.7	9	0	0	1422.66	27	38
Microsomal glutathione S-transferase 3	MGST3	MGST3_HUMAN	16.5	99.8%	2	2	5	0.00%	18.4%	IASGLGLAWIVGR	99.7%	51.9	25	48.8	4	0	0	1312.77	85	97
Microsomal glutathione S-transferase 3	MGST3	MGST3_HUMAN	16.5	99.8%	2	2	5	0.00%	18.4%	VLYAYGYYTGEPSKR	99.1%	34.3	25	34.3	1	0	0	1766.87	98	112
Microtubule-associated protein 1B	MAP1B	MAP1B_HUMAN	270.6	100.0%	3	3	5	0.00%	1.5%	AVLDALLEGK	99.7%	42	25	32.7	2	0	0	1028.60	2400	2409
Microtubule-associated protein 1B	MAP1B	MAP1B_HUMAN	270.6	100.0%	3	3	5	0.00%	1.5%	DLTGQVPTPVVK	98.4%	31.8	25	28.9	1	0	0	1253.71	520	531
Microtubule-associated protein 1B	MAP1B	MAP1B_HUMAN	270.6	100.0%	3	3	5	0.00%	1.5%	SVGNTIDPVILFQK	99.7%	59.4	25	55	2	0	0	1530.85	401	414
Microtubule-associated protein RP/EB family member 2	MAPRE2	MARE2_HUMAN	37.0	99.8%	2	2	2	0.00%	6.7%	FQDNLDFIQWFK	99.7%	49	25	49	1	0	0	1600.78	144	155
Microtubule-associated protein RP/EB family member 2	MAPRE2	MARE2_HUMAN	37.0	99.8%	2	2	2	0.00%	6.7%	LALEGVEKER	99.7%	46.4	25	29.6	1	0	0	1143.64	256	265
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	11	11	14	0.01%	2.5%	AEQESGLYR	98.0%	30.8	25	7.74	1	0	0	1052.50	3546	3554
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	11	11	14	0.01%	2.5%	ALEFGEPVLLVGDTGCGK	99.7%	58.2	25	58.2	1	0	0	1861.94	1379	1396
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	11	11	14	0.01%	2.5%	ALVLANPEVSLWR	99.7%	57.5	25	57.5	1	0	0	1467.83	234	246
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	11	11	14	0.01%	2.5%	APAVQDLLTR	99.7%	62.7	25	53.5	1	0	0	1083.62	3340	3349
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	11	11	14	0.01%	2.5%	FLNGLEILLAK	99.7%	69.7	25	64.8	1	0	0	1230.75	3773	3783
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	11	11	14	0.01%	2.5%	FMLFATQNPPGLYGGR	96.5%	28.5	25	27.7	1	0	0	1768.88	1189	1204
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	11	11	14	0.01%	2.5%	IISAISELLER	99.7%	42.9	25	39.2	1	0	0	1243.73	4574	4584
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	11	11	14	0.01%	2.5%	LLEEAQLQDLEK	99.7%	52.8	25	52.8	1	0	0	1428.76	222	233
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	11	11	14	0.01%	2.5%	SLLQAWGLILR	99.7%	55.5	25	46.8	2	0	0	1269.77	2860	2870
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	11	11	14	0.01%	2.5%	SLTTLSEQWIILR	99.5%	36.5	25	20	2	0	0	1559.88	4242	4254
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	11	11	14	0.01%	2.5%	TSLVEYLAAVTGR	99.7%	65.8	25	45.9	2	0	0	1379.75	336	348
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	21	0.02%	17.6%	AMVEAVQLIADGK	99.7%	80.1	25	74.1	2	0	0	1344.72	197	209
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	21	0.02%	17.6%	ANSTEYGLASGVFTR	99.7%	82.5	25	68.1	2	0	0	1572.77	848	862
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	21	0.02%	17.6%	DLGEEALNEYLK	99.7%	78.9	25	68.9	2	0	0	1393.68	904	915
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	21	0.02%	17.6%	EESFGPIMVISK	99.7%	60.6	25	60.6	2	0	0	1336.68	824	835
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	21	0.02%	17.6%	GVINIIPGSGGIAGQR	99.7%	53.5	25	53.5	2	0	0	1508.85	642	657
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	21	0.02%	17.6%	LEAGTVFINTYNK	99.7%	77.2	25	64.4	1	0	0	1469.76	874	886
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	21	0.02%	17.6%	LGFTGSTPIGK	99.7%	68.6	25	63.3	2	0	0	1077.59	667	677
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	21	0.02%	17.6%	LLQYCETGVK	99.5%	36.9	25	34	1	0	0	1210.61	779	788
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	21	0.02%	17.6%	SAACLAAGNTLVLKPAQVTPLTALK	99.7%	54.5	25	46.7	0	1	0	2508.42	605	629
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	21	0.02%	17.6%	SPLIIFNDCELDK	99.7%	55.2	25	48	2	0	0	1563.77	699	711
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	21	0.02%	17.6%	TDVAAPFGGVK	99.7%	53.6	25	45.6	2	0	0	1061.56	887	897
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	21	0.02%	17.6%	VSYASLADVDK	99.7%	55.9	25	54.3	2	0	0	1167.59	474	484
Mitochondrial 2-oxodicarboxylate carrier	SLC25A21	ODC_HUMAN	33.3	99.8%	2	2	2	0.00%	8.7%	IQGPQPVPGEIK	99.3%	35.3	25	28.7	1	0	0	1262.71	235	246
Mitochondrial 2-oxodicarboxylate carrier	SLC25A21	ODC_HUMAN	33.3	99.8%	2	2	2	0.00%	8.7%	NTFAEQPSTVGYAR	99.7%	60.3	25	49.5	1	0	0	1540.74	142	155
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	39	0.04%	53.2%	AVIGMTAGATGAFVGTPAEVALIR	99.7%	105	25	105	4	2	0	2289.23	123	146
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	39	0.04%	53.2%	AVVVNAAQLASYSQSK	99.7%	131	25	124	2	0	0	1635.87	191	206
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	39	0.04%	53.2%	EEGVLTLWR	99.1%	34	25	27	2	0	0	1102.59	174	182
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	39	0.04%	53.2%	FLFGGLAGMGATVFVQPLDLVK	99.7%	51.8	25	51.8	2	0	0	2296.24	25	46
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	39	0.04%	53.2%	GIYTGLSAGLLR	99.7%	79.9	25	74.2	2	0	0	1220.70	79	90
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	39	0.04%	53.2%	ITREEGVLTLWR	99.7%	36.1	25	30.7	0	2	0	1472.82	171	182
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	39	0.04%	53.2%	LGIYTVLFER	99.7%	88.2	25	82.3	5	0	0	1210.68	99	108
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	39	0.04%	53.2%	LTGADGTPPGFLLK	99.7%	68	25	61.7	4	0	0	1386.76	109	122
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	39	0.04%	53.2%	MIDGKPEYK	98.8%	33	25	19	3	0	0	1096.53	252	260
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	39	0.04%	53.2%	MTADGRLPADQR	98.4%	31.8	25	22.9	1	1	0	1330.65	147	158
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	39	0.04%	53.2%	NGLDVLFK	99.7%	51.3	25	36.8	2	0	0	905.51	261	268
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	39	0.04%	53.2%	NVFNALIR	99.4%	35.8	25	23.7	2	0	0	946.55	163	170

Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	39	0.04%	53.2%	TSFHALTSILK	99.7%	57.7	25	48.9	2	2	0	1217.69	63	73
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	19	39	0.04%	53.2%	YEGFFSLWK	97.1%	29.2	25	26	1	0	0	1176.57	272	280
Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20	MCAT_HUMAN	32.9	100.0%	5	5	9	0.01%	15.6%	EGITGLYR	99.7%	42.4	25	18.3	2	0	0	908.48	66	73
Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20	MCAT_HUMAN	32.9	100.0%	5	5	9	0.01%	15.6%	ELIRDEGVTSLYK	99.7%	44.8	25	43.6	2	0	0	1522.81	255	267
Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20	MCAT_HUMAN	32.9	100.0%	5	5	9	0.01%	15.6%	GTVLTLMR	99.7%	47.9	25	34	2	0	0	906.51	171	178
Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20	MCAT_HUMAN	32.9	100.0%	5	5	9	0.01%	15.6%	KLYQEFGIR	99.7%	42.3	25	29.7	2	0	0	1153.64	158	166
Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20	MCAT_HUMAN	32.9	100.0%	5	5	9	0.01%	15.6%	YTGTLDCAK	99.4%	36.2	25	25.5	1	0	0	1028.47	149	157
Mitochondrial carrier homolog 2	MTCH2	MTCH2_HUMAN	33.3	100.0%	3	3	4	0.00%	14.2%	GLFTGLTPR	99.7%	54.7	25	40.2	2	0	0	961.55	69	77
Mitochondrial carrier homolog 2	MTCH2	MTCH2_HUMAN	33.3	100.0%	3	3	4	0.00%	14.2%	LCSGVLGTVVHGK	97.9%	30.6	25	27.4	1	0	0	1326.72	78	90
Mitochondrial carrier homolog 2	MTCH2	MTCH2_HUMAN	33.3	100.0%	3	3	4	0.00%	14.2%	VLQHYQESDKGEELGPGNVQK	99.7%	40.3	25	40.3	0	1	0	2355.16	91	111
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	16	29	0.03%	48.4%	FAIYETVR	99.7%	39.9	25	35.8	2	0	0	998.53	79	86
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	16	29	0.03%	48.4%	GALVTVGQLSCYDQAK	99.7%	108	25	108	2	0	0	1709.85	171	186
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	16	29	0.03%	48.4%	GEYQGVFHCAVETAK	99.7%	57.6	25	57.6	2	2	0	1695.78	232	246
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	16	29	0.03%	48.4%	GSQGPLPFHEK	99.7%	48.9	25	39.1	2	0	0	1196.61	92	102
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	16	29	0.03%	48.4%	LFSGATMASSR	99.7%	68.5	25	63.1	2	0	0	1143.55	160	170
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	16	29	0.03%	48.4%	LGPLAFYK	99.7%	55.3	25	40.8	2	0	0	908.52	247	254
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	16	29	0.03%	48.4%	NYAHALDGLYR	99.7%	47.8	25	47.8	2	1	0	1292.64	140	150
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	16	29	0.03%	48.4%	QMTYSLTR	99.7%	60.9	25	51.4	3	0	0	999.49	71	78
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	16	29	0.03%	48.4%	TDGILALYSGLSASLCR	99.7%	97.7	25	93.6	2	0	0	1796.92	54	70
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	16	29	0.03%	48.4%	VHLQTQQEVK	99.7%	48.2	25	45.6	2	1	0	1209.66	32	41
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	16	29	0.03%	48.4%	VLLGSVSGLAGGFVGTPADLVNVR	99.7%	81.8	25	81.8	2	2	0	2298.28	103	126
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	4	4	5	0.00%	21.7%	KLYPTVGKPSSS	99.1%	34.2	25	28.7	1	0	0	1263.69	155	166
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	4	4	5	0.00%	21.7%	SVDFLLDSSLR	99.7%	56.9	25	40.1	1	0	0	1251.66	144	154
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	4	4	5	0.00%	21.7%	SVDFLLDSSLRK	99.7%	41.8	25	33.3	1	0	0	1379.75	144	155
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	4	4	5	0.00%	21.7%	YLGYANEVGEAFR	99.7%	78.6	25	78.6	2	0	0	1488.71	21	33
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	8	9	16	0.02%	25.1%	GAAVNLTLVTPEK	99.7%	88.1	25	82.1	2	0	0	1312.75	68	80
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	8	9	16	0.02%	25.1%	GLGATLLR	99.1%	33.9	25	15.1	2	0	0	800.50	189	196
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	8	9	16	0.02%	25.1%	GVNEDTYSGILDCAR	99.7%	62.1	25	62.1	2	0	0	1669.75	259	273
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	8	9	16	0.02%	25.1%	HEGPSAFLK	95.4%	27.4	25	20.1	1	0	0	985.51	278	286
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	8	9	16	0.02%	25.1%	IQLQDAGR	99.7%	45.2	25	23.1	2	0	0	900.49	129	136
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	8	9	16	0.02%	25.1%	LAANDFFR	99.7%	57.7	25	46.2	2	0	0	953.48	84	91
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	8	9	16	0.02%	25.1%	SEGYFGMYR	99.7%	50.4	25	50.4	2	0	0	1109.47	59	67
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	8	9	16	0.02%	25.1%	VYTSMSDCLIK	99.7%	47.8	25	40.3	3	0	0	1316.62	45	55
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	10	19	0.02%	30.6%	AQGPQQQPGSEGPSYAK	99.7%	66.7	25	64	4	0	0	1729.81	48	64
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	10	19	0.02%	30.6%	DISCLNRDPAR	94.5%	26.8	25	13.4	1	0	0	1316.64	233	243
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	10	19	0.02%	30.6%	IPDEFDNDPILVQQLR	99.7%	93	25	78.3	2	0	0	1911.98	98	113
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	10	19	0.02%	30.6%	QNLFLGSLTSR	99.7%	57.4	25	47.6	2	0	0	1235.67	335	345
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	10	19	0.02%	30.6%	RAPDQAAEIGSR	99.7%	55.1	25	47.1	2	0	0	1270.65	32	43
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	10	19	0.02%	30.6%	SNKQNLFLGSLTSR	99.7%	62.5	25	62.5	1	0	0	1564.84	332	345
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	10	19	0.02%	30.6%	TIALNGVEDVR	99.7%	65.9	25	57.5	2	0	0	1186.64	285	295
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	10	19	0.02%	30.6%	TVLEHYALEDDPLAAFK	99.7%	39.3	25	39.3	1	2	0	1931.98	296	312
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	9	10	19	0.02%	30.6%	VLLDLSAFLK	99.7%	50.2	25	50.2	2	0	0	1118.68	275	284
Mitochondrial import receptor subunit TOM22 homolog	TOMM22	TOM22_HUMAN	15.5	100.0%	2	2	3	0.00%	19.7%	LQMEQQQQLQQR	95.3%	27.4	25	26.9	1	0	0	1557.78	106	117
Mitochondrial import receptor subunit TOM22 homolog	TOMM22	TOM22_HUMAN	15.5	100.0%	2	2	3	0.00%	19.7%	SAAGATFDLSLFVAQK	99.7%	48.1	25	41.8	2	0	0	1625.85	61	76
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	9	14	24	0.02%	24.9%	CKELFPIQMEGVK	99.7%	45.4	25	34.8	1	0	0	1578.80	90	102
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	9	14	24	0.02%	24.9%	ELFPIQMEGVK	99.7%	52.5	25	42.1	3	0	0	1290.68	92	102
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	9	14	24	0.02%	24.9%	FQCGFGLTIG	96.3%	28.3	25	26.1	1	0	0	1099.52	352	361
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	9	14	24	0.02%	24.9%	FVNWQVDGEYR	99.7%	50	25	47.3	2	0	0	1412.66	185	195
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	9	14	24	0.02%	24.9%	GSVDSNWIVGATLEK	99.7%	122	25	111	3	0	0	1575.80	316	330
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	9	14	24	0.02%	24.9%	MAIQTQQSK	99.4%	36	25	29.1	1	0	0	1050.53	176	184
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	9	14	24	0.02%	24.9%	MQDTSVSFGYQLDLPK	99.7%	88.7	25	87.9	4	0	0	1828.88	294	309

Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	9	14	24	0.02%	24.9%	NKFQCGFGLTIG	98.9%	33.3	25	33.3	2	0	0	1341.66	350	361
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	9	14	24	0.02%	24.9%	RPGEEGTVMSLAGK	99.7%	88.2	25	78.8	4	3	0	1431.73	240	253
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	19	20	45	0.04%	29.4%	AAMDNSEIAGEKK	95.4%	27.5	25	23.1	1	0	0	1379.65	258	270
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	19	20	45	0.04%	29.4%	AVDEAADALLK	99.7%	67.2	25	53.7	4	0	0	1115.59	287	297
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	19	20	45	0.04%	29.4%	ELDSITPEVLPGWK	99.7%	61	25	56.6	4	0	0	1583.83	372	385
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	19	20	45	0.04%	29.4%	ERPPEEVAAR	99.7%	45.4	25	39.5	4	0	0	1153.60	196	205
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	19	20	45	0.04%	29.4%	EVAGAKPHITAAEGK	99.7%	52.5	25	32.6	2	0	0	1478.80	316	330
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	19	20	45	0.04%	29.4%	GIEQAVQSHAVAEEEAR	99.7%	105	25	105	2	0	0	1823.89	548	564
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	19	20	45	0.04%	29.4%	GVYSEETLR	99.7%	49.5	25	38.9	2	0	0	1053.52	624	632
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	19	20	45	0.04%	29.4%	ISSVSEVMK	98.1%	31	25	20	2	0	0	995.51	111	119
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	19	20	45	0.04%	29.4%	LFEMVLGPAAYNVPLPK	99.1%	34	25	33.7	1	0	0	1859.01	85	101
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	19	20	45	0.04%	29.4%	LHNMIVDLDNVVK	99.7%	62.2	25	55.8	1	0	0	1509.81	331	343
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	19	20	45	0.04%	29.4%	LSEQELQFR	99.7%	80.3	25	52.9	2	0	0	1149.59	517	525
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	19	20	45	0.04%	29.4%	RIDQLNR	97.0%	29.2	25	0	1	0	0	914.52	411	417
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	19	20	45	0.04%	29.4%	SEFEQNLSEK	99.7%	51.4	25	45.7	2	0	0	1210.56	507	516
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	19	20	45	0.04%	29.4%	SLEDALR	95.7%	27.7	25	9.79	1	0	0	803.43	223	229
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	19	20	45	0.04%	29.4%	TSSAETPTIPLGSAVEAIK	99.7%	89.5	25	85.2	4	0	0	1872.00	582	600
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	19	20	45	0.04%	29.4%	TVEGALKER	99.7%	39.8	25	28.1	3	0	0	1002.56	276	284
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	19	20	45	0.04%	29.4%	VAMIDETR	99.7%	42.3	25	35.6	2	0	0	934.47	645	652
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	19	20	45	0.04%	29.4%	VVSQYHELVVQAR	99.7%	90.6	25	85.4	2	2	0	1527.83	354	366
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	19	20	45	0.04%	29.4%	YSTSGSSGLTTGK	99.7%	66	25	64.4	3	0	0	1245.60	33	45
Mitochondrial inner membrane protein OXA1L	OXA1L	OXA1L_HUMAN	48.5	100.0%	5	6	10	0.01%	11.5%	ASSEMALYQK	99.7%	55.7	25	53.3	3	0	0	1127.54	198	207
Mitochondrial inner membrane protein OXA1L	OXA1L	OXA1L_HUMAN	48.5	100.0%	5	6	10	0.01%	11.5%	CLIFPLIVTGQR	99.7%	67.3	25	56.2	2	0	0	1416.80	153	164
Mitochondrial inner membrane protein OXA1L	OXA1L	OXA1L_HUMAN	48.5	100.0%	5	6	10	0.01%	11.5%	LAGDHIEYYK	99.7%	51.7	25	42.3	2	0	0	1208.59	188	197
Mitochondrial inner membrane protein OXA1L	OXA1L	OXA1L_HUMAN	48.5	100.0%	5	6	10	0.01%	11.5%	NQLELAAR	99.4%	36	25	14.8	2	0	0	914.51	387	394
Mitochondrial inner membrane protein OXA1L	OXA1L	OXA1L_HUMAN	48.5	100.0%	5	6	10	0.01%	11.5%	SKYPWHDTLG	95.4%	27.5	25	27.5	1	0	0	1203.58	426	435
Mitochondrial ornithine transporter 1	SLC25A15	ORNT1_HUMAN	32.7	100.0%	4	4	5	0.00%	15.6%	DGPLGFYHGLSSTLLR	99.6%	38.3	25	38.3	1	0	0	1732.90	164	179
Mitochondrial ornithine transporter 1	SLC25A15	ORNT1_HUMAN	32.7	100.0%	4	4	5	0.00%	15.6%	IQVLSMSGK	97.1%	29.3	25	6.53	1	0	0	962.53	237	245
Mitochondrial ornithine transporter 1	SLC25A15	ORNT1_HUMAN	32.7	100.0%	4	4	5	0.00%	15.6%	LQTMYEMETSGK	99.3%	35.2	25	35.2	1	0	0	1417.63	134	145
Mitochondrial ornithine transporter 1	SLC25A15	ORNT1_HUMAN	32.7	100.0%	4	4	5	0.00%	15.6%	SQNTVWSVIK	99.7%	55	25	43.7	2	0	0	1161.63	149	158
Mitochondrial pyruvate carrier 2	MPC2	MPC2_HUMAN	14.3	99.8%	2	3	6	0.01%	17.3%	LLDKVELMLPEK	98.7%	32.4	25	18.3	1	0	0	1427.82	16	27
Mitochondrial pyruvate carrier 2	MPC2	MPC2_HUMAN	14.3	99.8%	2	3	6	0.01%	17.3%	TVFFWAPIMK	99.7%	38.5	25	31.2	5	0	0	1239.66	40	49
Mitochondrial Rho GTPase 2	RHOT2	MIRO2_HUMAN	68.1	100.0%	4	4	8	0.01%	6.6%	ILLLGEAQVGK	99.7%	70.1	25	37.5	2	0	0	1140.70	7	17
Mitochondrial Rho GTPase 2	RHOT2	MIRO2_HUMAN	68.1	100.0%	4	4	8	0.01%	6.6%	NISELFYYAQK	99.2%	34.9	25	19.5	2	0	0	1375.69	154	164
Mitochondrial Rho GTPase 2	RHOT2	MIRO2_HUMAN	68.1	100.0%	4	4	8	0.01%	6.6%	SAFLQAFLGR	99.7%	64.8	25	56.9	2	0	0	1109.61	430	439
Mitochondrial Rho GTPase 2	RHOT2	MIRO2_HUMAN	68.1	100.0%	4	4	8	0.01%	6.6%	VPIILVGNK	99.5%	36.4	25	0	2	0	0	952.62	111	119
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	20	39	0.04%	47.9%	DSIIYLTADSPNVMTTFR	99.7%	95	25	90.7	6	0	0	2044.01	285	302
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	20	39	0.04%	47.9%	EFIEMWR	95.2%	27.2	25	24.4	2	0	0	1010.48	96	102
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	20	39	0.04%	47.9%	EVPEHITEEELK	99.7%	42.8	25	34.7	2	0	0	1452.72	107	118
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	20	39	0.04%	47.9%	LLETTEEDKQK	99.7%	53.2	25	49.5	3	0	0	1333.68	165	175
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	20	39	0.04%	47.9%	LLLTSTEK	96.1%	28.1	25	15.8	1	0	0	904.54	269	276
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	20	39	0.04%	47.9%	LNLATECLPLDK	98.8%	33	25	12.9	1	0	0	1386.73	329	340
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	20	39	0.04%	47.9%	NESTPPSEELELDKWK	99.7%	62.5	25	52.6	2	1	0	1901.91	52	67
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	20	39	0.04%	47.9%	NLTLDQMIR	99.7%	48.5	25	36.7	2	0	0	1103.59	350	358
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	20	39	0.04%	47.9%	NMDIAMGWK	99.4%	35.6	25	18.9	2	0	0	1065.49	186	194
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	20	39	0.04%	47.9%	NNGNWQEALQFVPK	99.7%	49.7	25	45.5	2	0	0	1644.81	365	378
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	20	39	0.04%	47.9%	NVDPFHIYFCNLK	99.1%	34.2	25	30.7	2	0	0	1666.80	237	249
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	20	39	0.04%	47.9%	SMQPGTSLAK	99.7%	46.2	25	35.7	3	0	0	1019.52	316	325
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	20	39	0.04%	47.9%	SSVQEECVSTISSSK	97.7%	30.2	25	30.2	1	0	0	1627.75	72	86
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	20	39	0.04%	47.9%	SSVQEECVSTISSSKDEDPLAATR	99.7%	52.5	25	52.5	0	2	0	2596.20	72	95
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	20	39	0.04%	47.9%	TLMECVSNTAK	99.7%	60.5	25	57.5	3	0	0	1253.59	119	129

Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	20	39	0.04%	47.9%	VYVIGSFVDK	99.7%	60.8	25	59.7	2	0	0	1126.61	306	315
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	20	39	0.04%	47.9%	YLQWEIGNK	99.7%	50.1	25	44.6	2	0	0	1150.59	341	349
Mitochondrial ribonuclease P protein 3	KIAA0391	MRRP3_HUMAN	67.3	100.0%	4	4	8	0.01%	7.7%	DVIDGGDQYRK	99.5%	36.9	25	36.9	1	0	0	1265.61	375	385
Mitochondrial ribonuclease P protein 3	KIAA0391	MRRP3_HUMAN	67.3	100.0%	4	4	8	0.01%	7.7%	EALLLLEDIKK	99.7%	43.2	25	36.7	2	0	0	1284.78	228	238
Mitochondrial ribonuclease P protein 3	KIAA0391	MRRP3_HUMAN	67.3	100.0%	4	4	8	0.01%	7.7%	ESQLLLNVVSQLAK	99.7%	81.5	25	66.2	2	0	0	1541.89	422	435
Mitochondrial ribonuclease P protein 3	KIAA0391	MRRP3_HUMAN	67.3	100.0%	4	4	8	0.01%	7.7%	LLDILSYLR	99.7%	68.4	25	68.4	3	0	0	1105.66	301	309
Mitogen-activated protein kinase kinase kinase 7	MAP3K7	M3K7_HUMAN	67.2	100.0%	3	3	4	0.00%	5.9%	DLKPPNLLLVAGGTVLK	95.6%	27.6	25	26.5	1	0	0	1748.07	156	172
Mitogen-activated protein kinase kinase kinase 7	MAP3K7	M3K7_HUMAN	67.2	100.0%	3	3	4	0.00%	5.9%	KAFIVELR	98.3%	31.5	25	13.2	1	0	0	975.60	72	79
Mitogen-activated protein kinase kinase kinase 7	MAP3K7	M3K7_HUMAN	67.2	100.0%	3	3	4	0.00%	5.9%	VQTEIALLLQR	99.7%	54.7	25	10.9	2	0	0	1283.77	536	546
Mitotic checkpoint protein BUB3	BUB3	BUB3_HUMAN	37.2	100.0%	5	5	7	0.01%	18.6%	LNQPPEDGISSVK	99.7%	50	25	48.7	2	0	0	1383.71	9	21
Mitotic checkpoint protein BUB3	BUB3	BUB3_HUMAN	37.2	100.0%	5	5	7	0.01%	18.6%	QGYVLSSIEGR	99.7%	75.3	25	68	2	0	0	1208.63	192	202
Mitotic checkpoint protein BUB3	BUB3	BUB3_HUMAN	37.2	100.0%	5	5	7	0.01%	18.6%	TPCNAGTFSQPEK	99.7%	74.2	25	64.9	1	0	0	1436.65	127	139
Mitotic checkpoint protein BUB3	BUB3	BUB3_HUMAN	37.2	100.0%	5	5	7	0.01%	18.6%	VAVEYLDPSPEVQK	99.7%	46.1	25	43.2	1	0	0	1573.81	203	216
Mitotic checkpoint protein BUB3	BUB3	BUB3_HUMAN	37.2	100.0%	5	5	7	0.01%	18.6%	VYTLSVSGDR	99.7%	49.7	25	41.6	1	0	0	1096.56	140	149
MKI67 FHA domain-interacting nucleolar phosphoprotein	NIFK	MK67I_HUMAN	34.2	99.8%	2	2	4	0.00%	9.2%	GIDYDFPSLILQK	99.7%	42.3	25	42.3	2	0	0	1508.80	180	192
MKI67 FHA domain-interacting nucleolar phosphoprotein	NIFK	MK67I_HUMAN	34.2	99.8%	2	2	4	0.00%	9.2%	GYAFVEFESEDVAK	99.7%	68.3	25	60.6	2	0	0	1590.73	87	100
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	8	8	14	0.01%	8.0%	EDLILSLR	99.7%	54.8	25	18.8	2	0	0	958.56	239	246
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	8	8	14	0.01%	8.0%	EVFQTASER	99.7%	49.6	25	37.8	2	0	0	1066.52	308	316
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	8	8	14	0.01%	8.0%	FAEFLLPLLIEK	99.7%	59.9	25	47.9	2	0	0	1432.85	255	266
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	8	8	14	0.01%	8.0%	FQPFQDGSSGQR	99.7%	46	25	34.5	2	0	0	1353.62	701	712
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	8	8	14	0.01%	8.0%	GEWFLLGSPGS	95.2%	27.2	25	17.9	1	0	0	1149.56	1020	1030
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	8	8	14	0.01%	8.0%	LLQAAAGASAR	99.7%	75.3	25	71.8	3	0	0	1028.58	374	384
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	8	8	14	0.01%	8.0%	NLLVAFR	97.3%	29.5	25	18.8	1	0	0	832.50	189	195
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	8	8	14	0.01%	8.0%	NVEIPQLNQLMR	99.6%	38.3	25	38.3	1	0	0	1454.78	728	739
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	6	8	19	0.02%	25.3%	CTAPQYVDFVMSSVQK	99.7%	53	25	52.3	3	2	0	1875.86	105	120
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	6	8	19	0.02%	25.3%	EFNLLDPK	99.7%	45.2	25	31	2	0	0	975.51	188	195
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	6	8	19	0.02%	25.3%	EFPSSFESLVR	99.7%	62.2	25	59.9	4	0	0	1297.64	135	145
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	6	8	19	0.02%	25.3%	ELVVLPR	99.7%	43.1	25	15.9	2	0	0	825.52	42	48
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	6	8	19	0.02%	25.3%	ITDFQFK	97.9%	30.5	25	11.5	2	0	0	898.47	35	41
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	6	8	19	0.02%	25.3%	LVTDEDVFPTK	99.7%	87.3	25	76.7	4	0	0	1263.65	121	131
Monocarboxylate transporter 1	SLC16A1	MOT1_HUMAN	53.9	100.0%	3	3	12	0.01%	6.6%	DLHDANTDLIGR	99.7%	57.5	25	52.2	7	0	0	1339.66	225	236
Monocarboxylate transporter 1	SLC16A1	MOT1_HUMAN	53.9	100.0%	3	3	12	0.01%	6.6%	ESKEEETSIDVAGKPNEVTK	99.7%	42.2	25	41.7	0	4	0	2190.08	460	479
Monocarboxylate transporter 1	SLC16A1	MOT1_HUMAN	53.9	100.0%	3	3	12	0.01%	6.6%	KDLHDANTDLIGR	99.1%	25.9	25	25.9	0	1	0	1467.76	224	236
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	24	27	48	0.05%	30.0%	AEIDLVCELAK	99.7%	68.8	25	60.6	2	0	0	1260.65	808	818
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	24	27	48	0.05%	30.0%	ASGLVPNVVVLVATVR	99.7%	51.6	25	51.6	2	1	0	1593.97	730	745
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	24	27	48	0.05%	30.0%	AVIELLEK	99.7%	51.2	25	24.9	2	0	0	914.56	206	213
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	24	27	48	0.05%	30.0%	DFILPISDVR	99.7%	72.6	25	60.1	2	0	0	1174.65	926	935
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	24	27	48	0.05%	30.0%	DIELSPEAQAK	99.7%	58.9	25	47.2	2	0	0	1200.61	881	891
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	24	27	48	0.05%	30.0%	DVDGVTDINLGK	99.7%	72	25	62.9	2	0	0	1245.63	178	189
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	24	27	48	0.05%	30.0%	EFSEIQLAR	99.7%	66.6	25	37	2	0	0	1092.57	531	539
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	24	27	48	0.05%	30.0%	EIGLLADEIEIYGK	99.7%	87	25	87	3	0	0	1562.83	380	393
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	24	27	48	0.05%	30.0%	EVLSLLQEK	99.7%	47.6	25	42.9	2	0	0	1058.61	84	92
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	24	27	48	0.05%	30.0%	FQFLYDVQVPIVDK	99.7%	104	25	98.7	2	0	0	1710.91	855	868
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	24	27	48	0.05%	30.0%	GDAHECFVSPVAK	99.7%	30.1	25	25.8	0	2	0	1416.66	193	205
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	24	27	48	0.05%	30.0%	ILHENTQTDK	99.7%	44.2	25	44	1	0	0	1198.61	507	516
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	24	27	48	0.05%	30.0%	IQNMVSSGR	99.7%	39.4	25	28.7	2	0	0	991.50	327	335
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	24	27	48	0.05%	30.0%	KITIGQGNTEK	99.7%	42.1	25	31.9	2	0	0	1188.66	586	596
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	24	27	48	0.05%	30.0%	LDIDPSTITWQR	99.7%	50.7	25	47.6	1	0	0	1444.74	564	575
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	24	27	48	0.05%	30.0%	LQPLSPVPSDIEISR	99.7%	90.8	25	90.8	2	0	0	1650.91	353	367
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	24	27	48	0.05%	30.0%	LVPLVNGVR	99.1%	34.2	25	31.2	2	0	0	966.61	522	530
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	24	27	48	0.05%	30.0%	MHGGGPSVTAGVPLKK	95.0%	20.5	25	20.5	0	1	0	1535.84	749	764

Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	24	27	48	0.05%	30.0%	SGQPVTADDLGVTGALTVLMK	99.7%	91.4	25	91.4	3	1	0	2073.09	639	659
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	24	27	48	0.05%	30.0%	TDPSTLTEEEVSK	99.7%	87.2	25	78.7	2	0	0	1435.68	548	560
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	24	27	48	0.05%	30.0%	TIAQAVYGAK	99.7%	61.6	25	42.7	2	0	0	1021.57	871	880
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	24	27	48	0.05%	30.0%	VLNALKPEK	99.6%	38	25	34	1	0	0	1011.62	169	177
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	24	27	48	0.05%	30.0%	YTQQGFGNLPICMAK	99.7%	61.2	25	61.2	2	0	0	1727.82	895	909
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	24	27	48	0.05%	30.0%	YVLVAGITPTPLGEGK	99.7%	101	25	101	2	0	0	1614.91	414	429
Motile sperm domain-containing protein 2	MOSPD2	MSPD2_HUMAN	59.7	100.0%	4	4	7	0.01%	8.5%	EISVNDLNESSIPR	99.7%	67.6	25	65.3	1	0	0	1572.79	74	87
Motile sperm domain-containing protein 2	MOSPD2	MSPD2_HUMAN	59.7	100.0%	4	4	7	0.01%	8.5%	LIAFWLER	99.7%	54.9	25	43.9	2	0	0	1047.60	128	135
Motile sperm domain-containing protein 2	MOSPD2	MSPD2_HUMAN	59.7	100.0%	4	4	7	0.01%	8.5%	TLIVLTNVTK	99.7%	56.2	25	56.2	2	0	0	1101.69	348	357
Motile sperm domain-containing protein 2	MOSPD2	MSPD2_HUMAN	59.7	100.0%	4	4	7	0.01%	8.5%	TWLGPEAVSLLK	99.7%	44.4	25	20.9	2	0	0	1313.75	200	211
mRNA export factor	RAE1	RAE1L_HUMAN	41.0	100.0%	4	5	8	0.01%	13.6%	CWEVQDSGQTIPK	99.7%	63.9	25	58.2	2	0	0	1547.72	68	80
mRNA export factor	RAE1	RAE1L_HUMAN	41.0	100.0%	4	5	8	0.01%	13.6%	NAAEELKPR	99.6%	38.3	25	31.1	2	0	0	1027.55	357	365
mRNA export factor	RAE1	RAE1L_HUMAN	41.0	100.0%	4	5	8	0.01%	13.6%	QNKPTGFALGSIEGR	99.7%	32.1	25	30.9	0	1	0	1574.83	225	239
mRNA export factor	RAE1	RAE1L_HUMAN	41.0	100.0%	4	5	8	0.01%	13.6%	SSNPMMVLQLPER	99.7%	47.6	25	36.7	3	0	0	1501.75	160	172
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	9	11	17	0.02%	39.7%	GEVGLLFTNR	99.7%	50.1	25	44.5	2	0	0	1105.60	98	107
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	9	11	17	0.02%	39.7%	GVVTLLSDYEVCK	99.7%	75.1	25	75.1	2	0	0	1482.75	165	177
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	9	11	17	0.02%	39.7%	LFGYEMAEFK	99.7%	46.8	25	46.1	2	0	0	1234.58	192	201
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	9	11	17	0.02%	39.7%	QNLIEELRK	99.4%	36.3	25	11.5	2	0	0	1142.65	24	32
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	9	11	17	0.02%	39.7%	SPSDEYKDNLHQVSK	99.7%	29.3	25	29.3	0	2	0	1746.83	80	94
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	9	11	17	0.02%	39.7%	TKEEVNEWFTK	99.7%	43.9	25	39.1	1	0	0	1410.69	108	118
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	9	11	17	0.02%	39.7%	VMMVALGR	99.2%	34.6	25	27.7	2	0	0	876.48	72	79
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	9	11	17	0.02%	39.7%	YLFIFSVANMR	99.7%	48	25	46.9	3	0	0	1360.71	39	49
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	9	11	17	0.02%	39.7%	YTEMDYAR	98.8%	32.8	25	32.8	1	0	0	1064.44	119	126
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	8	8	13	0.01%	24.2%	ASILNTWISLK	99.7%	66.4	25	60.6	2	0	0	1245.72	404	414
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	8	8	13	0.01%	24.2%	DQITAGNAAR	99.1%	34.3	25	24.8	2	0	0	1016.51	37	46
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	8	8	13	0.01%	24.2%	EIVLADVIDNDSWR	99.7%	98.8	25	93	2	0	0	1644.82	202	215
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	8	8	13	0.01%	24.2%	EVTPEGLQMVK	94.9%	27	25	15.7	1	0	0	1230.64	236	246
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	8	8	13	0.01%	24.2%	ITSCIFQLLQEAGIK	99.7%	74.9	25	66.3	1	0	0	1720.93	60	74
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	8	8	13	0.01%	24.2%	TKEVYELLDSPGK	99.7%	78.1	25	66	2	0	0	1478.77	18	30
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	8	8	13	0.01%	24.2%	VTSAHKGPDETLR	97.3%	29.5	25	25.5	2	0	0	1410.73	299	311
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	8	8	13	0.01%	24.2%	VVVLMGSTSDLGHCEK	99.7%	68.1	25	68.1	1	0	0	1731.84	268	283
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	43	0.04%	18.6%	AGALHAQVER	99.2%	34.6	25	25.6	1	0	0	1051.56	897	906
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	43	0.04%	18.6%	ALVDILSEVSK	99.7%	61	25	50.3	1	0	0	1173.67	180	190
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	43	0.04%	18.6%	AQDSSLHMPER	98.8%	32.8	25	32.8	1	0	0	1286.58	433	443
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	43	0.04%	18.6%	ATLQEILPEVLK	99.7%	49.5	25	42.6	2	0	0	1353.80	191	202
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	43	0.04%	18.6%	EIPSATQSPISK	99.7%	57.9	25	49.1	2	0	0	1257.67	1156	1167
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	43	0.04%	18.6%	ELEAHSAEAR	95.8%	27.8	25	26	1	0	0	1112.53	582	591
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	43	0.04%	18.6%	EVVEQGLLK	99.7%	47.5	25	37.7	3	0	0	1014.58	287	295
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	43	0.04%	18.6%	FLSPPALQGYVAWLR	99.7%	49.3	25	49.3	1	0	0	1717.94	397	411
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	43	0.04%	18.6%	GNTAEGCVHETQEK	99.7%	75.5	25	69.6	2	0	0	1559.68	936	949
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	43	0.04%	18.6%	HQACLLLQK	99.3%	35	25	20.3	2	0	0	1110.61	1028	1036
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	43	0.04%	18.6%	KPTSQIPETK	99.3%	35.2	25	25	2	0	0	1128.63	489	498
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	43	0.04%	18.6%	LITGLGVGR	99.7%	55.7	25	43.8	2	0	0	885.55	77	85
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	43	0.04%	18.6%	LLGAALPLLTK	99.7%	52.1	25	52.1	4	0	0	1109.73	308	318
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	43	0.04%	18.6%	LPAIALDLLR	99.7%	65.4	25	46.3	2	0	0	1094.69	264	273
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	43	0.04%	18.6%	LVGSVNLFSDENVPR	99.7%	102	25	96.6	2	0	0	1645.85	232	246
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	43	0.04%	18.6%	MQFWPASYLCFR	98.8%	32.8	25	32.8	2	0	0	1605.73	296	307
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	43	0.04%	18.6%	QLMGQVLAK	99.7%	54.6	25	36.5	1	0	0	987.57	1054	1062
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	43	0.04%	18.6%	SPAPGAPTR	98.6%	32.1	25	30.9	1	0	0	853.45	1232	1240
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	43	0.04%	18.6%	SPLSALAR	99.7%	43.3	25	16.3	2	0	0	814.48	1290	1297
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	43	0.04%	18.6%	SPSLLQSGAK	99.7%	40.3	25	27.1	2	0	0	987.55	1308	1317

Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	43	0.04%	18.6%	TLGVQRPK	99.0%	33.6	25	29.7	1	0	0	898.55	1141	1148
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	43	0.04%	18.6%	VLDLVEVLVTK	99.7%	87.7	25	87.7	2	0	0	1227.76	828	838
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	43	0.04%	18.6%	VYSTALSSFLTK	99.7%	95.9	25	85	4	0	0	1316.71	977	988
Myosin light polypeptide 6	MYL6	MYL6_HUMAN	16.9	100.0%	2	2	6	0.01%	15.9%	ALGQNPTNAEVLK	99.7%	57.4	25	51	4	0	0	1354.73	38	50
Myosin light polypeptide 6	MYL6	MYL6_HUMAN	16.9	100.0%	2	2	6	0.01%	15.9%	ILYSQCGDVMR	99.7%	45.2	25	45.2	2	0	0	1357.62	27	37
Myosin-10	MYH10	MYH10_HUMAN	229.0	100.0%	3	3	3	0.00%	1.8%	ALELDPNLYR	99.7%	40	25	40	1	0	0	1203.64	753	762
Myosin-10	MYH10	MYH10_HUMAN	229.0	100.0%	3	3	3	0.00%	1.8%	QLLQANPILESFGNAK	99.7%	65.1	25	64.7	1	0	0	1742.94	217	232
Myosin-10	MYH10	MYH10_HUMAN	229.0	100.0%	3	3	3	0.00%	1.8%	VKPLLQVTR	98.5%	31.8	25	31.8	1	0	0	1053.68	841	849
Myosin-9	MYH9	MYH9_HUMAN	226.5	100.0%	4	4	6	0.01%	3.1%	IIGLDQVAGMSETALPGAFK	98.2%	31.2	25	31.2	1	0	0	2018.06	618	637
Myosin-9	MYH9	MYH9_HUMAN	226.5	100.0%	4	4	6	0.01%	3.1%	QLLQANPILEAFGNAK	99.7%	87.4	25	87.4	2	0	0	1726.95	210	225
Myosin-9	MYH9	MYH9_HUMAN	226.5	100.0%	4	4	6	0.01%	3.1%	RGDLPFVVPR	98.7%	32.5	25	22.1	1	0	0	1155.66	1923	1932
Myosin-9	MYH9	MYH9_HUMAN	226.5	100.0%	4	4	6	0.01%	3.1%	VISGVLQLGNIVFK	99.7%	60	25	60	2	0	0	1486.90	342	355
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	14	0.01%	9.5%	AGFVPVYLR	99.5%	36.8	25	28.7	2	0	0	1021.58	726	734
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	14	0.01%	9.5%	ALQLLQMYYEGR	99.7%	44.1	25	44.1	1	0	0	1484.76	644	655
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	14	0.01%	9.5%	ASEVFLQR	99.7%	58.4	25	35	2	0	0	949.51	521	528
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	14	0.01%	9.5%	EELEALFLPYDLK	99.7%	53.7	25	51.2	1	0	0	1579.83	811	823
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	14	0.01%	9.5%	ILIENGVAER	99.7%	50.5	25	38.2	2	0	0	1113.63	12	21
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	14	0.01%	9.5%	LDYLGVSYGLTPR	99.7%	69.1	25	55.2	1	0	0	1453.77	706	718
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	14	0.01%	9.5%	LFNEVQEK	94.8%	27	25	5.28	1	0	0	1006.52	905	912
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	14	0.01%	9.5%	QQSAQSQVSTTAENK	99.7%	101	25	89.4	2	0	0	1606.77	433	447
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	14	0.01%	9.5%	SLFVVVGDR	99.7%	46.7	25	36.7	2	0	0	991.56	24	32
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	5	5	6	0.01%	6.8%	EANSIIITPGYGLCAAK	99.7%	44	25	44	1	0	0	1777.92	923	939
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	5	5	6	0.01%	6.8%	FFTGQITAAGK	99.6%	38.4	25	35.1	1	0	0	1140.60	214	224
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	5	5	6	0.01%	6.8%	GITHIGYTDLPSR	99.7%	40.2	25	30.7	1	0	0	1429.74	367	379
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	5	5	6	0.01%	6.8%	TSGTLISFIYPAQNPELLNK	99.7%	52	25	52	2	0	0	2206.18	147	166
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	5	5	6	0.01%	6.8%	VALSPAGVQNLVK	99.7%	41.1	25	36.5	1	0	0	1295.77	72	84
NAD(P)H-hydrate epimerase	APOA1BP	NNRE_HUMAN	31.7	99.8%	2	2	3	0.00%	10.4%	GNAGGIQPDLLISLTAPK	99.7%	38.7	25	31.4	1	0	0	1764.99	228	245
NAD(P)H-hydrate epimerase	APOA1BP	NNRE_HUMAN	31.7	99.8%	2	2	3	0.00%	10.4%	LFGYEPTIYYPK	99.7%	48.3	25	46.8	2	0	0	1490.76	133	144
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	7	7	11	0.01%	19.2%	FDKGPWLK	99.1%	34.2	25	7.64	2	0	0	990.54	278	285
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	7	7	11	0.01%	19.2%	FYDDPR	98.6%	32.2	25	32.2	1	0	0	812.36	117	122
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	7	7	11	0.01%	19.2%	ITSAYLQDIENAYK	99.7%	53	25	49	1	0	0	1628.82	229	242
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	7	7	11	0.01%	19.2%	LQSWLYSSR	99.7%	52.1	25	43.8	2	0	0	1139.58	131	139
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	7	7	11	0.01%	19.2%	QCVDHYNEVK	98.1%	30.9	25	26.4	1	0	0	1291.57	182	191
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	7	7	11	0.01%	19.2%	VITVDGNICTGK	99.7%	98.8	25	89.3	2	0	0	1276.66	59	70
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	7	7	11	0.01%	19.2%	VVEDIEYLK	99.7%	56.5	25	48.7	2	0	0	1107.59	269	277
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	99.8%	2	2	7	0.01%	16.6%	GLQQITGHGGLR	99.7%	71.7	25	59.1	6	0	0	1236.68	10	21
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	99.8%	2	2	7	0.01%	16.6%	IQEWIPPSTPYK	97.8%	30.4	25	22.5	1	0	0	1458.76	134	145
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	NDUAD_HUMAN	16.7	100.0%	5	5	8	0.01%	38.9%	ENLEEEAIIMK	99.7%	63.1	25	44.3	2	0	0	1318.66	89	99
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	NDUAD_HUMAN	16.7	100.0%	5	5	8	0.01%	38.9%	IALLPLLQAETDR	99.5%	36.4	25	36.4	1	0	0	1452.84	69	81
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	NDUAD_HUMAN	16.7	100.0%	5	5	8	0.01%	38.9%	LQIEDFEAR	99.7%	56.1	25	45.7	2	0	0	1120.56	60	68
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	NDUAD_HUMAN	16.7	100.0%	5	5	8	0.01%	38.9%	VGESVFHTTR	99.7%	80.1	25	74.6	2	0	0	1132.57	106	115
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	NDUAD_HUMAN	16.7	100.0%	5	5	8	0.01%	38.9%	WVPPLIGELYGLR	99.7%	42.6	25	33.9	1	0	0	1512.86	116	128
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	NDUFA2	NDUA2_HUMAN	10.9	100.0%	2	2	3	0.00%	20.2%	ALENVLSGKA	99.7%	64.9	25	35.9	2	0	0	1001.56	90	99
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	NDUFA2	NDUA2_HUMAN	10.9	100.0%	2	2	3	0.00%	20.2%	ANPDLPILIR	97.9%	30.6	25	26.2	1	0	0	1121.67	47	56
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	NDUFA4	NDUA4_HUMAN	9.4	100.0%	3	3	6	0.01%	37.0%	FYSVNVDYSK	99.7%	64.3	25	53	2	0	0	1221.58	64	73
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	NDUFA4	NDUA4_HUMAN	9.4	100.0%	3	3	6	0.01%	37.0%	LALFNPDVCWDR	99.7%	51.3	25	51.3	2	0	0	1505.72	36	47
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	NDUFA4	NDUA4_HUMAN	9.4	100.0%	3	3	6	0.01%	37.0%	LGPNDQYK	98.9%	33.1	25	29.5	2	0	0	934.46	56	63
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	NDUA5_HUMAN	13.5	100.0%	4	5	8	0.01%	31.0%	ILDVLEEIPK	99.7%	59.1	25	50.9	2	0	0	1168.68	31	40
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	NDUA5_HUMAN	13.5	100.0%	4	5	8	0.01%	31.0%	KYTEQITNEK	99.7%	40.7	25	40.2	2	0	0	1253.64	46	55
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	NDUA5_HUMAN	13.5	100.0%	4	5	8	0.01%	31.0%	TTGLVGLAVCNTPHER	99.7%	73.4	25	73.4	2	1	0	1724.88	8	23
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	NDUA5_HUMAN	13.5	100.0%	4	5	8	0.01%	31.0%	YTEQITNEK	99.7%	38.9	25	24.5	1	0	0	1125.54	47	55

NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	NDUFA6	NDUA6_HUMAN	17.9	100.0%	3	4	9	0.01%	18.8%	FFHETEAPRPK	99.7%	43.6	25	38.3	2	2	0	1358.69	132	142
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	NDUFA6	NDUA6_HUMAN	17.9	100.0%	3	4	9	0.01%	18.8%	GKIELEETIK	97.6%	30.1	25	19.5	1	0	0	1159.66	112	121
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	NDUFA6	NDUA6_HUMAN	17.9	100.0%	3	4	9	0.01%	18.8%	VVDLLVIK	99.7%	52.6	25	52.6	4	0	0	898.60	104	111
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	NDUFA7	NDUA7_HUMAN	12.6	99.8%	2	2	3	0.00%	16.8%	ALVSGKPAESSAVAATEK	99.7%	41.9	25	41.9	1	0	0	1715.92	75	92
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	NDUFA7	NDUA7_HUMAN	12.6	99.8%	2	2	3	0.00%	16.8%	ALVSGKPAESSAVAATEKK	99.6%	28.3	25	28.3	0	2	0	1844.01	75	93
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	7	8	13	0.01%	19.1%	FGPIPLGSLGWK	98.2%	31.3	25	31.3	1	0	0	1271.71	223	234
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	7	8	13	0.01%	19.1%	MGSQVIIPYR	99.7%	42.3	25	39.3	4	0	0	1179.62	76	85
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	7	8	13	0.01%	19.1%	NFDFEDVFVK	97.9%	30.5	25	19.6	1	0	0	1259.59	138	147
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	7	8	13	0.01%	19.1%	QPVYVVDVSK	99.5%	37	25	33.7	2	0	0	1133.62	238	247
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	7	8	13	0.01%	19.1%	SFAFVGPSR	99.7%	47.2	25	42.2	2	0	0	967.50	262	270
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	7	8	13	0.01%	19.1%	VFEISPFEPWITR	99.7%	39.4	25	31.5	1	0	0	1620.84	304	316
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	7	8	13	0.01%	19.1%	YVVNHLGR	98.6%	32.2	25	28.2	2	0	0	957.53	68	75
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3	NDUFB3	NDUB3_HUMAN	11.4	99.8%	2	2	2	0.00%	21.4%	IEGTPLETIQK	98.2%	31.2	25	23.4	1	0	0	1228.68	24	34
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3	NDUFB3	NDUB3_HUMAN	11.4	99.8%	2	2	2	0.00%	21.4%	SVSFSDVFFK	96.2%	28.2	25	21.4	1	0	0	1162.58	60	69
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	NDUFB4	NDUB4_HUMAN	15.2	100.0%	4	4	8	0.01%	41.1%	EYLLQYNDPNRR	99.6%	28.3	25	21.2	0	2	0	1580.78	46	57
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	NDUFB4	NDUB4_HUMAN	15.2	100.0%	4	4	8	0.01%	41.1%	GLIENPALLR	99.7%	64.9	25	55.3	2	0	0	1095.65	58	67
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	NDUFB4	NDUB4_HUMAN	15.2	100.0%	4	4	8	0.01%	41.1%	TINVYPNFRPTPK	99.7%	39.7	25	36.9	2	0	0	1546.84	73	85
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	NDUFB4	NDUB4_HUMAN	15.2	100.0%	4	4	8	0.01%	41.1%	TLPETLDPAEYNISPETR	99.7%	59.9	25	59.9	2	0	0	2046.00	13	30
NADH dehydrogenase [ubiquinone] 1 subunit C2	NDUFC2	NDUC2_HUMAN	14.2	99.8%	2	2	3	0.00%	16.8%	EDYLYAVR	99.0%	33.8	25	32.9	1	0	0	1028.50	78	85
NADH dehydrogenase [ubiquinone] 1 subunit C2	NDUFC2	NDUC2_HUMAN	14.2	99.8%	2	2	3	0.00%	16.8%	LHPEDFPEEDKK	98.6%	24.3	25	24.3	0	2	0	1483.71	95	106
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	3	3	5	0.00%	7.5%	EAYEAGLIGK	99.7%	47.7	25	47.7	2	0	0	1050.55	175	184
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	3	3	5	0.00%	7.5%	GGAGFPTGLK	99.4%	36	25	27.4	1	0	0	904.49	89	98
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	3	3	5	0.00%	7.5%	NACGSGYDFDVFVVR	99.7%	86.7	25	86.7	2	0	0	1705.76	185	199
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	4	4	6	0.01%	9.5%	IIAQCLNK	95.5%	27.5	25	16.4	1	0	0	959.53	343	350
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	4	4	6	0.01%	9.5%	LVMELSGEMVR	99.7%	54	25	52.2	1	0	0	1263.64	97	107
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	4	4	6	0.01%	9.5%	MFEFYER	99.4%	36.3	25	30.1	2	0	0	1021.44	210	216
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	4	4	6	0.01%	9.5%	NITLNFGPQHPAAHGVLR	99.7%	35.1	25	35.1	0	2	0	1942.04	79	96
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	16	0.02%	39.4%	AANWYER	99.7%	42.5	25	38	2	0	0	909.42	162	168
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	16	0.02%	39.4%	DFPLSGYVELR	99.7%	75.2	25	63.7	2	0	0	1295.66	201	211
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	16	0.02%	39.4%	FDLNSPWEAFPVYR	99.7%	61.7	25	59.6	2	0	0	1740.84	233	246
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	16	0.02%	39.4%	ILTDYGFEGHPFR	99.7%	54.1	25	50.7	2	0	0	1551.76	187	199
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	16	0.02%	39.4%	QLSAFGEYVAEILPK	99.7%	79.2	25	78.8	2	0	0	1664.89	57	71
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	16	0.02%	39.4%	SLVDLTAVDVPTR	99.7%	89	25	85.7	2	0	0	1385.76	110	122
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	16	0.02%	39.4%	TYTDELTPIESAVSVFK	99.7%	75.9	25	71.9	2	0	0	1899.96	145	161
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	16	0.02%	39.4%	VVAEPVELAQEFRK	99.7%	68.5	25	68.5	2	0	0	1614.89	219	232
NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	NDUFS6	NDUS6_HUMAN	13.7	99.8%	2	2	4	0.00%	21.8%	TGTCGYCGLQFR	99.5%	37	25	37	2	0	0	1419.61	109	120
NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	NDUFS6	NDUS6_HUMAN	13.7	99.8%	2	2	4	0.00%	21.8%	VIACDGGGGALGHPK	99.7%	60.2	25	57.1	2	0	0	1408.70	84	98
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	NDUS7_HUMAN	23.6	100.0%	4	6	12	0.01%	15.5%	KVYDQMPEPR	99.7%	41.5	25	41.5	2	0	0	1278.61	136	145
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	NDUS7_HUMAN	23.6	100.0%	4	6	12	0.01%	15.5%	LDDLVNWAR	99.7%	61.9	25	48.1	2	0	0	1101.57	67	75
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	NDUS7_HUMAN	23.6	100.0%	4	6	12	0.01%	15.5%	QSDVMIVAGTLTNK	99.7%	97.9	25	96.7	4	0	0	1476.77	116	129
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	NDUS7_HUMAN	23.6	100.0%	4	6	12	0.01%	15.5%	VYDQMPEPR	99.7%	60.1	25	60.1	4	0	0	1134.52	137	145
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	NDUS8_HUMAN	23.7	100.0%	5	5	10	0.01%	29.0%	EPATINYPFEK	96.8%	28.9	25	28.9	1	0	0	1308.65	78	88
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	NDUS8_HUMAN	23.7	100.0%	5	5	10	0.01%	29.0%	GLGMTLSYLFR	99.7%	61.3	25	54.5	2	0	0	1257.67	67	77
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	NDUS8_HUMAN	23.7	100.0%	5	5	10	0.01%	29.0%	LCEAICPAQAITIEAEPR	99.7%	86.3	25	86.3	2	0	0	2042.00	116	133
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	NDUS8_HUMAN	23.7	100.0%	5	5	10	0.01%	29.0%	TLLWTELFR	99.7%	57.9	25	51.3	2	0	0	1178.66	58	66
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	NDUS8_HUMAN	23.7	100.0%	5	5	10	0.01%	29.0%	YVNMQDPEMDMK	99.7%	48.4	25	41.5	3	0	0	1548.60	38	49
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	17	28	0.03%	24.5%	ALSEIAGMTLPYDTLDQVR	99.7%	81.7	25	78.2	3	0	0	2109.05	625	643
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	17	28	0.03%	24.5%	FASEIAGVDDLGTTGR	99.7%	129	25	124	2	0	0	1608.79	185	200
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	17	28	0.03%	24.5%	FAYDGLKR	99.7%	38.7	25	30.7	2	0	0	969.52	292	299
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	17	28	0.03%	24.5%	FEAPLFNAR	99.7%	45.2	25	35.8	2	0	0	1064.55	409	417
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	17	28	0.03%	24.5%	GLLTYTSWEDALSR	99.7%	81.3	25	73.4	2	0	0	1611.80	312	325

NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	17	28	0.03%	24.5%	GWNILTNSEK	99.7%	43	25	34.9	2	0	0	1161.59	99	108
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	17	28	0.03%	24.5%	ILQDIASGSHPFSQVLK	99.7%	61.6	25	61.6	1	1	0	1840.00	451	467
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	17	28	0.03%	24.5%	KPMVVLGSSALQR	98.0%	30.8	25	25.7	1	0	0	1385.79	471	483
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	17	28	0.03%	24.5%	NDGAAILAAVSSIAQK	99.7%	99.1	25	95.8	2	0	0	1528.83	484	499
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	17	28	0.03%	24.5%	SATYVNTEGR	99.7%	54	25	43.2	2	0	0	1097.52	593	602
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	17	28	0.03%	24.5%	VAGMLQSFQGK	99.7%	60.6	25	58	3	0	0	1181.60	326	336
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	17	28	0.03%	24.5%	VAVTPPGLAR	99.1%	34.1	25	34.1	2	0	0	980.59	608	617
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	17	28	0.03%	24.5%	VLFLLGADGGCITR	99.7%	90.8	25	86.8	2	0	0	1491.80	544	557
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	17	28	0.03%	24.5%	VVAACAMPVMK	99.7%	42.3	25	32.6	1	0	0	1208.58	88	98
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	7	9	14	0.01%	26.4%	AMIENFNAK	99.7%	47.3	25	34.8	2	0	0	1037.51	97	105
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	7	9	14	0.01%	26.4%	HVVLGAIENK	99.7%	44.1	25	42.2	2	0	0	1079.62	170	179
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	7	9	14	0.01%	26.4%	HVVLGAIENKVESK	98.3%	23.8	25	23.8	0	1	0	1522.86	170	183
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	7	9	14	0.01%	26.4%	MEEDPDDVPHGHITSLAVK	99.7%	41.1	25	37.2	0	2	0	2089.99	60	78
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	7	9	14	0.01%	26.4%	YVSLHVR	98.9%	33.1	25	26.2	2	0	0	873.49	106	112
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	7	9	14	0.01%	26.4%	YYADGEDAYAMK	99.7%	56.5	25	56.5	2	0	0	1396.57	137	148
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	7	9	14	0.01%	26.4%	YYADGEDAYAMKR	99.7%	54	25	53.5	3	0	0	1568.67	137	149
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	23	26	49	0.05%	24.5%	AIELATTLDESLTNR	99.7%	106	25	87	2	0	0	1646.86	783	797
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	23	26	49	0.05%	24.5%	ALKPANMLER	96.5%	28.5	25	13.1	1	0	0	1142.64	267	276
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	23	26	49	0.05%	24.5%	DLSLLQIQMR	99.7%	87.9	25	72.7	4	0	0	1216.67	119	128
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	23	26	49	0.05%	24.5%	EALEHLCTYEK	99.7%	51.5	25	35.1	2	0	0	1392.65	208	218
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	23	26	49	0.05%	24.5%	EEAYELVR	94.9%	27.1	25	19	1	0	0	1008.50	63	70
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	23	26	49	0.05%	24.5%	FAEHGETLAMK	99.7%	53.3	25	45	4	0	0	1233.59	42	52
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	23	26	49	0.05%	24.5%	FKECLDK	98.5%	31.9	25	18.2	1	0	0	939.46	306	312
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	23	26	49	0.05%	24.5%	FLLMLQSVK	99.7%	47	25	31.6	2	0	0	1094.63	688	696
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	23	26	49	0.05%	24.5%	GLTLNCLGK	99.5%	37.1	25	28	2	0	0	975.53	53	61
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	23	26	49	0.05%	24.5%	IAIEIYLK	99.7%	43.5	25	41	2	0	0	962.59	560	567
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	23	26	49	0.05%	24.5%	ILEEFRK	99.6%	37.8	25	30.3	2	0	0	934.54	170	176
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	23	26	49	0.05%	24.5%	KEEAYELVR	99.7%	55.1	25	48.7	2	0	0	1136.59	62	70
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	23	26	49	0.05%	24.5%	LEDAADVYR	99.7%	81.8	25	76	3	0	0	1051.51	240	248
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	23	26	49	0.05%	24.5%	LFGATNPK	98.7%	32.7	25	5.14	1	0	0	847.47	741	748
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	23	26	49	0.05%	24.5%	LFNTAVCESK	99.7%	66.2	25	57.9	2	0	0	1168.57	715	724
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	23	26	49	0.05%	24.5%	LPLNFLSGEK	99.6%	37.6	25	27.2	2	0	0	1117.63	296	305
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	23	26	49	0.05%	24.5%	MVYYLDPSSQK	99.7%	68.6	25	59.8	4	0	0	1346.63	771	781
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	23	26	49	0.05%	24.5%	NFNETFLKR	99.7%	46.8	25	29.3	2	0	0	1168.61	749	757
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	23	26	49	0.05%	24.5%	NPENWAYYK	99.7%	44.2	25	39.4	2	0	0	1184.54	254	262
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	23	26	49	0.05%	24.5%	RLPLNFLSGEK	99.7%	53.8	25	49.2	2	0	0	1273.73	295	305
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	23	26	49	0.05%	24.5%	VAIIEELVVGYETSLK	99.7%	59.5	25	57.7	2	0	0	1762.98	339	354
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	23	26	49	0.05%	24.5%	WDKDNLQILR	99.7%	38.3	25	26.3	0	2	0	1300.70	109	118
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	23	26	49	0.05%	24.5%	WMDEAQALDTADR	99.7%	70.9	25	70.9	2	0	0	1521.66	430	442
N-alpha-acetyltransferase 20	NAA20	NAA20_HUMAN	20.4	100.0%	5	6	9	0.01%	30.3%	AFTCDDLFR	97.0%	29.1	25	24.1	1	0	0	1144.51	6	14
N-alpha-acetyltransferase 20	NAA20	NAA20_HUMAN	20.4	100.0%	5	6	9	0.01%	30.3%	LMELLEEISER	99.7%	58.4	25	50.9	2	0	0	1361.70	92	102
N-alpha-acetyltransferase 20	NAA20	NAA20_HUMAN	20.4	100.0%	5	6	9	0.01%	30.3%	QLGYSVYR	99.4%	35.9	25	25.2	2	0	0	985.51	125	132
N-alpha-acetyltransferase 20	NAA20	NAA20_HUMAN	20.4	100.0%	5	6	9	0.01%	30.3%	SIIPLPHPVRPEDIE	97.2%	29.3	25	29.3	1	0	0	1711.94	164	178
N-alpha-acetyltransferase 20	NAA20	NAA20_HUMAN	20.4	100.0%	5	6	9	0.01%	30.3%	VSNQVAVNMYK	99.7%	45.9	25	45.9	3	0	0	1252.64	114	124
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	18	18	27	0.03%	20.7%	ALQQHLCVVQLTR	99.7%	50.8	25	41.1	0	1	0	1565.86	410	422
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	18	18	27	0.03%	20.7%	DIQYPFLGPVPTR	99.7%	57.6	25	57.3	2	0	0	1502.80	748	760
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	18	18	27	0.03%	20.7%	DTSEYIIQAYK	99.7%	74	25	74	2	0	0	1330.65	576	586
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	18	18	27	0.03%	20.7%	FINQLLGVVPLSTPTEDK	99.7%	52.5	25	52.5	2	0	0	1971.08	384	401
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	18	18	27	0.03%	20.7%	IPEFIAFR	99.7%	53.8	25	34.4	2	0	0	992.56	593	600
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	18	18	27	0.03%	20.7%	LALPADIR	99.7%	42.5	25	27	1	0	0	868.53	402	409
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	18	18	27	0.03%	20.7%	LISGLPSLNHPVEPK	99.7%	41.5	25	30	2	0	0	1600.91	696	710

N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	18	18	27	0.03%	20.7%	LLGLYHTMDK	97.8%	30.4	25	21	1	0	0	1206.62	423	432
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	18	18	27	0.03%	20.7%	LLLQQLEATLETGK	99.7%	62.1	25	62.1	1	0	0	1556.89	729	742
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	18	18	27	0.03%	20.7%	LNNSLHFAQVR	97.0%	22	25	17.7	0	1	0	1298.70	603	613
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	18	18	27	0.03%	20.7%	LSLEEETLWLR	99.7%	50.3	25	49	2	0	0	1388.74	678	688
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	18	18	27	0.03%	20.7%	LTSEIQSR	99.7%	40.3	25	25.3	2	0	0	933.50	224	231
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	18	18	27	0.03%	20.7%	SLLDQLKDVFSK	99.7%	56.1	25	52.5	1	0	0	1392.77	807	818
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	18	18	27	0.03%	20.7%	TMFLPLAER	97.9%	30.6	25	22.2	1	0	0	1093.57	171	179
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	18	18	27	0.03%	20.7%	VFVDLLPATQCTK	99.7%	62.4	25	55.4	2	0	0	1491.79	371	383
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	18	18	27	0.03%	20.7%	WPECNALSR	99.6%	37.5	25	31.1	1	0	0	1132.52	245	253
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	18	18	27	0.03%	20.7%	YQEALDVIR	99.7%	52.8	25	40.5	2	0	0	1106.58	209	217
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	18	18	27	0.03%	20.7%	YQHGLEFGK	97.6%	30	25	14.8	1	0	0	1078.53	446	454
Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACA	NACAM_HUMAN	205.4	99.8%	2	2	4	0.00%	1.4%	IEDLSQQAQLAAAEK	99.7%	106	25	99.3	2	0	0	1614.83	1991	2005
Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACA	NACAM_HUMAN	205.4	99.8%	2	2	4	0.00%	1.4%	SPASDTYIVFGEAK	99.7%	77.7	25	77.7	2	0	0	1484.73	1977	1990
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	15	16	26	0.03%	14.4%	AAEDLFVNIR	99.7%	81.2	25	60.6	2	0	0	1147.61	306	315
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	15	16	26	0.03%	14.4%	ASLGLADHR	99.7%	63.9	25	52.2	2	0	0	939.50	502	510
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	15	16	26	0.03%	14.4%	DEIIWLLR	99.7%	57.7	25	39.6	2	0	0	1057.60	380	387
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	15	16	26	0.03%	14.4%	ELATVLSDQPGLLGPK	99.7%	66.4	25	66.4	2	0	0	1637.91	352	367
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	15	16	26	0.03%	14.4%	EYLTSHLEIR	99.7%	49.2	25	38.9	2	0	0	1260.66	706	715
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	15	16	26	0.03%	14.4%	KFPAVETR	99.1%	34.4	25	17.2	2	0	0	947.53	63	70
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	15	16	26	0.03%	14.4%	LQAYTSVSK	99.7%	40.5	25	37.2	1	0	0	996.54	493	501
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	15	16	26	0.03%	14.4%	LVVENVDVLTQMR	99.7%	72.4	25	71.3	2	0	0	1531.82	869	881
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	15	16	26	0.03%	14.4%	MFQQCLELPSQSR	99.7%	39.5	25	34.4	1	0	0	1623.76	552	564
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	15	16	26	0.03%	14.4%	MTIIGVILSFR	95.9%	27.9	25	27.9	1	0	0	1265.73	907	917
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	15	16	26	0.03%	14.4%	NNNQQLAQLQK	99.7%	56.4	25	47.8	1	0	0	1298.68	71	81
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	15	16	26	0.03%	14.4%	QVEDGEVFDFR	99.7%	54.6	25	52.2	2	0	0	1340.61	474	484
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	15	16	26	0.03%	14.4%	SLSELLGPYGMK	99.7%	41.7	25	19.1	3	0	0	1310.67	838	849
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	15	16	26	0.03%	14.4%	SLSLCNMFLDEMAK	99.7%	42.3	25	42.3	2	0	0	1658.76	595	608
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	15	16	26	0.03%	14.4%	YGPVMQR	97.9%	30.6	25	18	1	0	0	850.42	422	428
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	8	8	12	0.01%	18.4%	DAAAVGNHVAK	99.7%	53.3	25	34.8	2	0	0	1052.55	353	363
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	8	8	12	0.01%	18.4%	EGQGNLPVR	95.3%	27.4	25	19.9	1	0	0	969.51	318	326
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	8	8	12	0.01%	18.4%	FTVVVATQLPESTSLR	99.7%	72.7	25	72.7	2	0	0	1747.96	123	138
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	8	8	12	0.01%	18.4%	GTIPDMIADSGK	98.4%	31.6	25	30.9	1	0	0	1204.59	327	338
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	8	8	12	0.01%	18.4%	LADVLWNSQIPLLICR	99.7%	44.7	25	44.7	1	0	0	1911.05	139	154
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	8	8	12	0.01%	18.4%	LLCSNSAFLR	99.7%	48	25	34.4	2	0	0	1180.61	382	391
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	8	8	12	0.01%	18.4%	TYGLVGYMR	99.5%	36.3	25	29.2	1	0	0	1059.53	155	163
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	8	8	12	0.01%	18.4%	YPGVSNYQVEEDIGK	99.7%	61.7	25	61.7	2	0	0	1697.80	442	456
Neuroblastoma-amplified sequence	NBAS	NBAS_HUMAN	268.6	100.0%	2	2	3	0.00%	0.8%	CSGALTVSSVK	96.8%	28.8	25	18.8	1	0	0	1108.57	406	416
Neuroblastoma-amplified sequence	NBAS	NBAS_HUMAN	268.6	100.0%	2	2	3	0.00%	0.8%	LLGLAELLR	99.7%	48.7	25	6.11	2	0	0	997.64	1262	1270
Neurochondrin	NCDN	NCDN_HUMAN	78.9	99.8%	2	2	3	0.00%	3.4%	IPILSTFLTAR	99.6%	37.3	25	37.3	2	0	0	1231.74	130	140
Neurochondrin	NCDN	NCDN_HUMAN	78.9	99.8%	2	2	3	0.00%	3.4%	NDSEQFAALLLVTK	96.0%	28	25	28	1	0	0	1548.83	48	61
Neurofilament light polypeptide	NEFL	NFL_HUMAN	61.5	99.8%	2	2	3	0.00%	6.8%	EYQDLLNVK	99.7%	54.4	25	47	8	0	0	1121.58	371	379
Neurofilament light polypeptide	NEFL	NFL_HUMAN	61.5	99.8%	2	2	3	0.00%	6.8%	LAAEDATNEK	99.7%	47.2	25	36.8	2	0	0	1061.51	148	157
Neurofilament light polypeptide	NEFL	NFL_HUMAN	61.5	99.8%	2	2	3	0.00%	6.8%	LLEGEETR	94.6%	26.9	25	11.7	1	0	0	946.48	392	399
Neurofilament light polypeptide	NEFL	NFL_HUMAN	61.5	99.8%	2	2	3	0.00%	6.8%	VLEAELLVLR	97.9%	30.6	25	28	1	0	0	1154.71	117	126
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	5	5	8	0.01%	8.0%	ATLEMVNHEK	99.7%	49.2	25	41.3	2	0	0	1171.58	159	168
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	5	5	8	0.01%	8.0%	EYQDLLNVK	99.7%	54.4	25	47	8	0	0	1121.58	383	391
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	5	5	8	0.01%	8.0%	HLREYQDLLNVK	99.7%	33.5	25	24.2	0	1	0	1527.83	380	391
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	5	5	8	0.01%	8.0%	LLEGEETR	94.6%	26.9	25	11.7	1	0	0	946.48	404	411
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	5	5	8	0.01%	8.0%	LRDDTEAAIR	99.7%	51.2	25	39.9	2	0	0	1159.61	195	204
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	5	5	8	0.01%	8.0%	VEEHEETFEEK	99.2%	34.8	25	30.3	1	0	0	1405.61	883	893
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	5	5	8	0.01%	8.0%	VQSLQDEVAFLR	99.7%	86.3	25	76.5	2	0	0	1404.75	224	235

Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	5	5	8	0.01%	8.0%	VSGSPSSGFR	97.8%	30.4	25	21.5	1	0	0	980.48	27	36
Neutral alpha-glucosidase AB	GANAB	GANAB_HUMAN	106.9	100.0%	3	3	5	0.00%	3.3%	LVAIVDPHIK	99.6%	38.3	25	33.2	1	0	0	1104.68	463	472
Neutral alpha-glucosidase AB	GANAB	GANAB_HUMAN	106.9	100.0%	3	3	5	0.00%	3.3%	SLLLSVNAR	99.7%	49.2	25	42	2	0	0	972.58	165	173
Neutral alpha-glucosidase AB	GANAB	GANAB_HUMAN	106.9	100.0%	3	3	5	0.00%	3.3%	VLLVLELQGLQK	99.7%	66.7	25	66.7	2	0	0	1352.85	85	96
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	39	0.04%	19.6%	EVLDSFLDLAR	99.7%	83.2	25	75.7	8	0	0	1277.67	179	189
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	39	0.04%	19.6%	GPAGDATVASEK	99.7%	67	25	54.5	2	0	0	1102.54	526	537
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	39	0.04%	19.6%	GPAGDATVASEKESVM	99.7%	71.2	25	71.2	3	0	0	1564.72	526	541
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	39	0.04%	19.6%	IVEMEDVGLLFAR	99.7%	86.4	25	85.1	4	0	0	1491.79	289	301
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	39	0.04%	19.6%	LGPEGELLIR	99.7%	73.7	25	67.7	4	0	0	1096.64	248	257
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	39	0.04%	19.6%	LSAFVFPGELLLR	99.7%	66	25	66	3	0	0	1461.85	86	98
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	39	0.04%	19.6%	NIFPSNLVSAAFR	99.7%	56.3	25	49.2	5	0	0	1435.77	190	202
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	39	0.04%	19.6%	SELPLDPLPVPTEEGNPLLK	99.7%	66.4	25	66.4	6	0	0	2158.16	503	522
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	9	9	39	0.04%	19.6%	STEPELIQVK	99.7%	52.6	25	41.6	4	0	0	1143.63	493	502
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	7	7	11	0.01%	11.4%	DASGQPIFNASAK	99.7%	63.8	25	60.5	2	0	0	1305.64	323	335
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	7	7	11	0.01%	11.4%	EGLGLDVER	99.7%	53.1	25	37.2	2	0	0	987.51	589	597
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	7	7	11	0.01%	11.4%	GAVEDVISR	99.7%	55	25	36.3	1	0	0	945.50	525	533
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	7	7	11	0.01%	11.4%	LLTDGYACEVR	99.7%	58.3	25	40.4	1	0	0	1296.63	235	245
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	7	7	11	0.01%	11.4%	SESHTDLTFSR	99.7%	49.3	25	40.6	1	0	0	1279.59	616	626
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	7	7	11	0.01%	11.4%	TNPEYIYAPLK	99.7%	40.1	25	38.3	2	0	0	1308.68	212	222
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	7	7	11	0.01%	11.4%	VILESEVIAEAVGVK	99.7%	71.2	25	65.1	2	0	0	1555.89	482	496
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	9	9	12	0.01%	17.2%	AVSDWLIASVEGR	99.7%	69.9	25	54.4	2	0	0	1402.73	195	207
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	9	9	12	0.01%	17.2%	DPEFVFYDQLK	99.7%	38.6	25	38.6	1	0	0	1400.67	501	511
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	9	9	12	0.01%	17.2%	EGTLQHAFLR	99.7%	47.6	25	30.4	1	0	0	1171.62	330	339
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	9	9	12	0.01%	17.2%	ELETVAAHQFPEVR	99.7%	67.9	25	58.5	2	0	0	1625.83	340	353
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	9	9	12	0.01%	17.2%	IIAEALTR	99.7%	59.5	25	37.8	2	0	0	886.54	417	424
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	9	9	12	0.01%	17.2%	LLDFSYEQYQK	99.7%	59.5	25	59.4	1	0	0	1433.69	89	99
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	9	9	12	0.01%	17.2%	NAVLNTEAR	99.7%	43.1	25	36.2	1	0	0	987.52	65	73
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	9	9	12	0.01%	17.2%	QSAGAVVIILPR	99.7%	63.3	25	46.9	1	0	0	1223.75	103	114
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	9	9	12	0.01%	17.2%	TMAAEVLSR	99.7%	61.4	25	50.3	1	0	0	977.51	74	82
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	13	15	26	0.03%	36.3%	AVPEGFVIPR	98.2%	31.1	25	29.5	1	0	0	1084.62	118	127
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	13	15	26	0.03%	36.3%	DLLNCSFK	99.7%	45.3	25	44.6	1	0	0	996.48	393	400
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	13	15	26	0.03%	36.3%	DVYKEHFQDDVFNEK	99.7%	38.1	25	38.1	0	2	0	1912.87	85	99
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	13	15	26	0.03%	36.3%	GVSSQETAGIGASAHLVNFK	99.7%	53.9	25	53.9	0	2	0	1973.01	197	216
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	13	15	26	0.03%	36.3%	GWNYILEK	99.7%	39.2	25	24.7	2	0	0	1022.53	100	107
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	13	15	26	0.03%	36.3%	KFPVTENSK	98.4%	31.6	25	18.7	2	0	0	1049.56	331	339
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	13	15	26	0.03%	36.3%	MWSIENIAFGSGGGLLQK	99.7%	104	25	98.3	2	0	0	1923.96	372	389
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	13	15	26	0.03%	36.3%	SYSFDEIRK	99.5%	36.8	25	24	2	0	0	1144.56	470	478
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	13	15	26	0.03%	36.3%	TPAGNFVTLEEGKGDLEEYGQDLLHTVFK	99.7%	87.2	25	87.2	0	2	0	3207.58	435	463
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	13	15	26	0.03%	36.3%	VIQGDGVDINTLQEIVEGMK	99.7%	125	25	125	4	0	0	2158.11	350	369
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	13	15	26	0.03%	36.3%	VKYEETVFYGLQYILNK	99.7%	95.4	25	95.4	1	2	0	2107.11	52	68
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	13	15	26	0.03%	36.3%	YEETVFYGLQYILNK	99.7%	94.3	25	90	1	0	0	1879.95	54	68
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	13	15	26	0.03%	36.3%	YLLETSGNLDGLEYK	99.7%	96.8	25	91.3	2	0	0	1714.85	175	189
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	15	23	61	0.06%	38.4%	AAPGAEFAPNKR	99.7%	76.3	25	71.7	4	0	0	1228.64	457	468
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	15	23	61	0.06%	38.4%	AGEVFIHK	99.7%	51.8	25	33	5	0	0	900.49	100	107
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	15	23	61	0.06%	38.4%	AVVIVDDR	99.7%	38.9	25	26.3	3	0	0	886.50	177	184
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	15	23	61	0.06%	38.4%	DKGFGFIR	99.1%	34.3	25	26.6	2	0	0	939.50	108	115
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	15	23	61	0.06%	38.4%	EKLEMEMEAAR	99.7%	49.7	25	39.6	4	0	0	1336.62	294	304
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	15	23	61	0.06%	38.4%	FACHSASLTVR	99.7%	56.7	25	49.4	4	3	0	1248.62	143	153
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	15	23	61	0.06%	38.4%	FAQPGSFEYEYAMR	99.7%	78.3	25	71.4	5	0	0	1711.74	257	270
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	15	23	61	0.06%	38.4%	FGQAATMEGIGAIGGTPPAFNR	99.7%	82.3	25	80.6	3	3	0	2179.06	435	456
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	15	23	61	0.06%	38.4%	GIVEFSGKPAAR	99.7%	52	25	47.2	5	0	0	1231.68	191	202

Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	15	23	61	0.06%	38.4%	LFVGNLPPDITEEEMR	99.7%	46	25	42.5	2	0	0	1859.92	76	91
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	15	23	61	0.06%	38.4%	MEELHNQEVQK	99.7%	62.8	25	27	4	0	0	1384.65	326	336
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	15	23	61	0.06%	38.4%	MGQMAMGGAMGINNR	99.7%	62.9	25	59.9	5	0	0	1602.65	384	398
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	15	23	61	0.06%	38.4%	NLPQYVSNELLEEAFSVFGQVER	99.7%	61.6	25	61.6	1	0	0	2668.33	154	176
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	15	23	61	0.06%	38.4%	RMEELHNQEVQK	99.7%	38.8	25	30.1	0	3	0	1540.75	325	336
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	15	23	61	0.06%	38.4%	VELDNMPLR	99.7%	70.7	25	51	5	0	0	1086.56	127	135
Nuclear autoantigenic sperm protein	NASP	NASP_HUMAN	85.2	99.8%	2	2	3	0.00%	2.5%	EAQLYAAQAHLK	98.3%	31.4	25	26.6	1	0	0	1342.71	536	547
Nuclear autoantigenic sperm protein	NASP	NASP_HUMAN	85.2	99.8%	2	2	3	0.00%	2.5%	SIEVIENR	99.4%	36.3	25	29.9	2	0	0	959.52	610	617
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	5	5	13	0.01%	7.1%	ANNYNEAVYLVR	99.7%	43.7	25	35.4	1	0	0	1425.71	118	129
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	5	5	13	0.01%	7.1%	ATNDEIFSILK	99.7%	52.8	25	44.4	3	0	0	1250.66	512	522
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	5	5	13	0.01%	7.1%	IFANTESYLK	99.7%	44.2	25	30.7	2	0	0	1185.62	195	204
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	5	5	13	0.01%	7.1%	NLFLVIFQR	99.7%	54.6	25	50.5	4	0	0	1149.68	708	716
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	5	5	13	0.01%	7.1%	NYNFGGEFVEAMIR	99.7%	109	25	101	3	0	0	1646.76	97	110
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	8	8	14	0.01%	4.6%	AVQAQGGESQQEAQR	99.7%	91.5	25	91.4	2	0	0	1586.75	1574	1588
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	8	8	14	0.01%	4.6%	DSAQTSVTQAQR	99.7%	77.8	25	62.9	2	0	0	1291.62	632	643
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	8	8	14	0.01%	4.6%	HQVEQLSSSLK	99.7%	42	25	37.7	2	0	0	1255.66	551	561
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	8	8	14	0.01%	4.6%	LADDLSTLQEK	99.7%	64	25	53.4	2	0	0	1232.64	898	908
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	8	8	14	0.01%	4.6%	LEILQQQLQVANEAR	99.7%	77.6	25	73.1	1	0	0	1752.96	617	631
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	8	8	14	0.01%	4.6%	LGHELQQAGLK	99.7%	41.4	25	36	1	0	0	1193.66	1655	1665
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	8	8	14	0.01%	4.6%	LLQAETASNSAR	99.7%	68.7	25	60.1	2	0	0	1260.65	1271	1282
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	8	8	14	0.01%	4.6%	SAPASQASLR	99.7%	46.7	25	35.6	2	0	0	987.52	1840	1849
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	17	0.02%	11.9%	AIYAALSGNLK	99.7%	56.7	25	39.3	2	0	0	1120.64	426	436
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	17	0.02%	11.9%	EADLDVATITK	99.7%	73.2	25	63.2	2	0	0	1175.62	627	637
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	17	0.02%	11.9%	GHLDALTADVK	99.4%	36.3	25	36.3	1	0	0	1139.61	804	814
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	17	0.02%	11.9%	IQSALEEESVFAVTAVNASEK	99.7%	69.8	25	69.8	2	0	0	2222.12	230	250
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	17	0.02%	11.9%	SGFGEISSPVIR	99.7%	41.4	25	36.4	2	0	0	1248.66	4	15
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	17	0.02%	11.9%	TVVEALFQR	99.7%	53.1	25	46.3	2	0	0	1062.59	251	259
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	17	0.02%	11.9%	TYIQLLIR	99.7%	52.8	25	32.7	2	0	0	1019.62	575	582
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	17	0.02%	11.9%	VFEELQATDK	99.7%	75.6	25	64.2	2	0	0	1179.59	492	501
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	17	0.02%	11.9%	VLLQASQDENFGNTTPR	99.7%	114	25	114	2	0	0	1889.94	32	48
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	14	14	28	0.03%	14.3%	AAFLQYCR	99.7%	54.5	25	39.8	2	0	0	1028.50	524	531
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	14	14	28	0.03%	14.3%	DGIQLSEYLPEVK	99.7%	51.7	25	46	2	0	0	1490.77	1111	1123
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	14	14	28	0.03%	14.3%	DLLQADQLGSLK	99.7%	79.1	25	69.8	2	0	0	1300.71	1124	1135
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	14	14	28	0.03%	14.3%	EYEIPSNLTPADVFFR	99.6%	37.3	25	37.3	2	0	0	1897.93	676	691
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	14	14	28	0.03%	14.3%	GLPLGSAVSSPVLFSPVGR	99.7%	73.7	25	73.7	2	0	0	1840.03	36	54
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	14	14	28	0.03%	14.3%	LAALASDFSEDMLQEK	99.7%	68.1	25	52	2	0	0	1767.85	976	991
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	14	14	28	0.03%	14.3%	LLLCEHAEK	99.6%	37.5	25	31.6	2	0	0	1112.58	638	646
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	14	14	28	0.03%	14.3%	LSAAIVLK	99.6%	37.6	25	21.8	2	0	0	814.54	647	654
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	14	14	28	0.03%	14.3%	NETIAQEDKIK	99.7%	47.2	25	26.3	2	0	0	1288.67	510	520
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	14	14	28	0.03%	14.3%	NSGLVSITSR	99.7%	83.4	25	81.1	2	0	0	1033.56	467	476
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	14	14	28	0.03%	14.3%	SNPYFEFVLK	99.7%	50.2	25	44.4	2	0	0	1243.64	1136	1145
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	14	14	28	0.03%	14.3%	SSFYSLTSSNISK	99.7%	97.2	25	83.1	2	0	0	1420.70	284	296
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	14	14	28	0.03%	14.3%	TFGSSLPVK	99.6%	37.8	25	33.7	2	0	0	935.52	83	91
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	14	14	28	0.03%	14.3%	VAYPQADSNLR	99.7%	50.6	25	42.6	2	0	0	1233.62	788	798
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	9	9	21	0.02%	7.3%	DLLILQQLLMR	99.7%	48.9	25	48.9	3	0	0	1355.81	733	743
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	9	9	21	0.02%	7.3%	GFNPAQPLNIR	95.8%	27.8	25	23.2	2	0	0	1226.66	690	700
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	9	9	21	0.02%	7.3%	LLSTYLER	99.7%	60.3	25	44.2	2	0	0	994.56	1291	1298
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	9	9	21	0.02%	7.3%	LLTGWMPTAIR	99.7%	53.7	25	43.5	2	0	0	1258.70	266	276
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	9	9	21	0.02%	7.3%	LPLTPVFEGLAFK	99.7%	53.2	25	36.6	3	0	0	1431.82	1237	1249
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	9	9	21	0.02%	7.3%	MNLTQLYGSNTAGYIVCR	99.7%	45.4	25	45.4	1	0	0	2060.99	701	718
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	9	9	21	0.02%	7.3%	SEDGEIVSTPR	99.7%	67	25	67	3	0	0	1189.57	949	959

Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	9	9	21	0.02%	7.3%	SFVELSGAER	99.7%	53.2	25	40.8	1	0	0	1094.55	44	53
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	9	9	21	0.02%	7.3%	TAPLLLSYYLIK	99.7%	50.8	25	47.4	4	0	0	1394.83	766	777
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	29	0.03%	10.1%	AQIEQVIANCEHK	99.7%	74.4	25	71.2	2	0	0	1539.76	1207	1219
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	29	0.03%	10.1%	ASTEGVAIQGQQGTR	99.7%	88.3	25	80	2	0	0	1502.76	70	84
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	29	0.03%	10.1%	DACDGHEIGR	99.7%	42	25	33.4	2	0	0	1129.47	1484	1493
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	29	0.03%	10.1%	DLPSADSVQYR	99.7%	41.6	25	33.8	2	0	0	1250.60	572	582
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	29	0.03%	10.1%	ENLFMDLLR	99.7%	60.6	25	44.5	2	0	0	1150.59	860	868
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	29	0.03%	10.1%	FQDDNVEGDKVSK	98.0%	30.7	25	8.95	2	0	0	1480.69	1733	1745
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	29	0.03%	10.1%	FTDELMEQGLTYK	99.7%	71.5	25	70.5	1	0	0	1574.74	173	185
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	29	0.03%	10.1%	IQQGALELLR	99.7%	64.7	25	56.7	2	0	0	1140.67	1566	1575
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	29	0.03%	10.1%	KADNVVNIAR	99.7%	49.5	25	35.9	1	0	0	1099.62	892	901
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	29	0.03%	10.1%	KPVSTTNLQDPGVLGCPR	99.4%	26.8	25	26.8	0	1	0	1939.01	1013	1030
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	29	0.03%	10.1%	LPGLQATVR	99.7%	60.6	25	54.2	2	0	0	954.57	322	330
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	29	0.03%	10.1%	LTAPEDVFSK	99.2%	34.6	25	33.2	1	0	0	1106.57	1452	1461
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	29	0.03%	10.1%	LVGDFTHDQSISQK	99.7%	51.5	25	51.5	1	0	0	1574.78	933	946
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	29	0.03%	10.1%	MLALALLDR	99.7%	49.6	25	37.5	2	0	0	1031.59	1494	1502
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	29	0.03%	10.1%	QCLGLLSR	95.1%	27.2	25	8.12	1	0	0	946.51	1714	1721
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	29	0.03%	10.1%	QYIATIHSR	99.7%	41.6	25	32.7	2	0	0	1088.58	305	313
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	29	0.03%	10.1%	SVSGFLHFDTATK	98.7%	32.5	25	29.3	1	0	0	1409.71	1165	1177
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	18	18	29	0.03%	10.1%	YSFIQALVR	99.7%	71.8	25	63.2	2	0	0	1096.61	1993	2001
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	7	7	11	0.01%	12.3%	DAAFATLVSDR	99.7%	85.7	25	79.8	2	0	0	1165.58	495	505
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	7	7	11	0.01%	12.3%	DVDVYSQILR	99.7%	66	25	55.9	2	0	0	1207.63	60	69
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	7	7	11	0.01%	12.3%	FADAASLLLSLMTSR	99.7%	60.6	25	51.5	1	0	0	1595.85	553	567
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	7	7	11	0.01%	12.3%	IMLGDEAALLEQK	99.7%	58.2	25	55.7	1	0	0	1430.76	286	298
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	7	7	11	0.01%	12.3%	IPLNTEQK	95.9%	27.9	25	12.4	1	0	0	942.53	442	449
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	7	7	11	0.01%	12.3%	LGSALSWSIR	99.7%	87.5	25	68.1	2	0	0	1089.61	483	492
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	7	7	11	0.01%	12.3%	QVIFSAEQTYELMR	99.7%	68.2	25	68.2	2	0	0	1714.85	589	602
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	45	0.04%	27.0%	AFDIIER	99.7%	39.1	25	25.5	2	0	0	863.46	710	716
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	45	0.04%	27.0%	AQHQLGEFK	97.5%	29.8	25	29.8	1	0	0	1057.54	341	349
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	45	0.04%	27.0%	AVYCIIGR	99.7%	38.8	25	29.5	2	0	0	951.51	389	396
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	45	0.04%	27.0%	CGDLLAASQVVNR	99.7%	77	25	64.5	2	0	0	1402.71	328	340
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	45	0.04%	27.0%	CVSELVIESR	99.5%	37	25	12.2	1	0	0	1191.60	569	578
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	45	0.04%	27.0%	DNALLSAIEESR	99.7%	92.4	25	87.2	2	0	0	1317.66	107	118
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	45	0.04%	27.0%	EALQYFYFLR	99.7%	51.7	25	43.3	5	0	0	1349.69	546	555
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	45	0.04%	27.0%	ESMLVEWEQVK	99.7%	52.2	25	41.7	1	0	0	1377.67	131	141
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	45	0.04%	27.0%	FTSDTKPIINK	99.7%	61.2	25	45.1	3	0	0	1263.69	601	611
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	45	0.04%	27.0%	GLDISHISQR	99.7%	62.3	25	59.2	2	0	0	1125.60	68	77
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	45	0.04%	27.0%	LLMLYTR	99.7%	44.5	25	42.1	2	0	0	909.52	531	537
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	45	0.04%	27.0%	LLSPVVPQISAPQSNK	99.7%	63.1	25	63.1	2	0	0	1677.95	645	660
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	45	0.04%	27.0%	LTLSQFQK	99.7%	50.9	25	42.1	3	0	0	964.55	435	442
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	45	0.04%	27.0%	LVPLNQESVEER	99.7%	67.2	25	62.4	2	0	0	1412.74	719	730
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	45	0.04%	27.0%	NLQEIQQAGER	99.7%	65.6	25	29.2	2	0	0	1285.65	32	42
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	45	0.04%	27.0%	NMALSIAER	99.7%	53.3	25	40.1	2	0	0	1004.52	665	673
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	45	0.04%	27.0%	QMTDVLLTPATDALK	99.7%	80	25	61.1	3	0	0	1616.86	229	243
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	45	0.04%	27.0%	SSGQSAQLLSHEPGDPPCLR	99.7%	45.3	25	37.2	0	2	0	2136.01	505	524
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	45	0.04%	27.0%	TLITFAGMIPYR	99.7%	73	25	73	5	0	0	1398.75	791	802
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	20	21	45	0.04%	27.0%	VIEDRDSQLR	96.3%	28.3	25	14.9	1	0	0	1230.64	777	786
Nuclear pore complex protein Nup98-Nup96	NUP98	NUP98_HUMAN	197.6	100.0%	5	5	12	0.01%	3.1%	EASGDLPEAQIVK	99.7%	50.6	25	39.7	2	0	0	1356.70	1255	1267
Nuclear pore complex protein Nup98-Nup96	NUP98	NUP98_HUMAN	197.6	100.0%	5	5	12	0.01%	3.1%	LALLLSQFVGSQSVR	99.7%	71.7	25	70	6	0	0	1617.93	1358	1372
Nuclear pore complex protein Nup98-Nup96	NUP98	NUP98_HUMAN	197.6	100.0%	5	5	12	0.01%	3.1%	LYQTPLELK	96.7%	28.8	25	21.5	1	0	0	1104.63	1214	1222
Nuclear pore complex protein Nup98-Nup96	NUP98	NUP98_HUMAN	197.6	100.0%	5	5	12	0.01%	3.1%	SITADPLDYR	97.9%	30.6	25	14.1	1	0	0	1150.57	1514	1523

Nuclear pore complex protein Nup98-Nup96	NUP98	NUP98_HUMAN	197.6	100.0%	5	5	12	0.01%	3.1%	SLVGGLLQSK	99.7%	52	25	47.5	2	0	0	1001.60	1043	1052
Nuclear pore membrane glycoprotein 210	NUP210	PO210_HUMAN	205.1	100.0%	4	4	4	0.00%	2.9%	AVDPTSGQLYGLAR	99.7%	46.5	25	38.9	1	0	0	1447.75	1259	1272
Nuclear pore membrane glycoprotein 210	NUP210	PO210_HUMAN	205.1	100.0%	4	4	4	0.00%	2.9%	GVAIGQTSLTASVTNK	99.7%	45.9	25	45.9	1	0	0	1546.84	1048	1063
Nuclear pore membrane glycoprotein 210	NUP210	PO210_HUMAN	205.1	100.0%	4	4	4	0.00%	2.9%	VFGAPEVLENLEVK	99.6%	38	25	38	1	0	0	1543.84	1711	1724
Nuclear pore membrane glycoprotein 210	NUP210	PO210_HUMAN	205.1	100.0%	4	4	4	0.00%	2.9%	VGQALELPLR	99.7%	45.6	25	45.6	1	0	0	1095.65	549	558
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	7	8	13	0.01%	13.4%	AQFFVEDASTASALK	99.7%	116	25	110	2	0	0	1584.79	159	173
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	7	8	13	0.01%	13.4%	AWLLSMIQSK	99.7%	76.5	25	62.2	2	0	0	1176.64	133	142
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	7	8	13	0.01%	13.4%	GSYFGTENLK	99.7%	42	25	28.8	1	0	0	1115.54	375	384
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	7	8	13	0.01%	13.4%	ILNLSGNELK	99.7%	43.8	25	32.7	2	0	0	1100.63	295	304
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	7	8	13	0.01%	13.4%	LDDMSSIVQK	99.7%	55.1	25	45.5	3	0	0	1151.56	280	289
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	7	8	13	0.01%	13.4%	LNVVAFLNELPK	99.7%	80.2	25	75.5	2	0	0	1356.79	460	471
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	7	8	13	0.01%	13.4%	SDPDLVAQNIDVVLNR	99.2%	34.8	25	34.4	1	0	0	1767.92	234	249
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	8	9	18	0.02%	36.4%	EDVFVHQTAIK	99.7%	50.8	25	45.6	2	0	0	1286.67	82	92
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	8	9	18	0.02%	36.4%	GAEAANVTGPGGVPVQGSK	99.7%	112	25	112	2	0	0	1695.87	119	137
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	8	9	18	0.02%	36.4%	NDTKEDVFVHQTAIK	99.7%	92.2	25	90.3	2	2	0	1744.89	78	92
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	8	9	18	0.02%	36.4%	NEGSESAPEGQAQQR	99.7%	71.6	25	68.4	2	0	0	1587.70	171	185
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	8	9	18	0.02%	36.4%	NGYGFINR	99.7%	53	25	45.4	3	0	0	940.46	70	77
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	8	9	18	0.02%	36.4%	NYQQNYQNSESGEKNEGSESAPEGQAQQR	99.7%	68.1	25	68.1	0	2	0	3257.40	157	185
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	8	9	18	0.02%	36.4%	RPQYSNPPVQGEVMEGADNQGAGEQGRPVR	99.7%	48.8	25	47.3	0	1	0	3239.53	205	234
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	8	9	18	0.02%	36.4%	SVGDGETVEFDVVEGEK	99.7%	99.9	25	91.9	2	0	0	1795.82	102	118
Nucleolar and coiled-body phosphoprotein 1	NOLC1	NOLC1_HUMAN	73.6	99.8%	2	2	3	0.00%	3.4%	DNQLSEVANK	99.7%	43	25	32.7	1	0	0	1117.55	24	33
Nucleolar and coiled-body phosphoprotein 1	NOLC1	NOLC1_HUMAN	73.6	99.8%	2	2	3	0.00%	3.4%	VAGGAAPSKPASAK	98.4%	31.8	25	31.8	2	0	0	1211.67	497	510
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	12	24	0.02%	13.8%	DLIGCLQK	96.4%	28.4	25	12.6	1	0	0	946.50	214	221
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	12	24	0.02%	13.8%	DREIQLEISGK	99.7%	56.2	25	48.7	2	0	0	1287.69	627	637
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	12	24	0.02%	13.8%	LFHEVVQAFR	99.7%	37.1	25	37.1	2	2	0	1245.67	169	178
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	12	24	0.02%	13.8%	LSNVNLQEK	99.7%	46.5	25	36	3	0	0	1044.57	508	516
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	12	24	0.02%	13.8%	MLQPSSSPLWGK	98.4%	31.6	25	17.4	1	0	0	1346.68	234	245
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	12	24	0.02%	13.8%	NSVPVTVAMVER	99.7%	77.1	25	65.4	4	0	0	1301.69	145	156
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	12	24	0.02%	13.8%	QVQQLLGK	99.7%	41	25	28.6	2	0	0	913.55	569	576
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	12	24	0.02%	13.8%	SPDKPGGSPSASR	98.8%	32.8	25	31.2	1	0	0	1242.61	49	61
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	12	24	0.02%	13.8%	VLAFLVLSR	99.7%	67.9	25	67.9	4	0	0	1017.65	311	319
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	12	24	0.02%	13.8%	VQENSAYICSR	99.7%	72.5	25	68.9	2	0	0	1326.61	577	587
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	7	7	12	0.01%	10.9%	DLSSSEPVHAK	95.3%	27.4	25	19.1	1	0	0	1169.58	113	123
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	7	7	12	0.01%	10.9%	FLQGDSFLNEDLNQLIK	99.7%	58	25	58	2	0	0	1994.02	761	777
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	7	7	12	0.01%	10.9%	FYLENLEQMVK	99.7%	54.5	25	33.9	1	0	0	1413.71	307	317
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	7	7	12	0.01%	10.9%	LGQASLGVIK	99.7%	71.5	25	34.5	2	0	0	985.60	394	403
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	7	7	12	0.01%	10.9%	NYEVRPEMLK	99.0%	33.6	25	22	2	0	0	1278.65	413	422
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	7	7	12	0.01%	10.9%	SPLLPAVLEGLAK	99.7%	48.5	25	48.5	2	0	0	1307.79	512	524
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	7	7	12	0.01%	10.9%	YSSEVATESPLDFTK	99.7%	73.6	25	73.6	2	0	0	1673.79	779	793
Nucleolar complex protein 4 homolog	NOC4L	NOC4L_HUMAN	58.5	100.0%	4	4	7	0.01%	8.0%	LFGALLER	99.7%	55.8	25	33.9	2	0	0	918.54	56	63
Nucleolar complex protein 4 homolog	NOC4L	NOC4L_HUMAN	58.5	100.0%	4	4	7	0.01%	8.0%	LGELLGHPSFQVK	99.7%	40.9	25	38.5	2	0	0	1424.79	103	115
Nucleolar complex protein 4 homolog	NOC4L	NOC4L_HUMAN	58.5	100.0%	4	4	7	0.01%	8.0%	REPTVSSFYVK	99.1%	34.2	25	26.1	1	0	0	1312.69	222	232
Nucleolar complex protein 4 homolog	NOC4L	NOC4L_HUMAN	58.5	100.0%	4	4	7	0.01%	8.0%	RLEAVLASR	99.7%	48.8	25	32.8	2	0	0	1014.61	17	25
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	7	7	9	0.01%	11.7%	ADVDVQPYAFTTK	99.7%	71.9	25	71.9	2	0	0	1454.72	191	203
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	7	7	9	0.01%	11.7%	FTQQNYHDR	99.7%	45.5	25	36.5	2	0	0	1208.54	53	61
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	7	7	9	0.01%	11.7%	IAELSEDDQK	99.2%	34.8	25	22.9	1	0	0	1147.55	296	305
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	7	7	9	0.01%	11.7%	LALGQINIAK	99.7%	52.6	25	45.8	1	0	0	1040.65	94	103
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	7	7	9	0.01%	11.7%	LSQILTDFPK	99.7%	62.1	25	53.7	1	0	0	1161.65	62	71
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	7	7	9	0.01%	11.7%	QSLEYLEQVR	99.6%	37.8	25	25.9	1	0	0	1264.65	146	155
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	7	7	9	0.01%	11.7%	TLLLCGYPNVGK	99.7%	64	25	59.9	1	0	0	1334.71	170	181
Nucleolar MIF4G domain-containing protein 1	NOM1	NOM1_HUMAN	96.3	100.0%	4	4	7	0.01%	5.7%	ASGAGSEFQDQTR	98.9%	33.1	25	33.1	1	0	0	1353.60	532	544

Nucleolar MIF4G domain-containing protein 1	NOM1	NOM1_HUMAN	96.3	100.0%	4	4	7	0.01%	5.7%	NAGSGSETQLR	99.7%	46.2	25	31.1	2	0	0	1119.54	584	594
Nucleolar MIF4G domain-containing protein 1	NOM1	NOM1_HUMAN	96.3	100.0%	4	4	7	0.01%	5.7%	TAGPEQGPGLGGR	99.7%	46.7	25	45.2	2	0	0	1196.60	101	113
Nucleolar MIF4G domain-containing protein 1	NOM1	NOM1_HUMAN	96.3	100.0%	4	4	7	0.01%	5.7%	TYNPFYAFLASK	99.5%	36.7	25	36.7	2	0	0	1421.71	702	713
Nucleolar pre-ribosomal-associated protein 1	URB1	NPA1P_HUMAN	254.4	99.9%	2	2	2	0.00%	1.0%	AEAAGLIGWLK	99.7%	44	25	29.8	1	0	0	1128.64	2116	2126
Nucleolar pre-ribosomal-associated protein 1	URB1	NPA1P_HUMAN	254.4	99.9%	2	2	2	0.00%	1.0%	ISTINILLSTLK	99.7%	55.1	25	40.2	1	0	0	1315.82	237	248
Nucleolar protein 16	NOP16	NOP16_HUMAN	21.2	100.0%	3	3	5	0.00%	18.0%	DEKNYYQDTPK	95.8%	27.8	25	27.8	1	0	0	1400.63	136	146
Nucleolar protein 16	NOP16	NOP16_HUMAN	21.2	100.0%	3	3	5	0.00%	18.0%	FGYSVNR	98.4%	31.8	25	22.9	2	0	0	842.42	13	19
Nucleolar protein 16	NOP16	NOP16_HUMAN	21.2	100.0%	3	3	5	0.00%	18.0%	QNLAEMGLAVDPNR	99.7%	65.8	25	65	2	0	0	1543.75	51	64
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	11	16	0.02%	18.0%	IDCFSEVPTSVFGEK	99.6%	38.2	25	32.6	1	0	0	1714.80	382	396
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	11	16	0.02%	18.0%	IINDNATYCR	99.7%	38.6	25	37.9	2	0	0	1239.58	203	212
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	11	16	0.02%	18.0%	LIAHAGSLTNLAK	99.7%	52.9	25	52.9	1	0	0	1308.76	308	320
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	11	16	0.02%	18.0%	LREQVEER	99.4%	36	25	18.7	2	0	0	1058.56	397	404
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	11	16	0.02%	18.0%	MSQVAPSLSALIGEAVGAR	99.7%	43.7	25	43.7	2	0	0	1872.98	289	307
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	11	16	0.02%	18.0%	VLLGVGDPK	99.7%	41.9	25	36.7	2	0	0	897.54	91	99
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	11	16	0.02%	18.0%	VVSLSEYR	99.7%	42.7	25	34.3	2	0	0	952.51	271	278
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	11	16	0.02%	18.0%	YGLIFHSTFIGR	99.7%	49.2	25	49.2	1	2	0	1410.75	348	359
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	11	16	0.02%	18.0%	YPASTVQILGAEK	99.7%	53.7	25	42.3	1	0	0	1376.74	321	333
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	8	10	17	0.02%	19.1%	EAHEPLAVADAK	99.7%	42.3	25	31.9	2	0	0	1250.64	82	93
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	8	10	17	0.02%	19.1%	HAASTVQILGAEK	99.7%	67.3	25	59.5	1	0	0	1324.72	311	323
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	8	10	17	0.02%	19.1%	IISDNLTYCK	99.7%	50.1	25	45.7	2	0	0	1226.61	197	206
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	8	10	17	0.02%	19.1%	LIAHAGSLLNLAK	99.7%	43.1	25	43.1	2	2	0	1320.80	298	310
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	8	10	17	0.02%	19.1%	LSELLPEEVEAEVK	99.7%	51.9	25	49.5	2	0	0	1584.84	222	235
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	8	10	17	0.02%	19.1%	SQMDGLIPGVEPR	99.6%	37.9	25	37.8	2	0	0	1414.70	121	133
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	8	10	17	0.02%	19.1%	TQLYEYLQNR	99.7%	51.5	25	51.5	2	0	0	1327.66	269	278
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	8	10	17	0.02%	19.1%	YGLIYHASLVGQTSPK	99.7%	62.2	25	59.3	0	2	0	1733.92	338	353
Nucleolar protein 9	NOP9	NOP9_HUMAN	69.4	100.0%	3	3	4	0.00%	6.5%	GSSVDGSPLLLFLR	99.7%	49.1	25	36.2	2	0	0	1460.81	311	324
Nucleolar protein 9	NOP9	NOP9_HUMAN	69.4	100.0%	3	3	4	0.00%	6.5%	TLLQVLGGTILESER	99.7%	50.2	25	50.2	1	0	0	1628.92	209	223
Nucleolar protein 9	NOP9	NOP9_HUMAN	69.4	100.0%	3	3	4	0.00%	6.5%	VLDAIWSGAALR	98.2%	31.2	25	11.9	1	0	0	1271.71	564	575
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	AAVIGDVIR	99.7%	65.3	25	50.6	6	0	0	913.55	424	432
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	AEPSEVDMNSPK	96.9%	29	25	18.3	1	0	0	1319.58	62	73
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	APQVLVLAPTR	99.7%	69.7	25	69.7	6	0	0	1164.71	260	270
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	DFSDITKK	99.1%	34.3	25	22.7	2	0	0	953.49	279	286
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	DVESYIHR	99.7%	41.1	25	32.2	2	0	0	1018.50	517	524
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	EAQELSQNSAIK	99.7%	56.5	25	44.1	6	0	0	1317.66	450	461
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	EEYQLVQVEQK	99.7%	71.7	25	65.5	2	0	0	1392.70	545	555
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	EGAFSNFPISEETIK	99.7%	67.2	25	64.2	8	0	0	1668.81	185	199
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	ELKEQLGEEIDSK	99.7%	61.4	25	52.4	2	0	0	1517.77	656	668
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	GAVEALAAALAHISGATSVDQR	99.7%	31.5	25	31.5	0	1	0	2108.11	606	627
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	GLDIPEVDLVIQSSPPK	99.7%	71.1	25	70.1	2	0	0	1806.99	500	516
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	GRAPQVLVLAPTR	99.7%	68.2	25	68.2	2	0	0	1377.83	258	270
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	GVTFLFPIQAK	99.7%	80.6	25	50.5	2	0	0	1220.70	205	215
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	IGVPSATEIIK	99.7%	51.5	25	51.5	5	0	0	1127.67	563	573
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	KAEPSEVDMNSPK	99.7%	51.3	25	51.3	2	1	0	1447.67	61	73
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	LGVCFDVPTASVTEIQEK	99.7%	85.1	25	80.4	3	0	0	1992.99	679	696
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	LLDSVPPTAISHFK	99.7%	32.3	25	23	2	2	0	1524.84	582	595
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	LSVACFYGGTPYGGQFER	99.7%	81.3	25	80.7	2	0	0	2008.92	287	304
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	NEEPSEEEIDAPKPK	99.7%	69.2	25	61.5	1	2	0	1711.80	117	131
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	NGIDILVGTPGR	99.7%	80	25	70.8	2	0	0	1211.67	307	318
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	NGSFGVLVATNVAAR	99.7%	91.8	25	89.4	2	0	0	1475.80	485	499
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	QDAQSLHGDIPQK	99.7%	56.4	25	52.8	3	0	0	1436.71	462	474
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	SDAGLESDTAMK	99.7%	64.3	25	64	5	0	0	1240.54	7	18

Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	STYEQVDLIGK	99.7%	78.2	25	67.3	2	0	0	1252.64	392	402
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	STYEQVDLIGKK	99.7%	64.4	25	43.6	2	0	0	1380.74	392	403
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	TAITVEHLAIK	99.7%	84.3	25	80.3	4	0	0	1195.70	407	417
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	TFSFAIPLIEK	99.7%	71.6	25	69.6	6	0	0	1265.71	237	247
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	TIIFCETKK	94.7%	26.9	25	13.7	1	0	0	1139.61	441	449
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	29	33	91	0.09%	43.3%	WQLSVATEQPELEGPR	99.7%	72.3	25	72.3	2	0	0	1839.92	703	718
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	22	27	150	0.15%	31.4%	ALELTGLK	99.7%	58.6	25	43.4	9	0	0	844.51	363	370
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	22	27	150	0.15%	31.4%	ALVATPGKK	96.7%	28.7	25	28.6	2	0	0	884.56	117	125
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	22	27	150	0.15%	31.4%	EAMEDGEIDGNK	99.7%	56.1	25	56.1	2	0	0	1307.54	628	639
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	22	27	150	0.15%	31.4%	EAMEDGEIDGNKVTLDWAKPK	99.7%	30.2	25	30.2	0	1	0	2362.12	628	648
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	22	27	150	0.15%	31.4%	ESFDGSVR	99.7%	40.5	25	33.2	2	0	0	896.41	590	597
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	22	27	150	0.15%	31.4%	EVFEDAAEIR	99.7%	77.4	25	60.2	6	0	0	1178.57	411	420
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	22	27	150	0.15%	31.4%	FGYVDFESAEDLEK	99.7%	95.8	25	86.7	7	0	0	1648.74	349	362
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	22	27	150	0.15%	31.4%	GFGFVDFNSEEDAK	99.7%	87.8	25	87.8	12	0	0	1561.68	611	624
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	22	27	150	0.15%	31.4%	GIAYIEFK	99.7%	49	25	38	8	0	0	940.51	430	437
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	22	27	150	0.15%	31.4%	GLSEDTTEETLK	99.7%	84.6	25	70.3	5	0	0	1322.63	578	589
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	22	27	150	0.15%	31.4%	GLSEDTTEETLKESFDGSVR	99.7%	106	25	104	3	6	0	2200.03	578	597
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	22	27	150	0.15%	31.4%	GYAFIEFASFEDAK	99.7%	107	25	101	8	0	0	1594.74	524	537
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	22	27	150	0.15%	31.4%	KFGYVDFESAEDLEK	99.7%	85.6	25	79.5	3	0	0	1776.83	348	362
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	22	27	150	0.15%	31.4%	LELQGPR	99.7%	44.2	25	23.1	12	0	0	812.46	555	561
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	22	27	150	0.15%	31.4%	NDLAVVDVR	99.7%	82	25	70.5	12	0	0	1000.54	334	342
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	22	27	150	0.15%	31.4%	SISLYYTGEK	99.7%	62.1	25	52.2	10	0	0	1160.58	458	467
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	22	27	150	0.15%	31.4%	TEADAEKTFEEK	99.7%	73.6	25	61	7	0	0	1397.64	438	449
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	22	27	150	0.15%	31.4%	TGISDVFAK	99.7%	70.2	25	54.2	11	0	0	937.50	325	333
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	22	27	150	0.15%	31.4%	TLVLSNLSYSATEETLQEVFEK	99.7%	125	25	125	4	2	0	2501.27	487	508
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	22	27	150	0.15%	31.4%	VEGTEPTTAFNLFVGNLNFNK	99.7%	99.1	25	99.1	4	2	0	2312.16	298	318
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	22	27	150	0.15%	31.4%	VFGNEIK	98.7%	32.6	25	11.1	4	0	0	806.44	371	377
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	22	27	150	0.15%	31.4%	VTQDELKEVFEDAAEIR	99.7%	73.3	25	73.3	3	5	0	1991.99	404	420
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	8	13	48	0.05%	31.6%	DELHIVEAEAMNYEGSPIK	99.7%	41.7	25	41.4	0	2	0	2161.01	55	73
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	8	13	48	0.05%	31.6%	GPSSVEDIK	99.7%	73.4	25	65.4	8	0	0	931.47	240	248
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	8	13	48	0.05%	31.6%	GPSSVEDIKAK	99.7%	79.9	25	67.3	11	0	0	1130.61	240	250
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	8	13	48	0.05%	31.6%	LLSISGKR	99.7%	50.5	25	37.6	5	0	0	873.55	135	142
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	8	13	48	0.05%	31.6%	MQASIEK	98.7%	32.6	25	8.77	4	0	0	822.40	251	257
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	8	13	48	0.05%	31.6%	MSVQPTVSLGGFEITPPVVLR	99.7%	77.9	25	77.9	6	2	0	2227.22	81	101
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	8	13	48	0.05%	31.6%	MTDQEAIQDLWQWR	99.7%	73.2	25	73.2	4	0	0	1835.84	278	291
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	8	13	48	0.05%	31.6%	VDNDENEHQLSLR	99.7%	71.3	25	69.2	6	0	0	1568.73	33	45
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	4	4	6	0.01%	2.7%	CTLLLILLR	99.7%	47.5	25	47.5	2	0	0	1114.70	1160	1168
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	4	4	6	0.01%	2.7%	LLYPLGGQTNLR	96.8%	28.8	25	24.2	1	0	0	1344.76	501	512
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	4	4	6	0.01%	2.7%	LSMSLMEQLLK	98.5%	31.9	25	30.6	2	0	0	1292.70	1399	1409
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	4	4	6	0.01%	2.7%	VQRPPSAASAAPSSSK	99.7%	38.8	25	35.2	1	0	0	1540.81	1518	1533
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	5	8	17	0.02%	30.9%	GDFCIQVGR	99.7%	60.4	25	52.5	4	0	0	1051.50	106	114
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	5	8	17	0.02%	30.9%	GLVGEIIK	99.6%	38.4	25	27.2	1	0	0	828.52	19	26
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	5	8	17	0.02%	30.9%	GLVGEIIKR	99.7%	41.8	25	36.6	2	0	0	984.62	19	27
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	5	8	17	0.02%	30.9%	TFIAIKPDGVQR	99.7%	41.7	25	41.2	2	2	0	1344.76	7	18
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	5	8	17	0.02%	30.9%	VMLGETNPADSKPGTIR	99.7%	63.2	25	52	4	2	0	1785.92	89	105
Nucleoside diphosphate kinase, mitochondrial	NME4	NDKM_HUMAN	20.7	99.9%	2	2	4	0.00%	11.2%	GDFSVHISR	99.7%	41.8	25	33.5	2	0	0	1017.51	139	147
Nucleoside diphosphate kinase, mitochondrial	NME4	NDKM_HUMAN	20.7	99.9%	2	2	4	0.00%	11.2%	TLVAVKPDGVQR	99.7%	41.8	25	39.2	2	0	0	1282.75	40	51
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	4	5	13	0.01%	17.1%	FYEEVHDLER	99.7%	48	25	43.8	6	0	0	1336.62	95	104
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	4	5	13	0.01%	17.1%	GIPEFWLTVFK	99.7%	63.6	25	61	5	0	0	1336.73	166	176
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	4	5	13	0.01%	17.1%	LDGLVETPTGYIESLPR	99.7%	67.7	25	67.7	2	0	0	1859.98	56	72
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	4	5	13	0.01%	17.1%	NVDLLSDMVQEHDEPILK	99.7%	50.4	25	50.4	1	4	0	2095.04	177	194

Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	4	5	13	0.01%	17.1%	YAVLYQPLFDK	99.3%	35.5	25	35.5	1	0	0	1356.72	106	116
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	8	8	18	0.02%	24.8%	AAATAEEPDPK	99.7%	39.9	25	38.4	2	0	0	1099.53	147	157
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	8	8	18	0.02%	24.8%	FYEEVHDLER	99.7%	48	25	43.8	6	0	0	1336.62	84	93
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	8	8	18	0.02%	24.8%	GIPEFWFTIFR	99.7%	51.4	25	49	1	0	0	1412.74	158	168
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	8	8	18	0.02%	24.8%	LDNVPHTPSSYIETLPK	96.1%	21.2	25	18.3	0	1	0	1910.99	45	61
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	8	8	18	0.02%	24.8%	LTDQVMQNPR	99.7%	42.5	25	41.9	3	0	0	1201.60	27	36
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	8	8	18	0.02%	24.8%	QVPNESFFNFFNPLK	99.7%	62.6	25	60.3	1	0	0	1827.91	283	297
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	8	8	18	0.02%	24.8%	VLAALQER	99.7%	55.4	25	38.2	2	0	0	899.53	37	44
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	8	8	18	0.02%	24.8%	YAALYQPLFDK	99.7%	60	25	56.5	2	0	0	1328.69	95	105
Oligosaccharyltransferase complex subunit OSTC	OSTC	OSTC_HUMAN	16.8	99.8%	2	2	7	0.01%	14.1%	MKLPGYLMG	99.1%	33.9	25	19.3	3	0	0	1025.52	141	149
Oligosaccharyltransferase complex subunit OSTC	OSTC	OSTC_HUMAN	16.8	99.8%	2	2	7	0.01%	14.1%	VPFLVLECPNLK	99.7%	65.9	25	62.5	4	0	0	1428.79	7	18
Origin recognition complex subunit 3	ORC3	ORC3_HUMAN	82.3	99.9%	2	2	2	0.00%	3.9%	ENVVNFIDCLVR	99.7%	42.4	25	39	1	0	0	1477.75	553	564
Origin recognition complex subunit 3	ORC3	ORC3_HUMAN	82.3	99.9%	2	2	2	0.00%	3.9%	TTSSQWQSPPVVVILK	99.7%	39.3	25	29.1	1	0	0	1769.98	205	220
Origin recognition complex subunit 4	ORC4	ORC4_HUMAN	50.4	100.0%	3	3	3	0.00%	7.1%	LDILELLEK	99.7%	49.5	25	25.3	1	0	0	1085.65	196	204
Origin recognition complex subunit 4	ORC4	ORC4_HUMAN	50.4	100.0%	3	3	3	0.00%	7.1%	LLLDNTQIMNALQK	99.7%	60.6	25	60.6	1	0	0	1614.89	404	417
Origin recognition complex subunit 4	ORC4	ORC4_HUMAN	50.4	100.0%	3	3	3	0.00%	7.1%	SVQEVLQK	99.1%	34	25	14.7	1	0	0	930.53	261	268
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	4	4	5	0.00%	9.2%	AMQTVYLR	99.7%	40.1	25	27.4	1	0	0	981.52	264	271
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	4	4	5	0.00%	9.2%	ESQVSILQSLFGER	99.7%	80.4	25	74	2	0	0	1592.83	12	25
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	4	4	5	0.00%	9.2%	LLLEQILNK	99.7%	40.3	25	33.7	1	0	0	1083.68	71	79
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	4	4	5	0.00%	9.2%	TYVTQTLLK	99.4%	35.6	25	34.5	1	0	0	1066.61	44	52
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	27	65	0.06%	49.7%	AFYNNVLGEYEEYITK	99.7%	75.5	25	68.1	3	0	0	1952.93	114	129
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	27	65	0.06%	49.7%	DNGLLAKPTHGDIIR	99.7%	40.7	25	40.7	0	2	0	1619.89	399	413
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	27	65	0.06%	49.7%	EDELRESIEIINK	99.7%	58.1	25	39.3	2	0	0	1587.82	422	434
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	27	65	0.06%	49.7%	FAPPLVIKEDELR	99.7%	64.1	25	61.5	2	2	0	1526.86	414	426
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	27	65	0.06%	49.7%	GIYLWDVEGR	99.7%	62.7	25	49.4	2	0	0	1207.61	67	76
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	27	65	0.06%	49.7%	GIYLWDVEGRK	99.7%	48	25	48	2	0	0	1335.71	67	77
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	27	65	0.06%	49.7%	GKGLLNAIVIK	96.9%	29	25	29	2	0	0	1125.74	373	383
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	27	65	0.06%	49.7%	GLLNAIVIK	99.7%	58.2	25	50.3	5	0	0	940.62	375	383
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	27	65	0.06%	49.7%	HQVLFIADEIQTGLAR	99.7%	109	25	96.4	2	2	0	1810.98	256	271
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	27	65	0.06%	49.7%	IVFAAGNFWGR	99.7%	61.4	25	61.4	6	0	0	1237.65	170	180
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	27	65	0.06%	49.7%	KTVQGPPTSDDIFER	99.7%	46.8	25	46.8	1	2	0	1689.84	32	46
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	27	65	0.06%	49.7%	KWGYTVK	98.0%	30.8	25	18	1	0	0	881.49	155	161
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	27	65	0.06%	49.7%	LPSDVVTAVR	99.7%	77.3	25	64.2	7	0	0	1056.60	363	372
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	27	65	0.06%	49.7%	NELMKLPSDVVTAVR	99.7%	42.5	25	36.4	1	2	0	1687.90	358	372
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	27	65	0.06%	49.7%	SQVDKLTLTSR	99.7%	62.4	25	51	3	2	0	1247.70	103	113
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	27	65	0.06%	49.7%	TVQGPPTSDDIFER	99.7%	78.2	25	75.8	2	0	0	1561.75	33	46
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	27	65	0.06%	49.7%	VAIAALEVLEEENLAENADK	99.7%	82.9	25	80.2	2	0	0	2141.10	332	351
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	27	65	0.06%	49.7%	VLPMNTGVEAGETACK	99.7%	87.9	25	85.2	4	0	0	1676.80	136	151
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	27	65	0.06%	49.7%	WLAVDYENVRPDIVLLGK	99.7%	78.5	25	78.5	2	2	0	2100.15	275	292
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	20	27	65	0.06%	49.7%	YGAHNYHPLPVALER	99.7%	46.2	25	46.2	2	0	0	1736.89	50	64
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	13	25	0.02%	32.2%	CQIIYPR	98.9%	33.4	25	19.9	2	0	0	949.49	341	347
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	13	25	0.02%	32.2%	ELEMIGFIENNVSK	99.7%	114	25	103	2	0	0	1622.81	355	368
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	13	25	0.02%	32.2%	HSNVVILTTSNITEK	99.7%	46.3	25	46.3	0	2	0	1655.90	290	304
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	13	25	0.02%	32.2%	IDVAFVDR	99.7%	64.8	25	40.8	2	0	0	934.50	305	312
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	13	25	0.02%	32.2%	IYLSCLEELMK	99.7%	65.8	25	55.9	2	0	0	1398.70	330	340
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	13	25	0.02%	32.2%	LSLLLNDISR	99.7%	76.7	25	52.7	2	0	0	1143.67	369	378
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	13	25	0.02%	32.2%	NVQSVSIIDTELK	99.7%	53.1	25	49.4	1	0	0	1445.78	69	81
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	13	25	0.02%	32.2%	QQLLTLR	99.7%	44.7	25	25	2	0	0	871.54	348	354
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	13	25	0.02%	32.2%	QYIGPPSAAAIFK	99.7%	47.5	25	42.9	2	0	0	1362.74	317	329
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	13	25	0.02%	32.2%	VVLLHGPPGTGK	99.7%	50.5	25	48.1	2	0	0	1174.69	174	185
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	13	25	0.02%	32.2%	VVNAVLTQIDQIKR	99.7%	70.9	25	70.9	2	2	0	1596.94	276	289

Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	13	25	0.02%	32.2%	YGQLIEINSHSLFSK	99.7%	39.3	25	35.4	0	2	0	1735.90	206	220
Paired amphipathic helix protein Sin3a	SIN3A	SIN3A_HUMAN	145.2	99.8%	2	2	3	0.00%	1.5%	LLFSNTAAQK	99.7%	38.8	25	24.8	2	0	0	1092.60	866	875
Paired amphipathic helix protein Sin3a	SIN3A	SIN3A_HUMAN	145.2	99.8%	2	2	3	0.00%	1.5%	SLLESTYQR	97.1%	29.2	25	20.6	1	0	0	1096.56	1044	1052
Pantothenate kinase 4	PANK4	PANK4_HUMAN	86.0	100.0%	5	5	8	0.01%	8.3%	AVASQPDSVDAAER	99.7%	65.2	25	62.8	1	0	0	1415.68	463	476
Pantothenate kinase 4	PANK4	PANK4_HUMAN	86.0	100.0%	5	5	8	0.01%	8.3%	GLLAGNVFDWGAK	99.7%	43.8	25	40.3	1	0	0	1347.71	560	572
Pantothenate kinase 4	PANK4	PANK4_HUMAN	86.0	100.0%	5	5	8	0.01%	8.3%	LLLVQTGSSSPCLDLSR	99.7%	83.3	25	83.3	2	0	0	1845.97	688	704
Pantothenate kinase 4	PANK4	PANK4_HUMAN	86.0	100.0%	5	5	8	0.01%	8.3%	VIQATGGGAYK	99.7%	38.6	25	21.5	2	0	0	1064.57	119	129
Pantothenate kinase 4	PANK4	PANK4_HUMAN	86.0	100.0%	5	5	8	0.01%	8.3%	VYFGGFFIR	99.5%	37.2	25	31.9	2	0	0	1105.58	319	327
Parafibromin	CDC73	CDC73_HUMAN	60.6	99.8%	2	2	3	0.00%	3.8%	NIFAILQSVK	99.7%	46.5	25	37.2	1	0	0	1132.67	248	257
Parafibromin	CDC73	CDC73_HUMAN	60.6	99.8%	2	2	3	0.00%	3.8%	SAPLEIGLQR	99.7%	50.5	25	49.6	2	0	0	1083.62	111	120
PC4 and SFRS1-interacting protein	PSIP1	PSIP1_HUMAN	60.1	99.8%	2	2	3	0.00%	3.0%	GQEEKQPK	99.3%	35.1	25	25.6	2	0	0	943.48	221	228
PC4 and SFRS1-interacting protein	PSIP1	PSIP1_HUMAN	60.1	99.8%	2	2	3	0.00%	3.0%	IDNLDVNR	97.1%	29.2	25	0	1	0	0	958.50	365	372
PCI domain-containing protein 2	PCID2	PCID2_HUMAN	46.0	100.0%	6	7	12	0.01%	17.5%	AIDSSNLKDDYSTAQR	99.7%	80.8	25	77.7	1	1	0	1783.85	194	209
PCI domain-containing protein 2	PCID2	PCID2_HUMAN	46.0	100.0%	6	7	12	0.01%	17.5%	CGIFLILEK	99.7%	45.5	25	39.7	2	0	0	1092.61	308	316
PCI domain-containing protein 2	PCID2	PCID2_HUMAN	46.0	100.0%	6	7	12	0.01%	17.5%	CQTVIVQSFLR	99.7%	42	25	27.7	2	0	0	1350.72	83	93
PCI domain-containing protein 2	PCID2	PCID2_HUMAN	46.0	100.0%	6	7	12	0.01%	17.5%	DGASCAELVSFK	99.7%	47.9	25	42.6	2	0	0	1283.59	21	32
PCI domain-containing protein 2	PCID2	PCID2_HUMAN	46.0	100.0%	6	7	12	0.01%	17.5%	MILIYLLPVK	99.7%	57.6	25	57.6	2	0	0	1202.76	250	259
PCI domain-containing protein 2	PCID2	PCID2_HUMAN	46.0	100.0%	6	7	12	0.01%	17.5%	VFANNADQQLVK	98.1%	30.9	25	25.5	2	0	0	1346.71	117	128
Peflin	PEF1	PEF1_HUMAN	30.4	99.8%	2	2	3	0.00%	8.5%	EKDTAVQGNIR	99.7%	43.7	25	38.3	1	0	0	1230.64	259	269
Peflin	PEF1	PEF1_HUMAN	30.4	99.8%	2	2	3	0.00%	8.5%	LSFEDFVTMTASR	99.7%	70.4	25	69.7	2	0	0	1503.71	270	282
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	6	6	11	0.01%	9.9%	LFDQPGDPLKR	98.2%	31.2	25	31.1	2	0	0	1285.69	378	388
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	6	6	11	0.01%	9.9%	SAYESQPIR	99.7%	49.4	25	24.7	1	0	0	1050.52	557	565
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	6	6	11	0.01%	9.9%	SELLNELMDSAK	99.7%	70.8	25	70.8	2	0	0	1349.66	608	619
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	6	6	11	0.01%	9.9%	SPALQVLR	99.7%	59.6	25	53.5	2	0	0	883.54	351	358
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	6	6	11	0.01%	9.9%	VEGTDVTGIEEVVIPK	99.7%	107	25	99.6	2	0	0	1684.90	46	61
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	6	6	11	0.01%	9.9%	VMSDFAINQEQK	99.7%	82.5	25	78	2	0	0	1409.67	649	660
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	9	14	27	0.03%	54.5%	ALSTGEKGFGYK	99.7%	38.9	25	28.4	2	0	0	1257.65	38	49
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	9	14	27	0.03%	54.5%	EGMNIVEAMER	99.7%	64.8	25	62.5	2	0	0	1278.58	134	144
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	9	14	27	0.03%	54.5%	IIPGFMCQGGDFTR	99.7%	63.2	25	63.2	4	0	0	1598.75	56	69
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	9	14	27	0.03%	54.5%	KITIADCGQLE	99.7%	66	25	58.3	1	0	0	1247.63	155	165
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	9	14	27	0.03%	54.5%	SIYGEKFEDENFILK	99.7%	74.2	25	68.6	2	0	0	1831.91	77	91
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	9	14	27	0.03%	54.5%	TEWLDGKHVVFGK	99.7%	45.2	25	37.7	1	2	0	1515.80	119	131
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	9	14	27	0.03%	54.5%	VKEGMNIVEAMER	99.7%	82.3	25	81.7	7	2	0	1505.75	132	144
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	9	14	27	0.03%	54.5%	VSFELFADK	99.7%	48.8	25	44	2	0	0	1055.54	20	28
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	9	14	27	0.03%	54.5%	VSFELFADKVPK	99.7%	69.6	25	65.1	2	0	0	1379.76	20	31
Peptidyl-prolyl cis-trans isomerase H	PPIH	PPIH_HUMAN	19.2	99.8%	2	2	4	0.00%	13.0%	IIDGLLVMR	99.7%	43.1	25	35.2	2	0	0	1029.61	144	152
Peptidyl-prolyl cis-trans isomerase H	PPIH	PPIH_HUMAN	19.2	99.8%	2	2	4	0.00%	13.0%	KIENVPTGPNNKPK	99.7%	44.1	25	43.6	0	2	0	1535.85	153	166
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	34	0.03%	52.8%	ADEGISFR	99.7%	53.8	25	40.4	2	0	0	894.43	121	128
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	34	0.03%	52.8%	ATAVMPDGQFK	99.7%	48.1	25	44	4	0	0	1180.57	17	27
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	34	0.03%	52.8%	ATAVMPDGQFKDISLSDYK	99.7%	29.5	25	27.2	1	2	0	2102.01	17	35
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	34	0.03%	52.8%	DISLSDYKGK	99.7%	45.2	25	42.5	2	0	0	1125.58	28	37
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	34	0.03%	52.8%	GLFIIDDKGILR	99.7%	58.4	25	58.4	6	2	0	1359.80	129	140
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	34	0.03%	52.8%	IGHPAPNFK	99.3%	35.4	25	32.6	3	0	0	980.53	8	16
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	34	0.03%	52.8%	LVQAFQFTDK	99.7%	61.4	25	51.5	2	0	0	1196.63	159	168
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	34	0.03%	52.8%	QGGLGPMNIPLVSDPK	99.7%	73	25	66.6	2	0	0	1638.85	94	109
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	34	0.03%	52.8%	QGGLGPMNIPLVSDPKR	99.7%	49.2	25	49.2	1	2	0	1794.95	94	110
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	34	0.03%	52.8%	QITVNDLPVGR	99.7%	71	25	60.2	2	0	0	1211.67	141	151
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	34	0.03%	52.8%	SVDETLR	98.3%	31.4	25	18.4	1	0	0	819.42	152	158
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	12	17	34	0.03%	52.8%	TIAQDYGVLK	99.7%	61.6	25	51	2	0	0	1107.60	111	120
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	6	6	10	0.01%	29.3%	ATAVVDGAFK	99.7%	45	25	41.2	2	0	0	978.53	17	26
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	6	6	10	0.01%	29.3%	ATAVVDGAFKEVK	99.7%	55	25	44.5	2	0	0	1334.73	17	29

Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	6	6	10	0.01%	29.3%	GLFIIDGK	99.4%	35.8	25	35.8	2	0	0	862.50	128	135
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	6	6	10	0.01%	29.3%	IGKPAPDFK	99.7%	39.8	25	32	1	0	0	972.55	8	16
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	6	6	10	0.01%	29.3%	LSEDYGVLK	99.7%	50.4	25	42.2	2	0	0	1023.54	111	119
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	6	6	10	0.01%	29.3%	LSEDYGVLKTDEGIAYR	99.7%	34.1	25	34.1	0	1	0	1928.96	111	127
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	6	6	10	0.01%	29.3%	QITVNDLPVGR	99.7%	71	25	60.2	2	0	0	1211.67	140	150
Peroxiredoxin-4	PRDX4	PRDX4_HUMAN	30.5	100.0%	4	4	6	0.01%	25.1%	DYGVYLEDSGHTLR	99.7%	53	25	53	2	0	0	1624.76	187	200
Peroxiredoxin-4	PRDX4	PRDX4_HUMAN	30.5	100.0%	4	4	6	0.01%	25.1%	GLFIIDDKGILR	99.7%	58.4	25	58.4	6	2	0	1359.80	201	212
Peroxiredoxin-4	PRDX4	PRDX4_HUMAN	30.5	100.0%	4	4	6	0.01%	25.1%	IPLLSDLTHQISK	99.7%	50.2	25	50.2	2	0	0	1464.84	174	186
Peroxiredoxin-4	PRDX4	PRDX4_HUMAN	30.5	100.0%	4	4	6	0.01%	25.1%	LVQAFQYTDK	98.7%	32.5	25	28.7	1	0	0	1212.63	231	240
Peroxiredoxin-4	PRDX4	PRDX4_HUMAN	30.5	100.0%	4	4	6	0.01%	25.1%	SVDETLR	98.3%	31.4	25	18.4	1	0	0	819.42	224	230
Peroxiredoxin-4	PRDX4	PRDX4_HUMAN	30.5	100.0%	4	4	6	0.01%	25.1%	VSVADHSLHLSK	98.2%	31.1	25	29.3	1	0	0	1292.70	67	78
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	12	15	26	0.03%	58.0%	DFTPVCTTELGR	99.7%	67.5	25	65.7	3	0	0	1395.66	42	53
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	12	15	26	0.03%	58.0%	DINAYNCEEPTEK	99.7%	73	25	73	2	0	0	1582.67	85	97
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	12	15	26	0.03%	58.0%	ELAILLGMLDPAEKDEK	99.7%	49.5	25	46.7	2	1	0	1885.00	109	125
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	12	15	26	0.03%	58.0%	FHDFLGDSWGILFSHPR	99.7%	45	25	45	0	1	0	2030.99	25	41
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	12	15	26	0.03%	58.0%	LPFPIIDDR	99.7%	58.8	25	46	2	0	0	1085.60	98	106
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	12	15	26	0.03%	58.0%	LPFPIIDDRNR	99.7%	30.3	25	16.3	1	2	0	1355.74	98	108
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	12	15	26	0.03%	58.0%	LSILYPATTGR	99.7%	62	25	43	2	0	0	1191.67	145	155
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	12	15	26	0.03%	58.0%	NFDEILR	99.7%	46.4	25	22.5	1	0	0	906.47	156	162
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	12	15	26	0.03%	58.0%	PGGLLLGDVAPNFEANTTVGR	99.7%	93.1	25	91.8	2	1	0	2098.09	2	22
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	12	15	26	0.03%	58.0%	VVFVFGPDK	99.7%	50.4	25	45.4	2	0	0	1007.56	133	141
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	12	15	26	0.03%	58.0%	VVFVFGPDKK	99.7%	56.9	25	56.9	2	0	0	1135.65	133	142
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	12	15	26	0.03%	58.0%	VVISLQLTAEK	99.7%	59.4	25	55.3	2	0	0	1200.72	163	173
Peroxisomal 2,4-dienoyl-CoA reductase	DECR2	DECR2_HUMAN	30.8	99.9%	2	2	3	0.00%	7.9%	GQALQVHAGSAK	99.7%	58.6	25	51.3	2	0	0	1166.63	171	182
Peroxisomal 2,4-dienoyl-CoA reductase	DECR2	DECR2_HUMAN	30.8	99.9%	2	2	3	0.00%	7.9%	LGGPQASLSTK	99.3%	35.4	25	28.6	1	0	0	1058.58	220	230
Peroxisomal membrane protein PMP34	SLC25A17	PM34_HUMAN	34.6	100.0%	4	4	7	0.01%	17.3%	AIATTVTYPLQTVQSILR	99.7%	50.9	25	50.9	3	0	0	1975.12	214	231
Peroxisomal membrane protein PMP34	SLC25A17	PM34_HUMAN	34.6	100.0%	4	4	7	0.01%	17.3%	LSSLDVFIIGAVAK	99.7%	68.2	25	68.2	2	0	0	1432.84	200	213
Peroxisomal membrane protein PMP34	SLC25A17	PM34_HUMAN	34.6	100.0%	4	4	7	0.01%	17.3%	LTAATFTVMGLK	94.5%	26.8	25	18.4	1	0	0	1268.69	291	302
Peroxisomal membrane protein PMP34	SLC25A17	PM34_HUMAN	34.6	100.0%	4	4	7	0.01%	17.3%	NILYLLHQR	99.7%	41.5	25	33.7	1	0	0	1169.68	249	257
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	12	0.01%	12.1%	GSATNYITR	99.7%	67	25	57.8	2	0	0	982.50	12	20
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	12	0.01%	12.1%	LAALEEQR	99.7%	54.7	25	42.5	2	0	0	929.51	496	503
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	12	0.01%	12.1%	LAQEEESEAKR	99.7%	51.4	25	46.9	2	0	0	1289.63	524	534
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	12	0.01%	12.1%	LEGQAQAEAK	99.7%	66.2	25	49.7	2	0	0	1044.53	250	259
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	12	0.01%	12.1%	LQLSLADFR	99.7%	51.9	25	45.6	2	0	0	1062.59	27	35
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	12	0.01%	12.1%	SFGGEVSWDK	99.7%	45.4	25	45.4	1	0	0	1111.51	349	358
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	12	0.01%	12.1%	SLCIGATYDVTDSR	99.7%	57.3	25	46.1	1	0	0	1557.72	359	372
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	9	11	19	0.02%	25.6%	DQHDTFFLRDPAEALQLPMDYVQR	99.7%	56.6	25	55.8	0	2	0	2905.39	272	295
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	9	11	19	0.02%	25.6%	FKPAYNPYTEPSMEVFSYHQGLK	99.7%	46.5	25	46.2	0	1	0	2733.30	405	427
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	9	11	19	0.02%	25.6%	LDAEPRPPPTQEAA	98.4%	31.6	25	31.5	1	0	0	1491.74	495	508
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	9	11	19	0.02%	25.6%	LGITQLR	99.7%	59.9	25	40.5	3	0	0	800.50	398	404
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	9	11	19	0.02%	25.6%	LLAEVTLK	95.9%	27.9	25	8.61	1	0	0	886.56	164	171
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	9	11	19	0.02%	25.6%	QETELSPEMISSGSWR	98.4%	31.6	25	31.6	1	0	0	1852.84	188	203
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	9	11	19	0.02%	25.6%	SLQALGEVIEAELR	99.7%	113	25	103	3	1	0	1527.84	43	56
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	9	11	19	0.02%	25.6%	VNLQMVYDSPLCR	99.7%	66.8	25	66.7	2	0	0	1594.77	482	494
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	9	11	19	0.02%	25.6%	VVDSMEDEVQR	99.7%	93	25	93	4	0	0	1306.59	128	138
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	21	0.02%	18.2%	ASEGPAFFPGR	99.7%	99.3	25	84	4	0	0	1135.55	537	547
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	21	0.02%	18.2%	DLLFQALGR	99.7%	63.3	25	42	4	0	0	1032.58	9	17
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	21	0.02%	18.2%	DRYDSFIELQEK	99.7%	53.3	25	35.7	2	0	0	1542.74	134	145
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	21	0.02%	18.2%	LFEISDIVIK	99.7%	53.2	25	36	2	0	0	1176.69	474	483
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	21	0.02%	18.2%	LGVLHPDVITK	99.7%	50	25	45.6	2	0	0	1191.71	561	571
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	21	0.02%	18.2%	LIITEETAK	99.7%	51.9	25	37.7	2	0	0	1017.58	108	116

Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	21	0.02%	18.2%	NIFIECTGTDFTK	99.7%	93	25	93	2	0	0	1545.73	250	262
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	21	0.02%	18.2%	TTLLPGLLK	99.4%	36.2	25	35.2	1	0	0	955.62	452	460
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	21	0.02%	18.2%	TYTIANQFPLNK	99.7%	50.2	25	45	1	0	0	1409.74	384	395
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	21	0.02%	18.2%	YDLLCLEGLVR	99.7%	53.3	25	46.9	1	0	0	1350.71	72	82
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	80	0.08%	36.5%	EKGSSASLVLK	99.7%	41.9	25	29.1	1	0	0	1118.64	294	304
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	80	0.08%	36.5%	FACFER	98.4%	31.6	25	27.9	4	0	0	829.37	235	240
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	80	0.08%	36.5%	FGFYEVFK	99.1%	34.3	25	29.1	4	0	0	1036.51	138	145
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	80	0.08%	36.5%	GIFNGFSVTLK	99.7%	72.4	25	65.3	4	0	0	1182.65	102	112
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	80	0.08%	36.5%	GIFNGFSVTLKEDGVR	99.7%	65	25	58.2	4	0	0	1738.91	102	117
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	80	0.08%	36.5%	GSSASLVLK	95.2%	27.3	25	16.1	1	0	0	861.50	296	304
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	80	0.08%	36.5%	GSSASLVLKR	99.7%	60.3	25	41.6	6	0	0	1017.61	296	305
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	80	0.08%	36.5%	GVAPLWMR	99.7%	49.2	25	39.6	12	0	0	945.50	219	226
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	80	0.08%	36.5%	GWAPTFLGYSMQGLCK	99.7%	77.1	25	77.1	6	0	0	1815.86	122	137
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	80	0.08%	36.5%	IQTQPGYANTLR	99.7%	67.5	25	54.6	10	0	0	1361.72	190	201
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	80	0.08%	36.5%	LPRPPPPEMPESLK	99.7%	37.7	25	35.9	0	2	0	1587.86	342	355
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	80	0.08%	36.5%	MQVDPQK	98.7%	32.5	25	22.7	3	0	0	845.42	93	99
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	80	0.08%	36.5%	MQVDPQKYK	99.6%	38	25	18.3	6	0	0	1152.57	93	101
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	80	0.08%	36.5%	MYKEEGLK	99.7%	44.1	25	30	7	0	0	997.50	207	214
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	80	0.08%	36.5%	TVEALYK	99.7%	44	25	22.5	2	0	0	823.46	241	247
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	80	0.08%	36.5%	VLYSNMLGEENTYLWR	99.7%	95.9	25	95.9	8	0	0	1987.96	146	161
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	6	7	13	0.01%	34.8%	AATALLEAGLAR	99.7%	98.2	25	83	2	0	0	1156.67	2	13
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	6	7	13	0.01%	34.8%	GVITMNEEYETR	99.7%	68.8	25	63.4	4	0	0	1441.66	67	78
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	6	7	13	0.01%	34.8%	IDPTVLLGALPLR	99.7%	65.4	25	65.2	2	0	0	1377.85	41	53
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	6	7	13	0.01%	34.8%	LGVEQLR	99.7%	45.1	25	21.7	2	0	0	814.48	90	96
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	6	7	13	0.01%	34.8%	LSTVDMTGIPTLDNLQK	99.7%	52.7	25	51.6	1	0	0	1845.96	97	113
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	6	7	13	0.01%	34.8%	QLVQDENVR	99.7%	52.7	25	42.2	2	0	0	1100.57	58	66
Phosphatidylinositide phosphatase SAC1	SACM1L	SAC1_HUMAN	67.0	100.0%	4	4	6	0.01%	6.3%	ASFVQTR	98.1%	31	25	14.6	1	0	0	808.43	251	257
Phosphatidylinositide phosphatase SAC1	SACM1L	SAC1_HUMAN	67.0	100.0%	4	4	6	0.01%	6.3%	ELSAQPEVHR	99.7%	48.9	25	36.3	2	0	0	1165.60	175	184
Phosphatidylinositide phosphatase SAC1	SACM1L	SAC1_HUMAN	67.0	100.0%	4	4	6	0.01%	6.3%	QVIINLINQK	99.7%	38.9	25	29	1	0	0	1182.72	302	311
Phosphatidylinositide phosphatase SAC1	SACM1L	SAC1_HUMAN	67.0	100.0%	4	4	6	0.01%	6.3%	TNVIQSLLAR	99.7%	48	25	40.5	2	0	0	1114.66	396	405
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	100.0%	7	7	23	0.02%	12.1%	ALYSTAMESIQGGAAR	99.7%	110	25	108	3	0	0	1625.80	352	367
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	100.0%	7	7	23	0.02%	12.1%	DCLVLESFK	99.7%	42.1	25	17.9	3	0	0	1110.55	305	313
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	100.0%	7	7	23	0.02%	12.1%	FMSNTVFR	95.6%	27.6	25	24.6	1	0	0	1001.49	438	445
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	100.0%	7	7	23	0.02%	12.1%	FYGLYCVQSGGK	99.7%	52.5	25	41.8	4	0	0	1378.65	220	231
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	100.0%	7	7	23	0.02%	12.1%	GVDASGETTYKK	99.7%	44.5	25	37.8	6	0	0	1255.62	62	73
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	100.0%	7	7	23	0.02%	12.1%	LLPGYYMNLNQNPR	99.7%	52.4	25	50.7	1	0	0	1708.85	201	214
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	100.0%	7	7	23	0.02%	12.1%	VVVMNNILPR	99.7%	52.7	25	36.9	5	0	0	1154.67	235	244
Phosphatidylserine synthase 1	PTDSS1	PTSS1_HUMAN	55.5	99.8%	2	2	4	0.00%	5.7%	AVLQFTPASWTYVR	99.7%	66.8	25	64.3	2	0	0	1638.86	263	276
Phosphatidylserine synthase 1	PTDSS1	PTSS1_HUMAN	55.5	99.8%	2	2	4	0.00%	5.7%	ILFIGGITAPTVR	99.7%	59.7	25	54.5	2	0	0	1357.82	324	336
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	4	4	12	0.01%	8.7%	AFVRPSGTEDVVR	99.7%	33.5	25	26.7	0	3	0	1432.75	493	505
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	4	4	12	0.01%	8.7%	MGLLAVLR	99.7%	60.8	25	45.5	4	0	0	872.54	42	49
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	4	4	12	0.01%	8.7%	QAVTPPGLQEAINDLVK	99.7%	56.1	25	56.1	2	0	0	1792.98	470	486
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	4	4	12	0.01%	8.7%	VISTTDAER	98.9%	33.3	25	28.2	3	0	0	991.51	461	469
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	16	18	46	0.05%	30.9%	AIDTTQLFSLPK	99.7%	84.7	25	73.8	2	0	0	1333.74	589	600
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	16	18	46	0.05%	30.9%	DEAGHFLWPGFGENAR	97.8%	22.9	25	22.4	0	2	0	1802.82	538	553
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	16	18	46	0.05%	30.9%	DFWEQEVR	97.7%	30.2	25	15.6	2	0	0	1108.51	601	608
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	16	18	46	0.05%	30.9%	EGALDLSGLR	99.7%	77.7	25	62.2	4	0	0	1030.55	579	588
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	16	18	46	0.05%	30.9%	EIISFGSGYGGNSLLGK	99.7%	111	25	111	4	0	0	1698.87	245	261
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	16	18	46	0.05%	30.9%	EVLAELEALER	99.7%	81	25	67.2	2	0	0	1271.68	625	635
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	16	18	46	0.05%	30.9%	GQLGNWMSPADFQR	99.7%	74.7	25	74.7	3	0	0	1606.74	129	142
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	16	18	46	0.05%	30.9%	GVPLVYEAFNWR	99.7%	51.5	25	47	2	0	0	1450.75	458	469

Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	16	18	46	0.05%	30.9%	LGTPVLQALGDGDFVK	99.7%	89.7	25	84.2	5	0	0	1629.89	194	209
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	16	18	46	0.05%	30.9%	SYLTEQVNQDLPK	99.7%	104	25	94.9	3	0	0	1534.77	612	624
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	16	18	46	0.05%	30.9%	TLIGHVPDQR	99.7%	40.7	25	32	2	0	0	1135.62	235	244
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	16	18	46	0.05%	30.9%	TMYVLPFSMGPVGSPLSR	99.7%	76.6	25	76.6	8	0	0	1970.97	156	173
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	16	18	46	0.05%	30.9%	VLDWICR	99.7%	47	25	35.4	2	0	0	961.49	554	560
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	16	18	46	0.05%	30.9%	VLSGDLGQLPTGIR	99.7%	98.9	25	91.6	2	0	0	1425.81	32	45
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	16	18	46	0.05%	30.9%	YNNCWLAR	98.4%	31.6	25	23.7	2	0	0	1096.50	89	96
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	16	18	46	0.05%	30.9%	YVAAAFPSACGK	97.5%	29.9	25	29.9	1	0	0	1241.60	297	308
Phosphoglycerate kinase 1	PGK1	PGK1_HUMAN	44.6	100.0%	4	4	6	0.01%	14.6%	ALESPERPFLAILGGAK	97.2%	22.2	25	22.2	0	1	0	1769.00	200	216
Phosphoglycerate kinase 1	PGK1	PGK1_HUMAN	44.6	100.0%	4	4	6	0.01%	14.6%	ITLPVDFVTADKFDENAK	99.7%	55.8	25	55.2	1	0	0	2023.04	280	297
Phosphoglycerate kinase 1	PGK1	PGK1_HUMAN	44.6	100.0%	4	4	6	0.01%	14.6%	LGDVYVNDAFGTAHR	99.7%	50.2	25	48.6	0	2	0	1634.79	157	171
Phosphoglycerate kinase 1	PGK1	PGK1_HUMAN	44.6	100.0%	4	4	6	0.01%	14.6%	VLPGVDALSNI	99.7%	45.7	25	45.7	2	0	0	1097.62	407	417
Phosphoglycerate mutase 1	PGAM1	PGAM1_HUMAN	28.8	100.0%	4	4	6	0.01%	17.7%	ALPFWNEEIVPQIK	99.5%	36.8	25	36.8	1	0	0	1683.91	163	176
Phosphoglycerate mutase 1	PGAM1	PGAM1_HUMAN	28.8	100.0%	4	4	6	0.01%	17.7%	AMEAVAAQGK	99.7%	40.3	25	31	2	0	0	975.49	242	251
Phosphoglycerate mutase 1	PGAM1	PGAM1_HUMAN	28.8	100.0%	4	4	6	0.01%	17.7%	HYGGLTGLNK	99.7%	42.6	25	33.4	1	0	0	1059.56	91	100
Phosphoglycerate mutase 1	PGAM1	PGAM1_HUMAN	28.8	100.0%	4	4	6	0.01%	17.7%	VLIAAHGNSLR	99.7%	52.1	25	52.1	2	0	0	1150.67	181	191
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	4	4	8	0.01%	12.8%	AVEMAAQR	99.7%	47.5	25	33.8	2	0	0	875.44	221	228
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	4	4	8	0.01%	12.8%	FIAGTGCLVR	99.7%	47.5	25	32.3	2	0	0	1093.58	211	220
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	4	4	8	0.01%	12.8%	GETAVPGAPEALR	99.7%	59.7	25	48.8	2	0	0	1267.66	42	54
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	4	4	8	0.01%	12.8%	LGFITNNSSK	99.7%	48.3	25	34.4	2	0	0	1080.57	63	72
Phosphoinositide 3-kinase regulatory subunit 4	PIK3R4	PI3R4_HUMAN	153.1	100.0%	2	2	2	0.00%	1.6%	FLELVQLK	99.5%	36.6	25	23.7	1	0	0	989.60	496	503
Phosphoinositide 3-kinase regulatory subunit 4	PIK3R4	PI3R4_HUMAN	153.1	100.0%	2	2	2	0.00%	1.6%	GVIDLAALGITGR	99.7%	40.9	25	37.7	1	0	0	1255.74	817	829
Phosphomannomutase 2	PMM2	PMM2_HUMAN	28.1	100.0%	2	2	3	0.00%	8.9%	IGVVGGSDFEK	99.7%	43.8	25	43.8	2	0	0	1107.57	41	51
Phosphomannomutase 2	PMM2	PMM2_HUMAN	28.1	100.0%	2	2	3	0.00%	8.9%	NGMLNVSPIGR	95.3%	27.4	25	19.7	1	0	0	1173.60	124	134
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	7	12	0.01%	30.9%	AGLTHIITMDLHQK	99.7%	61.4	25	0	0	2	0	1577.85	125	138
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	7	12	0.01%	30.9%	EIQGFFSFPVDNLR	99.2%	34.7	25	26.5	2	0	0	1668.84	139	152
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	7	12	0.01%	30.9%	EKPPITVVGDVGGR	99.7%	38	25	38	2	2	0	1423.79	237	250
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	7	12	0.01%	30.9%	GQDIFIIQTIPR	99.7%	95.1	25	86.8	2	0	0	1400.79	57	68
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	7	12	0.01%	30.9%	IYVMATHGILSAEAPR	99.7%	41	25	29.8	0	2	0	1728.91	280	295
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	7	12	0.01%	30.9%	NIIGVIPYFPYSK	99.7%	63.7	25	63.7	2	0	0	1510.83	91	103
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	7	12	0.01%	30.9%	SVVYQETNGETR	99.7%	54.3	25	43.5	2	0	0	1382.65	37	48
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	7	12	0.01%	30.9%	VFSANSTAACTELAK	99.7%	70.7	25	66.4	2	0	0	1569.76	10	24
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	10	17	31	0.03%	37.1%	AGLTHLITMDLHQK	99.7%	61.4	25	0	0	2	0	1577.85	137	150
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	10	17	31	0.03%	37.1%	EIQGFFNIPVDNLR	99.7%	77.1	25	68.7	2	0	0	1661.86	151	164
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	10	17	31	0.03%	37.1%	EKPPITVVGDVGGR	99.7%	38	25	38	2	2	0	1423.79	250	263
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	10	17	31	0.03%	37.1%	GGLVLFSANSNSSCMELSK	99.7%	68.7	25	68.7	1	0	0	2000.94	18	36
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	10	17	31	0.03%	37.1%	IFVMATHGLLSSDAPR	99.7%	72	25	65.3	4	4	0	1714.89	293	308
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	10	17	31	0.03%	37.1%	LLASMMCK	99.7%	44.6	25	35.6	4	0	0	953.46	129	136
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	10	17	31	0.03%	37.1%	SIIGVIPYFPYSK	99.7%	43	25	36.5	2	0	0	1483.82	103	115
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	10	17	31	0.03%	37.1%	SVAAIHPSLEIPMLIPK	99.7%	30.1	25	30.1	2	1	0	1816.04	233	249
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	10	17	31	0.03%	37.1%	TVDISMILSEAIR	99.7%	68	25	62.6	3	0	0	1463.78	338	350
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	10	17	31	0.03%	37.1%	VQVYQEPNR	98.7%	32.4	25	23	2	0	0	1132.57	49	57
Phosphoribosyltransferase domain-containing protein 1	PRTFDC1	PRDC1_HUMAN	25.7	99.8%	2	2	4	0.00%	10.7%	DIGYSDIMVLCVLK	99.7%	69	25	65.6	2	0	0	1625.83	63	76
Phosphoribosyltransferase domain-containing protein 1	PRTFDC1	PRDC1_HUMAN	25.7	99.8%	2	2	4	0.00%	10.7%	FCADLVEHLK	99.7%	49.4	25	38.8	2	0	0	1231.61	81	90
Phosphorylase b kinase regulatory subunit beta	PHKB	KPBB_HUMAN	124.9	99.8%	2	2	2	0.00%	2.5%	LLADELISPK	99.4%	35.8	25	25.4	1	0	0	1098.64	453	462
Phosphorylase b kinase regulatory subunit beta	PHKB	KPBB_HUMAN	124.9	99.8%	2	2	2	0.00%	2.5%	STLLLYQSPTTGLFPTK	99.7%	46	25	46	1	0	0	1867.02	58	74
Phosphoserine aminotransferase	PSAT1	SERC_HUMAN	40.4	100.0%	6	6	9	0.01%	18.4%	ALELNMLSLK	99.7%	60.2	25	58.7	2	0	0	1131.64	324	333
Phosphoserine aminotransferase	PSAT1	SERC_HUMAN	40.4	100.0%	6	6	9	0.01%	18.4%	ASLYNAVTIEDVQK	99.7%	77.6	25	74	1	0	0	1550.81	343	356
Phosphoserine aminotransferase	PSAT1	SERC_HUMAN	40.4	100.0%	6	6	9	0.01%	18.4%	CADYVVTGAWSAK	99.7%	53.2	25	53.2	1	0	0	1427.66	98	110
Phosphoserine aminotransferase	PSAT1	SERC_HUMAN	40.4	100.0%	6	6	9	0.01%	18.4%	ELLAVPDNYK	94.7%	26.9	25	26.9	1	0	0	1161.62	62	71
Phosphoserine aminotransferase	PSAT1	SERC_HUMAN	40.4	100.0%	6	6	9	0.01%	18.4%	FGTINIVHPK	99.7%	60.8	25	58.3	2	0	0	1125.64	118	127

Phosphoserine aminotransferase	PSAT1	SERC_HUMAN	40.4	100.0%	6	6	9	0.01%	18.4%	QVVNFGPGPAK	99.6%	37.4	25	27.2	2	0	0	1113.61	6	16
Plakophilin-1	PKP1	PKP1_HUMAN	82.9	99.8%	2	2	3	0.00%	3.1%	LDAEVPTR	99.7%	41	25	30.4	1	0	0	900.48	486	493
Plakophilin-1	PKP1	PKP1_HUMAN	82.9	99.8%	2	2	3	0.00%	3.1%	SPNQNVQQAAAGALR	99.7%	81.5	25	72.7	2	0	0	1524.79	298	312
Plasma membrane calcium-transporting ATPase 1	ATP2B1	AT2B1_HUMAN	138.8	100.0%	4	4	4	0.00%	5.2%	EASDIILTDDNFTSIVK	99.7%	60.7	25	60	1	0	0	1880.95	824	840
Plasma membrane calcium-transporting ATPase 1	ATP2B1	AT2B1_HUMAN	138.8	100.0%	4	4	4	0.00%	5.2%	QVVAVTGDGTNDGPALK	99.7%	79.9	25	73.2	1	0	0	1641.84	790	806
Plasma membrane calcium-transporting ATPase 1	ATP2B1	AT2B1_HUMAN	138.8	100.0%	4	4	4	0.00%	5.2%	SSLYEGLEKPESR	99.7%	51.6	25	37.8	1	0	0	1494.74	1164	1176
Plasma membrane calcium-transporting ATPase 1	ATP2B1	AT2B1_HUMAN	138.8	100.0%	4	4	4	0.00%	5.2%	YGDLLPADGILIQGNDLK	97.9%	30.5	25	13.2	1	0	0	1915.02	220	237
Plastin-3	PLS3	PLST_HUMAN	70.8	100.0%	2	2	2	0.00%	3.8%	ANDDIIVNWVNR	99.7%	42.4	25	42.4	1	0	0	1428.72	519	530
Plastin-3	PLS3	PLST_HUMAN	70.8	100.0%	2	2	2	0.00%	3.8%	INNFSADIKDSK	99.7%	61.9	25	54	1	0	0	1351.69	289	300
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	AALAHSEEVTASQVAATK	99.7%	29	25	22.6	0	1	0	1783.92	2744	2761
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	APVPASELLASGVLSR	99.7%	102	25	102	2	0	0	1566.89	3447	3462
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	AQLEPVASPAK	99.3%	35	25	30.9	1	0	0	1110.62	1428	1438
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	AVVQLKPR	95.8%	27.8	25	17.2	1	0	0	910.58	927	934
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	DVAEVDTVRR	95.2%	27.3	25	21	1	0	0	1159.61	3146	3155
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	ELIPTEEALR	98.9%	33.2	25	31	2	0	0	1170.64	3926	3935
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	ESADPLGAWLQDAR	99.7%	64.4	25	59	1	0	0	1528.74	1351	1364
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	FAEQTLR	96.2%	28.2	25	19.3	1	0	0	864.46	2310	2316
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	GLLSAEVAR	99.7%	42.3	25	19	2	0	0	915.53	3850	3858
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	IIITVVEEQEQK	99.7%	60.8	25	55.6	2	0	0	1428.79	3095	3106
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	IISLETYNLLR	99.7%	47	25	39.2	2	0	0	1334.77	3794	3804
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	LAAEQELIR	99.7%	39.8	25	23.8	2	0	0	1042.59	1846	1854
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	LAAIGEATR	99.7%	48	25	28.5	2	0	0	901.51	1976	1984
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	LAQGHTTVDELAR	99.7%	49.9	25	46.6	0	2	0	1410.73	2809	2821
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	LKAEATEAAR	94.7%	26.9	25	15.2	1	0	0	1059.58	2349	2358
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	LKQSAEEQAQAR	99.7%	42.7	25	38.5	2	0	0	1358.70	2254	2265
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	LQAEEVAQQK	99.7%	47.6	25	35.8	2	0	0	1143.60	1783	1792
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	LQEAGILSAEELQR	99.7%	89.9	25	86.9	2	0	0	1556.83	2795	2808
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	LQLEACETR	98.8%	33.1	25	24.9	2	0	0	1119.55	1131	1139
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	LRAETEQGEQQR	99.7%	58.8	25	46.6	2	0	0	1444.71	1855	1866
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	LSVAAQEAAR	99.7%	81.1	25	58.7	2	0	0	1015.55	2420	2429
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	LSVYAALQR	99.7%	71.8	25	61.6	1	0	0	1020.58	2847	2855
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	QLAEEDLAQQR	99.7%	39.6	25	38.6	1	0	0	1300.65	2432	2442
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	QLLEEELAR	98.3%	31.5	25	24.4	1	0	0	1100.59	1867	1875
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	QVEEEILALK	99.7%	47.7	25	21.6	2	0	0	1171.66	2059	2068
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	RQELEAELAK	94.9%	27.1	25	4.51	1	0	0	1186.64	1887	1896
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	SAEAELQSKR	99.3%	35.6	25	30.2	1	0	0	1118.58	1710	1719
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	SDEGQLSPATR	99.0%	33.9	25	24.7	1	0	0	1160.55	714	724
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	SIQEELQQLR	99.7%	67.6	25	44.6	2	0	0	1243.66	1554	1563
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	SKEQAELEAAR	99.7%	50.2	25	43.5	2	0	0	1231.63	2098	2108
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	SLVPAAELLESR	99.7%	41.8	25	35.6	2	0	0	1284.72	3116	3127
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	SQVEEELFSVR	99.7%	79	25	69.4	2	0	0	1322.66	2361	2371
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	TPVEVPVGGFK	95.7%	27.7	25	27.7	1	0	0	1129.63	3374	3384
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	VLADPSDDTK	98.7%	32.4	25	22.6	1	0	0	1060.52	2979	2988
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	VPVDVAYQR	97.0%	29.1	25	22.6	2	0	0	1046.56	3620	3628
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	VPVDVAYR	99.7%	44.8	25	33.7	2	0	0	918.50	2961	2968
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	VQSGSESVIQEYVDLR	99.7%	101	25	95.2	1	0	0	1808.90	1442	1457
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	38	38	59	0.06%	8.8%	VTLVQTLEIQR	99.7%	72.1	25	60.9	1	0	0	1299.76	2565	2575
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	99.8%	2	3	4	0.00%	5.6%	ASVHTLSGHTNAVATVR	99.7%	56	25	55.3	0	2	0	1720.91	321	337
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	99.8%	2	3	4	0.00%	5.6%	GPQNATDSYVHK	99.7%	47.4	25	39.3	1	1	0	1316.62	69	80
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	13	13	25	0.02%	15.2%	AEPVEVVAPR	99.7%	48.5	25	45.1	2	0	0	1066.59	487	496
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	13	13	25	0.02%	15.2%	AMVEYEIDLQK	99.7%	64.4	25	58.5	2	0	0	1338.66	685	695

Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	13	13	25	0.02%	15.2%	ELLIFNK	99.7%	38.5	25	25.5	1	0	0	876.52	263	269
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	13	13	25	0.02%	15.2%	GIYFADMVSK	99.7%	44.6	25	35.6	2	0	0	1130.56	894	903
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	13	13	25	0.02%	15.2%	KGDEVDGVDEVAK	99.7%	68.4	25	59.8	2	0	0	1360.66	209	221
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	13	13	25	0.02%	15.2%	KPPLLNNADSVQAK	99.7%	55.5	25	53.7	2	0	0	1494.83	748	761
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	13	13	25	0.02%	15.2%	LQLLEDDKENR	99.6%	38.1	25	36.3	1	0	0	1372.71	572	582
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	13	13	25	0.02%	15.2%	MAIMVQSPMFDGK	99.4%	35.7	25	35.7	1	0	0	1454.68	35	47
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	13	13	25	0.02%	15.2%	QQVPSGESAILDR	99.7%	73.5	25	65.7	2	0	0	1399.72	270	282
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	13	13	25	0.02%	15.2%	TLGDFAAEYAK	99.7%	61	25	61	2	0	0	1185.58	109	119
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	13	13	25	0.02%	15.2%	TTNFAGILSQGLR	99.7%	90.1	25	76.8	2	0	0	1377.75	866	878
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	13	13	25	0.02%	15.2%	VFSATLGLVDIVK	99.7%	70.2	25	49.8	4	0	0	1361.80	552	564
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	13	13	25	0.02%	15.2%	VVSEDFLQDVSASTK	99.7%	124	25	124	2	0	0	1624.81	453	467
Poly(A) RNA polymerase, mitochondrial	MTPAP	PAPD1_HUMAN	66.2	100.0%	2	2	3	0.00%	3.6%	SPPILPTLDSLK	99.7%	43.6	25	43.6	2	0	0	1280.75	392	403
Poly(A) RNA polymerase, mitochondrial	MTPAP	PAPD1_HUMAN	66.2	100.0%	2	2	3	0.00%	3.6%	TVLIHCPEK	99.3%	35.2	25	29.5	1	0	0	1096.58	77	85
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	9	22	0.02%	26.4%	AITIAGVPQSVTECVK	99.7%	60.6	25	57.4	2	0	0	1672.89	145	160
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	9	22	0.02%	26.4%	ESTGAQVQVAGDMLPNSTER	99.7%	93.7	25	93.7	6	1	0	2105.98	125	144
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	9	22	0.02%	26.4%	IANPVEGSSGR	99.7%	68.8	25	62.2	2	0	0	1086.55	315	325
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	9	22	0.02%	26.4%	IITLTGPTNAIFK	99.7%	69.3	25	63.8	2	0	0	1388.82	58	70
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	9	22	0.02%	26.4%	INISEGNCPER	99.7%	49.1	25	49.1	5	0	0	1288.60	47	57
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	9	22	0.02%	26.4%	LVVPATQCGSLIGK	98.6%	32.4	25	21.8	2	0	0	1442.80	102	115
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	9	22	0.02%	26.4%	QGANINEIR	99.7%	73.8	25	64.7	2	0	0	1014.53	298	306
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	17	0.02%	23.3%	AITIAGIPQSIIECVK	99.7%	41.4	25	39.1	2	0	0	1712.96	145	160
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	17	0.02%	23.3%	ESTGAQVQVAGDMLPNSTER	99.7%	93.7	25	93.7	6	1	0	2105.98	125	144
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	17	0.02%	23.3%	IANPVEGSTDR	99.7%	82.6	25	77	3	0	0	1158.58	323	333
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	17	0.02%	23.3%	IITLAGPTNAIFK	99.7%	62.3	25	62.3	7	0	0	1358.80	58	70
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	17	0.02%	23.3%	INISEGNCPER	99.7%	49.1	25	49.1	5	0	0	1288.60	47	57
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	17	0.02%	23.3%	LVVPASQCGSLIGK	99.7%	69.4	25	69.4	5	0	0	1428.79	102	115
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	19	0.02%	16.8%	GYGFIEYEK	99.7%	50.7	25	50.2	3	0	0	1105.52	268	276
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	19	0.02%	16.8%	KQESTVMVLR	99.7%	50.2	25	43.6	2	0	0	1206.65	458	467
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	19	0.02%	16.8%	KVVAEVYDQER	99.7%	73.9	25	69.5	2	0	0	1335.69	541	551
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	19	0.02%	16.8%	LGLPPLTPEQQEALQK	99.3%	35.5	25	33.5	2	0	0	1761.97	54	69
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	19	0.02%	16.8%	QGEEEDAEIIVK	99.7%	70.2	25	60.4	2	0	0	1359.66	503	514
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	19	0.02%	16.8%	SIDMSWDSVTMK	99.7%	38.6	25	38.6	1	0	0	1415.62	157	168
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	19	0.02%	16.8%	VVAEVYDQER	99.7%	69.9	25	65.3	2	0	0	1207.60	542	551
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	19	0.02%	16.8%	VYVGSIYYELGEDTIR	99.7%	105	25	101	3	0	0	1876.93	131	146
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	19	0.02%	16.8%	YAMEQSIK	99.7%	45.4	25	31.8	2	0	0	969.47	73	80
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	22	30	95	0.09%	34.1%	AKEFTNVYIK	99.6%	28.7	25	17.3	2	2	0	1212.66	187	196
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	22	30	95	0.09%	34.1%	ALDTMNFDVIK	99.7%	92.1	25	83.8	4	0	0	1266.64	68	78
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	22	30	95	0.09%	34.1%	ALYDTFSAFGNILSCK	99.7%	112	25	110	5	0	0	1806.87	114	129
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	22	30	95	0.09%	34.1%	EFSPFGTITSAK	99.7%	60.3	25	51.2	4	0	0	1284.65	313	324
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	22	30	95	0.09%	34.1%	EFTNVYIK	97.3%	29.6	25	8.96	1	0	0	1013.53	189	196
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	22	30	95	0.09%	34.1%	FGPALSVK	99.7%	54.8	25	13.9	6	0	0	818.48	214	221
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	22	30	95	0.09%	34.1%	FSPAGPILSIR	99.7%	58.8	25	55.9	5	0	0	1157.67	31	41
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	22	30	95	0.09%	34.1%	GFGFVCFSSPEEATK	99.7%	81.1	25	81.1	6	0	0	1662.75	334	348
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	22	30	95	0.09%	34.1%	GFGFVSFER	99.7%	54.9	25	41.8	8	0	0	1045.51	232	240
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	22	30	95	0.09%	34.1%	GYGFVHFETQEAAER	99.7%	84	25	80.3	2	4	0	1740.80	139	153
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	22	30	95	0.09%	34.1%	IMWSQR	95.4%	27.5	25	0	1	0	0	820.41	84	89
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	22	30	95	0.09%	34.1%	IVATKPLYVALAQR	99.7%	81.1	25	79.2	4	5	0	1542.94	357	370
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	22	30	95	0.09%	34.1%	KEFSPFGTITSAK	99.7%	80.5	25	80.5	2	2	0	1412.74	312	324
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	22	30	95	0.09%	34.1%	LFPLIQAMHPTLAGK	99.7%	86.3	25	85.1	4	0	0	1652.92	566	580
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	22	30	95	0.09%	34.1%	NLDDGIDDER	99.7%	48.1	25	41.5	2	0	0	1161.50	300	309
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	22	30	95	0.09%	34.1%	NLDDGIDDERLR	99.7%	56.1	25	46.1	2	0	0	1430.69	300	311

Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	22	30	95	0.09%	34.1%	QAHLTNQYMQR	99.7%	54.9	25	51.7	4	2	0	1405.66	375	385
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	22	30	95	0.09%	34.1%	SGVGNIFIK	99.7%	76.1	25	51.5	7	0	0	934.54	96	104
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	22	30	95	0.09%	34.1%	SKVDEAVAVLQAHQAK	99.7%	56.7	25	55.1	0	2	0	1693.92	605	620
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	22	30	95	0.09%	34.1%	SLGYAYVNFQQPADAER	99.7%	120	25	120	4	0	0	1928.91	51	67
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	22	30	95	0.09%	34.1%	VDEAVAVLQAHQAK	99.7%	56.2	25	56.2	1	0	0	1478.80	607	620
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	22	30	95	0.09%	34.1%	YQGVNLYVK	99.7%	43.5	25	43.5	4	0	0	1083.58	291	299
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	4	4	7	0.01%	18.8%	AKEFTNVYIK	99.6%	28.7	25	17.3	2	2	0	1212.66	187	196
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	4	4	7	0.01%	18.8%	ALDTMNFDVIK	99.7%	92.1	25	83.8	4	0	0	1266.64	68	78
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	4	4	7	0.01%	18.8%	ALYDTFSAFGNILSCK	99.7%	112	25	110	5	0	0	1806.87	114	129
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	4	4	7	0.01%	18.8%	EFSPFGSITSAK	99.7%	69.7	25	69.7	2	0	0	1270.63	313	324
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	4	4	7	0.01%	18.8%	EFTNVYIK	97.3%	29.6	25	8.96	1	0	0	1013.53	189	196
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	4	4	7	0.01%	18.8%	FSPAGPVLSIR	99.7%	59.2	25	51.4	2	0	0	1143.65	31	41
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	4	4	7	0.01%	18.8%	GFGFVCFSSPEEATK	99.7%	81.1	25	81.1	6	0	0	1662.75	334	348
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	4	4	7	0.01%	18.8%	IMWSQR	95.4%	27.5	25	0	1	0	0	820.41	84	89
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	4	4	7	0.01%	18.8%	IVGSKPLYVALAQR	99.7%	37	25	13.9	0	1	0	1514.91	357	370
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	4	4	7	0.01%	18.8%	SLGYAYVNFQQPADAER	99.7%	120	25	120	4	0	0	1928.91	51	67
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	4	4	7	0.01%	18.8%	YQGVNLYIK	99.7%	46.1	25	33.7	2	0	0	1097.60	291	299
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	4	4	7	0.01%	13.6%	GVVLFPWQAR	98.4%	31.7	25	24.3	2	0	0	1172.66	92	101
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	4	4	7	0.01%	13.6%	LENLDSDVVQLR	99.7%	66.8	25	62.9	2	0	0	1400.74	269	280
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	4	4	7	0.01%	13.6%	SQTEAVTFLANHDDSR	99.7%	38.6	25	38.6	1	0	0	1790.83	150	165
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	4	4	7	0.01%	13.6%	VLETVGVFEVPK	99.7%	58.7	25	51	2	0	0	1316.75	61	72
Polynucleotide 5'-hydroxyl-kinase NOL9	NOL9	NOL9_HUMAN	79.3	99.8%	2	2	2	0.00%	4.1%	ALLLLPVEQGFTFSGICR	96.9%	28.9	25	28.9	1	0	0	2021.09	124	141
Polynucleotide 5'-hydroxyl-kinase NOL9	NOL9	NOL9_HUMAN	79.3	99.8%	2	2	2	0.00%	4.1%	LIGVYTDFAFR	99.7%	41.3	25	36.7	1	0	0	1301.69	496	506
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	7	8	12	0.01%	20.7%	GQPIYIQFSNHK	98.8%	33.1	25	32.3	1	0	0	1431.74	123	134
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	7	8	12	0.01%	20.7%	HQNVQLPR	99.6%	37.5	25	32.7	2	0	0	991.54	411	418
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	7	8	12	0.01%	20.7%	IAIPGLAGAGNSVLLVSNLNPER	99.7%	101	25	101	2	0	0	2275.28	326	348
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	7	8	12	0.01%	20.7%	IIVENLFYPVTLDVLHQIFSK	99.7%	37.1	25	37.1	0	2	0	2488.39	186	206
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	7	8	12	0.01%	20.7%	KLPIDVTEGEVISLGLPFGK	99.7%	41.7	25	41.7	0	2	0	2112.20	65	84
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	7	8	12	0.01%	20.7%	VTNLLMLK	99.7%	44	25	0	1	0	0	947.56	85	92
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	7	8	12	0.01%	20.7%	VTPQSLFILFGVYGDVQR	99.7%	65.2	25	65.2	1	1	0	2039.10	349	366
Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	FIP1_HUMAN	66.5	100.0%	3	3	3	0.00%	7.9%	MGLEVIPVTSTTNK	99.7%	43.2	25	38.2	1	0	0	1489.79	197	210
Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	FIP1_HUMAN	66.5	100.0%	3	3	3	0.00%	7.9%	TGAPQYGSYGTAPVNLNIK	99.7%	49.3	25	36.9	1	0	0	1950.99	105	123
Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	FIP1_HUMAN	66.5	100.0%	3	3	3	0.00%	7.9%	TGNSEKETALPSTK	99.7%	29.2	25	27.1	0	1	0	1462.74	241	254
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	5	7	16	0.02%	48.0%	GTAYVVYEDIFDAK	99.7%	81.2	25	81.2	3	0	0	1590.77	58	71
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	5	7	16	0.02%	48.0%	ITAEEMYDIFGK	99.7%	99.2	25	93.7	7	0	0	1416.67	30	41
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	5	7	16	0.02%	48.0%	NACDHLSGFNVCNR	99.7%	64	25	64	2	1	0	1663.71	72	85
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	5	7	16	0.02%	48.0%	YGINTDPPK	99.7%	39.1	25	29.7	1	0	0	1004.50	117	125
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	5	7	16	0.02%	48.0%	YLVVLYYNANR	99.7%	83.2	25	74.6	2	0	0	1387.74	86	96
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	11	13	23	0.02%	28.6%	ATVLTTER	99.5%	36.9	25	23.6	2	0	0	890.49	180	187
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	11	13	23	0.02%	28.6%	FIASTGMDR	99.7%	48.8	25	46.2	3	0	0	997.48	489	497
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	11	13	23	0.02%	28.6%	ILTGGADKNVVVFDK	99.7%	82.3	25	80.6	2	2	0	1575.87	237	251
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	11	13	23	0.02%	28.6%	IWSVPNASCVQVVR	99.7%	77.8	25	69.8	2	0	0	1614.84	290	303
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	11	13	23	0.02%	28.6%	KVTSVVFHPSQDLVFSASPDATIR	99.7%	73	25	73	0	2	0	2601.37	266	289
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	11	13	23	0.02%	28.6%	QELSHALYQHDAACR	99.7%	70	25	70	0	2	0	1798.83	101	115
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	11	13	23	0.02%	28.6%	SSEQILATLK	99.7%	73.8	25	54.1	2	0	0	1089.62	252	261
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	11	13	23	0.02%	28.6%	TLQLDNNFEVK	99.7%	61.1	25	50.6	2	0	0	1320.68	429	439
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	11	13	23	0.02%	28.6%	TVPEELVKPEELSK	99.7%	65.1	25	61.7	2	0	0	1597.87	193	206
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	11	13	23	0.02%	28.6%	VTSVVFHPSQDLVFSASPDATIR	95.1%	20.5	25	18.6	0	1	0	2473.27	267	289
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	11	13	23	0.02%	28.6%	YIAENGTDPINNQPLSEEQLIDIK	99.7%	36.8	25	34.4	0	1	0	2714.35	33	56
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	19	21	36	0.04%	21.3%	AAELETDIR	99.7%	63.1	25	25.6	1	0	0	1017.52	379	387
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	19	21	36	0.04%	21.3%	AAQDLCEEALR	99.7%	54	25	40	1	0	0	1275.60	693	703

Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	19	21	36	0.04%	21.3%	AAVELEEPEDAR	99.7%	58.3	25	55.4	2	0	0	1328.63	409	420
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	19	21	36	0.04%	21.3%	AEVLWLMGAK	99.7%	58.3	25	49.9	2	0	0	1117.61	607	616
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	19	21	36	0.04%	21.3%	AGSVATCQAVMR	99.7%	49.7	25	43.2	3	0	0	1266.59	516	527
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	19	21	36	0.04%	21.3%	AIYAYALQVFPSK	99.7%	72.2	25	57.5	2	0	0	1470.80	561	573
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	19	21	36	0.04%	21.3%	AVIGIGIEEEDRK	99.7%	58.3	25	56.6	2	0	0	1428.77	528	540
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	19	21	36	0.04%	21.3%	AVVAQAVR	99.7%	39.4	25	35.2	2	0	0	813.49	360	367
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	19	21	36	0.04%	21.3%	EAYNQGLKK	95.4%	27.4	25	22.3	1	0	0	1050.56	730	738
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	19	21	36	0.04%	21.3%	ESLEALLQR	99.7%	56.8	25	39	2	0	0	1058.58	591	599
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	19	21	36	0.04%	21.3%	HYEDFPK	98.4%	31.8	25	26.8	2	0	0	935.43	704	710
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	19	21	36	0.04%	21.3%	IDSDLGDAWAFFYK	99.7%	87.1	25	87.1	2	0	0	1647.77	870	883
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	19	21	36	0.04%	21.3%	IQQQFSDLKR	99.7%	47.5	25	33.1	2	1	0	1262.69	138	147
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	19	21	36	0.04%	21.3%	LESENDEYER	99.7%	50.9	25	50.9	2	0	0	1283.54	651	660
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	19	21	36	0.04%	21.3%	LETYENAR	99.7%	47.1	25	32.3	2	0	0	995.48	443	450
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	19	21	36	0.04%	21.3%	LEWVQDNIR	99.7%	43.7	25	30.7	2	0	0	1172.61	684	692
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	19	21	36	0.04%	21.3%	LSQVSDSVSGQTVVDPK	99.7%	102	25	84.1	2	0	0	1745.89	255	271
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	19	21	36	0.04%	21.3%	NIANTLMAK	97.4%	29.7	25	23.5	1	0	0	975.53	794	802
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	19	21	36	0.04%	21.3%	WLAGDVPAAR	99.1%	34.1	25	32.5	2	0	0	1055.56	619	628
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	AISAANLHLR	99.7%	49.7	25	39.3	2	0	0	1065.62	2077	2086
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	ANPALYVLR	99.7%	45.7	25	42.9	2	0	0	1016.59	1736	1744
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	AQIAGYLYGVSPPDNPQVK	99.7%	75.3	25	75.1	1	0	0	2017.04	2122	2140
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	DINLQDEDWNEFNDINK	99.7%	59.2	25	59.2	1	0	0	2121.94	285	301
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	DNPNLLFNMCGFECR	98.1%	31	25	31	1	0	0	1886.80	1181	1195
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	EAVVNTQELLDLLVK	99.7%	80	25	75.1	1	0	0	1683.95	1276	1290
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	EQSQLTATQTR	99.7%	64.4	25	46.2	2	0	0	1262.63	2035	2045
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	FGDLILK	99.7%	40.9	25	25.2	1	0	0	805.48	1902	1908
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	FICISDLR	99.7%	49	25	40.8	2	0	0	1023.53	2114	2121
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	FNTGPVGK	99.4%	35.6	25	17.7	2	0	0	819.44	616	623
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	GSELQLPFQACLK	99.7%	60.8	25	50.5	2	0	0	1490.77	1886	1898
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	GTYFPTWEGLFWEK	99.7%	59.2	25	59.2	2	0	0	1760.83	1492	1505
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	IDLTLLNR	99.7%	55	25	37.9	2	0	0	957.57	988	995
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	IIHTSVWAGQK	99.7%	41.3	25	33.8	1	0	0	1239.68	1821	1831
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	ISLIQIFR	99.7%	64	25	53.3	4	0	0	989.61	1571	1578
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	LIVDHNIADYMTAK	99.7%	62.7	25	62.2	3	0	0	1603.82	999	1012
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	LKEAYSVK	96.6%	28.6	25	14.8	1	0	0	937.54	846	853
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	LLILALER	99.7%	59.4	25	59.4	3	0	0	940.62	838	845
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	LTPSGYEWGR	98.3%	31.4	25	31.4	1	0	0	1165.56	2230	2239
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	LVVDSHVQYR	99.7%	64.7	25	61	1	0	0	1215.65	556	565
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	QILMASGSTTFTK	99.7%	74	25	72.4	3	0	0	1384.71	1246	1258
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	QQIAEIEK	99.7%	38.5	25	27.7	2	0	0	958.52	2024	2031
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	QTDVGITHFR	99.7%	51.3	25	42.5	2	0	0	1173.60	1345	1354
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	RALDIPLVK	99.1%	34.3	25	28.6	2	0	0	1024.65	420	428
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	TIIITCSFTPGSCTLTAYK	99.7%	61.4	25	61.4	2	0	0	2134.06	2211	2229
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	TISSYTAFSR	99.7%	42.2	25	38.1	2	0	0	1132.56	1926	1935
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	VPGLPTPIENMILR	97.6%	30.1	25	30.1	1	0	0	1549.88	728	741
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	VQMLLSDR	99.3%	35	25	27.2	1	0	0	961.51	2259	2266
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	VWLFFMR	95.8%	27.8	25	27.8	1	0	0	998.53	636	642
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	YIQPWESEFIDSQR	99.7%	55.2	25	53.2	2	0	0	1797.84	1371	1384
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	31	33	55	0.05%	14.7%	YYVLNALK	96.3%	28.2	25	22.7	2	0	0	983.56	453	460
Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16	DHX38	PRP16_HUMAN	140.5	100.0%	2	2	2	0.00%	1.9%	DATSDLAIIAR	99.5%	36.9	25	21.6	1	0	0	1145.62	435	445
Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16	DHX38	PRP16_HUMAN	140.5	100.0%	2	2	2	0.00%	1.9%	SLNTDVLFGLLR	99.7%	77.3	25	63	1	0	0	1347.76	658	669
Pre-mRNA-splicing factor SPF27	BCAS2	SPF27_HUMAN	26.1	100.0%	2	2	3	0.00%	11.6%	EAAAALVEEETRR	96.5%	28.5	25	21.6	1	0	0	1444.74	30	42

Pre-mRNA-splicing factor SPF27	BCAS2	SPF27_HUMAN	26.1	100.0%	2	2	3	0.00%	11.6%	TIVQLENEIYQIK	99.7%	69.8	25	50.1	2	0	0	1590.87	198	210
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	6	6	10	0.01%	11.2%	AAQEFFQR	99.6%	37.9	25	33	2	0	0	996.49	222	229
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	6	6	10	0.01%	11.2%	GDTGVFLQYTHAR	99.7%	62.4	25	51.2	1	0	0	1464.72	457	469
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	6	6	10	0.01%	11.2%	IVVEFSSPNVAK	99.7%	48	25	37.8	2	0	0	1289.71	127	138
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	6	6	10	0.01%	11.2%	SSQDFQPR	98.1%	31	25	22.3	1	0	0	964.45	512	519
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	6	6	10	0.01%	11.2%	TVLQQVIEDGSK	99.7%	68.9	25	63	2	0	0	1316.71	100	111
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	6	6	10	0.01%	11.2%	VGLAALIIQDFK	99.7%	64.9	25	64.9	2	0	0	1287.77	427	438
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	12	12	22	0.02%	30.2%	APILIATDVASR	99.7%	81.3	25	81.3	8	0	0	1226.71	469	480
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	12	12	22	0.02%	30.2%	APLPDLYPFGTMR	99.7%	41.1	25	41.1	2	0	0	1477.75	69	81
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	12	12	22	0.02%	30.2%	DMVGIAQTGSGK	99.7%	77.7	25	69.1	2	0	0	1179.57	210	221
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	12	12	22	0.02%	30.2%	ELAQQVQQVADDYGK	99.7%	99.9	25	97.6	2	0	0	1691.82	255	269
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	12	12	22	0.02%	30.2%	GDGPICLVLAPTR	99.7%	71.2	25	67.7	2	0	0	1368.73	242	254
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	12	12	22	0.02%	30.2%	GLDVEDVK	99.3%	35.4	25	25.1	2	0	0	874.45	481	488
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	12	12	22	0.02%	30.2%	GTAYTFFTPGNLK	99.7%	72.8	25	71.4	2	0	0	1416.72	516	528
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	12	12	22	0.02%	30.2%	GVEICIATPGR	99.7%	86.1	25	57.6	2	0	0	1172.61	294	304
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	12	12	22	0.02%	30.2%	IVDQIRPDR	95.7%	27.7	25	13.7	2	0	0	1111.62	342	350
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	12	12	22	0.02%	30.2%	LIDFLESGK	99.7%	51	25	45.4	2	0	0	1021.56	305	313
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	12	12	22	0.02%	30.2%	LMQLVDHR	99.7%	39.5	25	29.1	1	0	0	1011.54	548	555
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	12	12	22	0.02%	30.2%	LTPYEVDELRR	97.0%	29.1	25	24.5	1	0	0	1390.73	144	154
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	12	12	22	0.02%	30.2%	MLDMGFEPQIR	99.7%	72.6	25	66.2	5	0	0	1336.64	330	340
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	12	12	22	0.02%	30.2%	NFYVEHPEVAR	99.7%	53.4	25	45.9	2	0	0	1360.66	133	143
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	12	12	22	0.02%	30.2%	QLAEDFLR	99.7%	60.6	25	32.4	2	0	0	991.52	365	372
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	12	12	22	0.02%	30.2%	QTLMWSATWPK	99.7%	71.7	25	63.5	3	0	0	1348.67	351	361
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	12	12	22	0.02%	30.2%	SSQSSSQQFSGIGR	99.7%	107	25	103	2	0	0	1455.68	671	684
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	12	12	22	0.02%	30.2%	STCIYGGAPK	99.7%	62.7	25	49	4	0	0	1053.50	275	284
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	12	12	22	0.02%	30.2%	TIIFVETKR	99.3%	35	25	35	2	0	0	1106.66	421	429
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	12	12	22	0.02%	30.2%	VLEEANQAINPK	99.7%	77.7	25	71.9	2	0	0	1325.71	536	547
Probable ATP-dependent RNA helicase DDX20	DDX20	DDX20_HUMAN	92.2	99.7%	2	2	3	0.00%	2.4%	VLISTDLTSR	99.7%	52.5	25	52.5	2	0	0	1104.63	362	371
Probable ATP-dependent RNA helicase DDX20	DDX20	DDX20_HUMAN	92.2	99.7%	2	2	3	0.00%	2.4%	VVNSYPLAHK	94.6%	26.9	25	23.9	1	0	0	1127.62	282	291
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	99.8%	2	2	3	0.00%	2.8%	AQPLSLEELLAK	99.1%	34.2	25	28.5	1	0	0	1311.75	139	150
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	99.8%	2	2	3	0.00%	2.8%	TLEEKEQEEAR	99.7%	41.4	25	41.1	2	0	0	1361.65	329	339
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	5	5	7	0.01%	6.9%	EAVVQEPER	99.4%	36.2	25	32.2	2	0	0	1056.53	642	650
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	5	5	7	0.01%	6.9%	ELGIQVHSVTR	99.3%	35.4	25	25.6	1	0	0	1238.69	300	310
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	5	5	7	0.01%	6.9%	IFVNSNTDVAPFLR	99.7%	58	25	47.7	2	0	0	1592.84	423	436
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	5	5	7	0.01%	6.9%	SADFNPDFVFTEK	98.9%	33.1	25	32.3	1	0	0	1516.70	79	91
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	5	5	7	0.01%	6.9%	VLVLVPTR	97.4%	29.8	25	26.8	1	0	0	896.59	292	299
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	5	5	7	0.01%	11.5%	GSFADLGLEPR	99.7%	39.5	25	30	1	0	0	1161.59	126	136
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	5	5	7	0.01%	11.5%	LLGQPSLDSLPIPAPR	99.7%	46.4	25	46.4	2	0	0	1673.96	190	205
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	5	5	7	0.01%	11.5%	SPDEPLPVVR	99.3%	35.5	25	33.5	1	0	0	1108.60	28	37
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	5	5	7	0.01%	11.5%	TLSYLLPLLQR	99.7%	43.9	25	43.9	1	0	0	1316.79	179	189
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	5	5	7	0.01%	11.5%	VASPDAVTTITSSK	99.7%	51.2	25	49.4	2	0	0	1376.73	344	357
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	4	4	7	0.01%	7.2%	DVLVATDVASK	99.7%	59.8	25	44.5	2	0	0	1117.61	484	494
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	4	4	7	0.01%	7.2%	LLQEDSSPLLR	95.7%	27.7	25	27.7	1	0	0	1270.70	283	293
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	4	4	7	0.01%	7.2%	MVYLLECLQK	99.7%	49	25	42.3	2	0	0	1296.67	421	430
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	4	4	7	0.01%	7.2%	SALVKPVTINVGR	99.7%	52.4	25	52.4	0	2	0	1353.82	388	400
Probable ATP-dependent RNA helicase DDX46	DDX46	DDX46_HUMAN	117.4	99.8%	2	2	3	0.00%	1.9%	LLVATSVAAR	99.7%	40	25	23.4	1	0	0	1000.61	672	681
Probable ATP-dependent RNA helicase DDX46	DDX46	DDX46_HUMAN	117.4	99.8%	2	2	3	0.00%	1.9%	TIAFLLPMFR	98.2%	31.2	25	31.2	2	0	0	1208.69	423	432
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	6	6	11	0.01%	15.8%	IQIEAIPLALQGR	99.7%	101	25	88.3	2	0	0	1421.85	50	62
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	6	6	11	0.01%	15.8%	LFALVLTPTR	99.7%	53.3	25	45.5	2	0	0	1130.69	93	102
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	6	6	11	0.01%	15.8%	LIDHLENTK	99.1%	34.3	25	34.3	1	0	0	1082.58	153	161
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	6	6	11	0.01%	15.8%	LQQYYIFIPSK	99.7%	60.7	25	44	2	0	0	1399.76	238	248

Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	6	6	11	0.01%	15.8%	SILLATDVASR	99.7%	39.9	25	28.7	1	0	0	1145.65	315	325
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	6	6	11	0.01%	15.8%	TGAFALPILNALLETPQR	99.7%	67	25	67	3	0	0	1925.09	75	92
Probable ATP-dependent RNA helicase DDX49	DDX49	DDX49_HUMAN	54.2	99.8%	2	2	3	0.00%	4.4%	ILIATDVASR	99.7%	66.4	25	46.7	2	0	0	1058.62	301	310
Probable ATP-dependent RNA helicase DDX49	DDX49	DDX49_HUMAN	54.2	99.8%	2	2	3	0.00%	4.4%	TAAFVLPILQK	98.5%	31.8	25	28.3	1	0	0	1200.74	53	63
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	20	22	61	0.06%	34.4%	APILIATDVASR	99.7%	81.3	25	81.3	8	0	0	1226.71	392	403
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	20	22	61	0.06%	34.4%	DGWPAMGIHGDK	96.9%	28.9	25	21.6	2	0	0	1283.58	364	375
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	20	22	61	0.06%	34.4%	ELAQQVQQVAAEYCR	99.7%	86.8	25	86.8	3	0	0	1792.86	178	192
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	20	22	61	0.06%	34.4%	FVINYDYPNSSEDYIHR	98.8%	25	25	24.6	0	1	0	2131.97	412	428
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	20	22	61	0.06%	34.4%	GDGPICLVLAPTR	99.7%	71.2	25	67.7	2	0	0	1368.73	165	177
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	20	22	61	0.06%	34.4%	GLDVEDVK	99.3%	35.4	25	25.1	2	0	0	874.45	404	411
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	20	22	61	0.06%	34.4%	GVEICIATPGR	99.7%	86.1	25	57.6	2	0	0	1172.61	217	227
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	20	22	61	0.06%	34.4%	IVDQIRPDR	95.7%	27.7	25	13.7	2	0	0	1111.62	265	273
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	20	22	61	0.06%	34.4%	LIDFLECGK	99.7%	64.2	25	59.1	4	0	0	1094.56	228	236
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	20	22	61	0.06%	34.4%	LLQLVEDR	99.7%	64.8	25	42.5	4	0	0	985.57	471	478
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	20	22	61	0.06%	34.4%	LMEEIMSEKENK	99.7%	45.4	25	40.2	2	0	0	1480.70	332	343
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	20	22	61	0.06%	34.4%	MLDMGFEPQIR	99.7%	72.6	25	66.2	5	0	0	1336.64	253	263
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	20	22	61	0.06%	34.4%	QTLMWSATWPK	99.7%	71.7	25	63.5	3	0	0	1348.67	274	284
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	20	22	61	0.06%	34.4%	QVSDLISVLR	99.7%	79.6	25	64.2	6	0	0	1129.66	452	461
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	20	22	61	0.06%	34.4%	STCIYGGAPK	99.7%	62.7	25	49	4	0	0	1053.50	198	207
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	20	22	61	0.06%	34.4%	TAQEVETYR	99.7%	56.6	25	45.4	1	0	0	1096.53	69	77
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	20	22	61	0.06%	34.4%	TGTAYTFFTPNNIK	99.7%	91.2	25	77.6	4	0	0	1574.79	438	451
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	20	22	61	0.06%	34.4%	TIVFVETK	99.3%	35.1	25	28.1	2	0	0	936.54	344	351
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	20	22	61	0.06%	34.4%	TIVFVETKR	99.7%	47.7	25	47.7	2	0	0	1092.64	344	352
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	20	22	61	0.06%	34.4%	TTYLVLDEADR	99.7%	78.7	25	70.4	2	0	0	1295.65	242	252
Probable ATP-dependent RNA helicase DDX52	DDX52	DDX52_HUMAN	67.5	100.0%	2	2	3	0.00%	4.7%	GFNPPVLVFVQSIER	99.7%	44.5	25	44.5	2	0	0	1701.93	410	424
Probable ATP-dependent RNA helicase DDX52	DDX52	DDX52_HUMAN	67.5	100.0%	2	2	3	0.00%	4.7%	TLAFSIPILMQLK	99.5%	36.4	25	36.4	1	0	0	1474.87	216	228
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	6	6	8	0.01%	6.0%	DLEDESTPIVK	99.7%	44.9	25	29.5	1	0	0	1245.62	940	950
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	6	6	8	0.01%	6.0%	DSPTLSNSGIR	99.7%	47.7	25	38.5	1	0	0	1146.58	898	908
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	6	6	8	0.01%	6.0%	GFQEDSEIR	99.7%	39.8	25	22.8	2	0	0	1080.50	208	216
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	6	6	8	0.01%	6.0%	LGDASIAAPFTSK	99.7%	41.1	25	36.7	1	0	0	1277.67	951	963
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	6	6	8	0.01%	6.0%	LGSTDLCYIAAVK	99.7%	52.3	25	49.2	1	0	0	1410.73	642	654
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	6	6	8	0.01%	6.0%	SPQENLVPCDVLLLR	99.7%	46.6	25	36.2	2	0	0	1752.93	328	342
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	10	11	17	0.02%	16.0%	DSKPHFTTVFQNSVYK	99.3%	26.5	25	26.5	0	1	0	1897.94	653	668
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	10	11	17	0.02%	16.0%	ICWTVTR	99.6%	38	25	24.3	2	0	0	935.48	133	139
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	10	11	17	0.02%	16.0%	IMDLIGIQTK	99.7%	66.3	25	49.1	3	0	0	1131.64	123	132
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	10	11	17	0.02%	16.0%	IVYSMYSR	99.7%	41.2	25	37.7	2	0	0	1018.50	587	594
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	10	11	17	0.02%	16.0%	LTEYPLVINTLK	99.7%	40.4	25	40.4	2	0	0	1403.81	92	103
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	10	11	17	0.02%	16.0%	TEMGLYYSYFK	99.7%	41.5	25	41.5	1	0	0	1401.64	62	72
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	10	11	17	0.02%	16.0%	TPLCNLLVK	99.7%	52.7	25	48.5	2	0	0	1057.61	644	652
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	10	11	17	0.02%	16.0%	VLEVVKE	99.1%	34.2	25	6.36	1	0	0	815.49	669	675
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	10	11	17	0.02%	16.0%	VMWTPPLR	98.2%	31.2	25	28.5	2	0	0	999.54	205	212
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	10	11	17	0.02%	16.0%	YSTKPDAVFAGAMPTMASVK	99.7%	36.1	25	29.4	0	1	0	2104.01	544	563
Probable cytosolic iron-sulfur protein assembly protein CIAO1	CIAO1	CIAO1_HUMAN	37.8	100.0%	3	4	8	0.01%	10.9%	EPGLLASCSDDGEVAFWK	99.7%	51.2	25	51.2	2	0	0	1980.90	315	332
Probable cytosolic iron-sulfur protein assembly protein CIAO1	CIAO1	CIAO1_HUMAN	37.8	100.0%	3	4	8	0.01%	10.9%	MKDSLVLLGR	99.7%	54.8	25	47.8	4	0	0	1131.66	1	10
Probable cytosolic iron-sulfur protein assembly protein CIAO1	CIAO1	CIAO1_HUMAN	37.8	100.0%	3	4	8	0.01%	10.9%	SVLSEGHQR	99.7%	41.5	25	30	2	0	0	1012.52	54	62
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	4	4	8	0.01%	13.1%	LQVLVGDVLK	99.7%	50.6	25	17.3	2	0	0	1083.68	107	116
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	4	4	8	0.01%	13.1%	LSINTQLLAR	99.7%	72.4	25	57.7	2	0	0	1128.67	175	184
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	4	4	8	0.01%	13.1%	NPLIINSIIDK	99.7%	46.9	25	46.9	2	0	0	1239.73	41	51
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	4	4	8	0.01%	13.1%	SSAVQQLLEK	99.7%	48.1	25	30.4	2	0	0	1102.61	244	253
Probable glutamate--tRNA ligase, mitochondrial	EARS2	SYEM_HUMAN	58.7	100.0%	4	4	7	0.01%	6.3%	GGPAGPYQQSQR	99.7%	53.1	25	46.2	2	0	0	1245.60	109	120
Probable glutamate--tRNA ligase, mitochondrial	EARS2	SYEM_HUMAN	58.7	100.0%	4	4	7	0.01%	6.3%	NMSQEQVAQK	99.7%	58.6	25	58.6	2	0	0	1162.55	169	178

Probable glutamate--tRNA ligase, mitochondrial	EARS2	SYEM_HUMAN	58.7	100.0%	4	4	7	0.01%	6.3%	RGGPAGPYQQSQR	97.8%	30.4	25	27.7	1	0	0	1401.70	108	120
Probable glutamate--tRNA ligase, mitochondrial	EARS2	SYEM_HUMAN	58.7	100.0%	4	4	7	0.01%	6.3%	TALYNYIFAK	99.7%	46.3	25	38.7	2	0	0	1203.64	56	65
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	11	12	18	0.02%	12.6%	EEVDLTGSVPVHAK	99.7%	57.8	25	42.5	2	0	0	1480.76	615	628
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	11	12	18	0.02%	12.6%	FYVLSMFPYPSGK	99.7%	53.7	25	53.7	3	0	0	1535.76	84	96
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	11	12	18	0.02%	12.6%	IPVPQQVAR	97.2%	29.4	25	27.6	1	0	0	1007.60	853	861
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	11	12	18	0.02%	12.6%	LLAQGLIK	97.3%	29.5	25	0	2	0	0	855.57	593	600
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	11	12	18	0.02%	12.6%	LPSGQYLQR	99.7%	70.2	25	58.6	1	0	0	1061.57	606	614
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	11	12	18	0.02%	12.6%	LSSSAEFTGMTR	99.7%	70.7	25	65	1	0	0	1302.60	408	419
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	11	12	18	0.02%	12.6%	QDAFLALTQK	99.0%	33.9	25	30.7	1	0	0	1134.62	420	429
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	11	12	18	0.02%	12.6%	SPQPQLLSNK	99.7%	41.5	25	29.5	1	0	0	1111.61	711	720
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	11	12	18	0.02%	12.6%	TALINFLVQD	99.7%	43.2	25	40.5	2	0	0	1133.62	894	903
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	11	12	18	0.02%	12.6%	TDALPGVLR	99.7%	42.8	25	36.1	2	0	0	941.54	682	690
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	11	12	18	0.02%	12.6%	VYTISDTIAR	99.7%	50.5	25	39.8	2	0	0	1138.61	104	113
Probable proline--tRNA ligase, mitochondrial	PARS2	SYPM_HUMAN	53.3	100.0%	3	3	4	0.00%	7.4%	FGYPFVIIAGK	99.7%	47.2	25	38	2	0	0	1211.68	428	438
Probable proline--tRNA ligase, mitochondrial	PARS2	SYPM_HUMAN	53.3	100.0%	3	3	4	0.00%	7.4%	QLPFLLYQVTR	95.2%	27.3	25	21	1	0	0	1377.79	176	186
Probable proline--tRNA ligase, mitochondrial	PARS2	SYPM_HUMAN	53.3	100.0%	3	3	4	0.00%	7.4%	VIDQEMQAIGGQK	99.7%	46.2	25	34.9	1	0	0	1416.72	104	116
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	6	6	10	0.01%	21.6%	AVDPEDDFQR	99.7%	59	25	58	2	0	0	1191.53	95	104
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	6	6	10	0.01%	21.6%	ESYDDVSSFR	99.7%	62.2	25	62.2	2	0	0	1204.51	263	272
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	6	6	10	0.01%	21.6%	GLLKPGLNVVLEGPK	96.3%	28.3	25	28.3	1	0	0	1533.94	30	44
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	6	6	10	0.01%	21.6%	QAQAAVLAVLPR	99.7%	89	25	88.7	2	0	0	1236.74	111	122
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	6	6	10	0.01%	21.6%	RPTDYFAEMAK	99.7%	42.9	25	32	2	0	0	1328.63	132	142
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	6	6	10	0.01%	21.6%	VQTEVLQK	98.1%	30.9	25	9.04	1	0	0	944.54	180	187
Probable serine carboxypeptidase CPVL	CPVL	CPVL_HUMAN	54.2	100.0%	4	4	6	0.01%	9.5%	FLSLPEVR	99.7%	39	25	38.4	2	0	0	960.55	332	339
Probable serine carboxypeptidase CPVL	CPVL	CPVL_HUMAN	54.2	100.0%	4	4	6	0.01%	9.5%	GGGHILPYDQPLR	95.2%	20.6	25	10.3	0	1	0	1422.75	445	457
Probable serine carboxypeptidase CPVL	CPVL	CPVL_HUMAN	54.2	100.0%	4	4	6	0.01%	9.5%	NNDFYVTGESYAGK	99.7%	102	25	102	2	0	0	1564.69	195	208
Probable serine carboxypeptidase CPVL	CPVL	CPVL_HUMAN	54.2	100.0%	4	4	6	0.01%	9.5%	SDSEVAGYIR	99.7%	76.3	25	67.1	1	0	0	1096.53	424	433
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	4	4	7	0.01%	16.7%	ISNDPSPGYNIEQMAK	99.7%	39.6	25	39.6	1	0	0	1763.83	170	185
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	4	4	7	0.01%	16.7%	PAVLGFEGSANK	99.7%	73.8	25	64.7	2	0	0	1189.62	2	13
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	4	4	7	0.01%	16.7%	TPLSDSGVTQR	99.7%	60.7	25	40.6	2	0	0	1160.59	313	323
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	4	4	7	0.01%	16.7%	TYVTPPGTGFLPGDTAR	99.7%	53.6	25	44.3	2	0	0	1749.88	31	47
Probable tRNA pseudouridine synthase 1	TRUB1	TRUB1_HUMAN	37.3	99.8%	2	2	2	0.00%	6.3%	GPTSAELLNR	99.7%	59	25	52.8	1	0	0	1057.56	79	88
Probable tRNA pseudouridine synthase 1	TRUB1	TRUB1_HUMAN	37.3	99.8%	2	2	2	0.00%	6.3%	GVLVVGIGSGTK	99.7%	43.9	25	36.9	1	0	0	1086.65	126	137
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	8	9	17	0.02%	3.4%	ELLAFQTSEK	99.7%	49.2	25	39.2	2	0	0	1165.61	1436	1445
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	8	9	17	0.02%	3.4%	FSEYLLECPSAEVR	99.7%	74.6	25	68.8	1	0	0	1699.80	2100	2113
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	8	9	17	0.02%	3.4%	GWLVDLLNK	99.7%	47.8	25	0	2	0	0	1057.60	219	227
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	8	9	17	0.02%	3.4%	LYSVVSQLIR	99.7%	85.6	25	65.1	2	0	0	1177.69	2228	2237
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	8	9	17	0.02%	3.4%	SGGLPLVLSMLTR	99.7%	69.6	25	69.6	4	0	0	1343.77	1120	1132
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	8	9	17	0.02%	3.4%	VLGGSFADQK	99.7%	49.1	25	41.2	2	0	0	1021.53	1713	1722
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	8	9	17	0.02%	3.4%	VPGQEETVK	99.3%	35.4	25	29	2	0	0	986.52	321	329
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	8	9	17	0.02%	3.4%	VVIQSNDDIASR	99.7%	65.8	25	62	2	0	0	1316.68	777	788
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	99.8%	2	2	3	0.00%	3.2%	FLLEYIAPMTEK	99.7%	50.8	25	50.8	2	0	0	1454.76	615	626
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	99.8%	2	2	3	0.00%	3.2%	SEDYVDIVQGR	99.7%	52.1	25	44.7	1	0	0	1280.61	431	441
Profilin-1	PFN1	PROF1_HUMAN	15.1	99.8%	2	2	4	0.00%	20.0%	DSLLQDGEFSMDLR	99.7%	65.1	25	65.1	3	0	0	1625.75	76	89
Profilin-1	PFN1	PROF1_HUMAN	15.1	99.8%	2	2	4	0.00%	20.0%	STGGAPTFNVTVTK	99.7%	39.8	25	32	1	0	0	1379.72	92	105
Profilin-2	PFN2	PROF2_HUMAN	15.0	99.8%	2	2	6	0.01%	19.3%	EGFFTNGLTLGAK	99.7%	51.3	25	50.1	2	0	0	1354.70	57	69
Profilin-2	PFN2	PROF2_HUMAN	15.0	99.8%	2	2	6	0.01%	19.3%	SQGGEPTYNVAVGR	99.7%	66.1	25	63.3	4	0	0	1434.70	92	105
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	13	13	23	0.02%	18.4%	DLQQSIAR	99.4%	35.8	25	17	2	0	0	930.50	708	715
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	13	13	23	0.02%	18.4%	DTIVLLCKPEPELNAAIPSANPAK	98.6%	24.3	25	22.3	0	1	0	2561.36	518	541
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	13	13	23	0.02%	18.4%	ELPELLQR	99.7%	49.6	25	44.2	2	0	0	997.57	439	446
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	13	13	23	0.02%	18.4%	FYNELTEILVR	99.7%	75.5	25	67.3	2	0	0	1396.75	676	686
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	13	13	23	0.02%	18.4%	LANQAADYFGDAFK	99.7%	89.5	25	86.3	2	0	0	1530.72	216	229

Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	13	13	23	0.02%	18.4%	NIQVSHQEFSK	99.6%	37.4	25	31.7	2	0	0	1316.66	628	638
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	13	13	23	0.02%	18.4%	SLLSNLDEVKK	99.7%	53.2	25	30.8	2	0	0	1245.71	554	564
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	13	13	23	0.02%	18.4%	STPVNVPISQK	99.7%	43.8	25	34.3	2	0	0	1169.65	340	350
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	13	13	23	0.02%	18.4%	SVIEQGGIQTVDQLIK	99.7%	99.7	25	88.2	2	0	0	1727.95	423	438
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	13	13	23	0.02%	18.4%	TMQGSEVVNVLK	99.7%	74.2	25	61.1	2	0	0	1320.68	542	553
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	13	13	23	0.02%	18.4%	TPSNELYKPLR	95.1%	27.2	25	27.2	1	0	0	1317.72	479	489
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	13	13	23	0.02%	18.4%	TSEVDLAKPLVK	99.7%	48.3	25	40.5	2	0	0	1299.75	12	23
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	13	13	23	0.02%	18.4%	YYDQICSIEPK	98.7%	32.7	25	28.6	1	0	0	1415.65	71	81
Programmed cell death protein 10	PDCD10	PDC10_HUMAN	24.7	100.0%	3	3	6	0.01%	14.2%	AINVFVSANR	99.7%	57.2	25	39.4	2	0	0	1090.60	187	196
Programmed cell death protein 10	PDCD10	PDC10_HUMAN	24.7	100.0%	3	3	6	0.01%	14.2%	IPDEINDR	99.7%	65.2	25	60.4	2	0	0	971.48	117	124
Programmed cell death protein 10	PDCD10	PDC10_HUMAN	24.7	100.0%	3	3	6	0.01%	14.2%	SVEVNFTESLLR	99.7%	90.5	25	83.6	2	0	0	1393.73	71	82
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	80	0.08%	60.3%	AAELIANSLATAGDGLIELR	99.7%	106	25	83.9	7	4	0	1998.09	220	239
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	80	0.08%	60.3%	AAIISAEGDSK	99.7%	69.7	25	62.6	4	0	0	1061.55	209	219
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	80	0.08%	60.3%	AATFGLILDDVSLTHLTFGK	99.7%	59.2	25	59.2	2	0	0	2119.14	158	177
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	80	0.08%	60.3%	AVIFDRFR	98.9%	33.4	25	29.3	1	0	0	1023.57	36	43
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	80	0.08%	60.3%	DLQNVNITLR	99.7%	74.7	25	56.4	6	0	0	1185.66	84	93
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	80	0.08%	60.3%	EFTEAVEAK	99.7%	48.3	25	36.7	4	0	0	1023.50	178	186
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	80	0.08%	60.3%	FDAGELITQR	99.7%	84.1	25	70.6	13	0	0	1149.59	134	143
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	80	0.08%	60.3%	IFTSIGEDYDER	99.7%	93.6	25	86.5	5	0	0	1444.66	106	117
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	80	0.08%	60.3%	ILFRPVASQLPR	99.7%	58.3	25	48.8	4	8	0	1396.84	94	105
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	80	0.08%	60.3%	KAAIISAEGDSK	99.7%	61	25	57.1	4	0	0	1189.64	208	219
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	80	0.08%	60.3%	KLEAAEDIAYQLSR	99.7%	131	25	124	4	0	0	1606.84	240	253
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	80	0.08%	60.3%	LEAAEDIAYQLSR	99.7%	92.5	25	88.2	2	0	0	1478.75	241	253
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	80	0.08%	60.3%	NITYLPAGQSVLLQLPQ	99.7%	69.1	25	69	4	0	0	1855.03	256	272
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	80	0.08%	60.3%	QVSDDLTER	99.7%	61.3	25	56.3	4	0	0	1062.51	149	157
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	80	0.08%	60.3%	VLPSITTEILK	99.7%	67.2	25	58.2	4	0	0	1213.74	118	128
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	21	65	0.06%	51.2%	AQFLVEK	99.3%	35.4	25	16.3	2	0	0	834.47	210	216
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	21	65	0.06%	51.2%	AQVSLLIR	99.3%	35.1	25	23	7	0	0	899.57	158	165
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	21	65	0.06%	51.2%	DLAGRLPAGPR	99.6%	38.4	25	35.9	2	0	0	1122.64	7	17
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	21	65	0.06%	51.2%	DLQMVNISLR	99.7%	69.2	25	52.1	7	0	0	1188.64	98	107
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	21	65	0.06%	51.2%	ESVFTVEGGHR	99.7%	89.3	25	73.9	2	2	0	1217.59	38	48
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	21	65	0.06%	51.2%	EYTAAVEAK	99.7%	65	25	59	3	0	0	981.49	192	200
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	21	65	0.06%	51.2%	FNASQLITQR	99.7%	81	25	69.8	9	0	0	1177.63	148	157
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	21	65	0.06%	51.2%	IGGVQQDTILAEGLHFR	99.7%	52	25	52	0	2	0	1853.99	55	71
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	21	65	0.06%	51.2%	IVQAEGEAEAAK	99.7%	93.2	25	80.7	2	0	0	1215.62	225	236
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	21	65	0.06%	51.2%	LGLDYEER	99.7%	56.9	25	43.6	6	0	0	994.48	124	131
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	21	65	0.06%	51.2%	LLLGAGAVAYGVR	99.7%	95.8	25	81.7	8	0	0	1259.75	25	37
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	21	65	0.06%	51.2%	MLGEALSK	99.6%	38.3	25	20.3	2	0	0	848.45	237	244
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	21	65	0.06%	51.2%	QKIVQAEGEAEAAK	99.7%	45.8	25	42.7	2	0	0	1471.78	223	236
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	21	65	0.06%	51.2%	VLPSIVNEVLK	99.0%	33.8	25	21.4	2	0	0	1210.74	132	142
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	21	65	0.06%	51.2%	VLSRPNAQELPSMYQR	99.7%	63.7	25	60.6	3	4	0	1888.97	108	123
Prolactin-inducible protein	PIP	PIP_HUMAN	16.6	100.0%	3	3	18	0.02%	25.3%	ELGICPDDAAVIPIK	98.4%	31.8	25	24.7	1	0	0	1610.85	119	133
Prolactin-inducible protein	PIP	PIP_HUMAN	16.6	100.0%	3	3	18	0.02%	25.3%	FYTIEILKVE	99.7%	52.2	25	45.6	5	0	0	1254.70	137	146
Prolactin-inducible protein	PIP	PIP_HUMAN	16.6	100.0%	3	3	18	0.02%	25.3%	TVQIAAVVDVIR	99.7%	68.8	25	64.1	12	0	0	1283.77	107	118
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	10	12	33	0.03%	44.4%	AEDNADTLALVFEAPNQEK	99.7%	85.9	25	85.9	2	0	0	2074.99	92	110
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	10	12	33	0.03%	44.4%	ATPLSSTVTLSMSADVPLVVEYK	99.7%	41.3	25	39.2	1	0	0	2424.26	218	240
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	10	12	33	0.03%	44.4%	DLSHIGDAVVISCAK	99.7%	76.2	25	76.2	4	1	0	1584.81	150	164
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	10	12	33	0.03%	44.4%	FSASGELGNGNIK	99.7%	97.6	25	87.4	4	0	0	1293.64	169	181
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	10	12	33	0.03%	44.4%	IADMGHLK	99.7%	48.9	25	39.4	3	0	0	884.47	241	248
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	10	12	33	0.03%	44.4%	LVQGSILK	97.5%	29.8	25	11.1	2	0	0	857.55	6	13
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	10	12	33	0.03%	44.4%	LVQGSILKK	99.7%	53.6	25	19.9	3	0	0	985.64	6	14

Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	10	12	33	0.03%	44.4%	MPSGEFAR	99.7%	42.4	25	31.4	6	0	0	910.41	139	146
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	10	12	33	0.03%	44.4%	NLAMGVNLTSMSK	99.7%	92.8	25	78.4	4	0	0	1381.68	65	77
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	10	12	33	0.03%	44.4%	SEGFDTYR	99.3%	35.4	25	28.8	3	0	0	974.42	54	61
Proline-, glutamic acid- and leucine-rich protein 1	PELP1	PELP1_HUMAN	119.7	99.8%	2	2	3	0.00%	2.7%	GSPDGSLQTGKPSAPK	97.8%	30.3	25	22.1	1	0	0	1526.78	480	495
Proline-, glutamic acid- and leucine-rich protein 1	PELP1	PELP1_HUMAN	119.7	99.8%	2	2	3	0.00%	2.7%	LLLLESVSGLLQPR	99.7%	42.2	25	42.2	2	0	0	1537.93	35	48
Prolyl 3-hydroxylase 1	LEPRE1	P3H1_HUMAN	83.4	100.0%	5	5	8	0.01%	7.5%	DLSFFGGLLR	99.7%	64.4	25	51.1	2	0	0	1124.61	106	115
Prolyl 3-hydroxylase 1	LEPRE1	P3H1_HUMAN	83.4	100.0%	5	5	8	0.01%	7.5%	EPPAYTFR	98.1%	31	25	20	1	0	0	980.48	603	610
Prolyl 3-hydroxylase 1	LEPRE1	P3H1_HUMAN	83.4	100.0%	5	5	8	0.01%	7.5%	LTNVAATSGDGYR	99.7%	82.3	25	82.3	2	0	0	1324.65	489	501
Prolyl 3-hydroxylase 1	LEPRE1	P3H1_HUMAN	83.4	100.0%	5	5	8	0.01%	7.5%	SPYNYLQVAYFK	98.8%	32.7	25	21.7	1	0	0	1492.75	144	155
Prolyl 3-hydroxylase 1	LEPRE1	P3H1_HUMAN	83.4	100.0%	5	5	8	0.01%	7.5%	TVTAEVQPQCGR	99.7%	76.2	25	69.4	2	0	0	1345.65	636	647
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	7	7	10	0.01%	16.1%	DPEGFVGHPVNAFK	99.7%	53.6	25	42.6	1	0	0	1513.74	73	86
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	7	7	10	0.01%	16.1%	GVAVDYLPER	99.7%	49.8	25	49.8	2	0	0	1118.58	277	286
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	7	7	10	0.01%	16.1%	HAACPVLVGNK	99.7%	43.5	25	32.8	2	0	0	1165.61	500	510
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	7	7	10	0.01%	16.1%	LLELDPEHQR	98.5%	31.9	25	31.9	1	0	0	1249.65	231	240
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	7	7	10	0.01%	16.1%	LQDTYNLDTDTISK	99.7%	105	25	104	2	0	0	1626.79	137	150
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	7	7	10	0.01%	16.1%	QYFPNDEDQVGAAK	99.7%	42.8	25	36.6	1	0	0	1581.72	119	132
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	7	7	10	0.01%	16.1%	SFLTAEDCFELGK	99.6%	37.9	25	37.9	1	0	0	1516.70	160	172
Proteasomal ATPase-associated factor 1	PAAF1	PAAF1_HUMAN	42.2	100.0%	3	3	8	0.01%	9.4%	GGILDTAIVDR	99.7%	74.3	25	63.4	2	0	0	1129.62	177	187
Proteasomal ATPase-associated factor 1	PAAF1	PAAF1_HUMAN	42.2	100.0%	3	3	8	0.01%	9.4%	GGLGVSSSTDGTMK	99.7%	68.9	25	68.9	2	0	0	1296.61	104	117
Proteasomal ATPase-associated factor 1	PAAF1	PAAF1_HUMAN	42.2	100.0%	3	3	8	0.01%	9.4%	SGAPVLSLLSVR	99.7%	64	25	56.6	4	0	0	1198.72	321	332
Proteasomal ubiquitin receptor ADRM1	ADRM1	ADRM1_HUMAN	42.2	99.8%	2	2	5	0.00%	5.9%	SQSAAVTPSSTTSSTR	99.7%	68.1	25	68.1	4	0	0	1567.76	211	226
Proteasomal ubiquitin receptor ADRM1	ADRM1	ADRM1_HUMAN	42.2	99.8%	2	2	5	0.00%	5.9%	VPQCPSGR	98.3%	31.4	25	28.4	1	0	0	900.44	85	92
Proteasome activator complex subunit 3	PSME3	PSME3_HUMAN	29.5	100.0%	5	5	8	0.01%	26.4%	ITSEAEDLVANFFPK	99.7%	48.5	25	43	2	0	0	1680.85	22	36
Proteasome activator complex subunit 3	PSME3	PSME3_HUMAN	29.5	100.0%	5	5	8	0.01%	26.4%	NQYVTLHDMILK	99.7%	38.4	25	38.2	1	0	0	1490.77	226	237
Proteasome activator complex subunit 3	PSME3	PSME3_HUMAN	29.5	100.0%	5	5	8	0.01%	26.4%	SNQQLVDIIEK	99.7%	64.3	25	56.4	1	0	0	1286.70	111	121
Proteasome activator complex subunit 3	PSME3	PSME3_HUMAN	29.5	100.0%	5	5	8	0.01%	26.4%	TVESEAASYLDQISR	99.7%	82.9	25	60.9	2	0	0	1668.81	167	181
Proteasome activator complex subunit 3	PSME3	PSME3_HUMAN	29.5	100.0%	5	5	8	0.01%	26.4%	TVTEIDEKEYISLR	99.7%	69.2	25	67.2	2	0	0	1695.88	205	218
Proteasome assembly chaperone 3	PSMG3	PSMG3_HUMAN	13.1	99.8%	2	2	3	0.00%	18.0%	AVLLAVAVK	98.1%	31	25	22.2	1	0	0	883.60	94	102
Proteasome assembly chaperone 3	PSMG3	PSMG3_HUMAN	13.1	99.8%	2	2	3	0.00%	18.0%	NLVAFVSQEAGNR	99.7%	80.7	25	74.1	2	0	0	1404.72	81	93
Proteasome subunit alpha type-1	PSMA1	PSA1_HUMAN	29.6	100.0%	2	2	2	0.00%	8.4%	LLCNFMR	99.1%	34	25	31.3	1	0	0	953.47	83	89
Proteasome subunit alpha type-1	PSMA1	PSA1_HUMAN	29.6	100.0%	2	2	2	0.00%	8.4%	NQYDNDVTVWSPQGR	99.7%	68.3	25	65.9	1	0	0	1778.81	4	18
Proteasome subunit alpha type-3	PSMA3	PSA3_HUMAN	28.4	100.0%	3	3	8	0.01%	11.8%	CKDGVVFGVEK	99.5%	36.9	25	12.5	2	0	0	1237.62	42	52
Proteasome subunit alpha type-3	PSMA3	PSA3_HUMAN	28.4	100.0%	3	3	8	0.01%	11.8%	SNFGYNIPLK	99.6%	38.1	25	29.8	4	0	0	1152.60	101	110
Proteasome subunit alpha type-3	PSMA3	PSA3_HUMAN	28.4	100.0%	3	3	8	0.01%	11.8%	VFQVEYAMK	99.7%	48.2	25	42.8	2	0	0	1114.56	21	29
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	10	14	35	0.03%	38.7%	ATCIGNNSAAAVSMLK	99.7%	105	25	83.9	8	0	0	1607.79	161	176
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	10	14	35	0.03%	38.7%	EVEQLIK	94.9%	27.1	25	13.3	1	0	0	858.49	232	238
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	10	14	35	0.03%	38.7%	LLDEVFFSEK	99.7%	61.1	25	56.4	4	0	0	1226.63	55	64
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	10	14	35	0.03%	38.7%	LNEDMACSVAGITSDANVLTNELR	99.7%	61.8	25	61.8	2	0	0	2609.22	68	91
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	10	14	35	0.03%	38.7%	LSAEKVEIATLTR	99.7%	86.9	25	73.4	4	2	0	1430.82	206	218
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	10	14	35	0.03%	38.7%	QAYTQFGGK	99.7%	40.4	25	31.4	3	0	0	999.49	119	127
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	10	14	35	0.03%	38.7%	QDYKEGEMTLK	99.7%	45.9	25	36.8	3	0	0	1341.64	177	187
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	10	14	35	0.03%	38.7%	QKEVEQLIK	99.7%	38.6	25	23.8	2	0	0	1114.65	230	238
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	10	14	35	0.03%	38.7%	TTIFSPEGR	99.6%	37.3	25	24	3	0	0	1007.52	9	17
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	10	14	35	0.03%	38.7%	VEIATLTR	99.7%	55.3	25	31.4	3	0	0	902.53	211	218
Proteasome subunit alpha type-5	PSMA5	PSA5_HUMAN	26.4	100.0%	4	6	11	0.01%	22.4%	AIGSASEGAQSSLQEVYHK	99.7%	91.8	25	91.8	2	2	0	1961.96	169	187
Proteasome subunit alpha type-5	PSMA5	PSA5_HUMAN	26.4	100.0%	4	6	11	0.01%	22.4%	GVNTFSPEGR	99.7%	44.9	25	32.9	1	0	0	1063.52	11	20
Proteasome subunit alpha type-5	PSMA5	PSA5_HUMAN	26.4	100.0%	4	6	11	0.01%	22.4%	ITSPLMEPSSIEK	99.7%	59.8	25	55.7	4	0	0	1447.74	54	66
Proteasome subunit alpha type-5	PSMA5	PSA5_HUMAN	26.4	100.0%	4	6	11	0.01%	22.4%	LFQVEYAIEAIK	99.7%	76.5	25	64.6	2	0	0	1423.78	21	32
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	5	6	11	0.01%	25.0%	ALLEVVQSGGK	99.7%	77.1	25	68.9	2	0	0	1100.63	194	204
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	5	6	11	0.01%	25.0%	LTVEDPVTVEYITR	99.7%	89.7	25	83.4	2	0	0	1634.86	96	109
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	5	6	11	0.01%	25.0%	LYQTDPSGTYHAWK	99.3%	35.3	25	29.4	1	0	0	1666.79	144	157

Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	5	6	11	0.01%	25.0%	NIELAVMR	99.7%	41.3	25	32.4	4	0	0	945.52	205	212
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	5	6	11	0.01%	25.0%	NYTDEAIETDDLTIK	99.7%	145	25	145	2	0	0	1740.82	175	189
Proteasome subunit beta type-5	PSMB5	PSB5_HUMAN	28.5	100.0%	4	4	5	0.00%	13.7%	ATAGAYIASQTVK	99.7%	61.4	25	59.2	2	0	0	1280.68	79	91
Proteasome subunit beta type-5	PSMB5	PSB5_HUMAN	28.5	100.0%	4	4	5	0.00%	13.7%	ATAGAYIASQTVKK	99.7%	53.9	25	51.8	1	0	0	1408.78	79	92
Proteasome subunit beta type-5	PSMB5	PSB5_HUMAN	28.5	100.0%	4	4	5	0.00%	13.7%	HGVIVAADSR	96.8%	28.8	25	23.6	1	0	0	1024.55	69	78
Proteasome subunit beta type-5	PSMB5	PSB5_HUMAN	28.5	100.0%	4	4	5	0.00%	13.7%	VSSDNVADLHEK	99.7%	54.3	25	43.6	1	0	0	1313.63	246	257
Proteasome subunit beta type-6	PSMB6	PSB6_HUMAN	25.4	100.0%	2	2	4	0.00%	8.8%	LAAIAESGVER	99.7%	69.9	25	57.5	2	0	0	1115.61	210	220
Proteasome subunit beta type-6	PSMB6	PSB6_HUMAN	25.4	100.0%	2	2	4	0.00%	8.8%	TTTGSYIANR	99.7%	59.2	25	53.8	2	0	0	1083.54	54	63
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	17	17	29	0.03%	10.9%	AGEQLAPFLPQLVPR	99.7%	60.9	25	56.1	3	0	0	1635.92	1112	1126
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	17	17	29	0.03%	10.9%	AIACVVTACSAELEK	99.7%	93.4	25	89.4	2	0	0	1621.79	1591	1605
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	17	17	29	0.03%	10.9%	ALSINTLVK	99.1%	34	25	19.7	1	0	0	958.59	1272	1280
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	17	17	29	0.03%	10.9%	ESSCLALNDLLR	99.7%	47.8	25	32.2	1	0	0	1390.70	1180	1191
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	17	17	29	0.03%	10.9%	HSVATAADLELK	97.6%	30	25	26.3	1	0	0	1254.67	274	285
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	17	17	29	0.03%	10.9%	IVAISCAADILK	99.7%	78.8	25	65.3	2	0	0	1273.72	1633	1644
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	17	17	29	0.03%	10.9%	LLSMAYSAVGK	99.7%	56.4	25	46.2	2	0	0	1139.61	415	425
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	17	17	29	0.03%	10.9%	LMSALLSGLTDR	99.7%	80.9	25	72.8	1	0	0	1276.69	1401	1412
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	17	17	29	0.03%	10.9%	LSSTQEGVR	99.7%	49.3	25	29.4	2	0	0	976.51	47	55
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	17	17	29	0.03%	10.9%	MSEQQDLER	99.5%	36.7	25	31.1	1	0	0	1151.50	771	779
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	17	17	29	0.03%	10.9%	NGPLPIPSEGSGFTK	99.7%	46.2	25	46.2	2	0	0	1500.77	823	837
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	17	17	29	0.03%	10.9%	SASPFNLAEKPK	99.7%	50.3	25	42.9	2	0	0	1288.69	157	168
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	17	17	29	0.03%	10.9%	TEALSVIELLLK	99.7%	108	25	95.6	3	0	0	1328.80	1785	1796
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	17	17	29	0.03%	10.9%	TLMSSGQMAPSSSNK	99.7%	43.8	25	43.8	2	0	0	1557.69	632	646
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	17	17	29	0.03%	10.9%	TPDGQGLSTYK	98.4%	31.6	25	25.2	1	0	0	1166.57	1057	1067
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	17	17	29	0.03%	10.9%	VYLGDIPLK	99.7%	46.8	25	43.6	2	0	0	1017.60	305	313
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	17	17	29	0.03%	10.9%	YLLLLAAGDPR	99.7%	66.1	25	58.1	1	0	0	1201.69	517	527
Protein arginine N-methyltransferase 1	PRMT1	ANM1_HUMAN	41.5	100.0%	5	5	7	0.01%	18.6%	GKVEEVELPVEK	99.7%	55.2	25	51.2	2	0	0	1355.74	134	145
Protein arginine N-methyltransferase 1	PRMT1	ANM1_HUMAN	41.5	100.0%	5	5	7	0.01%	18.6%	QLVTNACLIK	98.9%	33.4	25	20.8	2	0	0	1159.65	234	243
Protein arginine N-methyltransferase 1	PRMT1	ANM1_HUMAN	41.5	100.0%	5	5	7	0.01%	18.6%	TGFSTSPESPYTHWK	99.7%	49.5	25	44	1	0	0	1724.79	289	303
Protein arginine N-methyltransferase 1	PRMT1	ANM1_HUMAN	41.5	100.0%	5	5	7	0.01%	18.6%	VEDLTFTSPFCLQVK	94.8%	27	25	22.7	1	0	0	1783.89	252	266
Protein arginine N-methyltransferase 1	PRMT1	ANM1_HUMAN	41.5	100.0%	5	5	7	0.01%	18.6%	VIGIECSSISDYAVK	99.7%	43.3	25	37.5	1	0	0	1640.82	104	118
Protein arginine N-methyltransferase 3	PRMT3	ANM3_HUMAN	59.9	99.8%	2	2	2	0.00%	4.7%	AVIPEAVVEVLDPK	98.9%	33.4	25	33.4	1	0	0	1478.85	397	410
Protein arginine N-methyltransferase 3	PRMT3	ANM3_HUMAN	59.9	99.8%	2	2	2	0.00%	4.7%	VVFSTGPQSTK	97.0%	29.1	25	17.1	1	0	0	1150.61	467	477
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	AAILPTSIFLTNK	99.7%	105	25	105	33	0	0	1388.81	228	240
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	AAILPTSIFLTNKK	99.7%	67.5	25	67.5	7	7	0	1516.91	228	241
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	ADIIVSELLGSFADNELSPECLDGAQHFLK	99.7%	95.5	25	77.4	0	1	0	3288.61	429	458
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	DDGVSIPGEYTSFLAPISSSK	99.7%	80.9	25	80.9	14	0	0	2170.06	459	479
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	DDIIENAPTTHTEEYSGEEK	99.7%	89.7	25	89.7	2	3	0	2278.00	165	184
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	DLNCVPEIADTLGAVAK	99.7%	97.4	25	94	31	2	0	1785.91	19	35
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	DPEAQFEMPYVVR	99.7%	72.2	25	72.2	5	0	0	1580.74	493	505
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	DPIKYSQYQQAIYK	99.7%	69.2	25	67.8	2	2	0	1744.89	330	343
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	DPMIDNNR	99.7%	41.6	25	29.1	6	0	0	974.44	527	534
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	DRDPEAQFEMPYVVR	99.7%	53.8	25	52.4	3	7	0	1851.87	491	505
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	DTNVQVLMVLGAGR	99.7%	105	25	91.7	5	0	0	1488.78	355	368
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	DWNTLIVGK	99.7%	60.4	25	44.7	17	0	0	1045.57	77	85
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	EFCSYLQYLEYLSQNRPPPNAYELFAK	99.7%	97.4	25	97.4	0	1	0	3340.60	276	302
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	EFIQEPAK	99.7%	45.6	25	21.3	19	0	0	961.50	53	60
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	EGQTICVR	99.7%	43.7	25	39.2	20	0	0	962.47	594	601
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	EWVAPEK	97.3%	29.5	25	23.7	1	0	0	858.44	422	428
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	GPLVNASLR	99.7%	75.5	25	66.1	10	0	0	926.54	369	377
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	GYEDYLQSPLQPLMDNLESQTYEVFEKDPIK	99.7%	64.4	25	64.4	0	7	0	3689.76	303	333
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	IAVALEIGADLPSNHVIDR	99.7%	75.8	25	75.8	4	6	0	2003.09	202	220

Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	IKLYAVEK	99.7%	41.1	25	18.4	8	0	0	963.59	386	393
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	KGFPVLSK	99.7%	56.5	25	29.8	14	0	0	875.54	241	248
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	KVWYEWAVTAPVCSAIHNPTGR	99.7%	84.8	25	84.8	0	2	0	2542.27	610	631
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	LEVQFIITGTNHHSEK	99.7%	48.7	25	41.7	0	1	0	1852.96	260	275
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	LSPWIRPDSK	98.3%	31.5	25	28.7	3	0	0	1198.66	86	95
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	QGFDFLCMPVFHPR	99.7%	62.4	25	62.4	10	20	0	1750.82	36	49
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	REFIQEPAK	99.7%	45.2	25	25	3	0	0	1117.60	52	60
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	SDLLLSGR	99.7%	40.1	25	22.2	6	0	0	860.48	69	76
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	SDLLLSGRDWNTLIVGK	99.7%	88.4	25	88.4	8	10	0	1887.03	69	85
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	TLCDYSK	99.1%	34	25	34	2	0	0	886.40	194	200
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	TLCDYSKR	99.7%	43.5	25	34.7	6	0	0	1042.50	194	201
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	TWMWWHNFR	99.7%	49.4	25	41.3	12	4	0	1363.62	185	193
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	VPEEEKDTNVQVLMVLGAGR	99.7%	95.7	25	95.7	4	10	0	2184.13	349	368
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	VPLVAPEDLR	99.7%	60.1	25	54.7	15	0	0	1108.64	155	164
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	VPLVAPEDLRDDIIENAPTTHTEEYSGEEK	99.7%	65.1	25	65.1	0	1	0	3367.62	155	184
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	VWYEWAVTAPVCSAIHNPTGR	99.7%	47.4	25	47.4	0	2	0	2414.17	611	631
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	WLGEPIK	99.5%	36.9	25	24.4	3	0	0	842.48	221	227
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	58	379	0.38%	61.7%	YSQYQQAIYK	99.7%	66.2	25	66.2	20	0	0	1291.63	334	343
Protein CIP2A	KIAA1524	CIP2A_HUMAN	102.2	100.0%	6	6	7	0.01%	7.2%	ALALAQADR	99.7%	59.8	25	49.5	1	0	0	928.52	648	656
Protein CIP2A	KIAA1524	CIP2A_HUMAN	102.2	100.0%	6	6	7	0.01%	7.2%	DGVPGLNIEELIEK	96.4%	28.4	25	15.3	1	0	0	1525.81	590	603
Protein CIP2A	KIAA1524	CIP2A_HUMAN	102.2	100.0%	6	6	7	0.01%	7.2%	LITPLAFALTSDNR	99.7%	75.2	25	75.2	2	0	0	1531.85	509	522
Protein CIP2A	KIAA1524	CIP2A_HUMAN	102.2	100.0%	6	6	7	0.01%	7.2%	LQDLLETK	99.7%	50.5	25	36.8	1	0	0	959.54	640	647
Protein CIP2A	KIAA1524	CIP2A_HUMAN	102.2	100.0%	6	6	7	0.01%	7.2%	SEANATQLLR	99.7%	61.7	25	41.2	1	0	0	1102.59	22	31
Protein CIP2A	KIAA1524	CIP2A_HUMAN	102.2	100.0%	6	6	7	0.01%	7.2%	SLLLTVSQYK	99.7%	60.1	25	53.5	1	0	0	1151.67	9	18
Protein CMSS1	CMSS1	CMS1_HUMAN	31.9	100.0%	2	2	3	0.00%	7.5%	QGGLNLSPLK	99.7%	42.8	25	29.5	1	0	0	1026.59	222	231
Protein CMSS1	CMSS1	CMS1_HUMAN	31.9	100.0%	2	2	3	0.00%	7.5%	VVHLGVGTPGR	99.7%	59	25	59	2	0	0	1091.63	205	215
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	4	5	9	0.01%	12.0%	LLASANLEEVTMK	99.7%	75.7	25	73.1	3	0	0	1418.76	332	344
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	4	5	9	0.01%	12.0%	NVGQFSGFPFEK	99.7%	49	25	49	2	0	0	1356.66	126	137
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	4	5	9	0.01%	12.0%	SGVNSELVKR	99.7%	48.7	25	35.2	2	0	0	1088.61	169	178
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	4	5	9	0.01%	12.0%	SICEVLDLER	99.7%	62.4	25	53.8	2	0	0	1233.61	159	168
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	3	3	4	0.00%	2.4%	ELGEYFLFDPK	97.1%	29.3	25	28.8	1	0	0	1357.67	1117	1127
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	3	3	4	0.00%	2.4%	LNAILFK	97.4%	29.7	25	19.3	1	0	0	818.51	937	943
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	3	3	4	0.00%	2.4%	TAQNLSIFLGSFR	99.7%	64.8	25	64.8	2	0	0	1453.78	856	868
Protein disulfide-isomerase A6	PDIA6	PDIA6_HUMAN	48.1	99.8%	2	2	2	0.00%	6.1%	GSFSEQGINEFLR	99.7%	53.4	25	35	1	0	0	1483.72	374	386
Protein disulfide-isomerase A6	PDIA6	PDIA6_HUMAN	48.1	99.8%	2	2	2	0.00%	6.1%	TGEAIVDAALSALR	99.7%	61.4	25	54.7	1	0	0	1386.76	119	132
Protein DJ-1	PARK7	PARK7_HUMAN	19.9	100.0%	3	5	9	0.01%	24.3%	DVVICPDASLEDAKK	99.6%	37.7	25	32.8	1	0	0	1659.83	49	63
Protein DJ-1	PARK7	PARK7_HUMAN	19.9	100.0%	3	5	9	0.01%	24.3%	GAEEMETVIPVDVMR	99.7%	48.4	25	47	4	0	0	1691.80	13	27
Protein DJ-1	PARK7	PARK7_HUMAN	19.9	100.0%	3	5	9	0.01%	24.3%	VTVAGLAGKDPVQCSR	99.7%	43.6	25	43.3	2	2	0	1657.87	33	48
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	6	6	11	0.01%	5.3%	ADLTALFLPR	99.7%	67.5	25	58.5	3	0	0	1116.64	875	884
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	6	6	11	0.01%	5.3%	GAQATLSSTTK	99.7%	72.4	25	65.5	2	0	0	1064.56	661	671
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	6	6	11	0.01%	5.3%	KFESLFPGK	98.1%	30.9	25	30.9	1	0	0	1052.58	1007	1015
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	6	6	11	0.01%	5.3%	LLQSLLDTR	99.7%	55.4	25	48.7	2	0	0	1058.62	765	773
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	6	6	11	0.01%	5.3%	NQLTSLPSAICK	99.6%	37.7	25	13.4	1	0	0	1331.70	279	290
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	6	6	11	0.01%	5.3%	VGLGLGYLELPQINYK	99.7%	47.6	25	47.6	2	0	0	1776.99	731	746
Protein KRI1 homolog	KRI1	KRI1_HUMAN	82.6	100.0%	4	4	7	0.01%	6.5%	EEAETPAEATGKPQR	99.7%	58	25	55.5	2	0	0	1613.78	593	607
Protein KRI1 homolog	KRI1	KRI1_HUMAN	82.6	100.0%	4	4	7	0.01%	6.5%	LQAFGLNPK	99.6%	37.6	25	22.6	2	0	0	987.56	674	682
Protein KRI1 homolog	KRI1	KRI1_HUMAN	82.6	100.0%	4	4	7	0.01%	6.5%	LQETSSQSYVEEQK	99.7%	103	25	99.1	1	0	0	1655.78	145	158
Protein KRI1 homolog	KRI1	KRI1_HUMAN	82.6	100.0%	4	4	7	0.01%	6.5%	VNAAFAAR	99.5%	37	25	27.7	2	0	0	819.45	12	19
Protein KTI12 homolog	KTI12	KTI12_HUMAN	38.6	100.0%	2	2	3	0.00%	5.7%	FEAPDSR	96.6%	28.7	25	21.3	1	0	0	821.38	216	222
Protein KTI12 homolog	KTI12	KTI12_HUMAN	38.6	100.0%	2	2	3	0.00%	5.7%	PLVVFCGLPYSGK	99.5%	36.9	25	36	2	0	0	1436.76	2	14
Protein mago nashi homolog 2	MAGOHB	MGN2_HUMAN	17.3	99.8%	2	2	2	0.00%	14.2%	IGSLIDVNQSK	99.7%	72.7	25	61.5	1	0	0	1173.65	106	116

Protein mago nashi homolog 2	MAGOHB	MGN2_HUMAN	17.3	99.8%	2	2	2	0.00%	14.2%	VFYYLVQDLK	99.7%	41.7	25	28.9	1	0	0	1287.70	123	132
Protein MON2 homolog	MON2	MON2_HUMAN	190.5	99.8%	2	2	3	0.00%	1.1%	AVAVESIHR	99.7%	39.8	25	14.6	1	0	0	981.55	353	361
Protein MON2 homolog	MON2	MON2_HUMAN	190.5	99.8%	2	2	3	0.00%	1.1%	LQLLLLNPLK	99.7%	47.9	25	47.9	2	0	0	1164.77	862	871
Protein NipSnap homolog 1	NIPSNAP1	NIPS1_HUMAN	33.3	100.0%	4	6	9	0.01%	16.2%	DAHSTLLSK	95.1%	27.2	25	23.1	1	0	0	971.52	57	65
Protein NipSnap homolog 1	NIPSNAP1	NIPS1_HUMAN	33.3	100.0%	4	6	9	0.01%	16.2%	FSGGYPALMDCMNK	99.7%	45.8	25	45.8	2	0	0	1622.66	128	141
Protein NipSnap homolog 1	NIPSNAP1	NIPS1_HUMAN	33.3	100.0%	4	6	9	0.01%	16.2%	GWDENVYYTVPLVR	99.7%	58.9	25	57.5	2	0	0	1710.85	255	268
Protein NipSnap homolog 1	NIPSNAP1	NIPS1_HUMAN	33.3	100.0%	4	6	9	0.01%	16.2%	MGPNIYELR	99.7%	70.2	25	60.4	4	0	0	1092.55	180	188
Protein NipSnap homolog 2	GBAS	NIPS2_HUMAN	33.7	100.0%	3	4	6	0.01%	10.8%	ICQEVLPK	99.5%	36.7	25	16.3	2	0	0	986.53	92	99
Protein NipSnap homolog 2	GBAS	NIPS2_HUMAN	33.7	100.0%	3	4	6	0.01%	10.8%	SGPNIYELR	99.7%	62.1	25	56.8	2	0	0	1048.54	182	190
Protein NipSnap homolog 2	GBAS	NIPS2_HUMAN	33.7	100.0%	3	4	6	0.01%	10.8%	YEGGYPALTEVMNK	99.7%	52.2	25	52.2	2	0	0	1571.74	130	143
Protein Njmu-R1	C17orf75	NJMU_HUMAN	44.6	100.0%	3	3	4	0.00%	7.3%	AIQDTNNLKR	94.5%	26.8	25	19.8	1	0	0	1172.64	326	335
Protein Njmu-R1	C17orf75	NJMU_HUMAN	44.6	100.0%	3	3	4	0.00%	7.3%	GGNPFLFR	99.7%	42.8	25	22.2	1	0	0	907.48	309	316
Protein Njmu-R1	C17orf75	NJMU_HUMAN	44.6	100.0%	3	3	4	0.00%	7.3%	NVIAVLEEFMK	99.7%	56.2	25	54.5	2	0	0	1292.69	379	389
Protein odr-4 homolog	ODR4	ODR4_HUMAN	51.1	100.0%	4	4	6	0.01%	12.1%	AFVSGLLIGQCSSQK	99.7%	61.5	25	58.8	1	0	0	1594.83	24	38
Protein odr-4 homolog	ODR4	ODR4_HUMAN	51.1	100.0%	4	4	6	0.01%	12.1%	GNTQATSHSFDVR	99.0%	33.9	25	33.9	2	0	0	1419.66	243	255
Protein odr-4 homolog	ODR4	ODR4_HUMAN	51.1	100.0%	4	4	6	0.01%	12.1%	STATVQICSGSVNLK	99.7%	67.2	25	55.5	1	0	0	1564.80	268	282
Protein odr-4 homolog	ODR4	ODR4_HUMAN	51.1	100.0%	4	4	6	0.01%	12.1%	VLTQLLLNSDHR	99.7%	62.3	25	55.4	2	0	0	1408.79	256	267
Protein pelota homolog	PELO	PELO_HUMAN	43.4	100.0%	4	4	5	0.00%	9.6%	FYEQVVQAIQR	99.7%	48.4	25	39.8	1	0	0	1380.73	185	195
Protein pelota homolog	PELO	PELO_HUMAN	43.4	100.0%	4	4	5	0.00%	9.6%	GTNIQENEYVK	95.4%	27.5	25	23.2	1	0	0	1294.63	85	95
Protein pelota homolog	PELO	PELO_HUMAN	43.4	100.0%	4	4	5	0.00%	9.6%	KVQTESSTGSVGSNR	99.7%	63.2	25	54.7	1	0	0	1536.76	46	60
Protein pelota homolog	PELO	PELO_HUMAN	43.4	100.0%	4	4	5	0.00%	9.6%	VQTESSTGSVGSNR	99.7%	71.4	25	62.6	2	0	0	1408.67	47	60
Protein phosphatase 1B	PPM1B	PPM1B_HUMAN	52.6	100.0%	4	6	12	0.01%	9.8%	IQNAGGSVMIQR	99.7%	70.3	25	60.8	4	0	0	1289.66	180	191
Protein phosphatase 1B	PPM1B	PPM1B_HUMAN	52.6	100.0%	4	6	12	0.01%	9.8%	NVIEAVYSR	99.7%	56.9	25	50.6	4	0	0	1050.56	361	369
Protein phosphatase 1B	PPM1B	PPM1B_HUMAN	52.6	100.0%	4	6	12	0.01%	9.8%	SGSALELSVENVK	99.7%	85.3	25	79.4	1	0	0	1332.70	91	103
Protein phosphatase 1B	PPM1B	PPM1B_HUMAN	52.6	100.0%	4	6	12	0.01%	9.8%	SGSTAVGVMISPK	99.7%	53.6	25	31.6	3	0	0	1233.65	130	142
Protein phosphatase 1F	PPM1F	PPM1F_HUMAN	49.8	99.8%	2	2	4	0.00%	6.8%	HVSLPSFNQLFGLSDPVNR	99.7%	31	25	31	0	2	0	2127.10	173	191
Protein phosphatase 1F	PPM1F	PPM1F_HUMAN	49.8	99.8%	2	2	4	0.00%	6.8%	YAAVHVHTNAAR	99.7%	31.3	25	29.8	0	2	0	1309.68	208	219
Protein QIL1	QIL1	QIL1_HUMAN	13.1	99.8%	2	2	4	0.00%	9.3%	EGWEYVK	97.6%	30	25	22.1	2	0	0	910.43	108	114
Protein QIL1	QIL1	QIL1_HUMAN	13.1	99.8%	2	2	4	0.00%	9.3%	EYSKEGWEYVK	99.7%	40.4	25	38	2	0	0	1417.66	104	114
Protein RCC2	RCC2	RCC2_HUMAN	56.1	99.8%	2	2	2	0.00%	5.8%	AGGAAVVITEPEHTKER	99.7%	53.8	25	53.8	0	1	0	1764.92	78	94
Protein RCC2	RCC2	RCC2_HUMAN	56.1	99.8%	2	2	2	0.00%	5.8%	LGHAEQKDEMVPR	97.8%	22.9	25	18.4	0	1	0	1525.74	362	374
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	5	5	9	0.01%	3.2%	IPLLLTSLSFK	99.7%	56	25	56	3	0	0	1231.77	1178	1188
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	5	5	9	0.01%	3.2%	LGPSVVGLAR	99.7%	75.7	25	68.1	2	0	0	968.59	1343	1352
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	5	5	9	0.01%	3.2%	LKDGVLAYAR	99.7%	39.4	25	30.8	1	0	0	1105.64	386	395
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	5	5	9	0.01%	3.2%	TSIIEAQYLR	99.7%	57.6	25	48.3	1	0	0	1193.65	437	446
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	5	5	9	0.01%	3.2%	TTEPGVTGLLLAVEGPAAK	99.7%	95.2	25	91.9	2	0	0	1824.01	982	1000
Protein S100-A8	S100A8	S10A8_HUMAN	10.8	99.8%	2	2	15	0.01%	23.7%	ALNSIIDVYHK	99.7%	65.2	25	57.4	6	0	0	1272.69	8	18
Protein S100-A8	S100A8	S10A8_HUMAN	10.8	99.8%	2	2	15	0.01%	23.7%	LLETECPQYIR	99.7%	64.3	25	54.4	9	0	0	1421.71	37	47
Protein SAAL1	SAAL1	SAAL1_HUMAN	53.6	100.0%	2	2	3	0.00%	4.4%	VDLPLIDSLIR	99.7%	79.8	25	77.1	2	0	0	1253.75	348	358
Protein SAAL1	SAAL1	SAAL1_HUMAN	53.6	100.0%	2	2	3	0.00%	4.4%	VLQNMEQCQK	99.4%	36.2	25	36.2	1	0	0	1277.60	359	368
Protein SCO2 homolog, mitochondrial	SCO2	SCO2_HUMAN	29.8	99.8%	2	2	4	0.00%	10.5%	QGPAETGGQGQPQGPGLR	99.7%	63	25	62.5	2	0	0	1734.85	41	58
Protein SCO2 homolog, mitochondrial	SCO2	SCO2_HUMAN	29.8	99.8%	2	2	4	0.00%	10.5%	SAEQISDSVR	99.7%	58.7	25	39.6	2	0	0	1091.53	246	255
Protein SEC13 homolog	SEC13	SEC13_HUMAN	35.5	99.8%	2	2	2	0.00%	8.7%	GQGSVSASVTEGQQNEQ	99.6%	38.1	25	37.2	1	0	0	1705.76	306	322
Protein SEC13 homolog	SEC13	SEC13_HUMAN	35.5	99.8%	2	2	2	0.00%	8.7%	NGGQILIADLR	99.7%	54.3	25	49.8	1	0	0	1169.66	44	54
Protein SET	SET	SET_HUMAN	33.5	100.0%	4	4	7	0.01%	15.5%	EFHLNESGDPSSK	99.7%	49.6	25	46.7	2	0	0	1446.65	155	167
Protein SET	SET	SET_HUMAN	33.5	100.0%	4	4	7	0.01%	15.5%	IDFYFDENPYFENK	99.7%	75.3	25	75.3	2	0	0	1840.81	137	150
Protein SET	SET	SET_HUMAN	33.5	100.0%	4	4	7	0.01%	15.5%	LRQPFFQK	96.5%	28.5	25	17.2	1	0	0	1063.60	76	83
Protein SET	SET	SET_HUMAN	33.5	100.0%	4	4	7	0.01%	15.5%	VEVTEFEDIK	99.7%	66.1	25	56.6	2	0	0	1208.60	123	132
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	5	6	12	0.01%	8.7%	DVLLDVAYAYGK	99.7%	81.6	25	76.9	2	0	0	1326.69	293	304
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	5	6	12	0.01%	8.7%	ELQSVEQEVR	99.7%	67.2	25	53.5	2	0	0	1216.62	164	173
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	5	6	12	0.01%	8.7%	LLGSLYALGIPK	99.7%	61.6	25	61.6	2	0	0	1244.76	149	160

Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	5	6	12	0.01%	8.7%	LSFHQTQVSQR	99.7%	61.8	25	52.2	2	0	0	1330.69	305	315
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	5	6	12	0.01%	8.7%	VLVMLAAQSR	99.7%	79.8	25	74.3	4	0	0	1087.63	261	270
Protein transport protein Sec23A	SEC23A	SC23A_HUMAN	86.2	100.0%	2	2	2	0.00%	3.3%	GPQVQQPPPSNR	99.6%	37.7	25	36.9	1	0	0	1304.67	217	228
Protein transport protein Sec23A	SEC23A	SC23A_HUMAN	86.2	100.0%	2	2	2	0.00%	3.3%	MVVPVAALFTPLK	99.7%	51.4	25	51.4	1	0	0	1385.82	34	46
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	8	17	0.02%	10.9%	AFSPTTVNTGR	99.7%	53.9	25	40.1	4	0	0	1150.59	195	205
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	8	17	0.02%	10.9%	ETSMVHELNR	99.7%	59.1	25	52.1	2	0	0	1215.58	406	415
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	8	17	0.02%	10.9%	GQYNTYPIK	99.7%	47.6	25	30.5	6	0	0	1083.55	274	282
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	8	17	0.02%	10.9%	IIEVGDTPK	99.7%	42.6	25	34.6	2	0	0	971.54	99	107
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	8	17	0.02%	10.9%	IIEVGDTPKDR	99.7%	46.3	25	34.9	1	1	0	1242.67	99	109
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	8	17	0.02%	10.9%	TWIEVSGSSAK	96.7%	28.8	25	25.8	1	0	0	1164.59	378	388
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	8	8	14	0.01%	10.8%	ALIPLALEGTDVGQTK	99.7%	106	25	106	2	0	0	1625.91	692	707
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	8	8	14	0.01%	10.8%	DNALTLLIK	99.7%	42.1	25	5.74	1	0	0	1000.60	313	321
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	8	8	14	0.01%	10.8%	LDQAVLDLQR	99.7%	76.7	25	61.1	2	0	0	1170.65	108	117
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	8	8	14	0.01%	10.8%	LLDMGETDLMLAALR	99.7%	59.9	25	38.9	2	0	0	1677.86	203	217
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	8	8	14	0.01%	10.8%	LLVLYSGEDDELLQR	99.7%	79.6	25	70.1	2	0	0	1762.92	822	836
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	8	8	14	0.01%	10.8%	TVATLSILGTR	99.7%	69.8	25	68.8	1	0	0	1131.67	230	240
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	8	8	14	0.01%	10.8%	VEQMFQILLDPEEK	99.7%	66.9	25	51.1	2	0	0	1718.87	153	166
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	8	8	14	0.01%	10.8%	VFLALVEEVEDR	99.7%	85.5	25	79.9	2	0	0	1418.75	670	681
Protein virilizer homolog	KIAA1429	VIR_HUMAN	202.0	100.0%	2	2	3	0.00%	1.3%	LLELILLDQTVR	99.7%	90.5	25	90.5	2	0	0	1425.87	534	545
Protein virilizer homolog	KIAA1429	VIR_HUMAN	202.0	100.0%	2	2	3	0.00%	1.3%	VVTAGSAILQK	94.7%	26.9	25	20.2	1	0	0	1086.65	546	556
Protein YIF1A	YIF1A	YIF1A_HUMAN	32.0	99.8%	2	2	4	0.00%	9.2%	TAALGPDSMGGPVPR	99.7%	72	25	65.6	2	0	0	1441.71	251	265
Protein YIF1A	YIF1A	YIF1A_HUMAN	32.0	99.8%	2	2	4	0.00%	9.2%	YFFAVDTAYVAK	99.7%	79.6	25	72.6	2	0	0	1394.70	93	104
Protein YIF1B	YIF1B	YIF1B_HUMAN	34.4	99.8%	2	2	6	0.01%	8.0%	ILADAAAEGVPVR	99.7%	70.9	25	64.7	4	0	0	1281.72	271	283
Protein YIF1B	YIF1B	YIF1B_HUMAN	34.4	99.8%	2	2	6	0.01%	8.0%	YYFAVDTMYVGR	98.5%	32.1	25	31.6	2	0	0	1484.69	111	122
Pumilio homolog 1	PUM1	PUM1_HUMAN	126.5	100.0%	4	4	8	0.01%	4.3%	FFEFGSLEQK	99.7%	47.3	25	39.4	2	0	0	1231.60	905	914
Pumilio homolog 1	PUM1	PUM1_HUMAN	126.5	100.0%	4	4	8	0.01%	4.3%	GNVLVLSQHK	99.7%	39.4	25	32.6	2	0	0	1094.63	1067	1076
Pumilio homolog 1	PUM1	PUM1_HUMAN	126.5	100.0%	4	4	8	0.01%	4.3%	SASSASSLFSPSSTLFSSSR	99.7%	58	25	57.8	2	0	0	1992.95	797	816
Pumilio homolog 1	PUM1	PUM1_HUMAN	126.5	100.0%	4	4	8	0.01%	4.3%	YISAAPGAEAK	99.5%	37	25	31.3	2	0	0	1077.56	784	794
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	26	30	65	0.06%	30.8%	AFFESHPAPSAER	99.7%	46.6	25	45.7	2	1	0	1445.68	870	882
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	26	30	65	0.06%	30.8%	AGIISTVEVLK	99.7%	80.1	25	72.9	2	0	0	1129.68	628	638
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	26	30	65	0.06%	30.8%	ATFDISLVVPK	99.7%	78.2	25	68.2	2	0	0	1189.68	198	208
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	26	30	65	0.06%	30.8%	DAESIHQYLLQR	99.7%	65.6	25	58.1	2	0	0	1472.75	901	912
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	26	30	65	0.06%	30.8%	DLSLPPVDR	97.7%	30.2	25	30.2	1	0	0	1011.55	607	615
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	26	30	65	0.06%	30.8%	DNWEELYNR	99.7%	52.3	25	44.3	1	0	0	1238.54	833	841
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	26	30	65	0.06%	30.8%	DYFNVPYPLPK	99.7%	51.3	25	50.8	3	0	0	1352.69	294	304
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	26	30	65	0.06%	30.8%	ETALLIDPK	99.7%	55.6	25	40.5	2	0	0	999.57	328	336
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	26	30	65	0.06%	30.8%	FALEVAAK	99.6%	38	25	19	2	0	0	848.49	280	287
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	26	30	65	0.06%	30.8%	GMNMYLTK	99.3%	35.4	25	30.4	2	0	0	957.45	460	467
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	26	30	65	0.06%	30.8%	IDFVGELNDK	99.7%	66.8	25	44.4	2	0	0	1149.58	146	155
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	26	30	65	0.06%	30.8%	ILMDKPEMNVVLK	99.1%	34	25	28.4	1	0	0	1561.83	559	571
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	26	30	65	0.06%	30.8%	KPYPDDENLVEVK	99.7%	72.2	25	58.1	2	0	0	1545.78	222	234
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	26	30	65	0.06%	30.8%	LGLQNDLFSLAR	99.7%	92.7	25	74.2	4	0	0	1346.74	616	627
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	26	30	65	0.06%	30.8%	LNLGTVGFYR	99.7%	73.1	25	61.3	5	0	0	1139.62	581	590
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	26	30	65	0.06%	30.8%	LSVEGFAVDK	99.7%	45.2	25	36.5	4	0	0	1064.56	854	863
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	26	30	65	0.06%	30.8%	QILSADLR	99.7%	49.3	25	35.5	2	0	0	915.53	737	744
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	26	30	65	0.06%	30.8%	SPVYLTVLK	99.7%	57	25	53.9	2	0	0	1019.61	745	753
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	26	30	65	0.06%	30.8%	TIQQCCENILLNAAWLK	99.7%	51.7	25	51.7	2	0	0	2075.04	883	899
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	26	30	65	0.06%	30.8%	TQYSSAMLESLLPGIR	99.7%	53.7	25	42.4	4	0	0	1781.91	591	606
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	26	30	65	0.06%	30.8%	VALSNMNVIDR	99.7%	85.1	25	73.2	4	0	0	1231.65	211	221
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	26	30	65	0.06%	30.8%	VLGATLLPDLIQK	99.7%	83.8	25	83.8	5	0	0	1380.85	782	794
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	26	30	65	0.06%	30.8%	VTLSFPSTLQTGTGTLK	99.7%	69.4	25	69.4	2	0	0	1750.96	129	145

Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	26	30	65	0.06%	30.8%	YAAVTQFEATDAR	99.7%	107	25	107	2	0	0	1442.69	173	185
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	26	30	65	0.06%	30.8%	YAAVTQFEATDARR	99.0%	33.8	25	33.8	1	1	0	1598.79	173	186
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	26	30	65	0.06%	30.8%	YQGGFLISR	99.7%	67.7	25	62.3	2	0	0	1040.55	842	850
Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial	CLPP	CLPP_HUMAN	30.2	100.0%	3	4	7	0.01%	12.3%	AYDIYSR	97.1%	29.2	25	10.8	1	0	0	887.43	72	78
Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial	CLPP	CLPP_HUMAN	30.2	100.0%	3	4	7	0.01%	12.3%	GQATDIAIQAEEIMK	99.7%	75.2	25	75.2	4	0	0	1617.82	186	200
Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial	CLPP	CLPP_HUMAN	30.2	100.0%	3	4	7	0.01%	12.3%	QSLQVIESAMER	99.7%	67.8	25	62.7	2	0	0	1390.70	215	226
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	AIFQQPPVGVR	99.7%	65.2	25	57	2	0	0	1211.69	715	725
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	AIVLAAIFR	99.7%	63.4	25	63.4	4	0	0	973.62	886	894
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	ATISLSDSDLLR	99.7%	81.4	25	72.3	2	0	0	1290.69	1116	1127
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	AVAGWEEVLR	99.7%	57.5	25	50	2	0	0	1129.60	942	951
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	CNVIITQPR	99.7%	41.7	25	25.5	1	0	0	1100.59	484	492
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	DPFSSSLQNR	99.7%	61.7	25	56.3	2	0	0	1150.55	909	918
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	DVNTDFLLILLK	99.7%	69.8	25	63.1	4	0	0	1403.81	565	576
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	ENYLEENLLYAPSLR	99.7%	50.1	25	50.1	2	0	0	1823.92	959	973
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	EYLTTLGQR	99.7%	52.8	25	42.3	2	0	0	1080.57	865	873
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	FKPNSVTYR	99.7%	42.4	25	32.3	2	0	0	1111.59	1041	1049
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	GGALLFCTVGILLR	99.7%	69	25	60.2	2	0	0	1489.86	529	542
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	GVLMAGLYPNLIQVR	99.7%	51.5	25	51.5	3	0	0	1643.93	1017	1031
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	IPQLLLER	99.7%	65.1	25	48.1	2	0	0	981.61	467	474
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	ISAVSVAQR	99.7%	62	25	28.3	2	0	0	930.54	494	502
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	LQEALGMHESK	99.7%	59.8	25	48.7	4	0	0	1242.61	688	698
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	LQSDDILPLGK	99.7%	44.7	25	32.9	2	0	0	1198.67	378	388
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	LSQSLLELWR	99.7%	42.5	25	38.3	2	0	0	1244.70	413	422
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	LVLMSATGDNER	99.7%	74.3	25	71.6	3	0	0	1321.64	587	598
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	MVPFQVPEILR	99.6%	37.7	25	35.3	3	0	0	1328.74	803	813
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	NLLNSVIGR	99.7%	54.7	25	43.5	2	0	0	985.58	55	63
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	NLMQFHTVGTK	97.7%	30.1	25	28.6	2	0	0	1291.65	264	274
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	NVGFQVR	97.1%	29.2	25	21.1	1	0	0	819.45	514	520
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	QAAAAACQLFK	99.1%	34	25	29	2	0	0	1178.60	112	122
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	RISAVSVAQR	99.7%	43.7	25	18.7	1	0	0	1086.64	493	502
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	SGNILLHK	99.7%	45.6	25	27.3	2	0	0	881.52	1052	1059
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	SVEVEGYGSK	99.7%	50.7	25	50.2	2	0	0	1054.51	96	105
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	TPLENLVLQAK	99.7%	60.4	25	58.7	2	0	0	1225.72	814	824
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	VIQIATSSSTAK	99.7%	80.7	25	74.4	3	0	0	1205.67	252	263
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	29	33	65	0.06%	25.0%	VSCLETVWVSR	99.7%	74.2	25	63.9	2	0	0	1335.67	763	773
Putative ATP-dependent RNA helicase DHX57	DHX57	DHX57_HUMAN	155.6	99.8%	2	2	2	0.00%	1.7%	QFTELLSDIGFAR	99.7%	48.5	25	45.5	1	0	0	1496.77	1165	1177
Putative ATP-dependent RNA helicase DHX57	DHX57	DHX57_HUMAN	155.6	99.8%	2	2	2	0.00%	1.7%	YVLQDGSPYMR	99.4%	36.1	25	29.9	1	0	0	1328.63	741	751
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	4	4	5	0.00%	5.3%	EAGQCFESFLVVR	99.7%	68.7	25	55.4	2	0	0	1541.74	12	24
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	4	4	5	0.00%	5.3%	ETGDPGGQLVLAGDPR	99.4%	35.8	25	27.2	1	0	0	1581.79	667	682
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	4	4	5	0.00%	5.3%	IANLAYVTK	99.7%	40.7	25	30.5	1	0	0	992.58	63	71
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	4	4	5	0.00%	5.3%	LDLQQGQNLLQGLSK	99.7%	45.5	25	45.5	1	0	0	1654.91	953	967
Putative methyltransferase NSUN5	NSUN5	NSUN5_HUMAN	46.7	99.8%	2	2	5	0.00%	6.1%	VLVYELLLGK	99.7%	56.1	25	52.8	4	0	0	1146.71	73	82
Putative methyltransferase NSUN5	NSUN5	NSUN5_HUMAN	46.7	99.8%	2	2	5	0.00%	6.1%	YSAVLDAVIASAGLLR	99.7%	45.9	25	45.9	1	0	0	1618.92	46	61
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	8	10	17	0.02%	17.5%	ALDQSDNDMSAVYR	99.7%	79.2	25	79.2	4	0	0	1584.70	536	549
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	8	10	17	0.02%	17.5%	CDLFIQEGAR	99.7%	57.5	25	47.3	2	0	0	1208.57	303	312
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	8	10	17	0.02%	17.5%	DLVLGPSGVLQGIRPGK	99.7%	72	25	72	2	0	0	1706.00	339	355
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	8	10	17	0.02%	17.5%	FFGTEDHAWIK	99.1%	34.1	25	31.8	1	0	0	1350.65	46	56
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	8	10	17	0.02%	17.5%	FQQAVDAVEEFLR	99.7%	96.3	25	87	2	0	0	1551.78	79	91
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	8	10	17	0.02%	17.5%	GLYEDCSSCFQAMGK	99.7%	65.7	25	65.7	3	0	0	1752.70	408	422
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	8	10	17	0.02%	17.5%	TAEKCDLFIQEGAR	99.7%	42.8	25	36.3	0	1	0	1637.80	299	312
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	8	10	17	0.02%	17.5%	TSFFLGEVGNAAK	99.7%	88.4	25	80.7	2	0	0	1340.68	423	435

Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	7	9	23	0.02%	9.4%	EAMNDPLLER	98.7%	32.6	25	25.2	1	0	0	1187.57	244	253
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	7	9	23	0.02%	9.4%	FTDILVR	95.7%	27.7	25	20.5	1	0	0	863.50	146	152
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	7	9	23	0.02%	9.4%	HQSFVLVGETGSGK	99.7%	47.3	25	47.3	2	0	0	1445.74	153	166
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	7	9	23	0.02%	9.4%	SLMSADNVR	99.1%	34	25	26.9	1	0	0	992.48	653	661
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	7	9	23	0.02%	9.4%	SNLGSVVLQLK	99.7%	76.2	25	67.9	2	0	0	1157.69	505	515
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	7	9	23	0.02%	9.4%	TLATDILMGVLK	99.7%	97	25	82.1	10	0	0	1290.73	266	277
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	7	9	23	0.02%	9.4%	YGVIILDEAHER	99.7%	54.6	25	53.2	3	3	0	1414.73	254	265
Putative ribonuclease	YBEY	YBEY_HUMAN	19.3	99.9%	2	2	3	0.00%	12.0%	AVLDELGRR	97.6%	30	25	20.2	2	0	0	1028.58	143	151
Putative ribonuclease	YBEY	YBEY_HUMAN	19.3	99.9%	2	2	3	0.00%	12.0%	FDLGIICVDNK	97.6%	30	25	21.6	1	0	0	1293.65	35	45
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	26	0.03%	16.6%	DLAQALINR	99.7%	42	25	39	2	0	0	1013.57	323	331
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	26	0.03%	16.6%	ELLLSAIDSVNATSK	99.7%	119	25	116	4	0	0	1560.85	493	507
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	26	0.03%	16.6%	GADSELSTVPSVTK	99.7%	85.3	25	72.8	1	0	0	1390.71	656	669
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	26	0.03%	16.6%	GISAGAVQTAGK	99.7%	75.1	25	74.7	3	0	0	1059.58	80	91
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	26	0.03%	16.6%	GVNLDPLGK	98.0%	30.7	25	28.9	1	0	0	912.52	332	340
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	26	0.03%	16.6%	IQDIVGILR	99.7%	67.6	25	46.7	4	0	0	1026.63	243	251
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	26	0.03%	16.6%	LGVTNTIISHYDGR	99.1%	25.8	25	25.6	0	1	0	1545.80	432	445
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	26	0.03%	16.6%	LVPTGLDFGQEGFTR	99.7%	80.9	25	78.2	4	0	0	1636.83	539	553
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	26	0.03%	16.6%	NTGVILANDANAER	99.7%	94.6	25	87.9	1	0	0	1457.73	408	421
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	26	0.03%	16.6%	SVVGNLHR	99.2%	34.7	25	25.2	2	0	0	881.50	424	431
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	11	11	26	0.03%	16.6%	TQASSSFQDSSQPAGK	99.7%	71.1	25	70.9	3	0	0	1625.74	670	685
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	3	3	5	0.00%	3.9%	ISHLSGSGSGDER	96.2%	28.2	25	28.2	1	0	0	1301.61	204	216
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	3	3	5	0.00%	3.9%	QDGGTAPVASASPK	97.7%	30.2	25	20.9	1	0	0	1285.64	770	783
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	3	3	5	0.00%	3.9%	VGAGAGAAPFR	99.7%	61.8	25	49.5	3	0	0	973.52	349	359
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	11	13	39	0.04%	41.1%	CMTNTPVVVR	99.7%	60.8	25	45.7	7	0	0	1176.59	120	129
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	11	13	39	0.04%	41.1%	EGATVYATGTHAQVEDGR	99.7%	51.7	25	49.2	0	3	0	1861.87	130	147
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	11	13	39	0.04%	41.1%	ELQSMADQEQVSPAAIK	99.7%	73.2	25	62.5	2	0	0	1844.91	267	283
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	11	13	39	0.04%	41.1%	ELQSMADQEQVSPAAIKK	99.6%	28.4	25	28.4	0	3	0	1989.00	267	284
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	11	13	39	0.04%	41.1%	GFTAAGVLAAHK	99.7%	67.9	25	58.9	4	0	0	1142.63	18	29
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	11	13	39	0.04%	41.1%	IMASSPDMDLATVSALR	99.7%	68.3	25	68.3	3	0	0	1777.88	30	46
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	11	13	39	0.04%	41.1%	LDSPAGTALSPSGHTK	99.7%	82.3	25	70.3	4	3	0	1538.78	292	307
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	11	13	39	0.04%	41.1%	LGAQALLGAAK	99.7%	90.1	25	83.3	4	0	0	1012.62	205	215
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	11	13	39	0.04%	41.1%	LSAFRPAPR	99.6%	37.7	25	30.2	1	0	0	1014.58	108	116
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	11	13	39	0.04%	41.1%	SLLINAVEASCIR	99.7%	85.4	25	79.1	6	0	0	1445.78	252	264
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	11	13	39	0.04%	41.1%	TILDKVK	96.5%	28.5	25	17.8	1	0	0	816.52	285	291
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	11	13	39	0.04%	41.1%	VKLDSPAGTALSPSGHTK	99.7%	40.8	25	25.7	0	4	0	1765.94	290	307
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	10	14	29	0.03%	33.4%	ELQSMADQEK	99.7%	46	25	36	4	0	0	1194.53	267	276
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	10	14	29	0.03%	33.4%	GFTAAGILSAHK	99.7%	66.8	25	58.8	3	0	0	1172.64	18	29
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	10	14	29	0.03%	33.4%	IIASSPEMNLPTVSALR	99.7%	82.5	25	76.1	3	0	0	1814.97	30	46
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	10	14	29	0.03%	33.4%	ISPAALKK	95.2%	27.3	25	24.1	1	0	0	827.54	277	284
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	10	14	29	0.03%	33.4%	LESPTVSTLTPSSPGK	99.7%	71.1	25	55	2	0	0	1600.84	292	307
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	10	14	29	0.03%	33.4%	LMAFQPAPK	99.7%	45.8	25	32.8	4	0	0	1002.54	108	116
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	10	14	29	0.03%	33.4%	MGVNLTR	99.7%	40.2	25	15.6	2	0	0	806.42	48	54
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	10	14	29	0.03%	33.4%	MLLDSEQHPCQLK	99.7%	45.2	25	45.2	2	0	0	1614.76	216	228
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	10	14	29	0.03%	33.4%	SLLINAVEASCIR	99.7%	85.4	25	79.1	6	0	0	1445.78	252	264
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	10	14	29	0.03%	33.4%	VKLESPTVSTLTPSSPGK	99.7%	76	25	69	2	0	0	1828.01	290	307
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	6	9	17	0.02%	24.8%	AATMSAVEAATCR	99.7%	79.5	25	79.3	2	0	0	1354.61	255	267
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	6	9	17	0.02%	24.8%	IAAQTLLGTAK	99.7%	95.7	25	95.7	2	0	0	1086.65	208	218
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	6	9	17	0.02%	24.8%	MAGAIAQGLIR	99.7%	77.9	25	68.2	4	0	0	1116.62	19	29
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	6	9	17	0.02%	24.8%	MGMPSSLAHR	99.7%	49.2	25	37.4	3	0	0	1086.52	198	207
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	6	9	17	0.02%	24.8%	RVGFVGAGR	98.6%	32.3	25	26.1	2	0	0	918.53	10	18
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	6	9	17	0.02%	24.8%	VEAQHILASAPTDR	99.7%	99.7	25	99.7	2	2	0	1507.79	33	46

Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	7	7	11	0.01%	7.6%	AEAEAQAEELSFPR	99.7%	111	25	106	2	0	0	1547.73	929	942
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	7	7	11	0.01%	7.6%	ALAVSDLNR	99.4%	36	25	12.1	1	0	0	958.53	1062	1070
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	7	7	11	0.01%	7.6%	DAHQSLLATR	99.7%	46.3	25	29	2	0	0	1111.59	572	581
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	7	7	11	0.01%	7.6%	DFTATFGPLDSLNTR	99.7%	91.8	25	90.8	2	0	0	1654.81	1022	1036
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	7	7	11	0.01%	7.6%	GANAVGYTNYPDNVVFK	99.7%	47	25	47	1	0	0	1828.89	645	661
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	7	7	11	0.01%	7.6%	GTPLDTEVPMER	97.2%	29.4	25	29.3	1	0	0	1344.65	819	830
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	7	7	11	0.01%	7.6%	TSTAPAASPNVR	99.7%	53.7	25	40	2	0	0	1171.61	19	30
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	16	18	31	0.03%	35.9%	AAASTDYYK	99.7%	39.3	25	39.3	2	0	0	989.46	236	244
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	16	18	31	0.03%	35.9%	AAASTDYYKR	99.7%	68.4	25	57.4	2	0	0	1145.56	236	245
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	16	18	31	0.03%	35.9%	AHGFTFTR	98.9%	33.2	25	33.2	1	0	0	936.47	120	127
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	16	18	31	0.03%	35.9%	EILAELTGR	99.7%	48	25	36	2	0	0	1001.56	133	141
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	16	18	31	0.03%	35.9%	EILAELTGRK	99.7%	41.9	25	34.3	1	0	0	1129.66	133	142
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	16	18	31	0.03%	35.9%	GANQWIK	99.7%	45.5	25	31	2	0	0	816.44	379	385
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	16	18	31	0.03%	35.9%	GDFIPGLR	95.3%	27.3	25	13.4	1	0	0	874.48	246	253
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	16	18	31	0.03%	35.9%	GPILMELQTYR	99.7%	68.7	25	68.7	2	0	0	1320.70	278	288
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	16	18	31	0.03%	35.9%	LEEGPPVTTVLTR	99.7%	80.6	25	74.4	3	0	0	1411.78	46	58
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	16	18	31	0.03%	35.9%	LPCIFICENNR	99.7%	63.4	25	61.7	2	0	0	1435.68	216	226
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	16	18	31	0.03%	35.9%	NFYGGNGIVGAQVPLGAGIALACK	99.7%	40.4	25	40.4	0	1	0	2347.22	159	182
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	16	18	31	0.03%	35.9%	RGDFIPGLR	98.9%	33.2	25	21.3	2	0	0	1030.58	245	253
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	16	18	31	0.03%	35.9%	SKSDPIMLLK	96.6%	28.7	25	15.1	1	0	0	1147.64	312	321
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	16	18	31	0.03%	35.9%	TREEIQEVR	99.5%	36.8	25	13.2	2	0	0	1159.61	303	311
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	16	18	31	0.03%	35.9%	VDGMDILCVR	99.7%	73.7	25	66.3	3	0	0	1177.57	254	263
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	16	18	31	0.03%	35.9%	YGMGTSVER	99.7%	58.5	25	52.2	4	0	0	1015.45	227	235
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	9	12	23	0.02%	30.4%	DFLIPIGK	95.5%	27.6	25	19.3	1	0	0	902.53	220	227
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	9	12	23	0.02%	30.4%	DIIFAIKK	99.5%	36.8	25	27.6	2	0	0	947.59	348	355
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	9	12	23	0.02%	30.4%	EGVECEVINMR	99.7%	67.1	25	65.9	4	0	0	1351.60	259	269
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	9	12	23	0.02%	30.4%	ILEDNSIPQVK	99.7%	63.6	25	45.8	2	0	0	1255.69	337	347
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	9	12	23	0.02%	30.4%	IMEGPAFNFLDAPAVR	99.7%	80.3	25	77.9	4	0	0	1747.88	309	324
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	9	12	23	0.02%	30.4%	TYYMSGGLQPVPIVFR	99.7%	57.9	25	55.2	4	0	0	1843.94	130	145
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	9	12	23	0.02%	30.4%	VFLLGEEVAQYDGAYK	99.7%	43.9	25	43.9	2	0	0	1801.90	53	68
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	9	12	23	0.02%	30.4%	VTGADVPMPYAK	99.7%	44.7	25	33.4	2	0	0	1248.63	325	336
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	9	12	23	0.02%	30.4%	VVSPWNSEDAK	99.6%	38	25	24.2	2	0	0	1231.60	174	184
Pyruvate dehydrogenase protein X component, mitochondrial	PDHX	ODPX_HUMAN	54.1	99.8%	2	2	4	0.00%	4.6%	HSLDASQGTATGPR	99.7%	66.7	25	60.8	2	0	0	1397.68	195	208
Pyruvate dehydrogenase protein X component, mitochondrial	PDHX	ODPX_HUMAN	54.1	99.8%	2	2	4	0.00%	4.6%	VVDDELATR	99.7%	47.8	25	40.4	2	0	0	1017.52	477	485
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	AEGSDVANAVLDGADCIMLSGETAK	99.7%	87.9	25	87.9	4	4	0	2494.14	343	367
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	AGKPVICATQMLESMIK	99.7%	41.9	25	41.2	2	4	0	1876.97	320	336
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	CCSGAIIVLTK	99.7%	78.7	25	72.4	4	0	0	1221.63	423	433
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	CDENILWLDYK	99.7%	98.8	25	98.2	2	0	0	1468.68	152	162
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	DPVQEAWAEDVDLR	99.7%	95.5	25	94.9	2	0	0	1642.77	476	489
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	EAEAAIYHLQLFEELR	99.5%	27.4	25	26.9	0	1	0	1931.99	384	399
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	EAEAAIYHLQLFEELRR	99.7%	57.5	25	55.5	0	3	0	2088.09	384	400
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	FDEILEASDGIMVAR	99.7%	111	25	109	3	0	0	1665.82	280	294
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	FGVEQDVDMVFASFIR	99.7%	126	25	121	15	4	0	1859.90	231	246
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	GADFLVTEVENGGSLGSK	99.7%	132	25	130	6	0	0	1779.88	189	206
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	GADFLVTEVENGGSLGSKK	99.7%	70.8	25	64	2	3	0	1907.97	189	207
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	GDLGIEIPAEK	99.7%	73.8	25	47.9	13	0	0	1141.61	295	305
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	GDYPLEAVR	99.7%	67.8	25	57.6	12	0	0	1019.52	368	376
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	GIFPVLCK	98.1%	30.9	25	12.9	1	0	0	933.52	468	475
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	GIFPVLCKDPVQEAWAEDVDLR	99.7%	57.2	25	57.2	2	2	0	2557.28	468	489
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	GSGTAEVELK	99.7%	61.3	25	41	3	0	0	990.51	126	135
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	GSGTAEVELKK	99.7%	55.2	25	41.7	12	0	0	1118.61	126	136

Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	GVNLPGAAVDLPAVSEK	99.7%	125	25	123	2	0	0	1636.89	208	224
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	GVNLPGAAVDLPAVSEKDIQDLK	99.7%	30.8	25	30.8	0	3	0	2349.27	208	230
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	ITLDNAYMEK	99.7%	66.5	25	65.3	6	0	0	1197.58	142	151
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	IYVDDGLISLQVK	99.7%	109	25	107	11	0	0	1462.82	174	186
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	KGVNLPGAAVDLPAVSEK	99.7%	44.8	25	41.5	1	2	0	1764.99	207	224
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	LAPITSDPTEATAVGAVEASFK	99.7%	133	25	133	4	3	0	2175.12	401	422
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	LDIDSPPITAR	99.7%	71.2	25	65.7	16	0	0	1197.65	33	43
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	LNFSHGTHEYHAETIK	99.7%	40	25	40	1	2	0	1883.90	74	89
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	MQHLIAR	99.7%	43.1	25	10.3	12	0	0	884.48	377	383
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	NTGIICTIGPASR	99.7%	99.6	25	96.2	14	0	0	1359.71	44	56
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	RFDEILEASDGIMVAR	99.7%	98	25	94	6	6	0	1821.92	279	294
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	SVETLKEMIK	99.7%	54.5	25	43.1	8	0	0	1177.65	57	66
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	TATESFASDPILYRPVAVALDTK	99.7%	55.1	25	55.1	2	8	0	2465.29	93	115
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	TATESFASDPILYRPVAVALDTKGPEIR	99.7%	50.3	25	50.3	0	2	0	3017.59	93	120
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	220	0.22%	65.3%	VNFAMNVGK	99.7%	68.3	25	58.9	7	0	0	979.50	490	498
Queuine tRNA-ribosyltransferase subunit QTRTD1	QTRTD1	QTRD1_HUMAN	46.7	100.0%	3	3	6	0.01%	8.7%	GVDLFESFFPYQVTER	99.7%	79.8	25	78.3	2	0	0	1933.93	267	282
Queuine tRNA-ribosyltransferase subunit QTRTD1	QTRTD1	QTRD1_HUMAN	46.7	100.0%	3	3	6	0.01%	8.7%	LQEESEVLQK	99.7%	55.7	25	45.6	2	0	0	1202.63	177	186
Queuine tRNA-ribosyltransferase subunit QTRTD1	QTRTD1	QTRD1_HUMAN	46.7	100.0%	3	3	6	0.01%	8.7%	SLLFLDNCLR	99.7%	49.5	25	38.2	2	0	0	1250.66	167	176
Rab3 GTPase-activating protein non-catalytic subunit	RAB3GAP2	RBGPR_HUMAN	156.0	100.0%	4	4	4	0.00%	3.2%	VAQFLVIYAPR	99.7%	60.3	25	60.3	1	0	0	1276.74	461	471
Rab3 GTPase-activating protein non-catalytic subunit	RAB3GAP2	RBGPR_HUMAN	156.0	100.0%	4	4	4	0.00%	3.2%	VILLDVAR	98.3%	31.5	25	14.4	1	0	0	898.57	408	415
Rab3 GTPase-activating protein non-catalytic subunit	RAB3GAP2	RBGPR_HUMAN	156.0	100.0%	4	4	4	0.00%	3.2%	VSSLQAEPLPR	99.7%	54.3	25	44.1	1	0	0	1196.66	914	924
Rab3 GTPase-activating protein non-catalytic subunit	RAB3GAP2	RBGPR_HUMAN	156.0	100.0%	4	4	4	0.00%	3.2%	VVSAAVQAQHSATK	99.7%	43.8	25	38	1	0	0	1396.75	1220	1233
Rab-like protein 2A	RABL2A	RBL2A_HUMAN	26.1	99.8%	2	2	3	0.00%	11.0%	IICLGDSAVGK	99.7%	56.5	25	52.3	1	0	0	1132.60	24	34
Rab-like protein 2A	RABL2A	RBL2A_HUMAN	26.1	99.8%	2	2	3	0.00%	11.0%	TILVDFWDTAGQER	99.7%	67.7	25	61	2	0	0	1650.81	69	82
Ragulator complex protein LAMTOR1	LAMTOR1	LTOR1_HUMAN	17.7	99.8%	2	2	3	0.00%	15.5%	IAAYAYSALSQIR	99.7%	55.5	25	44.2	2	0	0	1426.77	135	147
Ragulator complex protein LAMTOR1	LAMTOR1	LTOR1_HUMAN	17.7	99.8%	2	2	3	0.00%	15.5%	LAVLSSSLTHWK	98.0%	30.7	25	22.9	1	0	0	1341.75	92	103
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	15	16	32	0.03%	28.8%	AFNSSSFNSNTFLTR	99.7%	99.3	25	86.1	3	0	0	1692.80	501	515
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	15	16	32	0.03%	28.8%	GAVAIADAIR	99.7%	70.3	25	56.5	4	0	0	956.55	280	289
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	15	16	32	0.03%	28.8%	GAVAMAETLK	99.7%	41	25	18.6	3	0	0	990.53	252	261
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	15	16	32	0.03%	28.8%	ILAAALTECHR	99.7%	46.6	25	41.3	2	0	0	1254.66	161	171
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	15	16	32	0.03%	28.8%	LLVHMGLLK	97.5%	29.9	25	28	1	0	0	1023.64	516	524
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	15	16	32	0.03%	28.8%	LNNCGMGIGGGK	99.7%	44.9	25	38.3	1	0	0	1177.55	149	160
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	15	16	32	0.03%	28.8%	LNTAEDAKDVIK	99.7%	47.5	25	31.6	1	0	0	1316.71	32	43
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	15	16	32	0.03%	28.8%	MAVQDAVDALMQK	99.7%	49	25	47.8	2	0	0	1419.70	488	500
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	15	16	32	0.03%	28.8%	QVEVINFGDCLVR	99.7%	69.3	25	68.7	2	0	0	1548.78	265	277
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	15	16	32	0.03%	28.8%	SKGAVAIADAIR	96.6%	28.6	25	25	1	0	0	1171.68	278	289
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	15	16	32	0.03%	28.8%	SSACFTLQELK	99.7%	51.6	25	45.7	2	0	0	1283.63	138	148
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	15	16	32	0.03%	28.8%	SSVLIAQQTDTSDPEK	99.7%	86.2	25	81.2	1	0	0	1718.84	453	468
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	15	16	32	0.03%	28.8%	TQVAGGQLSFK	99.7%	56.8	25	46.9	4	0	0	1135.61	16	26
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	15	16	32	0.03%	28.8%	VINLNDNTFTEK	99.7%	61.5	25	54.5	2	0	0	1407.71	240	251
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	15	16	32	0.03%	28.8%	VSSVFKDEATVR	99.7%	82.4	25	70.3	3	0	0	1337.71	476	487
Ran-specific GTPase-activating protein	RANBP1	RANG_HUMAN	23.3	100.0%	3	3	5	0.00%	15.4%	FASENDLPEWK	96.0%	28	25	16.9	1	0	0	1335.62	58	68
Ran-specific GTPase-activating protein	RANBP1	RANG_HUMAN	23.3	100.0%	3	3	5	0.00%	15.4%	FLNAENAQK	99.7%	56.3	25	38.4	2	0	0	1034.53	142	150
Ran-specific GTPase-activating protein	RANBP1	RANG_HUMAN	23.3	100.0%	3	3	5	0.00%	15.4%	TLEEDEEELFK	99.7%	68.1	25	63.9	2	0	0	1381.64	40	50
Ras GTPase-activating protein-binding protein 1	G3BP1	G3BP1_HUMAN	52.2	100.0%	3	3	4	0.00%	9.7%	EAGEQGDIEPR	99.7%	50.5	25	49.7	2	0	0	1200.55	321	331
Ras GTPase-activating protein-binding protein 1	G3BP1	G3BP1_HUMAN	52.2	100.0%	3	3	4	0.00%	9.7%	FMQTFVLAPEGSVANK	99.4%	35.8	25	35.5	1	0	0	1738.88	108	123
Ras GTPase-activating protein-binding protein 1	G3BP1	G3BP1_HUMAN	52.2	100.0%	3	3	4	0.00%	9.7%	SSSPAPADIAQTVQEDLR	99.7%	54.7	25	54.7	1	0	0	1884.93	230	247
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	13	13	22	0.02%	9.5%	ALESGDVNTVWK	99.7%	60	25	49.8	2	0	0	1318.66	466	477
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	13	13	22	0.02%	9.5%	ALQSPALGLR	99.7%	41.8	25	38.8	2	0	0	1025.61	327	336
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	13	13	22	0.02%	9.5%	ATFYGEQVDYYK	99.7%	57.3	25	57.3	1	0	0	1483.67	1517	1528
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	13	13	22	0.02%	9.5%	FALGIFAINEAVESGDVGK	99.7%	52.6	25	52.6	1	0	0	1937.00	623	641

Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	13	13	22	0.02%	9.5%	GLQQQNSDWYLK	99.7%	38.5	25	31.2	1	0	0	1479.72	337	348
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	13	13	22	0.02%	9.5%	GVLLEIEDLQVNQFK	99.7%	44.9	25	37.9	2	0	0	1744.95	1572	1586
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	13	13	22	0.02%	9.5%	ILAIGLINEALDEGDAQK	99.7%	87.3	25	81.7	2	0	0	1883.01	539	556
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	13	13	22	0.02%	9.5%	LAAVALINAAIQK	99.7%	90.2	25	76.4	2	0	0	1295.80	389	401
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	13	13	22	0.02%	9.5%	LGNFFSPK	99.7%	45.1	25	39.7	2	0	0	909.48	81	88
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	13	13	22	0.02%	9.5%	LIFQMPQNK	96.6%	28.6	25	24.3	1	0	0	1118.60	989	997
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	13	13	22	0.02%	9.5%	LIVDVIR	98.8%	32.8	25	2.81	2	0	0	827.54	1391	1397
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	13	13	22	0.02%	9.5%	LQQTYAALNSK	99.7%	55.2	25	45.5	2	0	0	1236.66	1506	1516
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	13	13	22	0.02%	9.5%	TLQALQIPAAK	99.7%	73.9	25	65	2	0	0	1153.69	557	567
Ras suppressor protein 1	RSU1	RSU1_HUMAN	31.5	100.0%	2	2	2	0.00%	6.1%	HMQANPEPPK	98.0%	30.7	25	30.7	1	0	0	1148.55	249	258
Ras suppressor protein 1	RSU1	RSU1_HUMAN	31.5	100.0%	2	2	2	0.00%	6.1%	LQILSLR	96.4%	28.4	25	17.8	1	0	0	842.55	159	165
Ras-related protein Rab-10	RAB10	RAB10_HUMAN	22.5	99.9%	2	2	4	0.00%	17.0%	AFLTLAEDILR	99.7%	55.5	25	46	2	0	0	1261.72	162	172
Ras-related protein Rab-10	RAB10	RAB10_HUMAN	22.5	99.9%	2	2	4	0.00%	17.0%	LQIWDTAGQER	99.7%	61.3	25	0	6	0	0	1316.66	60	70
Ras-related protein Rab-10	RAB10	RAB10_HUMAN	22.5	99.9%	2	2	4	0.00%	17.0%	NIDEHANEDVER	99.5%	37.1	25	36.2	2	0	0	1440.64	106	117
Ras-related protein Rab-13	RAB13	RAB13_HUMAN	22.8	99.8%	2	2	3	0.00%	9.9%	SIKENASAGVER	99.7%	56.8	25	44.4	2	0	0	1260.65	105	116
Ras-related protein Rab-13	RAB13	RAB13_HUMAN	22.8	99.8%	2	2	3	0.00%	9.9%	TITTAYYR	96.6%	28.6	25	8.87	1	0	0	988.51	72	79
Ras-related protein Rab-18	RAB18	RAB18_HUMAN	23.0	100.0%	4	4	7	0.01%	24.3%	GAQGVILVYDVTR	99.7%	40.5	25	40.5	1	0	0	1390.77	80	92
Ras-related protein Rab-18	RAB18	RAB18_HUMAN	23.0	100.0%	4	4	7	0.01%	24.3%	IIQTPGLWESENQNK	99.7%	44	25	38	2	0	0	1756.89	169	183
Ras-related protein Rab-18	RAB18	RAB18_HUMAN	23.0	100.0%	4	4	7	0.01%	24.3%	ILIIGESGVGK	99.7%	49.2	25	19.1	2	0	0	1085.66	11	21
Ras-related protein Rab-18	RAB18	RAB18_HUMAN	23.0	100.0%	4	4	7	0.01%	24.3%	LAIWDTAGQER	99.7%	66.5	25	60.7	2	0	0	1259.64	59	69
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	5	7	17	0.02%	33.3%	EFADSLGIPFLETSAK	99.7%	64.6	25	50	1	0	0	1724.87	138	153
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	5	7	17	0.02%	33.3%	LQIWDTAGQER	99.7%	61.3	25	0	6	0	0	1316.66	59	69
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	5	7	17	0.02%	33.3%	MGPGAASGGERPNLK	99.7%	57.7	25	46.9	4	2	0	1441.72	173	187
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	5	7	17	0.02%	33.3%	NATNVEQAFMTMAAEIK	99.7%	48.1	25	20	2	0	0	1900.88	154	170
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	5	7	17	0.02%	33.3%	QWLQEIDR	99.7%	50.1	25	24.4	2	0	0	1087.55	101	108
Ras-related protein Rab-23	RAB23	RAB23_HUMAN	26.7	100.0%	2	2	2	0.00%	10.5%	TIGVDFLER	98.0%	30.7	25	30.7	1	0	0	1049.56	41	49
Ras-related protein Rab-23	RAB23	RAB23_HUMAN	26.7	100.0%	2	2	2	0.00%	10.5%	VVAEVGDIPTVLVQNK	99.7%	46.5	25	46.5	1	0	0	1680.95	107	122
Ras-related protein Rab-32	RAB32	RAB32_HUMAN	25.0	100.0%	3	3	6	0.01%	15.1%	DNINIEEAAR	99.7%	67.5	25	61.6	2	0	0	1144.56	177	186
Ras-related protein Rab-32	RAB32	RAB32_HUMAN	25.0	100.0%	3	3	6	0.01%	15.1%	EAVGAFVVFDISR	99.7%	60.1	25	60.1	2	0	0	1409.74	98	110
Ras-related protein Rab-32	RAB32	RAB32_HUMAN	25.0	100.0%	3	3	6	0.01%	15.1%	LQLWDIAGQER	99.7%	47.4	25	36.8	2	0	0	1328.70	77	87
Ras-related protein Rab-5A	RAB5A	RAB5A_HUMAN	23.7	99.7%	2	2	3	0.00%	16.3%	GVDLTEPTQPTR	99.7%	59	25	48.2	2	0	0	1313.67	198	209
Ras-related protein Rab-5A	RAB5A	RAB5A_HUMAN	23.7	99.7%	2	2	3	0.00%	16.3%	LVLLGESAVGK	98.5%	32	25	24.6	1	0	0	1085.66	23	33
Ras-related protein Rab-5A	RAB5A	RAB5A_HUMAN	23.7	99.7%	2	2	3	0.00%	16.3%	NEPQNPGANSAR	94.7%	26.9	25	26.1	1	0	0	1254.58	184	195
Ras-related protein Rab-5C	RAB5C	RAB5C_HUMAN	23.5	100.0%	3	3	4	0.00%	18.1%	LVLLGESAVGK	98.5%	32	25	24.6	1	0	0	1085.66	24	34
Ras-related protein Rab-5C	RAB5C	RAB5C_HUMAN	23.5	100.0%	3	3	4	0.00%	18.1%	QASPNIVIALAGNK	99.7%	46	25	45.4	2	0	0	1395.80	122	135
Ras-related protein Rab-5C	RAB5C	RAB5C_HUMAN	23.5	100.0%	3	3	4	0.00%	18.1%	TAMNVNEIFMAIAK	99.7%	46.1	25	2.03	1	0	0	1568.78	167	180
Ras-related protein Rab-6A	RAB6A	RAB6A_HUMAN	23.6	100.0%	2	3	4	0.00%	16.3%	ELNVMFIETSAK	99.7%	44.3	25	44.3	2	0	0	1397.70	147	158
Ras-related protein Rab-6A	RAB6A	RAB6A_HUMAN	23.6	100.0%	2	3	4	0.00%	16.3%	LQLWDTAGQER	99.7%	61.3	25	0	6	0	0	1316.66	64	74
Ras-related protein Rab-6A	RAB6A	RAB6A_HUMAN	23.6	100.0%	2	3	4	0.00%	16.3%	LVFLGEQSVGK	99.7%	65.2	25	48.4	2	0	0	1176.66	16	26
Ras-related protein Rab-7a	RAB7A	RAB7A_HUMAN	23.5	100.0%	3	3	5	0.00%	18.4%	DPENFPFVVLGNK	99.5%	36.4	25	36.4	1	0	0	1475.75	114	126
Ras-related protein Rab-7a	RAB7A	RAB7A_HUMAN	23.5	100.0%	3	3	5	0.00%	18.4%	EAINVEQAFQTIAR	99.7%	73.6	25	69.8	2	0	0	1589.83	158	171
Ras-related protein Rab-7a	RAB7A	RAB7A_HUMAN	23.5	100.0%	3	3	5	0.00%	18.4%	VIILGDSGVGK	99.7%	38.6	25	23.7	2	0	0	1057.63	11	21
Ras-related protein Rab-9A	RAB9A	RAB9A_HUMAN	22.8	99.8%	2	2	3	0.00%	12.4%	DATNVAAAFEEAVR	99.7%	83.7	25	74.7	1	0	0	1463.71	157	170
Ras-related protein Rab-9A	RAB9A	RAB9A_HUMAN	22.8	99.8%	2	2	3	0.00%	12.4%	VILLGDGGVGK	99.7%	62.7	25	38.5	2	0	0	1027.61	10	20
Ras-related protein R-Ras2	RRAS2	RRAS2_HUMAN	23.4	100.0%	2	2	3	0.00%	11.3%	LVVVGGGGVGK	99.2%	34.9	25	33.9	1	0	0	941.58	17	27
Ras-related protein R-Ras2	RRAS2	RRAS2_HUMAN	23.4	100.0%	2	2	3	0.00%	11.3%	QVTQEEGQQLAR	99.7%	67.9	25	57.2	2	0	0	1386.70	136	147
Regulation of nuclear pre-mRNA domain-containing protein 1A	RPRD1A	RPR1A_HUMAN	35.7	100.0%	2	2	2	0.00%	5.5%	IQSLPDLSR	99.5%	36.4	25	27.6	1	0	0	1028.57	283	291
Regulation of nuclear pre-mRNA domain-containing protein 1A	RPRD1A	RPR1A_HUMAN	35.7	100.0%	2	2	2	0.00%	5.5%	VLSIWEER	99.7%	40.1	25	35.4	1	0	0	1031.55	107	114
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	11	11	18	0.02%	10.7%	ADSVVVLLCR	99.7%	41.1	25	38.3	2	0	0	1131.62	201	210
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	11	11	18	0.02%	10.7%	AGLSQSLFER	99.7%	65.1	25	43.3	2	0	0	1107.58	689	698
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	11	11	18	0.02%	10.7%	IPSEQEQLR	99.7%	42.7	25	19.2	2	0	0	1099.57	245	253

Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	11	11	18	0.02%	10.7%	KLVNTINPGAR	99.7%	44.6	25	33.3	1	0	0	1182.70	929	939
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	11	11	18	0.02%	10.7%	LMQGDEICLR	99.0%	33.5	25	27.2	1	0	0	1234.59	367	376
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	11	11	18	0.02%	10.7%	LVNTINPGAR	99.3%	35.2	25	22	1	0	0	1054.60	930	939
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	11	11	18	0.02%	10.7%	TVLQRPLSLIQGPPGTGK	99.7%	37.7	25	37.7	0	2	0	1862.09	492	509
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	11	11	18	0.02%	10.7%	TVTSATIVYHLAR	99.7%	107	25	99.1	2	0	0	1431.80	510	522
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	11	11	18	0.02%	10.7%	VPDNYGDEIAIELR	99.7%	73.2	25	73.2	2	0	0	1603.80	394	407
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	11	11	18	0.02%	10.7%	YEDAYQYQNIFGPLVK	99.7%	54.6	25	54.6	2	0	0	1947.95	296	311
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	11	11	18	0.02%	10.7%	YGVIIVGNPK	99.7%	61	25	61	1	0	0	1059.62	879	888
Regulatory-associated protein of mTOR	RPTOR	RPTOR_HUMAN	149.0	100.0%	5	5	7	0.01%	4.6%	ALETIGANLQK	99.7%	41.7	25	30.3	1	0	0	1157.65	98	108
Regulatory-associated protein of mTOR	RPTOR	RPTOR_HUMAN	149.0	100.0%	5	5	7	0.01%	4.6%	LDDQIFLNR	99.7%	49.4	25	43.2	2	0	0	1133.60	1013	1021
Regulatory-associated protein of mTOR	RPTOR	RPTOR_HUMAN	149.0	100.0%	5	5	7	0.01%	4.6%	LYSLLSDPIPEVR	99.7%	39	25	22.1	1	0	0	1501.83	604	616
Regulatory-associated protein of mTOR	RPTOR	RPTOR_HUMAN	149.0	100.0%	5	5	7	0.01%	4.6%	QDLLVASLFR	99.7%	64.9	25	43.8	2	0	0	1161.66	339	348
Regulatory-associated protein of mTOR	RPTOR	RPTOR_HUMAN	149.0	100.0%	5	5	7	0.01%	4.6%	VLDTSSLTQSAPASPTNK	99.7%	58.2	25	58.2	1	0	0	1816.93	850	867
Replication factor C subunit 1	RFC1	RFC1_HUMAN	128.3	100.0%	4	4	7	0.01%	4.2%	AALLSGPPGVGK	99.0%	33.5	25	32.8	2	0	0	1066.63	646	657
Replication factor C subunit 1	RFC1	RFC1_HUMAN	128.3	100.0%	4	4	7	0.01%	4.2%	AIVAESLNNTSIK	99.7%	54.1	25	49.8	1	0	0	1359.75	688	700
Replication factor C subunit 1	RFC1	RFC1_HUMAN	128.3	100.0%	4	4	7	0.01%	4.2%	GGIQELIGLIK	99.7%	45.9	25	42.3	2	0	0	1140.70	732	742
Replication factor C subunit 1	RFC1	RFC1_HUMAN	128.3	100.0%	4	4	7	0.01%	4.2%	IIDEDGLLNLIR	99.7%	47.7	25	26.4	2	0	0	1383.78	469	480
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	9	10	17	0.02%	30.8%	APGSAGHYELPWVEK	99.7%	33.6	25	33.6	0	2	0	1640.81	27	41
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	9	10	17	0.02%	30.8%	EGNVPNIIIAGPPGTGK	99.7%	68	25	66.5	2	0	0	1633.89	66	82
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	9	10	17	0.02%	30.8%	FALACNASDKIIEPIQSR	99.7%	46.2	25	44.6	0	2	0	2033.05	167	184
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	9	10	17	0.02%	30.8%	IAEGVNSLLQMAGLLAR	99.7%	71.7	25	67.6	3	0	0	1755.98	327	343
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	9	10	17	0.02%	30.8%	IIEPIQSR	99.7%	42.8	25	28.4	1	0	0	955.56	177	184
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	9	10	17	0.02%	30.8%	LNEIVGNEDTVSR	99.7%	99.5	25	99.5	2	0	0	1445.72	47	59
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	9	10	17	0.02%	30.8%	LTDAQILTR	99.7%	87.8	25	77.1	2	0	0	1030.59	193	201
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	9	10	17	0.02%	30.8%	TTSILCLAR	99.7%	47.8	25	34	2	0	0	1034.57	83	91
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	9	10	17	0.02%	30.8%	VCDEPHPLLVK	96.7%	28.7	25	23.6	1	0	0	1306.68	254	264
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	11	13	21	0.02%	31.7%	AIYHLEAFVAK	99.7%	52.1	25	33.7	2	0	0	1261.69	328	338
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	11	13	21	0.02%	31.7%	ALLMCEACR	99.7%	44.5	25	44.5	3	0	0	1123.51	226	234
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	11	13	21	0.02%	31.7%	EGLNLPSQLAHR	99.7%	55.6	25	43.8	2	0	0	1334.72	203	214
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	11	13	21	0.02%	31.7%	ETANAIVSQQTPQR	99.7%	111	25	101	2	0	0	1542.79	257	270
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	11	13	21	0.02%	31.7%	IEHQTITTPSK	94.7%	26.9	25	15.9	1	0	0	1254.67	69	79
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	11	13	21	0.02%	31.7%	LDYHKEQAAQLR	99.7%	41.4	25	35.7	1	1	0	1471.77	16	27
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	11	13	21	0.02%	31.7%	LILCCNSTSK	99.1%	33.9	25	33.9	2	0	0	1195.58	161	170
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	11	13	21	0.02%	31.7%	TVAQSQQLETNSQR	99.7%	110	25	100	2	0	0	1589.79	114	127
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	11	13	21	0.02%	31.7%	VVIQEMLK	99.7%	50.1	25	26.3	2	0	0	959.56	106	113
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	11	13	21	0.02%	31.7%	VVLLTEVDK	99.3%	35	25	30.6	1	0	0	1015.60	131	139
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	11	13	21	0.02%	31.7%	VVLLTEVDKLTK	99.7%	64.2	25	64.2	2	0	0	1357.83	131	142
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	18	0.02%	28.1%	AITFLQSATR	99.7%	79.2	25	73.5	2	0	0	1107.62	241	250
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	18	0.02%	28.1%	ELFGPELFR	99.7%	52.1	25	36.5	2	0	0	1107.58	94	102
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	18	0.02%	28.1%	GTSISTKPPLTK	99.7%	47.7	25	32	2	0	0	1229.71	7	18
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	18	0.02%	28.1%	ISDEGIAYLVK	99.7%	87.4	25	80.8	2	0	0	1207.66	222	232
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	18	0.02%	28.1%	SLEGADLPNLLFYGPPGTGK	99.7%	57.7	25	57.3	2	0	0	2046.05	65	84
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	18	0.02%	28.1%	TSTILAAAR	99.7%	59.5	25	49.8	2	0	0	903.53	85	93
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	18	0.02%	28.1%	VITDIAGVIPAEK	99.7%	79.1	25	65.5	2	0	0	1325.77	261	273
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	18	0.02%	28.1%	VLELNASDER	99.7%	66.1	25	57.2	2	0	0	1145.58	105	114
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	18	0.02%	28.1%	VSEGDLRK	99.6%	37.6	25	14.8	2	0	0	903.49	233	240
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	7	8	13	0.01%	21.8%	ALNILQSTNMAFGK	99.7%	84.4	25	70.6	4	0	0	1523.79	216	229
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	7	8	13	0.01%	21.8%	ALVTLSSGDMR	99.7%	69	25	60	2	0	0	1149.59	204	214
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	7	8	13	0.01%	21.8%	FCLICNYLSK	99.7%	41.1	25	38.4	2	0	0	1317.63	151	160
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	7	8	13	0.01%	21.8%	FGPLTPELMVPR	98.9%	33.4	25	33.4	1	0	0	1356.73	174	185
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	7	8	13	0.01%	21.8%	GPILSFASTR	99.7%	61.8	25	56.5	2	0	0	1048.58	103	112

Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	7	8	13	0.01%	21.8%	TSTILACAK	99.7%	38.5	25	30.5	1	0	0	964.51	67	75
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	7	8	13	0.01%	21.8%	VDFPSSVR	96.9%	29	25	19.9	1	0	0	906.47	291	298
Required for meiotic nuclear division protein 1 homolog	RMND1	RMND1_HUMAN	51.6	100.0%	3	3	6	0.01%	7.6%	DAANILVMGVENSAK	99.7%	58.9	25	58.9	2	0	0	1531.78	205	219
Required for meiotic nuclear division protein 1 homolog	RMND1	RMND1_HUMAN	51.6	100.0%	3	3	6	0.01%	7.6%	EGDPGTIFFFR	99.7%	39.4	25	39.4	2	0	0	1285.62	220	230
Required for meiotic nuclear division protein 1 homolog	RMND1	RMND1_HUMAN	51.6	100.0%	3	3	6	0.01%	7.6%	IGELFALR	99.7%	47.3	25	35	2	0	0	918.54	353	360
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	5	5	9	0.01%	23.3%	AEELHYPLGER	99.2%	34.8	25	33.6	1	0	0	1313.65	25	35
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	5	5	9	0.01%	23.3%	EALLGVQEDVDEYVK	99.7%	90.9	25	90.9	2	0	0	1706.85	42	56
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	5	5	9	0.01%	23.3%	QLHDDYFYHDEL	99.7%	38.8	25	35.4	2	0	0	1594.68	306	317
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	5	5	9	0.01%	23.3%	VIDFDENTALDDAEEESFRK	99.7%	32.5	25	32.5	0	2	0	2343.06	130	149
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	5	5	9	0.01%	23.3%	WDPTANEDPEWILVEK	99.7%	64.8	25	62.4	2	0	0	1941.92	217	232
Retinoid-inducible serine carboxypeptidase	SCPEP1	RISC_HUMAN	50.8	100.0%	2	2	3	0.00%	4.4%	MAAGIGLELYK	99.7%	46.6	25	43.8	2	0	0	1165.63	172	182
Retinoid-inducible serine carboxypeptidase	SCPEP1	RISC_HUMAN	50.8	100.0%	2	2	3	0.00%	4.4%	SLETSAFVK	96.5%	28.5	25	14.5	1	0	0	981.53	408	416
Ribonuclease P protein subunit p14	RPP14	RPP14_HUMAN	13.7	99.8%	2	2	3	0.00%	13.7%	ICSSGLVK	97.5%	29.8	25	20.8	1	0	0	863.47	77	84
Ribonuclease P protein subunit p14	RPP14	RPP14_HUMAN	13.7	99.8%	2	2	3	0.00%	13.7%	PAPAATYER	99.3%	35	25	35	2	0	0	975.49	2	10
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	5	5	8	0.01%	26.8%	AVVLEYFTR	99.7%	49.8	25	47.1	1	0	0	1097.60	55	63
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	5	5	8	0.01%	26.8%	CPSYVGITGILLQETK	99.7%	57.4	25	57.4	2	0	0	1778.94	147	162
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	5	5	8	0.01%	26.8%	EANDSDVQPSGAQR	99.7%	80.2	25	73.6	2	0	0	1473.66	13	26
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	5	5	8	0.01%	26.8%	LFDIKPEQQR	99.3%	35.2	25	27.1	1	0	0	1273.69	86	95
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	5	5	8	0.01%	26.8%	SVIYHALSQK	99.7%	44.9	25	35.3	2	0	0	1145.63	3	12
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	9	10	23	0.02%	43.7%	AALLHGETR	99.7%	44.5	25	40.2	2	0	0	967.53	227	235
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	9	10	23	0.02%	43.7%	GLAFELVYSPAIK	99.7%	60.4	25	57.5	4	0	0	1407.79	149	161
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	9	10	23	0.02%	43.7%	GPYDVANLGLLFGLSESDAK	99.7%	49.2	25	49.2	1	0	0	2066.04	199	218
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	9	10	23	0.02%	43.7%	KTAFGIISTVK	99.7%	52.1	25	52	2	0	0	1164.70	236	246
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	9	10	23	0.02%	43.7%	LTIIVSDPSHCNVLR	97.4%	29.7	25	29.7	1	0	0	1723.92	77	91
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	9	10	23	0.02%	43.7%	LYDVVAVFPK	99.7%	72.1	25	72.1	4	0	0	1150.65	99	108
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	9	10	23	0.02%	43.7%	NVIISSAAERPLEIR	99.7%	56	25	45.2	2	0	0	1667.94	184	198
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	9	10	23	0.02%	43.7%	RPPINVAIDR	99.7%	38.7	25	21.4	3	0	0	1150.67	139	148
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	9	10	23	0.02%	43.7%	YTISSALNLMQICK	99.7%	91.7	25	84.9	4	0	0	1641.83	168	181
Ribonuclease P protein subunit p38	RPP38	RPP38_HUMAN	31.8	100.0%	3	3	4	0.00%	11.0%	NTTDFVDEVR	99.7%	55	25	43.5	2	0	0	1195.56	185	194
Ribonuclease P protein subunit p38	RPP38	RPP38_HUMAN	31.8	100.0%	3	3	4	0.00%	11.0%	QASVTLQPLK	99.7%	39.1	25	23.4	1	0	0	1084.64	251	260
Ribonuclease P protein subunit p38	RPP38	RPP38_HUMAN	31.8	100.0%	3	3	4	0.00%	11.0%	QLAIGVNEVTR	94.7%	26.9	25	16.1	1	0	0	1199.67	112	122
Ribonuclease P/MRP protein subunit POP5	POP5	POP5_HUMAN	18.8	99.8%	2	2	3	0.00%	15.3%	LSLDDRVLSSLVR	98.1%	30.9	25	30.9	1	0	0	1472.84	22	34
Ribonuclease P/MRP protein subunit POP5	POP5	POP5_HUMAN	18.8	99.8%	2	2	3	0.00%	15.3%	YLNAYTGIVLLR	99.7%	72.7	25	66.8	2	0	0	1395.80	57	68
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	7	7	12	0.01%	8.1%	AGPEGTSQEIPK	99.7%	65.7	25	53.2	2	0	0	1213.61	89	100
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	7	7	12	0.01%	8.1%	EMLGPVTFIWK	99.0%	33.8	25	28.9	2	0	0	1320.70	303	313
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	7	7	12	0.01%	8.1%	ISDQDLNR	98.3%	31.4	25	9.93	1	0	0	960.47	567	574
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	7	7	12	0.01%	8.1%	LGWGSGWDVLLPK	99.7%	56.7	25	53.2	1	0	0	1427.77	612	624
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	7	7	12	0.01%	8.1%	NQPTNVTLSSGFVADR	99.7%	86.9	25	86.9	2	0	0	1705.85	15	30
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	7	7	12	0.01%	8.1%	SSNSLVFQTLPR	99.7%	67.8	25	56.9	2	0	0	1348.72	126	137
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	7	7	12	0.01%	8.1%	YITASTFAQAR	99.7%	45	25	38.3	2	0	0	1228.63	101	111
Ribonucleoside-diphosphate reductase subunit M2 B	RRM2B	RIR2B_HUMAN	40.7	100.0%	2	2	3	0.00%	7.1%	EFLFNAIETMPYVK	98.6%	32.4	25	32.4	1	0	0	1701.86	153	166
Ribonucleoside-diphosphate reductase subunit M2 B	RRM2B	RIR2B_HUMAN	40.7	100.0%	2	2	3	0.00%	7.1%	FSQEVQVPEAR	99.7%	64.1	25	54.3	2	0	0	1289.65	111	121
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	5	6	10	0.01%	17.6%	IFSGSSHQDLSQK	99.7%	70.2	25	64.4	2	0	0	1433.70	6	18
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	5	6	10	0.01%	17.6%	MVLVGDVKDR	99.7%	52.2	25	45.3	3	0	0	1147.61	205	214
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	5	6	10	0.01%	17.6%	NCTIVSPDAGGAK	99.7%	63.8	25	55.5	2	0	0	1289.62	164	176
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	5	6	10	0.01%	17.6%	RVTSIADR	95.6%	27.7	25	17.1	1	0	0	917.52	177	184
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	5	6	10	0.01%	17.6%	VTAVIPCFPYAR	99.7%	38.8	25	38.8	2	0	0	1393.73	85	96
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	2	2	2	0.00%	18.2%	FSNQETSVEIGESVR	99.7%	62.9	25	62.9	1	0	0	1681.80	35	49
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	2	2	2	0.00%	18.2%	MVLVGDVKDR	99.7%	52.2	25	45.3	3	0	0	1147.61	205	214
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	2	2	2	0.00%	18.2%	NCIIVSPDAGGAK	99.5%	37	25	37	1	0	0	1301.65	164	176
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	2	2	2	0.00%	18.2%	RVTSIADR	95.6%	27.7	25	17.1	1	0	0	917.52	177	184

Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	2	2	2	0.00%	18.2%	VTAVIPCFPYAR	99.7%	38.8	25	38.8	2	0	0	1393.73	85	96
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	5	5	8	0.01%	8.0%	FVNLISER	99.7%	60.5	25	40.7	2	0	0	977.54	122	129
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	5	5	8	0.01%	8.0%	GCYFVLDWLQK	99.7%	51.2	25	51.2	1	0	0	1428.70	172	182
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	5	5	8	0.01%	8.0%	LLDVTGGLGTDELR	99.7%	91.4	25	87.3	2	0	0	1458.78	99	112
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	5	5	8	0.01%	8.0%	SGNELPLAVASTADLIR	99.7%	95.6	25	83.7	2	0	0	1726.93	80	96
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	5	5	8	0.01%	8.0%	VECVLAELK	99.7%	39.6	25	17.7	1	0	0	1060.57	304	312
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	10	10	17	0.02%	19.2%	AAESETPGKSPEK	99.7%	56.1	25	45.9	2	0	0	1330.65	418	430
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	10	10	17	0.02%	19.2%	AVDALLTHCK	99.7%	48.6	25	46.3	2	0	0	1127.59	39	48
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	10	10	17	0.02%	19.2%	EINDCIGGTVLNISK	99.7%	84.7	25	81	2	0	0	1632.83	193	207
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	10	10	17	0.02%	19.2%	LLPSLIGR	99.2%	34.6	25	24.5	2	0	0	868.56	164	171
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	10	10	17	0.02%	19.2%	LLSSFDFFLTDAR	99.7%	85.1	25	84.7	2	0	0	1531.78	148	160
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	10	10	17	0.02%	19.2%	RLLPSLIGR	98.8%	32.9	25	27.4	1	0	0	1024.66	163	171
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	10	10	17	0.02%	19.2%	TPANEKVEIQK	99.7%	45.1	25	41	1	0	0	1256.68	375	385
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	10	10	17	0.02%	19.2%	TVSQIISLQTLK	99.7%	58.4	25	58.4	2	0	0	1330.79	125	136
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	10	10	17	0.02%	19.2%	TVSQIISLQTLKK	99.7%	39.2	25	39.2	1	0	0	1458.89	125	137
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	10	10	17	0.02%	19.2%	VPVSVNLLSK	99.7%	47.8	25	45.3	2	0	0	1055.65	179	188
Ribosomal protein S6 kinase alpha-1	RPS6KA1	KS6A1_HUMAN	82.7	99.8%	2	2	3	0.00%	4.1%	DPSEEIEILLR	99.7%	48.8	25	41.9	2	0	0	1313.69	455	465
Ribosomal protein S6 kinase alpha-1	RPS6KA1	KS6A1_HUMAN	82.7	99.8%	2	2	3	0.00%	4.1%	EASFVLHTIGK	99.7%	48	25	41.1	1	0	0	1201.66	511	521
Ribosomal protein S6 kinase alpha-1	RPS6KA1	KS6A1_HUMAN	82.7	99.8%	2	2	3	0.00%	4.1%	ICDFGFAK	99.7%	51.6	25	0	2	0	0	957.45	555	562
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	6	7	10	0.01%	9.3%	EASAVLFTITK	99.7%	47	25	47	2	0	0	1179.66	515	525
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	6	7	10	0.01%	9.3%	FSLSGGYWNSVSDTAK	99.7%	64.3	25	63.2	1	0	0	1718.80	638	653
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	6	7	10	0.01%	9.3%	GAMAATYSALNR	99.7%	51.4	25	51.4	2	0	0	1241.59	701	712
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	6	7	10	0.01%	9.3%	ICDFGFAK	99.7%	51.6	25	0	2	0	0	957.45	559	566
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	6	7	10	0.01%	9.3%	NQSPVLEPVGR	98.2%	31.2	25	26.8	1	0	0	1195.64	713	723
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	6	7	10	0.01%	9.3%	PLAQLADPWQK	99.7%	44.4	25	44.4	2	0	0	1266.68	2	12
Ribosomal RNA processing protein 1 homolog A	RRP1	RRP1_HUMAN	52.8	99.8%	2	2	3	0.00%	4.8%	LAGNEQVTR	99.7%	65.3	25	51.9	2	0	0	987.52	17	25
Ribosomal RNA processing protein 1 homolog A	RRP1	RRP1_HUMAN	52.8	99.8%	2	2	3	0.00%	4.8%	VGAEELTADQNLK	99.7%	57.6	25	46.4	1	0	0	1387.71	180	192
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	8	8	15	0.01%	13.6%	AGPGSLELCGLPSQK	99.7%	40.3	25	37.2	1	0	0	1513.77	575	589
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	8	8	15	0.01%	13.6%	ELLADQNLK	97.3%	29.6	25	21.5	2	0	0	1043.57	183	191
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	8	8	15	0.01%	13.6%	ETGGFSQEELLK	99.7%	52.7	25	41	2	0	0	1337.66	42	53
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	8	8	15	0.01%	13.6%	GSPTGGAQLLK	98.2%	31.3	25	24.4	1	0	0	1028.57	512	522
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	8	8	15	0.01%	13.6%	SILVSPTGPSR	98.8%	32.8	25	25.2	2	0	0	1113.63	702	712
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	8	8	15	0.01%	13.6%	SSTATHPPGPAVQLNK	99.7%	47.6	25	44.1	2	0	0	1604.84	661	676
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	8	8	15	0.01%	13.6%	TPTSSPASSPLVAK	99.7%	70.4	25	70.4	3	0	0	1342.72	728	741
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	8	8	15	0.01%	13.6%	VFCVEEEDSESSLQK	99.7%	91.1	25	84.2	2	0	0	1785.78	384	398
Ribosome biogenesis protein BRX1 homolog	BRIX1	BRX1_HUMAN	41.4	99.7%	2	2	2	0.00%	5.7%	FLVQNIHTLAELK	99.7%	75.6	25	66	1	0	0	1525.87	141	153
Ribosome biogenesis protein BRX1 homolog	BRIX1	BRX1_HUMAN	41.4	99.7%	2	2	2	0.00%	5.7%	FVLNLIK	94.7%	26.9	25	26.9	1	0	0	846.54	236	242
Ribosome production factor 2 homolog	RPF2	RPF2_HUMAN	35.6	100.0%	3	3	5	0.00%	10.1%	GPTVSNIR	98.1%	30.9	25	24	2	0	0	843.47	169	176
Ribosome production factor 2 homolog	RPF2	RPF2_HUMAN	35.6	100.0%	3	3	5	0.00%	10.1%	NISHDTFGTTYGR	99.7%	43.7	25	43.7	1	0	0	1468.68	253	265
Ribosome production factor 2 homolog	RPF2	RPF2_HUMAN	35.6	100.0%	3	3	5	0.00%	10.1%	THLASDDLYK	99.0%	33.5	25	33.2	2	0	0	1162.57	228	237
RING finger protein 219	RNF219	RN219_HUMAN	81.1	100.0%	5	5	7	0.01%	7.9%	FAVAALQSK	99.7%	41.5	25	29.4	2	0	0	934.54	217	225
RING finger protein 219	RNF219	RN219_HUMAN	81.1	100.0%	5	5	7	0.01%	7.9%	KIQSSLSSASPSK	99.7%	61	25	43.7	1	0	0	1319.72	710	722
RING finger protein 219	RNF219	RN219_HUMAN	81.1	100.0%	5	5	7	0.01%	7.9%	NLSLESQIK	99.7%	43	25	16.4	2	0	0	1031.57	117	125
RING finger protein 219	RNF219	RN219_HUMAN	81.1	100.0%	5	5	7	0.01%	7.9%	SLDLDGLSK	99.1%	34.2	25	15.8	1	0	0	947.50	561	569
RING finger protein 219	RNF219	RN219_HUMAN	81.1	100.0%	5	5	7	0.01%	7.9%	TILDPLTLVQGNQNEDK	99.7%	68	25	68	1	0	0	1897.99	126	142
RNA 3'-terminal phosphate cyclase	RTCA	RTCA_HUMAN	39.3	100.0%	5	5	11	0.01%	15.6%	AFVAGVLPFK	99.7%	48.6	25	39.5	2	0	0	1048.62	196	205
RNA 3'-terminal phosphate cyclase	RTCA	RTCA_HUMAN	39.3	100.0%	5	5	11	0.01%	15.6%	DLYVNIQPVQEPK	99.7%	85.8	25	85.8	2	0	0	1542.82	224	236
RNA 3'-terminal phosphate cyclase	RTCA	RTCA_HUMAN	39.3	100.0%	5	5	11	0.01%	15.6%	FGFIFNCDIK	99.7%	55.1	25	47	2	0	0	1260.61	147	156
RNA 3'-terminal phosphate cyclase	RTCA	RTCA_HUMAN	39.3	100.0%	5	5	11	0.01%	15.6%	QLNPINLTER	99.7%	56.1	25	43.7	2	0	0	1197.66	177	186
RNA 3'-terminal phosphate cyclase	RTCA	RTCA_HUMAN	39.3	100.0%	5	5	11	0.01%	15.6%	VSTALSCLLGLPLR	99.7%	59.3	25	54.4	3	0	0	1499.86	22	35
RNA 3'-terminal phosphate cyclase-like protein	RCL1	RCL1_HUMAN	40.8	99.8%	2	2	4	0.00%	6.2%	GVTNDQVDPSVDVLK	99.7%	49.7	25	43.8	2	0	0	1585.81	119	133

RNA 3'-terminal phosphate cyclase-like protein	RCL1	RCL1_HUMAN	40.8	99.8%	2	2	4	0.00%	6.2%	LLLEEIYR	99.7%	53	25	50.9	2	0	0	1048.60	282	289
RNA methyltransferase-like protein 1	RNMTL1	RMTL1_HUMAN	47.0	100.0%	3	3	6	0.01%	8.3%	EKQPLEESASR	99.7%	46.2	25	35.6	2	0	0	1273.64	72	82
RNA methyltransferase-like protein 1	RNMTL1	RMTL1_HUMAN	47.0	100.0%	3	3	6	0.01%	8.3%	KAPSEASAQEQR	99.7%	68.1	25	54.5	2	0	0	1301.64	60	71
RNA methyltransferase-like protein 1	RNMTL1	RMTL1_HUMAN	47.0	100.0%	3	3	6	0.01%	8.3%	VVFPSGEVVEQK	99.7%	54.3	25	44.3	2	0	0	1317.70	40	51
RNA polymerase II-associated factor 1 homolog	PAF1	PAF1_HUMAN	60.0	100.0%	4	4	6	0.01%	9.4%	AGVQSGTNALLVVK	99.7%	75.4	25	69	2	0	0	1356.78	339	352
RNA polymerase II-associated factor 1 homolog	PAF1	PAF1_HUMAN	60.0	100.0%	4	4	6	0.01%	9.4%	GYEENYFFIFR	99.7%	50.1	25	50.1	2	0	0	1484.68	306	316
RNA polymerase II-associated factor 1 homolog	PAF1	PAF1_HUMAN	60.0	100.0%	4	4	6	0.01%	9.4%	VTPVEVMPVFPDFK	99.7%	38.9	25	34.3	1	0	0	1604.84	199	212
RNA polymerase II-associated factor 1 homolog	PAF1	PAF1_HUMAN	60.0	100.0%	4	4	6	0.01%	9.4%	YGISNEKPEVK	98.4%	31.8	25	30.1	1	0	0	1263.66	144	154
RNA polymerase-associated protein CTR9 homolog	CTR9	CTR9_HUMAN	133.5	99.8%	2	2	2	0.00%	1.8%	FDLALAATEAR	99.7%	71.2	25	57.5	1	0	0	1177.62	805	815
RNA polymerase-associated protein CTR9 homolog	CTR9	CTR9_HUMAN	133.5	99.8%	2	2	2	0.00%	1.8%	LATSVLKDEK	98.2%	31.1	25	27.4	1	0	0	1103.63	764	773
RNA pseudouridylate synthase domain-containing protein 3	RPUSD3	RUSD3_HUMAN	38.5	100.0%	3	3	5	0.00%	8.8%	SGPLGDQPFAGLLPK	99.7%	38.9	25	38.9	2	0	0	1496.81	54	68
RNA pseudouridylate synthase domain-containing protein 3	RPUSD3	RUSD3_HUMAN	38.5	100.0%	3	3	5	0.00%	8.8%	TLQCLGLR	99.7%	41.6	25	16	2	0	0	960.53	342	349
RNA pseudouridylate synthase domain-containing protein 3	RPUSD3	RUSD3_HUMAN	38.5	100.0%	3	3	5	0.00%	8.8%	VGTVLGQR	96.6%	28.7	25	11.8	1	0	0	829.49	268	275
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	9	10	18	0.02%	23.3%	AIKVEQATKPSFESGR	99.7%	47.9	25	47.8	0	2	0	1747.93	78	93
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	9	10	18	0.02%	23.3%	DRDYSDHPSGGSYR	99.6%	37.3	25	37.3	1	0	0	1611.68	269	282
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	9	10	18	0.02%	23.3%	GFAFVTFESPADAK	99.7%	98	25	64.4	2	0	0	1486.72	50	63
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	9	10	18	0.02%	23.3%	GPPPSYGGSSR	99.7%	67.7	25	64.8	2	0	0	1061.50	299	309
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	9	10	18	0.02%	23.3%	IVEVLLMK	99.7%	53	25	50.5	4	0	0	944.59	34	41
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	9	10	18	0.02%	23.3%	LFIGGLNTETNEK	99.7%	84.5	25	71.8	2	0	0	1435.74	10	22
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	9	10	18	0.02%	23.3%	REPLPSR	97.6%	30	25	12	1	0	0	854.48	196	202
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	9	10	18	0.02%	23.3%	RGPPPPPR	99.7%	41.9	25	37.3	2	0	0	873.51	94	101
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	9	10	18	0.02%	23.3%	VEQATKPSFESGR	99.7%	52.9	25	48.4	2	0	0	1435.72	81	93
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	AHLSENELEALEK	99.7%	51.2	25	51.2	2	0	0	1482.74	794	806
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	ASNIVMLR	99.7%	60.7	25	48.6	1	0	0	903.51	127	134
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	CGVQNFK	99.7%	46	25	31.6	2	0	0	852.40	222	228
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	DGDYRDQDYR	95.2%	20.6	25	20.6	0	1	0	1302.53	99	108
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	DGLGSDNIGSR	99.7%	67.9	25	60.4	5	0	0	1090.51	854	864
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	EKYGIPEPPEPK	99.4%	35.9	25	26.9	2	0	0	1383.72	823	834
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	ESATADAGYAILEK	99.7%	117	25	111	5	0	0	1438.71	686	699
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	GDPTGAGPEASLEPGADSVSMQAFSR	99.7%	68.4	25	68.4	3	2	0	2550.14	473	498
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	GFAFVEFSHLQDATR	99.7%	121	25	115	6	5	0	1724.84	172	186
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	GLVAAYSGESDSEEEQER	99.7%	138	25	132	3	0	0	1955.85	727	744
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	GQLQSHGVQAR	99.7%	60.6	25	53.8	14	0	0	1180.62	147	157
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	GSSYGVTSTESYK	99.7%	77.2	25	77.2	2	0	0	1365.62	903	915
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	GSSYGVTSTESYKETLHK	96.0%	21.1	25	19.9	0	1	0	1973.95	903	920
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	HQQLSGLHK	97.5%	29.9	25	25.7	2	0	0	1047.57	777	785
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	INEDWLCNK	99.7%	61.6	25	35.5	5	0	0	1191.55	213	221
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	KQGIVTPIEAQTR	99.7%	59.6	25	59.6	2	1	0	1440.82	881	893
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	KYGGISTASVDFEQPTR	99.7%	91.9	25	91.9	2	2	0	1855.92	837	853
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	LACLLCR	99.7%	49.1	25	32.1	4	0	0	905.47	759	765
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	LDQQTLPLGGR	99.7%	84.4	25	75.1	6	0	0	1197.66	253	263
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	MLPQAATEDDIR	99.7%	79.5	25	71.1	6	0	0	1359.66	135	146
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	MLQAMGWK	99.7%	42	25	31.1	4	0	0	964.47	865	872
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	NSFQPISSLR	99.7%	57.2	25	32.7	4	0	0	1148.61	671	680
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	NSFQPISSLRDDER	99.6%	28.8	25	28.8	0	1	0	1663.80	671	684
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	QGIVTPIEAQTR	99.7%	64	25	51.3	3	0	0	1312.72	882	893
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	QNLEIHR	99.7%	44.4	25	26.5	1	0	0	909.49	786	792
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	SEAEQKLPLGTR	99.7%	70.5	25	50.3	10	2	0	1328.72	241	252
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	TINVEFAK	99.7%	44.4	25	37.1	2	0	0	921.50	376	383
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	TYVPALEQSADGHK	99.7%	63.7	25	61.6	4	0	0	1515.74	614	627
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	TYVPALEQSADGHKETGAPSK	99.4%	27.3	25	26	0	2	0	2186.07	614	634

RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	VSMHYSDPKPK	99.7%	32.5	25	30.1	0	3	0	1304.63	202	212
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	YGGISTASVDFEQPTR	99.7%	96.1	25	95.6	3	0	0	1727.82	838	853
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	32	41	124	0.12%	34.6%	YGIPEPPEPK	96.3%	28.3	25	26.5	1	0	0	1126.58	825	834
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	7	7	16	0.02%	14.5%	ASYVAPLTAQPATYR	99.7%	69.7	25	62.2	2	0	0	1608.84	224	238
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	7	7	16	0.02%	14.5%	IFVGNVSAACTSQELR	99.7%	136	25	130	4	0	0	1751.87	81	96
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	7	7	16	0.02%	14.5%	INVELSTK	99.2%	34.7	25	28	4	0	0	903.51	142	149
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	7	7	16	0.02%	14.5%	KGPGLAVQSGDK	99.3%	35.4	25	25.1	2	0	0	1156.63	153	164
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	7	7	16	0.02%	14.5%	TQPMTAQAASYR	99.7%	38.7	25	27.1	1	0	0	1340.63	263	274
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	7	7	16	0.02%	14.5%	TQSSASLAASYAAQQHPQAAASYR	99.7%	73.1	25	73.1	0	1	0	2465.18	518	541
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	7	7	16	0.02%	14.5%	YSGSYNDYLR	99.7%	73.5	25	73.5	2	0	0	1237.55	648	657
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	6	7	14	0.01%	8.3%	EKEELEEIR	99.7%	41.4	25	22.4	2	0	0	1174.60	539	547
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	6	7	14	0.01%	8.3%	FPVAPLIPYPLITK	99.7%	41.2	25	41.2	2	0	0	1568.95	248	261
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	6	7	14	0.01%	8.3%	GAIEVLIR	99.7%	44.4	25	26.7	2	0	0	870.54	209	216
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	6	7	14	0.01%	8.3%	LGASNSPGQPNSVK	99.7%	46.4	25	40.8	2	0	0	1355.69	672	685
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	6	7	14	0.01%	8.3%	LLAEGHPDPDAELQR	99.7%	55.5	25	54.4	2	2	0	1660.83	550	564
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	6	7	14	0.01%	8.3%	LLHDLQIGEK	99.6%	37.6	25	34.4	2	0	0	1165.66	146	155
RNA-binding protein 26	RBM26	RBM26_HUMAN	113.6	100.0%	2	2	3	0.00%	2.5%	AEAEAAAVHGAR	99.6%	38.1	25	34.3	2	0	0	1152.58	936	947
RNA-binding protein 26	RBM26	RBM26_HUMAN	113.6	100.0%	2	2	3	0.00%	2.5%	EGSTQQLQTTSPK	99.4%	36.1	25	33.4	1	0	0	1404.70	606	618
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	8	8	14	0.01%	10.5%	AAEGVSAADMAK	99.7%	53.5	25	53.5	2	0	0	1120.53	454	465
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	8	8	14	0.01%	10.5%	FNQLVEQYK	99.7%	43.7	25	26.5	2	0	0	1168.60	730	738
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	8	8	14	0.01%	10.5%	KLLLSATSGEK	97.5%	29.9	25	20.1	1	0	0	1146.67	505	515
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	8	8	14	0.01%	10.5%	LINNNPEIFGPLK	99.5%	36.5	25	36.5	2	0	0	1468.82	559	571
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	8	8	14	0.01%	10.5%	LLLSATSGEK	99.6%	38.3	25	35.3	2	0	0	1018.58	506	515
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	8	8	14	0.01%	10.5%	QQLSSEQVSR	99.6%	37.5	25	28.5	2	0	0	1161.59	709	718
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	8	8	14	0.01%	10.5%	SEQLEELFSQVGPVK	99.7%	71.7	25	59.3	2	0	0	1689.87	17	31
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	8	8	14	0.01%	10.5%	TVAVDWAVAK	99.3%	35.1	25	18.5	1	0	0	1059.58	183	192
RNA-binding protein 39	RBM39	RBM39_HUMAN	59.4	100.0%	4	4	9	0.01%	10.0%	DLEEFFSTVGK	99.7%	58.4	25	50.7	4	0	0	1271.62	168	178
RNA-binding protein 39	RBM39	RBM39_HUMAN	59.4	100.0%	4	4	9	0.01%	10.0%	TDASSASSFLDSDELER	99.7%	70	25	70	1	0	0	1829.80	330	346
RNA-binding protein 39	RBM39	RBM39_HUMAN	59.4	100.0%	4	4	9	0.01%	10.0%	TGIDLGTTGR	99.7%	53.8	25	50.7	2	0	0	990.52	347	356
RNA-binding protein 39	RBM39	RBM39_HUMAN	59.4	100.0%	4	4	9	0.01%	10.0%	VLGVPIIVQASQAEK	99.7%	90.2	25	90.2	2	0	0	1551.91	218	232
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	7	7	12	0.01%	17.6%	AEDAVEAIR	99.7%	63.1	25	38	2	0	0	973.49	121	129
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	7	7	12	0.01%	17.6%	GLDNTEFQGK	99.7%	49.2	25	44.2	2	0	0	1108.53	130	139
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	7	7	12	0.01%	17.6%	GLDNTEFQGKR	99.7%	42.4	25	35.4	2	0	0	1264.63	130	140
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	7	7	12	0.01%	17.6%	LFIGNLPR	99.7%	53.8	25	13.1	2	0	0	929.56	4	11
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	7	7	12	0.01%	17.6%	LHGVNINVEASK	99.1%	34	25	26.9	1	0	0	1280.70	60	71
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	7	7	12	0.01%	17.6%	VADLTEQYNEQYGAVR	99.7%	101	25	101	2	0	0	1855.88	183	198
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	7	7	12	0.01%	17.6%	VLECDIIK	99.7%	40.5	25	21	1	0	0	989.53	28	35
RNA-binding protein FUS	FUS	FUS_HUMAN	53.4	99.8%	2	3	4	0.00%	5.9%	AAIDWFDGKEFSGNPIK	99.7%	65.1	25	63.1	1	1	0	1894.93	349	365
RNA-binding protein FUS	FUS	FUS_HUMAN	53.4	99.8%	2	3	4	0.00%	5.9%	GEATVSFDDPPSAK	99.7%	89	25	81.3	2	0	0	1420.66	335	348
RNA-binding protein Musashi homolog 1	MSI1	MSI1H_HUMAN	39.1	99.8%	2	3	4	0.00%	8.3%	GFGFVTFESEDIVEK	99.1%	34.4	25	34.4	1	0	0	1703.82	151	165
RNA-binding protein Musashi homolog 1	MSI1	MSI1H_HUMAN	39.1	99.8%	2	3	4	0.00%	8.3%	GFGFVTFMDQAGVDK	99.7%	68.8	25	64.9	3	0	0	1634.75	62	76
RNA-binding protein PNO1	PNO1	PNO1_HUMAN	27.9	99.8%	2	2	3	0.00%	9.5%	AEEGFTQVTR	99.7%	43.5	25	30.7	1	0	0	1137.55	12	21
RNA-binding protein PNO1	PNO1	PNO1_HUMAN	27.9	99.8%	2	2	3	0.00%	9.5%	TAICNLILGNPPSK	99.7%	55.3	25	43	2	0	0	1497.81	223	236
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	4	4	9	0.01%	14.7%	GYAFVQYSNER	99.7%	58	25	52.2	2	0	0	1333.62	56	66
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	4	4	9	0.01%	14.7%	LQASNVTNKNDPK	99.7%	44.4	25	33.4	1	0	0	1428.74	5	17
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	4	4	9	0.01%	14.7%	SNIDALLSR	99.7%	50.1	25	31.1	2	0	0	988.54	199	207
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	4	4	9	0.01%	14.7%	VFIGNLNTALVK	99.7%	70	25	0	4	0	0	1288.76	23	34
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	7	8	13	0.01%	24.0%	ANCIDSTASAEAVFASEVK	99.7%	57.5	25	54.7	1	0	0	1969.92	266	284
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	7	8	13	0.01%	24.0%	IVALNAHTFLR	99.7%	51.3	25	43.7	2	0	0	1254.73	245	255
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	7	8	13	0.01%	24.0%	NLVPGESVYGEK	99.3%	35.2	25	30.4	2	0	0	1291.65	110	121
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	7	8	13	0.01%	24.0%	NLVPGESVYGEKR	99.7%	61.1	25	56.9	2	0	0	1447.75	110	122

rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	7	8	13	0.01%	24.0%	SGRDLINLAK	99.2%	34.5	25	18.6	1	0	0	1086.63	196	205
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	7	8	13	0.01%	24.0%	TNIIPVIEDAR	99.7%	70.8	25	0	2	0	0	1240.69	208	218
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	7	8	13	0.01%	24.0%	VSISEGDDKIEYR	99.7%	72.2	25	72.2	2	1	0	1510.74	123	135
RRP12-like protein	RRP12	RRP12_HUMAN	143.7	100.0%	4	4	7	0.01%	3.3%	RAVLETIR	98.4%	31.6	25	13	2	0	0	957.58	711	718
RRP12-like protein	RRP12	RRP12_HUMAN	143.7	100.0%	4	4	7	0.01%	3.3%	SWLLPVIR	99.1%	34	25	10.6	1	0	0	983.60	567	574
RRP12-like protein	RRP12	RRP12_HUMAN	143.7	100.0%	4	4	7	0.01%	3.3%	TYLTITDTQLVNSLLEK	99.7%	59	25	59	2	0	0	1952.06	719	735
RRP12-like protein	RRP12	RRP12_HUMAN	143.7	100.0%	4	4	7	0.01%	3.3%	VLATQPGPGR	99.7%	51.3	25	44.1	2	0	0	995.56	1129	1138
RUN and FYVE domain-containing protein 1	RUFY1	RUFY1_HUMAN	79.8	99.8%	2	2	3	0.00%	3.1%	AQNAESSLQQK	99.2%	34.8	25	34.8	1	0	0	1203.60	470	480
RUN and FYVE domain-containing protein 1	RUFY1	RUFY1_HUMAN	79.8	99.8%	2	2	3	0.00%	3.1%	SFFGPLELVEK	99.3%	35.3	25	30.1	2	0	0	1265.68	172	182
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	8	8	14	0.01%	23.0%	ALESSIAPIVIFASNR	99.7%	66.8	25	66.8	2	0	0	1687.94	318	333
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	8	8	14	0.01%	23.0%	AVLLAGPPGTGK	99.7%	54.6	25	50.8	2	0	0	1080.64	65	76
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	8	8	14	0.01%	23.0%	EACGVIVELIK	99.7%	51.9	25	36.3	2	0	0	1230.68	47	57
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	8	8	14	0.01%	23.0%	GLGLDESGLAK	99.7%	47.7	25	39	2	0	0	1059.57	23	33
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	8	8	14	0.01%	23.0%	LDPSIFESLQK	99.7%	61.3	25	48.9	1	0	0	1276.68	172	182
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	8	8	14	0.01%	23.0%	QAASGLVGQENAR	99.7%	77	25	67.7	2	0	0	1300.66	34	46
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	8	8	14	0.01%	23.0%	TALALAIAQELGSK	99.7%	112	25	112	2	0	0	1385.80	77	90
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	8	8	14	0.01%	23.0%	VPFCPMVGSEVYSTEIK	99.7%	58.8	25	53.5	1	0	0	1942.93	91	107
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	12	22	0.02%	31.1%	AAGVVLEMIR	99.7%	62	25	46.4	2	0	0	1058.60	55	64
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	12	22	0.02%	31.1%	ALESDMAPVLIMATNR	99.7%	84	25	82.3	2	0	0	1731.88	315	330
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	12	22	0.02%	31.1%	AVLIAGQPGTGK	99.7%	66.8	25	57.5	2	0	0	1111.65	72	83
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	12	22	0.02%	31.1%	DKVQAGDVITIDK	99.7%	61.1	25	47.6	2	0	0	1401.76	185	197
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	12	22	0.02%	31.1%	EVVHTVSLHEIDVINSR	99.7%	40	25	40	0	1	0	1947.03	237	253
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	12	22	0.02%	31.1%	FVQCPDGELQK	99.7%	51.5	25	44.3	2	0	0	1320.63	224	234
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	12	22	0.02%	31.1%	GTEVQVDDIKR	99.7%	57.4	25	39.6	2	0	0	1259.66	418	428
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	12	22	0.02%	31.1%	LLIVSTTPYSEK	99.7%	61.8	25	52.2	2	0	0	1350.75	354	365
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	12	22	0.02%	31.1%	LLIVSTTPYSEKDTK	99.7%	57.8	25	57.8	2	0	0	1694.92	354	368
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	12	22	0.02%	31.1%	TQGFLALFSGDTGEIK	99.7%	96.1	25	91.6	2	0	0	1683.86	254	269
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	12	22	0.02%	31.1%	TTEMETIYDLGTK	99.7%	41	25	41	1	0	0	1517.70	165	177
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	12	22	0.02%	31.1%	VYSLFLDESR	99.7%	59.9	25	48.1	2	0	0	1228.62	429	438
S1 RNA-binding domain-containing protein 1	SRBD1	SRBD1_HUMAN	111.8	100.0%	2	2	4	0.00%	2.5%	ETEAYFADLIMK	99.7%	52.9	25	52.9	2	0	0	1430.69	603	614
S1 RNA-binding domain-containing protein 1	SRBD1	SRBD1_HUMAN	111.8	100.0%	2	2	4	0.00%	2.5%	LFNDDNTIPFIIR	99.7%	62.9	25	54.6	2	0	0	1577.83	235	247
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	7	9	14	0.01%	19.5%	DLDLKKPIYQR	99.4%	36.1	25	31.4	1	0	0	1388.79	363	373
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	7	9	14	0.01%	19.5%	FVIGGPQGDAGLTGR	99.7%	99.9	25	93.9	2	0	0	1444.75	250	264
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	7	9	14	0.01%	19.5%	FVIGGPQGDAGLTGRK	97.3%	22.4	25	19.4	0	1	0	1572.85	250	265
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	7	9	14	0.01%	19.5%	NFDLRPGVIVR	95.0%	27.1	25	24.5	1	0	0	1285.74	352	362
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	7	9	14	0.01%	19.5%	TGMILLAGEITSR	99.7%	86.2	25	80.1	4	0	0	1361.75	62	74
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	7	9	14	0.01%	19.5%	TQVTVQYMQDR	99.7%	48.9	25	46.9	1	0	0	1368.66	182	192
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	7	9	14	0.01%	19.5%	YLDEDTIYHLQPSGR	99.7%	75.8	25	75.7	2	2	0	1806.87	235	249
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	22	31	59	0.06%	23.8%	AEIGIAMGSGTAVAK	99.7%	81.8	25	77.5	2	0	0	1391.72	713	727
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	22	31	59	0.06%	23.8%	AMGVVVATGVNTEIGK	99.7%	71.4	25	53.8	3	0	0	1561.83	219	234
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	22	31	59	0.06%	23.8%	ANACNSVIK	96.2%	28.2	25	18.8	1	0	0	976.49	468	476
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	22	31	59	0.06%	23.8%	EFDELNPSAQR	99.7%	63.7	25	59.8	2	0	0	1305.61	656	666
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	22	31	59	0.06%	23.8%	EFTLEFSR	99.7%	52.9	25	37.8	3	0	0	1028.50	482	489
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	22	31	59	0.06%	23.8%	EWGSGSDTLR	99.7%	44	25	35.9	2	0	0	1107.51	550	559
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	22	31	59	0.06%	23.8%	GAPEGVIDR	99.7%	46.6	25	42.1	2	0	0	913.47	515	523
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	22	31	59	0.06%	23.8%	HTDPVPDPR	95.9%	27.9	25	20.3	1	0	0	1033.51	190	198
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	22	31	59	0.06%	23.8%	IGIFGQDEDVTSK	99.7%	79.4	25	75.6	2	0	0	1408.70	638	650
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	22	31	59	0.06%	23.8%	IRDEMVATEQER	99.7%	60.2	25	50.7	4	0	0	1476.71	235	246
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	22	31	59	0.06%	23.8%	ISLPVILMDETLK	99.7%	88.6	25	87.4	7	0	0	1471.84	972	984
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	22	31	59	0.06%	23.8%	KAEIGIAMGSGTAVAK	99.7%	69.8	25	68.8	2	3	0	1519.82	712	727
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	22	31	59	0.06%	23.8%	LDEFGEQLSK	99.7%	50	25	34.4	2	0	0	1165.57	253	262

Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	22	31	59	0.06%	23.8%	NMLFSGTNIAAGK	99.7%	79.6	25	73.8	5	0	0	1323.67	206	218
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	22	31	59	0.06%	23.8%	NYLEPGKECVQPATK	98.9%	33.1	25	32.8	1	0	0	1733.85	989	1003
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	22	31	59	0.06%	23.8%	RIGIFGQDEDVTSK	99.4%	35.6	25	35.6	1	0	0	1564.80	637	650
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	22	31	59	0.06%	23.8%	SLPSVETLGCTSVICSDK	99.7%	101	25	101	2	0	0	1952.93	335	352
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	22	31	59	0.06%	23.8%	SMSVYCTPNKPSR	99.7%	58.3	25	58.3	2	0	0	1526.71	493	505
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	22	31	59	0.06%	23.8%	TGTLTTNQMSVCR	99.7%	63.9	25	61.8	3	0	0	1468.69	353	365
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	22	31	59	0.06%	23.8%	VDQSILTGESVSVIK	99.7%	89.9	25	81.8	4	0	0	1574.86	175	189
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	22	31	59	0.06%	23.8%	VGEATETALTCLVEK	99.7%	119	25	108	3	0	0	1620.82	437	451
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	22	31	59	0.06%	23.8%	VIMITGDNK	98.6%	32.2	25	2.56	2	0	0	990.53	620	628
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	23	54	0.05%	24.0%	DQIIDSLKR	99.7%	41.9	25	25.2	4	0	0	1087.61	80	88
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	23	54	0.05%	24.0%	EPAVLMGILGIYK	99.7%	44.1	25	44.1	4	0	0	1403.80	539	551
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	23	54	0.05%	24.0%	GVQQLTR	98.3%	31.3	25	6.54	2	0	0	801.46	89	95
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	23	54	0.05%	24.0%	IMGFDFCVSSTNPSEQEPK	99.7%	64.5	25	64.5	3	0	0	2172.96	194	212
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	23	54	0.05%	24.0%	LGSSSLTNIPEEVR	99.7%	77.9	25	54.2	2	0	0	1501.79	288	301
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	23	54	0.05%	24.0%	LILPELGPVFK	99.7%	44.6	25	35.3	4	0	0	1225.76	408	418
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	23	54	0.05%	24.0%	LLTVQHPLEESR	99.7%	64.5	25	59.1	4	1	0	1421.77	101	112
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	23	54	0.05%	24.0%	MVHGNITPENIILNK	99.7%	50.1	25	50.1	1	2	0	1692.91	174	188
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	23	54	0.05%	24.0%	NACLQTSSLAVR	99.7%	84.5	25	70.2	4	0	0	1319.67	494	505
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	23	54	0.05%	24.0%	QEVAVFVFDKK	99.7%	49	25	37.5	3	0	0	1309.72	59	69
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	23	54	0.05%	24.0%	QQEPIQILLIFLQK	99.7%	57.5	25	57.5	2	1	0	1711.02	419	432
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	23	54	0.05%	24.0%	SLDIGNQMNVSEEMK	99.7%	78.7	25	78.7	1	0	0	1694.77	622	636
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	23	54	0.05%	24.0%	SQQPLKPQVHTPVATVK	95.4%	20.7	25	20.7	0	1	0	1858.05	698	714
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	23	54	0.05%	24.0%	VNSLVCLGK	99.7%	57.4	25	45	3	0	0	989.54	506	514
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	23	54	0.05%	24.0%	VTADVTSAVMGNPVTR	99.7%	117	25	103	7	0	0	1633.82	15	30
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	23	54	0.05%	24.0%	VTNIGNQQIDK	99.7%	60.7	25	46.6	4	0	0	1229.65	637	647
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	17	23	54	0.05%	24.0%	YGLLQVSEGLSFLHSSVK	99.3%	26.5	25	25.4	0	1	0	1964.05	156	173
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	6	6	11	0.01%	12.0%	FGQDIISPLLSVK	99.7%	75.8	25	74.3	3	0	0	1416.81	51	63
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	6	6	11	0.01%	12.0%	GTAAEMVAVK	99.7%	68.2	25	57.6	2	0	0	976.51	215	224
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	6	6	11	0.01%	12.0%	LTSAVSSLPELLEK	99.7%	70.5	25	53.7	2	0	0	1486.84	382	395
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	6	6	11	0.01%	12.0%	QQNLPVTR	97.5%	29.9	25	18.8	1	0	0	955.53	542	549
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	6	6	11	0.01%	12.0%	SYDLTPVDKFWQK	99.7%	41.3	25	41.3	2	0	0	1626.82	316	328
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	6	6	11	0.01%	12.0%	VNLEESSGVENSPAGARPK	99.7%	88.8	25	88.8	1	0	0	1940.97	292	310
Sentrin-specific protease 3	SENP3	SENP3_HUMAN	65.0	100.0%	3	4	5	0.00%	6.1%	GLVLQLIQSYQR	95.8%	27.8	25	16.2	1	0	0	1417.82	358	369
Sentrin-specific protease 3	SENP3	SENP3_HUMAN	65.0	100.0%	3	4	5	0.00%	6.1%	LGLLGALMAEDGVR	99.7%	75.7	25	75.7	3	0	0	1414.77	197	210
Sentrin-specific protease 3	SENP3	SENP3_HUMAN	65.0	100.0%	3	4	5	0.00%	6.1%	STSLTFHWK	98.7%	32.5	25	19	1	0	0	1106.56	141	149
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	7	7	14	0.01%	13.8%	FINDQYEK	98.4%	31.7	25	21.3	1	0	0	1056.50	382	389
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	7	7	14	0.01%	13.8%	LEPKPQPPVAEATPR	99.7%	33.1	25	33.1	0	2	0	1629.90	223	237
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	7	7	14	0.01%	13.8%	QVENAGAIGPSR	99.7%	47.9	25	39.6	2	0	0	1198.62	118	129
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	7	7	14	0.01%	13.8%	RTELSIDISSK	96.9%	29	25	13.9	1	0	0	1248.68	107	117
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	7	7	14	0.01%	13.8%	VPEVPTAPATDAAPK	99.7%	59.9	25	54.1	3	0	0	1463.77	172	186
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	7	7	14	0.01%	13.8%	VVNIVPVIAK	99.4%	36.1	25	36.1	2	0	0	1051.69	436	445
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	7	7	14	0.01%	13.8%	YLQEEVNINR	99.7%	58.9	25	48.1	3	0	0	1277.65	390	399
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	9	9	14	0.01%	24.5%	AACFAIQK	99.7%	49.4	25	37	2	0	0	908.47	190	197
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	9	9	14	0.01%	24.5%	ECINFASFNFLGLLDNPR	99.7%	92.3	25	92.3	1	0	0	2127.03	99	116
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	9	9	14	0.01%	24.5%	EQEIEDQKNPR	99.7%	54.7	25	51.5	2	0	0	1385.67	223	233
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	9	9	14	0.01%	24.5%	HNDMADLER	99.6%	37.8	25	37.8	2	0	0	1100.48	211	219
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	9	9	14	0.01%	24.5%	IFLEESLSFGVLGEHGR	99.6%	28.1	25	25.1	0	2	0	1889.98	271	287
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	9	9	14	0.01%	24.5%	LLQEIVDQCMNR	99.7%	57.3	25	57.3	1	0	0	1518.74	411	422
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	9	9	14	0.01%	24.5%	RGDIVFVDR	97.1%	29.2	25	10.7	1	0	0	1076.58	181	189
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	9	9	14	0.01%	24.5%	TEEAIIYSYGFATIASAIPAYSK	99.0%	33.8	25	33.8	1	0	0	2466.24	158	180
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	9	9	14	0.01%	24.5%	YGVGTCGPR	99.7%	54.2	25	49.2	2	0	0	966.45	128	136

Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	12	27	0.03%	41.1%	DAEDAVYGR	99.6%	38.2	25	31.9	2	0	0	995.44	66	74
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	12	27	0.03%	41.1%	DGTGVVEFVR	99.7%	66.7	25	49.8	3	0	0	1078.55	155	164
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	12	27	0.03%	41.1%	DIEDVFYK	98.2%	31.3	25	30.7	1	0	0	1028.49	31	38
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	12	27	0.03%	41.1%	EAGDVCYADVYR	99.7%	69.1	25	69.1	2	0	0	1417.61	143	154
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	12	27	0.03%	41.1%	EDMTYAVR	97.2%	29.4	25	27.4	1	0	0	984.45	166	173
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	12	27	0.03%	41.1%	GGPPFAFVEFEDPR	99.7%	49.2	25	49.2	2	0	0	1564.74	52	65
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	12	27	0.03%	41.1%	IYVGNLPPDIR	99.7%	64.6	25	52.8	6	0	0	1256.70	18	28
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	12	27	0.03%	41.1%	KEDMTYAVR	99.7%	52.7	25	47.8	4	0	0	1112.54	165	173
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	12	27	0.03%	41.1%	LRVEFPR	99.5%	36.8	25	25	4	0	0	916.54	84	90
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	12	27	0.03%	41.1%	SHEGETAYIR	99.7%	39.9	25	39.9	3	0	0	1162.55	182	191
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	12	27	0.03%	41.1%	TKDIEDVFYK	99.7%	55.6	25	53.7	2	0	0	1257.64	29	38
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	12	27	0.03%	41.1%	YGAIRDIDLK	97.4%	29.7	25	12.4	1	0	0	1163.64	39	48
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	99.8%	2	3	7	0.01%	18.3%	AFGYYGPLR	99.7%	49.9	25	40.2	4	0	0	1043.53	29	37
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	99.8%	2	3	7	0.01%	18.3%	NPPGFAFVEFEDPRDAADAVR	99.7%	38.8	25	38.8	1	2	0	2320.10	44	64
Serine/arginine-rich splicing factor 5	SRSF5	SRSF5_HUMAN	31.3	99.8%	2	2	4	0.00%	8.8%	LIVENLSSR	99.7%	50.6	25	37.3	2	0	0	1030.59	110	118
Serine/arginine-rich splicing factor 5	SRSF5	SRSF5_HUMAN	31.3	99.8%	2	2	4	0.00%	8.8%	LNEGVVEFASYGDLK	99.7%	82.3	25	81.9	2	0	0	1640.82	144	158
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	10	12	21	0.02%	43.9%	DAEDAIYGR	95.9%	27.9	25	18.5	1	0	0	1009.46	64	72
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	10	12	21	0.02%	43.9%	DGVGMVEYLR	99.7%	63.8	25	54	4	0	0	1154.55	145	154
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	10	12	21	0.02%	43.9%	EAGDVCYADVQK	99.7%	72.9	25	72.9	2	0	0	1354.59	133	144
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	10	12	21	0.02%	43.9%	EKDLEDLFYK	99.7%	56.7	25	48.1	2	0	0	1299.65	27	36
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	10	12	21	0.02%	43.9%	HGLVPFAFVR	99.7%	43.6	25	41.5	1	0	0	1142.65	49	58
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	10	12	21	0.02%	43.9%	IYVGNLPTDVR	99.7%	55.3	25	46.3	2	0	0	1246.68	16	26
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	10	12	21	0.02%	43.9%	KEDMEYALR	98.1%	30.9	25	29.6	2	0	0	1154.55	155	163
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	10	12	21	0.02%	43.9%	LRVEFPR	99.5%	36.8	25	25	4	0	0	916.54	82	88
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	10	12	21	0.02%	43.9%	NGYDYGQCR	99.7%	41.8	25	40.5	1	0	0	1132.45	73	81
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	10	12	21	0.02%	43.9%	SHEGETSYIR	99.7%	40.2	25	39.4	2	0	0	1178.54	172	181
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	14	18	35	0.03%	41.1%	AERDILVEADSLWVVK	99.7%	43.3	25	42.4	0	2	0	1843.00	136	151
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	14	18	35	0.03%	41.1%	AKDLILR	99.5%	37.2	25	20.9	3	0	0	828.53	353	359
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	14	18	35	0.03%	41.1%	DIKPDNLLLDSK	99.7%	47.4	25	44.9	2	2	0	1370.75	212	223
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	14	18	35	0.03%	41.1%	DILVEADSLWVVK	99.7%	85	25	85	4	0	0	1486.82	139	151
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	14	18	35	0.03%	41.1%	DTGHVYAMK	99.7%	42.5	25	27.7	2	0	0	1021.48	110	118
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	14	18	35	0.03%	41.1%	DWVFINYTYK	99.7%	58.6	25	0	3	0	0	1348.66	437	446
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	14	18	35	0.03%	41.1%	FCCEWEHR	99.7%	54.5	25	54.5	2	2	0	1223.47	360	367
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	14	18	35	0.03%	41.1%	IGAPGVEEIK	99.7%	68	25	54.4	2	0	0	1012.57	368	377
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	14	18	35	0.03%	41.1%	LGLEDFESLK	99.7%	54.7	25	54.7	2	0	0	1150.60	84	93
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	14	18	35	0.03%	41.1%	LSDFGLCTGLK	99.7%	64.5	25	62.2	4	0	0	1210.61	228	238
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	14	18	35	0.03%	41.1%	LSDFGLCTGLKK	99.7%	65.6	25	61.1	4	2	0	1338.71	228	239
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	14	18	35	0.03%	41.1%	NLNHSLPSDFTFQNMNSK	99.7%	47.9	25	46.2	0	2	0	2093.97	248	265
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	14	18	35	0.03%	41.1%	QLAFSTVGTPDYIAPEVFMQTGYNK	99.7%	56.2	25	56.2	1	2	0	2777.35	277	301
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	14	18	35	0.03%	41.1%	RFEGLTAR	99.7%	47.8	25	36	2	0	0	949.52	447	454
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	14	18	35	0.03%	41.1%	SNSFFEGVDWEHIR	99.7%	34	25	34	0	2	0	1722.79	378	391
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	14	18	35	0.03%	41.1%	VMEEEGLKDEEK	99.7%	69.3	25	54.5	2	0	0	1435.66	51	62
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	14	18	35	0.03%	41.1%	VTLENFYSNLIAQHEER	99.7%	69.7	25	66.7	1	2	0	2063.02	25	41
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	14	18	35	0.03%	41.1%	VTLENFYSNLIAQHEEREMR	99.4%	27.3	25	27.3	0	1	0	2495.20	25	44
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	18	22	57	0.06%	35.1%	AKDLILR	99.5%	37.2	25	20.9	3	0	0	828.53	354	360
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	18	22	57	0.06%	35.1%	DIKPDNLLLDAK	99.7%	47	25	43.4	4	1	0	1354.76	213	224
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	18	22	57	0.06%	35.1%	DILVEADGAWVVK	99.7%	92.4	25	80.2	2	0	0	1414.76	140	152
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	18	22	57	0.06%	35.1%	DTGHIYAMK	99.7%	47.4	25	35.5	4	0	0	1035.49	111	119
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	18	22	57	0.06%	35.1%	DWVFLNYTYK	99.7%	58.6	25	0	3	0	0	1348.66	435	444
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	18	22	57	0.06%	35.1%	ERPAAIPIEIK	99.4%	35.6	25	29.3	4	0	0	1236.73	393	403
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	18	22	57	0.06%	35.1%	FCIDSENR	99.7%	53.1	25	47	4	0	0	1040.45	361	368

Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	18	22	57	0.06%	35.1%	FEGLTQR	99.7%	42	25	29.1	3	0	0	850.44	446	452
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	18	22	57	0.06%	35.1%	GHPFFEGVDWEHIR	99.7%	43.6	25	43.6	0	1	0	1725.81	379	392
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	18	22	57	0.06%	35.1%	LGLDDFESLK	99.7%	58.7	25	58.7	4	0	0	1136.58	85	94
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	18	22	57	0.06%	35.1%	LSDFGLCTGLK	99.7%	64.5	25	62.2	4	0	0	1210.61	229	239
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	18	22	57	0.06%	35.1%	LSDFGLCTGLKK	99.7%	65.6	25	61.1	4	2	0	1338.71	229	240
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	18	22	57	0.06%	35.1%	LTLENFYSNLILQHEER	99.7%	50.4	25	49.4	2	2	0	2119.08	26	42
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	18	22	57	0.06%	35.1%	LTLENFYSNLILQHEERETR	98.8%	24.8	25	21.9	0	1	0	2505.27	26	45
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	18	22	57	0.06%	35.1%	MFYSFQDKR	99.7%	55.1	25	45.6	2	0	0	1221.57	153	161
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	18	22	57	0.06%	35.1%	NLTHNPPSDFSFQNMNSK	99.7%	69.2	25	69.2	0	4	0	2077.94	249	266
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	18	22	57	0.06%	35.1%	RFEGLTQR	99.7%	47	25	32.3	2	0	0	1006.54	445	452
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	18	22	57	0.06%	35.1%	TRLGLDDFESLK	99.7%	59	25	52.7	1	0	0	1393.73	83	94
Serine/threonine-protein kinase D1	PRKD1	KPCD1_HUMAN	101.7	99.8%	2	2	3	0.00%	5.3%	EIPLSEILSLEPVK	98.5%	32	25	32	1	0	0	1566.90	465	478
Serine/threonine-protein kinase D1	PRKD1	KPCD1_HUMAN	101.7	99.8%	2	2	3	0.00%	5.3%	FLITQILVALR	99.7%	41.5	25	41.5	2	0	0	1286.82	685	695
Serine/threonine-protein kinase D1	PRKD1	KPCD1_HUMAN	101.7	99.8%	2	2	3	0.00%	5.3%	LCDFGFAR	99.7%	53	25	35.4	2	0	0	985.46	725	732
Serine/threonine-protein kinase D1	PRKD1	KPCD1_HUMAN	101.7	99.8%	2	2	3	0.00%	5.3%	SVVGTPAYLAPEVLR	99.7%	60.1	25	49	2	0	0	1571.88	742	756
Serine/threonine-protein kinase D2	PRKD2	KPCD2_HUMAN	96.8	100.0%	5	5	10	0.01%	7.4%	EFVLLPAASELAHVK	99.6%	37.5	25	29.3	2	0	0	1623.91	56	70
Serine/threonine-protein kinase D2	PRKD2	KPCD2_HUMAN	96.8	100.0%	5	5	10	0.01%	7.4%	FLITQILVALR	99.7%	41.5	25	41.5	2	0	0	1286.82	653	663
Serine/threonine-protein kinase D2	PRKD2	KPCD2_HUMAN	96.8	100.0%	5	5	10	0.01%	7.4%	LCDFGFAR	99.7%	53	25	35.4	2	0	0	985.46	693	700
Serine/threonine-protein kinase D2	PRKD2	KPCD2_HUMAN	96.8	100.0%	5	5	10	0.01%	7.4%	NEVAILQSLR	99.7%	64.6	25	44.9	2	0	0	1142.65	597	606
Serine/threonine-protein kinase D2	PRKD2	KPCD2_HUMAN	96.8	100.0%	5	5	10	0.01%	7.4%	SVVGTPAYLAPEVLLNQGYNR	99.7%	52.2	25	52.2	2	0	0	2261.19	710	730
Serine/threonine-protein kinase D3	PRKD3	KPCD3_HUMAN	100.5	99.8%	2	3	3	0.00%	4.9%	FMVTQILVALR	99.7%	57.9	25	57.5	2	0	0	1290.76	678	688
Serine/threonine-protein kinase D3	PRKD3	KPCD3_HUMAN	100.5	99.8%	2	3	3	0.00%	4.9%	LCDFGFAR	99.7%	53	25	35.4	2	0	0	985.46	718	725
Serine/threonine-protein kinase D3	PRKD3	KPCD3_HUMAN	100.5	99.8%	2	3	3	0.00%	4.9%	SVVGTPAYLAPEVLR	99.7%	60.1	25	49	2	0	0	1571.88	735	749
Serine/threonine-protein kinase D3	PRKD3	KPCD3_HUMAN	100.5	99.8%	2	3	3	0.00%	4.9%	YITHESDDAR	99.1%	34.2	25	16	1	0	0	1206.54	852	861
Serine/threonine-protein kinase MST4	MST4	MST4_HUMAN	46.5	100.0%	4	4	7	0.01%	12.0%	AANVLLSEQGDVK	99.7%	62.5	25	53	2	0	0	1343.72	147	159
Serine/threonine-protein kinase MST4	MST4	MST4_HUMAN	46.5	100.0%	4	4	7	0.01%	12.0%	ADIWSLGITAIELAK	99.7%	76.7	25	62.1	2	0	0	1600.89	200	214
Serine/threonine-protein kinase MST4	MST4	MST4_HUMAN	46.5	100.0%	4	4	7	0.01%	12.0%	SIAVAEAACPGITDK	99.7%	65.6	25	63.3	1	0	0	1502.75	384	398
Serine/threonine-protein kinase MST4	MST4	MST4_HUMAN	46.5	100.0%	4	4	7	0.01%	12.0%	VLFLIPK	99.2%	34.8	25	34.8	2	0	0	829.55	227	233
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	4	4	6	0.01%	1.7%	DASAVSLSESK	99.7%	51	25	31	1	0	0	1093.54	911	921
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	4	4	6	0.01%	1.7%	LFDAPEAPLPSR	98.1%	31	25	31	1	0	0	1312.69	1121	1132
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	4	4	6	0.01%	1.7%	TLDQSPELR	98.8%	33	25	31.5	2	0	0	1058.55	1162	1170
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	4	4	6	0.01%	1.7%	VLGLLGALDPYK	99.7%	51.8	25	51.8	2	0	0	1258.74	887	898
Serine/threonine-protein kinase Nek7	NEK7	NEK7_HUMAN	34.6	99.8%	2	2	2	0.00%	5.3%	GQFSEVYR	99.7%	40.7	25	40.7	1	0	0	985.47	43	50
Serine/threonine-protein kinase Nek7	NEK7	NEK7_HUMAN	34.6	99.8%	2	2	2	0.00%	5.3%	LGDLGLGR	99.7%	43.1	25	18.5	1	0	0	800.46	177	184
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	5	5	9	0.01%	11.0%	IPISLVLR	99.7%	52.8	25	49.4	2	0	0	910.61	432	439
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	5	5	9	0.01%	11.0%	LLSGGSVLDIIK	99.7%	60.1	25	45.2	2	0	0	1214.74	94	105
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	5	5	9	0.01%	11.0%	RPTAAELLR	95.2%	27.3	25	19.1	1	0	0	1026.61	279	287
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	5	5	9	0.01%	11.0%	SGVLDESTIATILR	99.7%	85	25	84.3	2	0	0	1474.81	115	128
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	5	5	9	0.01%	11.0%	TAQALSSGSGSQETK	99.7%	65.2	25	55	2	0	0	1451.70	417	431
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	128	0.13%	37.9%	AMEIASQR	99.7%	53.9	25	38.3	6	0	0	905.45	402	409
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	128	0.13%	37.9%	ATVEQVLDPR	99.7%	61.7	25	60.3	10	0	0	1127.61	156	165
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	128	0.13%	37.9%	DCANVNDFFMR	99.7%	80.8	25	80.8	11	0	0	1388.57	360	370
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	128	0.13%	37.9%	DKYVSGEFR	98.8%	32.9	25	27.5	1	0	0	1100.54	221	229
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	128	0.13%	37.9%	DMDIIMK	99.5%	36.4	25	30.1	2	0	0	865.42	443	449
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	128	0.13%	37.9%	EANVYHASTANGESR	99.7%	80.8	25	80.8	8	0	0	1605.73	191	205
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	128	0.13%	37.9%	ELFEFVTDPSITHENMDAYLSK	99.7%	42.3	25	42.2	0	3	0	2586.21	380	401
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	128	0.13%	37.9%	ELYLQVIQYMR	99.7%	75.5	25	62.6	12	0	0	1455.77	302	312
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	128	0.13%	37.9%	GIITEINGCISTGK	99.7%	69.3	25	62.8	4	0	0	1462.76	177	190
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	128	0.13%	37.9%	GYVWNGGSNPQANR	99.7%	48.8	25	48.8	2	0	0	1519.70	82	95
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	128	0.13%	37.9%	HSVAVMTVR	99.7%	48	25	45.5	11	0	0	1015.54	371	379
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	128	0.13%	37.9%	INLDKLNVTDSVINK	99.7%	99	25	99	6	6	0	1685.94	120	134

Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	128	0.13%	37.9%	LNTAEIPCPEPIMLR	99.7%	81.7	25	57.5	9	0	0	1753.90	257	271
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	128	0.13%	37.9%	LNVTDSVINK	99.7%	83.5	25	67	8	0	0	1102.61	125	134
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	128	0.13%	37.9%	NYERDMDIIMK	96.2%	28.2	25	15.8	1	0	0	1459.66	439	449
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	128	0.13%	37.9%	SSQDHVDEEVFKR	99.7%	66.8	25	62.7	4	6	0	1575.74	415	427
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	128	0.13%	37.9%	TSILVFK	99.6%	37.5	25	29.6	4	0	0	807.50	212	218
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	128	0.13%	37.9%	TSILVFKDR	99.7%	54	25	54	3	0	0	1078.63	212	220
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	128	0.13%	37.9%	VPALLENQVEER	99.7%	87.3	25	87.3	10	0	0	1396.74	482	493
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	128	0.13%	37.9%	VVPGQFDDADSSDSENR	99.7%	85.1	25	85.1	1	0	0	1837.78	11	27
Serine/threonine-protein kinase ULK3	ULK3	ULK3_HUMAN	53.4	99.8%	2	2	2	0.00%	5.1%	ASVENLLTEIEILK	99.7%	40.7	25	40.7	1	0	0	1571.89	54	67
Serine/threonine-protein kinase ULK3	ULK3	ULK3_HUMAN	53.4	99.8%	2	2	2	0.00%	5.1%	ATALVVQAVK	99.2%	34.7	25	22.6	1	0	0	999.62	284	293
Serine/threonine-protein kinase VRK1	VRK1	VRK1_HUMAN	45.5	100.0%	4	4	4	0.00%	11.9%	ASNLLLNYK	99.7%	48.6	25	38.2	1	0	0	1035.58	180	188
Serine/threonine-protein kinase VRK1	VRK1	VRK1_HUMAN	45.5	100.0%	4	4	4	0.00%	11.9%	KTVLQLSLR	99.7%	44.9	25	44.9	1	0	0	1057.67	152	160
Serine/threonine-protein kinase VRK1	VRK1	VRK1_HUMAN	45.5	100.0%	4	4	4	0.00%	11.9%	NPDQVYLVDYGLAYR	99.7%	60.7	25	58.5	1	0	0	1785.88	189	203
Serine/threonine-protein kinase VRK1	VRK1	VRK1_HUMAN	45.5	100.0%	4	4	4	0.00%	11.9%	VEPSDNGPLFTELK	99.7%	38.6	25	35.6	1	0	0	1545.78	72	85
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	4	4	6	0.01%	8.1%	ESSLTEPVIVGLLK	99.5%	36.9	25	32.9	1	0	0	1484.86	354	367
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	4	4	6	0.01%	8.1%	FLESPDFQPNIAK	99.7%	57.1	25	51.8	1	0	0	1505.76	220	232
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	4	4	6	0.01%	8.1%	TVETEAVQMLK	99.7%	45.2	25	35.8	2	0	0	1248.65	550	560
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	4	4	6	0.01%	8.1%	VLPIMFPALYR	99.7%	52.1	25	52.1	2	0	0	1319.75	442	452
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	7	9	12	0.01%	13.2%	ELVSDANQHVK	99.5%	37	25	27.2	2	0	0	1239.63	332	342
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	7	9	12	0.01%	13.2%	LAGGDWFTSR	99.7%	51.7	25	28.6	1	0	0	1109.54	135	144
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	7	9	12	0.01%	13.2%	LSTIALALGVER	99.7%	83.8	25	68.8	2	0	0	1242.74	35	46
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	7	9	12	0.01%	13.2%	LTQDQDVDVK	99.7%	56.8	25	48.4	2	0	0	1160.58	567	576
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	7	9	12	0.01%	13.2%	MAGDPVANVR	99.7%	49	25	45.2	2	0	0	1029.51	528	537
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	7	9	12	0.01%	13.2%	VLAMSGDPNYLHR	99.7%	39.1	25	38	1	1	0	1488.73	486	498
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	7	9	12	0.01%	13.2%	YMVADKFTELQK	99.7%	42.5	25	38.9	1	0	0	1472.75	261	272
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	4	4	8	0.01%	16.1%	GAGWLFGAK	99.7%	43.6	25	27.8	2	0	0	906.48	211	219
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	4	4	8	0.01%	16.1%	LVTVWSAPNYCYR	99.7%	44.2	25	44.2	2	0	0	1628.79	252	264
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	4	4	8	0.01%	16.1%	QITQVYGFYDECQTK	99.7%	39.9	25	39.9	2	0	0	1879.85	118	132
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	4	4	8	0.01%	16.1%	VTNEFVHINNLK	99.7%	69	25	69	2	0	0	1427.76	220	231
Serine/threonine-protein phosphatase 6 regulatory subunit 1	PPP6R1	PP6R1_HUMAN	96.7	99.8%	2	2	2	0.00%	2.2%	LGQPPGVR	97.7%	30.1	25	18.7	1	0	0	823.48	656	663
Serine/threonine-protein phosphatase 6 regulatory subunit 1	PPP6R1	PP6R1_HUMAN	96.7	99.8%	2	2	2	0.00%	2.2%	VAGALVQNTEK	99.4%	35.8	25	28.1	1	0	0	1129.62	470	480
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	7	7	19	0.02%	27.0%	AIETTDIISR	99.7%	75.2	25	61.8	6	0	0	1118.61	153	162
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	7	7	19	0.02%	27.0%	ALQFPPEGWLR	96.5%	28.5	25	21.6	1	0	0	1313.70	241	251
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	7	7	19	0.02%	27.0%	EQAELTGLR	99.7%	49.3	25	35.5	4	0	0	1016.54	126	134
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	7	7	19	0.02%	27.0%	NVESGEEELASK	99.7%	78.4	25	78.3	4	0	0	1291.60	77	88
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	7	7	19	0.02%	27.0%	QEEDSYEIFICHANVIR	99.7%	38.1	25	38.1	0	1	0	2122.99	219	235
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	7	7	19	0.02%	27.0%	TLGDTGFMPPDK	99.7%	53.6	25	42.7	2	0	0	1278.60	274	285
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	7	7	19	0.02%	27.0%	VSTDLLR	98.1%	30.9	25	19.2	1	0	0	803.46	170	176
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	7	8	11	0.01%	27.1%	FSPDGELYASGSEDGTLR	99.7%	93.2	25	89.2	2	0	0	1900.86	273	290
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	7	8	11	0.01%	27.1%	IYDLNKPEAEPK	99.7%	41.7	25	39.6	2	1	0	1416.74	126	137
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	7	8	11	0.01%	27.1%	LWDHATMTEVK	99.3%	35.3	25	35.3	1	0	0	1330.65	168	178
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	7	8	11	0.01%	27.1%	LWQTVVGK	99.2%	34.5	25	17.1	1	0	0	930.54	291	298
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	7	8	11	0.01%	27.1%	QGDTGDWIGTFLGHK	98.9%	25.2	25	23.9	0	2	0	1631.78	45	59
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	7	8	11	0.01%	27.1%	TVDFTQDSNYLLTGGQDK	99.7%	71.3	25	64.6	1	0	0	2001.94	105	122
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	7	8	11	0.01%	27.1%	YDYNSGEELESYK	99.7%	53.1	25	53.1	1	0	0	1596.67	250	262
Serpin B12	SERPINB12	SPB12_HUMAN	46.3	99.9%	2	2	2	0.00%	6.4%	ADLTGISPSPNLYLSK	98.7%	32.4	25	15.3	1	0	0	1675.89	328	343
Serpin B12	SERPINB12	SPB12_HUMAN	46.3	99.9%	2	2	2	0.00%	6.4%	TDYTLSIANR	99.7%	44.5	25	38.3	1	0	0	1153.58	108	117
Serpin B9	SERPINB9	SPB9_HUMAN	42.4	99.8%	2	2	2	0.00%	5.3%	AQLLELPYAR	98.5%	31.9	25	30.9	1	0	0	1173.66	214	223
Serpin B9	SERPINB9	SPB9_HUMAN	42.4	99.8%	2	2	2	0.00%	5.3%	LVLVNAIYFK	97.4%	29.6	25	29.6	1	0	0	1179.71	159	168
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	12	24	0.02%	31.6%	DTQSGSLLFIGR	99.7%	88.8	25	75.3	5	0	0	1293.68	394	405
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	12	24	0.02%	31.6%	GVVEVTHDLQK	99.7%	55	25	50.5	2	0	0	1224.66	309	319

Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	12	24	0.02%	31.6%	HLAGLGLTEAIDK	99.7%	55.9	25	55.9	2	0	0	1337.74	320	332
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	12	24	0.02%	31.6%	HLAGLGLTEAIDKNK	99.7%	54.1	25	54.1	0	2	0	1579.88	320	334
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	12	24	0.02%	31.6%	KPAAAAAPGTAEK	99.7%	42.4	25	39.3	2	0	0	1182.65	23	35
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	12	24	0.02%	31.6%	LFYADHPFIFLVR	99.7%	44.2	25	44.2	2	1	0	1637.88	381	393
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	12	24	0.02%	31.6%	LQIVEMPLAHK	99.7%	45.2	25	33.2	1	0	0	1294.72	253	263
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	12	24	0.02%	31.6%	LSSLIILMPHHVEPLER	99.7%	29.5	25	29.5	0	1	0	1984.11	264	280
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	12	24	0.02%	31.6%	LYGPSSVSFADDFVR	99.7%	86.4	25	82.2	3	0	0	1659.80	134	148
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	12	24	0.02%	31.6%	SAGLAFSLYQAMAK	99.7%	83.6	25	75.1	2	0	0	1457.75	47	60
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	12	24	0.02%	31.6%	SYTVGVMMMHR	99.7%	38.7	25	38.7	1	0	0	1311.60	229	239
Serrate RNA effector molecule homolog	SRRT	SRRT_HUMAN	100.7	100.0%	4	4	6	0.01%	4.1%	AEIISLCK	98.2%	31.3	25	18.3	1	0	0	933.51	435	442
Serrate RNA effector molecule homolog	SRRT	SRRT_HUMAN	100.7	100.0%	4	4	6	0.01%	4.1%	ESLSEEEAQK	99.7%	39.3	25	32.9	2	0	0	1149.53	678	687
Serrate RNA effector molecule homolog	SRRT	SRRT_HUMAN	100.7	100.0%	4	4	6	0.01%	4.1%	LIHTLDDR	99.7%	54	25	30	1	0	0	982.53	527	534
Serrate RNA effector molecule homolog	SRRT	SRRT_HUMAN	100.7	100.0%	4	4	6	0.01%	4.1%	VALSEPQPER	99.7%	50.6	25	49.7	2	0	0	1125.59	450	459
Serum albumin	ALB	ALBU_HUMAN	69.4	100.0%	5	6	10	0.01%	8.4%	FQNALLVR	98.5%	31.8	25	6.11	1	0	0	960.56	427	434
Serum albumin	ALB	ALBU_HUMAN	69.4	100.0%	5	6	10	0.01%	8.4%	KVPQVSTPTLVEVSR	99.7%	47.3	25	47.3	1	3	0	1639.94	438	452
Serum albumin	ALB	ALBU_HUMAN	69.4	100.0%	5	6	10	0.01%	8.4%	LVAASQAALGL	99.7%	58.2	25	58.2	1	0	0	1013.60	599	609
Serum albumin	ALB	ALBU_HUMAN	69.4	100.0%	5	6	10	0.01%	8.4%	LVNEVTEFAK	99.7%	38.5	25	33.2	2	0	0	1149.62	66	75
Serum albumin	ALB	ALBU_HUMAN	69.4	100.0%	5	6	10	0.01%	8.4%	YLYEIAR	99.7%	40.8	25	32.1	2	0	0	927.49	162	168
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	11	12	22	0.02%	33.8%	ADKEGDYYVLNGSK	99.3%	35	25	35	1	0	0	1558.74	192	205
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	11	12	22	0.02%	33.8%	ASSTCPLTFENVK	99.7%	56.3	25	54.3	2	0	0	1453.70	257	269
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	11	12	22	0.02%	33.8%	ATYLPQLTTEK	99.7%	48.7	25	48.7	2	0	0	1264.68	160	170
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	11	12	22	0.02%	33.8%	CIEWMGGVGYTK	99.6%	37.3	25	37.3	1	0	0	1400.63	385	396
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	11	12	22	0.02%	33.8%	FAQEQIAPLVSTMDENSKMEK	99.6%	28.1	25	28.1	0	2	0	2428.14	71	91
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	11	12	22	0.02%	33.8%	GITSFLVDR	99.7%	38.8	25	25.9	2	0	0	1007.55	231	239
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	11	12	22	0.02%	33.8%	IGTIYEGASNIQLNTIAK	99.7%	85	25	79.6	2	0	0	1906.03	409	426
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	11	12	22	0.02%	33.8%	LLEAGKPFIK	99.7%	48.6	25	35.2	2	0	0	1115.68	356	365
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	11	12	22	0.02%	33.8%	VPEANILGQIGHGYK	99.7%	75	25	72.7	2	2	0	1595.85	270	284
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	11	12	22	0.02%	33.8%	YAIGSLNEGR	99.7%	64.6	25	52	2	0	0	1079.55	285	294
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	11	12	22	0.02%	33.8%	YYASEIAGQTTSK	99.7%	108	25	101	2	0	0	1418.68	372	384
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	11	12	33	0.03%	36.3%	ANHFFTVTDPR	99.7%	45.2	25	35.5	1	0	0	1304.64	25	35
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	11	12	33	0.03%	36.3%	HVSPLIGR	99.7%	38.9	25	32.4	2	0	0	878.52	171	178
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	11	12	33	0.03%	36.3%	IQESHPELR	99.7%	53.4	25	40.6	3	0	0	1108.57	306	314
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	11	12	33	0.03%	36.3%	IQESHPELRR	99.4%	27	25	24.3	0	1	0	1264.68	306	315
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	11	12	33	0.03%	36.3%	NILLTNEQLESAR	99.7%	107	25	97.7	4	0	0	1500.80	36	48
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	11	12	33	0.03%	36.3%	QAITQVVVSR	99.7%	80.1	25	72.6	4	0	0	1100.64	224	233
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	11	12	33	0.03%	36.3%	QGIVPPGLTENELWR	99.7%	75.9	25	73.7	4	0	0	1708.90	56	70
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	11	12	33	0.03%	36.3%	SSMSVTSLEAELQAK	99.7%	91.8	25	91.6	4	0	0	1596.78	291	305
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	11	12	33	0.03%	36.3%	VGIPVTDENGNR	99.7%	59.8	25	57.5	3	0	0	1270.64	203	214
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	11	12	33	0.03%	36.3%	WDQSTFIGR	99.7%	59.9	25	0	2	0	0	1109.54	16	24
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	11	12	33	0.03%	36.3%	YIYDSAFHPDTGEK	99.7%	74.2	25	70.7	4	1	0	1642.74	73	86
Sideroflexin-2	SFXN2	SFXN2_HUMAN	36.2	99.8%	2	2	4	0.00%	7.8%	AAAIGITQVVISR	99.7%	53.5	25	44.9	2	0	0	1298.78	220	232
Sideroflexin-2	SFXN2	SFXN2_HUMAN	36.2	99.8%	2	2	4	0.00%	7.8%	YGELEPYVYFNK	99.7%	50.8	25	50.8	2	0	0	1521.73	309	320
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	99.9%	2	2	3	0.00%	8.0%	DAVPAFIEPNVR	99.7%	39.9	25	35.1	2	0	0	1327.70	19	30
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	99.9%	2	2	3	0.00%	8.0%	SLATVHPDSSNLIPK	97.7%	30.2	25	29.5	1	0	0	1578.85	92	106
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	4	5	11	0.01%	23.5%	GDLLFLTNR	99.7%	73.7	25	53.8	2	0	0	1048.58	64	72
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	4	5	11	0.01%	23.5%	GDNNAVDDRGLYK	99.7%	44.9	25	44	2	0	0	1436.68	115	127
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	4	5	11	0.01%	23.5%	MLSLDFLDDVRR	98.9%	25.2	25	21.1	0	3	0	1495.76	1	12
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	4	5	11	0.01%	23.5%	VGEIVVFR	99.7%	67.3	25	63.3	4	0	0	918.54	79	86
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	8	15	0.01%	35.4%	FDDKYTLK	99.6%	37.9	25	26.2	2	0	0	1029.53	166	173
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	8	15	0.01%	35.4%	FFDHSGTLVMDAYEPEISR	99.7%	33.4	25	33.4	0	2	0	2230.01	196	214
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	8	15	0.01%	35.4%	IDDKPVKIDK	99.6%	38.4	25	20.4	2	0	0	1170.67	41	50

Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	8	15	0.01%	35.4%	IDKWDGSAVK	99.7%	48.9	25	31.2	2	0	0	1118.58	48	57
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	8	15	0.01%	35.4%	LHDSLAIER	99.7%	51.3	25	43.7	2	0	0	1053.57	215	223
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	8	15	0.01%	35.4%	SGLLDKWK	99.7%	53.7	25	37.8	1	0	0	946.54	33	40
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	8	15	0.01%	35.4%	SIFLVAHR	99.7%	38.6	25	31	2	0	0	942.55	138	145
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	8	15	0.01%	35.4%	YVENFGLIDGR	99.7%	56	25	41.8	2	0	0	1282.64	74	84
Signal peptidase complex subunit 3	SPCS3	SPCS3_HUMAN	20.3	100.0%	3	3	6	0.01%	17.8%	NNALNQVVLWDK	99.7%	59.8	25	43.4	2	0	0	1413.75	97	108
Signal peptidase complex subunit 3	SPCS3	SPCS3_HUMAN	20.3	100.0%	3	3	6	0.01%	17.8%	NVEDFTGPR	99.7%	53.4	25	47.4	3	0	0	1034.49	50	58
Signal peptidase complex subunit 3	SPCS3	SPCS3_HUMAN	20.3	100.0%	3	3	6	0.01%	17.8%	YFFFDDGNGLK	98.9%	33.5	25	31.7	1	0	0	1322.61	127	137
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	4	5	11	0.01%	28.7%	EVNKFQMAYSNLLR	99.7%	41.1	25	30.9	1	2	0	1712.88	75	88
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	4	5	11	0.01%	28.7%	FQMAYSNLLR	99.7%	47.8	25	32.9	2	0	0	1242.63	79	88
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	4	5	11	0.01%	28.7%	TSGSVYITLKK	99.7%	46.9	25	46.9	2	0	0	1196.69	22	32
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	4	5	11	0.01%	28.7%	VLLESEQFLTELTR	99.7%	87.1	25	86.8	4	0	0	1677.91	2	15
Signal recognition particle 19 kDa protein	SRP19	SRP19_HUMAN	16.2	99.8%	2	2	3	0.00%	18.8%	SVMLYAAEMIPK	99.1%	34.2	25	25.9	1	0	0	1384.69	103	114
Signal recognition particle 19 kDa protein	SRP19	SRP19_HUMAN	16.2	99.8%	2	2	3	0.00%	18.8%	TGGADQSLQQGEGSK	99.7%	72.6	25	61.7	2	0	0	1462.68	122	136
Signal recognition particle 9 kDa protein	SRP9	SRP09_HUMAN	10.1	100.0%	3	3	6	0.01%	34.9%	LYLADPMK	96.8%	28.9	25	21.5	2	0	0	950.50	17	24
Signal recognition particle 9 kDa protein	SRP9	SRP09_HUMAN	10.1	100.0%	3	3	6	0.01%	34.9%	PQYQTWEEFSR	99.7%	51.5	25	47.5	1	0	0	1470.66	2	12
Signal recognition particle 9 kDa protein	SRP9	SRP09_HUMAN	10.1	100.0%	3	3	6	0.01%	34.9%	VTDDLVCLVYK	99.7%	62.9	25	50.6	3	0	0	1324.68	42	52
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	8	10	13	0.01%	13.5%	AGAVEQLR	98.7%	32.6	25	14.6	1	0	0	843.47	459	466
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	8	10	13	0.01%	13.5%	ALADHSMAQTPR	97.5%	29.9	25	29.1	2	0	0	1313.63	569	580
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	8	10	13	0.01%	13.5%	DAAGIAMEAIAFAR	99.7%	75.8	25	59.2	3	0	0	1406.71	497	510
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	8	10	13	0.01%	13.5%	GTLGGMFGMLK	99.7%	42.5	25	36	1	0	0	1111.56	315	325
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	8	10	13	0.01%	13.5%	LIDGIVLTK	97.2%	29.4	25	16	1	0	0	971.61	581	589
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	8	10	13	0.01%	13.5%	MLDFFTIFSK	99.7%	48.9	25	43	3	0	0	1248.63	1	10
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	8	10	13	0.01%	13.5%	NQGFDVVLVDTAGR	99.7%	91.1	25	80.6	1	0	0	1490.76	511	524
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	8	10	13	0.01%	13.5%	TMVQLFEK	99.6%	37.9	25	30.4	1	0	0	995.52	485	492
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	24	0.02%	50.9%	AIVFVVDSAAFQR	99.7%	83	25	80.2	4	0	0	1422.77	138	150
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	24	0.02%	50.9%	AVLLVGLCDSGK	99.7%	81.4	25	71.2	2	0	0	1231.67	66	77
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	24	0.02%	50.9%	DTQTSITDSCAVYR	99.7%	84.2	25	84.2	2	0	0	1616.72	91	104
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	24	0.02%	50.9%	GDVGSADIQDLEK	99.7%	81.9	25	70.2	2	0	0	1346.64	253	265
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	24	0.02%	50.9%	GNSLTLIDLPGHESLR	99.7%	53.4	25	53.4	2	2	0	1721.92	110	125
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	24	0.02%	50.9%	LIQQQLEK	99.7%	39.8	25	9.35	2	0	0	999.58	192	199
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	24	0.02%	50.9%	LLTGLYR	99.5%	36.9	25	1.3	1	0	0	835.50	84	90
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	24	0.02%	50.9%	LQFLER	99.4%	35.6	25	0	2	0	0	805.46	126	131
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	24	0.02%	50.9%	NTPSFLIACNK	99.7%	50.7	25	45.6	2	0	0	1264.64	171	181
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	24	0.02%	50.9%	SAAPSTLDSSSTAPAQLGK	99.7%	88.1	25	88.1	1	0	0	1788.90	209	227
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	24	0.02%	50.9%	VADGGGAGGTFQPYLDTLR	99.7%	83	25	83	2	0	0	1894.93	9	27
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	9	9	16	0.02%	16.6%	AAIEAFNK	99.0%	33.6	25	22.2	1	0	0	863.46	206	213
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	9	9	16	0.02%	16.6%	ALLQQQPEDDSKR	96.1%	21.2	25	21.2	0	1	0	1527.78	405	417
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	9	9	16	0.02%	16.6%	DLPDVQELITQVR	99.7%	51.2	25	42.1	2	0	0	1525.82	509	521
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	9	9	16	0.02%	16.6%	FETFCLDPSLVTK	99.7%	82.8	25	77.3	2	0	0	1556.77	558	570
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	9	9	16	0.02%	16.6%	LASAFTEEQAVLYNQR	99.7%	83.2	25	74.3	2	0	0	1839.92	221	236
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	9	9	16	0.02%	16.6%	LFESMLSECR	99.7%	54.5	25	48.1	3	0	0	1271.58	336	345
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	9	9	16	0.02%	16.6%	SPRPQDLIR	98.1%	31	25	16.3	1	0	0	1081.61	418	426
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	9	9	16	0.02%	16.6%	VEEISPNIR	99.7%	46	25	41.6	3	0	0	1056.57	237	245
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	9	9	16	0.02%	16.6%	YANEVNSDAGAFK	99.7%	46.4	25	40.3	1	0	0	1385.63	492	504
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	4	4	6	0.01%	6.6%	SPAHLSLIR	99.7%	45.8	25	27	2	0	0	993.58	443	451
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	4	4	6	0.01%	6.6%	TEEALQLYNQIIK	99.7%	66.2	25	62.7	2	0	0	1562.84	242	254
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	4	4	6	0.01%	6.6%	TIESANQQTDKLK	99.7%	60	25	55.5	1	0	0	1475.77	100	112
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	4	4	6	0.01%	6.6%	YGQNGDFTR	94.6%	26.9	25	20.1	1	0	0	1057.47	21	29
Signal transducer and activator of transcription 1-alpha/beta	STAT1	STAT1_HUMAN	87.3	100.0%	3	3	4	0.00%	4.5%	LQELNYNLK	96.9%	29	25	20.2	1	0	0	1134.62	351	359
Signal transducer and activator of transcription 1-alpha/beta	STAT1	STAT1_HUMAN	87.3	100.0%	3	3	4	0.00%	4.5%	NLSFFLTPPCAR	98.8%	33	25	23.3	1	0	0	1422.72	483	494

Signal transducer and activator of transcription 1-alpha/beta	STAT1	STAT1_HUMAN	87.3	100.0%	3	3	4	0.00%	4.5%	TELISVSEVHPSR	99.7%	60	25	52.8	2	0	0	1453.76	704	716
Signal transducer and activator of transcription 3	STAT3	STAT3_HUMAN	88.1	100.0%	4	4	7	0.01%	8.3%	GLSIEQLTTLAEK	99.7%	91.7	25	79.8	2	0	0	1402.78	519	531
Signal transducer and activator of transcription 3	STAT3	STAT3_HUMAN	88.1	100.0%	4	4	7	0.01%	8.3%	LLQTAATAAQQGGQANHPTAAVVTEK	99.7%	83	25	82.4	0	2	0	2576.34	115	140
Signal transducer and activator of transcription 3	STAT3	STAT3_HUMAN	88.1	100.0%	4	4	7	0.01%	8.3%	TQIQSVEPYTK	99.0%	33.7	25	9.79	1	0	0	1293.67	632	642
Signal transducer and activator of transcription 3	STAT3	STAT3_HUMAN	88.1	100.0%	4	4	7	0.01%	8.3%	VVENLQDDFDFNYK	99.7%	90.1	25	80.6	2	0	0	1745.80	164	177
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	6	7	13	0.01%	49.3%	DVAYQYVK	96.9%	29	25	22.1	2	0	0	985.50	96	103
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	6	7	13	0.01%	49.3%	ISVFRPGLR	98.2%	31.1	25	24.3	2	0	0	1044.63	87	95
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	6	7	13	0.01%	49.3%	NPVTIFSLATNEMWR	99.7%	50.3	25	45.6	3	0	0	1794.88	52	66
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	6	7	13	0.01%	49.3%	QATTIIADNIIFLSDQTK	99.7%	54.4	25	54.4	2	0	0	1992.07	128	145
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	6	7	13	0.01%	49.3%	SGDSEVYQLGDVSQK	99.7%	114	25	107	2	0	0	1611.75	67	81
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	6	7	13	0.01%	49.3%	VGQDPVLR	99.7%	56.4	25	51.1	2	0	0	883.50	39	46
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	11	11	22	0.02%	10.4%	DIFLFITR	98.0%	30.8	25	24.1	2	0	0	1024.58	115	122
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	11	11	22	0.02%	10.4%	DLALVNDQLLGFVR	99.7%	73.6	25	71.2	4	0	0	1572.87	391	404
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	11	11	22	0.02%	10.4%	EINSDQATQGNISSDR	99.7%	57.3	25	57.3	1	0	0	1734.79	1220	1235
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	11	11	22	0.02%	10.4%	EVQLAQIFEPLSR	99.7%	62.8	25	56.7	2	0	0	1529.83	751	763
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	11	11	22	0.02%	10.4%	FNDIHVPVR	99.7%	39	25	32.6	1	0	0	1096.59	332	340
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	11	11	22	0.02%	10.4%	IETDLPQIR	99.7%	41.4	25	25.4	1	0	0	1084.60	709	717
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	11	11	22	0.02%	10.4%	LLVACCLADIFR	99.7%	64	25	64	3	0	0	1450.75	88	99
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	11	11	22	0.02%	10.4%	LYTVCDVALCVINSK	99.7%	72.4	25	72.4	2	0	0	1754.88	1075	1089
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	11	11	22	0.02%	10.4%	SIEGTADDEEEGVSPDTAIR	99.7%	62.3	25	52.8	2	0	0	2090.94	638	657
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	11	11	22	0.02%	10.4%	STLIPILHQK	98.5%	31.8	25	0	2	0	0	1149.70	718	727
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	11	11	22	0.02%	10.4%	TVTAAGAENIQQK	99.7%	78.8	25	57.1	2	0	0	1330.70	1240	1252
Small nuclear ribonucleoprotein E	SNRPE	RUXE_HUMAN	10.8	100.0%	4	6	13	0.01%	42.4%	GDNITLLQSVSN	99.7%	60.8	25	50.6	2	0	0	1260.64	81	92
Small nuclear ribonucleoprotein E	SNRPE	RUXE_HUMAN	10.8	100.0%	4	6	13	0.01%	42.4%	IMLKGDNITLLQSVSN	99.7%	53.2	25	53.2	4	0	0	1745.95	77	92
Small nuclear ribonucleoprotein E	SNRPE	RUXE_HUMAN	10.8	100.0%	4	6	13	0.01%	42.4%	IQVWLYEQVNMR	99.7%	58.2	25	58.2	2	0	0	1594.80	31	42
Small nuclear ribonucleoprotein E	SNRPE	RUXE_HUMAN	10.8	100.0%	4	6	13	0.01%	42.4%	VMVQPINLIFR	99.7%	47.8	25	44.6	5	0	0	1345.77	13	23
Small nuclear ribonucleoprotein F	SNRPF	RUXF_HUMAN	9.7	100.0%	3	3	6	0.01%	33.7%	CNNVLYIR	99.7%	57.5	25	39.7	4	0	0	1051.54	66	73
Small nuclear ribonucleoprotein F	SNRPF	RUXF_HUMAN	9.7	100.0%	3	3	6	0.01%	33.7%	GVEEEEEDGEMRE	99.7%	40.8	25	40.8	1	0	0	1553.59	74	86
Small nuclear ribonucleoprotein F	SNRPF	RUXF_HUMAN	9.7	100.0%	3	3	6	0.01%	33.7%	LKWGMEYK	98.8%	33	25	16.1	1	0	0	1054.54	23	30
Small nuclear ribonucleoprotein Sm D1	SNRPD1	SMD1_HUMAN	13.3	100.0%	4	7	20	0.02%	37.8%	EPVQLETLSIR	99.7%	56.8	25	37.1	2	0	0	1284.72	51	61
Small nuclear ribonucleoprotein Sm D1	SNRPD1	SMD1_HUMAN	13.3	100.0%	4	7	20	0.02%	37.8%	LSHETVTIELK	99.7%	53.2	25	44.3	4	2	0	1269.71	10	20
Small nuclear ribonucleoprotein Sm D1	SNRPD1	SMD1_HUMAN	13.3	100.0%	4	7	20	0.02%	37.8%	NGTQVHGTITGVDVSMNTHLK	99.7%	78.7	25	78.7	0	6	0	2209.10	21	41
Small nuclear ribonucleoprotein Sm D1	SNRPD1	SMD1_HUMAN	13.3	100.0%	4	7	20	0.02%	37.8%	NREPVQLETLSIR	99.7%	58.9	25	55.5	4	2	0	1554.86	49	61
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	10	15	28	0.03%	68.6%	AFDRHCNMVLENVK	99.7%	30.8	25	30.8	0	3	0	1732.83	58	71
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	10	15	28	0.03%	68.6%	EEEEFNTGPLSVLTQSVK	99.7%	97.6	25	97.6	2	0	0	2006.99	20	37
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	10	15	28	0.03%	68.6%	EMWTEVPK	97.8%	30.4	25	28.6	2	0	0	1019.49	72	79
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	10	15	28	0.03%	68.6%	GDSVIVVLR	99.7%	71.4	25	56	4	0	0	957.57	103	111
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	10	15	28	0.03%	68.6%	GDSVIVVLRNPLIAGK	99.7%	42.4	25	42.4	2	0	0	1650.99	103	118
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	10	15	28	0.03%	68.6%	HCNMVLENVK	99.7%	54.9	25	54.5	4	0	0	1243.59	62	71
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	10	15	28	0.03%	68.6%	MFLRGDSVIVVLR	99.7%	35.6	25	35.2	1	2	0	1520.86	99	111
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	10	15	28	0.03%	68.6%	NNTQVLINCR	99.7%	78.8	25	67.7	2	0	0	1231.62	38	47
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	10	15	28	0.03%	68.6%	REEEEFNTGPLSVLTQSVK	99.7%	70.5	25	70.5	1	2	0	2163.09	19	37
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	10	15	28	0.03%	68.6%	SEMTPEELQK	99.7%	56.3	25	47.5	3	0	0	1191.56	9	18
Small nuclear ribonucleoprotein Sm D3	SNRPD3	SMD3_HUMAN	13.9	100.0%	3	4	8	0.01%	31.7%	FLILPDMLK	99.7%	40.3	25	18.2	4	0	0	1105.63	70	78
Small nuclear ribonucleoprotein Sm D3	SNRPD3	SMD3_HUMAN	13.9	100.0%	3	4	8	0.01%	31.7%	VAQLEQVYIR	99.7%	79.6	25	70	2	0	0	1218.68	55	64
Small nuclear ribonucleoprotein Sm D3	SNRPD3	SMD3_HUMAN	13.9	100.0%	3	4	8	0.01%	31.7%	VLHEAEGHIVTCETNTGEVYR	99.7%	81.3	25	81.3	0	2	0	2414.14	9	29
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN	24.6	100.0%	4	5	12	0.01%	15.0%	GENLVSMTVEGPPPK	99.7%	55.1	25	49.1	4	0	0	1554.78	74	88
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN	24.6	100.0%	4	5	12	0.01%	15.0%	GENLVSMTVEGPPPKDTGIAR	99.7%	37	25	37	0	1	0	2168.10	74	94
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN	24.6	100.0%	4	5	12	0.01%	15.0%	IFIGTFK	97.1%	29.3	25	16.5	2	0	0	825.49	26	32
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN	24.6	100.0%	4	5	12	0.01%	15.0%	VLGLVLLR	99.7%	67	25	67	5	0	0	882.61	66	73
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	23	27	73	0.07%	29.0%	ADIGVAMGIAGSDVSK	99.7%	114	25	108	4	0	0	1490.75	728	743

Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	23	27	73	0.07%	29.0%	AVAGDASESALLK	99.7%	94.4	25	84.2	6	0	0	1231.65	446	458
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	23	27	73	0.07%	29.0%	AVFQANQENLPILK	99.7%	80.3	25	67	4	0	0	1584.87	431	444
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	23	27	73	0.07%	29.0%	CIELCCGSVK	99.7%	42.8	25	31.7	2	0	0	1225.54	459	468
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	23	27	73	0.07%	29.0%	DGPNALTPPPTTPEWIK	99.5%	36.9	25	36.7	2	0	0	1833.94	75	91
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	23	27	73	0.07%	29.0%	GIVVYTGDR	99.7%	55	25	49.6	4	0	0	979.52	256	264
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	23	27	73	0.07%	29.0%	GVGIISEGNETVEDIAAR	99.7%	133	25	122	3	0	0	1829.92	630	647
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	23	27	73	0.07%	29.0%	IVEIPFNSTNK	95.1%	27.2	25	25.7	1	0	0	1261.68	477	487
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	23	27	73	0.07%	29.0%	LIFDNLKK	99.7%	43.3	25	31.9	2	0	0	990.60	767	774
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	23	27	73	0.07%	29.0%	LIIVEGCQR	99.7%	55.3	25	45.5	5	0	0	1087.59	699	707
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	23	27	73	0.07%	29.0%	LNIPVSQVNPR	99.7%	59.8	25	58.7	7	0	0	1236.71	648	658
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	23	27	73	0.07%	29.0%	MSINAEEVVVGDLVEVK	99.7%	72.1	25	68.7	3	0	0	1846.95	178	194
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	23	27	73	0.07%	29.0%	NIAFFSTNCVEGTAR	99.7%	103	25	99.7	2	0	0	1686.79	241	255
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	23	27	73	0.07%	29.0%	NLEAVETLGSTSTICSDK	99.7%	92.3	25	92.3	2	0	0	1924.92	360	377
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	23	27	73	0.07%	29.0%	NMVPQQALVIR	99.7%	52.3	25	47.3	4	0	0	1268.71	163	173
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	23	27	73	0.07%	29.0%	NPNTSEPQHLLVMK	99.7%	61.6	25	52.1	3	0	0	1607.82	495	508
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	23	27	73	0.07%	29.0%	QGAIVAVTGDGVNDSPALK	99.7%	110	25	106	2	0	0	1811.95	708	726
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	23	27	73	0.07%	29.0%	SPDFTNENPLETR	99.7%	82.5	25	76.3	4	0	0	1519.70	228	240
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	23	27	73	0.07%	29.0%	TSATWLALSR	99.7%	86.9	25	74	4	0	0	1105.60	414	423
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	23	27	73	0.07%	29.0%	VDNSSLTGESEPQTR	99.7%	103	25	89.7	3	0	0	1619.75	213	227
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	23	27	73	0.07%	29.0%	VIMVTGDHPITAK	99.7%	59.6	25	56.1	2	0	0	1397.75	613	625
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	23	27	73	0.07%	29.0%	YGTDLSR	98.1%	31	25	16.5	2	0	0	811.39	55	61
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	23	27	73	0.07%	29.0%	YHTEIVFAR	99.7%	39.5	25	28.4	2	0	0	1135.59	684	692
Sodium/potassium-transporting ATPase subunit beta-3	ATP1B3	AT1B3_HUMAN	31.5	99.8%	2	2	4	0.00%	8.6%	LFIYNPTTGEFLGR	99.7%	71	25	68.5	2	0	0	1627.85	18	31
Sodium/potassium-transporting ATPase subunit beta-3	ATP1B3	AT1B3_HUMAN	31.5	99.8%	2	2	4	0.00%	8.6%	SLNQSLAEWK	98.6%	32.3	25	22.1	2	0	0	1175.61	8	17
Sorting and assembly machinery component 50 homolog	SAMM50	SAM50_HUMAN	52.0	100.0%	4	4	6	0.01%	10.7%	ICDGVQFGAGIR	99.7%	77	25	70.8	1	0	0	1292.64	456	467
Sorting and assembly machinery component 50 homolog	SAMM50	SAM50_HUMAN	52.0	100.0%	4	4	6	0.01%	10.7%	SSLSHAMVIDSR	99.7%	72.4	25	55.6	1	0	0	1302.65	256	267
Sorting and assembly machinery component 50 homolog	SAMM50	SAM50_HUMAN	52.0	100.0%	4	4	6	0.01%	10.7%	TKDDIIICEIGDVFK	99.7%	98.6	25	83.3	2	0	0	1765.90	58	72
Sorting and assembly machinery component 50 homolog	SAMM50	SAM50_HUMAN	52.0	100.0%	4	4	6	0.01%	10.7%	VTGQFPWSSLR	99.5%	36.9	25	29.7	2	0	0	1277.66	195	205
Sorting nexin-2	SNX2	SNX2_HUMAN	58.5	99.8%	2	2	3	0.00%	4.1%	ELSANTAAFAK	99.7%	56.5	25	50.4	1	0	0	1122.58	336	346
Sorting nexin-2	SNX2	SNX2_HUMAN	58.5	99.8%	2	2	3	0.00%	4.1%	QFLESSELPR	99.7%	51.2	25	35.7	2	0	0	1205.62	260	269
Sorting nexin-9	SNX9	SNX9_HUMAN	66.6	100.0%	2	2	2	0.00%	3.7%	FGSAIPIPSLPDK	96.1%	28.1	25	19	1	0	0	1341.74	301	313
Sorting nexin-9	SNX9	SNX9_HUMAN	66.6	100.0%	2	2	2	0.00%	3.7%	IYDYNSVIR	99.7%	53	25	42.6	1	0	0	1142.58	560	568
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	SPTN1_HUMAN	284.5	100.0%	4	4	5	0.00%	1.7%	DVDEIEAWISEK	99.2%	34.5	25	34	1	0	0	1433.68	1559	1570
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	SPTN1_HUMAN	284.5	100.0%	4	4	5	0.00%	1.7%	EANQQQQFNR	94.6%	26.9	25	15.2	1	0	0	1262.59	676	685
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	SPTN1_HUMAN	284.5	100.0%	4	4	5	0.00%	1.7%	LFGAAEVQR	99.7%	44.7	25	25.8	1	0	0	990.54	251	259
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	SPTN1_HUMAN	284.5	100.0%	4	4	5	0.00%	1.7%	SQLLGSAHEVQR	99.7%	54.4	25	43.1	2	0	0	1324.70	1226	1237
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	7	7	9	0.01%	3.8%	ALVADSHPESER	99.7%	46.8	25	46.5	1	0	0	1310.63	1657	1668
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	7	7	9	0.01%	3.8%	GNLEVLLFTIQSK	99.7%	45.9	25	45.9	1	0	0	1461.83	360	372
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	7	7	9	0.01%	3.8%	LILEVHQFSR	99.7%	44.2	25	24.8	1	0	0	1241.70	2015	2024
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	7	7	9	0.01%	3.8%	LVSQDNFGFDLPAVEAATK	99.7%	47.7	25	47.7	2	0	0	2022.02	444	462
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	7	7	9	0.01%	3.8%	SQNIVTDSSSLSAEAIR	99.7%	91.6	25	83.4	1	0	0	1777.89	1548	1564
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	7	7	9	0.01%	3.8%	VLDNAIETEK	99.5%	37	25	37	1	0	0	1131.59	293	302
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	7	7	9	0.01%	3.8%	VQAVVAVAR	99.5%	36.8	25	25.9	2	0	0	912.56	478	486
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	4	4	6	0.01%	12.9%	AAFVLPEFAR	98.7%	32.5	25	25.6	2	0	0	1120.61	286	295
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	4	4	6	0.01%	12.9%	FLPGMAIGYSSSK	99.7%	49.2	25	33.4	2	0	0	1357.68	136	148
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	4	4	6	0.01%	12.9%	YQDILVFR	95.8%	27.8	25	20	1	0	0	1053.57	48	55
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	4	4	6	0.01%	12.9%	YYNSDVHR	99.7%	40.2	25	38.7	1	0	0	1053.47	278	285
Sphingomyelin phosphodiesterase 4	SMPD4	NSMA3_HUMAN	93.4	100.0%	4	4	6	0.01%	4.5%	FDFPVSYLPGPVK	99.6%	38.2	25	38.2	1	0	0	1465.77	107	119
Sphingomyelin phosphodiesterase 4	SMPD4	NSMA3_HUMAN	93.4	100.0%	4	4	6	0.01%	4.5%	LAQLITQAK	99.7%	60.7	25	53.3	1	0	0	985.60	557	565
Sphingomyelin phosphodiesterase 4	SMPD4	NSMA3_HUMAN	93.4	100.0%	4	4	6	0.01%	4.5%	LFVGFLNR	99.7%	43.1	25	39.2	2	0	0	965.56	444	451
Sphingomyelin phosphodiesterase 4	SMPD4	NSMA3_HUMAN	93.4	100.0%	4	4	6	0.01%	4.5%	LSEAQLR	99.4%	35.7	25	3.42	2	0	0	816.46	632	638

Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	7	10	23	0.02%	40.1%	EGNGPVTQWK	99.0%	33.6	25	20.8	2	0	0	1115.55	64	73
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	7	10	23	0.02%	40.1%	GTVLDQVPVNPSLYLIK	99.7%	52.6	25	34.7	4	0	0	1856.05	74	90
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	7	10	23	0.02%	40.1%	IMPDSNDSPPAEREPGEVVDSLVGK	99.7%	29.4	25	26.2	0	1	0	2654.26	192	216
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	7	10	23	0.02%	40.1%	ISDAHLADTMIGK	99.7%	63.7	25	59.4	2	0	0	1371.69	123	135
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	7	10	23	0.02%	40.1%	SSVGPSKPVSQPR	99.7%	57.5	25	42.2	4	4	0	1325.72	38	50
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	7	10	23	0.02%	40.1%	VSALEVLPDR	99.7%	77.4	25	64.3	4	0	0	1098.62	108	117
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	7	10	23	0.02%	40.1%	YDGFDCVYGLELNKDER	99.7%	33	25	33	1	1	0	2092.93	91	107
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	24	27	63	0.06%	22.8%	AIVNVIGMHK	99.7%	45.2	25	44.2	3	0	0	1097.61	999	1008
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	24	27	63	0.06%	22.8%	ATVNTFGYIAK	99.7%	65.5	25	64.3	2	0	0	1184.63	1076	1086
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	24	27	63	0.06%	22.8%	DTPGHGSGWAETPR	99.7%	38.5	25	36.8	1	2	0	1467.66	302	315
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	24	27	63	0.06%	22.8%	EIISNLAK	99.2%	34.7	25	12.9	1	0	0	887.52	595	602
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	24	27	63	0.06%	22.8%	EVMLILIR	99.7%	56.9	25	38.6	7	0	0	986.61	768	775
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	24	27	63	0.06%	22.8%	GDTPGHATPGHGGATSSAR	99.7%	57.1	25	57.1	0	3	0	1733.80	271	289
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	24	27	63	0.06%	22.8%	GGDSIGETPTPGASK	99.7%	52.5	25	46.4	4	0	0	1373.65	319	333
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	24	27	63	0.06%	22.8%	ICFELLELLK	99.7%	58.8	25	55.4	3	0	0	1277.72	1058	1067
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	24	27	63	0.06%	22.8%	ILVVIEPLLIDEDYYAR	99.7%	69.4	25	69.4	1	0	0	2034.12	574	590
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	24	27	63	0.06%	22.8%	IYNDDKNTYIR	99.7%	57.5	25	49.8	3	0	0	1414.70	1287	1297
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	24	27	63	0.06%	22.8%	IYNSIYIGSQDALIAHYPR	99.7%	49.8	25	45.1	0	2	0	2194.13	1268	1286
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	24	27	63	0.06%	22.8%	LDPFADGGKTPDPK	98.8%	32.9	25	31.8	1	0	0	1457.73	133	146
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	24	27	63	0.06%	22.8%	MTPPIKDLLPR	99.7%	43.9	25	32.6	1	0	0	1296.73	1009	1019
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	24	27	63	0.06%	22.8%	QLVDTTVELANK	99.7%	89.6	25	81.5	4	0	0	1330.72	832	843
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	24	27	63	0.06%	22.8%	QQAADLISR	99.7%	58.4	25	46.2	4	0	0	1001.54	949	957
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	24	27	63	0.06%	22.8%	SLVEIIEHGLVDEQQK	99.7%	47.8	25	35.7	2	0	0	1836.97	685	700
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	24	27	63	0.06%	22.8%	SRWDETPASQMGGSTPVLTPGK	99.7%	33	25	33	0	1	0	2318.11	336	357
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	24	27	63	0.06%	22.8%	TEILPPFFK	99.7%	47	25	29.3	2	0	0	1091.61	808	816
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	24	27	63	0.06%	22.8%	THEDIEAQIR	99.7%	49.4	25	43.9	2	0	0	1211.60	7	16
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	24	27	63	0.06%	22.8%	TMIISPER	99.1%	34.3	25	22.7	2	0	0	962.50	125	132
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	24	27	63	0.06%	22.8%	VGAAEIISR	99.7%	75.7	25	39.6	4	0	0	915.53	844	852
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	24	27	63	0.06%	22.8%	VLPPPAGYVPIR	99.6%	37.6	25	32.5	1	0	0	1278.76	414	425
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	24	27	63	0.06%	22.8%	VPELNVQNGVLK	99.7%	63.4	25	58.8	3	0	0	1309.75	1138	1149
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	24	27	63	0.06%	22.8%	VQENCIDLVGR	99.7%	74.5	25	70.3	4	0	0	1302.65	1031	1041
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	3	3	6	0.01%	3.5%	AAVLLEQER	99.7%	59.2	25	53.2	2	0	0	1028.57	184	192
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	3	3	6	0.01%	3.5%	KPGDLSDELR	99.7%	57.6	25	41.5	2	0	0	1129.59	605	614
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	3	3	6	0.01%	3.5%	LAEIGAPIQGNR	99.6%	38	25	38	2	0	0	1238.69	36	47
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	18	39	0.04%	16.7%	DYIVVGSDSGR	99.7%	63.5	25	51.5	2	0	0	1167.56	76	86
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	18	39	0.04%	16.7%	FGNICVVR	99.7%	56.8	25	44.7	2	0	0	964.50	1050	1057
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	18	39	0.04%	16.7%	FLAVGLVDNTVR	99.7%	78.6	25	67.2	4	0	0	1303.74	604	615
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	18	39	0.04%	16.7%	FSNTGEDWYVLVGVAK	99.7%	83.1	25	81	2	0	0	1784.89	896	911
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	18	39	0.04%	16.7%	IVILEYQPSK	99.7%	64.1	25	54.8	2	0	0	1189.68	87	96
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	18	39	0.04%	16.7%	LGAVFNQVAFPLQYTPR	99.7%	75.7	25	75.7	5	0	0	1921.03	770	786
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	18	39	0.04%	16.7%	LPPNTNDEVDEDPTGNK	99.7%	47.1	25	47.1	1	0	0	1854.84	1058	1074
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	18	39	0.04%	16.7%	MFLYNLTLQR	99.7%	61.4	25	56.8	3	0	0	1298.69	1	10
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	18	39	0.04%	16.7%	MQGQEAVLAMSSR	99.7%	77.7	25	76	3	0	0	1407.67	706	718
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	18	39	0.04%	16.7%	NENQLIIFADDTYPR	99.7%	80.9	25	80.9	1	0	0	1808.88	1017	1031
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	18	39	0.04%	16.7%	NFGDQPDIR	99.7%	44.7	25	39.8	2	0	0	1061.50	260	268
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	18	39	0.04%	16.7%	SVAGGFVYTYK	99.7%	61.3	25	49.5	3	0	0	1191.60	919	929
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	18	39	0.04%	16.7%	SWLSYSYQSR	99.7%	45.6	25	41.2	2	0	0	1276.60	719	728
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	18	39	0.04%	16.7%	TPVEEVPAAIAPFQGR	99.7%	69.3	25	61.3	2	0	0	1681.89	943	958
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	18	39	0.04%	16.7%	TVLDPVTGDLSDTR	99.7%	94.5	25	92.8	3	0	0	1488.75	677	690
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	16	18	39	0.04%	16.7%	VIVSDVQESFIWVR	99.7%	66.1	25	58.4	2	0	0	1676.90	1000	1013
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	3	3	6	0.01%	12.5%	AVIDLNNR	99.7%	41.1	25	31.6	2	0	0	914.51	126	133

Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	3	3	6	0.01%	12.5%	NPQNSSQSADGLR	99.7%	78.2	25	75.1	2	0	0	1373.64	54	66
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	3	3	6	0.01%	12.5%	QYEMGECTR	99.7%	48.9	25	36.6	2	0	0	1173.47	157	165
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	13	26	0.03%	26.9%	ELLTSFGPLK	98.7%	32.6	25	22.4	2	0	0	1104.63	277	286
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	13	26	0.03%	26.9%	GAKEEHGGLIR	99.6%	37.6	25	27.2	2	0	0	1166.63	68	78
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	13	26	0.03%	26.9%	IFVEFTSVFDCQK	99.7%	81.3	25	81.3	2	0	0	1619.78	432	444
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	13	26	0.03%	26.9%	LFIGGLPNYLNDDQVK	99.7%	57.9	25	47.9	2	0	0	1805.94	261	276
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	13	26	0.03%	26.9%	LGGLTQAPGNPVLAVQINQDK	99.7%	71	25	71	2	0	0	2133.17	175	195
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	13	26	0.03%	26.9%	NFAFLEFR	99.7%	57.2	25	42.4	2	0	0	1043.53	196	203
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	13	26	0.03%	26.9%	SIEIPRPVDGVEVPGCGK	99.7%	70.3	25	65.8	2	2	0	1908.99	414	431
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	13	26	0.03%	26.9%	SVDETTQAMAFDGIIFQGQSLK	99.7%	83.8	25	83.5	4	2	0	2402.15	204	225
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	13	26	0.03%	26.9%	YCDPDSYHR	99.7%	57	25	57	2	2	0	1212.47	463	471
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	6	6	8	0.01%	11.7%	AELDDTPMR	99.7%	45.8	25	37.5	1	0	0	1063.47	350	358
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	6	6	8	0.01%	11.7%	AVVIVDDR	99.7%	38.9	25	26.3	3	0	0	886.50	400	407
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	6	6	8	0.01%	11.7%	FATHAAALSVR	99.7%	57.6	25	45.8	1	0	0	1143.63	366	376
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	6	6	8	0.01%	11.7%	FGQGGAGPVGGQGPR	99.7%	52.7	25	44.8	2	0	0	1341.67	667	681
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	6	6	8	0.01%	11.7%	GIVEFASKPAAR	99.1%	34.3	25	34.3	1	0	0	1245.70	414	425
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	6	6	8	0.01%	11.7%	LFVGNLPADITEDEFKR	97.9%	23.1	25	21	0	1	0	1964.01	299	315
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	6	6	8	0.01%	11.7%	YGEPGEVFINK	99.7%	51.3	25	48.5	2	0	0	1252.62	320	330
SRA stem-loop-interacting RNA-binding protein, mitochondrial	SLIRP	SLIRP_HUMAN	12.3	99.8%	2	2	4	0.00%	25.7%	GLGWVQFSSEEGLR	99.7%	43.3	25	43.3	2	0	0	1564.78	61	74
SRA stem-loop-interacting RNA-binding protein, mitochondrial	SLIRP	SLIRP_HUMAN	12.3	99.8%	2	2	4	0.00%	25.7%	NALQQENHIIDGVK	99.7%	62.7	25	61.8	2	0	0	1578.82	75	88
SRSF protein kinase 2	SRPK2	SRPK2_HUMAN	77.5	99.8%	2	2	3	0.00%	3.5%	AADLLVNPLDPR	99.7%	43.4	25	43.4	2	0	0	1293.72	508	519
SRSF protein kinase 2	SRPK2	SRPK2_HUMAN	77.5	99.8%	2	2	3	0.00%	3.5%	TVSASSTGDLPK	99.4%	36.3	25	28.2	1	0	0	1162.60	492	503
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	9	16	0.02%	34.8%	AEQINQAAGEASAVLAK	99.7%	118	25	117	2	0	0	1670.87	234	250
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	9	16	0.02%	34.8%	APVPGTPDSLSSGSSR	99.7%	65.6	25	63	2	0	0	1514.74	322	337
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	9	16	0.02%	34.8%	ASYGVEDPEYAVTQLAQTTMR	99.7%	94.4	25	94	2	1	0	2330.10	115	135
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	9	16	0.02%	34.8%	ATVLESEGTR	99.7%	70.6	25	59.9	2	0	0	1062.54	202	211
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	9	16	0.02%	34.8%	DVQGTDASLDEELDRVK	99.7%	94	25	84.1	2	0	0	1889.91	338	354
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	9	16	0.02%	34.8%	ESAINVAEGKK	99.7%	55.4	25	41	2	0	0	1145.62	212	222
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	9	16	0.02%	34.8%	ILEPGLNILIPVLDR	99.7%	71.4	25	71.4	1	0	0	1675.02	58	72
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	9	16	0.02%	34.8%	NTVVLFVPQQEAWVVER	99.7%	68.5	25	68.5	2	0	0	2014.08	35	51
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	19	47	0.05%	33.9%	AQFEGIVTDLIR	99.7%	86.8	25	80.1	5	0	0	1361.74	349	360
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	19	47	0.05%	33.9%	ASNGDAWVEAHGK	99.7%	73.4	25	73.4	2	0	0	1341.62	147	159
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	19	47	0.05%	33.9%	DAGQISGLNVLR	99.7%	82.1	25	66.3	3	0	0	1242.68	207	218
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	19	47	0.05%	33.9%	LLGQFTLIGIPPAPR	99.7%	45.6	25	45.6	4	0	0	1592.95	499	513
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	19	47	0.05%	33.9%	LYSPSQIGAFVLMK	99.7%	63.3	25	63.3	3	0	0	1569.83	160	173
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	19	47	0.05%	33.9%	MKETAENYLGHTAK	99.7%	63.5	25	58.2	1	0	0	1592.77	174	187
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	19	47	0.05%	33.9%	NAVITVPAYFNDSQR	99.7%	65.5	25	64.6	2	0	0	1694.85	188	202
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	19	47	0.05%	33.9%	QAASSLQQASLK	99.7%	84.3	25	75.8	4	0	0	1231.66	635	646
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	19	47	0.05%	33.9%	QAVTNPNNTFYATK	99.7%	71.6	25	70.7	2	0	0	1568.77	108	121
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	19	47	0.05%	33.9%	RYDDPEVQK	99.7%	44.7	25	34.5	2	0	0	1149.55	127	135
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	19	47	0.05%	33.9%	SDIGEVILVGGMTR	99.7%	88.3	25	87.7	4	0	0	1446.76	378	391
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	19	47	0.05%	33.9%	SQVFSTAADGQTQVEIK	99.7%	116	25	109	4	0	0	1808.90	469	485
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	19	47	0.05%	33.9%	STNGDTFLGGEDFDQALLR	99.7%	100	25	92.4	2	0	0	2055.96	266	284
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	19	47	0.05%	33.9%	TTPSVVAFTADGER	99.7%	117	25	111	2	0	0	1450.72	86	99
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	19	47	0.05%	33.9%	VINEPTAAALAYGLDK	99.7%	120	25	115	3	0	0	1645.88	219	234
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	19	47	0.05%	33.9%	VLENAEGAR	99.7%	56.7	25	42.9	2	0	0	958.50	77	85
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	19	47	0.05%	33.9%	VQQTVQDLFGR	99.7%	49.9	25	46.3	2	0	0	1290.68	395	405
Striatin-interacting protein 1	STRIP1	STRP1_HUMAN	95.6	100.0%	2	2	3	0.00%	2.4%	ILLAAAPTSK	99.7%	63.3	25	51.3	2	0	0	984.61	527	536
Striatin-interacting protein 1	STRIP1	STRP1_HUMAN	95.6	100.0%	2	2	3	0.00%	2.4%	LLDGLEVTAR	99.7%	72.6	25	61.9	1	0	0	1086.62	129	138
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	15	17	34	0.03%	13.5%	DLIHGAPVGKPAANR	96.9%	21.9	25	21.9	0	1	0	1515.84	63	77
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	15	17	34	0.03%	13.5%	HLALNLQEK	97.4%	29.7	25	24.6	2	0	0	1065.61	726	734

Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	15	17	34	0.03%	13.5%	LGIQLDFEK	99.6%	37.8	25	32.4	1	0	0	1062.58	817	825
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	15	17	34	0.03%	13.5%	LNEQQSVLQR	99.7%	74	25	53.9	4	0	0	1214.65	1010	1019
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	15	17	34	0.03%	13.5%	LVIDVIR	97.5%	29.9	25	10.6	1	0	0	827.54	593	599
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	15	17	34	0.03%	13.5%	LYHNEVEIEK	99.5%	36.7	25	30.3	1	0	0	1273.64	228	237
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	15	17	34	0.03%	13.5%	NFLVFQGAVESIAMK	99.7%	67.8	25	60	4	0	0	1653.87	132	146
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	15	17	34	0.03%	13.5%	NMDAIIVDSEK	99.6%	37.8	25	32.7	1	0	0	1234.60	541	551
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	15	17	34	0.03%	13.5%	SGELAQEYDKR	99.7%	53.2	25	45.9	3	0	0	1295.62	161	171
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	15	17	34	0.03%	13.5%	SGVISGGASDLK	99.6%	38	25	24.1	2	0	0	1090.57	649	660
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	15	17	34	0.03%	13.5%	SKLESELANFGPR	99.7%	84.2	25	72	2	1	0	1447.75	735	747
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	15	17	34	0.03%	13.5%	SNLMDAISFVLGEK	99.7%	70	25	64.5	3	0	0	1523.78	39	52
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	15	17	34	0.03%	13.5%	TALFEEISR	99.7%	66.3	25	61.3	4	0	0	1065.56	152	160
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	15	17	34	0.03%	13.5%	TVALDGTLFQK	99.7%	67.1	25	46	3	0	0	1192.66	638	648
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	15	17	34	0.03%	13.5%	YSQSDLEQTK	99.7%	52.7	25	40.6	1	0	0	1198.56	714	723
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	ALNHEIEELEK	99.7%	39.1	25	33.6	2	0	0	1324.67	276	286
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	AMNVLTEAEER	99.7%	45.1	25	35.4	3	0	0	1278.60	987	997
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	ASNLQDLVYK	98.0%	30.8	25	23.8	2	0	0	1150.61	59	68
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	ASVSITFDNSDKK	99.7%	59.4	25	49	1	0	0	1411.71	77	89
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	DQEALEAVKR	99.7%	40.2	25	31.2	2	0	0	1158.61	447	456
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	DTSATTALELVAGER	99.7%	99.2	25	86.5	2	0	0	1533.78	534	548
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	EGMFNNANVLFK	99.6%	37.4	25	31.6	2	0	0	1383.67	1147	1158
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	ENLTELSGGQR	99.7%	82.1	25	70.4	2	0	0	1203.60	1080	1090
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	FQELKDVQDELR	99.7%	54.7	25	52.3	2	0	0	1519.78	678	689
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	FVDGVSTVAR	99.7%	91.2	25	78.1	2	0	0	1050.56	1161	1170
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	GLVASLISVK	99.7%	68.8	25	68.8	2	0	0	986.62	524	533
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	IKELDHNISK	99.7%	40.7	25	29.5	2	0	0	1196.66	910	919
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	ILTTIEDLDQKK	99.7%	87.6	25	74.1	2	2	0	1416.79	1015	1026
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	ITDGLHALQEASNK	99.7%	55.1	25	50.2	1	0	0	1496.77	355	368
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	LKETYEALLAR	99.7%	67.3	25	53.5	2	0	0	1306.74	492	502
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	LQEELSENDKK	99.7%	42.6	25	37.9	1	0	0	1332.66	263	273
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	LYNVVVDTEVTGK	99.7%	58.5	25	55.6	1	0	0	1436.76	549	561
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	LYNVVVDTEVTGKK	99.7%	64	25	63.9	1	0	0	1564.86	549	562
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	QKEVITAQDTVIK	97.7%	30.3	25	24.6	1	0	0	1472.83	878	890
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	QQLEAVNEAIK	99.7%	54.1	25	41.6	2	0	0	1242.67	838	848
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	SAEELKEMQDK	99.7%	49.7	25	41.3	2	0	0	1307.61	249	259
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	SIILEGFK	96.0%	28	25	28	1	0	0	906.53	5	12
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	SLEDALAEAQR	99.7%	80.8	25	65	2	0	0	1202.60	298	308
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	SQAASILTK	99.7%	44.4	25	31.8	2	0	0	918.53	669	677
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	SSYLEYQK	98.3%	31.4	25	25	1	0	0	1017.49	215	222
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	TEEADLLQTK	99.7%	48.2	25	38.5	2	0	0	1147.58	723	732
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	TIEESEETLK	99.7%	51.3	25	48.1	2	0	0	1178.58	751	760
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	TILEEEITPTIQK	99.7%	67.6	25	61.9	2	0	0	1514.83	197	209
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	TVTLGGDVFDPHGTLSGGAR	99.7%	44.5	25	44.5	0	2	0	1956.98	649	668
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	YLINGVNANNTR	99.7%	38.5	25	29.4	1	0	0	1348.70	115	126
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	55	0.05%	28.5%	YTIIPLNK	97.5%	29.9	25	26.7	1	0	0	961.57	573	580
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	AELGTDLLSQLSLEDQK	97.7%	30.2	25	30.2	1	0	0	1859.96	779	795
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	AKLDELSAK	99.7%	40.5	25	18.2	2	0	0	974.55	237	245
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	ALDQFVNFSEQK	99.7%	78.6	25	76	2	0	0	1425.70	986	997
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	ALEYTIYNQELNETR	99.7%	72.7	25	57.6	2	0	0	1856.90	222	236
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	DLEDTEANKEK	99.7%	45.7	25	39.2	2	0	0	1291.60	419	429
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	DQTIVDPFSSK	99.7%	52.3	25	12.4	2	0	0	1236.61	16	26
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	DTAYPETNDAIPMISK	99.7%	47.1	25	47.1	4	0	0	1781.83	597	612

Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	EENAEQQALAAK	99.7%	81.8	25	69.3	2	0	0	1301.63	475	486
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	ELGSLPQEAFEK	99.7%	54.4	25	42.5	2	0	0	1347.68	945	956
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	EMQQLSGGQK	96.2%	28.2	25	21	1	0	0	1105.53	1111	1120
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	GALTGGYYDTR	99.7%	74.1	25	64.4	2	0	0	1173.55	662	672
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	INQMATAPDSQR	99.7%	66.9	25	63.6	4	0	0	1347.63	144	155
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	KAEEELGELEAK	99.7%	87.3	25	76.5	2	0	0	1345.68	684	695
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	KEESISLMK	98.7%	32.5	25	17.6	1	0	0	1064.57	172	180
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	LALLHEGTGPR	99.7%	48.1	25	46.7	2	0	0	1163.65	62	72
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	LFYHIVDSDEVSTK	99.7%	62.3	25	50.2	2	1	0	1652.82	558	571
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	MNLPGEVTFLPLNK	99.7%	82.9	25	74.5	4	0	0	1588.84	579	592
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	NDVMNLLESAGFSR	99.7%	102	25	96.9	4	0	0	1552.74	119	132
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	NFSEVFQK	99.0%	33.8	25	15.2	2	0	0	998.49	1039	1046
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	QKELAETEPK	96.1%	28.1	25	20.2	1	0	0	1172.62	341	350
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	QVIIQGFR	99.7%	50.2	25	35.2	2	0	0	960.56	5	12
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	SEDLDNSIDKTEAGIK	99.7%	71.8	25	71.8	2	0	0	1734.84	880	895
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	SIMELMNVLELR	99.7%	41.4	25	31.7	1	0	0	1447.76	1013	1024
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	SLDQAINDK	99.7%	46.2	25	38.9	2	0	0	1003.51	401	409
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	SMEVSTQLAR	99.7%	50.2	25	37.6	4	0	0	1121.56	635	644
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	SYRDQTIVDPFSSK	99.4%	36.3	25	33.1	1	0	0	1642.81	13	26
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	VETYLNENLR	99.7%	54.1	25	27.1	2	0	0	1250.64	828	837
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	34	61	0.06%	26.4%	VSHIDVITAEMAK	99.7%	69.4	25	62.9	2	0	0	1413.74	1195	1207
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	20	20	32	0.03%	17.6%	ELEANVLATAPDK	99.7%	47.3	25	46.9	1	0	0	1370.72	841	853
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	20	20	32	0.03%	17.6%	FTASIQR	98.5%	31.9	25	20.7	2	0	0	822.45	821	827
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	20	20	32	0.03%	17.6%	FTQLDLEDVQVR	99.7%	77.4	25	75.9	2	0	0	1462.75	390	401
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	20	20	32	0.03%	17.6%	HNTAVSQLTK	99.7%	48.2	25	38.4	2	0	0	1098.59	513	522
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	20	20	32	0.03%	17.6%	IAEMETQKEK	96.3%	28.3	25	14.9	1	0	0	1206.60	334	343
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	20	20	32	0.03%	17.6%	IFNLSGGEK	95.3%	27.3	25	14	1	0	0	964.51	1188	1196
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	20	20	32	0.03%	17.6%	IHEDTKEINEK	99.7%	51.7	25	47.6	2	0	0	1355.68	344	354
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	20	20	32	0.03%	17.6%	LHNTIVEINNHK	99.3%	26.6	25	24.5	0	1	0	1431.77	887	898
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	20	20	32	0.03%	17.6%	LLEENVSAFK	99.7%	44.4	25	34	2	0	0	1149.62	858	867
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	20	20	32	0.03%	17.6%	LTQEETNFK	99.7%	55.2	25	48.4	2	0	0	1109.55	565	573
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	20	20	32	0.03%	17.6%	NAQFIIISLR	99.7%	53.7	25	44.2	2	0	0	1174.69	1243	1252
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	20	20	32	0.03%	17.6%	NTNAAEESLPEIQK	99.7%	69.7	25	69.1	2	0	0	1543.76	975	988
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	20	20	32	0.03%	17.6%	QAFYFALR	96.8%	28.9	25	12.9	1	0	0	1015.54	706	713
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	20	20	32	0.03%	17.6%	QLDECASAITK	99.7%	48.3	25	41.9	2	0	0	1235.59	912	922
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	20	20	32	0.03%	17.6%	QNIGVATFIGLDK	99.7%	60.9	25	59.4	2	0	0	1375.76	661	673
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	20	20	32	0.03%	17.6%	SNNIINETTTR	99.7%	56.6	25	43	2	0	0	1262.63	435	445
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	20	20	32	0.03%	17.6%	SNVIDSMLFVFGYR	99.4%	36.2	25	29.1	1	0	0	1663.81	120	133
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	20	20	32	0.03%	17.6%	VAELDKITYER	99.7%	42.7	25	36.7	1	0	0	1336.71	1107	1117
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	20	20	32	0.03%	17.6%	VIQENEHALQK	99.7%	74.2	25	73.5	2	0	0	1308.69	999	1009
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	20	20	32	0.03%	17.6%	VVTLQGQIIEQSGTMTGGGSK	99.7%	106	25	106	1	0	0	2091.08	737	757
Structural maintenance of chromosomes protein 6	SMC6	SMC6_HUMAN	126.3	100.0%	3	3	4	0.00%	3.1%	LYFDNLLSQR	99.7%	39.2	25	28.3	1	0	0	1268.66	943	952
Structural maintenance of chromosomes protein 6	SMC6	SMC6_HUMAN	126.3	100.0%	3	3	4	0.00%	3.1%	SATGSVVSTR	99.0%	33.8	25	24.9	1	0	0	964.51	158	167
Structural maintenance of chromosomes protein 6	SMC6	SMC6_HUMAN	126.3	100.0%	3	3	4	0.00%	3.1%	SAVLTALIVGLGGR	99.7%	40.4	25	37.5	2	0	0	1326.81	83	96
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	SDHB	SDHB_HUMAN	31.6	100.0%	4	4	6	0.01%	15.7%	CGPMVLDALIK	99.0%	33.7	25	21.8	1	0	0	1232.64	68	78
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	SDHB	SDHB_HUMAN	31.6	100.0%	4	4	6	0.01%	15.7%	IKNEVDSTLTFR	99.7%	46.6	25	46.6	2	0	0	1422.76	79	90
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	SDHB	SDHB_HUMAN	31.6	100.0%	4	4	6	0.01%	15.7%	LQDPFSLYR	99.5%	36.9	25	29.5	1	0	0	1138.59	234	242
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	SDHB	SDHB_HUMAN	31.6	100.0%	4	4	6	0.01%	15.7%	YLGPAVLMQAYR	99.7%	75.8	25	71.5	2	0	0	1381.73	206	217
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	6	9	16	0.02%	22.0%	GGQTHLGLPVFNTVK	99.7%	50.1	25	49.9	2	1	0	1567.86	91	105
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	6	9	16	0.02%	22.0%	IICQGFTGK	99.7%	42.8	25	34.6	2	0	0	1023.53	58	66
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	6	9	16	0.02%	22.0%	LIGPNCPGVINPGECK	99.7%	82.7	25	79.4	2	0	0	1724.85	167	182

Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	6	9	16	0.02%	22.0%	LVGGTTPGK	99.2%	34.5	25	28	2	0	0	829.48	82	90
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	6	9	16	0.02%	22.0%	MGHAGAIIAGGK	99.7%	54.7	25	51.6	4	0	0	1082.58	297	308
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	6	9	16	0.02%	22.0%	QGTFHSQQALEYGTK	99.7%	51.5	25	51.5	1	2	0	1694.81	67	81
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	11	23	0.02%	25.3%	CDVIAQGIVMAVK	99.7%	85.6	25	70.3	2	0	0	1403.74	384	396
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	11	23	0.02%	25.3%	DLEIKIPVVVR	99.7%	45.2	25	45.2	2	0	0	1280.79	397	407
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	11	23	0.02%	25.3%	EQALQLAQK	99.7%	51	25	43.9	3	0	0	1028.57	217	225
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	11	23	0.02%	25.3%	ICNQVLVCER	99.7%	67.7	25	60.4	4	0	0	1290.63	151	160
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	11	23	0.02%	25.3%	ILACDDLDEAAR	99.7%	75.3	25	64.6	2	0	0	1361.64	427	438
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	11	23	0.02%	25.3%	INFDSNSAYR	99.7%	68.9	25	66.1	2	0	0	1186.55	275	284
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	11	23	0.02%	25.3%	IVFSPEEAK	98.4%	31.7	25	27.4	1	0	0	1019.54	121	129
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	11	23	0.02%	25.3%	LSEIVTLAK	99.7%	59.3	25	41	2	0	0	973.59	443	451
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	11	23	0.02%	25.3%	LYSLFLK	99.7%	43.9	25	31.3	1	0	0	883.53	243	249
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	11	23	0.02%	25.3%	MGFPPNIVESAAENMVK	99.7%	53.9	25	48.8	2	0	0	1833.89	226	242
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	11	23	0.02%	25.3%	SPDEAYAIAK	99.7%	75.7	25	73.5	2	0	0	1064.53	79	88
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	12	15	32	0.03%	31.5%	DPNVVGQLAK	99.7%	45.9	25	41.2	2	0	0	1040.57	109	118
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	12	15	32	0.03%	31.5%	EAQVYQAFK	99.7%	44.1	25	37.2	3	0	0	1083.55	339	347
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	12	15	32	0.03%	31.5%	ELELKVPLVVR	99.2%	34.6	25	33.8	2	1	0	1294.81	382	392
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	12	15	32	0.03%	31.5%	ETYLAILMDR	99.7%	44.5	25	38.5	2	0	0	1240.62	151	160
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	12	15	32	0.03%	31.5%	FFVADTANEALEAAK	99.7%	131	25	123	4	0	0	1596.79	59	73
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	12	15	32	0.03%	31.5%	ILNNSGLPITSAIDLEDAAK	99.7%	76.3	25	75.8	2	0	0	2055.10	404	423
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	12	15	32	0.03%	31.5%	INFDDNAEFR	99.7%	64.2	25	56.3	4	0	0	1240.56	260	269
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	12	15	32	0.03%	31.5%	LEGTNVQEAQK	99.7%	68.1	25	53.8	1	0	0	1216.62	393	403
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	12	15	32	0.03%	31.5%	LYNLFLK	98.5%	32	25	20.8	1	0	0	910.54	228	234
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	12	15	32	0.03%	31.5%	MAENLGFVGPLK	99.7%	71.3	25	61.2	4	0	0	1275.68	207	218
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	12	15	32	0.03%	31.5%	QMIGYNLATK	99.7%	52.1	25	41.6	4	0	0	1138.59	119	128
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	12	15	32	0.03%	31.5%	VMVAEALDISR	99.7%	88.6	25	78	2	0	0	1203.64	140	150
SUMO-activating enzyme subunit 2	UBA2	SAE2_HUMAN	71.2	100.0%	2	2	4	0.00%	4.2%	QFILVMNALDNR	99.7%	60.8	25	54	2	0	0	1433.76	108	119
SUMO-activating enzyme subunit 2	UBA2	SAE2_HUMAN	71.2	100.0%	2	2	4	0.00%	4.2%	VLVVGAGGIGCELLK	99.7%	80.8	25	80.8	2	0	0	1484.85	20	34
SUN domain-containing protein 2	SUN2	SUN2_HUMAN	80.3	100.0%	5	5	9	0.01%	9.1%	DSSPHFQAEQR	99.7%	44.7	25	43.9	2	0	0	1301.59	265	275
SUN domain-containing protein 2	SUN2	SUN2_HUMAN	80.3	100.0%	5	5	9	0.01%	9.1%	IGLADYALESGGASVISTR	99.7%	122	25	122	2	0	0	1879.98	544	562
SUN domain-containing protein 2	SUN2	SUN2_HUMAN	80.3	100.0%	5	5	9	0.01%	9.1%	ILTHVAEMQGK	97.4%	29.7	25	29	1	0	0	1242.65	492	502
SUN domain-containing protein 2	SUN2	SUN2_HUMAN	80.3	100.0%	5	5	9	0.01%	9.1%	IQEELSALR	99.7%	53	25	34.6	2	0	0	1058.58	355	363
SUN domain-containing protein 2	SUN2	SUN2_HUMAN	80.3	100.0%	5	5	9	0.01%	9.1%	LTTAASLLDVFVLTR	99.7%	54.5	25	54.5	2	0	0	1619.94	191	205
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	34	0.03%	17.0%	AIGNTELENK	99.7%	47.9	25	37.7	2	0	0	1088.56	1013	1022
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	34	0.03%	17.0%	DVDFEGTDEPIFGK	99.7%	63.8	25	61	2	0	0	1568.71	65	78
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	34	0.03%	17.0%	EAIQCVDNNQSVLVSAHTSAGK	99.4%	27.2	25	27.2	0	1	0	2328.12	146	167
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	34	0.03%	17.0%	EIEEYIHKPK	99.6%	38.1	25	19.1	1	0	0	1285.68	639	648
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	34	0.03%	17.0%	EYPFILDAFQR	99.7%	61.7	25	53.2	3	0	0	1398.71	135	145
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	34	0.03%	17.0%	GIVILMVDEK	99.7%	65.6	25	61.7	4	0	0	1132.63	533	542
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	34	0.03%	17.0%	KAQIAIDIK	99.4%	35.7	25	22.7	1	0	0	999.62	825	833
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	34	0.03%	17.0%	LDFNTDEEK	98.4%	31.6	25	31.2	2	0	0	1110.50	409	417
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	34	0.03%	17.0%	LDFNTDEEKK	98.3%	31.5	25	22.6	1	0	0	1238.59	409	418
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	34	0.03%	17.0%	LGFATSSDVIEMK	99.7%	65.9	25	57.7	3	0	0	1413.69	861	873
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	34	0.03%	17.0%	LTEQLAGPLR	99.7%	79.9	25	65	2	0	0	1097.63	924	933
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	34	0.03%	17.0%	MTDVFEGSIIR	99.7%	73.5	25	67.6	3	0	0	1267.64	985	995
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	34	0.03%	17.0%	NFQPVIIFSFSK	99.7%	55	25	54.1	4	0	0	1426.77	385	396
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	34	0.03%	17.0%	RLEELLR	98.8%	32.8	25	10.2	1	0	0	928.56	999	1005
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	34	0.03%	17.0%	SFYQFQHYR	99.7%	50.7	25	42.9	2	0	0	1275.59	588	596
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	34	0.03%	17.0%	TVLQMDELK	97.4%	29.7	25	16.2	1	0	0	1076.57	844	852
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	17	20	34	0.03%	17.0%	YCLPFLQPGR	99.5%	37	25	24.9	1	0	0	1250.64	649	658
Suppressor of SWI4 1 homolog	PPAN	SSF1_HUMAN	53.2	100.0%	3	3	5	0.00%	8.0%	LPGGPTLTFQVK	99.7%	72.9	25	71.4	2	0	0	1257.72	102	113

Suppressor of SWI4 1 homolog	PPAN	SSF1_HUMAN	53.2	100.0%	3	3	5	0.00%	8.0%	TEEELQAILEAK	99.7%	49.2	25	38.5	1	0	0	1373.72	304	315
Suppressor of SWI4 1 homolog	PPAN	SSF1_HUMAN	53.2	100.0%	3	3	5	0.00%	8.0%	VGGSDEEASGIPSR	99.7%	56.9	25	53.8	2	0	0	1360.63	356	369
Surfeit locus protein 4	SURF4	SURF4_HUMAN	30.4	100.0%	4	4	8	0.01%	18.2%	GQNDLMGTAEDFADQFLR	99.7%	63.6	25	63.6	2	0	0	2043.91	2	19
Surfeit locus protein 4	SURF4	SURF4_HUMAN	30.4	100.0%	4	4	8	0.01%	18.2%	LCLISTFLEDGIR	99.7%	81.9	25	73.3	4	0	0	1536.81	31	43
Surfeit locus protein 4	SURF4	SURF4_HUMAN	30.4	100.0%	4	4	8	0.01%	18.2%	QYLPHVAR	98.7%	32.7	25	25.9	1	0	0	983.54	23	30
Surfeit locus protein 4	SURF4	SURF4_HUMAN	30.4	100.0%	4	4	8	0.01%	18.2%	SMFAGVPTMR	98.6%	32.1	25	30.7	1	0	0	1112.52	140	149
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	8	8	13	0.01%	8.5%	ALNIVDQEGSLLGK	99.7%	70.3	25	69.9	2	0	0	1456.80	215	228
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	8	8	13	0.01%	8.5%	APSSLSDAVPQR	99.7%	67.1	25	62.3	2	0	0	1227.63	570	581
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	8	8	13	0.01%	8.5%	ATTGTQTLLSSGTR	99.7%	54.9	25	46.5	1	0	0	1393.73	696	709
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	8	8	13	0.01%	8.5%	FGIEIIK	98.4%	31.6	25	15.8	1	0	0	819.50	328	334
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	8	8	13	0.01%	8.5%	GADQKPTSADCAVR	98.2%	31.2	25	28.7	1	0	0	1475.69	646	659
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	8	8	13	0.01%	8.5%	IPLGLDLK	98.1%	31.1	25	13.2	2	0	0	868.55	298	305
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	8	8	13	0.01%	8.5%	VDNEFLNMLLDK	99.7%	42	25	36	2	0	0	1450.72	398	409
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	8	8	13	0.01%	8.5%	YSLSGSVAHSR	99.7%	64.1	25	59.3	2	0	0	1163.58	63	73
Survival motor neuron protein	SMN1	SMN_HUMAN	31.8	100.0%	3	3	4	0.00%	12.6%	GTGQSDDSDIWDDTALIK	99.7%	67.8	25	67.8	1	0	0	1936.88	24	41
Survival motor neuron protein	SMN1	SMN_HUMAN	31.8	100.0%	3	3	4	0.00%	12.6%	LGPGKPGLK	97.5%	29.8	25	26.8	1	0	0	866.55	205	213
Survival motor neuron protein	SMN1	SMN_HUMAN	31.8	100.0%	3	3	4	0.00%	12.6%	NTAASLQQWK	99.6%	37.8	25	32.7	2	0	0	1146.59	84	93
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	20	33	0.03%	15.9%	ANYAVDAYFR	99.7%	49.7	25	40.6	1	0	0	1189.56	740	749
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	20	33	0.03%	15.9%	CNELQDIEK	99.7%	44.6	25	29.1	2	0	0	1148.53	891	899
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	20	33	0.03%	15.9%	DFNQFIK	97.8%	30.4	25	10.4	1	0	0	911.46	849	855
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	20	33	0.03%	15.9%	DIDILNSAGK	99.7%	65	25	37.1	2	0	0	1045.55	431	440
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	20	33	0.03%	15.9%	EIQEPDPTYEEK	99.7%	48	25	40.1	1	0	0	1477.67	72	83
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	20	33	0.03%	15.9%	FITDNTVEER	99.7%	56.8	25	46.6	2	0	0	1223.59	607	616
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	20	33	0.03%	15.9%	LDGQTPHDER	94.8%	27	25	27	1	0	0	1167.54	529	538
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	20	33	0.03%	15.9%	LDSIVIQQGR	99.7%	66.7	25	52.1	2	0	0	1128.64	627	636
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	20	33	0.03%	15.9%	LLNILMQLR	99.7%	48	25	36.7	5	0	0	1113.68	446	454
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	20	33	0.03%	15.9%	LRLDSIVIQQGR	99.7%	45.4	25	45.4	1	1	0	1397.82	625	636
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	20	33	0.03%	15.9%	NPELPNAAQAQK	99.7%	50.5	25	43.8	2	0	0	1280.66	803	814
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	20	33	0.03%	15.9%	QNLLSVGDYR	99.7%	59.8	25	36	2	0	0	1164.60	133	142
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	20	33	0.03%	15.9%	QTELFAHFIQPAAQK	99.7%	40.1	25	37.1	1	0	0	1728.91	98	112
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	20	33	0.03%	15.9%	SVCLIGDKEQR	99.7%	60.4	25	32.9	2	0	0	1304.66	257	267
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	20	33	0.03%	15.9%	VLDILEDYCMWR	99.5%	36.3	25	36.3	1	0	0	1612.75	511	522
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	20	33	0.03%	15.9%	VLIFSQMTR	99.7%	66.5	25	60.2	4	0	0	1094.60	502	510
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	20	33	0.03%	15.9%	YLVIDEAHR	99.7%	40.2	25	37.8	2	0	0	1115.58	304	312
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	SMARCD2	SMRD2_HUMAN	58.9	100.0%	2	2	2	0.00%	4.9%	IHETIESINQLK	97.2%	29.4	25	24.8	1	0	0	1424.77	440	451
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	SMARCD2	SMRD2_HUMAN	58.9	100.0%	2	2	2	0.00%	4.9%	IITDVIGNPEEERR	99.7%	29	25	27.4	0	1	0	1640.86	481	494
Symplekin	SYMPK	SYMPK_HUMAN	141.2	100.0%	8	8	13	0.01%	8.1%	ATNLCFAER	99.7%	46.7	25	34.9	2	0	0	1081.51	965	973
Symplekin	SYMPK	SYMPK_HUMAN	141.2	100.0%	8	8	13	0.01%	8.1%	AVACSGAAQVR	99.7%	38.8	25	23.5	1	0	0	1089.55	575	585
Symplekin	SYMPK	SYMPK_HUMAN	141.2	100.0%	8	8	13	0.01%	8.1%	ETAAGGLTLKEER	95.4%	27.4	25	23.1	1	0	0	1374.72	1230	1242
Symplekin	SYMPK	SYMPK_HUMAN	141.2	100.0%	8	8	13	0.01%	8.1%	LGGFVMNILSR	95.2%	27.3	25	21.8	1	0	0	1206.67	1012	1022
Symplekin	SYMPK	SYMPK_HUMAN	141.2	100.0%	8	8	13	0.01%	8.1%	TPSPAAEDAREPEAK	99.3%	35.1	25	35.1	1	0	0	1568.76	1257	1271
Symplekin	SYMPK	SYMPK_HUMAN	141.2	100.0%	8	8	13	0.01%	8.1%	TVIQSLTMYPR	99.5%	37	25	33.6	1	0	0	1324.69	1001	1011
Symplekin	SYMPK	SYMPK_HUMAN	141.2	100.0%	8	8	13	0.01%	8.1%	VVDLLNQAALITNDSK	99.7%	93.9	25	93.9	2	0	0	1713.94	36	51
Symplekin	SYMPK	SYMPK_HUMAN	141.2	100.0%	8	8	13	0.01%	8.1%	VVLEAPLITESALEVVR	99.7%	92.8	25	92.8	4	0	0	1838.06	667	683
Syntaxin-18	STX18	STX18_HUMAN	38.7	100.0%	2	2	3	0.00%	6.9%	LIGEMNSLFDEVR	99.7%	44.4	25	44.4	2	0	0	1522.76	242	254
Syntaxin-18	STX18	STX18_HUMAN	38.7	100.0%	2	2	3	0.00%	6.9%	TCSEAIQQLR	99.7%	55.1	25	40.5	1	0	0	1205.59	106	115
Syntaxin-binding protein 1	STXBP1	STXB1_HUMAN	67.6	99.8%	2	2	2	0.00%	3.0%	ISEQTYQLSR	99.7%	60.7	25	49.2	1	0	0	1224.62	468	477
Syntaxin-binding protein 1	STXBP1	STXB1_HUMAN	67.6	99.8%	2	2	2	0.00%	3.0%	SQLLILDR	99.3%	35.2	25	16.2	1	0	0	957.57	228	235
Syntaxin-binding protein 2	STXBP2	STXB2_HUMAN	66.5	100.0%	3	3	5	0.00%	6.4%	ADTPSLGEGPEK	99.2%	34.9	25	29.5	2	0	0	1200.57	214	225
Syntaxin-binding protein 2	STXBP2	STXB2_HUMAN	66.5	100.0%	3	3	5	0.00%	6.4%	LIVPVLLDAAVPAYDK	99.7%	48.4	25	48.4	2	0	0	1696.99	388	403
Syntaxin-binding protein 2	STXBP2	STXB2_HUMAN	66.5	100.0%	3	3	5	0.00%	6.4%	YETTGLSEAR	99.7%	41.4	25	37.3	1	0	0	1126.54	266	275

TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	5	6	11	0.01%	15.2%	FGGNPGGFGNQGGFGNSR	99.7%	113	25	104	2	0	0	1726.77	276	293
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	5	6	11	0.01%	15.2%	FTEYETQVK	99.7%	48.6	25	29	3	0	0	1144.55	152	160
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	5	6	11	0.01%	15.2%	GISVHISNAEPK	99.7%	60.5	25	56.8	2	0	0	1251.67	252	263
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	5	6	11	0.01%	15.2%	KMDETDASSAVK	99.7%	40.7	25	36.8	2	0	0	1281.60	84	95
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	5	6	11	0.01%	15.2%	TSDLIVLGLPWK	99.7%	70.1	25	62	2	0	0	1341.78	103	114
Target of EGR1 protein 1	TOE1	TOE1_HUMAN	56.5	100.0%	3	3	5	0.00%	6.7%	ALLNLPGTQTSGEAK	99.7%	48.3	25	46.5	2	0	0	1499.81	348	362
Target of EGR1 protein 1	TOE1	TOE1_HUMAN	56.5	100.0%	3	3	5	0.00%	6.7%	SILSLGLACFK	99.7%	59.8	25	48.8	2	0	0	1208.67	96	106
Target of EGR1 protein 1	TOE1	TOE1_HUMAN	56.5	100.0%	3	3	5	0.00%	6.7%	YAAEFHAR	99.5%	36.7	25	31.4	1	0	0	964.46	231	238
TATA box-binding protein-like protein 1	TBPL1	TBPL1_HUMAN	20.9	99.8%	2	2	2	0.00%	12.4%	IICTGATSEEEAK	99.7%	43.8	25	43.8	1	0	0	1408.66	66	78
TATA box-binding protein-like protein 1	TBPL1	TBPL1_HUMAN	20.9	99.8%	2	2	2	0.00%	12.4%	ITATIWSSGK	99.7%	39.6	25	26.4	1	0	0	1063.58	56	65
TATA-box-binding protein	TBP	TBP_HUMAN	37.7	99.8%	2	2	3	0.00%	7.4%	AEIYEAFENIYPILK	98.5%	31.8	25	31.8	1	0	0	1812.94	319	333
TATA-box-binding protein	TBP	TBP_HUMAN	37.7	99.8%	2	2	3	0.00%	7.4%	TTALIFSSGK	99.7%	43.5	25	43.5	2	0	0	1024.57	209	218
TBC1 domain family member 15	TBC1D15	TBC15_HUMAN	79.5	99.8%	2	2	3	0.00%	3.0%	TQLIQLSTLLR	99.7%	73.1	25	71	2	0	0	1285.78	497	507
TBC1 domain family member 15	TBC1D15	TBC15_HUMAN	79.5	99.8%	2	2	3	0.00%	3.0%	VTNYIFDSLR	99.7%	59	25	38.5	1	0	0	1227.64	253	262
TBC1 domain family member 4	TBC1D4	TBCD4_HUMAN	146.6	100.0%	3	3	5	0.00%	3.1%	EVILVLSAPFLR	99.7%	39.7	25	39.7	1	0	0	1356.83	81	92
TBC1 domain family member 4	TBC1D4	TBCD4_HUMAN	146.6	100.0%	3	3	5	0.00%	3.1%	LLPADALVNCDLLLR	99.7%	58.3	25	57.3	2	0	0	1695.95	1268	1282
TBC1 domain family member 4	TBC1D4	TBCD4_HUMAN	146.6	100.0%	3	3	5	0.00%	3.1%	QAFSTAAALQSAK	99.7%	45.5	25	34.2	2	0	0	1293.68	435	447
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	AFHNEAQVNPER	99.7%	71.8	25	71.8	4	2	0	1411.67	469	480
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	AFHNEAQVNPERK	99.7%	42.4	25	36.3	4	4	0	1539.77	469	481
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	DCLINAAK	99.7%	47.2	25	28.4	3	0	0	904.46	146	153
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	DDKHGSYEDAVHSGALND	99.7%	78.1	25	78.1	2	3	0	1929.82	539	556
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	DNKQAGVFEPTIVK	99.7%	45.4	25	37.7	2	0	0	1545.83	497	510
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	EQLAIAEFAR	99.7%	68.4	25	61.2	11	0	0	1147.61	434	443
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	EVGDGTTSVVIIAAELLK	99.7%	86.7	25	86.7	2	0	0	1815.01	85	102
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	FATEAAITILR	99.7%	87.9	25	65.1	16	0	0	1205.69	516	526
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	GANDFMCDEMER	99.7%	72.4	25	50	10	0	0	1490.53	379	390
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	HGSYEDAVHSGALND	99.7%	86.8	25	81.4	2	0	0	1571.67	542	556
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	IACLDFSLQK	99.7%	74.3	25	66.5	5	0	0	1194.62	234	243
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	ICDDELILIK	99.7%	64.2	25	52.1	5	0	0	1231.66	356	365
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	IHPTSVISGYR	99.7%	40.1	25	37	1	0	0	1229.66	112	122
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	IIGINGDFFANMVVDAVLAIK	99.7%	48.8	25	48.8	1	0	0	2236.20	160	180
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	ILATGANVILTTGGIDDMCLK	99.7%	122	25	122	4	4	0	2192.13	278	298
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	LGVQVVITDPEK	99.7%	73.8	25	71.4	2	0	0	1297.74	248	259
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	LGVQVVITDPEKLDQIR	99.7%	58.5	25	55.8	2	4	0	1923.09	248	264
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	LLEVEHPAAK	99.7%	59.9	25	50	6	0	0	1106.62	64	73
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	MLVDDIGDVTITNDGATILK	99.7%	150	25	141	4	3	0	2120.08	44	63
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	QAGVFEPTIVK	99.7%	49.2	25	40.1	4	0	0	1188.66	500	510
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	SLHDALCVVK	99.7%	41.8	25	28.6	3	0	0	1141.60	391	400
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	SLHDALCVVKR	99.7%	48.1	25	46.4	2	0	0	1297.70	391	401
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	SLLVIPNTLAVNAAQDSTDLVAK	99.7%	107	25	107	9	2	0	2353.30	444	466
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	SQNVMAAASIANIVK	99.7%	134	25	128	4	0	0	1532.81	19	33
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	SSLGPVGLDK	99.7%	62.2	25	27.4	4	0	0	972.54	34	43
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	SVVPGGGAVEAALSIYLENYATSMGSR	99.7%	59.2	25	59.2	1	1	0	2699.33	407	433
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	TSASIILR	99.7%	66.8	25	54.2	2	0	0	860.52	371	378
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	VLCELADLQDK	99.7%	78.2	25	71.5	2	0	0	1303.66	74	84
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	VLCELADLQDKEVGDGTTSVVIIAAELLK	99.7%	76.8	25	76.8	0	3	0	3099.65	74	102
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	WIGLDLSNGKPR	98.9%	25	25	18	0	2	0	1355.74	485	496
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	YFVEAGAMAVR	99.7%	64.6	25	52.3	4	0	0	1213.60	299	309
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	32	47	151	0.15%	65.1%	YPVNSVNILK	99.7%	60.6	25	43.7	2	0	0	1146.65	190	199
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	25	41	0.04%	51.2%	AAHSEGNTTAGLDMR	99.7%	79.2	25	79.2	2	3	0	1530.70	467	481
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	25	41	0.04%	51.2%	AGADEERAETAR	97.9%	30.5	25	26.1	2	0	0	1275.59	14	25

T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	25	41	0.04%	51.2%	DASLMVTNDGATILK	99.7%	58	25	53.2	1	0	0	1548.79	58	72
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	25	41	0.04%	51.2%	EALLSSAVDHGSDEVK	99.7%	95.5	25	86.9	2	2	0	1656.81	139	154
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	25	41	0.04%	51.2%	EAVAMESYAK	96.6%	28.6	25	28.6	1	0	0	1098.51	432	441
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	25	41	0.04%	51.2%	EGTIGDMAILGITESFQVK	99.7%	84.9	25	84.9	1	0	0	2009.03	482	500
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	25	41	0.04%	51.2%	GATQQILDEAER	99.7%	97.5	25	92.2	2	0	0	1330.66	377	388
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	25	41	0.04%	51.2%	HGINCFINR	99.7%	51.1	25	41.8	2	0	0	1130.55	285	293
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	25	41	0.04%	51.2%	ILIANTGMDTDKIK	99.7%	73.8	25	60.1	4	0	0	1532.84	237	250
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	25	41	0.04%	51.2%	KIHPQTIIAGWR	99.7%	50.5	25	50.5	0	2	0	1419.82	120	131
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	25	41	0.04%	51.2%	LALVTGGEIASTFDHPELVK	98.8%	24.9	25	24.9	0	2	0	2097.12	323	342
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	25	41	0.04%	51.2%	LKGSGNLEAIHIIK	99.7%	41.5	25	32.7	0	2	0	1492.88	190	203
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	25	41	0.04%	51.2%	LTSFIGAIAIGDLVK	99.7%	134	25	125	1	0	0	1517.89	26	40
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	25	41	0.04%	51.2%	MLPTIIADNAGYDSADLVAQLR	99.7%	137	25	137	2	2	0	2347.20	445	466
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	25	41	0.04%	51.2%	QLIYNYPEQLFGAAGVMAIEHADFAGVER	99.7%	51.8	25	51.8	0	2	0	3209.57	294	322
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	25	41	0.04%	51.2%	VAEIEHAEKEK	99.7%	50.1	25	42.5	2	0	0	1282.66	264	274
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	25	41	0.04%	51.2%	VLVDMSR	99.7%	44.8	25	28.3	2	0	0	819.44	83	89
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	18	25	41	0.04%	51.2%	VQDDEVGDGTTSVTVLAAELLR	99.7%	127	25	125	2	0	0	2288.16	90	111
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	32	103	0.10%	61.8%	AFADAMEVIPSTLAENAGLNPISTVTELR	99.7%	47.3	25	45.6	0	1	0	3030.55	453	481
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	32	103	0.10%	61.8%	ALIAGGGAPEIELALR	99.7%	92.7	25	92.7	11	0	0	1550.89	420	435
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	32	103	0.10%	61.8%	AQDIEAGDGTTSVVIIAGSLLDSCTK	99.7%	105	25	105	2	2	0	2621.30	97	122
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	32	103	0.10%	61.8%	AYILNLVK	99.7%	40.9	25	35.1	2	0	0	933.58	281	288
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	32	103	0.10%	61.8%	DALSDLALHFLNK	99.7%	102	25	89.5	9	2	0	1456.78	307	319
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	32	103	0.10%	61.8%	DIEREDIEFICK	99.7%	55.8	25	55.8	2	0	0	1566.75	327	338
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	32	103	0.10%	61.8%	FSNISAAK	99.7%	44.8	25	32.5	2	0	0	837.45	35	42
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	32	103	0.10%	61.8%	GAYQDRDKPAQIR	99.7%	43.4	25	43.4	1	2	0	1517.78	22	34
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	32	103	0.10%	61.8%	GDVTITNDGATILK	99.7%	48.3	25	36.2	1	0	0	1417.75	66	79
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	32	103	0.10%	61.8%	GIEILTDMSRPVELSDRETLLNSATTSLNSK	99.7%	69.6	25	69.6	0	3	0	3390.74	144	174
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	32	103	0.10%	61.8%	GIHPTIISESFQK	99.7%	46.1	25	40	0	2	0	1456.78	127	139
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	32	103	0.10%	61.8%	IDDVVNTR	99.7%	54.8	25	47	2	0	0	931.48	532	539
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	32	103	0.10%	61.8%	IGLIQFCLSAPK	99.7%	67.7	25	63.2	10	0	0	1346.75	246	257
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	32	103	0.10%	61.8%	LGGTIDDCELVEGLVLTQK	99.7%	94.7	25	94.7	2	0	0	2060.06	214	232
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	32	103	0.10%	61.8%	LVIEEAER	99.7%	55.6	25	48.7	5	0	0	958.52	396	403
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	32	103	0.10%	61.8%	MIQDGKGDVTITNDGATILK	99.7%	58.7	25	51.1	2	4	0	2090.08	60	79
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	32	103	0.10%	61.8%	MLVELSK	99.7%	39.8	25	2.57	4	0	0	819.46	90	96
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	32	103	0.10%	61.8%	QMQVLHPAAR	99.7%	54.5	25	42.5	4	0	0	1150.62	80	89
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	32	103	0.10%	61.8%	SIHDALCVIR	99.7%	68.8	25	0	4	0	0	1183.63	404	413
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	32	103	0.10%	61.8%	TDMDNQIVVSDYAQMDR	99.7%	71.8	25	71.8	1	0	0	2016.86	258	274
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	32	103	0.10%	61.8%	TGCNVLLIQK	99.7%	52.5	25	33.6	6	0	0	1145.63	293	302
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	32	103	0.10%	61.8%	TLSGMESYCVR	99.7%	67	25	67	8	0	0	1302.58	442	452
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	32	103	0.10%	61.8%	VIDPATATSVDLR	99.7%	83.7	25	71.9	8	0	0	1357.73	194	206
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	32	103	0.10%	61.8%	VVSQYSSLLSPMSVNAVMK	99.7%	96.4	25	96.4	5	0	0	2072.04	175	193
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	AVTIFIR	99.7%	44.9	25	17.1	5	0	0	819.51	382	388
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	CPTLEQYAMR	99.7%	59.6	25	59.6	3	0	0	1268.58	440	449
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	DKMLVIEQCK	99.7%	44.6	25	32.2	2	0	0	1279.64	369	378
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	DTEPLIQTAK	99.5%	37.1	25	37.1	1	0	0	1115.59	161	170
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	DVDFELIK	98.2%	31.3	25	15.4	1	0	0	978.51	203	210
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	DVDFELIKVEGK	99.7%	72.5	25	63.7	2	0	0	1391.74	203	214
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	EKFEEMIQQIK	99.7%	48.8	25	43.8	2	0	0	1438.72	283	293
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	EMNPALGIDCLHK	99.7%	84	25	79.9	4	2	0	1497.72	484	496
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	ETGANLAICQWGFDDEANHLLLQNNLPAVR	99.7%	42.2	25	42.2	0	1	0	3379.65	294	323
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	FEEMIQQIK	99.7%	52.5	25	38.3	4	0	0	1165.59	285	293
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	FSELTAEK	99.7%	55.5	25	44.9	2	0	0	924.47	345	352

T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	GVIVDKDFSHPQMPK	99.7%	82	25	82	4	4	0	1697.87	227	241
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	HKLDVTSVEDYK	98.6%	24.4	25	22.5	0	1	0	1433.73	264	275
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	IADGYEQAAR	99.7%	87.8	25	80.5	11	0	0	1093.53	133	142
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	IAILTCPFEPPKPK	99.7%	48	25	48	2	0	0	1610.90	248	261
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	IDDIRKPGESEE	99.6%	37.9	25	36.3	1	0	0	1387.67	530	541
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	ISDSVLVDIKDTEPLIQTAK	99.7%	56.1	25	45	0	2	0	2185.20	151	170
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	KQQISLATQMVR	99.7%	69.1	25	67.5	4	4	0	1418.78	514	525
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	LDVTSVEDYK	99.7%	62.2	25	58.9	2	0	0	1168.57	266	275
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	LGFAGLVQEISFGTTK	99.7%	131	25	129	10	0	0	1667.90	353	368
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	LMGLEALK	99.7%	45.5	25	26	4	0	0	874.51	28	35
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	LMVELSK	99.7%	38.5	25	11.1	2	0	0	819.46	90	96
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	MIIEEAKR	99.7%	47.5	25	27.2	3	0	0	989.54	393	400
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	MLVIEQCK	99.7%	45	25	28	2	0	0	1036.52	371	378
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	QQHVIETLIGK	98.2%	31.2	25	26.8	1	0	0	1265.72	503	513
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	QQISLATQMVR	99.7%	59.8	25	52.6	4	0	0	1290.68	515	525
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	RDVDFELIK	99.7%	44.2	25	7.8	2	0	0	1134.62	202	210
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	SLHDALCVIR	99.7%	68.8	25	0	4	0	0	1183.63	401	410
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	TSLGPNGLDK	99.7%	59.4	25	54.4	2	0	0	1001.53	50	59
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	30	43	102	0.10%	52.5%	WVGGPEIELIAIATGGR	99.7%	86.4	25	85.3	4	0	0	1738.95	324	340
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	22	26	73	0.07%	47.3%	ALEIIPR	99.7%	40.9	25	38.5	4	0	0	811.50	441	447
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	22	26	73	0.07%	47.3%	ATISNDGATILK	99.7%	45.9	25	32.4	2	0	0	1203.66	56	67
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	22	26	73	0.07%	47.3%	CQVFEETQIGGER	99.7%	90.7	25	81.8	3	0	0	1552.71	345	357
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	22	26	73	0.07%	47.3%	GGAEQFMEETER	99.7%	76.7	25	74.4	6	0	0	1383.58	376	387
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	22	26	73	0.07%	47.3%	IALLNVELELK	99.7%	71.4	25	60.9	2	0	0	1254.77	237	247
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	22	26	73	0.07%	47.3%	IKEIAVTVK	99.7%	43.5	25	36.5	1	0	0	1000.64	136	144
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	22	26	73	0.07%	47.3%	INALTAASEAACLIVSVDETIK	99.7%	101	25	101	2	4	0	2289.20	500	521
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	22	26	73	0.07%	47.3%	INALTAASEAACLIVSVDETIKNPR	99.7%	73.3	25	73.3	0	3	0	2656.40	500	524
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	22	26	73	0.07%	47.3%	LLDVVHPAAK	99.7%	45.2	25	37.8	4	0	0	1062.63	68	77
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	22	26	73	0.07%	47.3%	LPIGDVATQYFADR	99.7%	74.9	25	74.9	3	0	0	1565.80	293	306
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	22	26	73	0.07%	47.3%	LPIGDVATQYFADRDMFCAGR	99.7%	30.6	25	30.6	0	1	0	2403.12	293	313
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	22	26	73	0.07%	47.3%	MVVDAVMMLDDLLQLK	99.7%	128	25	77.8	5	0	0	1849.95	178	193
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	22	26	73	0.07%	47.3%	QLCDNAGFDATNILNK	99.7%	111	25	94.8	2	0	0	1793.85	448	463
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	22	26	73	0.07%	47.3%	QQLLIGAYAK	99.7%	71.4	25	59.3	3	0	0	1104.64	431	440
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	22	26	73	0.07%	47.3%	SLHDAIMIVR	99.2%	34.6	25	23.2	3	0	0	1170.63	388	397
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	22	26	73	0.07%	47.3%	SQDAEVGDGTTSVTLLAAEFLK	99.7%	133	25	133	4	0	0	2252.13	85	106
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	22	26	73	0.07%	47.3%	TATQLAVNK	99.7%	63.7	25	53.7	4	0	0	945.54	127	135
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	22	26	73	0.07%	47.3%	TCTFILR	99.7%	45.1	25	19.4	3	0	0	910.48	369	375
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	22	26	73	0.07%	47.3%	TFSYAGFEMQPK	99.7%	70.4	25	70.4	4	0	0	1405.65	219	230
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	22	26	73	0.07%	47.3%	VPEEDLKR	99.7%	56.4	25	46.8	4	0	0	985.53	314	321
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	22	26	73	0.07%	47.3%	VQGGALEDSQLVAGVAFK	99.7%	97	25	97	2	0	0	1788.95	200	217
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	22	26	73	0.07%	47.3%	YNFFTGCPK	99.7%	62.1	25	50.4	4	0	0	1133.51	358	366
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	ACTILLR	99.7%	53.1	25	32.4	2	0	0	846.49	371	377
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	ALDDMISTLK	99.7%	71.9	25	65.4	6	0	0	1106.58	129	138
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	ALDDMISTLKK	99.7%	57.2	25	51.2	5	2	0	1234.67	129	139
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	AMTGVEQWPYR	99.7%	64.6	25	63.4	6	0	0	1353.63	428	438
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	ANITAIRR	95.9%	27.9	25	22.2	2	0	0	914.55	307	314
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	AVAQALEVIPR	99.7%	84.6	25	64.2	14	0	0	1166.69	439	449
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	EILSEVER	99.7%	47.9	25	14.8	6	0	0	974.52	382	389
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	EIQVQHPAAK	99.7%	54.5	25	42.8	10	0	0	1120.61	69	78
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	ELGIWEPLAVK	99.7%	66.8	25	59.8	3	0	0	1254.71	492	502
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	GISDLAQHYLMR	99.7%	80.6	25	80.6	10	3	0	1403.71	295	306

T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	IDDIVSGHK	99.7%	51.4	25	36.8	6	0	0	983.52	519	527
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	IDDIVSGHKK	98.2%	31.1	25	18.8	2	0	0	1111.61	519	528
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	IGDEYFTFITDCK	99.7%	53.6	25	53.6	1	0	0	1608.73	355	367
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	IGDEYFTFITDCKDPK	99.7%	39.1	25	38.3	2	0	0	1948.90	355	370
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	IPGGIIEDSCVLR	99.7%	90.7	25	79.2	6	0	0	1428.75	204	216
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	IVLLDSSLEYK	99.7%	79	25	69.6	6	0	0	1279.71	238	248
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	IVLLDSSLEYKK	99.7%	64.2	25	61.4	4	1	0	1407.81	238	249
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	KGESQTDIEITR	99.7%	89.1	25	52.5	2	2	0	1376.70	249	260
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	MLLDPMGGIVMTNDGNAILR	99.7%	104	25	104	15	4	0	2131.07	49	68
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	MVQFEENGR	99.5%	36.6	25	34.2	1	0	0	1109.50	182	190
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	MVQFEENGRK	99.7%	47.2	25	35.8	2	0	0	1237.60	182	191
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	NLQDAMQVCR	99.7%	66.2	25	53.7	10	0	0	1234.57	390	399
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	NVLLDPQLVPGGGASEMAVAHALTEK	99.7%	30.7	25	27.5	0	3	0	2633.36	400	425
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	SMIEISR	99.7%	40.2	25	17.3	2	0	0	835.43	79	85
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	TAVETAVLLLR	99.7%	107	25	92.6	6	0	0	1185.72	508	518
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	TLIQNCGASTIR	99.7%	73.2	25	58.5	4	0	0	1333.69	450	461
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	VEKIPGGIIEDSCVLR	99.7%	41	25	38	0	2	0	1784.96	201	216
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	28	43	155	0.15%	48.4%	WSSLACNIALDAVK	99.7%	102	25	92.7	5	0	0	1547.79	168	181
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	13	0.01%	19.0%	AIADTGANVVVTGGK	99.7%	76.8	25	70.1	1	0	0	1372.74	282	296
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	13	0.01%	19.0%	APGFAQMLK	95.9%	27.9	25	21.2	1	0	0	962.51	8	16
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	13	0.01%	19.0%	AVDDGVNTFK	99.7%	68.1	25	60.8	2	0	0	1065.52	391	400
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	13	0.01%	19.0%	DIDEVSSLLR	99.7%	52.7	25	41.9	2	0	0	1146.60	156	165
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	13	0.01%	19.0%	DMLEAGILDTYLGK	99.7%	57.3	25	57.2	1	0	0	1538.78	491	504
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	13	0.01%	19.0%	FAEAFEAIPR	99.7%	68.1	25	61.5	2	0	0	1150.59	441	450
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	13	0.01%	19.0%	LFVTNDAATILR	99.7%	96.2	25	87.3	2	0	0	1333.75	63	74
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	13	0.01%	19.0%	LVPGGGATEIELAK	97.9%	30.6	25	20.9	1	0	0	1354.76	408	421
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	13	0.01%	19.0%	LYAVHQEGNK	96.1%	28	25	24.9	1	0	0	1158.59	467	476
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	98	0.10%	46.1%	ALQFLEEVK	99.7%	55.7	25	49.7	2	0	0	1076.60	130	138
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	98	0.10%	46.1%	AQAALAVNISAAR	99.7%	93.4	25	89.4	8	0	0	1255.71	16	28
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	98	0.10%	46.1%	AQLGVQAFADALLIIPK	99.7%	92.2	25	91.8	4	0	0	1768.04	433	449
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	98	0.10%	46.1%	DGNVLLHEMQIQHPTASLIAK	99.7%	36.6	25	32.6	0	4	0	2331.21	59	79
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	98	0.10%	46.1%	EGIVALRR	99.5%	36.9	25	22.8	2	0	0	913.56	308	315
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	98	0.10%	46.1%	EMDRETLIDVAR	99.7%	38.2	25	34.3	3	4	0	1463.72	142	153
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	98	0.10%	46.1%	ETLIDVAR	95.0%	27.1	25	22.1	1	0	0	916.51	146	153
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	98	0.10%	46.1%	GFVVINQK	96.4%	28.4	25	6.14	1	0	0	904.53	288	295
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	98	0.10%	46.1%	GIDPFSLDALSK	99.7%	80.9	25	33.2	10	0	0	1262.66	296	307
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	98	0.10%	46.1%	GLQDVLR	99.5%	36.5	25	13.1	2	0	0	800.46	29	35
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	98	0.10%	46.1%	GLVLDHGAR	99.7%	59.5	25	46.2	11	0	0	937.52	209	217
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	98	0.10%	46.1%	HKSETDTSLIR	99.7%	32.1	25	28.8	1	1	0	1286.67	198	208
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	98	0.10%	46.1%	IITEGFEAAK	99.7%	56.3	25	29.6	5	0	0	1078.58	118	127
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	98	0.10%	46.1%	IITEGFEAAKEK	99.7%	67.3	25	56.8	2	0	0	1335.72	118	129
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	98	0.10%	46.1%	MLVSGAGDIK	99.7%	59.6	25	33.8	6	0	0	990.53	46	55
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	98	0.10%	46.1%	NAIDDGCVVPGAGAVEVAMAEALIK	99.7%	35.6	25	31.3	0	1	0	2470.23	400	424
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	98	0.10%	46.1%	QADLYISEGLHPR	99.7%	105	25	102	5	2	0	1498.77	105	117
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	98	0.10%	46.1%	SETDTSLIR	99.7%	62.7	25	48.4	6	0	0	1021.52	200	208
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	98	0.10%	46.1%	TEVNSGFFYK	99.7%	53	25	48.9	2	0	0	1191.57	242	251
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	98	0.10%	46.1%	VATAQDDITGDGTTSNVLIIGELLK	99.7%	101	25	101	3	3	0	2544.34	80	104
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	98	0.10%	46.1%	VCGDSDKGFVVINQK	99.7%	78.3	25	71.5	2	2	0	1665.83	281	295
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	98	0.10%	46.1%	VLAQNSGFDLQETLVK	99.7%	103	25	102	5	0	0	1761.94	450	465
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	11	11	20	0.02%	6.6%	CVWSPLASPSTSILK	97.6%	30	25	30	1	0	0	1645.86	2169	2183
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	11	11	20	0.02%	6.6%	GASSPYGAPGTPR	99.7%	65.5	25	65.5	1	0	0	1217.59	399	411

Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	11	11	20	0.02%	6.6%	IGISDISSLSEK	99.7%	56.8	25	52.5	2	0	0	1248.67	1700	1711
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	11	11	20	0.02%	6.6%	ITSELSEANALELLSK	99.7%	99.3	25	87.7	4	0	0	1717.92	88	103
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	11	11	20	0.02%	6.6%	LIAEQTLQENLIEK	99.7%	96.6	25	90.6	2	0	0	1641.91	1468	1481
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	11	11	20	0.02%	6.6%	LVSDIIDPVALEIPLSK	99.7%	64.7	25	63.2	2	0	0	1822.06	2399	2415
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	11	11	20	0.02%	6.6%	SLIDNFALNPDILCSAK	99.7%	65.5	25	65.5	2	0	0	1890.96	299	315
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	11	11	20	0.02%	6.6%	SQEDEISSPVNK	99.7%	61.8	25	46	1	0	0	1332.63	2189	2200
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	11	11	20	0.02%	6.6%	TIGDLSTLTASEIK	99.7%	80.1	25	76.1	2	0	0	1448.78	2329	2342
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	11	11	20	0.02%	6.6%	TLGETSANAETEQNKK	99.7%	91.7	25	86.5	2	0	0	1720.83	1489	1504
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	11	11	20	0.02%	6.6%	YAEYSFTSLPVPESNLR	99.7%	43.5	25	43.5	1	0	0	1972.97	1659	1675
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	6	6	9	0.01%	7.2%	LAAVQLLQFLAPK	99.7%	50.7	25	47.5	2	0	0	1411.87	116	128
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	6	6	9	0.01%	7.2%	LLLQHAPLR	99.7%	48.7	25	40.2	1	0	0	1060.66	866	874
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	6	6	9	0.01%	7.2%	LQNATPTNFK	96.7%	28.8	25	28.8	1	0	0	1133.60	25	34
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	6	6	9	0.01%	7.2%	SLQATALR	99.4%	36.2	25	16	1	0	0	859.50	591	598
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	6	6	9	0.01%	7.2%	SQNFDILQSAISK	99.7%	97.2	25	90.4	2	0	0	1450.75	747	759
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	6	6	9	0.01%	7.2%	VGPEELPVVGQLLR	98.8%	33	25	33	2	0	0	1505.87	852	865
Tetratricopeptide repeat protein 19, mitochondrial	TTC19	TTC19_HUMAN	42.5	99.8%	2	2	4	0.00%	5.5%	GQLENAEQLFK	99.7%	39	25	18.6	2	0	0	1276.65	150	160
Tetratricopeptide repeat protein 19, mitochondrial	TTC19	TTC19_HUMAN	42.5	99.8%	2	2	4	0.00%	5.5%	LASIYAAQNR	99.7%	62.4	25	50	2	0	0	1106.60	185	194
Tetratricopeptide repeat protein 27	TTC27	TTC27_HUMAN	96.6	99.8%	2	2	3	0.00%	3.2%	DISQLQIDLTGALGK	99.7%	72	25	70.6	1	0	0	1571.86	259	273
Tetratricopeptide repeat protein 27	TTC27	TTC27_HUMAN	96.6	99.8%	2	2	3	0.00%	3.2%	FWAIQTSALILR	99.7%	40.6	25	37.3	2	0	0	1418.82	381	392
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	4	4	6	0.01%	3.3%	ASELNPESIYSVFK	99.6%	38.4	25	38.4	1	0	0	1583.80	624	637
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	4	4	6	0.01%	3.3%	CLLTSAIYALQGR	99.7%	43.2	25	37.1	1	0	0	1465.78	1162	1174
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	4	4	6	0.01%	3.3%	SGPGLIGLGIK	99.7%	52.3	25	41.8	2	0	0	1011.62	271	281
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	4	4	6	0.01%	3.3%	SNPDQPAVILLLR	99.0%	33.7	25	33.7	2	0	0	1435.83	1355	1367
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	30	0.03%	26.4%	HEDMTLLVR	99.7%	54.4	25	43.2	3	0	0	1113.57	355	363
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	30	0.03%	26.4%	IHSDTFASGGER	99.7%	61.2	25	49.8	2	0	0	1276.59	337	348
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	30	0.03%	26.4%	LSQLGLDAGK	99.7%	60.8	25	43	2	0	0	1001.56	218	227
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	30	0.03%	26.4%	LWSVDHGEQSVVTAP	99.5%	36.5	25	34.5	2	0	0	1624.80	490	504
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	30	0.03%	26.4%	QTSLDAVAQAVVDR	99.7%	114	25	98.9	2	0	0	1472.77	320	333
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	30	0.03%	26.4%	QVGIICGQESTR	99.7%	42.2	25	39.1	2	0	0	1347.67	230	241
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	30	0.03%	26.4%	SFLESIDDALAEK	99.7%	90.4	25	81.5	4	0	0	1437.71	116	128
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	30	0.03%	26.4%	VLLQAFDVVER	99.7%	81.3	25	71.9	4	0	0	1288.73	105	115
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	30	0.03%	26.4%	VTNFVAQR	99.7%	51.3	25	33.6	5	0	0	934.51	76	83
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	30	0.03%	26.4%	VYPVSVPYSSAQSTSK	99.7%	44.6	25	44.1	2	0	0	1699.85	387	402
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	11	12	30	0.03%	26.4%	YGYTDIDLLSAAK	99.7%	96.6	25	96.6	2	0	0	1429.72	250	262
Thioredoxin	TXN	THIO_HUMAN	11.7	100.0%	5	5	10	0.01%	40.0%	CMPTFQFFK	98.2%	31.2	25	31.2	1	0	0	1205.55	73	81
Thioredoxin	TXN	THIO_HUMAN	11.7	100.0%	5	5	10	0.01%	40.0%	EKLEATINELV	99.7%	60.4	25	57.7	4	0	0	1258.69	95	105
Thioredoxin	TXN	THIO_HUMAN	11.7	100.0%	5	5	10	0.01%	40.0%	TAFQEALDAAGDK	99.7%	89.1	25	89.1	2	0	0	1336.64	9	21
Thioredoxin	TXN	THIO_HUMAN	11.7	100.0%	5	5	10	0.01%	40.0%	VGEFSGANK	99.7%	46.2	25	38.6	2	0	0	908.45	86	94
Thioredoxin	TXN	THIO_HUMAN	11.7	100.0%	5	5	10	0.01%	40.0%	VGEFSGANKEK	96.5%	28.5	25	15.3	1	0	0	1165.58	86	96
Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3	PRDX3_HUMAN	27.7	99.8%	2	2	5	0.00%	10.2%	DYGVLLEGSGLALR	99.7%	83	25	77.5	2	0	0	1462.79	171	184
Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3	PRDX3_HUMAN	27.7	99.8%	2	2	5	0.00%	10.2%	GLFIIDPNGVIK	99.7%	52.7	25	39.6	3	0	0	1285.75	185	196
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	12	12	21	0.02%	8.9%	AEGGYFGQIR	99.7%	59.7	25	53.8	2	0	0	1097.54	711	720
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	12	12	21	0.02%	8.9%	ASVHCLETGEYTHIR	99.6%	28.1	25	28.1	0	1	0	1772.84	1107	1121
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	12	12	21	0.02%	8.9%	CIFSAIDAVYCAR	99.7%	81.1	25	79.2	2	0	0	1545.72	986	998
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	12	12	21	0.02%	8.9%	EKTPATTPEAR	98.2%	31.1	25	25.9	1	0	0	1200.62	1283	1293
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	12	12	21	0.02%	8.9%	FLCCMLETVTR	99.7%	49.7	25	45.3	1	0	0	1429.66	1042	1052
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	12	12	21	0.02%	8.9%	FLQLCIFPR	99.7%	55.4	25	36.5	2	0	0	1193.65	977	985
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	12	12	21	0.02%	8.9%	FVELVHQQK	99.7%	42.9	25	33.4	2	0	0	1127.62	999	1007
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	12	12	21	0.02%	8.9%	LDPETLESLGLIK	99.7%	62.7	25	52.6	2	0	0	1427.80	127	139
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	12	12	21	0.02%	8.9%	LGLLEALLK	99.7%	61.4	25	53	4	0	0	969.63	346	354
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	12	12	21	0.02%	8.9%	TPNFSTLLCYDR	99.7%	63.2	25	62.9	1	0	0	1486.70	1008	1019

THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	12	12	21	0.02%	8.9%	VFSDIIYTVASCTENEASR	99.7%	46.6	25	46.6	1	0	0	2162.01	1020	1038
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	12	12	21	0.02%	8.9%	VLNLGQALER	99.7%	66.1	25	57	2	0	0	1112.64	1137	1146
THO complex subunit 3	THOC3	THOC3_HUMAN	38.8	100.0%	3	4	8	0.01%	8.6%	TASVFLLEKDR	99.7%	55.8	25	52.9	2	0	0	1278.71	78	88
THO complex subunit 3	THOC3	THOC3_HUMAN	38.8	100.0%	3	4	8	0.01%	8.6%	TLSFSHDGK	95.6%	27.7	25	10.3	2	0	0	991.48	271	279
THO complex subunit 3	THOC3	THOC3_HUMAN	38.8	100.0%	3	4	8	0.01%	8.6%	YVLGMQELFR	99.7%	69	25	59.6	4	0	0	1255.65	34	43
THO complex subunit 4	ALYREF	THOC4_HUMAN	26.9	100.0%	3	4	10	0.01%	15.2%	MDMSLDDIIK	99.2%	34.5	25	31.8	2	0	0	1180.56	5	14
THO complex subunit 4	ALYREF	THOC4_HUMAN	26.9	100.0%	3	4	10	0.01%	15.2%	QQLSAEELDAQLDAYNAR	99.7%	124	25	123	2	2	0	2034.97	236	253
THO complex subunit 4	ALYREF	THOC4_HUMAN	26.9	100.0%	3	4	10	0.01%	15.2%	SLGTADVHFER	99.7%	82	25	70.6	4	0	0	1231.61	145	155
THO complex subunit 6 homolog	THOC6	THOC6_HUMAN	37.5	99.9%	2	2	2	0.00%	6.5%	CVNQWQLSGELK	98.9%	33.4	25	18.5	1	0	0	1461.72	279	290
THO complex subunit 6 homolog	THOC6	THOC6_HUMAN	37.5	99.9%	2	2	2	0.00%	6.5%	VLTAAGNSCR	99.7%	40	25	30.6	1	0	0	1048.52	316	325
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	5	5	7	0.01%	8.2%	FLGDIEVWDQAEK	97.9%	30.6	25	25.8	1	0	0	1549.75	505	517
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	5	5	7	0.01%	8.2%	GFQEVVTPNIFNSR	99.7%	60.2	25	57.3	1	0	0	1607.82	368	381
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	5	5	7	0.01%	8.2%	LADFGVLHR	99.7%	48.8	25	37.3	1	0	0	1027.57	434	442
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	5	5	7	0.01%	8.2%	NELSGALTGLTR	99.7%	74.2	25	53.5	2	0	0	1231.66	443	454
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	5	5	7	0.01%	8.2%	TVYSVFGFSFK	99.7%	41.4	25	38.2	2	0	0	1281.65	485	495
Threonine--tRNA ligase, mitochondrial	TARS2	SYTM_HUMAN	81.0	100.0%	3	3	4	0.00%	4.3%	AEASGGLGGLTR	99.7%	66.1	25	54.7	1	0	0	1088.57	439	450
Threonine--tRNA ligase, mitochondrial	TARS2	SYTM_HUMAN	81.0	100.0%	3	3	4	0.00%	4.3%	LADFGALHR	99.7%	58.2	25	45.8	1	0	0	999.54	430	438
Threonine--tRNA ligase, mitochondrial	TARS2	SYTM_HUMAN	81.0	100.0%	3	3	4	0.00%	4.3%	VYNALVAFIR	99.7%	69.8	25	64.6	2	0	0	1165.67	331	340
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	6	7	10	0.01%	13.4%	AANNIASLLTK	99.7%	48	25	36.8	2	0	0	1115.64	359	369
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	6	7	10	0.01%	13.4%	AAVYVLIR	99.6%	37.5	25	22.6	1	0	0	904.56	477	484
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	6	7	10	0.01%	13.4%	AVLLTQDTK	99.5%	36.9	25	28.6	2	0	0	988.57	441	449
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	6	7	10	0.01%	13.4%	NWNLYPACLR	94.9%	27	25	20.9	1	0	0	1306.64	419	428
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	6	7	10	0.01%	13.4%	TGSVDIIVTDLPFGK	99.7%	45.8	25	45.8	2	0	0	1561.85	397	411
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	6	7	10	0.01%	13.4%	TPQAFVHPSEQDGER	98.8%	33.1	25	33.1	1	1	0	1697.79	485	499
Thymidine kinase, cytosolic	TK1	KITH_HUMAN	25.5	100.0%	2	3	6	0.01%	11.5%	GQIQVILGPMFSGK	99.7%	38.9	25	38.9	4	0	0	1490.80	19	32
Thymidine kinase, cytosolic	TK1	KITH_HUMAN	25.5	100.0%	2	3	6	0.01%	11.5%	TVIVAALDGTFQR	99.7%	80.1	25	73.1	2	0	0	1390.77	118	130
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	7	8	17	0.02%	7.4%	ASAVSELSPR	99.7%	65.3	25	59.1	3	0	0	1016.54	236	245
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	7	8	17	0.02%	7.4%	EESAASGGAAYTK	99.7%	55.6	25	51.5	2	0	0	1241.56	334	346
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	7	8	17	0.02%	7.4%	EESAASGGAAYTKR	98.8%	32.7	25	32.7	1	0	0	1397.67	334	347
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	7	8	17	0.02%	7.4%	EQTFSGGTSQDTK	99.7%	55.2	25	48.5	2	0	0	1385.62	203	215
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	7	8	17	0.02%	7.4%	GSFSDTGLGDGK	99.7%	64.4	25	63.2	3	0	0	1140.52	376	387
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	7	8	17	0.02%	7.4%	SIFQHIQSAQSQR	99.7%	57.1	25	49.8	1	1	0	1529.78	609	621
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	7	8	17	0.02%	7.4%	SPLQSVVVR	99.7%	45.9	25	33	4	0	0	984.58	253	261
Torsin-1A-interacting protein 1	TOR1AIP1	TOIP1_HUMAN	66.2	100.0%	3	3	4	0.00%	6.7%	FESFPAGSTLIFYK	99.7%	39.6	25	39.6	1	0	0	1606.82	481	494
Torsin-1A-interacting protein 1	TOR1AIP1	TOIP1_HUMAN	66.2	100.0%	3	3	4	0.00%	6.7%	SELGNQSPSTSSR	99.7%	40.5	25	40.5	1	0	0	1349.63	309	321
Torsin-1A-interacting protein 1	TOR1AIP1	TOIP1_HUMAN	66.2	100.0%	3	3	4	0.00%	6.7%	SQPAILLLTAAR	99.7%	63.1	25	63.1	2	0	0	1253.76	405	416
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	6	7	10	0.01%	26.9%	ATTPADGEEPAPEAEALAAAR	99.7%	86.5	25	86.5	2	1	0	2037.97	6	26
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	6	7	10	0.01%	26.9%	DYIQSTMETEK	99.2%	34.9	25	34.9	2	0	0	1360.59	124	134
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	6	7	10	0.01%	26.9%	FLSGLELVK	99.0%	33.8	25	27.8	1	0	0	1005.60	32	40
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	6	7	10	0.01%	26.9%	GVDLYVLEK	99.7%	69.4	25	50	1	0	0	1035.57	197	205
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	6	7	10	0.01%	26.9%	TIGQVLAR	95.4%	27.4	25	8.36	1	0	0	857.52	145	152
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	6	7	10	0.01%	26.9%	TPQGLSNLAK	99.7%	51.1	25	41.4	2	0	0	1028.57	135	144
TraB domain-containing protein	TRABD	TRABD_HUMAN	42.3	99.8%	2	2	4	0.00%	5.9%	AIAALSFWQK	99.7%	60.1	25	47.2	2	0	0	1134.63	200	209
TraB domain-containing protein	TRABD	TRABD_HUMAN	42.3	99.8%	2	2	4	0.00%	5.9%	TVTQLVAEDGSR	99.7%	74.8	25	65.4	2	0	0	1275.65	63	74
Trafficking protein particle complex subunit 1	TRAPPC1	TPPC1_HUMAN	16.8	100.0%	5	6	8	0.01%	37.9%	DGFLAFQTSR	99.7%	53.1	25	38.5	2	0	0	1141.56	59	68
Trafficking protein particle complex subunit 1	TRAPPC1	TPPC1_HUMAN	16.8	100.0%	5	6	8	0.01%	37.9%	LHYYETPTGIK	99.7%	42.2	25	29.9	1	0	0	1321.68	71	81
Trafficking protein particle complex subunit 1	TRAPPC1	TPPC1_HUMAN	16.8	100.0%	5	6	8	0.01%	37.9%	NPLCPLGQTVQSELFR	99.7%	41.9	25	41.9	1	0	0	1858.95	112	127
Trafficking protein particle complex subunit 1	TRAPPC1	TPPC1_HUMAN	16.8	100.0%	5	6	8	0.01%	37.9%	SRLDSYVR	99.7%	39.3	25	32.3	2	0	0	995.53	128	135
Trafficking protein particle complex subunit 1	TRAPPC1	TPPC1_HUMAN	16.8	100.0%	5	6	8	0.01%	37.9%	TVHNLYLFDR	99.7%	33.1	25	30.3	1	1	0	1277.66	2	11
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	6	6	9	0.01%	3.8%	AVATYHANTER	99.7%	46.7	25	34.4	2	0	0	1232.60	503	513
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	6	6	9	0.01%	3.8%	DTALETALNAK	99.7%	62.5	25	50.3	2	0	0	1146.60	427	437

Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	6	6	9	0.01%	3.8%	ELPEYYELIR	99.7%	41.6	25	40	1	0	0	1324.68	1493	1502
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	6	6	9	0.01%	3.8%	GLDPVEILQER	99.7%	60.6	25	52.7	2	0	0	1268.68	360	370
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	6	6	9	0.01%	3.8%	LCTVNSVEEK	98.8%	32.8	25	20.6	1	0	0	1178.57	1204	1213
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	6	6	9	0.01%	3.8%	VIQAGMFDQK	95.5%	27.6	25	21.5	1	0	0	1136.58	1228	1237
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	99.9%	2	3	6	0.01%	8.9%	AEWQVYKEEISR	99.7%	47.1	25	45.8	2	2	0	1537.76	105	116
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	99.9%	2	3	6	0.01%	8.9%	SAYNVYVAER	99.7%	59.4	25	46.7	2	0	0	1171.57	160	169
Transcription initiation factor TFIID subunit 4	TAF4	TAF4_HUMAN	110.1	100.0%	3	3	7	0.01%	4.0%	ALSAVSAQAAAAQK	99.7%	76.2	25	58	2	0	0	1286.71	804	817
Transcription initiation factor TFIID subunit 4	TAF4	TAF4_HUMAN	110.1	100.0%	3	3	7	0.01%	4.0%	ELNSSPQPYLVPFLK	99.7%	39.4	25	39.4	2	0	0	1731.93	644	658
Transcription initiation factor TFIID subunit 4	TAF4	TAF4_HUMAN	110.1	100.0%	3	3	7	0.01%	4.0%	ILATNSELVGTLTR	99.7%	68.6	25	64.6	3	0	0	1487.84	852	865
Transcriptional activator protein Pur-alpha	PURA	PURA_HUMAN	34.9	100.0%	4	5	6	0.01%	20.8%	FFFDVGSNK	99.7%	53.9	25	53.9	2	0	0	1060.51	231	239
Transcriptional activator protein Pur-alpha	PURA	PURA_HUMAN	34.9	100.0%	4	5	6	0.01%	20.8%	GPGLGSTQGQTIALPAQGLIEFR	99.7%	43.9	25	43.9	1	1	0	2311.24	177	199
Transcriptional activator protein Pur-alpha	PURA	PURA_HUMAN	34.9	100.0%	4	5	6	0.01%	20.8%	LIDDYGVEEEPAELPEGTSLTVDNKR	99.7%	74.2	25	71.1	0	1	0	2889.40	205	230
Transcriptional activator protein Pur-alpha	PURA	PURA_HUMAN	34.9	100.0%	4	5	6	0.01%	20.8%	VSEVKPTYR	95.3%	27.4	25	17.5	1	0	0	1078.59	246	254
Transcriptional activator protein Pur-beta	PURB	PURB_HUMAN	33.2	100.0%	4	4	8	0.01%	14.4%	FFFDVGCNK	99.7%	45.1	25	45.1	2	0	0	1133.51	232	240
Transcriptional activator protein Pur-beta	PURB	PURB_HUMAN	33.2	100.0%	4	4	8	0.01%	14.4%	GGGEQETQELASK	99.7%	71.9	25	61	2	0	0	1333.62	25	37
Transcriptional activator protein Pur-beta	PURB	PURB_HUMAN	33.2	100.0%	4	4	8	0.01%	14.4%	GGGGGPCGFQPASR	96.2%	28.2	25	28.2	2	0	0	1304.58	11	24
Transcriptional activator protein Pur-beta	PURB	PURB_HUMAN	33.2	100.0%	4	4	8	0.01%	14.4%	VSEVKPSYR	99.1%	34.1	25	23.8	2	0	0	1064.57	247	255
Transducin beta-like protein 3	TBL3	TBL3_HUMAN	89.0	100.0%	3	3	7	0.01%	4.7%	AALEALLPYTER	99.7%	43.8	25	37.2	2	0	0	1346.73	755	766
Transducin beta-like protein 3	TBL3	TBL3_HUMAN	89.0	100.0%	3	3	7	0.01%	4.7%	LLLFSSATDAAIR	99.7%	57.1	25	57.1	2	0	0	1377.77	166	178
Transducin beta-like protein 3	TBL3	TBL3_HUMAN	89.0	100.0%	3	3	7	0.01%	4.7%	VNILEVASGAVLR	99.7%	104	25	95.1	3	0	0	1340.79	47	59
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	17	29	0.03%	23.9%	DSAQNSVIIVDK	99.7%	79.2	25	70.6	2	0	0	1288.67	194	205
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	17	29	0.03%	23.9%	GFVEPDHYVVVGAQR	99.7%	79.9	25	78.4	1	2	0	1672.84	395	409
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	17	29	0.03%	23.9%	ILNIFGVIK	99.7%	55.2	25	40.9	2	0	0	1016.65	386	394
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	17	29	0.03%	23.9%	LAVDEEENADNNTK	99.7%	77.9	25	64.2	2	0	0	1561.70	40	53
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	17	29	0.03%	23.9%	LLNENSYVPR	99.7%	67.2	25	53.5	2	0	0	1204.63	146	155
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	17	29	0.03%	23.9%	LTTDFGNAEK	99.7%	60.4	25	44.2	2	0	0	1095.53	656	665
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	17	29	0.03%	23.9%	LTVSNVLK	99.0%	33.6	25	21.6	2	0	0	873.54	375	382
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	17	29	0.03%	23.9%	LVYLVENPGGYVAYSK	99.7%	79.8	25	78.4	2	0	0	1771.93	209	224
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	17	29	0.03%	23.9%	QVDGDNSHVEMK	97.0%	29.1	25	22.2	1	0	0	1358.60	28	39
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	17	29	0.03%	23.9%	SAFSNLFGGEPLSYTR	99.7%	78.3	25	78.3	2	0	0	1745.85	7	22
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	17	29	0.03%	23.9%	SGVGTALLLK	99.7%	46	25	33.8	2	0	0	958.59	419	428
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	17	29	0.03%	23.9%	SSGLPNIPVQTISR	99.7%	50.6	25	44.2	2	0	0	1468.81	326	339
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	17	29	0.03%	23.9%	VEYHFLSPYVSPK	99.7%	38.5	25	38.5	1	1	0	1565.80	681	693
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	17	29	0.03%	23.9%	VSASPLLYTLIEK	99.7%	74.8	25	74.8	1	0	0	1433.83	496	508
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	15	17	29	0.03%	23.9%	YNSQLLSFVR	99.7%	68.5	25	68.4	2	0	0	1226.65	614	623
Transformation/transcription domain-associated protein	TRRAP	TRRAP_HUMAN	437.6	99.9%	2	2	3	0.00%	0.6%	ACQLPLFSYIVER	99.7%	53.4	25	51.8	2	0	0	1595.83	1132	1144
Transformation/transcription domain-associated protein	TRRAP	TRRAP_HUMAN	437.6	99.9%	2	2	3	0.00%	0.6%	TLSFLAYIIR	99.7%	39.7	25	34	1	0	0	1196.70	287	296
Transgelin-2	TAGLN2	TAGL2_HUMAN	22.4	100.0%	2	2	4	0.00%	12.6%	GASQAGMTGYGMPR	99.7%	45.8	25	45.8	2	0	0	1415.60	183	196
Transgelin-2	TAGLN2	TAGL2_HUMAN	22.4	100.0%	2	2	4	0.00%	12.6%	NFSDNQLQEGK	99.7%	46.2	25	46.2	2	0	0	1279.59	161	171
Transitional endoplasmic reticulum ATPase	VCP	TERA_HUMAN	89.3	100.0%	6	6	9	0.01%	9.4%	AIANECQANFISIK	99.7%	46.8	25	46.8	1	0	0	1578.79	530	543
Transitional endoplasmic reticulum ATPase	VCP	TERA_HUMAN	89.3	100.0%	6	6	9	0.01%	9.4%	ESIESEIRR	97.7%	30.1	25	16.4	1	0	0	1118.58	701	709
Transitional endoplasmic reticulum ATPase	VCP	TERA_HUMAN	89.3	100.0%	6	6	9	0.01%	9.4%	GILLYGPPGTGK	99.7%	53.9	25	0	2	0	0	1172.67	240	251
Transitional endoplasmic reticulum ATPase	VCP	TERA_HUMAN	89.3	100.0%	6	6	9	0.01%	9.4%	LAGESESNLRK	95.4%	27.5	25	14.6	1	0	0	1203.63	278	288
Transitional endoplasmic reticulum ATPase	VCP	TERA_HUMAN	89.3	100.0%	6	6	9	0.01%	9.4%	LDQLIYIPLPDEK	99.0%	33.7	25	33.7	2	0	0	1556.86	639	651
Transitional endoplasmic reticulum ATPase	VCP	TERA_HUMAN	89.3	100.0%	6	6	9	0.01%	9.4%	NAPAIIFIDELDAIAPK	99.7%	39.7	25	37	2	0	0	1811.00	296	312
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	6	6	10	0.01%	23.0%	AQNKPFYVVAESFK	95.8%	21	25	21	0	1	0	1627.85	221	234
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	6	6	10	0.01%	23.0%	DGATILTHAYSR	99.7%	64.3	25	59.7	2	0	0	1304.66	121	132
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	6	6	10	0.01%	23.0%	DKGETIQGLR	99.7%	65.6	25	50.5	2	0	0	1116.60	37	46
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	6	6	10	0.01%	23.0%	FISLASLEYSDYSK	99.7%	85.4	25	75.8	1	0	0	1622.79	75	88
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	6	6	10	0.01%	23.0%	IGTNQMAVCAK	99.7%	52	25	46.8	2	0	0	1208.58	210	220
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	6	6	10	0.01%	23.0%	VLEAAVAAK	99.7%	47.2	25	27.5	2	0	0	871.52	137	145

Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	5	5	8	0.01%	20.8%	AVTGTHTLALAAK	99.7%	79.1	25	75.3	2	0	0	1253.72	247	259
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	5	5	8	0.01%	20.8%	FVAPEEVLPFTEGDILEK	99.6%	38	25	38	2	0	0	2033.05	288	305
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	5	5	8	0.01%	20.8%	LSPQFPNEEDSFHK	99.2%	34.6	25	34.6	1	0	0	1674.78	274	287
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	5	5	8	0.01%	20.8%	MTAAQPSETTVGNMVR	99.7%	44.1	25	42.6	1	0	0	1708.80	68	83
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	5	5	8	0.01%	20.8%	SDESDQQESLHK	99.7%	41.4	25	33.6	2	0	0	1402.61	100	111
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	6	6	11	0.01%	12.2%	ASPSTAGETPSGVK	99.7%	49	25	43.8	2	0	0	1288.64	129	142
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	6	6	11	0.01%	12.2%	ASPSTAGETPSGVKR	99.6%	37.7	25	37.7	2	0	0	1444.74	129	143
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	6	6	11	0.01%	12.2%	ILQEAWTEGR	99.7%	72.9	25	53.9	2	0	0	1202.62	345	354
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	6	6	11	0.01%	12.2%	LGLQYSQGLVSGSNAR	99.7%	83.9	25	83.9	2	0	0	1649.86	210	225
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	6	6	11	0.01%	12.2%	VGTAQLALVAR	99.7%	97.9	25	74.2	2	0	0	1098.66	418	428
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	6	6	11	0.01%	12.2%	VSLFSHLPQYSR	98.8%	32.8	25	31.9	1	0	0	1433.75	177	188
Translation initiation factor eIF-2B subunit epsilon	EIF2B5	EI2BE_HUMAN	80.4	100.0%	4	4	4	0.00%	5.8%	GYNPAEVGAAGK	99.5%	37.1	25	31.2	1	0	0	1133.56	482	493
Translation initiation factor eIF-2B subunit epsilon	EIF2B5	EI2BE_HUMAN	80.4	100.0%	4	4	4	0.00%	5.8%	IITSELYR	99.7%	41.6	25	30.7	1	0	0	994.56	122	129
Translation initiation factor eIF-2B subunit epsilon	EIF2B5	EI2BE_HUMAN	80.4	100.0%	4	4	4	0.00%	5.8%	VFQNEVLGTLQR	99.7%	66.7	25	57.4	1	0	0	1403.76	552	563
Translation initiation factor eIF-2B subunit epsilon	EIF2B5	EI2BE_HUMAN	80.4	100.0%	4	4	4	0.00%	5.8%	YCALLLPLLK	99.6%	38.3	25	38.3	1	0	0	1203.72	617	626
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	5	5	8	0.01%	15.3%	GADIKDCLIGSGQR	99.7%	40.8	25	36.3	1	0	0	1489.74	418	431
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	5	5	8	0.01%	15.3%	KGQDSIEPVPGQK	99.7%	51.9	25	48.3	2	0	0	1382.73	134	146
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	5	5	8	0.01%	15.3%	LLSALCPEEPPVHSSAQIVSK	99.7%	29.5	25	29.5	0	1	0	2262.18	329	349
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	5	5	8	0.01%	15.3%	SELIPYLVR	99.4%	36.2	25	29.9	2	0	0	1089.63	226	234
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	5	5	8	0.01%	15.3%	VGFEEVIVVTTR	99.7%	79	25	79	2	0	0	1348.75	46	57
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	AALLETLSLLLAK	99.7%	72.2	25	72.2	2	0	0	1355.85	2324	2336
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	ADYTSHLR	99.7%	40.2	25	28.4	2	0	0	962.47	2184	2191
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	AGSVELLGAMAYCAPK	99.7%	103	25	100	2	0	0	1637.80	1515	1530
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	AIITALGVER	99.7%	65.6	25	43.6	2	0	0	1042.63	1872	1881
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	ALADENEFVR	99.7%	66.7	25	57.4	2	0	0	1163.57	1785	1794
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	ALGTLVSHVTLR	99.7%	73	25	59.4	2	1	0	1266.75	915	926
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	ALVAVLLSR	99.7%	91.6	25	82	3	0	0	941.61	568	576
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	ASLLDPVPEVR	99.7%	42.1	25	38	2	0	0	1195.67	1664	1674
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	AVMSNLSAHGVK	99.7%	60.5	25	54.5	3	0	0	1213.64	1485	1496
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	AYSDQAIVNLLK	99.7%	95.6	25	71.7	2	0	0	1334.73	2610	2621
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	CGLALALNK	99.7%	42.1	25	18.7	1	0	0	959.53	1235	1243
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	CLQTLLDTK	99.4%	36	25	29.1	1	0	0	1091.58	1595	1603
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	FTPYVGPIIPCILK	98.0%	30.8	25	30.8	1	0	0	1617.91	1771	1784
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	GAAYGLAGLVK	99.7%	57.2	25	45.5	2	0	0	1019.59	1396	1406
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	GIKEEVQLTSK	99.7%	50.5	25	37.6	1	0	0	1231.69	819	829
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	GVTSILPVLR	98.5%	31.9	25	31.9	1	0	0	1054.66	2260	2269
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	HLDQIIPR	99.6%	37.4	25	31.4	2	0	0	991.57	705	712
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	ILPEIIPILEEGLR	99.7%	63	25	61.9	2	0	0	1604.96	1960	1973
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	LFCLTLHR	99.5%	36.5	25	23	2	0	0	1059.58	53	60
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	LISIHIK	99.0%	33.7	25	20.1	2	0	0	823.54	2374	2380
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	LMDEAVLALR	99.7%	68.4	25	52.9	4	0	0	1130.62	314	323
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	LMEIYQEK	99.7%	45.1	25	38.3	2	0	0	1053.53	1201	1208
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	LMPEIVATASK	98.8%	32.9	25	24.4	1	0	0	1159.64	1735	1745
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	LSSFWQLIVDEK	99.3%	35	25	14.7	1	0	0	1464.77	510	521
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	LTEVLTDSHVK	99.7%	52.6	25	43.3	2	0	0	1241.67	1543	1553
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	LTSADALRPSVVSITGPLIR	99.7%	31.3	25	31	0	1	0	2066.20	2293	2312
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	LYRPPPVLDALGR	99.7%	45.1	25	35.9	2	2	0	1466.85	1209	1221
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	NAPNDASYDAVR	99.7%	61.8	25	61.8	2	0	0	1292.59	1305	1316
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	NLLHSLQSSGIGSK	99.7%	64	25	53.5	2	2	0	1440.78	88	101
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	QAGAEALSQAVAR	99.7%	82.2	25	63.1	2	0	0	1271.67	1177	1189
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	QLSSCLPNIVPK	99.7%	39.8	25	37.6	1	0	0	1355.74	1531	1542

Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	SALLDFYMK	99.7%	39.2	25	32.4	3	0	0	1087.55	221	229
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	SGAAQGLAEVMAGLGVEK	99.7%	87.7	25	69.3	1	0	0	1687.87	1714	1731
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	SLVSGLIR	99.7%	44.5	25	16.4	1	0	0	844.53	2192	2199
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	VDENGPELLPR	99.7%	53.3	25	45.9	2	0	0	1238.64	1027	1037
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	VDIAPHVR	95.3%	27.3	25	27.3	1	0	0	906.52	1746	1753
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	VDPLFTELLNGIR	99.7%	56.8	25	49.6	2	0	0	1486.83	2381	2393
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	VISESPPDQWEAR	99.7%	45.6	25	44.5	2	0	0	1513.73	1222	1234
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	VLAFLSSVAGDALTR	99.7%	95	25	95	2	0	0	1519.85	2093	2107
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	VLAGLYMGR	99.7%	47.8	25	41.1	1	0	0	979.54	1885	1893
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	VLPLEALVTDAGEVTEAGK	99.7%	97.5	25	97.5	3	2	0	1912.03	617	635
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	42	49	84	0.08%	18.1%	YLLDSCAPLLR	99.7%	59.9	25	53.3	2	0	0	1320.70	241	251
Translin-associated protein X	TSNAX	TSNAX_HUMAN	33.1	99.8%	2	3	5	0.00%	7.9%	DVNSSSPVMLAFK	99.7%	51.1	25	42	2	0	0	1394.70	28	40
Translin-associated protein X	TSNAX	TSNAX_HUMAN	33.1	99.8%	2	3	5	0.00%	7.9%	SLISMDEINK	99.7%	47.7	25	33.4	3	0	0	1149.58	141	150
Translocation protein SEC63 homolog	SEC63	SEC63_HUMAN	88.0	100.0%	5	5	5	0.00%	7.8%	AYAALTDEESR	99.7%	52.8	25	41.2	1	0	0	1225.57	148	158
Translocation protein SEC63 homolog	SEC63	SEC63_HUMAN	88.0	100.0%	5	5	5	0.00%	7.8%	LIMVLAGASEFDPQYNK	99.7%	38.9	25	38.9	1	0	0	1895.96	246	262
Translocation protein SEC63 homolog	SEC63	SEC63_HUMAN	88.0	100.0%	5	5	5	0.00%	7.8%	LSQMAVQGLQQFK	99.7%	50.8	25	44.5	1	0	0	1493.78	369	381
Translocation protein SEC63 homolog	SEC63	SEC63_HUMAN	88.0	100.0%	5	5	5	0.00%	7.8%	VLLLSHLAR	99.7%	51.4	25	51.4	1	0	0	1021.65	303	311
Translocation protein SEC63 homolog	SEC63	SEC63_HUMAN	88.0	100.0%	5	5	5	0.00%	7.8%	YSGDQILIR	99.7%	52.4	25	39.2	1	0	0	1064.57	218	226
Translocator protein	TSPO	TSPOA_HUMAN	18.8	99.8%	2	2	3	0.00%	9.5%	ELGGFTEK	99.7%	42.9	25	15	2	0	0	880.44	70	77
Translocator protein	TSPO	TSPOA_HUMAN	18.8	99.8%	2	2	3	0.00%	9.5%	FVHGEGLR	95.3%	27.3	25	23.1	1	0	0	914.48	25	32
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	8	10	16	0.02%	41.6%	FFDEESYSLLR	99.7%	72.6	25	68.5	2	0	0	1405.66	106	116
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	8	10	16	0.02%	41.6%	FFDEESYSLLRK	99.7%	52	25	44.9	2	1	0	1533.76	106	117
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	8	10	16	0.02%	41.6%	GQDVGRYQVSWSLDHK	97.4%	22.4	25	22.4	0	1	0	1874.91	80	95
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	8	10	16	0.02%	41.6%	NNEDISIIPPLFTVSVDHR	99.7%	42.7	25	39.9	0	2	0	2166.12	121	139
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	8	10	16	0.02%	41.6%	NRVQNMALYADVGGK	97.5%	29.9	25	25.6	1	0	0	1651.82	59	73
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	8	10	16	0.02%	41.6%	SAHAGTYEVR	95.3%	27.4	25	18.2	1	0	0	1090.53	96	105
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	8	10	16	0.02%	41.6%	VQNMALYADVGGK	99.7%	85.9	25	78.9	4	0	0	1365.68	61	73
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	8	10	16	0.02%	41.6%	YQVSWSLDHK	99.7%	42.5	25	30.8	2	0	0	1262.62	86	95
Transmembrane 9 superfamily member 3	TM9SF3	TM9S3_HUMAN	67.9	100.0%	3	3	6	0.01%	5.4%	NLSGQPNFPCR	99.7%	45	25	42.3	1	0	0	1289.61	419	429
Transmembrane 9 superfamily member 3	TM9SF3	TM9S3_HUMAN	67.9	100.0%	3	3	6	0.01%	5.4%	YFSLPFCVGSK	99.5%	37	25	35.7	3	0	0	1304.63	60	70
Transmembrane 9 superfamily member 3	TM9SF3	TM9S3_HUMAN	67.9	100.0%	3	3	6	0.01%	5.4%	YLDPSFFQHR	99.7%	52.1	25	42.4	2	0	0	1309.63	211	220
Transmembrane and coiled-coil domain-containing protein 1	TMCO1	TMCO1_HUMAN	21.2	99.8%	2	2	3	0.00%	12.2%	ILGLAPSR	97.0%	29.2	25	14.7	1	0	0	826.51	161	168
Transmembrane and coiled-coil domain-containing protein 1	TMCO1	TMCO1_HUMAN	21.2	99.8%	2	2	3	0.00%	12.2%	LPFTPLSYIQGLSHR	99.7%	42.3	25	41.4	0	2	0	1728.94	117	131
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	99.8%	2	2	4	0.00%	10.5%	IPDQLVILDMK	99.7%	53.1	25	41.7	2	0	0	1284.72	117	127
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	99.8%	2	2	4	0.00%	10.5%	ITDSAGHILYSK	99.7%	44.7	25	44.4	2	0	0	1304.68	76	87
Transmembrane emp24 domain-containing protein 7	TMED7	TMED7_HUMAN	25.2	99.8%	2	2	3	0.00%	9.8%	QCFYEDIAQGTK	99.5%	36.8	25	36.8	1	0	0	1459.65	47	58
Transmembrane emp24 domain-containing protein 7	TMED7	TMED7_HUMAN	25.2	99.8%	2	2	3	0.00%	9.8%	SVIDYQTHFR	99.7%	49.8	25	31.3	2	0	0	1265.63	160	169
Transmembrane protein 11, mitochondrial	TMEM11	TMM11_HUMAN	21.5	99.8%	2	2	3	0.00%	12.5%	LPLHTLTSSTPVVLVR	99.2%	26.1	25	26.1	0	2	0	1733.03	146	161
Transmembrane protein 11, mitochondrial	TMEM11	TMM11_HUMAN	21.5	99.8%	2	2	3	0.00%	12.5%	YIVIEPTR	97.8%	30.3	25	11.3	1	0	0	990.56	59	66
Transmembrane protein 201	TMEM201	TM201_HUMAN	72.2	100.0%	4	4	6	0.01%	6.9%	ALLLSHQFK	99.7%	40.5	25	33.7	1	0	0	1056.62	184	192
Transmembrane protein 201	TMEM201	TM201_HUMAN	72.2	100.0%	4	4	6	0.01%	6.9%	EADQTHAQNFSSAVK	99.7%	59.8	25	52.6	2	0	0	1632.76	195	209
Transmembrane protein 201	TMEM201	TM201_HUMAN	72.2	100.0%	4	4	6	0.01%	6.9%	EEGRYDEEVEVYR	95.9%	21.1	25	21.1	0	1	0	1672.74	142	154
Transmembrane protein 201	TMEM201	TM201_HUMAN	72.2	100.0%	4	4	6	0.01%	6.9%	SPVQVILLR	99.7%	49.3	25	44.3	2	0	0	1024.65	210	218
Transmembrane protein 209	TMEM209	TM209_HUMAN	62.9	99.8%	2	2	3	0.00%	4.5%	FQYQLACR	99.7%	44.4	25	31.9	2	0	0	1085.52	289	296
Transmembrane protein 209	TMEM209	TM209_HUMAN	62.9	99.8%	2	2	3	0.00%	4.5%	MGCPELQIGEASITSLK	99.7%	41.1	25	39.3	1	0	0	1833.91	365	381
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	5	6	16	0.02%	22.7%	ALLANALTSALR	99.7%	100	25	96.4	5	0	0	1213.73	58	69
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	5	6	16	0.02%	22.7%	GSNSLPLLR	99.7%	47.2	25	35	2	0	0	956.55	135	143
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	5	6	16	0.02%	22.7%	LCLQSIAFISR	99.7%	66.3	25	57.2	2	0	0	1307.71	231	241
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	5	6	16	0.02%	22.7%	LDTAMWLSR	99.7%	65.7	25	42.2	3	0	0	1092.55	23	31
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	5	6	16	0.02%	22.7%	SVLDKLSANQQNILK	99.7%	79.1	25	74.2	2	2	0	1670.94	144	158
Transmembrane protein 97	TMEM97	TMM97_HUMAN	20.8	99.8%	2	2	3	0.00%	9.7%	ELYPVEFR	99.7%	44.5	25	31.4	2	0	0	1052.54	37	44

Transmembrane protein 97	TMEM97	TMM97_HUMAN	20.8	99.8%	2	2	3	0.00%	9.7%	SPYYKYEEK	96.3%	28.3	25	24.3	1	0	0	1206.57	164	172
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	25	0.02%	14.8%	ALVMLLEVR	99.7%	69.7	25	50.9	4	0	0	1043.63	246	254
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	25	0.02%	14.8%	ATVGILITTIASK	99.7%	115	25	115	3	0	0	1287.79	116	128
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	25	0.02%	14.8%	ESQSPDTTIQR	99.7%	44.6	25	35.4	2	0	0	1261.60	29	39
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	25	0.02%	14.8%	FLQFFK	95.0%	27.1	25	17.3	1	0	0	829.46	187	192
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	25	0.02%	14.8%	FSDQFPLPLK	99.7%	49.4	25	45.9	2	0	0	1191.64	880	889
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	25	0.02%	14.8%	GELQNWPDLLPK	99.7%	52.1	25	37.4	2	0	0	1409.74	129	140
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	25	0.02%	14.8%	QSSFALLGDLTK	99.7%	83.5	25	75.6	2	0	0	1279.69	693	704
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	25	0.02%	14.8%	SECLNNIGDSSPLIR	99.7%	92.3	25	89.2	2	0	0	1674.81	101	115
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	25	0.02%	14.8%	SITCWTLSR	97.0%	29.1	25	17.5	1	0	0	1123.56	464	472
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	25	0.02%	14.8%	SNILTLMYQCMQDK	99.7%	64.8	25	64.8	2	0	0	1744.81	674	687
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	25	0.02%	14.8%	TLLENTAITIGR	99.7%	72.6	25	57.3	2	0	0	1301.74	774	785
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	25	0.02%	14.8%	YSDIDIILLK	99.7%	52.2	25	44	2	0	0	1192.68	318	327
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	9	9	16	0.02%	12.6%	ASFWLGELQR	99.7%	42.7	25	30.4	1	0	0	1206.63	30	39
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	9	9	16	0.02%	12.6%	ETTVGAVTVTHK	99.7%	61.8	25	56.4	2	0	0	1242.67	882	893
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	9	9	16	0.02%	12.6%	GTALVLAR	99.7%	59.6	25	39	2	0	0	800.50	564	571
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	9	9	16	0.02%	12.6%	IFTELCETFLEK	99.7%	79.3	25	60.1	2	0	0	1529.76	298	309
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	9	9	16	0.02%	12.6%	IVCTPGQGLGDLR	99.7%	54.5	25	50.9	2	0	0	1385.72	310	322
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	9	9	16	0.02%	12.6%	LPETVHTAVR	99.7%	73.4	25	58.6	2	0	0	1122.63	469	478
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	9	9	16	0.02%	12.6%	SLDSFLLSPEAAVGLLK	99.7%	73.3	25	73	2	0	0	1759.98	547	563
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	9	9	16	0.02%	12.6%	SVDPENNPTLVEVLEGVVR	99.7%	61.2	25	61.2	2	0	0	2066.08	450	468
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	9	9	16	0.02%	12.6%	VIQEIWPVLSETLNK	99.5%	36.8	25	36.8	1	0	0	1768.98	637	651
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	9	11	22	0.02%	29.3%	FFVMTSLR	99.7%	50.3	25	27.4	4	0	0	1000.53	199	206
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	9	11	22	0.02%	29.3%	FGMFEFLSNHMR	99.3%	35.3	25	35.3	2	0	0	1531.68	102	113
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	9	11	22	0.02%	29.3%	FIHDQTSPNPK	99.7%	36	25	34.5	2	2	0	1283.64	150	160
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	9	11	22	0.02%	29.3%	GLSSLLYGSIPK	99.7%	56.1	25	35.9	2	0	0	1234.70	86	97
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	9	11	22	0.02%	29.3%	GTYQGLTATVLK	99.7%	64.3	25	56.4	2	0	0	1251.69	179	190
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	9	11	22	0.02%	29.3%	MQGLEAHK	98.9%	33.4	25	18	2	0	0	913.46	248	255
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	9	11	22	0.02%	29.3%	NTWDCGLQILK	99.7%	55.8	25	48.2	2	0	0	1347.67	258	268
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	9	11	22	0.02%	29.3%	SHGVLGLYR	99.5%	36.8	25	36.8	2	0	0	1001.55	77	85
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	9	11	22	0.02%	29.3%	TQLQLDER	99.7%	43.7	25	26.6	2	0	0	1002.52	51	58
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	23	31	68	0.07%	39.2%	ADMVIEAVFEDLSLK	99.7%	96.4	25	90.3	4	0	0	1679.86	441	455
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	23	31	68	0.07%	39.2%	ALMGLYHGQVLCK	99.7%	66.5	25	62.5	2	0	0	1489.77	338	350
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	23	31	68	0.07%	39.2%	ALTSFER	99.7%	43	25	28.1	2	0	0	823.43	416	422
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	23	31	68	0.07%	39.2%	CLAPMMSEVIR	97.4%	29.6	25	19.9	2	0	0	1306.63	550	560
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	23	31	68	0.07%	39.2%	DATLTALDR	99.7%	81.7	25	43.3	2	0	0	975.51	391	399
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	23	31	68	0.07%	39.2%	DGPGFYTTR	99.7%	45.1	25	29.5	2	0	0	1013.47	541	549
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	23	31	68	0.07%	39.2%	DLNSDMDSILASLK	99.7%	86.2	25	79.2	3	0	0	1521.75	647	660
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	23	31	68	0.07%	39.2%	DSIFSNLTGQLDYQGFEK	99.7%	88.9	25	84.8	2	0	0	2061.98	423	440
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	23	31	68	0.07%	39.2%	DTSASAVAVGLK	99.7%	90.2	25	71.4	4	0	0	1118.61	520	531
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	23	31	68	0.07%	39.2%	FGELVMTK	99.7%	46.6	25	34.9	2	0	0	940.48	327	334
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	23	31	68	0.07%	39.2%	FGGGNPELLTQMVSK	99.7%	84	25	76.2	4	0	0	1577.80	611	625
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	23	31	68	0.07%	39.2%	GFYIYQEGVK	99.7%	65.9	25	61.8	2	0	0	1203.60	635	644
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	23	31	68	0.07%	39.2%	ILQEGVDPK	99.7%	47.2	25	37.4	3	0	0	998.55	561	569
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	23	31	68	0.07%	39.2%	LTAYAMTIPFVR	99.7%	73.4	25	67.6	7	0	0	1382.75	268	279
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	23	31	68	0.07%	39.2%	MGLVDQLVEPLGPGLKPPEER	99.7%	54.6	25	54.6	0	2	0	2290.21	215	235
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	23	31	68	0.07%	39.2%	MQLLEIITTEK	99.7%	83.1	25	71.8	5	0	0	1318.73	506	516
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	23	31	68	0.07%	39.2%	MVGVPAALDMMLTGR	99.7%	77.5	25	75.3	4	0	0	1561.79	191	205
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	23	31	68	0.07%	39.2%	SEVSSDEDIQFR	99.7%	83.6	25	82.4	2	0	0	1411.63	665	676
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	23	31	68	0.07%	39.2%	TGIEQGSDAGYLCESQK	99.7%	111	25	111	2	0	0	1842.82	310	326
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	23	31	68	0.07%	39.2%	TIEYLEEVAITFAK	99.7%	92.9	25	85.2	3	0	0	1626.86	236	249

Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	23	31	68	0.07%	39.2%	TLQEVTQLSQEAQR	99.7%	91.1	25	81.7	2	1	0	1630.84	112	125
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	23	31	68	0.07%	39.2%	TVLGTPEVLLGALPGAGGTQR	99.7%	76	25	75.9	2	2	0	2007.12	167	187
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	23	31	68	0.07%	39.2%	VIGMHYFSPVDK	99.7%	39.7	25	29.8	2	0	0	1392.70	494	505
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	33	0.03%	38.4%	AALTGLLHR	99.7%	55.6	25	42.2	2	0	0	951.57	82	90
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	33	0.03%	38.4%	DFMYVSQDPKDQLLLGPTYATPK	99.6%	28.6	25	28.3	0	2	0	2627.31	339	361
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	33	0.03%	38.4%	DLMPHDLAR	99.1%	34	25	26.5	1	0	0	1083.53	73	81
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	33	0.03%	38.4%	DNGIRPSSLEQMAK	97.8%	30.4	25	28.6	1	0	0	1561.76	278	291
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	33	0.03%	38.4%	DQLLLGPTYATPK	99.7%	55.9	25	55.8	2	0	0	1416.77	349	361
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	33	0.03%	38.4%	EAALGAGFSDK	99.7%	57.6	25	46.9	2	0	0	1065.52	118	128
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	33	0.03%	38.4%	EGGQYGLVAACAAGGQGHAMIVEAYPK	99.7%	70.8	25	70.8	0	3	0	2721.28	448	474
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	33	0.03%	38.4%	EVVDYIIFGTVIQEVK	99.7%	79.5	25	75.7	3	0	0	1852.01	96	111
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	33	0.03%	38.4%	FNNWGGSLSLGHPFGATGCR	99.7%	52.9	25	52.9	0	2	0	2134.99	417	436
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	33	0.03%	38.4%	KLMLDLNK	99.6%	37.6	25	9.43	2	0	0	990.57	181	188
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	33	0.03%	38.4%	LAAAFAVSR	99.7%	67.9	25	57.5	2	0	0	905.52	230	238
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	33	0.03%	38.4%	LMLDLNK	99.1%	33.9	25	19.7	1	0	0	862.47	182	188
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	33	0.03%	38.4%	LVMAAANR	99.7%	50.6	25.3	42.4	2	0	0	845.47	437	444
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	33	0.03%	38.4%	NVVVVDGVR	99.7%	61.9	25	51.7	2	0	0	956.55	53	61
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	33	0.03%	38.4%	TPFLLSGTSYK	99.7%	56.7	25	50.8	2	0	0	1213.65	62	72
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	33	0.03%	38.4%	TPFLLSGTSYKDLMPHDLAR	99.7%	35.7	25	35.7	0	2	0	2278.15	62	81
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	17	18	33	0.03%	38.4%	VGLPPLEK	99.5%	36.8	25	36.8	2	0	0	852.52	409	416
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	69	0.07%	27.1%	AAGFKDPLLASGTDGVGTK	99.7%	55.5	25	55.5	1	2	0	1804.94	481	499
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	69	0.07%	27.1%	AFAHITGGGLLENIPR	99.7%	34.4	25	30.2	0	2	0	1665.91	677	692
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	69	0.07%	27.1%	AIAFLQQPR	99.7%	44.4	25	27.7	7	0	0	1043.60	425	433
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	69	0.07%	27.1%	AVQEIMQEK	99.7%	39.2	25	33.3	3	0	0	1091.54	170	178
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	69	0.07%	27.1%	ENLISALEEAKK	99.7%	51.5	25	37.1	4	0	0	1344.74	394	405
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	69	0.07%	27.1%	EQTEQILR	99.7%	41.2	25	24.7	2	0	0	1016.54	744	751
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	69	0.07%	27.1%	ESGVDIAAGNMLVK	99.7%	72.3	25	59.9	4	0	0	1403.72	439	452
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	69	0.07%	27.1%	FGDPECQVILPLLK	99.7%	58.5	25	58.5	7	0	0	1628.87	293	306
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	69	0.07%	27.1%	GDTVATLSER	99.7%	41.9	25	18.7	1	0	0	1048.53	966	975
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	69	0.07%	27.1%	GVEITGFPEAQALGLEVFHAGTALK	98.5%	24.1	25	16.8	0	1	0	2555.35	351	375
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	69	0.07%	27.1%	IKDTVLQR	99.7%	44.5	25	22.5	2	0	0	972.58	250	257
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	69	0.07%	27.1%	ILSGPFVQK	99.4%	35.8	25	0	2	0	0	988.58	898	906
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	69	0.07%	27.1%	ISNTAISISDHTALAQFCK	99.7%	53.6	25	52.6	0	3	0	2077.04	45	63
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	69	0.07%	27.1%	IYSHSLLPVLR	99.7%	45.8	25	38.2	2	2	0	1297.76	661	671
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	69	0.07%	27.1%	LDLSVTEAVVAGIAK	99.7%	96.9	25	81.7	2	0	0	1485.85	543	557
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	69	0.07%	27.1%	MLNIHPSLLPSFK	99.7%	50.7	25	42.9	3	0	0	1512.82	911	923
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	69	0.07%	27.1%	SAGVQCFGPTAEAAQLESSKR	99.7%	30	25	30	0	3	0	2194.06	88	108
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	69	0.07%	27.1%	TFNCGVGAVLVVSK	99.7%	90.9	25	85.9	2	0	0	1450.77	730	743
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	69	0.07%	27.1%	VDLGGFAGLFDLK	99.7%	92.8	25	90.4	6	0	0	1351.73	468	480
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	69	0.07%	27.1%	VLAVTAIR	99.7%	58.1	25	24.5	4	0	0	842.55	386	393
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	69	0.07%	27.1%	VLEFNCR	99.7%	39.7	25	34.5	4	0	0	937.46	286	292
Triosephosphate isomerase	TPI1	TPIS_HUMAN	30.8	100.0%	2	2	5	0.00%	9.8%	TATPQQAQEVHEK	99.7%	56.9	25	56.3	3	0	0	1466.72	213	225
Triosephosphate isomerase	TPI1	TPIS_HUMAN	30.8	100.0%	2	2	5	0.00%	9.8%	VVLAYEPVWAIGTGK	99.7%	72.8	25	64.3	2	0	0	1602.89	198	212
TRMT1-like protein	TRMT1L	TRM1L_HUMAN	81.7	100.0%	5	5	7	0.01%	9.4%	NLGIVSVTSTDISSLYAK	99.7%	90.5	25	90.5	2	0	0	1868.00	391	408
TRMT1-like protein	TRMT1L	TRM1L_HUMAN	81.7	100.0%	5	5	7	0.01%	9.4%	QLIFCTLAALAEER	99.7%	85.7	25	82.5	1	0	0	1634.86	261	274
TRMT1-like protein	TRMT1L	TRM1L_HUMAN	81.7	100.0%	5	5	7	0.01%	9.4%	SSYIAASTAKPPK	99.7%	52.1	25	46.3	2	0	0	1320.72	214	226
TRMT1-like protein	TRMT1L	TRM1L_HUMAN	81.7	100.0%	5	5	7	0.01%	9.4%	TTDDTTTDNYIAQGK	99.7%	67.2	25	67.2	1	0	0	1643.74	595	609
TRMT1-like protein	TRMT1L	TRM1L_HUMAN	81.7	100.0%	5	5	7	0.01%	9.4%	VSVEFEGYR	99.7%	65.4	25	57.1	1	0	0	1085.53	148	156
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	15	17	39	0.04%	24.4%	EDPFVFIPEDDPLFPPIEK	99.7%	41.2	25	41.2	1	0	0	2244.11	517	535
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	15	17	39	0.04%	24.4%	FHQFLVSETESGNISR	99.7%	34.2	25	32.7	0	1	0	1850.90	145	160
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	15	17	39	0.04%	24.4%	FYALDPSFPR	97.4%	29.7	25	29.7	2	0	0	1212.60	536	545

tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	15	17	39	0.04%	24.4%	GAEQLAEGGR	99.7%	79.6	25	66.8	2	0	0	987.49	306	315
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	15	17	39	0.04%	24.4%	IITVSMEDVK	99.7%	65.6	25	55.3	4	0	0	1134.61	619	628
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	15	17	39	0.04%	24.4%	ILCDVPCSGDGTMR	99.7%	44.4	25	36.4	2	0	0	1580.69	265	278
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	15	17	39	0.04%	24.4%	ILDMCAAPGSK	99.7%	43.7	25	38.2	1	0	0	1178.55	180	190
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	15	17	39	0.04%	24.4%	ILLTQENPFFR	99.7%	85.4	25	85.1	6	0	0	1377.75	629	639
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	15	17	39	0.04%	24.4%	KLSSETYSQAK	99.7%	53.5	25	52.4	4	0	0	1241.64	640	650
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	15	17	39	0.04%	24.4%	LAQEGIYTLYPFINSR	99.7%	65.4	25	65.4	4	2	0	1884.99	603	618
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	15	17	39	0.04%	24.4%	LQQQQRPEDAEDGAEGGGK	99.2%	26.3	25	26.3	0	1	0	2012.93	10	28
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	15	17	39	0.04%	24.4%	LSSETYSQAK	99.7%	63.4	25	54.9	2	0	0	1113.54	641	650
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	15	17	39	0.04%	24.4%	MMGLEVLGEK	99.7%	45.5	25	43.6	2	0	0	1106.56	701	710
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	15	17	39	0.04%	24.4%	NNSGEEFDCAFR	99.7%	71.6	25	71.6	2	0	0	1445.58	591	602
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	15	17	39	0.04%	24.4%	SEGALELADVSNELPGLK	99.7%	106	25	97.7	3	0	0	1841.95	339	356
tRNA pseudouridine synthase A, mitochondrial	PUS1	TRUA_HUMAN	47.5	99.8%	2	2	4	0.00%	4.9%	APGLGLVLER	99.6%	37.6	25	32.8	2	0	0	1024.62	328	337
tRNA pseudouridine synthase A, mitochondrial	PUS1	TRUA_HUMAN	47.5	99.8%	2	2	4	0.00%	4.9%	LSAETLQQVNR	99.7%	50.5	25	40.4	2	0	0	1258.68	224	234
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	7	8	12	0.01%	16.6%	GGGVGGFLPAMK	99.7%	52.5	25	38	2	0	0	1090.57	56	67
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	7	8	12	0.01%	16.6%	GMAAAGNYAWVNR	99.7%	81.5	25	68.6	1	0	0	1380.65	309	321
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	7	8	12	0.01%	16.6%	LVMEEAPESYK	99.7%	42.9	25	35.7	1	0	0	1311.61	466	476
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	7	8	12	0.01%	16.6%	MLQADPNKVSAR	99.7%	65.2	25	62.2	1	0	0	1329.69	199	210
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	7	8	12	0.01%	16.6%	QIGNVAALPGIVHR	99.0%	25.4	25	24.7	0	1	0	1444.84	68	81
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	7	8	12	0.01%	16.6%	SYNDELQFLEK	99.7%	62.5	25	35.5	2	0	0	1385.66	4	14
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	7	8	12	0.01%	16.6%	VEQHVVDGKER	99.7%	51.6	25	46	2	2	0	1295.67	358	368
Tropomyosin alpha-3 chain	TPM3	TPM3_HUMAN	33.0	99.8%	2	2	2	0.00%	8.1%	AADAEAEVASLNR	99.7%	44.3	25	41.7	1	0	0	1316.64	79	91
Tropomyosin alpha-3 chain	TPM3	TPM3_HUMAN	33.0	99.8%	2	2	2	0.00%	8.1%	IQLVEEELDR	99.1%	34.2	25	34.2	1	0	0	1243.65	93	102
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	16	0.02%	68.1%	AFVHWYVGEGMEEGEFSEAR	99.7%	87.4	25	87.4	2	7	0	2330.02	403	422
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	16	0.02%	68.1%	AFVHWYVGEGMEEGEFSEAREDMAALEK	99.7%	82	25	82	0	4	0	3217.42	403	430
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	16	0.02%	68.1%	AVCMLSNTTAIAEAWAR	99.7%	124	25	108	19	8	0	1880.90	374	390
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	16	0.02%	68.1%	AVFVDLEPTVIDEVR	99.7%	116	25	116	38	4	0	1701.91	65	79
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	16	0.02%	68.1%	AYHEQLSVAEITNACFEPANQMVK	99.7%	72.1	25	72.1	1	10	0	2750.29	281	304
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	16	0.02%	68.1%	DVNAAIATIK	99.7%	81.4	25	64.4	15	0	0	1015.58	327	336
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	16	0.02%	68.1%	EDMAALEK	99.7%	51.6	25	34.3	4	0	0	906.42	423	430
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	16	0.02%	68.1%	EIIDLVLDR	99.7%	79.8	25	73.4	37	0	0	1085.62	113	121
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	16	0.02%	68.1%	FDGALNVDLTEFQTNLVPYPR	99.7%	124	25	124	12	1	0	2409.21	244	264
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	16	0.02%	68.1%	FDLMYAK	99.7%	48.3	25	28.8	6	0	0	903.43	395	401
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	16	0.02%	68.1%	GDVVPKDVNAAIATIK	96.1%	28.1	25	26.8	1	0	0	1610.91	321	336
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	16	0.02%	68.1%	IHFPLATYAPVISAEK	99.7%	98.5	25	93.5	8	9	0	1756.96	265	280
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	16	0.02%	68.1%	LADQCTGLQGFLVFHSFGGGTGSGFTSLLMER	99.7%	114	25	114	0	24	0	3390.63	125	156
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	16	0.02%	68.1%	LDHKFDLMYAK	99.7%	56.8	25	43.6	8	9	0	1380.70	391	401
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	16	0.02%	68.1%	LIGQIVSSITASLR	99.7%	95.7	25	94.6	2	0	0	1457.87	230	243
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	16	0.02%	68.1%	LSVDYGKK	99.7%	50.4	25	39	9	0	0	909.50	157	164
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	16	0.02%	68.1%	NLDIERPTYTNLNR	99.7%	51.1	25	43.2	13	11	0	1718.88	216	229
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	16	0.02%	68.1%	QLFHPEQLITGK	99.7%	36.5	25	0	3	3	0	1410.77	85	96
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	16	0.02%	68.1%	QLFHPEQLITGKEDAANNYAR	99.7%	76.6	25	76.6	3	4	0	2415.21	85	105
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	16	0.02%	68.1%	RNLDIERPTYTNLNR	99.7%	30.7	25	30.7	1	2	0	1874.98	215	229
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	16	0.02%	68.1%	TIGGGDDSFNTFFSETGAGK	99.7%	108	25	108	24	0	0	2007.89	41	60
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	16	0.02%	68.1%	TIQFVDWCPTGFK	99.7%	88.4	25	83.6	14	0	0	1598.77	340	352
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	16	0.02%	68.1%	VGINYQPPTVVPGGDLAK	99.7%	60.1	25	60.1	18	0	0	1824.99	353	370
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	16	0.02%	68.1%	YMACCLLYR	99.7%	52.5	25	51.8	21	0	0	1265.55	312	320
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	25	47	380	0.38%	68.3%	AFVHWYVGEGMEEGEFSEAR	99.7%	87.4	25	87.4	2	7	0	2330.02	403	422
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	25	47	380	0.38%	68.3%	AFVHWYVGEGMEEGEFSEAREDMAALEK	99.7%	82	25	82	0	4	0	3217.42	403	430
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	25	47	380	0.38%	68.3%	AVCMLSNTTAIAEAWAR	99.7%	124	25	108	19	8	0	1880.90	374	390
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	25	47	380	0.38%	68.3%	AVFVDLEPTVIDEVR	99.7%	116	25	116	38	4	0	1701.91	65	79

Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	25	47	380	0.38%	68.3%	AYHEQLSVAEITNACFEPANQMVK	99.7%	72.1	25	72.1	1	10	0	2750.29	281	304
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	25	47	380	0.38%	68.3%	DVNAAIATIK	99.7%	81.4	25	64.4	15	0	0	1015.58	327	336
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	25	47	380	0.38%	68.3%	EDMAALEK	99.7%	51.6	25	34.3	4	0	0	906.42	423	430
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	25	47	380	0.38%	68.3%	EIIDLVLDR	99.7%	79.8	25	73.4	37	0	0	1085.62	113	121
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	25	47	380	0.38%	68.3%	FDGALNVDLTEFQTNLVPYPR	99.7%	124	25	124	12	1	0	2409.21	244	264
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	25	47	380	0.38%	68.3%	FDLMYAK	99.7%	48.3	25	28.8	6	0	0	903.43	395	401
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	25	47	380	0.38%	68.3%	GDVVPKDVNAAIATIK	96.1%	28.1	25	26.8	1	0	0	1610.91	321	336
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	25	47	380	0.38%	68.3%	IHFPLATYAPVISAEK	99.7%	98.5	25	93.5	8	9	0	1756.96	265	280
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	25	47	380	0.38%	68.3%	LADQCTGLQGFLVFHSFGGGTGSGFTSLLMER	99.7%	114	25	114	0	24	0	3390.63	125	156
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	25	47	380	0.38%	68.3%	LDHKFDLMYAK	99.7%	56.8	25	43.6	8	9	0	1380.70	391	401
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	25	47	380	0.38%	68.3%	LISQIVSSITASLR	99.7%	105	25	105	16	4	0	1487.88	230	243
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	25	47	380	0.38%	68.3%	LSVDYGKK	99.7%	50.4	25	39	9	0	0	909.50	157	164
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	25	47	380	0.38%	68.3%	NLDIERPTYTNLNR	99.7%	51.1	25	43.2	13	11	0	1718.88	216	229
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	25	47	380	0.38%	68.3%	QLFHPEQLITGK	99.7%	36.5	25	0	3	3	0	1410.77	85	96
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	25	47	380	0.38%	68.3%	QLFHPEQLITGKEDAANNYAR	99.7%	76.6	25	76.6	3	4	0	2415.21	85	105
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	25	47	380	0.38%	68.3%	RNLDIERPTYTNLNR	99.7%	30.7	25	30.7	1	2	0	1874.98	215	229
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	25	47	380	0.38%	68.3%	RSIQFVDWCPTGFK	99.7%	44.2	25	44.2	1	0	0	1740.85	339	352
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	25	47	380	0.38%	68.3%	SIQFVDWCPTGFK	99.7%	92.8	25	91.3	20	0	0	1584.75	340	352
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	25	47	380	0.38%	68.3%	TIGGGDDSFNTFFSETGAGK	99.7%	108	25	108	24	0	0	2007.89	41	60
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	25	47	380	0.38%	68.3%	VGINYQPPTVVPGGDLAK	99.7%	60.1	25	60.1	18	0	0	1824.99	353	370
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	25	47	380	0.38%	68.3%	YMACCLLYR	99.7%	52.5	25	51.8	21	0	0	1265.55	312	320
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	68.4%	AFVHWYVGEGMEEGEFSEAR	99.7%	87.4	25	87.4	2	7	0	2330.02	403	422
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	68.4%	AFVHWYVGEGMEEGEFSEAREDMAALEK	99.7%	82	25	82	0	4	0	3217.42	403	430
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	68.4%	AVCMLSNTTAVAEAWAR	99.7%	49.3	25	44.8	1	4	0	1850.89	374	390
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	68.4%	AVFVDLEPTVIDEVR	99.7%	116	25	116	38	4	0	1701.91	65	79
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	68.4%	AYHEQLTVAEITNACFEPANQMVK	98.9%	25	25	25	0	4	0	2764.31	281	304
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	68.4%	DVNAAIATIK	99.7%	81.4	25	64.4	15	0	0	1015.58	327	336
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	68.4%	EDMAALEK	99.7%	51.6	25	34.3	4	0	0	906.42	423	430
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	68.4%	EIIDLVLDR	99.7%	79.8	25	73.4	37	0	0	1085.62	113	121
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	68.4%	FDGALNVDLTEFQTNLVPYPR	99.7%	124	25	124	12	1	0	2409.21	244	264
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	68.4%	FDLMYAK	99.7%	48.3	25	28.8	6	0	0	903.43	395	401
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	68.4%	GDVVPKDVNAAIATIK	96.1%	28.1	25	26.8	1	0	0	1610.91	321	336
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	68.4%	IHFPLATYAPVISAEK	99.7%	98.5	25	93.5	8	9	0	1756.96	265	280
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	68.4%	LADQCTGLQGFLVFHSFGGGTGSGFTSLLMER	99.7%	114	25	114	0	24	0	3390.63	125	156
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	68.4%	LDHKFDLMYAK	99.7%	56.8	25	43.6	8	9	0	1380.70	391	401
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	68.4%	LISQIVSSITASLR	99.7%	105	25	105	16	4	0	1487.88	230	243
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	68.4%	LSVDYGKK	99.7%	50.4	25	39	9	0	0	909.50	157	164
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	68.4%	NLDIERPTYTNLNR	99.7%	51.1	25	43.2	13	11	0	1718.88	216	229
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	68.4%	QLFHPEQLITGK	99.7%	36.5	25	0	3	3	0	1410.77	85	96
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	68.4%	QLFHPEQLITGKEDAANNYAR	99.7%	76.6	25	76.6	3	4	0	2415.21	85	105
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	68.4%	RNLDIERPTYTNLNR	99.7%	30.7	25	30.7	1	2	0	1874.98	215	229
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	68.4%	TIGGGDDSFNTFFSETGAGK	99.7%	108	25	108	24	0	0	2007.89	41	60
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	68.4%	TIQFVDWCPTGFK	99.7%	88.4	25	83.6	14	0	0	1598.77	340	352
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	68.4%	VGINYQPPTVVPGGDLAK	99.7%	60.1	25	60.1	18	0	0	1824.99	353	370
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	9	0.01%	68.4%	YMACCLLYR	99.7%	52.5	25	51.8	21	0	0	1265.55	312	320
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	AILVDLEPGTMDSVR	99.7%	90.9	25	88.3	36	0	0	1631.83	63	77
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	ALTVPELTQQVFDAK	99.7%	78	25	78	18	4	0	1659.90	283	297
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	98.8	25	0	0	8	0	3311.53	123	154
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	EIVHIQAGQCGNQIGAK	99.7%	72	25	0	4	4	0	1822.92	3	19
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	EVDEQMLNVQNK	99.7%	88.2	25	87.5	19	0	0	1462.68	325	336
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	FPGQLNADLR	99.7%	58.6	25	45.4	14	0	0	1130.60	242	251

Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	FPGQLNADLRK	99.7%	42.1	25	34.7	7	6	0	1258.69	242	252
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	FWEVISDEHGIDPTGTYHGDSDLQLDR	99.7%	81.4	25	38.3	0	5	0	3102.41	20	46
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	GHYTEGAELVDSVLDVVR	99.7%	147	25	147	4	7	0	1958.98	104	121
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	GHYTEGAELVDSVLDVVRK	99.7%	130	25	111	2	5	0	2087.08	104	122
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	IMNTFSVVPSPK	99.7%	96	25	88	23	0	0	1319.70	163	174
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	IREEYPDR	99.7%	39.2	25	23	7	0	0	1077.53	155	162
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	ISEQFTAMFR	99.7%	85.1	25	76	24	0	0	1229.60	381	390
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	ISVYYNEATGGK	99.7%	83.3	25	83.3	26	0	0	1301.64	47	58
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	KEAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	77.8	25	0	0	2	0	3455.62	122	154
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	KLAVNMVPFPR	99.7%	62.5	25	60.2	6	3	0	1271.73	252	262
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	LAVNMVPFPR	99.7%	79.2	25	68.3	29	0	0	1143.63	253	262
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	LHFFMPGFAPLTSR	99.7%	62.1	25	45.2	16	13	0	1620.84	263	276
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	LTTPTYGDLNHLVSATMSGVTTCLR	99.7%	127	25	127	2	15	0	2708.34	217	241
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	MAVTFIGNSTAIQELFK	99.7%	119	25	112	15	2	0	1885.97	363	379
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	MAVTFIGNSTAIQELFKR	99.7%	115	25	115	7	17	0	2026.08	363	380
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	MREIVHIQAGQCGNQIGAK	99.7%	71.8	25	0	0	10	0	2110.06	1	19
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	MSMKEVDEQMLNVQNK	99.7%	57.2	25	32.7	9	20	0	1955.89	321	336
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	NMMAACDPR	99.7%	55.1	25	55.1	18	0	0	1065.43	298	306
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	NSSYFVEWIPNNVK	99.7%	78.3	25	64.4	15	0	0	1696.83	337	350
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	RISEQFTAMFR	99.7%	57.6	25	51.3	2	2	0	1385.70	380	390
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	SGPFGQIFRPDNFVFGQSGAGNNWAK	99.7%	91.1	25	91.1	2	15	0	2798.34	78	103
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	TAVCDIPPR	99.7%	59	25	49.1	27	0	0	1028.52	351	359
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	99.7%	65.2	25	65.2	0	1	0	4593.11	175	213
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	30	62	479	0.48%	83.1%	YLTVAAVFR	99.7%	78.8	25	74.6	8	0	0	1039.59	310	318
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	AILVDLEPGTMDSVR	99.7%	90.9	25	88.3	36	0	0	1631.83	63	77
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	ALTVPELTQQMFDSK	99.7%	95.8	25	37.9	9	0	0	1707.86	283	297
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	EIVHIQAGQCGNQIGAK	99.7%	72	25	0	4	4	0	1822.92	3	19
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	EVDEQMLNVQNK	99.7%	88.2	25	87.5	19	0	0	1462.68	325	336
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	FPGQLNADLR	99.7%	58.6	25	45.4	14	0	0	1130.60	242	251
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	FPGQLNADLRK	99.7%	42.1	25	34.7	7	6	0	1258.69	242	252
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	GHYTEGAELVDSVLDVVR	99.7%	147	25	147	4	7	0	1958.98	104	121
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	GHYTEGAELVDSVLDVVRK	99.7%	130	25	111	2	5	0	2087.08	104	122
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	IMNTFSVMPSPK	99.7%	88.1	25	77.8	9	0	0	1351.67	163	174
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	INVYYNEATGNK	99.7%	69.2	25	64.8	4	0	0	1385.67	47	58
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	IREEYPDR	99.7%	39.2	25	23	7	0	0	1077.53	155	162
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	ISEQFTAMFR	99.7%	85.1	25	76	24	0	0	1229.60	381	390
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	KLAVNMVPFPR	99.7%	62.5	25	60.2	6	3	0	1271.73	252	262
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	LAVNMVPFPR	99.7%	79.2	25	68.3	29	0	0	1143.63	253	262
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	LHFFMPGFAPLTSR	99.7%	62.1	25	45.2	16	13	0	1620.84	263	276
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	LTTPTYGDLNHLVSATMSGVTTCLR	99.7%	127	25	127	2	15	0	2708.34	217	241
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	MREIVHIQAGQCGNQIGAK	99.7%	71.8	25	0	0	10	0	2110.06	1	19
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	MSATFIGNSTAIQELFK	99.7%	129	25	9.92	9	0	0	1873.94	363	379
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	MSATFIGNSTAIQELFKR	99.7%	63.4	25	8.33	1	8	0	2014.04	363	380
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	MSMKEVDEQMLNVQNK	99.7%	57.2	25	32.7	9	20	0	1955.89	321	336
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	NMMAACDPR	99.7%	55.1	25	55.1	18	0	0	1065.43	298	306
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	NSSYFVEWIPNNVK	99.7%	78.3	25	64.4	15	0	0	1696.83	337	350
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	RISEQFTAMFR	99.7%	57.6	25	51.3	2	2	0	1385.70	380	390
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	SGPFGQIFRPDNFVFGQSGAGNNWAK	99.7%	91.1	25	91.1	2	15	0	2798.34	78	103
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	TAVCDIPPR	99.7%	59	25	49.1	27	0	0	1028.52	351	359
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	99.7%	65.2	25	65.2	0	1	0	4593.11	175	213
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	27	0.03%	69.7%	YLTVAAIFR	99.7%	78.7	25	66.5	5	0	0	1053.61	310	318

Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	6	0.01%	39.3%	AILVDLEPGTMDSVR	99.7%	90.9	25	88.3	36	0	0	1631.83	63	77
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	6	0.01%	39.3%	ALTVPELTQQMFDAK	99.7%	80.2	25	79.1	16	1	0	1691.87	283	297
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	6	0.01%	39.3%	EIVHIQAGQCGNQIGAK	99.7%	72	25	0	4	4	0	1822.92	3	19
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	6	0.01%	39.3%	FPGQLNADLR	99.7%	58.6	25	45.4	14	0	0	1130.60	242	251
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	6	0.01%	39.3%	FPGQLNADLRK	99.7%	42.1	25	34.7	7	6	0	1258.69	242	252
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	6	0.01%	39.3%	GHYTEGAELVDSVLDVVR	99.7%	147	25	147	4	7	0	1958.98	104	121
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	6	0.01%	39.3%	GHYTEGAELVDSVLDVVRK	99.7%	130	25	111	2	5	0	2087.08	104	122
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	6	0.01%	39.3%	IMNTFSVVPSPK	99.7%	96	25	88	23	0	0	1319.70	163	174
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	6	0.01%	39.3%	ISEQFTAMFR	99.7%	85.1	25	76	24	0	0	1229.60	381	390
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	6	0.01%	39.3%	KLAVNMVPFPR	99.7%	62.5	25	60.2	6	3	0	1271.73	252	262
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	6	0.01%	39.3%	LATPTYGDLNHLVSATMSGVTTSLR	99.7%	34.9	25	34.9	0	1	0	2605.33	217	241
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	6	0.01%	39.3%	LAVNMVPFPR	99.7%	79.2	25	68.3	29	0	0	1143.63	253	262
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	6	0.01%	39.3%	MREIVHIQAGQCGNQIGAK	99.7%	71.8	25	0	0	10	0	2110.06	1	19
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	6	0.01%	39.3%	MSSTFIGNSTAIQELFK	99.7%	111	25	0	4	0	0	1873.94	363	379
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	6	0.01%	39.3%	MSSTFIGNSTAIQELFKR	98.9%	33.5	25	0	1	0	0	2030.04	363	380
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	6	0.01%	39.3%	NMMAACDPR	99.7%	55.1	25	55.1	18	0	0	1065.43	298	306
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	6	0.01%	39.3%	NSSYFVEWIPNNVK	99.7%	78.3	25	64.4	15	0	0	1696.83	337	350
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	6	0.01%	39.3%	RISEQFTAMFR	99.7%	57.6	25	51.3	2	2	0	1385.70	380	390
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	ALTVPELTQQMFDAK	99.7%	80.2	25	79.1	16	1	0	1691.87	283	297
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	AVLVDLEPGTMDSVR	99.7%	104	25	89.8	14	0	0	1617.82	63	77
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	98.8	25	0	0	8	0	3311.53	123	154
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	EIVHLQAGQCGNQIGAK	99.7%	72	25	0	4	4	0	1822.92	3	19
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	FPGQLNADLR	99.7%	58.6	25	45.4	14	0	0	1130.60	242	251
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	FPGQLNADLRK	99.7%	42.1	25	34.7	7	6	0	1258.69	242	252
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	FWEVISDEHGIDPTGTYHGDSDLQLER	99.7%	80	25	78.5	0	2	0	3116.42	20	46
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	GHYTEGAELVDAVLDVVR	99.7%	114	25	114	1	2	0	1942.99	104	121
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	IMNTFSVVPSPK	99.7%	96	25	88	23	0	0	1319.70	163	174
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	INVYYNEATGGNYVPR	99.7%	91.7	25	90.4	1	0	0	1829.88	47	62
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	IREEFPDR	97.4%	29.7	25	19.3	1	0	0	1061.54	155	162
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	ISEQFTAMFR	99.7%	85.1	25	76	24	0	0	1229.60	381	390
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	KEAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	77.8	25	0	0	2	0	3455.62	122	154
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	KLAVNMVPFPR	99.7%	62.5	25	60.2	6	3	0	1271.73	252	262
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	LAVNMVPFPR	99.7%	79.2	25	68.3	29	0	0	1143.63	253	262
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	LHFFMPGFAPLTSR	99.7%	62.1	25	45.2	16	13	0	1620.84	263	276
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	LTTPTYGDLNHLVSATMSGVTTCLR	99.7%	127	25	127	2	15	0	2708.34	217	241
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	MAATFIGNSTAIQELFK	99.7%	71.6	25	10.9	6	0	0	1857.94	363	379
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	MAATFIGNSTAIQELFKR	99.7%	85.8	25	1.25	4	0	0	2014.04	363	380
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	MREIVHLQAGQCGNQIGAK	99.7%	71.8	25	0	0	10	0	2110.06	1	19
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	NMMAACDPR	99.7%	55.1	25	55.1	18	0	0	1065.43	298	306
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	NSSYFVEWIPNNVK	99.7%	78.3	25	64.4	15	0	0	1696.83	337	350
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	RISEQFTAMFR	99.7%	57.6	25	51.3	2	2	0	1385.70	380	390
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	SGPFGQIFRPDNFVFGQSGAGNNWAK	99.7%	91.1	25	91.1	2	15	0	2798.34	78	103
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	TAVCDIPPR	99.7%	59	25	49.1	27	0	0	1028.52	351	359
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	99.7%	65.2	25	65.2	0	1	0	4593.11	175	213
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	6	15	0.01%	80.4%	YLTVAAVFR	99.7%	78.8	25	74.6	8	0	0	1039.59	310	318
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	ALTVPELTQQMFDAK	99.7%	80.2	25	79.1	16	1	0	1691.87	283	297
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	AVLVDLEPGTMDSVR	99.7%	104	25	89.8	14	0	0	1617.82	63	77
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	98.8	25	0	0	8	0	3311.53	123	154
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	EIVHLQAGQCGNQIGAK	99.7%	72	25	0	4	4	0	1822.92	3	19
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	EVDEQMLNVQNK	99.7%	88.2	25	87.5	19	0	0	1462.68	325	336
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	FPGQLNADLR	99.7%	58.6	25	45.4	14	0	0	1130.60	242	251

Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	FPGQLNADLRK	99.7%	42.1	25	34.7	7	6	0	1258.69	242	252
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	FWEVISDEHGIDPTGTYHGDSDLQLER	99.7%	80	25	78.5	0	2	0	3116.42	20	46
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	GHYTEGAELVDSVLDVVR	99.7%	147	25	147	4	7	0	1958.98	104	121
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	GHYTEGAELVDSVLDVVRK	99.7%	130	25	111	2	5	0	2087.08	104	122
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	IMNTFSVVPSPK	99.7%	96	25	88	23	0	0	1319.70	163	174
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	INVYYNEATGGK	99.7%	82.3	25	68.3	9	0	0	1328.65	47	58
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	IREEYPDR	99.7%	39.2	25	23	7	0	0	1077.53	155	162
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	ISEQFTAMFR	99.7%	85.1	25	76	24	0	0	1229.60	381	390
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	KEAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	77.8	25	0	0	2	0	3455.62	122	154
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	KLAVNMVPFPR	99.7%	62.5	25	60.2	6	3	0	1271.73	252	262
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	LAVNMVPFPR	99.7%	79.2	25	68.3	29	0	0	1143.63	253	262
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	LHFFMPGFAPLTSR	99.7%	62.1	25	45.2	16	13	0	1620.84	263	276
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	LTTPTYGDLNHLVSATMSGVTTCLR	99.7%	127	25	127	2	15	0	2708.34	217	241
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	MREIVHLQAGQCGNQIGAK	99.7%	71.8	25	0	0	10	0	2110.06	1	19
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	MSATFIGNSTAIQELFK	99.7%	129	25	9.92	9	0	0	1873.94	363	379
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	MSATFIGNSTAIQELFKR	99.7%	63.4	25	8.33	1	8	0	2014.04	363	380
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	MSMKEVDEQMLNVQNK	99.7%	57.2	25	32.7	9	20	0	1955.89	321	336
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	NMMAACDPR	99.7%	55.1	25	55.1	18	0	0	1065.43	298	306
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	NSSYFVEWIPNNVK	99.7%	78.3	25	64.4	15	0	0	1696.83	337	350
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	RISEQFTAMFR	99.7%	57.6	25	51.3	2	2	0	1385.70	380	390
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	SGPFGQIFRPDNFVFGQSGAGNNWAK	99.7%	91.1	25	91.1	2	15	0	2798.34	78	103
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	TAVCDIPPR	99.7%	59	25	49.1	27	0	0	1028.52	351	359
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	99.7%	65.2	25	65.2	0	1	0	4593.11	175	213
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	60	0.06%	82.9%	YLTVAAVFR	99.7%	78.8	25	74.6	8	0	0	1039.59	310	318
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	7	0.01%	46.6%	AALVDLEPGTMDSVR	99.7%	49.2	25	42.3	1	0	0	1589.78	63	77
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	7	0.01%	46.6%	ALTVPELTQQMFDAR	99.7%	53.9	25	53.9	3	0	0	1719.87	283	297
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	7	0.01%	46.6%	FPGQLNADLR	99.7%	58.6	25	45.4	14	0	0	1130.60	242	251
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	7	0.01%	46.6%	FPGQLNADLRK	99.7%	42.1	25	34.7	7	6	0	1258.69	242	252
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	7	0.01%	46.6%	GHYTEGAELVDAVLDVVR	99.7%	114	25	114	1	2	0	1942.99	104	121
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	7	0.01%	46.6%	IMNTFSVMPSPK	99.7%	88.1	25	77.8	9	0	0	1351.67	163	174
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	7	0.01%	46.6%	IREEFPDR	97.4%	29.7	25	19.3	1	0	0	1061.54	155	162
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	7	0.01%	46.6%	KLAVNMVPFPR	99.7%	62.5	25	60.2	6	3	0	1271.73	252	262
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	7	0.01%	46.6%	LAVNMVPFPR	99.7%	79.2	25	68.3	29	0	0	1143.63	253	262
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	7	0.01%	46.6%	LHFFMPGFAPLTSR	99.7%	62.1	25	45.2	16	13	0	1620.84	263	276
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	7	0.01%	46.6%	LTTPTYGDLNHLVSATMSGVTTSLR	99.7%	47.6	25	47.6	0	1	0	2635.34	217	241
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	7	0.01%	46.6%	MASTFIGNSTAIQELFK	99.7%	62.4	25	0.19	7	0	0	1857.94	363	379
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	7	0.01%	46.6%	MASTFIGNSTAIQELFKR	98.9%	33.5	25	0	2	0	0	2030.04	363	380
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	7	0.01%	46.6%	NMMAACDPR	99.7%	55.1	25	55.1	18	0	0	1065.43	298	306
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	7	0.01%	46.6%	NSSYFVEWIPNNVK	99.7%	78.3	25	64.4	15	0	0	1696.83	337	350
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	7	0.01%	46.6%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	99.7%	65.2	25	65.2	0	1	0	4593.11	175	213
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	5	6	10	0.01%	14.0%	AVLLDLEPR	99.6%	38.4	25	34.4	2	0	0	1025.60	64	72
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	5	6	10	0.01%	14.0%	DVFFYQADDEHYIPR	99.7%	68.2	25	68.2	1	0	0	1914.87	49	63
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	5	6	10	0.01%	14.0%	KTTVLDVMR	99.7%	49	25	37.5	2	0	0	1062.60	287	295
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	5	6	10	0.01%	14.0%	LTQNADCVVVLDNTALNR	99.7%	95.1	25	91.7	1	0	0	2016.02	195	212
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	5	6	10	0.01%	14.0%	VIHSILNSPYAK	99.7%	41.3	25	35.7	2	2	0	1341.75	73	84
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	11	12	19	0.02%	10.9%	AAMTSLMDLTLLLAR	99.6%	38	25	15.9	1	0	0	1651.88	874	888
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	11	12	19	0.02%	10.9%	DAAAVLVSR	99.7%	49.5	25	22.9	2	0	0	901.51	205	213
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	11	12	19	0.02%	10.9%	GACSVGTNVR	99.7%	38.5	25	29.5	2	0	0	1020.49	455	464
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	11	12	19	0.02%	10.9%	ILQIAESYLIVSDK	99.7%	81.6	25	81.2	2	0	0	1591.89	189	202
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	11	12	19	0.02%	10.9%	IMCCVAQQASEK	99.7%	47.4	25	47.4	2	0	0	1424.63	902	913
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	11	12	19	0.02%	10.9%	ITQLLGLPTYR	99.7%	38.9	25	38.9	2	0	0	1274.75	969	979

Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	11	12	19	0.02%	10.9%	LDGNLLTQPGQAR	99.7%	49.6	25	42.8	2	0	0	1382.74	170	182
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	11	12	19	0.02%	10.9%	LPESNQTLLR	99.7%	54	25	39.3	1	0	0	1170.65	285	294
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	11	12	19	0.02%	10.9%	LQQVLTGLR	99.7%	61.6	25	40.5	2	0	0	1027.63	791	799
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	11	12	19	0.02%	10.9%	SDVASVNWSAPSQAFPR	99.7%	61.3	25	57.5	1	0	0	1818.88	952	968
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	11	12	19	0.02%	10.9%	VIEQLLVGLK	99.7%	63.3	25	63.3	2	0	0	1111.71	361	370
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	AFCEPGNVENNGVLSFIK	99.7%	78.6	25	70.5	2	0	0	1994.96	248	265
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	AMLESIGVPLEK	99.7%	84.1	25	70.1	4	0	0	1302.70	103	114
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	APWELLELR	99.7%	56.5	25	35.4	4	0	0	1126.63	85	93
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	DFAAEVVHPGDLK	99.7%	63.3	25	38.1	2	0	0	1397.71	298	310
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	EYTLDVYR	99.7%	41.2	25	33.8	2	0	0	1058.52	128	135
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	GTDYQLSK	99.7%	39.8	25	18.2	2	0	0	911.45	120	127
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	GVESQGMLLCASIEGINR	99.7%	93.8	25	84.8	3	1	0	1933.95	433	450
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	HPDADSLYVEK	99.7%	59	25	50.2	2	0	0	1273.61	381	391
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	HVLFPLK	99.3%	35.2	25	32.1	2	0	0	853.53	266	272
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	IDVGEAEPR	99.7%	68.5	25	55.1	3	0	0	985.50	392	400
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	IITVEKHPDADSLYVEK	99.7%	58	25	58	1	2	0	1957.03	375	391
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	ISEECIAQWK	99.7%	69	25	64.8	2	0	0	1263.60	497	506
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	KIFTFAEK	96.2%	28.2	25	24	1	0	0	983.56	190	197
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	KLASAAYPDPSK	99.7%	55.5	25	55.5	2	0	0	1247.66	335	346
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	LASAAYPDPSK	99.7%	75.9	25	64.8	2	0	0	1119.57	336	346
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	LLDPIREK	99.7%	43.3	25	27.4	2	0	0	983.59	320	327
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	LSSVVTQHDSK	99.7%	63.9	25	58.2	2	0	0	1200.62	136	146
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	LSSVVTQHDSKK	99.7%	48.3	25	42.8	2	1	0	1328.72	136	147
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	LVVVLCNLKPQK	99.7%	54.8	25	54.8	2	0	0	1410.85	419	430
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	MSSSEEESKIDLLDR	99.7%	39.1	25	32.9	2	1	0	1754.81	223	237
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	NLQEVLGEEK	99.7%	64.2	25	56.2	2	0	0	1158.60	17	26
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	NLQEVLGEEKLK	99.7%	43.5	25	29.4	2	0	0	1399.78	17	28
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	NSEPEEVIPSR	99.7%	73.3	25	62.4	2	0	0	1256.61	357	367
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	NSVEVALNK	99.7%	75.7	25	52.5	2	0	0	973.53	311	319
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	QVEPLDPPAGSAPGEHVFVK	99.7%	44.1	25	44.1	1	2	0	2074.06	451	470
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	SEFVILRDEK	99.7%	54	25	34.4	2	0	0	1235.66	273	282
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	TVVSGLVQFVPK	99.7%	86.9	25	78.2	2	0	0	1273.75	401	412
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	VDAQFGGIDQR	99.7%	85.7	25	75.9	2	0	0	1205.59	179	189
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	VHLMNPMVPGLTGSK	99.7%	52.9	25	52.9	6	0	0	1580.83	208	222
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	VSYYENVIK	99.7%	47.9	25	46	2	0	0	1114.58	94	102
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	31	40	75	0.07%	59.5%	YLPALGYSK	99.6%	38.3	25	23.4	1	0	0	1011.55	198	206
U1 small nuclear ribonucleoprotein A	SNRPA	SNRPA_HUMAN	31.3	99.8%	2	2	4	0.00%	6.4%	EVSSATNALR	99.7%	75	25	44.2	2	0	0	1047.54	61	70
U1 small nuclear ribonucleoprotein A	SNRPA	SNRPA_HUMAN	31.3	99.8%	2	2	4	0.00%	6.4%	GQAFVIFK	99.7%	44.8	25	36.3	2	0	0	909.52	53	60
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	6	6	11	0.01%	26.7%	GLLQSGQIPGR	99.7%	61	25	23.3	2	0	0	1125.64	222	232
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	6	6	11	0.01%	26.7%	KLDGFPLLR	99.7%	44.6	25	28.4	2	0	0	1058.64	56	64
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	6	6	11	0.01%	26.7%	LTAELIEQAAQYTNAVR	99.7%	60.4	25	60.4	2	0	0	1890.99	4	20
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	6	6	11	0.01%	26.7%	NAIANASTLAEVER	99.7%	96.9	25	96.4	2	0	0	1458.75	206	219
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	6	6	11	0.01%	26.7%	SLTYLSILR	99.7%	57.7	25	34.1	2	0	0	1065.63	114	122
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	6	6	11	0.01%	26.7%	TLLVNNNR	97.3%	29.5	25	19.2	1	0	0	943.53	68	75
U3 small nucleolar RNA-associated protein 15 homolog	UTP15	UTP15_HUMAN	58.4	99.8%	2	2	3	0.00%	3.7%	FLLLQGLVEK	99.7%	53.5	25	48.8	2	0	0	1159.71	463	472
U3 small nucleolar RNA-associated protein 15 homolog	UTP15	UTP15_HUMAN	58.4	99.8%	2	2	3	0.00%	3.7%	LLSGSLDRK	99.4%	35.8	25	0	1	0	0	988.58	263	271
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	19	31	86	0.09%	47.9%	ASEVMGPVEAAPEYR	99.7%	96.5	25	95.2	8	0	0	1605.76	77	91
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	19	31	86	0.09%	47.9%	FPELESLVPNALDYIR	99.7%	72.8	25	72.8	1	0	0	1875.99	122	137
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	19	31	86	0.09%	47.9%	IEEYISK	99.7%	39.2	25	33.6	2	0	0	881.46	67	73
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	19	31	86	0.09%	47.9%	IMGVAGGLTNLSK	99.7%	82.7	25	66.4	8	0	0	1260.70	231	243
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	19	31	86	0.09%	47.9%	IYEYVESR	99.7%	57.7	25	49.5	7	0	0	1058.52	204	211

U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	19	31	86	0.09%	47.9%	LEEACDMALELNASK	99.7%	74.2	25	74.2	4	0	0	1693.78	187	201
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	19	31	86	0.09%	47.9%	LGLTEIR	99.7%	56.6	25	16.5	2	0	0	801.48	366	372
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	19	31	86	0.09%	47.9%	LGLTEIRK	99.7%	61.7	25	47.5	6	0	0	929.58	366	373
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	19	31	86	0.09%	47.9%	MFAEIMMK	99.5%	36.5	25	36.5	4	0	0	1032.46	59	66
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	19	31	86	0.09%	47.9%	MPACNIMLLGAQR	99.7%	89.7	25	75.9	7	0	0	1490.73	244	256
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	19	31	86	0.09%	47.9%	MSFGEIEEDAYQEDLGFSLGHLGK	99.7%	59.4	25	58.3	0	3	0	2688.21	378	401
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	19	31	86	0.09%	47.9%	MSFIAPNLSIIIGASTAAK	99.7%	77.6	25	77.6	4	0	0	1921.05	212	230
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	19	31	86	0.09%	47.9%	QVKPLPAPLDGQR	99.7%	31.3	25	31.3	1	3	0	1418.81	339	351
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	19	31	86	0.09%	47.9%	RFPELESLVPNALDYIR	95.7%	20.9	25	18.5	0	1	0	2032.09	121	137
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	19	31	86	0.09%	47.9%	SSGTASSVAFTPLQGLEIVNPQAAEK	99.7%	69.1	25	69.1	2	3	0	2602.34	445	470
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	19	31	86	0.09%	47.9%	VDSFHESTEGK	99.7%	76.6	25	74.2	5	1	0	1235.55	305	315
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	19	31	86	0.09%	47.9%	VGYELKDEIER	99.7%	78.3	25	54	5	3	0	1350.69	316	326
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	19	31	86	0.09%	47.9%	VIVDANNLTVEIENELNIIHK	99.7%	39.2	25	36.7	0	2	0	2390.29	92	112
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	19	31	86	0.09%	47.9%	YFSSMAEFLK	99.7%	57.8	25	48.6	4	0	0	1238.58	479	488
U4/U6 small nuclear ribonucleoprotein Prp4	PRPF4	PRP4_HUMAN	58.5	99.8%	2	2	4	0.00%	4.8%	ALGEPITLFGEGPAER	99.7%	58.7	25	58.7	2	0	0	1656.86	114	129
U4/U6 small nuclear ribonucleoprotein Prp4	PRPF4	PRP4_HUMAN	58.5	99.8%	2	2	4	0.00%	4.8%	FLGTTCYDR	99.7%	50.7	25	50.6	2	0	0	1132.51	337	345
U4/U6.U5 tri-snRNP-associated protein 1	SART1	SNUT1_HUMAN	90.3	100.0%	7	7	11	0.01%	10.6%	EAAGTTAAAGTGGATEQPPR	99.7%	114	25	114	2	0	0	1813.87	12	31
U4/U6.U5 tri-snRNP-associated protein 1	SART1	SNUT1_HUMAN	90.3	100.0%	7	7	11	0.01%	10.6%	GLAAALLLCQNK	99.7%	58.1	25	49.9	1	0	0	1271.71	637	648
U4/U6.U5 tri-snRNP-associated protein 1	SART1	SNUT1_HUMAN	90.3	100.0%	7	7	11	0.01%	10.6%	IEYVDETGRK	98.6%	32.2	25	22.4	1	0	0	1209.61	710	719
U4/U6.U5 tri-snRNP-associated protein 1	SART1	SNUT1_HUMAN	90.3	100.0%	7	7	11	0.01%	10.6%	LEQGGTADGLR	99.7%	55.8	25	45.7	2	0	0	1116.56	351	361
U4/U6.U5 tri-snRNP-associated protein 1	SART1	SNUT1_HUMAN	90.3	100.0%	7	7	11	0.01%	10.6%	LQAQSLSTVGPR	99.7%	76.7	25	76.7	3	0	0	1256.70	374	385
U4/U6.U5 tri-snRNP-associated protein 1	SART1	SNUT1_HUMAN	90.3	100.0%	7	7	11	0.01%	10.6%	QLQQLQQLR	99.7%	39.7	25	30.3	1	0	0	1154.66	511	519
U4/U6.U5 tri-snRNP-associated protein 1	SART1	SNUT1_HUMAN	90.3	100.0%	7	7	11	0.01%	10.6%	TPYIVLSGSGK	97.0%	29.1	25	20.5	1	0	0	1121.62	781	791
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	AALETDENLLLCAPTGAGK	99.7%	112	25	102	2	0	0	1943.97	491	509
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	ANSNLVLQADR	99.7%	80.5	25	58.5	2	0	0	1200.63	15	25
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	DEPTGEVLSLVGK	99.7%	47.5	25	42.7	1	0	0	1343.71	34	46
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	DIDAFWLQR	99.7%	67.5	25	47.2	2	0	0	1163.58	262	270
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	DILCGAADEVLAVLK	99.7%	106	25	96.9	1	0	0	1586.85	130	144
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	DMCLEKDTLGLFLR	99.7%	63.7	25	63.7	1	0	0	1710.86	740	753
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	EEGWWVVIGDAK	99.7%	58.4	25	42.8	2	0	0	1388.68	2061	2072
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	EGSASTEVLR	99.7%	48.3	25	38	2	0	0	1048.53	754	763
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	FQIMNEIVYEK	99.7%	70.2	25	57.6	4	0	0	1413.71	701	711
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	FYDDAIVSQK	99.7%	61.9	25	53.1	2	0	0	1185.58	275	284
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	GNIIISTPEKWDILSR	99.3%	26.4	25	15.9	0	1	0	1842.01	1422	1437
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	GTQVYSPEK	96.4%	28.4	25	21.7	2	0	0	1008.50	830	838
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	IIYIAPMR	99.7%	42.6	25	33.2	3	0	0	976.56	538	545
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	IVALSSSLSNAK	99.7%	103	25	97.4	2	0	0	1189.68	1487	1498
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	KADEVLEILK	99.7%	53	25	38.9	2	0	0	1157.68	285	294
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	KPVIVFVPSR	99.7%	65.2	25	63	2	0	0	1141.71	1557	1566
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	LELSVHLQPITR	99.7%	29.2	25	21.8	1	2	0	1405.82	1184	1195
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	LIGLSATLPNYEDVATFLR	99.5%	36.6	25	36.6	2	0	0	2093.13	648	666
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	LTAIDILTTCAADIQR	99.7%	111	25	99.8	2	0	0	1774.94	1571	1586
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	LYDLNHNEIGELIR	99.7%	80.1	25	73.8	2	2	0	1698.88	1153	1166
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	MEADPELSK	97.5%	29.9	25	21.4	1	0	0	1019.47	350	358
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	MQLSAELQSDTEEILSK	99.7%	88.8	25	88.8	2	0	0	1921.94	1902	1918
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	MTQNPNYYNLQGISHR	99.3%	26.7	25	26.7	0	2	0	1935.91	1764	1779
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	NALLQLTDSQIADVAR	99.7%	122	25	120	2	0	0	1727.93	1994	2009
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	NIEMTQEDVR	99.7%	49.4	25	31.2	4	0	0	1234.57	638	647
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	NQVLVFVHSR	99.7%	61.9	25	58.4	2	0	0	1198.67	719	728
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	SLVQEMVGSFGK	99.7%	109	25	104	4	0	0	1281.65	546	557
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	SLVQEMVGSFGKR	99.7%	58.4	25	58.4	1	0	0	1437.75	546	558

U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	SNSLISIKR	99.7%	45.8	25	22.1	2	0	0	1017.61	2073	2081
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	SPTLYGISHDDLK	99.5%	36.3	25	36.3	1	0	0	1445.73	932	944
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	TGNFQVTELGR	99.7%	71.6	25	64.5	2	0	0	1221.62	976	986
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	TNLLLQAHLSR	99.7%	71.6	25	71.6	2	0	0	1265.73	1891	1901
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	TYTQLVR	98.7%	32.5	25	17.2	1	0	0	880.49	604	610
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	VELTITPDFQWDEK	99.7%	56.8	25	52.9	2	0	0	1720.84	1200	1213
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	VFSLSSEFK	99.7%	39	25	29.9	2	0	0	1043.54	1017	1025
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	VVLLTGETSTDLK	99.7%	106	25	100	2	0	0	1375.77	1405	1417
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	44	76	0.08%	20.5%	YAQAGFEGFK	99.7%	60.4	25	59.2	2	0	0	1117.53	470	479
Ubiquinol-cytochrome-c reductase complex assembly factor 1	UQCC1	UQCC1_HUMAN	34.6	100.0%	2	3	6	0.01%	7.0%	IIEAMGFTGPLK	99.7%	72.9	25	68.8	4	0	0	1276.70	96	107
Ubiquinol-cytochrome-c reductase complex assembly factor 1	UQCC1	UQCC1_HUMAN	34.6	100.0%	2	3	6	0.01%	7.0%	TDFEEFFLR	99.7%	52	25	47.3	2	0	0	1203.57	128	136
Ubiquitin carboxyl-terminal hydrolase 15	USP15	UBP15_HUMAN	112.4	100.0%	3	3	5	0.00%	3.1%	FSYVTPR	99.5%	37.1	25	31.2	1	0	0	869.45	354	360
Ubiquitin carboxyl-terminal hydrolase 15	USP15	UBP15_HUMAN	112.4	100.0%	3	3	5	0.00%	3.1%	QDTFSGTGFFPLDR	99.7%	50.3	25	49.3	2	0	0	1587.74	933	946
Ubiquitin carboxyl-terminal hydrolase 15	USP15	UBP15_HUMAN	112.4	100.0%	3	3	5	0.00%	3.1%	VEVYLTELK	99.7%	49.6	25	45.9	2	0	0	1093.61	129	137
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	5	5	5	0.00%	2.6%	LEAASSALGGPTLTHAVTR	99.7%	35.2	25	31.1	0	1	0	1851.99	877	895
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	5	5	5	0.00%	2.6%	LVSIPELLSAVK	97.2%	29.4	25	29.4	1	0	0	1268.78	358	369
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	5	5	5	0.00%	2.6%	SSQLNNPQFVWVVPALR	99.7%	59	25	59	1	0	0	1955.05	621	637
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	5	5	5	0.00%	2.6%	VAVATILEK	99.0%	33.5	25	33.5	1	0	0	943.58	2236	2244
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	5	5	5	0.00%	2.6%	VLYNLEVLSSK	99.7%	50.8	25	47.1	1	0	0	1264.71	1174	1184
Ubiquitin carboxyl-terminal hydrolase 7	USP7	UBP7_HUMAN	128.3	99.9%	2	2	2	0.00%	1.5%	HNYEGTLR	98.6%	32.2	25	23.9	1	0	0	989.48	855	862
Ubiquitin carboxyl-terminal hydrolase 7	USP7	UBP7_HUMAN	128.3	99.9%	2	2	2	0.00%	1.5%	SVPLALQR	99.7%	42	25	9.79	1	0	0	883.54	255	262
Ubiquitin conjugation factor E4 A	UBE4A	UBE4A_HUMAN	122.6	99.8%	2	2	3	0.00%	2.6%	DAQQSSSPAADNLR	99.7%	63.9	25	61.4	1	0	0	1459.68	545	558
Ubiquitin conjugation factor E4 A	UBE4A	UBE4A_HUMAN	122.6	99.8%	2	2	3	0.00%	2.6%	IFLITLDNSDPSLK	99.7%	71.6	25	46.8	2	0	0	1575.86	91	104
Ubiquitin conjugation factor E4 B	UBE4B	UBE4B_HUMAN	146.2	99.8%	2	2	3	0.00%	1.7%	ELFEEVISK	99.7%	42.1	25	31.8	2	0	0	1093.58	1181	1189
Ubiquitin conjugation factor E4 B	UBE4B	UBE4B_HUMAN	146.2	99.8%	2	2	3	0.00%	1.7%	YFSGPAITLENTR	99.5%	36.8	25	36.8	1	0	0	1468.74	611	623
Ubiquitin thioesterase OTUB1	OTUB1	OTUB1_HUMAN	31.3	99.8%	2	2	3	0.00%	8.9%	IQQEIAVQNPLVSER	99.7%	48.2	25	33.9	1	0	0	1723.93	37	51
Ubiquitin thioesterase OTUB1	OTUB1	OTUB1_HUMAN	31.3	99.8%	2	2	3	0.00%	8.9%	LLTSGYLQR	99.7%	53.6	25	47.8	2	0	0	1050.59	177	185
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	8	44	0.04%	56.4%	CCLTYCFNKPEDK	99.7%	46.8	25	46.8	4	0	0	1734.73	144	156
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	8	44	0.04%	56.4%	ECPSDECGAGVFMASHFDR	99.6%	38.2	25	38.2	1	1	0	2171.86	120	138
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	8	44	0.04%	56.4%	ESTLHLVLR	99.7%	62.9	25	50.1	2	0	0	1067.62	64	72
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	8	44	0.04%	56.4%	IQDKEGIPPDQQR	99.7%	42.6	25	42.6	2	0	0	1523.78	30	42
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	8	44	0.04%	56.4%	TITLEVEPSDTIENVK	99.7%	98.2	25	93.4	18	0	0	1787.93	12	27
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	8	44	0.04%	56.4%	TLSDYNIQK	99.7%	52.3	25	42.8	12	0	0	1081.55	55	63
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	8	44	0.04%	56.4%	YYKVDENGK	99.7%	39.2	25	25.2	4	0	0	1115.54	105	113
Ubiquitin-like modifier-activating enzyme 1	UBA1	UBA1_HUMAN	117.9	100.0%	5	5	8	0.01%	7.4%	AAVATFLQSVQVPEFTPK	98.8%	32.8	25	32.8	1	0	0	1933.04	785	802
Ubiquitin-like modifier-activating enzyme 1	UBA1	UBA1_HUMAN	117.9	100.0%	5	5	8	0.01%	7.4%	LAGTQPLEVLEAVQR	99.7%	70.1	25	70.1	2	0	0	1623.91	679	693
Ubiquitin-like modifier-activating enzyme 1	UBA1	UBA1_HUMAN	117.9	100.0%	5	5	8	0.01%	7.4%	LQTSSVLVSGLR	99.3%	35.2	25	35	1	0	0	1259.73	70	81
Ubiquitin-like modifier-activating enzyme 1	UBA1	UBA1_HUMAN	117.9	100.0%	5	5	8	0.01%	7.4%	SLVASLAEPDFVVTDFAK	99.7%	43.7	25	43.7	2	0	0	1909.00	305	322
Ubiquitin-like modifier-activating enzyme 1	UBA1	UBA1_HUMAN	117.9	100.0%	5	5	8	0.01%	7.4%	YFLVGAGAIGCELLK	99.7%	57.3	25	55.1	2	0	0	1610.86	471	485
Ubiquitin-protein ligase E3A	UBE3A	UBE3A_HUMAN	100.7	100.0%	6	6	8	0.01%	8.1%	EFVNLYSDYILNK	99.7%	76.5	25	68.3	2	0	0	1617.82	712	724
Ubiquitin-protein ligase E3A	UBE3A	UBE3A_HUMAN	100.7	100.0%	6	6	8	0.01%	8.1%	IGDSSQGDNNLQK	99.7%	40.1	25	38.3	1	0	0	1375.65	214	226
Ubiquitin-protein ligase E3A	UBE3A	UBE3A_HUMAN	100.7	100.0%	6	6	8	0.01%	8.1%	NLGLYYDNR	97.0%	29.1	25	23.4	1	0	0	1127.55	490	498
Ubiquitin-protein ligase E3A	UBE3A	UBE3A_HUMAN	100.7	100.0%	6	6	8	0.01%	8.1%	NLVNDDDAIVAASK	99.7%	59.5	25	53.1	1	0	0	1444.73	360	373
Ubiquitin-protein ligase E3A	UBE3A	UBE3A_HUMAN	100.7	100.0%	6	6	8	0.01%	8.1%	VFSSAEALVQSFR	99.7%	70.2	25	62	2	0	0	1440.75	156	168
Ubiquitin-protein ligase E3A	UBE3A	UBE3A_HUMAN	100.7	100.0%	6	6	8	0.01%	8.1%	VISNEFNSR	99.7%	43.4	25	40.1	1	0	0	1065.53	351	359
Ubiquitin-protein ligase E3C	UBE3C	UBE3C_HUMAN	123.9	100.0%	6	6	9	0.01%	6.1%	LPEFYDETLLR	99.7%	48.4	25	43.8	2	0	0	1395.72	1057	1067
Ubiquitin-protein ligase E3C	UBE3C	UBE3C_HUMAN	123.9	100.0%	6	6	9	0.01%	6.1%	MITGSMVPLLQVISR	99.7%	53.9	25	53.9	1	0	0	1644.92	470	484
Ubiquitin-protein ligase E3C	UBE3C	UBE3C_HUMAN	123.9	100.0%	6	6	9	0.01%	6.1%	NAIIIQSFIR	99.7%	63.8	25	52	2	0	0	1174.69	48	57
Ubiquitin-protein ligase E3C	UBE3C	UBE3C_HUMAN	123.9	100.0%	6	6	9	0.01%	6.1%	SGFNPNQGFFK	99.7%	42.5	25	36.7	1	0	0	1242.59	783	793
Ubiquitin-protein ligase E3C	UBE3C	UBE3C_HUMAN	123.9	100.0%	6	6	9	0.01%	6.1%	SLYLLINSK	99.7%	41.3	25	35.1	1	0	0	1050.62	210	218
Ubiquitin-protein ligase E3C	UBE3C	UBE3C_HUMAN	123.9	100.0%	6	6	9	0.01%	6.1%	VTQLYVPASR	99.7%	55.4	25	47.8	2	0	0	1133.63	639	648

UDP-glucose 6-dehydrogenase	UGDH	UGDH_HUMAN	55.0	99.8%	2	2	4	0.00%	3.9%	IAILGFAFK	99.3%	35.3	25	30	2	0	0	979.60	331	339
UDP-glucose 6-dehydrogenase	UGDH	UGDH_HUMAN	55.0	99.8%	2	2	4	0.00%	3.9%	VTVVDVNESR	99.7%	61.4	25	54.8	2	0	0	1117.58	32	41
UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	OGT	OGT1_HUMAN	116.9	100.0%	3	3	5	0.00%	3.2%	DSGNIPEAIASYR	99.5%	36.4	25	36.4	2	0	0	1392.68	441	453
UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	OGT	OGT1_HUMAN	116.9	100.0%	3	3	5	0.00%	3.2%	IIFSPVAPK	98.1%	30.9	25	15.5	1	0	0	971.59	900	908
UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	OGT	OGT1_HUMAN	116.9	100.0%	3	3	5	0.00%	3.2%	LVSIVADQLEK	99.7%	65.9	25	49.3	2	0	0	1214.70	489	499
Uncharacterized protein C11orf84	C11orf84	CK084_HUMAN	41.0	100.0%	3	3	6	0.01%	12.6%	DREVAEGGLPR	99.7%	54.4	25	40.7	2	0	0	1198.62	295	305
Uncharacterized protein C11orf84	C11orf84	CK084_HUMAN	41.0	100.0%	3	3	6	0.01%	12.6%	MPAEIVVLLDSEDNPSLPK	99.5%	37	25	37	1	0	0	2067.07	171	189
Uncharacterized protein C11orf84	C11orf84	CK084_HUMAN	41.0	100.0%	3	3	6	0.01%	12.6%	SNILEAWSEGVALLQDVR	99.7%	130	25	77.3	3	0	0	2000.04	126	143
Uncharacterized protein C19orf52	C19orf52	CS052_HUMAN	29.2	100.0%	5	5	7	0.01%	24.2%	AEAGDAVVAKPGVWAR	98.3%	31.4	25	31.4	1	0	0	1596.85	15	30
Uncharacterized protein C19orf52	C19orf52	CS052_HUMAN	29.2	100.0%	5	5	7	0.01%	24.2%	ESEAFVQR	99.7%	43.5	25	24.6	1	0	0	965.47	105	112
Uncharacterized protein C19orf52	C19orf52	CS052_HUMAN	29.2	100.0%	5	5	7	0.01%	24.2%	LALSQAHSLVQAEAPR	99.7%	61.3	25	59.5	0	2	0	1690.92	245	260
Uncharacterized protein C19orf52	C19orf52	CS052_HUMAN	29.2	100.0%	5	5	7	0.01%	24.2%	VLDVGFVGR	99.7%	49	25	49	2	0	0	961.55	163	171
Uncharacterized protein C19orf52	C19orf52	CS052_HUMAN	29.2	100.0%	5	5	7	0.01%	24.2%	VVGPQQLHSETNER	99.7%	50.5	25	50.5	1	0	0	1593.80	198	211
Uncharacterized protein C2orf47, mitochondrial	C2orf47	CB047_HUMAN	32.5	100.0%	5	6	10	0.01%	19.9%	EFTQGVKPDWTIAR	99.7%	68.7	25	60.4	2	2	0	1647.85	270	283
Uncharacterized protein C2orf47, mitochondrial	C2orf47	CB047_HUMAN	32.5	100.0%	5	6	10	0.01%	19.9%	FDLLEELVAK	99.7%	56.2	25	46	2	0	0	1176.65	164	173
Uncharacterized protein C2orf47, mitochondrial	C2orf47	CB047_HUMAN	32.5	100.0%	5	6	10	0.01%	19.9%	MIVLGFSNPINWVR	99.7%	57.2	25	57.2	1	0	0	1645.89	110	123
Uncharacterized protein C2orf47, mitochondrial	C2orf47	CB047_HUMAN	32.5	100.0%	5	6	10	0.01%	19.9%	QLLSASYEFQR	99.7%	63.1	25	61.3	2	0	0	1341.68	259	269
Uncharacterized protein C2orf47, mitochondrial	C2orf47	CB047_HUMAN	32.5	100.0%	5	6	10	0.01%	19.9%	VTSLPDNHK	97.5%	29.9	25	24.4	1	0	0	1010.53	183	191
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	8	8	12	0.01%	8.6%	EQLLQSNPVLEAFGNAK	99.7%	91.4	25	91.4	2	0	0	1857.97	140	156
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	8	8	12	0.01%	8.6%	IFLLTNNNLLLADQK	99.7%	97.2	25	97.2	2	0	0	1729.98	1007	1021
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	8	8	12	0.01%	8.6%	IIIAEVVNK	99.7%	54.2	25	42.4	2	0	0	998.62	987	995
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	8	8	12	0.01%	8.6%	LVMSYVAAVCGK	99.7%	46.3	25	46.3	1	0	0	1297.66	120	131
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	8	8	12	0.01%	8.6%	SEVPLVDVTK	99.7%	48.8	25	42.6	2	0	0	1086.60	1027	1036
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	8	8	12	0.01%	8.6%	SSALVIQSYIR	99.7%	71.5	25	59.3	1	0	0	1236.69	752	762
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	8	8	12	0.01%	8.6%	VSTTLNVAQAYYAR	99.7%	68.7	25	66.8	1	0	0	1556.81	336	349
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	8	8	12	0.01%	8.6%	YNYLSLDSAK	99.7%	40.7	25	35.4	1	0	0	1173.58	232	241
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	13	13	22	0.02%	15.9%	DGTIDFTPGSELLITK	99.7%	64.9	25	63.3	2	0	0	1706.89	1032	1047
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	13	13	22	0.02%	15.9%	GEELLSPLNLEQAAYAR	99.7%	67.7	25	59.5	2	0	0	1873.97	362	378
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	13	13	22	0.02%	15.9%	KYEAFLQR	99.7%	43.3	25	37.4	2	0	0	1054.57	667	674
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	13	13	22	0.02%	15.9%	LGTDEISPR	99.7%	83.5	25	65.8	2	0	0	987.51	901	909
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	13	13	22	0.02%	15.9%	LLQFYAETCPAPER	99.7%	76.2	25	59.7	2	0	0	1694.82	153	166
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	13	13	22	0.02%	15.9%	LLQSNPVLEAFGNAK	99.7%	61.1	25	61.1	2	0	0	1600.87	174	188
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	13	13	22	0.02%	15.9%	NPQSYLYLVK	95.5%	27.5	25	26.5	1	0	0	1224.66	260	269
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	13	13	22	0.02%	15.9%	QLLLTPNAVVIVEDAK	99.7%	40.1	25	39.1	2	0	0	1723.00	939	954
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	13	13	22	0.02%	15.9%	SAICIQSWWR	99.6%	37.7	25	30.1	1	0	0	1306.64	760	769
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	13	13	22	0.02%	15.9%	TSFLLNLR	99.7%	64.2	25	60.2	2	0	0	963.56	814	821
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	13	13	22	0.02%	15.9%	VLQALGSEPIQYAVPVVK	99.7%	39.4	25	39.4	1	0	0	1911.10	910	927
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	13	13	22	0.02%	15.9%	VNSININQGSITFAGGPGR	99.7%	65.6	25	65.6	1	0	0	1901.98	1013	1031
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	13	13	22	0.02%	15.9%	YLGLLENLR	99.7%	51.2	25	48	2	0	0	1090.63	648	656
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	5	5	7	0.01%	5.1%	NYDTTIHGK	96.8%	28.9	25	27.9	1	0	0	1048.51	367	375
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	5	5	7	0.01%	5.1%	SYIHEVAR	99.7%	41.2	25	33	2	0	0	974.51	738	745
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	5	5	7	0.01%	5.1%	TLFTLEELR	99.2%	34.6	25	27.6	2	0	0	1121.62	686	694
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	5	5	7	0.01%	5.1%	VTDEMFLEALNSK	94.6%	26.9	25	22.1	1	0	0	1496.73	466	478
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	5	5	7	0.01%	5.1%	VVSIIAELLSTK	99.7%	72.7	25	72.7	1	0	0	1272.78	296	307
Unconventional myosin-Ie	MYO1E	MYO1E_HUMAN	127.1	99.8%	2	2	3	0.00%	1.9%	VFDFLVDSINK	99.7%	47.9	25	47.9	2	0	0	1296.68	363	373
Unconventional myosin-Ie	MYO1E	MYO1E_HUMAN	127.1	99.8%	2	2	3	0.00%	1.9%	VPDQGAAGVR	97.0%	29.1	25	19.9	1	0	0	969.51	1020	1029
Unconventional myosin-Vb	MYO5B	MYO5B_HUMAN	213.7	100.0%	3	3	4	0.00%	1.8%	ILNLYTPLNEFEER	99.7%	52.1	25	49.5	2	0	0	1750.90	1775	1788
Unconventional myosin-Vb	MYO5B	MYO5B_HUMAN	213.7	100.0%	3	3	4	0.00%	1.8%	TIQAQLQER	99.4%	35.9	25	24.5	1	0	0	1086.59	1796	1804
Unconventional myosin-Vb	MYO5B	MYO5B_HUMAN	213.7	100.0%	3	3	4	0.00%	1.8%	YNISQLEEWLR	99.5%	36.7	25	25.8	1	0	0	1450.73	1714	1724
Unhealthy ribosome biogenesis protein 2 homolog	URB2	URB2_HUMAN	170.5	100.0%	3	3	4	0.00%	2.6%	ACPQIVTALTLLNR	99.4%	36	25	36	1	0	0	1569.88	1293	1306
Unhealthy ribosome biogenesis protein 2 homolog	URB2	URB2_HUMAN	170.5	100.0%	3	3	4	0.00%	2.6%	ADVQAVVSAVTLLR	99.7%	57.5	25	46.5	2	0	0	1441.84	1262	1275

Unhealthy ribosome biogenesis protein 2 homolog	URB2	URB2_HUMAN	170.5	100.0%	3	3	4	0.00%	2.6%	GEIAQNLLSLVK	99.7%	39.1	25	32.7	1	0	0	1284.75	868	879
UPF0420 protein C16orf58	C16orf58	CP058_HUMAN	51.0	99.9%	2	2	2	0.00%	3.6%	AALTVHQAR	99.7%	43.2	25	43.2	1	0	0	966.55	212	220
UPF0420 protein C16orf58	C16orf58	CP058_HUMAN	51.0	99.9%	2	2	2	0.00%	3.6%	KESWVVVK	97.7%	30.1	25	29.1	1	0	0	974.57	414	421
UPF0488 protein C8orf33	C8orf33	CH033_HUMAN	25.0	100.0%	2	2	5	0.00%	10.9%	AAAYSAQVQPVDGATR	99.7%	48.6	25	47	1	0	0	1604.80	183	198
UPF0488 protein C8orf33	C8orf33	CH033_HUMAN	25.0	100.0%	2	2	5	0.00%	10.9%	LPGPVSSAR	99.7%	52.4	25	21.6	4	0	0	883.50	28	36
UPF0668 protein C10orf76	C10orf76	CJ076_HUMAN	78.7	99.8%	2	2	2	0.00%	3.3%	LQDGLDQYER	97.1%	29.3	25	29.3	1	0	0	1236.59	636	645
UPF0668 protein C10orf76	C10orf76	CJ076_HUMAN	78.7	99.8%	2	2	2	0.00%	3.3%	VVNALQTLCALIR	99.7%	38.5	25	34.2	1	0	0	1470.85	97	109
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	15	0.01%	21.0%	AALGPLVTGLYDVQAFK	99.7%	89.8	25	89.8	2	0	0	1762.97	6	22
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	15	0.01%	21.0%	AAWEAYLSR	99.7%	49.3	25	25.2	2	0	0	1066.53	469	477
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	15	0.01%	21.0%	FADIGNTVK	99.4%	35.8	25	27.4	1	0	0	964.51	315	323
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	15	0.01%	21.0%	FGDFVLK	99.7%	38.8	25	28.6	2	0	0	825.45	23	29
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	15	0.01%	21.0%	IASWADLVNAHVVPGSGVVK	99.7%	52.6	25	52.6	0	2	0	2019.10	333	352
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	15	0.01%	21.0%	KVDAETVGR	99.7%	58.5	25	44.5	2	0	0	974.53	188	196
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	15	0.01%	21.0%	LHSVCTLSK	97.9%	30.6	25	27.6	1	0	0	1044.55	170	178
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	15	0.01%	21.0%	MLEILEQQK	99.7%	44.5	25	32.3	1	0	0	1131.61	179	187
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	15	0.01%	21.0%	SGLSSPIYIDLR	99.7%	64.6	25	49.8	2	0	0	1320.72	30	41
Uridine-cytidine kinase 2	UCK2	UCK2_HUMAN	29.3	100.0%	5	5	9	0.01%	21.8%	IVQLLGQNEVDYR	99.7%	77.6	25	73.3	1	0	0	1546.82	40	52
Uridine-cytidine kinase 2	UCK2	UCK2_HUMAN	29.3	100.0%	5	5	9	0.01%	21.8%	LFVDTDADTR	99.7%	47.6	25	43.6	2	0	0	1152.55	153	162
Uridine-cytidine kinase 2	UCK2	UCK2_HUMAN	29.3	100.0%	5	5	9	0.01%	21.8%	QVVILSQDSFYR	99.7%	78.2	25	69.4	2	0	0	1454.76	55	66
Uridine-cytidine kinase 2	UCK2	UCK2_HUMAN	29.3	100.0%	5	5	9	0.01%	21.8%	TVQIPVYDFVSHSR	99.7%	58.9	25	56.9	2	0	0	1647.85	106	119
Uridine-cytidine kinase 2	UCK2	UCK2_HUMAN	29.3	100.0%	5	5	9	0.01%	21.8%	YADVIIPR	99.7%	44.5	25	35.2	2	0	0	946.54	203	210
Uridine-cytidine kinase-like 1	UCKL1	UCKL1_HUMAN	61.1	100.0%	3	3	3	0.00%	6.9%	ADADPSPTSPPTAR	99.2%	34.5	25	29.2	1	0	0	1382.65	8	21
Uridine-cytidine kinase-like 1	UCKL1	UCKL1_HUMAN	61.1	100.0%	3	3	3	0.00%	6.9%	EAFAIGLGGGSASGK	99.7%	73.8	25	64.9	1	0	0	1321.67	97	111
Uridine-cytidine kinase-like 1	UCKL1	UCKL1_HUMAN	61.1	100.0%	3	3	3	0.00%	6.9%	IITTAVDKR	95.6%	27.7	25	26.9	1	0	0	1016.61	503	511
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	6	7	12	0.01%	24.2%	EITGIGPSTTTETETIAK	99.7%	77.9	25	77.9	2	0	0	1848.94	215	232
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	6	7	12	0.01%	24.2%	ELALPGELTQSR	99.7%	82.4	25	74.3	2	0	0	1313.71	94	105
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	6	7	12	0.01%	24.2%	FESPESQASAEQPEM	99.7%	40.5	25	40.5	1	0	0	1682.69	313	327
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	6	7	12	0.01%	24.2%	HYLFYDGESVSGK	99.7%	63	25	61.8	2	0	0	1501.70	39	51
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	6	7	12	0.01%	24.2%	LFLAGYDPTPTMR	99.7%	69	25	64.6	4	0	0	1497.74	250	262
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	6	7	12	0.01%	24.2%	QQEIILWR	99.0%	33.5	25	21.1	1	0	0	1085.61	289	296
Vacuolar protein sorting-associated protein 29	VPS29	VPS29_HUMAN	20.5	100.0%	3	3	5	0.00%	17.0%	GDFDENLNYPEQK	99.7%	39.2	25	39.2	2	0	0	1568.69	61	73
Vacuolar protein sorting-associated protein 29	VPS29	VPS29_HUMAN	20.5	100.0%	3	3	5	0.00%	17.0%	TLAGDVHIVR	99.7%	68.3	25	59.6	2	0	0	1080.62	51	60
Vacuolar protein sorting-associated protein 29	VPS29	VPS29_HUMAN	20.5	100.0%	3	3	5	0.00%	17.0%	VVTVGQFK	99.7%	43.4	25	36.4	1	0	0	877.51	74	81
Vacuolar protein sorting-associated protein 33B	VPS33B	VP33B_HUMAN	70.6	100.0%	3	3	6	0.01%	5.0%	FIFLTTAVTNSAR	99.7%	55.9	25	54.9	2	0	0	1440.78	595	607
Vacuolar protein sorting-associated protein 33B	VPS33B	VP33B_HUMAN	70.6	100.0%	3	3	6	0.01%	5.0%	IIEQVLER	98.7%	32.4	25	14.6	2	0	0	999.58	524	531
Vacuolar protein sorting-associated protein 33B	VPS33B	VP33B_HUMAN	70.6	100.0%	3	3	6	0.01%	5.0%	ITDAFSSLAK	98.1%	31	25	20.5	2	0	0	1052.56	471	480
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	7	7	15	0.01%	11.1%	AELAELPLR	99.7%	41.3	25	32	2	0	0	1011.58	574	582
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	7	7	15	0.01%	11.1%	ILVGTNLVR	99.7%	67.4	25	49.4	2	0	0	984.62	218	226
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	7	7	15	0.01%	11.1%	IPVDTYNNILTVLK	99.7%	77.3	25	72.6	4	0	0	1602.91	404	417
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	7	7	15	0.01%	11.1%	LFDIFSQQVATVIQSR	99.7%	76	25	68.1	2	0	0	1852.00	324	339
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	7	7	15	0.01%	11.1%	LNLEHIATSSAVSK	99.7%	54.9	25	54.9	1	0	0	1469.80	383	396
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	7	7	15	0.01%	11.1%	LSQLEGVNVER	99.7%	58.7	25	46.6	2	0	0	1243.66	227	237
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	7	7	15	0.01%	11.1%	SEDPDQQYLILNTAR	99.7%	94.4	25	87.2	2	0	0	1762.86	500	514
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	11	11	16	0.02%	9.0%	ADYNLTR	99.7%	39.4	25	26	1	0	0	852.42	1123	1129
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	11	11	16	0.02%	9.0%	ALSPLEEWLR	97.5%	29.9	25	22.6	2	0	0	1213.66	138	147
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	11	11	16	0.02%	9.0%	DINLDVNR	97.1%	29.2	25	0	1	0	0	958.50	935	942
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	11	11	16	0.02%	9.0%	DVSGPMPDSYSPR	99.7%	41.7	25	41.7	1	0	0	1407.62	291	303
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	11	11	16	0.02%	9.0%	EAFLQEVWK	99.7%	38.6	25	26	1	0	0	1149.59	410	418
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	11	11	16	0.02%	9.0%	KVDEAIALFQK	99.7%	67.2	25	64.4	1	0	0	1261.72	1252	1262
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	11	11	16	0.02%	9.0%	LHEEGIIYR	97.8%	30.5	25	25.2	1	0	0	1129.60	462	470
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	11	11	16	0.02%	9.0%	LQQTEAELR	99.7%	54.4	25	43.3	2	0	0	1087.57	1243	1251

Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	11	11	16	0.02%	9.0%	LSAAVTEAFVR	99.7%	95.2	25	87.8	2	0	0	1163.64	451	461
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	11	11	16	0.02%	9.0%	SSAQDPQAVLGALGR	99.7%	76.3	25	76.3	2	0	0	1469.77	123	137
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	11	11	16	0.02%	9.0%	VPLEVQEADEAK	99.7%	68.3	25	61.8	2	0	0	1327.67	1231	1242
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	6	7	14	0.01%	11.6%	FSFTLPYPVK	99.7%	42.5	25	38.8	2	0	0	1198.65	310	319
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	6	7	14	0.01%	11.6%	LESEGSPETLTNLR	99.7%	102	25	95	3	0	0	1545.78	133	146
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	6	7	14	0.01%	11.6%	LESEGSPETLTNLRK	99.7%	60.2	25	51.5	1	0	0	1673.87	133	147
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	6	7	14	0.01%	11.6%	LRLESEGSPETLTNLR	99.7%	81	25	74.7	2	2	0	1814.96	131	146
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	6	7	14	0.01%	11.6%	QVNITVQK	99.1%	34.2	25	23.9	2	0	0	929.54	77	84
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	6	7	14	0.01%	11.6%	VSQWWER	99.7%	47.6	25	33.8	2	0	0	990.48	86	92
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	4	4	15	0.01%	12.3%	LLETLFVHR	99.7%	56.1	25	36	4	0	0	1127.66	142	150
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	4	4	15	0.01%	12.3%	LPVGTTATLYFR	99.7%	73.1	25	69.5	4	0	0	1338.74	68	79
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	4	4	15	0.01%	12.3%	SLKDEDVLQK	99.7%	50.1	25	42.8	4	0	0	1174.63	58	67
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	4	4	15	0.01%	12.3%	YDFTSSR	97.0%	29.1	25	24.8	3	0	0	875.39	117	123
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	37	0.04%	25.0%	AENSSLNLIGK	99.7%	95	25	74.6	2	0	0	1145.62	188	198
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	37	0.04%	25.0%	GILLYGPPGCGK	99.7%	38.7	25	26.5	2	0	0	1231.65	255	266
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	37	0.04%	25.0%	GSMAGSTGVHDTVVNQLLSK	99.7%	36.1	25	34.2	0	1	0	2001.01	338	357
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	37	0.04%	25.0%	IAEESNFPFIK	99.7%	40	25	26.6	2	0	0	1294.67	556	566
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	37	0.04%	25.0%	KLLIIGTTSR	99.7%	46.8	25	38.8	2	0	0	1101.70	639	648
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	37	0.04%	25.0%	LLDYVPIGPR	99.7%	57.3	25	56	2	0	0	1142.66	608	617
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	37	0.04%	25.0%	LLIIGTTSR	99.7%	55.1	25	47.9	2	0	0	973.60	640	648
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	37	0.04%	25.0%	LQILHIHTAR	99.7%	47.3	25	31.6	2	1	0	1201.72	404	413
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	37	0.04%	25.0%	NFSGAELEGLVR	99.7%	79.1	25	59.4	2	0	0	1291.66	435	446
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	37	0.04%	25.0%	QSIINPDWNFEK	99.7%	60.8	25	55.7	2	0	0	1490.73	206	217
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	37	0.04%	25.0%	SQLSCVVVDDIER	99.7%	91.6	25	84.9	2	0	0	1519.74	595	607
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	37	0.04%	25.0%	TPLVSVLLEGPPHSGK	99.7%	42.9	25	42.9	2	2	0	1630.92	534	549
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	37	0.04%	25.0%	VEVDMEKAESLQVTR	99.3%	26.8	25	21.9	0	1	0	1733.87	463	477
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	37	0.04%	25.0%	VLDDGELLVQQTK	99.7%	85	25	85	4	0	0	1457.78	517	529
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	37	0.04%	25.0%	VVNGPEILNK	99.6%	38.3	25	32.2	2	0	0	1082.62	284	293
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	37	0.04%	25.0%	YVGESEANIR	99.7%	45.7	25	37.9	2	0	0	1137.55	294	303
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	37	0.04%	25.0%	YVGESEANIRK	99.7%	45.5	25	30.8	2	0	0	1265.65	294	304
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	DGQVINETSQHHDDLE	99.7%	61	25	61	5	2	0	1836.80	451	466
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	DNLAEDIMR	99.7%	60.1	25	53.7	4	0	0	1076.50	176	184
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	EEAENTLQSFR	99.7%	61	25	52.6	3	0	0	1323.62	197	207
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	EEAENTLQSFRQDVDNASLAR	99.7%	52.1	25	52.1	0	2	0	2393.13	197	217
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	EKLQEEMLQR	99.7%	50	25	39.2	4	0	0	1319.66	187	196
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	EMEENFAVEAANYQDTIGR	99.7%	127	25	127	8	3	0	2202.96	346	364
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	ETNLDSLPLVDTHSK	99.7%	47.8	25	46.1	2	2	0	1668.84	425	439
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	ETNLDSLPLVDTHSKR	99.7%	43.3	25	41	2	2	0	1824.95	425	440
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	EYQDLLNVK	99.7%	54.4	25	47	8	0	0	1121.58	382	390
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	FADLSEAANR	99.7%	74.5	25	60.7	5	0	0	1093.53	295	304
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	FADLSEAANRNNDALR	99.7%	34.2	25	32	0	1	0	1776.86	295	310
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	FANYIDK	97.9%	30.6	25	21.6	1	0	0	870.44	114	120
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	FANYIDKVR	99.7%	72.7	25	66.1	4	0	0	1125.61	114	122
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	FLEQQNK	97.3%	29.5	25	0	1	0	0	906.47	123	129
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	HLREYQDLLNVK	99.7%	33.5	25	24.2	0	1	0	1527.83	379	390
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	ILLAELEQLK	99.7%	67.9	25	60.6	7	0	0	1169.71	130	139
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	ILLAELEQLKGQGK	99.7%	58.9	25	52	4	4	0	1539.91	130	143
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	ISLPLPNFSSLNLR	99.7%	80.5	25	74.2	7	0	0	1570.90	411	424
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	KLLEGEESR	99.7%	62.4	25	42.4	4	0	0	1060.56	402	410
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	KVESLQEEIAFLK	99.7%	108	25	104	4	2	0	1533.85	223	235
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	LGDLYEEEMR	99.7%	63.2	25	61.3	6	0	0	1254.57	146	155

Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	LLEGEESR	99.7%	39.9	25	29.9	6	0	0	932.47	403	410
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	LLQDSVDFSLADAINTEFK	99.7%	110	25	106	19	7	0	2126.07	79	97
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	LQDEIQNMK	99.7%	52.8	25	49.5	4	0	0	1118.55	365	373
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	LQDEIQNMKEEMAR	99.7%	90.2	25	78.7	11	8	0	1734.82	365	378
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	LQEEMLQR	99.7%	44.7	25	29.8	4	0	0	1046.53	189	196
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	LQEEMLQREEAENTLQSFR	99.7%	68.6	25	68.6	2	4	0	2351.13	189	207
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	MALDIEIATYR	99.7%	93.5	25	34	4	0	0	1295.67	391	401
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	MALDIEIATYRK	99.7%	36.7	25	25.6	0	2	0	1423.76	391	402
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	MFGGPGTASRPSSSR	99.7%	40.5	25	36.4	2	4	0	1510.71	14	28
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	NLQEAEEWYK	99.7%	59.7	25	59.7	5	0	0	1309.61	283	292
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	QDVDNASLAR	99.7%	80.7	25	63.7	8	0	0	1088.53	208	217
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	QMREMEENFAVEAANYQDTIGR	99.7%	65.1	25	65.1	0	2	0	2634.16	343	364
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	QQYESVAAK	99.7%	60.5	25	46.6	4	0	0	1023.51	274	282
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	QVDQLTNDK	99.7%	59.7	25	29	2	0	0	1060.53	160	168
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	QVDQLTNDKAR	99.7%	56.9	25	40	4	2	0	1287.67	160	170
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	QVQSLTCEVDALK	99.7%	73	25	60.3	3	0	0	1490.75	322	334
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	QVQSLTCEVDALKGTNESLER	99.7%	77.8	25	77.8	2	3	0	2377.17	322	342
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	RQVDQLTNDK	99.7%	48.8	25	40.5	2	0	0	1216.63	159	168
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	SLYASSPGGVYATR	99.7%	114	25	114	11	0	0	1428.71	51	64
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	SRLGDLYEEEMR	96.5%	21.6	25	15.9	0	1	0	1497.70	144	155
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	SYVTTSTR	99.7%	46	25	39.9	2	0	0	914.46	29	36
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	TNEKVELQELNDR	99.7%	61.3	25	54.5	4	2	0	1587.80	101	113
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	TYSLGSALRPSTSR	99.7%	37	25	34.9	2	2	0	1495.79	37	50
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	VELQELNDR	99.7%	62.3	25	55.4	3	0	0	1115.57	105	113
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	46	77	250	0.25%	78.3%	VEVERDNLAEDIMR	99.7%	47.8	25	43.2	5	6	0	1704.82	171	184
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	6	7	14	0.01%	25.8%	GYGFGLIK	97.4%	29.6	25	24.9	1	0	0	854.48	21	28
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	6	7	14	0.01%	25.8%	KLETAVNLAWTAGNSNTR	99.7%	37.4	25	37.4	0	2	0	1946.01	201	218
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	6	7	14	0.01%	25.8%	LTFDSSFSPNTGK	99.7%	82.6	25	72.2	2	0	0	1400.67	97	109
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	6	7	14	0.01%	25.8%	LTFDSSFSPNTGKK	99.7%	82.7	25	77.2	3	1	0	1528.76	97	110
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	6	7	14	0.01%	25.8%	LTLSALLDGK	99.7%	83.5	25	0	13	0	0	1030.61	257	266
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	6	7	14	0.01%	25.8%	VTQSNFAVGYK	99.7%	72.5	25	65.2	2	0	0	1213.62	164	174
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	6	7	14	0.01%	25.8%	YQIDPDACFSAK	99.7%	66	25	64.8	3	0	0	1414.63	225	236
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	10	11	41	0.04%	42.5%	GFGFGLVK	98.7%	32.5	25	27.3	2	0	0	824.47	32	39
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	10	11	41	0.04%	42.5%	LTFDTTFSPNTGK	99.7%	110	25	92.8	4	0	0	1428.70	108	120
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	10	11	41	0.04%	42.5%	LTFDTTFSPNTGKK	99.7%	72	25	72	5	0	0	1556.80	108	121
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	10	11	41	0.04%	42.5%	LTLSALVDGK	99.7%	83.4	25	73.7	7	0	0	1016.60	268	277
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	10	11	41	0.04%	42.5%	NNFAVGYR	99.7%	52.8	25	46.6	4	0	0	940.46	178	185
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	10	11	41	0.04%	42.5%	SCSGVEFSTSGSSNTDTGK	99.7%	122	25	122	6	0	0	1907.79	46	64
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	10	11	41	0.04%	42.5%	TGDFQLHTNVNDGTEFGGSIYQK	99.7%	30.9	25	30.9	0	1	0	2528.17	186	208
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	10	11	41	0.04%	42.5%	VNNSSLIGVGYTQTLRPGVK	99.7%	98	25	98	3	3	0	2103.16	248	267
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	10	11	41	0.04%	42.5%	WCEYGLTFTEK	99.7%	55	25	55	2	0	0	1433.64	75	85
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	10	11	41	0.04%	42.5%	YQLDPTASISAK	99.7%	68.3	25	55.9	4	0	0	1293.67	236	247
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	13	47	0.05%	41.7%	GYGFGMVK	98.7%	32.5	25	21.4	2	0	0	874.41	21	28
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	13	47	0.05%	41.7%	IETSINLAWTAGSNNTR	99.7%	95.4	25	87.5	4	0	0	1847.92	202	218
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	13	47	0.05%	41.7%	LSQNNFALGYK	99.7%	69.4	25	61	6	0	0	1254.65	164	174
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	13	47	0.05%	41.7%	LTLDTIFVPNTGK	99.7%	83.8	25	83.8	5	0	0	1418.79	97	109
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	13	47	0.05%	41.7%	LTLDTIFVPNTGKK	99.7%	44	25	41.2	2	2	0	1546.88	97	110
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	13	47	0.05%	41.7%	LTLSALIDGK	99.7%	83.5	25	0	13	0	0	1030.61	257	266
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	13	47	0.05%	41.7%	SCSGVEFSTSGHAYTDTGK	99.7%	80.5	25	80.5	3	0	0	1990.84	35	53
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	13	47	0.05%	41.7%	VCNYGLTFTQK	99.7%	70.7	25	60.7	4	0	0	1330.65	64	74
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	13	47	0.05%	41.7%	VNNASLIGLGYTQTLRPGVK	99.7%	82.9	25	82.9	2	1	0	2101.18	237	256

Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	13	47	0.05%	41.7%	YKVCNYGLTFTQK	99.7%	48.6	25	48.6	2	0	0	1621.80	62	74
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	13	47	0.05%	41.7%	YMLDCR	96.2%	28.2	25	21.9	1	0	0	873.36	225	230
V-type proton ATPase 116 kDa subunit a isoform 1	ATP6V0A1	VPP1_HUMAN	96.4	99.8%	2	2	4	0.00%	2.8%	LGFVAGVINR	99.7%	68.5	25	59.8	3	0	0	1045.62	168	177
V-type proton ATPase 116 kDa subunit a isoform 1	ATP6V0A1	VPP1_HUMAN	96.4	99.8%	2	2	4	0.00%	2.8%	SVFIIFFQGDQLK	99.5%	37	25	25.8	1	0	0	1541.84	218	230
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	6	7	11	0.01%	10.9%	FTMVQVWPVR	99.7%	50	25	50	2	0	0	1262.67	203	212
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	6	7	11	0.01%	10.9%	GVNVSALSR	99.7%	61.6	25	45.6	2	0	0	902.51	121	129
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	6	7	11	0.01%	10.9%	LPANHPLLTGQR	99.0%	25.4	25	24.4	0	2	0	1316.74	221	232
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	6	7	11	0.01%	10.9%	TALVANTSNMPVAAR	99.7%	74.2	25	66.2	2	0	0	1515.79	309	323
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	6	7	11	0.01%	10.9%	TVISQSLSK	99.2%	34.9	25	19.7	1	0	0	962.55	257	265
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	6	7	11	0.01%	10.9%	VGHSELVGEIIR	99.7%	48.5	25	44.6	1	1	0	1308.73	45	56
V-type proton ATPase subunit d 1	ATP6V0D1	VA0D1_HUMAN	40.3	100.0%	3	3	6	0.01%	9.4%	LYPEGLAQLAR	99.7%	46.6	25	35.1	2	0	0	1230.68	247	257
V-type proton ATPase subunit d 1	ATP6V0D1	VA0D1_HUMAN	40.3	100.0%	3	3	6	0.01%	9.4%	NIVWIAECIAQR	99.7%	58.4	25	58.4	2	0	0	1472.77	328	339
V-type proton ATPase subunit d 1	ATP6V0D1	VA0D1_HUMAN	40.3	100.0%	3	3	6	0.01%	9.4%	NVADYYPEYK	99.2%	34.8	25	34.8	2	0	0	1261.57	266	275
V-type proton ATPase subunit H	ATP6V1H	VATH_HUMAN	55.9	100.0%	5	5	7	0.01%	14.5%	LLEVSDDPQVLAVAAHDVGEYVR	99.7%	29.6	25	29.6	0	1	0	2495.28	397	419
V-type proton ATPase subunit H	ATP6V1H	VATH_HUMAN	55.9	100.0%	5	5	7	0.01%	14.5%	QLQSEQPQTAAAR	99.7%	57	25	49.5	2	0	0	1427.72	470	482
V-type proton ATPase subunit H	ATP6V1H	VATH_HUMAN	55.9	100.0%	5	5	7	0.01%	14.5%	VSIFFDYAR	99.7%	60.7	25	54.5	2	0	0	1117.57	108	116
V-type proton ATPase subunit H	ATP6V1H	VATH_HUMAN	55.9	100.0%	5	5	7	0.01%	14.5%	YNALLAVQK	98.6%	32.3	25	23.4	1	0	0	1019.59	450	458
V-type proton ATPase subunit H	ATP6V1H	VATH_HUMAN	55.9	100.0%	5	5	7	0.01%	14.5%	YNIIPVLSDILQESVK	99.7%	81	25	77.4	1	0	0	1831.02	263	278
WASH complex subunit 7	KIAA1033	WASH7_HUMAN	136.4	100.0%	4	5	7	0.01%	3.4%	DLALFFSLNPIR	99.7%	48.7	25	43.1	1	0	0	1405.78	706	717
WASH complex subunit 7	KIAA1033	WASH7_HUMAN	136.4	100.0%	4	5	7	0.01%	3.4%	HLNTINIR	95.0%	27.2	25	26	1	0	0	980.56	814	821
WASH complex subunit 7	KIAA1033	WASH7_HUMAN	136.4	100.0%	4	5	7	0.01%	3.4%	LHYMFSALR	97.1%	29.2	25	5.92	1	0	0	1153.58	630	638
WASH complex subunit 7	KIAA1033	WASH7_HUMAN	136.4	100.0%	4	5	7	0.01%	3.4%	MLVDVFAPEFR	99.7%	51	25	42.5	4	0	0	1323.68	993	1003
WASH complex subunit strumpellin	KIAA0196	STRUM_HUMAN	134.3	100.0%	4	4	5	0.00%	4.3%	FTPVDESVTFIGR	99.7%	53.9	25	51.8	1	0	0	1467.75	811	823
WASH complex subunit strumpellin	KIAA0196	STRUM_HUMAN	134.3	100.0%	4	4	5	0.00%	4.3%	IVSCGNAIIAELLR	99.7%	54	25	54	2	0	0	1528.85	18	31
WASH complex subunit strumpellin	KIAA0196	STRUM_HUMAN	134.3	100.0%	4	4	5	0.00%	4.3%	LSEFIPAVFR	98.7%	32.5	25	29.5	1	0	0	1178.66	32	41
WASH complex subunit strumpellin	KIAA0196	STRUM_HUMAN	134.3	100.0%	4	4	5	0.00%	4.3%	TALNNTLDLSNVR	99.7%	70.9	25	70.5	1	0	0	1430.76	312	324
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	18	0.02%	19.3%	DYSGQGVVK	99.6%	37.5	25	29.8	2	0	0	952.47	397	405
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	18	0.02%	19.3%	FATASADGQIYIYDGK	99.7%	87.3	25	85.6	1	0	0	1719.82	204	219
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	18	0.02%	19.3%	IAVVGEGR	99.7%	44.4	25	33.2	2	0	0	800.46	117	124
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	18	0.02%	19.3%	LATGSDDNCAAFFEGPPFK	99.7%	67	25	67	2	0	0	2043.91	162	180
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	18	0.02%	19.3%	LYSILGTTLKDEGK	99.7%	78.6	25	58.7	2	1	0	1537.85	471	484
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	18	0.02%	19.3%	SIQCLTVHK	97.4%	29.7	25	18.9	1	0	0	1085.58	322	330
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	18	0.02%	19.3%	VFASLPQVER	99.7%	54.2	25	46.8	2	0	0	1145.63	8	17
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	18	0.02%	19.3%	YAPSGFYIASGDVSGK	99.7%	87	25	81.9	2	0	0	1618.77	66	81
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	18	0.02%	19.3%	YEYQPFAGK	98.3%	31.4	25	31.1	2	0	0	1102.52	96	104
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	18	0.02%	19.3%	YTSLMLR	99.2%	34.4	25	19.2	1	0	0	883.47	390	396
WD repeat-containing protein 5	WDR5	WDR5_HUMAN	36.6	99.8%	2	2	4	0.00%	7.5%	IWDTASGQCLK	99.7%	48.3	25	48.3	2	0	0	1278.61	197	207
WD repeat-containing protein 5	WDR5	WDR5_HUMAN	36.6	99.8%	2	2	4	0.00%	7.5%	TLIDDDNPPVSFVK	99.7%	70.3	25	67.2	2	0	0	1559.80	208	221
WD repeat-containing protein 6	WDR6	WDR6_HUMAN	121.7	99.8%	2	2	4	0.00%	1.7%	DGQLQPVLR	97.7%	30.2	25	25.4	2	0	0	1025.57	598	606
WD repeat-containing protein 6	WDR6	WDR6_HUMAN	121.7	99.8%	2	2	4	0.00%	1.7%	GLGVSALCFK	99.7%	46.7	25	46.7	2	0	0	1051.56	334	343
WD repeat-containing protein 82	WDR82	WDR82_HUMAN	35.1	99.9%	2	3	6	0.01%	10.9%	VVALSMSPVDDTFISGSLDK	99.7%	83.5	25	83.5	4	0	0	2097.04	110	129
WD repeat-containing protein 82	WDR82	WDR82_HUMAN	35.1	99.9%	2	3	6	0.01%	10.9%	YTHAANTVVYSSNK	99.7%	51.4	25	47.4	2	0	0	1554.75	71	84
Xanthine dehydrogenase/oxidase	XDH	XDH_HUMAN	146.4	100.0%	2	2	2	0.00%	1.2%	GVLEQLR	99.4%	35.8	25	18.4	1	0	0	814.48	329	335
Xanthine dehydrogenase/oxidase	XDH	XDH_HUMAN	146.4	100.0%	2	2	2	0.00%	1.2%	LDSPATPEK	99.7%	40.7	25	23.2	1	0	0	957.49	1297	1305
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	19	60	0.06%	19.8%	AFREEAIK	98.6%	32.3	25	9.43	1	0	0	963.53	641	648
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	19	60	0.06%	19.8%	ALQEKVEIK	95.2%	27.2	25	17	1	0	0	1057.63	661	669
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	19	60	0.06%	19.8%	ANPQVGVAFPHIK	99.6%	37.3	25	37.3	2	0	0	1377.76	401	413
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	19	60	0.06%	19.8%	CFSVLGFCK	99.7%	58.1	25	51.2	4	0	0	1117.52	339	347
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	19	60	0.06%	19.8%	EEASGSSVTAEEAK	99.7%	116	25	113	4	0	0	1394.63	689	702
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	19	60	0.06%	19.8%	EEASGSSVTAEEAKK	99.7%	102	25	92.3	5	0	0	1522.72	689	703
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	19	60	0.06%	19.8%	FFMGNQVLK	99.7%	41.8	25	39.9	5	0	0	1083.57	355	363

X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	19	60	0.06%	19.8%	HIEIFTDLSSR	99.7%	52.3	25	42.2	4	0	0	1317.68	131	141
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	19	60	0.06%	19.8%	KVITMFVQR	99.6%	37.8	25	32.7	2	0	0	1121.65	36	44
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	19	60	0.06%	19.8%	LFQCLLHR	99.7%	41.4	25	32.2	4	0	0	1086.59	490	497
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	19	60	0.06%	19.8%	LGGHGPSFPLK	99.7%	44.8	25	34.7	4	0	0	1109.61	185	195
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	19	60	0.06%	19.8%	SQLDIIIHSLK	99.7%	53	25	53	4	0	0	1266.74	145	155
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	19	60	0.06%	19.8%	SQLDIIIHSLKK	99.5%	27.9	25	27.7	0	1	0	1394.84	145	156
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	19	60	0.06%	19.8%	TDTLEDLFPTTK	99.7%	62.4	25	53.8	4	0	0	1380.69	470	481
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	19	60	0.06%	19.8%	TLFPLIEAK	99.7%	45.5	25	17.6	2	0	0	1031.61	535	543
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	19	60	0.06%	19.8%	VITMFVQR	99.7%	62.5	25	47.3	8	0	0	993.56	37	44
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	19	60	0.06%	19.8%	YGSDIVPFSK	99.7%	61.7	25	51.3	5	0	0	1112.56	316	325
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	16	33	0.03%	25.1%	DSLIFLVDASK	99.7%	87.5	25	79.3	5	0	0	1207.66	36	46
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	16	33	0.03%	25.1%	DTGIFLDLMHLK	99.7%	54	25	47.5	4	0	0	1402.74	195	206
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	16	33	0.03%	25.1%	EVAALCR	98.9%	33.2	25	21.4	1	0	0	818.42	393	399
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	16	33	0.03%	25.1%	IISSDRDLLAVVFYGTEK	99.6%	28.4	25	18.9	0	1	0	2026.09	75	92
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	16	33	0.03%	25.1%	ILELDQFK	99.7%	39.3	25	9.56	2	0	0	1005.56	116	123
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	16	33	0.03%	25.1%	ILELDQFKGQQGQK	99.7%	64.5	25	57.1	2	0	0	1631.88	116	129
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	16	33	0.03%	25.1%	IMATPEQVGK	99.7%	49.9	25	28.9	4	0	0	1089.56	452	461
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	16	33	0.03%	25.1%	IMLFTNEDNPHGNDSAK	99.7%	44	25	42.7	0	2	0	1902.87	166	182
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	16	33	0.03%	25.1%	KQELLEALTK	99.7%	67.3	25	56.6	2	0	0	1172.69	596	605
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	16	33	0.03%	25.1%	LGSLVDEFK	98.1%	31	25	23.2	1	0	0	1007.54	518	526
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	16	33	0.03%	25.1%	NIYVLQELDNPGAK	99.7%	135	25	126	4	0	0	1573.82	101	114
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	16	33	0.03%	25.1%	QELLEALTK	99.7%	44.1	25	27.9	2	0	0	1044.59	597	605
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	16	33	0.03%	25.1%	SDSFENPVLQQHFR	99.5%	27.5	25	27.1	0	1	0	1703.81	475	488
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	16	33	0.03%	25.1%	TFNTSTGGLLLPSDTKR	99.7%	98.7	25	97.3	2	0	0	1807.96	302	318
YEATS domain-containing protein 4	YEATS4	YETS4_HUMAN	26.5	100.0%	3	4	6	0.01%	16.7%	GVTIVKPIVYGNVAR	99.7%	33.6	25	29	2	2	0	1585.94	18	32
YEATS domain-containing protein 4	YEATS4	YETS4_HUMAN	26.5	100.0%	3	4	6	0.01%	16.7%	LFQSDTNAMLGK	99.7%	53.3	25	41.5	1	0	0	1324.66	120	131
YEATS domain-containing protein 4	YEATS4	YETS4_HUMAN	26.5	100.0%	3	4	6	0.01%	16.7%	MAEFGPDSGGR	99.7%	59.2	25	56.2	1	0	0	1123.48	5	15
YTH domain-containing family protein 2	YTHDF2	YTHD2_HUMAN	62.3	100.0%	3	3	7	0.01%	5.9%	LENNENKPVTNSR	98.6%	24.3	25	22.9	0	1	0	1514.76	515	527
YTH domain-containing family protein 2	YTHDF2	YTHD2_HUMAN	62.3	100.0%	3	3	7	0.01%	5.9%	LGSTEVASNVPK	99.7%	73.1	25	61.7	4	0	0	1201.64	194	205
YTH domain-containing family protein 2	YTHDF2	YTHD2_HUMAN	62.3	100.0%	3	3	7	0.01%	5.9%	SYSEDDIHR	99.7%	49.6	25	49.6	2	0	0	1121.49	417	425
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	99.8%	2	2	2	0.00%	4.2%	DFVVGALILR	99.7%	59.4	25	54.6	1	0	0	1102.66	183	192
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	99.8%	2	2	2	0.00%	4.2%	TLFILFR	96.1%	28.1	25	28.1	1	0	0	909.56	255	261
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	3	4	6	0.01%	12.9%	LADPAVTDFPAGK	99.7%	51.7	25	47.4	2	0	0	1301.67	225	237
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	3	4	6	0.01%	12.9%	TVASSLGQIPMQR	99.7%	44.7	25	41.7	3	0	0	1387.74	270	282
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	3	4	6	0.01%	12.9%	VCCALLISESQK	99.7%	59.4	25	59.4	1	0	0	1407.70	77	88
Zinc finger protein 768	ZNF768	ZN768_HUMAN	60.2	100.0%	3	3	4	0.00%	6.1%	AFSQSSDLIR	99.5%	36.5	25	11.3	2	0	0	1123.57	521	530
Zinc finger protein 768	ZNF768	ZN768_HUMAN	60.2	100.0%	3	3	4	0.00%	6.1%	FEPESPGFESR	96.5%	28.5	25	26.4	1	0	0	1281.57	79	89
Zinc finger protein 768	ZNF768	ZN768_HUMAN	60.2	100.0%	3	3	4	0.00%	6.1%	FGQSSVLAIHAR	99.7%	70	25	64.1	1	0	0	1285.70	438	449
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	99.8%	2	2	2	0.00%	2.3%	STAPAVAYDSK	98.0%	30.8	25	27.2	1	0	0	1109.55	148	158
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	99.8%	2	2	2	0.00%	2.3%	STPVTSAVQIPEVK	99.6%	37.7	25	34.4	1	0	0	1455.81	528	541

Table S-1-4. List of proteins identified in immunoprecipitation product of H7N9 NS1 (Replicate 1)

Protein name	Gene name	Accession number	M.W. (kDa)	Protein probability	No. of unique peptide	No. of unique spectra	No. of total spectra	Percentage of total spectra	Sequence coverage	Peptide sequence	Best peptide probability	Mascot			No. of spectra			Calculated +1H peptide mass (AMU)	Peptide index	
												ion score	identity score	delta ion score	+2H	+3H	+4H		start	stop
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	PDK1	PDK1_HUMAN	49.2	100.0%	3	3	4	0.00%	8.5%	AIYDFTDTVIR	99.7%	55.3	25	49.9	1	0	0	1313.67	134	144
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	PDK1	PDK1_HUMAN	49.2	100.0%	3	3	4	0.00%	8.5%	AVPLAGFGYGLPISR	99.7%	50.8	25	50.8	2	0	0	1517.85	349	363
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	PDK1	PDK1_HUMAN	49.2	100.0%	3	3	4	0.00%	8.5%	EISLLPDNLLR	96.8%	30.4	25	30.4	1	0	0	1282.74	93	103
10 kDa heat shock protein, mitochondrial	HSPE1	CH10_HUMAN	10.9	100.0%	3	3	6	0.01%	25.5%	GGEIQPVSVK	99.7%	49.7	25	37.6	2	0	0	1013.56	57	66
10 kDa heat shock protein, mitochondrial	HSPE1	CH10_HUMAN	10.9	100.0%	3	3	6	0.01%	25.5%	GKGGEIQPVSVK	99.6%	40.3	25	40.2	2	0	0	1198.68	55	66
10 kDa heat shock protein, mitochondrial	HSPE1	CH10_HUMAN	10.9	100.0%	3	3	6	0.01%	25.5%	VLQATVVAVGSGSK	99.7%	88.6	25	88.2	2	0	0	1315.76	41	54
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	AFIPAIDSFGFETDLR	99.7%	93.9	25	93.5	4	0	0	1798.90	873	888
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	CFAETPNKK	97.1%	30.9	25	30.6	1	0	0	1094.53	674	682
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	DSIVQGFQWGTR	99.7%	82	25	76.8	2	0	0	1393.69	764	775
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	EGPLCDELIR	99.7%	49	25	39.4	2	0	0	1201.59	776	785
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	FFDDPMLLELAK	99.7%	62	25	55.9	6	0	0	1438.73	952	963
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	GGGQIIPTAR	99.0%	35.7	25	22.6	4	0	0	969.55	804	813
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	GHVTQDAPIPGSPLYTIK	99.7%	106	25	106	2	2	0	1894.01	855	872
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	GLSEDVSISK	99.7%	46.9	25	32.7	3	0	0	1034.54	942	951
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	GNEEAQIFRPLK	99.7%	63.3	25	50.9	4	0	0	1401.75	570	581
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	IAVEPVNPSELPK	99.7%	60	25	53.5	3	0	0	1392.77	590	602
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	ILAQVVGDVDTSLPR	99.7%	99.4	25	93.9	2	0	0	1582.88	380	394
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	ILDAVVAQEPLHR	99.7%	61	25	59.5	2	3	0	1460.82	791	803
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	ITMIAEPLEK	99.7%	47.8	25	43.9	6	0	0	1144.63	685	694
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	IYADTFGDINYQEFAK	99.7%	117	25	116	4	0	0	1894.89	326	341
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	KGLSEDVSISK	99.7%	58.8	25	47	1	0	0	1162.63	941	951
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	LGEFFQTK	99.7%	51.1	25	42.2	4	0	0	969.50	714	721
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	MYSTDDGVQFHAFGR	97.7%	25.6	25	25.6	0	2	0	1746.75	481	495
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	SFVEFILEPLYK	99.7%	82.2	25	69.7	4	0	0	1484.80	368	379
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	SIVIRPLEPQPAPHLAR	99.7%	39.7	25	39.7	0	2	0	1894.10	915	931
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	STPVTVVLPDTK	99.7%	72.5	25	67.1	4	0	0	1256.71	183	194
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	TLDELGIHLTK	99.7%	68.2	25	63	4	0	0	1239.69	395	405
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	VADPVVTFCETVVETSSLK	99.7%	84.8	25	79.5	4	0	0	2081.05	655	673
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	VLGENYTLEDEEDSQICTVGR	99.7%	130	25	130	2	0	0	2427.10	509	529
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	VLSGTIHAGQPVK	99.7%	83.5	25	81.1	5	0	0	1306.75	496	508
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	VPAGNWVLIEGVDQPIVK	99.7%	64.1	25	64.1	2	2	0	1934.07	544	561
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	VVYSAFLMATPR	99.7%	58	25	46	3	0	0	1370.71	815	826
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	YDWDLLAAR	99.7%	66.6	25	59.9	4	0	0	1122.56	722	730
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	28	34	95	0.09%	36.1%	YHIEVNR	96.1%	29.5	25	7.39	2	0	0	930.48	537	543
14-3-3 protein beta/alpha	YWHAB	1433B_HUMAN	28.1	99.8%	2	2	2	0.00%	21.1%	AVTEQGHELSNEER	99.7%	101	25	92.9	1	0	0	1598.74	30	43
14-3-3 protein beta/alpha	YWHAB	1433B_HUMAN	28.1	99.8%	2	2	2	0.00%	21.1%	DSTLIMQLLR	99.0%	35.4	25	13.2	2	0	0	1205.66	215	224
14-3-3 protein beta/alpha	YWHAB	1433B_HUMAN	28.1	99.8%	2	2	2	0.00%	21.1%	EMQPTHPIR	99.7%	51.6	25	41.2	2	0	0	1108.56	161	169
14-3-3 protein beta/alpha	YWHAB	1433B_HUMAN	28.1	99.8%	2	2	2	0.00%	21.1%	VISSIEQK	99.7%	42.2	25	0	1	0	0	903.51	63	70
14-3-3 protein beta/alpha	YWHAB	1433B_HUMAN	28.1	99.8%	2	2	2	0.00%	21.1%	YLSEVASGDNK	99.7%	54.2	25	48.4	1	0	0	1182.56	130	140
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	7	7	13	0.01%	35.3%	DSTLIMQLLR	99.0%	35.4	25	13.2	2	0	0	1205.66	216	225
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	7	7	13	0.01%	35.3%	EAAENSLVAYK	99.7%	48.9	25	46.6	2	0	0	1194.60	143	153
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	7	7	13	0.01%	35.3%	HLIPAANTGESK	99.3%	37.4	25	23.7	1	0	0	1237.65	107	118
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	7	7	13	0.01%	35.3%	IISSIEQKEENK	99.7%	64	25	56.3	2	0	0	1417.75	62	73
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	7	7	13	0.01%	35.3%	LICCDILDVLDK	99.7%	64	25	59.2	2	0	0	1476.74	95	106
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	7	7	13	0.01%	35.3%	QMVETELK	99.7%	49.4	25	34.3	2	0	0	993.49	87	94

14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	7	7	13	0.01%	35.3%	VAGMDVELTVEER	99.7%	79.3	25	67.2	2	0	0	1463.70	30	42
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	7	7	13	0.01%	35.3%	YLAEFATGNDRK	99.7%	42.5	25	34.1	2	0	0	1384.69	131	142
14-3-3 protein gamma	YWHAG	1433G_HUMAN	28.3	100.0%	3	3	5	0.00%	23.9%	AYSEAHEISK	99.7%	55	25	48.2	2	0	0	1134.54	153	162
14-3-3 protein gamma	YWHAG	1433G_HUMAN	28.3	100.0%	3	3	5	0.00%	23.9%	DSTLIMQLLR	99.0%	35.4	25	13.2	2	0	0	1205.66	218	227
14-3-3 protein gamma	YWHAG	1433G_HUMAN	28.3	100.0%	3	3	5	0.00%	23.9%	MKGDYYR	98.2%	32.9	25	19.7	2	0	0	932.43	126	132
14-3-3 protein gamma	YWHAG	1433G_HUMAN	28.3	100.0%	3	3	5	0.00%	23.9%	NVTELNEPLSNEER	99.7%	86.6	25	86.6	2	0	0	1643.79	29	42
14-3-3 protein gamma	YWHAG	1433G_HUMAN	28.3	100.0%	3	3	5	0.00%	23.9%	VISSIEQK	99.7%	42.2	25	0	1	0	0	903.51	62	69
14-3-3 protein gamma	YWHAG	1433G_HUMAN	28.3	100.0%	3	3	5	0.00%	23.9%	YLAEVATGEK	99.3%	37.2	25	31.1	1	0	0	1080.56	133	142
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	5	5	7	0.01%	24.9%	AVTEQGAELSNEER	99.7%	102	25	89.4	2	0	0	1532.72	28	41
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	5	5	7	0.01%	24.9%	DSTLIMQLLR	99.0%	35.4	25	13.2	2	0	0	1205.66	213	222
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	5	5	7	0.01%	24.9%	EKVESELR	96.7%	30.3	25	16.5	1	0	0	989.53	84	91
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	5	5	7	0.01%	24.9%	EMQPTHPIR	99.7%	51.6	25	41.2	2	0	0	1108.56	159	167
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	5	5	7	0.01%	24.9%	VISSIEQK	99.7%	42.2	25	0	1	0	0	903.51	61	68
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	5	5	7	0.01%	24.9%	YLAEVACGDDR	99.7%	41.7	25	41.7	1	0	0	1268.56	128	138
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	5	5	7	0.01%	24.9%	YLAEVACGDDRK	99.7%	60.6	25	55.8	2	0	0	1396.65	128	139
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	8	8	15	0.01%	36.7%	DICNDVLSLLEK	99.7%	65.1	25	59.7	2	0	0	1418.72	92	103
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	8	8	15	0.01%	36.7%	DSTLIMQLLR	99.0%	35.4	25	13.2	2	0	0	1205.66	213	222
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	8	8	15	0.01%	36.7%	EMQPTHPIR	99.7%	51.6	25	41.2	2	0	0	1108.56	159	167
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	8	8	15	0.01%	36.7%	FLIPNASQAESK	99.3%	37.6	25	30.7	2	0	0	1304.68	104	115
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	8	8	15	0.01%	36.7%	MKGDYYR	98.2%	32.9	25	19.7	2	0	0	932.43	121	127
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	8	8	15	0.01%	36.7%	SVTEQGAELSNEER	99.7%	104	25	98.5	2	0	0	1548.71	28	41
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	8	8	15	0.01%	36.7%	VVSSIEQKTEGAEK	98.7%	34.4	25	26	1	0	0	1504.79	61	74
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	8	8	15	0.01%	36.7%	YLAEVAAGDDKK	99.7%	58.9	25	39.4	2	0	0	1279.65	128	139
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	6	6	10	0.01%	12.1%	AGQVFLEELGNHK	99.7%	89.4	25	85.2	2	0	0	1441.74	205	217
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	6	6	10	0.01%	12.1%	GEEVGELSR	99.7%	40.9	25	25.4	2	0	0	975.47	361	369
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	6	6	10	0.01%	12.1%	GGSRGEEVGELSR	99.7%	49	25	39.3	2	0	0	1332.65	357	369
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	6	6	10	0.01%	12.1%	LDCAQLK	98.5%	33.7	25	13.1	2	0	0	847.43	156	162
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	6	6	10	0.01%	12.1%	RPPGVLHCTTK	97.2%	24.8	25	10.2	0	1	0	1265.68	245	255
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	6	6	10	0.01%	12.1%	VIVDKYR	97.6%	31.6	25	21.1	1	0	0	892.53	69	75
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	33	0.03%	40.6%	ADHDFVVQEDFMK	99.7%	72.7	25	72.7	1	1	0	1596.70	357	369
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	33	0.03%	40.6%	ALQSVGQIVGEVLK	99.7%	86.3	25	83	4	0	0	1440.84	49	62
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	33	0.03%	40.6%	AVASQLDCNFLK	99.7%	65.5	25	57.8	2	0	0	1365.68	186	197
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	33	0.03%	40.6%	DKALQDYR	96.3%	29.8	25	21.1	1	0	0	1008.51	6	13
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	33	0.03%	40.6%	EVIELPLTNPELFQR	99.7%	69.8	25	69.8	2	0	0	1797.97	147	161
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	33	0.03%	40.6%	FSEGTSADR	99.7%	53.5	25	39.2	1	0	0	969.43	243	251
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	33	0.03%	40.6%	FSEGTSADREIQR	99.2%	36.9	25	33.1	1	0	0	1495.71	243	255
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	33	0.03%	40.6%	GCLLYGPPGTGK	99.7%	60.4	25	60.4	2	0	0	1219.61	169	180
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	33	0.03%	40.6%	HGEIDYEAIVK	99.7%	75.3	25	63.8	2	0	0	1273.64	323	333
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	33	0.03%	40.6%	IHAGPITK	98.9%	35	25	32.1	2	0	0	836.50	315	322
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	33	0.03%	40.6%	KIHIDLPNEQAR	99.7%	56.6	25	54.6	0	2	0	1433.79	298	309
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	33	0.03%	40.6%	NVCTEAGMFAIR	99.7%	70.5	25	63	4	0	0	1384.63	345	356
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	33	0.03%	40.6%	VALDMTTLTIMR	99.7%	95.9	25	95.9	4	0	0	1364.73	98	109
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	14	18	33	0.03%	40.6%	VVSSSIVDKYIGESAR	99.7%	66.1	25	66.1	2	2	0	1709.91	198	213
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	16	20	42	0.04%	45.0%	AICTEAGLMALR	99.7%	62.4	25	56.4	5	0	0	1321.66	397	408
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	16	20	42	0.04%	45.0%	APQETYADIGGLDNQIQEIK	99.7%	76.1	25	71.9	1	1	0	2203.09	179	198
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	16	20	42	0.04%	45.0%	AVANQTSATFLR	99.7%	77.5	25	66.4	5	0	0	1278.68	238	249
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	16	20	42	0.04%	45.0%	DDLSGADIK	99.7%	53.5	25	41.7	2	0	0	933.45	388	396
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	16	20	42	0.04%	45.0%	GVILYGPPGTGK	99.7%	58	25	0	5	0	0	1158.65	221	232
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	16	20	42	0.04%	45.0%	IETLDPALIRPGR	99.7%	34.2	25	27	0	3	0	1450.84	334	346
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	16	20	42	0.04%	45.0%	IFQIHTSR	99.7%	50	25	31.4	2	0	0	1001.55	364	371
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	16	20	42	0.04%	45.0%	KIEFPLPDEK	99.5%	31.5	25	19.7	0	1	0	1215.66	350	359

26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	16	20	42	0.04%	45.0%	KQEGTPEGLYL	99.7%	51.9	25	44.7	2	0	0	1234.63	430	440
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	16	20	42	0.04%	45.0%	KYEPPVPTR	98.2%	32.9	25	23.2	2	0	0	1086.59	24	32
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	16	20	42	0.04%	45.0%	LPLVTPHTQCR	99.7%	63.4	25	54.1	2	0	0	1321.70	49	59
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	16	20	42	0.04%	45.0%	MTLADDVTLDDLIMAK	99.7%	97.5	25	95.9	2	0	0	1780.87	372	387
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	16	20	42	0.04%	45.0%	NQEQMKPLEEK	96.3%	29.8	25	29.5	1	0	0	1389.67	81	91
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	16	20	42	0.04%	45.0%	NQEQMKPLEEKQEEER	99.7%	40.3	25	40.3	0	3	0	2044.96	81	96
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	16	20	42	0.04%	45.0%	SKENVLYK	95.9%	29.4	25	21.2	1	0	0	980.54	422	429
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	16	20	42	0.04%	45.0%	TMLELLNQLDGFDSR	99.7%	109	25	100	7	0	0	1751.86	308	322
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	16	20	42	0.04%	45.0%	VIMATNR	98.1%	32.8	25	18	3	0	0	804.44	327	333
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	16	20	42	0.04%	45.0%	VVGSELIQK	99.7%	81.6	25	67.1	2	0	0	972.57	250	258
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	54	0.05%	52.2%	AMEVDERPTEQYSDIGGLDK	99.7%	41.2	25	41.2	0	1	0	2269.03	174	193
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	54	0.05%	52.2%	APSIIFIDELDAIGTK	99.7%	67.9	25	64.8	2	0	0	1702.93	279	294
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	54	0.05%	52.2%	AVCVEAGMIALR	99.7%	72.6	25	69.3	3	0	0	1289.67	398	409
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	54	0.05%	52.2%	CTDDFNGAQCK	99.7%	60.5	25	60.5	2	0	0	1315.50	387	397
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	54	0.05%	52.2%	DSYLILETLPTEYDSR	99.7%	99.7	25	99.4	2	0	0	1914.93	156	171
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	54	0.05%	52.2%	EKFENLGIQPPK	99.6%	39.9	25	32.4	2	0	0	1399.76	210	221
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	54	0.05%	52.2%	FENLGIQPPK	99.7%	52.8	25	31.3	2	0	0	1142.62	212	221
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	54	0.05%	52.2%	GVLMYGPPGTGK	99.7%	74	25	66.7	4	0	0	1192.60	222	233
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	54	0.05%	52.2%	IMQIHSR	99.7%	42.5	25	27.5	2	0	0	884.48	365	371
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	54	0.05%	52.2%	KMNVSPDVNYEELAR	99.7%	75.3	25	67.9	0	4	0	1780.85	372	386
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	54	0.05%	52.2%	LAGPQLVQMFIGDGAK	99.7%	102	25	102	4	0	0	1644.88	251	266
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	54	0.05%	52.2%	LLDSEIK	98.3%	33.2	25	11.9	2	0	0	817.47	47	53
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	54	0.05%	52.2%	MSTEEIIQR	99.7%	73.6	25	50.2	4	0	0	1106.55	36	44
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	54	0.05%	52.2%	QIQELVEAIVLPMNHK	99.7%	38	25	38	0	2	0	1862.02	194	209
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	54	0.05%	52.2%	QTYFLPVIGLVDAEK	99.7%	81	25	67.9	6	0	0	1692.92	130	144
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	54	0.05%	52.2%	TMLELLNQLDGFQPNTQVK	99.7%	91.5	25	91.5	4	0	0	2189.13	309	327
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	54	0.05%	52.2%	VDILDPALLR	99.7%	63.6	25	49.3	4	0	0	1124.67	335	344
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	54	0.05%	52.2%	VIAATNRVDILDPALLR	99.7%	52.8	25	52.8	0	2	0	1850.09	328	344
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	19	24	54	0.05%	52.2%	VTHELQAMK	99.7%	49.3	25	37	2	0	0	1056.55	62	70
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	14	20	36	0.03%	38.0%	ADTLDPALLRPGR	99.0%	35.5	25	35.5	2	0	0	1394.78	314	326
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	14	20	36	0.03%	38.0%	AVAHHTTAAFIR	99.7%	73.1	25	68.9	2	2	0	1294.70	218	229
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	14	20	36	0.03%	38.0%	EAVELPLTHFELYK	99.7%	80.5	25	73.1	2	0	0	1688.89	179	192
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	14	20	36	0.03%	38.0%	EFLHAQEEVKR	99.7%	44.1	25	29.5	2	2	0	1385.72	71	81
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	14	20	36	0.03%	38.0%	ELLKPNASVALHK	99.7%	43.4	25	41.8	0	2	0	1419.83	122	134
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	14	20	36	0.03%	38.0%	ENAPAIIFIDEIDAIATK	99.7%	80.6	25	80.6	3	1	0	1944.03	256	273
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	14	20	36	0.03%	38.0%	FDAQTGADREVQR	99.5%	31.6	25	26.6	1	1	0	1492.71	275	287
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	14	20	36	0.03%	38.0%	GVLMYGPPGCGK	99.7%	61	25	61	4	0	0	1251.59	201	212
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	14	20	36	0.03%	38.0%	ILLELLNQMDGFDQNVNVK	99.7%	96.5	25	96.5	4	0	0	2219.14	288	306
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	14	20	36	0.03%	38.0%	ILSTIDR	97.4%	31.3	25	11.7	1	0	0	817.48	115	121
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	14	20	36	0.03%	38.0%	LIFSTITSK	97.7%	31.9	25	29	1	0	0	1009.59	343	351
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	14	20	36	0.03%	38.0%	RFDAQTGADR	99.2%	36.8	25	7.45	2	0	0	1136.54	274	283
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	14	20	36	0.03%	38.0%	RLIFSTITSK	98.7%	34.4	25	29.6	2	0	0	1165.69	342	351
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	14	20	36	0.03%	38.0%	VIMATNR	98.1%	32.8	25	18	3	0	0	804.44	307	313
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	14	20	36	0.03%	38.0%	VVGSEFVQK	99.7%	78.7	25	65.6	2	0	0	992.54	230	238
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	27	52	0.05%	56.1%	ALDEGDIALLK	99.7%	76.3	25	59.3	2	0	0	1157.64	24	34
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	27	52	0.05%	56.1%	ESDTGLAPPALWDLAADK	99.4%	38.5	25	38.5	2	0	0	1869.92	67	84
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	27	52	0.05%	56.1%	EVVETPLLHPER	99.7%	41.6	25	28.9	1	0	0	1418.76	189	200
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	27	52	0.05%	56.1%	FDDGAGGDNEVQR	99.7%	88.1	25	88.1	2	0	0	1379.58	285	297
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	27	52	0.05%	56.1%	FVNLGIEPPK	99.7%	60.9	25	36.4	4	0	0	1113.63	201	210
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	27	52	0.05%	56.1%	FVVDLSDQVAPTDIEEGMR	99.7%	86.5	25	76.8	2	0	0	2121.02	121	139
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	27	52	0.05%	56.1%	GVLLFGPPGTGK	99.7%	60.5	25	50.2	2	0	0	1142.66	211	222

26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	27	52	0.05%	56.1%	IATEKDFLEAVNK	99.7%	72	25	64	2	2	0	1477.79	403	415
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	27	52	0.05%	56.1%	IEFSLPDLEGR	99.7%	61.2	25	44.6	2	0	0	1275.66	341	351
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	27	52	0.05%	56.1%	IINADSEDPK	99.7%	52.8	25	39.4	2	0	0	1101.54	101	110
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	27	52	0.05%	56.1%	IINADSEDPKYIINVK	99.7%	86.3	25	86.3	2	0	0	1831.98	101	116
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	27	52	0.05%	56.1%	INELTGIK	99.7%	46.5	25	29.5	1	0	0	887.52	59	66
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	27	52	0.05%	56.1%	KINELTGIK	99.7%	47.4	25	25.9	2	0	0	1015.61	58	66
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	27	52	0.05%	56.1%	LCPNSTGAEIR	99.7%	44.8	25	36.1	2	0	0	1217.59	376	386
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	27	52	0.05%	56.1%	LREVVETPLLHPER	99.7%	48.6	25	43.1	0	2	0	1687.95	187	200
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	27	52	0.05%	56.1%	PDYLGADQRK	99.7%	60	25	43.7	2	0	0	1162.59	2	11
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	27	52	0.05%	56.1%	QTLQSEQPLQVAR	99.7%	63.6	25	51.3	2	0	0	1497.80	85	97
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	27	52	0.05%	56.1%	QVEDDIQQLLK	99.7%	89.8	25	72.8	2	0	0	1328.71	47	57
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	27	52	0.05%	56.1%	SVCTEAGMFAIR	99.7%	62	25	55.8	5	0	0	1341.63	387	398
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	27	52	0.05%	56.1%	TDACFIR	99.7%	50.4	25	40.1	2	0	0	882.41	233	239
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	27	52	0.05%	56.1%	TMLELINQLDGFDPR	99.7%	84.1	25	81.4	4	0	0	1761.88	298	312
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	27	52	0.05%	56.1%	TYGQSTYSR	99.4%	38.2	25	27.4	1	0	0	1062.49	35	43
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	27	52	0.05%	56.1%	VIGSELVQK	99.4%	38.2	25	26.9	2	0	0	972.57	240	248
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	19	26	59	0.06%	57.9%	AVAHHTDCTFIR	99.7%	58.3	25	44.1	2	2	0	1427.68	202	213
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	19	26	59	0.06%	57.9%	EELQLLQEQGSYVGEVVR	99.7%	77.6	25	76.8	1	0	0	2076.06	61	78
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	19	26	59	0.06%	57.9%	EHAPSIIFMDEIDSIGSSR	99.7%	39.4	25	39.4	0	1	0	2120.00	240	258
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	19	26	59	0.06%	57.9%	ELFVMAR	98.3%	33.1	25	27.1	4	0	0	865.46	233	239
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	19	26	59	0.06%	57.9%	FVVDVDKNIDINDVTPNCR	99.7%	41.9	25	39.5	0	2	0	2233.09	95	113
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	19	26	59	0.06%	57.9%	GVCTEAGMYALR	99.7%	63	25	63	4	0	0	1343.61	361	372
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	19	26	59	0.06%	57.9%	GVLLYGPPGTGK	99.7%	58	25	0	5	0	0	1158.65	185	196
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	19	26	59	0.06%	57.9%	IAELMPGASGAEVK	99.7%	63.5	25	54	4	0	0	1372.71	347	360
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	19	26	59	0.06%	57.9%	IDILDSALLRPGR	99.7%	56.3	25	53.4	2	2	0	1438.84	298	310
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	19	26	59	0.06%	57.9%	IEELQLIVNDK	99.7%	96.2	25	90.2	2	0	0	1313.73	28	38
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	19	26	59	0.06%	57.9%	LEGGSGGDSEVQR	99.7%	81.9	25	81.9	5	0	0	1290.59	259	271
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	19	26	59	0.06%	57.9%	NDSYTLHK	98.6%	33.9	25	30	2	0	0	977.47	118	125
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	19	26	59	0.06%	57.9%	RVHVTQEDFEMAVAK	99.7%	51.2	25	50.3	0	1	0	1775.87	375	389
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	19	26	59	0.06%	57.9%	TMLELLNQLDGFEATK	99.7%	105	25	99.8	4	0	0	1822.93	272	287
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	19	26	59	0.06%	57.9%	VALRNDSYTLHK	99.7%	35.3	25	21.6	0	2	0	1416.76	114	125
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	19	26	59	0.06%	57.9%	VDPLVSLMMVEK	99.7%	56.5	25	50.4	2	0	0	1360.72	131	142
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	19	26	59	0.06%	57.9%	VIMATNR	98.1%	32.8	25	18	3	0	0	804.44	291	297
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	19	26	59	0.06%	57.9%	VPDSTYEMIGGLDK	99.7%	89.3	25	82.2	4	0	0	1540.72	143	156
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	19	26	59	0.06%	57.9%	VSGSELVQK	99.7%	78.7	25	43.5	5	0	0	946.52	214	222
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	29.9%	AAVESLGFILFR	99.7%	92.1	25	91.1	5	0	0	1322.75	617	628
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	29.9%	DNLEWLAR	99.7%	53.1	25	48.2	2	0	0	1016.52	388	395
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	29.9%	DTSEDIEELVEPVAAHGPK	99.7%	88.9	25	85.2	2	0	0	2035.98	916	934
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	29.9%	EAINLLEPMTNDPVNYVR	99.7%	82.4	25	82.4	4	0	0	2104.04	667	684
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	29.9%	EALQLMATYLPK	99.5%	39.5	25	34.5	4	0	0	1377.74	418	429
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	29.9%	FTATASLGVIHK	96.2%	23.6	25	23.6	0	1	0	1244.70	402	413
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	29.9%	LCMSLMQNK	96.1%	29.6	25	27.4	1	0	0	1156.52	183	191
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	29.9%	LLHVAVSDVNDDVR	97.6%	25.5	25	25.5	0	1	0	1551.81	602	615
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	29.9%	LLHVAVSDVNDDVRR	99.7%	48	25	48	0	2	0	1707.91	602	616
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	29.9%	MEEADALIESLCR	99.7%	98.1	25	97.5	3	0	0	1536.70	560	572
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	29.9%	NAQAIEDMVGYAQETQHEK	99.7%	34.4	25	34.4	0	2	0	2161.98	525	543
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	29.9%	NNNTDLMILK	99.7%	41.3	25	24	3	0	0	1191.60	345	354
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	29.9%	QAIGIALETR	99.7%	61.2	25	45.6	2	0	0	1071.62	149	158
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	29.9%	QDVYDLLK	99.7%	51.2	25	24.3	2	0	0	993.53	491	498
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	29.9%	SNCKPSTFAYPAPLEVPK	99.7%	35	25	25.7	0	2	0	2006.01	804	821
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	29.9%	TILESNDVPGMLAYSLK	99.7%	95.1	25	92	2	0	0	1850.96	166	182

26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	29.9%	TPEASPEPK	99.7%	45.5	25	44.8	2	0	0	955.47	311	319
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	29.9%	TPEQCPSVVSLLSESYNPHVR	99.7%	70.3	25	70.3	0	2	0	2399.17	629	649
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	29.9%	TVGTPIASVPGSTNTGTVPGSEK	99.7%	55.8	25	53.8	1	0	0	2157.10	270	292
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	29.9%	VINDKHDDVMAK	99.7%	53.7	25	47.8	3	0	0	1384.69	716	727
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	29.9%	VLTMPETCR	97.5%	31.4	25	20.6	1	0	0	1106.53	891	899
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	22	27	49	0.05%	29.9%	VSTAVLSITAK	99.7%	93.8	25	90.3	2	0	0	1089.65	828	838
26S proteasome non-ATPase regulatory subunit 10	PSMD10	PSD10_HUMAN	24.4	100.0%	4	4	6	0.01%	29.2%	ASTNIQDTEGNTPLHLACDEERVEEAK	99.7%	64.7	25	61.3	0	2	0	3027.40	163	189
26S proteasome non-ATPase regulatory subunit 10	PSMD10	PSD10_HUMAN	24.4	100.0%	4	4	6	0.01%	29.2%	DHYEATAMHR	99.7%	36.3	25	35.6	0	1	0	1230.53	136	145
26S proteasome non-ATPase regulatory subunit 10	PSMD10	PSD10_HUMAN	24.4	100.0%	4	4	6	0.01%	29.2%	LEELKESILADK	99.7%	59	25	48.3	2	0	0	1387.77	19	30
26S proteasome non-ATPase regulatory subunit 10	PSMD10	PSD10_HUMAN	24.4	100.0%	4	4	6	0.01%	29.2%	LLVSQGASIYIENKEEK	99.3%	30.7	25	28.4	0	1	0	1921.03	190	206
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	8	8	12	0.01%	22.3%	EQSILELGSLLAK	99.7%	41.1	25	41.1	2	0	0	1400.80	47	59
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	8	8	12	0.01%	22.3%	IMLNTPEDVQALVSGK	99.7%	59	25	59	1	0	0	1714.90	259	274
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	8	8	12	0.01%	22.3%	LYDNLLEQNLIR	99.7%	68.3	25	64.8	2	0	0	1503.82	326	337
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	8	8	12	0.01%	22.3%	TYHALSNLPK	97.7%	31.8	25	25	1	0	0	1143.62	176	185
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	8	8	12	0.01%	22.3%	VQIEHISSLIK	99.7%	45.6	25	43.4	2	0	0	1266.74	345	355
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	8	8	12	0.01%	22.3%	VVDSLYNK	98.7%	34.2	25	31.8	1	0	0	937.50	410	417
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	8	8	12	0.01%	22.3%	YQEALHLGSQLLR	99.6%	32.7	25	28.1	0	1	0	1527.83	143	155
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	8	8	12	0.01%	22.3%	YVRPFLNSISK	98.5%	27.2	25	27.2	0	2	0	1323.74	72	82
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	9	10	19	0.02%	26.9%	DLPVSEQQER	99.7%	63	25	63	2	0	0	1200.59	187	196
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	9	10	19	0.02%	26.9%	GSIDEVDKR	99.1%	36.2	25	24.8	2	0	0	1018.52	322	330
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	9	10	19	0.02%	26.9%	LNIGDLQVTK	99.7%	63	25	49	2	0	0	1100.63	123	132
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	9	10	19	0.02%	26.9%	QLTFEEIAK	99.2%	36.9	25	28.6	1	0	0	1078.58	290	298
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	9	10	19	0.02%	26.9%	QMTDPNVALTFLEK	99.7%	69.4	25	69.1	4	0	0	1622.81	86	99
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	9	10	19	0.02%	26.9%	SSDEAVILCK	99.7%	59.4	25	37.3	2	0	0	1121.55	106	115
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	9	10	19	0.02%	26.9%	TAWGQQPDLAANEAQLLR	99.7%	93.1	25	92.2	2	0	0	1982.01	253	270
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	9	10	19	0.02%	26.9%	VLDLQQIK	99.7%	61.8	25	43.8	2	0	0	956.58	340	347
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	9	10	19	0.02%	26.9%	YYQTIGNHASYYK	99.7%	65.1	25	65.1	2	0	0	1607.75	162	174
26S proteasome non-ATPase regulatory subunit 14	PSMD14	PSDE_HUMAN	34.6	100.0%	6	9	13	0.01%	27.7%	AVAVVVDPIQSVK	99.7%	67.1	25	67.1	2	0	0	1324.78	140	152
26S proteasome non-ATPase regulatory subunit 14	PSMD14	PSDE_HUMAN	34.6	100.0%	6	9	13	0.01%	27.7%	AVEEEDKMTPEQLAIK	99.7%	68.1	25	68.1	3	1	0	1830.92	258	273
26S proteasome non-ATPase regulatory subunit 14	PSMD14	PSDE_HUMAN	34.6	100.0%	6	9	13	0.01%	27.7%	HYYSITINYR	99.4%	38.2	25	33.6	1	0	0	1329.66	199	208
26S proteasome non-ATPase regulatory subunit 14	PSMD14	PSDE_HUMAN	34.6	100.0%	6	9	13	0.01%	27.7%	LINANMMVLGHEPR	99.5%	32.3	25	30.2	0	1	0	1594.82	162	175
26S proteasome non-ATPase regulatory subunit 14	PSMD14	PSDE_HUMAN	34.6	100.0%	6	9	13	0.01%	27.7%	VIDVFAMPQSGTGVSVEAVDPVFQAK	99.7%	42.8	25	42.8	0	3	0	2707.37	69	94
26S proteasome non-ATPase regulatory subunit 14	PSMD14	PSDE_HUMAN	34.6	100.0%	6	9	13	0.01%	27.7%	VVIDAFR	99.7%	43.2	25	42.6	2	0	0	819.47	155	161
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	APVQPQQSPAAAPGGTDEKPSGK	99.7%	67.3	25	67.3	0	2	0	2218.11	9	31
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	AVPLALALISVSNPR	99.7%	54	25	54	2	2	0	1520.92	689	703
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	CALGVFR	96.4%	30	25	25.5	1	0	0	822.43	251	257
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	DIDENAYAK	99.7%	41.3	25	41.3	2	0	0	1038.47	220	228
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	DKAPVQPQQSPAAAPGGTDEKPSGK	99.7%	54.3	25	54.3	0	2	0	2461.23	7	31
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	DPNNLFMVR	99.7%	50.3	25	41.4	5	0	0	1121.54	755	763
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	DTSLYRPALEELRR	99.6%	33.4	25	29	0	1	0	1718.92	67	80
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	EDVLTLLLPVMGDSK	99.7%	93.2	25	86.9	5	0	0	1629.88	495	509
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	ELDIMEPK	99.3%	37.2	25	9.15	2	0	0	990.48	336	343
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	EPLLTLVK	97.2%	30.9	25	25.7	2	0	0	912.58	182	189
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	EWQELDDAEK	99.7%	46	25	42.7	2	0	0	1262.55	169	178
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	FAADIISVLAMTMSGER	99.7%	89.8	25	81.4	5	0	0	1843.89	121	137
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	FGGSGSQVDSAR	99.7%	116	25	105	5	0	0	1167.54	358	369
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	GTLTLCPYHSDR	99.7%	50.5	25	49.5	2	0	0	1419.67	774	785
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	LAQGLTHLGK	99.7%	46.5	25	46.5	2	0	0	1037.61	764	773
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	LGSIFGLGLAYAGSNR	99.7%	103	25	102	2	2	0	1595.85	479	494
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	LNILDTLSK	99.7%	55.5	25	34.4	2	0	0	1016.60	704	712
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	LVGSQEELASWGHEYVR	99.7%	42.5	25	39.8	0	1	0	1959.96	144	160

26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	MNLASSFVNGFVNAAFGQDK	99.7%	70.1	25	70.1	1	0	0	2133.01	370	389
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	NECDPALALLSDYVLHNSNTMR	99.7%	37.2	25	37.2	0	2	0	2549.18	457	478
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	QMAFMLGR	95.7%	29.2	25	20	1	0	0	953.47	293	300
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	SETELKDTYAR	99.3%	30.2	25	30.2	0	2	0	1312.64	546	556
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	SFANTLVDVCAYAGSGNVLK	99.7%	104	25	96.2	1	0	0	2086.03	589	608
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	SGALLACGIVNSGVR	99.7%	88.8	25	88.8	2	0	0	1473.78	442	456
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	SSTTSMTSVPKPLK	99.7%	66.5	25	63.9	4	0	0	1463.78	84	97
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	TITGFQTHTTPVLLAHGER	99.7%	42.5	25	42.5	0	2	0	2079.10	861	879
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	VGQAVDVVGQAGKPK	99.7%	96.6	25	85.4	6	1	0	1452.82	846	860
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	VQQLLHICSEHFDSK	96.1%	23.6	25	23.6	0	2	0	1840.90	609	623
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	YGEPTLR	98.2%	33	25	26.9	1	0	0	835.43	681	687
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	30	37	76	0.07%	42.8%	YLYSSEDYIK	99.7%	49.6	25	41.1	2	0	0	1280.60	432	441
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	23	28	53	0.05%	44.6%	AIQLEYSEAR	99.7%	80.1	25	75.2	2	0	0	1179.60	297	306
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	23	28	53	0.05%	44.6%	ALDLVAAK	99.3%	37.3	25	22.1	1	0	0	800.49	202	209
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	23	28	53	0.05%	44.6%	APQHTAVGFK	99.6%	39.6	25	37.6	2	0	0	1055.56	316	325
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	23	28	53	0.05%	44.6%	AVQGFFTSNNATR	99.7%	87.8	25	81.6	2	0	0	1412.69	116	128
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	23	28	53	0.05%	44.6%	CYYYHAR	96.2%	29.7	25	29.7	1	0	0	1032.44	210	216
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	23	28	53	0.05%	44.6%	DGVIEASINHEK	99.7%	57.5	25	42.8	2	0	0	1311.65	444	455
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	23	28	53	0.05%	44.6%	DLESAEERR	99.2%	36.6	25	28.7	2	0	0	1104.53	504	512
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	23	28	53	0.05%	44.6%	ELDTVTLEDIKEHVK	99.6%	32.7	25	32.7	0	2	0	1768.93	66	80
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	23	28	53	0.05%	44.6%	EMIDIYSTR	99.7%	55.1	25	39.7	4	0	0	1143.54	462	470
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	23	28	53	0.05%	44.6%	EPQLAFHQR	99.7%	56.5	25	40.9	2	0	0	1125.58	471	479
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	23	28	53	0.05%	44.6%	EQQDLEFAK	98.5%	33.8	25	25.8	1	0	0	1107.53	515	523
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	23	28	53	0.05%	44.6%	EREQQDLEFAK	99.7%	50	25	48.6	2	0	0	1392.68	513	523
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	23	28	53	0.05%	44.6%	FNQVLDQFGEK	99.7%	72.7	25	50.5	2	0	0	1324.65	375	385
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	23	28	53	0.05%	44.6%	HDADGQATLLNLLLR	99.7%	74.4	25	74.4	2	0	0	1649.90	242	256
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	23	28	53	0.05%	44.6%	ISDDLMQK	99.7%	61.8	25	40.7	4	0	0	949.47	187	194
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	23	28	53	0.05%	44.6%	ISLADIAQK	99.7%	63.5	25	21.9	1	0	0	958.56	417	425
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	23	28	53	0.05%	44.6%	LQLDSPEDAEFIVAK	99.7%	88.2	25	76	2	0	0	1674.86	426	440
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	23	28	53	0.05%	44.6%	MISLSYSR	99.7%	41.4	25	19.5	4	0	0	972.48	409	416
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	23	28	53	0.05%	44.6%	NYLHYSLYDQAEK	99.7%	77.5	25	66.2	2	0	0	1643.77	257	269
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	23	28	53	0.05%	44.6%	SLMPYFLLTQAVR	99.7%	86.5	25	71.5	6	0	0	1538.84	356	368
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	23	28	53	0.05%	44.6%	SVFPEQANNNEWAR	99.7%	77.9	25	77.2	2	0	0	1661.77	274	287
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	23	28	53	0.05%	44.6%	VYEFLDKLDVVR	99.7%	64.5	25	59	2	2	0	1495.82	217	228
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	23	28	53	0.05%	44.6%	YLYYTGR	96.7%	30.2	25	21.8	1	0	0	935.46	288	294
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	5	5	7	0.01%	17.8%	AAAASAAEAGIATTGTEDSDDALLK	99.7%	35.6	25	35.6	0	2	0	2320.12	238	262
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	5	5	7	0.01%	17.8%	ITFCTGIR	99.7%	43.6	25	34.5	2	0	0	967.50	84	91
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	5	5	7	0.01%	17.8%	LQAQQDAVNIVCHSK	99.3%	30.5	25	26.9	0	1	0	1710.86	26	40
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	5	5	7	0.01%	17.8%	NAMGSLASQATK	99.7%	85.4	25	76.8	1	0	0	1194.58	354	365
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	5	5	7	0.01%	17.8%	VSMEEQR	96.9%	30.6	25	16.3	1	0	0	878.40	222	228
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	39	0.04%	46.5%	DNNMAPYYEALCK	98.7%	34.5	25	34.5	1	0	0	1604.67	47	59
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	39	0.04%	46.5%	DWLFAPHYR	99.7%	42.3	25	34.9	2	0	0	1204.59	285	293
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	39	0.04%	46.5%	FLLSLPEHR	99.7%	55.3	25	49.9	2	0	0	1111.63	24	32
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	39	0.04%	46.5%	GAEILEVLHSLPAVR	99.7%	77.9	25	72.3	4	0	0	1603.92	243	257
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	39	0.04%	46.5%	GDAAVRDELMAAVR	99.7%	37.5	25	31	2	3	0	1473.75	33	46
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	39	0.04%	46.5%	IDKVNEIVETNRPDSK	99.7%	40	25	39.9	0	2	0	1856.97	347	362
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	39	0.04%	46.5%	IGLFYMDNDLITR	99.7%	83.1	25	83.1	4	0	0	1586.79	147	159
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	39	0.04%	46.5%	IHAYSQLLESYR	99.7%	45.5	25	34.6	2	1	0	1479.76	301	312
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	39	0.04%	46.5%	KGDLLLNR	99.7%	46.7	25	33.6	2	0	0	928.56	372	379
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	39	0.04%	46.5%	LDEELEDAEK	99.7%	62	25	47.3	1	0	0	1190.54	84	93
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	39	0.04%	46.5%	LDIVFYLLR	99.7%	63.6	25	42	2	0	0	1151.68	138	146

26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	39	0.04%	46.5%	NLGESEIR	96.4%	29.9	25	22	1	0	0	917.47	94	101
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	39	0.04%	46.5%	PLENLEEEGLPK	99.7%	63	25	60.1	2	0	0	1367.71	2	13
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	39	0.04%	46.5%	QYLFSLYECR	99.7%	68	25	58.1	2	0	0	1378.65	258	267
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	39	0.04%	46.5%	SLIEEGGDWDRR	97.9%	32.1	25	27.4	1	0	0	1432.68	166	177
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	39	0.04%	46.5%	VNEIVETNRPDSK	99.7%	68.6	25	52.6	2	1	0	1500.77	350	362
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	39	0.04%	46.5%	VYQGLYCVAIR	99.7%	77.1	25	77.1	2	0	0	1341.70	182	192
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	3	3	6	0.01%	9.1%	DIQTNVYIK	99.7%	48.5	25	38	2	0	0	1093.59	219	227
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	3	3	6	0.01%	9.1%	ILFTEATR	99.7%	42.7	25	27.1	2	0	0	950.53	282	289
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	3	3	6	0.01%	9.1%	LVLLELNFLPTTGTK	99.7%	59.2	25	59.2	2	0	0	1658.97	121	135
26S proteasome non-ATPase regulatory subunit 9	PSMD9	PSMD9_HUMAN	24.7	99.8%	2	3	5	0.00%	9.9%	ANYDVLESQK	99.7%	40.9	25	38	2	0	0	1166.57	39	48
26S proteasome non-ATPase regulatory subunit 9	PSMD9	PSMD9_HUMAN	24.7	99.8%	2	3	5	0.00%	9.9%	KLGQSESQGPPR	99.7%	49.6	25	49.4	2	1	0	1283.67	123	134
28S ribosomal protein S10, mitochondrial	MRPS10	RT10_HUMAN	23.0	100.0%	3	4	10	0.01%	18.9%	AVLDSYEYFAVLAAK	99.7%	82.3	25	78.9	3	0	0	1659.86	86	100
28S ribosomal protein S10, mitochondrial	MRPS10	RT10_HUMAN	23.0	100.0%	3	4	10	0.01%	18.9%	FTLLQSVHIYK	99.7%	63.5	25	56.5	2	0	0	1348.76	118	128
28S ribosomal protein S10, mitochondrial	MRPS10	RT10_HUMAN	23.0	100.0%	3	4	10	0.01%	18.9%	NLPEGVAMEVTK	99.7%	57.6	25	53.2	5	0	0	1287.66	163	174
28S ribosomal protein S11, mitochondrial	MRPS11	RT11_HUMAN	20.6	100.0%	4	6	10	0.01%	22.2%	FSIYPPIPGEESSLR	97.7%	31.8	25	30.8	1	0	0	1691.86	60	74
28S ribosomal protein S11, mitochondrial	MRPS11	RT11_HUMAN	20.6	100.0%	4	6	10	0.01%	22.2%	GTGIAAQTAGIAAAAR	99.7%	89.5	25	84.8	2	0	0	1399.77	123	138
28S ribosomal protein S11, mitochondrial	MRPS11	RT11_HUMAN	20.6	100.0%	4	6	10	0.01%	22.2%	KFEEIPIAHIK	99.7%	39.2	25	39.2	1	2	0	1324.76	79	89
28S ribosomal protein S11, mitochondrial	MRPS11	RT11_HUMAN	20.6	100.0%	4	6	10	0.01%	22.2%	KGTGIAAQTAGIAAAAR	99.7%	114	25	112	2	2	0	1527.86	122	138
28S ribosomal protein S12, mitochondrial	MRPS12	RT12_HUMAN	15.2	100.0%	3	4	8	0.01%	15.2%	GVVLCTFTR	99.6%	39.8	25	24.4	4	0	0	1052.56	60	68
28S ribosomal protein S12, mitochondrial	MRPS12	RT12_HUMAN	15.2	100.0%	3	4	8	0.01%	15.2%	KLGPTEGRPQLK	98.2%	26.5	25	18.8	1	1	0	1323.77	48	59
28S ribosomal protein S12, mitochondrial	MRPS12	RT12_HUMAN	15.2	100.0%	3	4	8	0.01%	15.2%	LGPTEGRPQLK	99.7%	45.2	25	33.7	2	0	0	1195.68	49	59
28S ribosomal protein S14, mitochondrial	MRPS14	RT14_HUMAN	15.1	100.0%	3	5	11	0.01%	28.9%	HLADHGQLSGIQR	99.7%	49.4	25	30.6	1	2	0	1431.75	113	125
28S ribosomal protein S14, mitochondrial	MRPS14	RT14_HUMAN	15.1	100.0%	3	5	11	0.01%	28.9%	ILQDVADEEIAALPR	99.7%	76.8	25	67.1	4	0	0	1652.89	66	80
28S ribosomal protein S14, mitochondrial	MRPS14	RT14_HUMAN	15.1	100.0%	3	5	11	0.01%	28.9%	MAYEYADER	99.7%	67.5	25	67.5	4	0	0	1163.47	43	51
28S ribosomal protein S15, mitochondrial	MRPS15	RT15_HUMAN	29.8	100.0%	4	4	7	0.01%	13.6%	IVANPEDTR	99.7%	49	25	39.4	2	0	0	1014.52	115	123
28S ribosomal protein S15, mitochondrial	MRPS15	RT15_HUMAN	29.8	100.0%	4	4	7	0.01%	13.6%	NTNYDVFEK	99.7%	50.6	25	39.3	2	0	0	1129.52	172	180
28S ribosomal protein S15, mitochondrial	MRPS15	RT15_HUMAN	29.8	100.0%	4	4	7	0.01%	13.6%	SYEEHLEK	97.4%	31.4	25	19.7	1	0	0	1034.48	138	145
28S ribosomal protein S15, mitochondrial	MRPS15	RT15_HUMAN	29.8	100.0%	4	4	7	0.01%	13.6%	YLLMSIDQR	99.7%	68.1	25	60.4	2	0	0	1138.59	155	163
28S ribosomal protein S16, mitochondrial	MRPS16	RT16_HUMAN	15.3	100.0%	3	4	8	0.01%	26.3%	AREVLLASQK	99.7%	51.2	25	43.9	2	0	0	1114.66	115	124
28S ribosomal protein S16, mitochondrial	MRPS16	RT16_HUMAN	15.3	100.0%	3	4	8	0.01%	26.3%	FVEQLGSYDPLPNSHGEK	99.7%	62.3	25	61.8	2	2	0	2016.97	47	64
28S ribosomal protein S16, mitochondrial	MRPS16	RT16_HUMAN	15.3	100.0%	3	4	8	0.01%	26.3%	LVALNLDR	99.7%	60	25	46.2	2	0	0	913.55	65	72
28S ribosomal protein S17, mitochondrial	MRPS17	RT17_HUMAN	14.5	99.8%	2	2	5	0.00%	15.4%	HELAEIVFK	99.7%	49.8	25	49.8	3	0	0	1085.60	79	87
28S ribosomal protein S17, mitochondrial	MRPS17	RT17_HUMAN	14.5	99.8%	2	2	5	0.00%	15.4%	NLEELNISSAQ	99.7%	81.5	25	64.8	2	0	0	1217.60	120	130
28S ribosomal protein S18a, mitochondrial	MRPS18A	RT18A_HUMAN	22.2	100.0%	4	4	10	0.01%	24.0%	ESPNPPNPSGQCPICR	99.7%	60.1	25	60.1	3	0	0	1809.80	59	74
28S ribosomal protein S18a, mitochondrial	MRPS18A	RT18A_HUMAN	22.2	100.0%	4	4	10	0.01%	24.0%	KITGLCQEEHR	98.7%	27.8	25	27.8	0	2	0	1370.68	103	113
28S ribosomal protein S18a, mitochondrial	MRPS18A	RT18A_HUMAN	22.2	100.0%	4	4	10	0.01%	24.0%	MPVGSPLLR	99.2%	36.5	25	24	1	0	0	969.56	174	182
28S ribosomal protein S18a, mitochondrial	MRPS18A	RT18A_HUMAN	22.2	100.0%	4	4	10	0.01%	24.0%	WAPGSVKPIYK	99.7%	40.9	25	32.1	4	0	0	1245.70	154	164
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	5	6	15	0.01%	24.4%	LTQAIQK	99.0%	35.8	25	16.1	1	0	0	801.48	150	156
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	5	6	15	0.01%	24.4%	LYQGHLQEESGPPPESMPK	99.7%	51.9	25	46.3	0	5	0	2140.00	219	237
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	5	6	15	0.01%	24.4%	TPAEASSTGQTGPQSAL	99.7%	75.7	25	75.7	2	0	0	1602.76	242	258
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	5	6	15	0.01%	24.4%	VVGNPCPICR	99.7%	50.7	25	43.8	3	0	0	1171.57	100	109
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	5	6	15	0.01%	24.4%	YLESEEYQER	99.7%	57.5	25	53.7	4	0	0	1345.59	58	67
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	7	8	12	0.01%	19.6%	DCGEYAHTR	99.6%	40.5	25	37.6	1	0	0	1108.45	161	169
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	7	8	12	0.01%	19.6%	FMEPYIFGSR	99.7%	52.3	25	47.3	4	0	0	1246.59	101	110
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	7	8	12	0.01%	19.6%	GGMLTNAR	98.9%	35.1	25	11.5	2	0	0	819.41	173	180
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	7	8	12	0.01%	19.6%	GIILFISR	99.7%	63.6	25	50.5	2	0	0	918.58	140	147
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	7	8	12	0.01%	19.6%	HSDFFNVK	99.7%	48.8	25	40.6	1	0	0	993.48	69	76
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	7	8	12	0.01%	19.6%	ILNEPLK	98.2%	32.9	25	18.7	1	0	0	826.50	62	68
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	7	8	12	0.01%	19.6%	LLFGPTVR	99.6%	40.6	25	27.5	1	0	0	902.55	181	188
28S ribosomal protein S21, mitochondrial	MRPS21	RT21_HUMAN	10.7	100.0%	3	5	12	0.01%	39.1%	ILTMDGLIEDIK	98.0%	32.3	25	23.4	1	0	0	1376.73	29	40
28S ribosomal protein S21, mitochondrial	MRPS21	RT21_HUMAN	10.7	100.0%	3	5	12	0.01%	39.1%	IYNMEMAR	99.7%	49.5	25	42.3	3	0	0	1027.47	63	70

28S ribosomal protein S21, mitochondrial	MRPS21	RT21_HUMAN	10.7	100.0%	3	5	12	0.01%	39.1%	TVMVQEGNVESAYR	99.7%	91.5	25	83.7	8	0	0	1598.75	11	24
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	14	26	0.02%	29.2%	DQAAEGINLIK	99.7%	67.3	25	57.9	2	0	0	1171.63	319	329
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	14	26	0.02%	29.2%	IDGLLIDQIQR	99.7%	74.3	25	51.6	2	0	0	1283.73	281	291
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	14	26	0.02%	29.2%	ILTPIIFKEENLR	99.7%	55.3	25	50.3	2	1	0	1585.93	204	216
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	14	26	0.02%	29.2%	KIDGLLIDQIQR	99.7%	43.5	25	28.3	0	2	0	1411.83	280	291
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	14	26	0.02%	29.2%	LMTQAQLEEATR	99.7%	95.7	25	82.2	4	0	0	1390.70	105	116
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	14	26	0.02%	29.2%	MIQVYFPK	99.7%	45.7	25	37.8	4	0	0	1041.54	192	199
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	14	26	0.02%	29.2%	MPPVLEER	99.7%	41	25	27	2	0	0	986.50	128	135
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	14	26	0.02%	29.2%	MTGLNLQK	99.4%	38	25	21.5	1	0	0	904.49	82	89
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	14	26	0.02%	29.2%	VPINDVLAEDK	99.7%	58.1	25	45.9	2	0	0	1212.65	136	146
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	14	26	0.02%	29.2%	VPINDVLAEDKILEGTETTK	99.7%	57.3	25	57.3	0	2	0	2185.16	136	155
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	11	14	26	0.02%	29.2%	YVFTDISYSIPHR	99.7%	71.2	25	71.2	2	0	0	1597.80	156	168
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	7	9	17	0.02%	35.8%	AFDLFNPNFK	99.7%	54.9	25	54.9	2	0	0	1212.60	84	93
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	7	9	17	0.02%	35.8%	AKFYSVYGSGQR	99.7%	65.2	25	64.2	2	1	0	1362.68	72	83
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	7	9	17	0.02%	35.8%	ALLAEGVILR	99.7%	69.1	25	38.5	2	0	0	1054.66	124	133
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	7	9	17	0.02%	35.8%	ALLAEGVILRR	95.6%	29.1	25	19.4	2	0	0	1210.76	124	134
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	7	9	17	0.02%	35.8%	FVEKYTELQK	99.3%	37.2	25	24.5	2	0	0	1284.68	99	108
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	7	9	17	0.02%	35.8%	LETVGSIFSR	99.7%	73.7	25	61.8	2	0	0	1108.60	6	15
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	7	9	17	0.02%	35.8%	LGETDEEKLFVETGK	99.7%	68.6	25	68.6	2	2	0	1694.85	109	123
28S ribosomal protein S24, mitochondrial	MRPS24	RT24_HUMAN	19.0	100.0%	5	5	9	0.01%	18.6%	GNQLEICAVVLR	99.7%	61.7	25	49.6	1	0	0	1371.74	114	125
28S ribosomal protein S24, mitochondrial	MRPS24	RT24_HUMAN	19.0	100.0%	5	5	9	0.01%	18.6%	LHLQTVPSK	99.7%	49.4	25	43.7	2	0	0	1022.60	153	161
28S ribosomal protein S24, mitochondrial	MRPS24	RT24_HUMAN	19.0	100.0%	5	5	9	0.01%	18.6%	RGNQLEICAVVLR	99.7%	39.5	25	34.8	0	2	0	1527.84	113	125
28S ribosomal protein S24, mitochondrial	MRPS24	RT24_HUMAN	19.0	100.0%	5	5	9	0.01%	18.6%	TVEDVFLR	99.7%	51.4	25	41.7	2	0	0	978.53	86	93
28S ribosomal protein S24, mitochondrial	MRPS24	RT24_HUMAN	19.0	100.0%	5	5	9	0.01%	18.6%	TVEDVFLRK	99.3%	37.2	25	26.1	2	0	0	1106.62	86	94
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	7	11	21	0.02%	49.7%	ECICEVEGQVPCPSLVPLPK	99.4%	38.3	25	37.2	1	0	0	2311.11	138	157
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	7	11	21	0.02%	49.7%	FVFFNIPQIQYK	95.1%	28.7	25	28.7	1	0	0	1543.83	47	58
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	7	11	21	0.02%	49.7%	NPWVQIMMFK	99.3%	37.7	25	37.2	4	0	0	1325.64	59	68
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	7	11	21	0.02%	49.7%	SNKEIMEHIR	99.7%	38.9	25	35.6	0	2	0	1272.64	94	103
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	7	11	21	0.02%	49.7%	TLQYLSQGNVVFK	99.7%	89.7	25	74.6	2	0	0	1496.81	12	24
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	7	11	21	0.02%	49.7%	TLQYLSQGNVVFKDSVK	99.7%	79.7	25	79.7	2	2	0	1926.03	12	28
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	7	11	21	0.02%	49.7%	VMTVNYNTHGELGEGAR	99.7%	85.4	25	80.8	4	3	0	1847.87	29	45
28S ribosomal protein S26, mitochondrial	MRPS26	RT26_HUMAN	24.2	100.0%	3	4	5	0.00%	18.5%	KAEEVQAWAQR	99.7%	50.4	25	44.2	1	2	0	1315.68	142	152
28S ribosomal protein S26, mitochondrial	MRPS26	RT26_HUMAN	24.2	100.0%	3	4	5	0.00%	18.5%	KNYNWAITR	99.7%	46.3	25	38.3	1	0	0	1165.61	185	193
28S ribosomal protein S26, mitochondrial	MRPS26	RT26_HUMAN	24.2	100.0%	3	4	5	0.00%	18.5%	VNMPPAVDPAEFFVLMER	99.7%	69.1	25	66	1	0	0	2062.01	42	59
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	8	8	15	0.01%	21.0%	EALDVLGAVLK	99.7%	85.7	25	79.7	2	0	0	1127.67	278	288
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	8	8	15	0.01%	21.0%	IESEGLLSLTTQLVK	99.7%	86.3	25	83.9	2	0	0	1630.93	347	361
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	8	8	15	0.01%	21.0%	KLPVSSLTISR	99.7%	50.1	25	46.7	2	0	0	1200.73	64	74
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	8	8	15	0.01%	21.0%	LIDNISSR	99.6%	40	25	4.86	2	0	0	917.51	75	82
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	8	8	15	0.01%	21.0%	LPQYLER	99.7%	42.8	25	27.4	2	0	0	918.50	327	333
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	8	8	15	0.01%	21.0%	LVEQLDIEETEQSK	99.7%	101	25	94.3	1	0	0	1660.83	313	326
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	8	8	15	0.01%	21.0%	NFGASLLLPGLK	99.7%	62.4	25	55.6	2	0	0	1229.73	203	214
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	8	8	15	0.01%	21.0%	VAASPEDIK	99.2%	36.6	25	28.1	2	0	0	929.49	266	274
28S ribosomal protein S28, mitochondrial	MRPS28	RT28_HUMAN	20.8	100.0%	3	3	12	0.01%	15.5%	AGGFASALER	99.7%	71.9	25	57.5	4	0	0	978.50	49	58
28S ribosomal protein S28, mitochondrial	MRPS28	RT28_HUMAN	20.8	100.0%	3	3	12	0.01%	15.5%	LLDLELTSR	99.7%	75.1	25	64.9	4	0	0	1059.60	144	152
28S ribosomal protein S28, mitochondrial	MRPS28	RT28_HUMAN	20.8	100.0%	3	3	12	0.01%	15.5%	NVESFASMLR	99.7%	69.8	25	65.4	4	0	0	1169.56	76	85
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	9	10	19	0.02%	22.6%	AYLPQELLGK	97.5%	31.5	25	19	2	0	0	1131.64	322	331
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	9	10	19	0.02%	22.6%	ELLFLSNANPSLLER	99.7%	104	25	103	2	0	0	1715.93	379	393
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	9	10	19	0.02%	22.6%	FDQPLEASTWLK	99.7%	81.7	25	68.2	2	0	0	1434.73	178	189
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	9	10	19	0.02%	22.6%	GSPLGEVVEQGITR	99.7%	75.6	25	69.8	2	0	0	1441.76	219	232
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	9	10	19	0.02%	22.6%	KAYLPQELLGK	99.4%	38.5	25	38.5	1	0	0	1259.74	321	331
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	9	10	19	0.02%	22.6%	NATDAVGIVLK	99.7%	72.4	25	64.2	2	0	0	1100.63	235	245

28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	9	10	19	0.02%	22.6%	NTSFAYPAIR	99.7%	47.6	25	36.5	2	0	0	1139.58	114	123
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	9	10	19	0.02%	22.6%	TFSEACLMVR	99.7%	41.8	25	41.5	4	0	0	1229.57	93	102
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	9	10	19	0.02%	22.6%	YLLYGEK	99.6%	39.8	25	30	2	0	0	885.47	124	130
28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	6	7	12	0.01%	20.0%	EAPETDTSPSLWDVEFAK	99.7%	76.4	25	76.4	2	0	0	2021.93	267	284
28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	6	7	12	0.01%	20.0%	HFMELVTCGLSK	96.5%	30.1	25	24.9	1	0	0	1437.69	349	360
28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	6	7	12	0.01%	20.0%	IQFDEGYDNYPGQEK	99.7%	94.6	25	94.6	2	0	0	1802.79	226	240
28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	6	7	12	0.01%	20.0%	ISFSNIISDMK	99.7%	78.1	25	68.4	4	0	0	1254.64	199	209
28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	6	7	12	0.01%	20.0%	SELLSQLQQHEEESR	97.7%	25.6	25	22.1	0	2	0	1812.87	175	189
28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	6	7	12	0.01%	20.0%	SLEATLGR	99.2%	36.7	25	19.3	1	0	0	846.47	128	135
28S ribosomal protein S33, mitochondrial	MRPS33	RT33_HUMAN	12.6	99.8%	2	2	4	0.00%	19.8%	LFGEVTRPTNSK	99.7%	49.3	25	40.8	2	0	0	1348.72	18	29
28S ribosomal protein S33, mitochondrial	MRPS33	RT33_HUMAN	12.6	99.8%	2	2	4	0.00%	19.8%	LFSELPLAK	99.7%	41.6	25	19.8	2	0	0	1017.60	36	44
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	6	7	18	0.02%	27.1%	AWGILTFK	99.7%	44.8	25	35.6	4	0	0	935.54	114	121
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	6	7	18	0.02%	27.1%	EQLNRPR	98.8%	34.7	25	22.9	1	0	0	912.50	23	29
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	6	7	18	0.02%	27.1%	LLQLLGR	99.7%	63.8	25	21.5	4	0	0	812.54	64	70
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	6	7	18	0.02%	27.1%	LPLFGLGR	99.6%	40.3	25	35.7	4	0	0	872.54	71	78
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	6	7	18	0.02%	27.1%	NGDTSTEEPMLNVQR	99.7%	65	25	65	2	0	0	1706.77	181	195
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	6	7	18	0.02%	27.1%	VRPDYTAQNLDHGK	99.7%	41.2	25	35.4	0	3	0	1613.80	100	113
28S ribosomal protein S35, mitochondrial	MRPS35	RT35_HUMAN	36.8	100.0%	7	8	12	0.01%	24.8%	EGNLELLK	98.2%	32.8	25	12.4	2	0	0	915.51	100	107
28S ribosomal protein S35, mitochondrial	MRPS35	RT35_HUMAN	36.8	100.0%	7	8	12	0.01%	24.8%	HFPIEIDSTDYVSSGPSVR	99.7%	86.5	25	82.3	1	0	0	2106.01	146	164
28S ribosomal protein S35, mitochondrial	MRPS35	RT35_HUMAN	36.8	100.0%	7	8	12	0.01%	24.8%	LSSLNLDDHAK	99.7%	76.8	25	58.5	2	0	0	1212.62	177	187
28S ribosomal protein S35, mitochondrial	MRPS35	RT35_HUMAN	36.8	100.0%	7	8	12	0.01%	24.8%	NEEENENSISQYK	99.7%	45.2	25	45.2	1	0	0	1583.68	301	313
28S ribosomal protein S35, mitochondrial	MRPS35	RT35_HUMAN	36.8	100.0%	7	8	12	0.01%	24.8%	NILETLLQMK	99.7%	64.2	25	52.7	2	0	0	1202.68	261	270
28S ribosomal protein S35, mitochondrial	MRPS35	RT35_HUMAN	36.8	100.0%	7	8	12	0.01%	24.8%	NMEINKEELLGTK	99.7%	62.5	25	56.7	3	0	0	1534.78	275	287
28S ribosomal protein S35, mitochondrial	MRPS35	RT35_HUMAN	36.8	100.0%	7	8	12	0.01%	24.8%	SVVSLKNEEENENSISQYK	99.7%	69.6	25	68.7	1	0	0	2197.06	295	313
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	8	9	17	0.02%	22.1%	EECGPLPIVVASPR	99.7%	78.5	25	73.9	2	0	0	1523.79	375	388
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	8	9	17	0.02%	22.1%	GAAGFSIGK	99.4%	37.8	25	20.1	2	0	0	807.44	252	260
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	8	9	17	0.02%	22.1%	GALAETGAGAK	99.7%	60.6	25	42.8	2	0	0	945.50	101	111
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	8	9	17	0.02%	22.1%	LTADELWK	99.7%	47.3	25	40.1	2	0	0	975.51	93	100
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	8	9	17	0.02%	22.1%	NGAVQTIAQR	99.7%	47.6	25	39.6	2	0	0	1057.57	151	160
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	8	9	17	0.02%	22.1%	VSGSINMLSLTQGLFR	99.7%	93.1	25	89.9	4	0	0	1738.92	336	351
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	8	9	17	0.02%	22.1%	YEDHTIFHDISLR	99.7%	36.1	25	36.1	0	2	0	1645.80	285	297
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	8	9	17	0.02%	22.1%	YGFLWPGLNVPLMK	99.7%	50.8	25	50.3	1	0	0	1650.87	137	150
28S ribosomal protein S6, mitochondrial	MRPS6	RT06_HUMAN	14.2	100.0%	4	5	6	0.01%	23.2%	AMQRPETAATLK	95.1%	28.7	25	22.9	1	0	0	1316.70	12	23
28S ribosomal protein S6, mitochondrial	MRPS6	RT06_HUMAN	14.2	100.0%	4	5	6	0.01%	23.2%	AMQRPETAATLKR	99.7%	40.1	25	28	0	3	0	1488.80	12	24
28S ribosomal protein S6, mitochondrial	MRPS6	RT06_HUMAN	14.2	100.0%	4	5	6	0.01%	23.2%	DLENLGER	98.5%	33.8	25	20.7	1	0	0	945.46	38	45
28S ribosomal protein S6, mitochondrial	MRPS6	RT06_HUMAN	14.2	100.0%	4	5	6	0.01%	23.2%	TIEALMDR	97.9%	32.2	25	22.6	1	0	0	964.48	25	32
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	6	7	13	0.01%	26.4%	FYQVPVPLPDR	99.7%	44.1	25	38	2	0	0	1330.72	167	177
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	6	7	13	0.01%	26.4%	KPVEELTEEEKYVR	99.7%	55.2	25	55	0	2	0	1748.91	53	66
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	6	7	13	0.01%	26.4%	LLEAFHNQGPVIK	99.7%	58.5	25	51.9	1	0	0	1465.82	209	221
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	6	7	13	0.01%	26.4%	LLEAFHNQGPVIKR	99.6%	33	25	28.3	0	1	0	1621.92	209	222
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	6	7	13	0.01%	26.4%	NCEPMIGLVPILK	98.3%	33.2	25	33.2	3	0	0	1483.80	151	163
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	6	7	13	0.01%	26.4%	TSSVFEDPVISK	99.7%	59.6	25	54.7	4	0	0	1308.67	82	93
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	9	10	16	0.02%	25.3%	AIAYLFPSGLFEK	99.7%	53.8	25	43.7	2	0	0	1455.79	107	119
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	9	10	16	0.02%	25.3%	ETYTEDFIKK	98.7%	34.5	25	22.4	2	0	0	1273.63	67	76
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	9	10	16	0.02%	25.3%	HDVTCTVSGGGR	99.7%	66.3	25	66.3	2	0	0	1245.56	326	337
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	9	10	16	0.02%	25.3%	HLANMMGEDPETFTQEDIDR	99.7%	36.8	25	36.8	0	1	0	2381.00	87	106
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	9	10	16	0.02%	25.3%	HPEQIFPR	97.7%	31.9	25	23.1	1	0	0	1023.54	127	134
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	9	10	16	0.02%	25.3%	LLTSQCGAAEEEFVQR	99.7%	102	25	99.6	2	0	0	1837.88	228	243
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	9	10	16	0.02%	25.3%	LSDLDYMQFIR	99.7%	78.1	25	77.8	4	0	0	1400.69	213	223
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	9	10	16	0.02%	25.3%	QIEEFNIGK	98.4%	33.4	25	22.2	1	0	0	1077.56	77	85
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	9	10	16	0.02%	25.3%	QIEEFNIGKR	99.6%	39.9	25	23.3	1	0	0	1233.66	77	86

2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	GCAT	KBL_HUMAN	45.3	100.0%	4	4	6	0.01%	13.4%	ALGGASGGYTTGPGPLVSLLR	99.7%	71.1	25	71.1	2	0	0	1944.06	266	286
2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	GCAT	KBL_HUMAN	45.3	100.0%	4	4	6	0.01%	13.4%	FICGTQSIHK	99.7%	47.2	25	33	1	0	0	1190.60	104	113
2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	GCAT	KBL_HUMAN	45.3	100.0%	4	4	6	0.01%	13.4%	GIFVIGFSYPVVPK	99.7%	43.9	25	43.9	2	0	0	1522.87	370	383
2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	GCAT	KBL_HUMAN	45.3	100.0%	4	4	6	0.01%	13.4%	GILEGELEGIR	99.7%	67.3	25	52.3	1	0	0	1185.65	29	39
2'-deoxynucleoside 5'-phosphate N-hydrolase 1	DNPH1	DNPH1_HUMAN	19.1	99.9%	2	3	3	0.00%	13.8%	FGTVLTEHVAAAELGAR	99.7%	72.7	25	67.3	1	1	0	1741.92	49	65
2'-deoxynucleoside 5'-phosphate N-hydrolase 1	DNPH1	DNPH1_HUMAN	19.1	99.9%	2	3	3	0.00%	13.8%	VLSAMIR	95.5%	29	25	10.6	1	0	0	805.46	126	132
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	COQ5	COQ5_HUMAN	37.1	100.0%	4	4	7	0.01%	15.6%	AQQNLSWEEIAK	99.7%	45	25	41.1	1	0	0	1416.71	142	153
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	COQ5	COQ5_HUMAN	37.1	100.0%	4	4	7	0.01%	15.6%	EYQNEEDSLGGSR	99.7%	74.8	25	69.1	2	0	0	1483.63	154	166
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	COQ5	COQ5_HUMAN	37.1	100.0%	4	4	7	0.01%	15.6%	FLCLEFSQVNNPLISR	99.7%	73	25	73	2	0	0	1937.00	242	257
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	COQ5	COQ5_HUMAN	37.1	100.0%	4	4	7	0.01%	15.6%	VYQVFESVAK	99.7%	60.9	25	55.1	2	0	0	1169.62	68	77
2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	BCKDHA	ODBA_HUMAN	50.5	99.8%	2	2	2	0.00%	6.7%	AVAENQPFLIEAMTYR	99.3%	37.4	25	37.4	1	0	0	1852.93	317	332
2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	BCKDHA	ODBA_HUMAN	50.5	99.8%	2	2	2	0.00%	6.7%	VDGNDVFAVYNATK	99.7%	75.3	25	75.3	1	0	0	1512.73	298	311
2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	BCKDHB	ODBB_HUMAN	43.1	100.0%	4	4	6	0.01%	13.5%	LGVSCEVIDLR	99.7%	77.2	25	62.3	2	0	0	1260.66	295	305
2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	BCKDHB	ODBB_HUMAN	43.1	100.0%	4	4	6	0.01%	13.5%	MNLFQSVTSALDNSLAK	99.7%	102	25	94.1	1	0	0	1854.93	71	87
2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	BCKDHB	ODBB_HUMAN	43.1	100.0%	4	4	6	0.01%	13.5%	SGDLFNCGSLTIR	99.7%	69.5	25	64.8	1	0	0	1439.69	171	183
2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	BCKDHB	ODBB_HUMAN	43.1	100.0%	4	4	6	0.01%	13.5%	TIIPWDVDTICK	98.3%	33.2	25	22.9	2	0	0	1460.75	306	317
39S ribosomal protein L1, mitochondrial	MRPL1	RM01_HUMAN	36.9	100.0%	4	4	5	0.00%	15.4%	FQILDFTSPK	99.3%	37.1	25	27.1	2	0	0	1195.64	109	118
39S ribosomal protein L1, mitochondrial	MRPL1	RM01_HUMAN	36.9	100.0%	4	4	5	0.00%	15.4%	NVEPFTSVLSLPYPFASEINK	99.7%	54.4	25	54.4	1	0	0	2352.21	136	156
39S ribosomal protein L1, mitochondrial	MRPL1	RM01_HUMAN	36.9	100.0%	4	4	5	0.00%	15.4%	QIYEVEK	96.9%	30.6	25	9.05	1	0	0	908.47	95	101
39S ribosomal protein L1, mitochondrial	MRPL1	RM01_HUMAN	36.9	100.0%	4	4	5	0.00%	15.4%	VAVFTENASEVK	99.7%	56.5	25	43.8	1	0	0	1293.67	157	168
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	10	10	17	0.02%	54.2%	AGLAMPGPPLGPVLGQR	99.7%	60.1	25	49.5	1	0	0	1646.91	26	42
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	10	10	17	0.02%	54.2%	AQDEAFALQDVPLSSVVR	99.7%	66.9	25	66.9	2	0	0	1945.00	125	142
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	10	10	17	0.02%	54.2%	DLSSEELAAFQK	99.7%	74.5	25	63.3	2	0	0	1337.66	158	169
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	10	10	17	0.02%	54.2%	DLSSEELAAFQKER	99.7%	61	25	61	2	0	0	1622.80	158	171
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	10	10	17	0.02%	54.2%	EADLAAQEEAAK	99.7%	55.5	25	51.1	1	0	0	1245.60	180	191
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	10	10	17	0.02%	54.2%	EADLAAQEEAAKK	99.7%	75.9	25	65.6	2	0	0	1373.69	180	192
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	10	10	17	0.02%	54.2%	GVSINQFCK	99.6%	40.3	25	29.2	2	0	0	1052.52	43	51
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	10	10	17	0.02%	54.2%	IGQPTVSYFLK	99.7%	54.9	25	52.2	2	0	0	1252.69	82	92
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	10	10	17	0.02%	54.2%	KPEVGGVIR	97.4%	31.2	25	26.8	2	0	0	954.57	13	21
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	10	10	17	0.02%	54.2%	QTGKEVAGLVTLK	95.4%	28.9	25	18.7	1	0	0	1343.79	103	115
39S ribosomal protein L12, mitochondrial	MRPL12	RM12_HUMAN	21.3	100.0%	3	3	5	0.00%	16.2%	KLVESLPQEIK	99.7%	72.3	25	58.2	2	0	0	1283.76	163	173
39S ribosomal protein L12, mitochondrial	MRPL12	RM12_HUMAN	21.3	100.0%	3	3	5	0.00%	16.2%	LTEAKPVDK	96.7%	30.3	25	25.2	1	0	0	1000.57	134	142
39S ribosomal protein L12, mitochondrial	MRPL12	RM12_HUMAN	21.3	100.0%	3	3	5	0.00%	16.2%	NYIQGINLVQAK	99.7%	62.5	25	55	2	0	0	1360.76	151	162
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	8	10	17	0.02%	46.6%	APQQWATFAR	99.7%	67.8	25	59	2	0	0	1175.60	7	16
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	8	10	17	0.02%	46.6%	IWYLLDGK	99.4%	38.5	25	19.7	1	0	0	1007.56	17	24
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	8	10	17	0.02%	46.6%	LAAMASIR	99.7%	61.2	25	48.3	2	0	0	848.47	31	38
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	8	10	17	0.02%	46.6%	LAIYGMLPK	99.5%	39.1	25	30.2	4	0	0	1021.58	106	114
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	8	10	17	0.02%	46.6%	LWTPPEDYRL	97.8%	32.1	25	21.1	1	0	0	1289.65	169	178
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	8	10	17	0.02%	46.6%	NLVEELPQPR	99.0%	35.8	25	28.6	2	0	0	1194.65	140	149
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	8	10	17	0.02%	46.6%	RLDEYTQEEIDAFPR	99.7%	35.3	25	34.7	0	1	0	1881.90	154	168
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	8	10	17	0.02%	46.6%	VYSSHTGYPGGFR	99.7%	72	25	69.8	2	2	0	1427.67	76	88
39S ribosomal protein L14, mitochondrial	MRPL14	RM14_HUMAN	15.9	100.0%	4	5	9	0.01%	37.2%	ALIVGHCMPGPR	99.6%	40.2	25	40.2	2	0	0	1323.67	84	95
39S ribosomal protein L14, mitochondrial	MRPL14	RM14_HUMAN	15.9	100.0%	4	5	9	0.01%	37.2%	FDSNNVVLIEDNGNPVGTR	99.7%	95.5	25	95.5	2	0	0	2060.00	100	118
39S ribosomal protein L14, mitochondrial	MRPL14	RM14_HUMAN	15.9	100.0%	4	5	9	0.01%	37.2%	VLAIAQNFV	99.7%	46.3	25	35.4	2	0	0	974.57	137	145
39S ribosomal protein L14, mitochondrial	MRPL14	RM14_HUMAN	15.9	100.0%	4	5	9	0.01%	37.2%	VVDNSALGNSPYHR	99.7%	63.2	25	52.7	2	1	0	1528.75	40	53
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	7	7	13	0.01%	28.7%	GVTIQPLKR	98.6%	33.9	25	19.4	2	0	0	1011.63	126	134
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	7	7	13	0.01%	28.7%	ILKPTDENLLK	99.5%	39.4	25	34	2	0	0	1283.76	282	292
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	7	7	13	0.01%	28.7%	LGFEGGQTPFYIR	99.7%	78.6	25	70.7	2	0	0	1484.75	65	77
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	7	7	13	0.01%	28.7%	LQYLIDLGR	99.7%	64.3	25	58.7	2	0	0	1090.63	101	109
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	7	7	13	0.01%	28.7%	SLDIVCKPVPFFLR	98.8%	28.2	25	28.2	0	1	0	1690.94	183	196
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	7	7	13	0.01%	28.7%	VDPSQPIDLTQLVNGR	99.7%	65	25	65	2	0	0	1751.93	110	125

39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	7	7	13	0.01%	28.7%	VSLANLKPNPGSK	99.7%	51.9	25	48.2	2	0	0	1324.76	22	34
39S ribosomal protein L16, mitochondrial	MRPL16	RM16_HUMAN	28.5	100.0%	5	5	9	0.01%	20.3%	GAIDHYVTPVK	99.7%	48	25	33.8	2	0	0	1199.64	145	155
39S ribosomal protein L16, mitochondrial	MRPL16	RM16_HUMAN	28.5	100.0%	5	5	9	0.01%	20.3%	IATANMLGIR	99.7%	81.4	25	64.5	2	0	0	1059.60	218	227
39S ribosomal protein L16, mitochondrial	MRPL16	RM16_HUMAN	28.5	100.0%	5	5	9	0.01%	20.3%	NNQNPWTFER	99.6%	39.9	25	39.8	1	0	0	1305.60	208	217
39S ribosomal protein L16, mitochondrial	MRPL16	RM16_HUMAN	28.5	100.0%	5	5	9	0.01%	20.3%	VLSPYDLTHK	98.2%	33	25	28	2	0	0	1172.63	229	238
39S ribosomal protein L16, mitochondrial	MRPL16	RM16_HUMAN	28.5	100.0%	5	5	9	0.01%	20.3%	VPAPFKPITR	99.7%	60.8	25	48.6	2	0	0	1125.68	124	133
39S ribosomal protein L17, mitochondrial	MRPL17	RM17_HUMAN	20.1	100.0%	3	3	7	0.01%	19.4%	LFQVLAPR	99.7%	60.6	25	48.3	4	0	0	943.57	89	96
39S ribosomal protein L17, mitochondrial	MRPL17	RM17_HUMAN	20.1	100.0%	3	3	7	0.01%	19.4%	MGLGPESR	99.7%	52.4	25	44	2	0	0	846.41	18	25
39S ribosomal protein L17, mitochondrial	MRPL17	RM17_HUMAN	20.1	100.0%	3	3	7	0.01%	19.4%	QSQEASNHSSHTAQTPGI	99.7%	52.5	25	45	1	0	0	1879.85	158	175
39S ribosomal protein L18, mitochondrial	MRPL18	RM18_HUMAN	20.6	100.0%	5	5	10	0.01%	24.4%	LQSAMTEGGVVLR	99.7%	72.8	25	60.5	2	0	0	1360.73	161	173
39S ribosomal protein L18, mitochondrial	MRPL18	RM18_HUMAN	20.6	100.0%	5	5	10	0.01%	24.4%	LQSAMTEGGVVLREPQR	99.7%	38.2	25	36.3	0	2	0	1886.98	161	177
39S ribosomal protein L18, mitochondrial	MRPL18	RM18_HUMAN	20.6	100.0%	5	5	10	0.01%	24.4%	NLELLSVAR	99.7%	64.7	25	37.2	2	0	0	1014.59	55	63
39S ribosomal protein L18, mitochondrial	MRPL18	RM18_HUMAN	20.6	100.0%	5	5	10	0.01%	24.4%	NVVACESIGR	99.7%	56.3	25	49	2	0	0	1104.55	121	130
39S ribosomal protein L18, mitochondrial	MRPL18	RM18_HUMAN	20.6	100.0%	5	5	10	0.01%	24.4%	VVVSASTR	99.7%	42.1	25	32.6	2	0	0	818.47	101	108
39S ribosomal protein L19, mitochondrial	MRPL19	RM19_HUMAN	33.5	100.0%	5	5	9	0.01%	17.5%	FDLCLTEQQMK	99.7%	44.9	25	44.9	1	0	0	1428.65	245	255
39S ribosomal protein L19, mitochondrial	MRPL19	RM19_HUMAN	33.5	100.0%	5	5	9	0.01%	17.5%	FLSPEFIPR	99.7%	43.6	25	36	2	0	0	1105.60	75	83
39S ribosomal protein L19, mitochondrial	MRPL19	RM19_HUMAN	33.5	100.0%	5	5	9	0.01%	17.5%	GLGATFILR	99.7%	64.6	25	49.3	2	0	0	947.57	144	152
39S ribosomal protein L19, mitochondrial	MRPL19	RM19_HUMAN	33.5	100.0%	5	5	9	0.01%	17.5%	ISQFLGICIQR	99.7%	66.8	25	60.5	2	0	0	1334.73	130	140
39S ribosomal protein L19, mitochondrial	MRPL19	RM19_HUMAN	33.5	100.0%	5	5	9	0.01%	17.5%	VTTADPYASGK	99.7%	49.6	25	45.7	2	0	0	1109.55	119	129
39S ribosomal protein L20, mitochondrial	MRPL20	RM20_HUMAN	17.4	100.0%	2	2	4	0.00%	14.8%	ITAASQEHGLK	99.7%	63.3	25	56.7	2	0	0	1154.62	72	82
39S ribosomal protein L20, mitochondrial	MRPL20	RM20_HUMAN	17.4	100.0%	2	2	4	0.00%	14.8%	VLADLAIYEPK	99.7%	82.5	25	68.9	2	0	0	1231.69	101	111
39S ribosomal protein L21, mitochondrial	MRPL21	RM21_HUMAN	22.8	100.0%	3	3	7	0.01%	15.6%	IVTTPQTVLR	99.7%	54.5	25	40.6	2	0	0	1127.68	185	194
39S ribosomal protein L21, mitochondrial	MRPL21	RM21_HUMAN	22.8	100.0%	3	3	7	0.01%	15.6%	LFAVVHFASR	99.7%	66.8	25	54.5	3	0	0	1146.64	95	104
39S ribosomal protein L21, mitochondrial	MRPL21	RM21_HUMAN	22.8	100.0%	3	3	7	0.01%	15.6%	VNEMIVTGQYGR	99.7%	64.9	25	41.4	2	0	0	1382.67	83	94
39S ribosomal protein L22, mitochondrial	MRPL22	RM22_HUMAN	23.6	100.0%	7	8	14	0.01%	33.5%	DKMWYLAK	98.3%	33.3	25	28.8	1	0	0	1054.54	79	86
39S ribosomal protein L22, mitochondrial	MRPL22	RM22_HUMAN	23.6	100.0%	7	8	14	0.01%	33.5%	EVLLEAQDMAVR	99.7%	87.7	25	79.7	4	0	0	1389.70	113	124
39S ribosomal protein L22, mitochondrial	MRPL22	RM22_HUMAN	23.6	100.0%	7	8	14	0.01%	33.5%	EYIQQLR	99.4%	37.8	25	0	2	0	0	949.51	192	198
39S ribosomal protein L22, mitochondrial	MRPL22	RM22_HUMAN	23.6	100.0%	7	8	14	0.01%	33.5%	LVEGPPPPPEPPK	99.7%	54.1	25	54.1	2	0	0	1353.74	172	184
39S ribosomal protein L22, mitochondrial	MRPL22	RM22_HUMAN	23.6	100.0%	7	8	14	0.01%	33.5%	RPAEIYHCR	98.6%	27.5	25	26	0	2	0	1201.59	63	71
39S ribosomal protein L22, mitochondrial	MRPL22	RM22_HUMAN	23.6	100.0%	7	8	14	0.01%	33.5%	SNLYIAESTSGR	99.7%	97.3	25	97.3	2	0	0	1297.64	132	143
39S ribosomal protein L22, mitochondrial	MRPL22	RM22_HUMAN	23.6	100.0%	7	8	14	0.01%	33.5%	VYCHYFVK	95.7%	29.2	25	18.5	1	0	0	1115.53	164	171
39S ribosomal protein L23, mitochondrial	MRPL23	RM23_HUMAN	17.8	99.9%	2	2	3	0.00%	14.4%	IPMEMTR	97.4%	31.4	25	21	1	0	0	909.42	44	50
39S ribosomal protein L23, mitochondrial	MRPL23	RM23_HUMAN	17.8	99.9%	2	2	3	0.00%	14.4%	NYLEGIYNVPVAAVR	99.7%	132	25	122	2	0	0	1677.90	55	69
39S ribosomal protein L24, mitochondrial	MRPL24	RM24_HUMAN	24.9	100.0%	3	3	5	0.00%	16.2%	ADGIVPETWIDGPK	97.8%	31.9	25	30.6	1	0	0	1497.76	162	175
39S ribosomal protein L24, mitochondrial	MRPL24	RM24_HUMAN	24.9	100.0%	3	3	5	0.00%	16.2%	GTMIPSEAPLLHR	99.7%	34.9	25	34.1	0	2	0	1437.75	106	118
39S ribosomal protein L24, mitochondrial	MRPL24	RM24_HUMAN	24.9	100.0%	3	3	5	0.00%	16.2%	KPTEIEWR	99.4%	38.7	25.3	28.3	2	0	0	1058.56	129	136
39S ribosomal protein L27, mitochondrial	MRPL27	RM27_HUMAN	16.1	99.9%	2	2	4	0.00%	14.2%	CLYALEEGIVR	99.7%	66.5	25	49.7	2	0	0	1322.68	88	98
39S ribosomal protein L27, mitochondrial	MRPL27	RM27_HUMAN	16.1	99.9%	2	2	4	0.00%	14.2%	NTEAVDLITR	99.7%	71.3	25	60.3	2	0	0	1131.60	110	119
39S ribosomal protein L28, mitochondrial	MRPL28	RM28_HUMAN	30.2	99.9%	2	2	4	0.00%	7.8%	LPGHYLR	99.4%	37.9	25	24.9	2	0	0	855.48	24	30
39S ribosomal protein L28, mitochondrial	MRPL28	RM28_HUMAN	30.2	99.9%	2	2	4	0.00%	7.8%	QDPQLHPEDPERR	98.2%	26.6	25	26.6	0	2	0	1616.78	172	184
39S ribosomal protein L3, mitochondrial	MRPL3	RM03_HUMAN	38.6	100.0%	3	4	6	0.01%	10.1%	MATLSVGGK	99.7%	41.8	25	31.5	3	0	0	863.47	142	150
39S ribosomal protein L3, mitochondrial	MRPL3	RM03_HUMAN	38.6	100.0%	3	4	6	0.01%	10.1%	QLVSDEDKAQLASK	99.7%	39.9	25	39.9	0	1	0	1531.80	63	76
39S ribosomal protein L3, mitochondrial	MRPL3	RM03_HUMAN	38.6	100.0%	3	4	6	0.01%	10.1%	RPGAVATGDIGR	99.5%	39	25	31.6	2	0	0	1169.64	239	250
39S ribosomal protein L32, mitochondrial	MRPL32	RM32_HUMAN	21.4	99.8%	2	2	2	0.00%	12.2%	HVLCAYCYEK	99.5%	39.3	25	39	1	0	0	1342.59	120	129
39S ribosomal protein L32, mitochondrial	MRPL32	RM32_HUMAN	21.4	99.8%	2	2	2	0.00%	12.2%	NNIDVCPECGHLK	99.7%	51.3	25	51.3	1	0	0	1555.70	105	117
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	5	6	11	0.01%	16.3%	ESLLLQVR	99.7%	57.9	25	35	2	0	0	957.57	216	223
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	5	6	11	0.01%	16.3%	ETYCPVIVDNLIQLCK	99.7%	60.3	25	60.3	2	0	0	1964.98	174	189
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	5	6	11	0.01%	16.3%	MILFAFGSALAQAR	99.7%	97.7	25	95.6	3	0	0	1495.81	313	326
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	5	6	11	0.01%	16.3%	VLEQPVVVQSVGTDGR	99.7%	87.7	25	87.7	2	0	0	1682.91	335	350
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	5	6	11	0.01%	16.3%	VYEIPGLEPITFAGK	99.7%	70.5	25	65.2	2	0	0	1633.88	49	63
39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	5	5	8	0.01%	17.4%	DLFHGATFVPR	99.7%	59.8	25	52.9	2	0	0	1259.65	160	170

39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	5	5	8	0.01%	17.4%	LAEYYGLYR	99.7%	70.9	25	57.2	2	0	0	1147.58	151	159
39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	5	5	8	0.01%	17.4%	LAFLLFK	98.8%	34.7	25	31.9	1	0	0	851.54	268	274
39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	5	5	8	0.01%	17.4%	QDQPIDFSEDARPSPCYQLAQR	99.7%	36.4	25	36.4	0	1	0	2621.21	275	296
39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	5	5	8	0.01%	17.4%	VAEGQVTCPYLPPFPAR	99.7%	59.5	25	54.9	2	0	0	1901.96	245	261
39S ribosomal protein L39, mitochondrial	MRPL39	RM39_HUMAN	38.7	100.0%	4	5	8	0.01%	13.6%	DAHALIYK	98.4%	33.4	25	25.3	1	0	0	930.50	205	212
39S ribosomal protein L39, mitochondrial	MRPL39	RM39_HUMAN	38.7	100.0%	4	5	8	0.01%	13.6%	DLPFETLEVEAK	99.7%	73.8	25	61.1	2	0	0	1390.71	213	224
39S ribosomal protein L39, mitochondrial	MRPL39	RM39_HUMAN	38.7	100.0%	4	5	8	0.01%	13.6%	IGDFIDVSEGPLIPR	99.7%	71.5	25	62.7	2	0	0	1627.87	257	271
39S ribosomal protein L39, mitochondrial	MRPL39	RM39_HUMAN	38.7	100.0%	4	5	8	0.01%	13.6%	TDPGTVFVMNK	98.9%	35.3	25	32.5	3	0	0	1224.59	73	83
39S ribosomal protein L4, mitochondrial	MRPL4	RM04_HUMAN	34.9	100.0%	3	3	7	0.01%	15.1%	ATENPEQVASEGLPEPVLR	99.7%	93	25	80.1	2	0	0	2036.03	31	49
39S ribosomal protein L4, mitochondrial	MRPL4	RM04_HUMAN	34.9	100.0%	3	3	7	0.01%	15.1%	GPTSYYYMLPMK	99.7%	53.8	25	23.4	3	0	0	1466.67	157	168
39S ribosomal protein L4, mitochondrial	MRPL4	RM04_HUMAN	34.9	100.0%	3	3	7	0.01%	15.1%	VGLADLHPDVFATAPR	99.7%	42	25	42	0	2	0	1678.89	77	92
39S ribosomal protein L40, mitochondrial	MRPL40	RM40_HUMAN	24.5	100.0%	2	2	4	0.00%	8.7%	DPNLFPFEK	99.2%	36.8	25	32.4	2	0	0	1106.55	165	173
39S ribosomal protein L40, mitochondrial	MRPL40	RM40_HUMAN	24.5	100.0%	2	2	4	0.00%	8.7%	VYTQVEFKR	99.7%	59.1	25	53.2	2	0	0	1169.63	198	206
39S ribosomal protein L41, mitochondrial	MRPL41	RM41_HUMAN	15.4	100.0%	5	6	9	0.01%	40.9%	DFKDGTFDPDNLEK	99.3%	37.2	25	34.7	1	1	0	1640.74	103	116
39S ribosomal protein L41, mitochondrial	MRPL41	RM41_HUMAN	15.4	100.0%	5	6	9	0.01%	40.9%	EMVPEFVVPDLTGFK	97.3%	31.2	25	31.2	1	0	0	1723.86	55	69
39S ribosomal protein L41, mitochondrial	MRPL41	RM41_HUMAN	15.4	100.0%	5	6	9	0.01%	40.9%	GIGFLTSGWR	99.6%	40.5	25	35.9	2	0	0	1093.58	40	49
39S ribosomal protein L41, mitochondrial	MRPL41	RM41_HUMAN	15.4	100.0%	5	6	9	0.01%	40.9%	LFQLYPR	99.7%	46.3	25	39.6	2	0	0	936.53	127	133
39S ribosomal protein L41, mitochondrial	MRPL41	RM41_HUMAN	15.4	100.0%	5	6	9	0.01%	40.9%	YGFEPTQEGK	99.6%	40.6	25	19.7	2	0	0	1155.53	117	126
39S ribosomal protein L43, mitochondrial	MRPL43	RM43_HUMAN	23.4	100.0%	5	5	9	0.01%	22.3%	EVIDFAR	99.7%	47	25	12.6	1	0	0	849.45	50	56
39S ribosomal protein L43, mitochondrial	MRPL43	RM43_HUMAN	23.4	100.0%	5	5	9	0.01%	22.3%	FLASVLHNGLGR	99.7%	73.8	25	68.1	2	0	0	1283.72	10	21
39S ribosomal protein L43, mitochondrial	MRPL43	RM43_HUMAN	23.4	100.0%	5	5	9	0.01%	22.3%	LADQSGLDVIR	99.7%	75.2	25	61.4	2	0	0	1186.64	104	114
39S ribosomal protein L43, mitochondrial	MRPL43	RM43_HUMAN	23.4	100.0%	5	5	9	0.01%	22.3%	SVEEISTLVQK	99.7%	61.9	25	41.8	2	0	0	1232.67	93	103
39S ribosomal protein L43, mitochondrial	MRPL43	RM43_HUMAN	23.4	100.0%	5	5	9	0.01%	22.3%	YVQQLQR	99.7%	50.8	25	39.3	2	0	0	934.51	22	28
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	8	9	16	0.02%	28.6%	EAVLLNLK	99.5%	39	25	32.5	2	0	0	899.56	113	120
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	8	9	16	0.02%	28.6%	IINPMGLLVEELK	99.7%	53.8	25	53.5	3	0	0	1468.84	234	246
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	8	9	16	0.02%	28.6%	LIAEGPGETVLVAEEEAAR	99.7%	103	25	103	2	0	0	1954.01	280	298
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	8	9	16	0.02%	28.6%	LQENFSLDLLK	99.7%	69.6	25	54	2	0	0	1319.72	79	89
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	8	9	16	0.02%	28.6%	LYGFTENR	99.7%	49.2	25	37.7	2	0	0	999.49	304	311
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	8	9	16	0.02%	28.6%	QQLGIEK	99.0%	35.7	25	14.6	1	0	0	815.46	106	112
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	8	9	16	0.02%	28.6%	QSGGTTALPLYFVGLYCDK	99.7%	72.9	25	72.9	2	0	0	2090.03	260	278
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	8	9	16	0.02%	28.6%	TAFVNSCYIK	99.7%	49.1	25	49.1	2	0	0	1202.59	90	99
39S ribosomal protein L45, mitochondrial	MRPL45	RM45_HUMAN	35.4	100.0%	4	4	8	0.01%	10.8%	IKDFPEK	98.7%	34.2	25	6.43	2	0	0	876.48	134	140
39S ribosomal protein L45, mitochondrial	MRPL45	RM45_HUMAN	35.4	100.0%	4	4	8	0.01%	10.8%	IKDYDANFK	99.7%	41	25	38	2	0	0	1113.56	125	133
39S ribosomal protein L45, mitochondrial	MRPL45	RM45_HUMAN	35.4	100.0%	4	4	8	0.01%	10.8%	QTLAIYDR	99.7%	67.9	25	55.2	2	0	0	979.52	220	227
39S ribosomal protein L45, mitochondrial	MRPL45	RM45_HUMAN	35.4	100.0%	4	4	8	0.01%	10.8%	TMASQVSIR	99.1%	36.3	25	27.9	2	0	0	1008.51	115	123
39S ribosomal protein L46, mitochondrial	MRPL46	RM46_HUMAN	31.7	100.0%	3	4	8	0.01%	12.9%	ALLLTGDFSQAGNK	99.7%	99.3	25	90.4	2	0	0	1434.76	236	249
39S ribosomal protein L46, mitochondrial	MRPL46	RM46_HUMAN	31.7	100.0%	3	4	8	0.01%	12.9%	SLYSDHELR	99.3%	37.5	25	20.6	2	0	0	1119.54	82	90
39S ribosomal protein L46, mitochondrial	MRPL46	RM46_HUMAN	31.7	100.0%	3	4	8	0.01%	12.9%	TLATLSENNMEAK	99.7%	75.7	25	60.3	4	0	0	1437.69	191	203
39S ribosomal protein L47, mitochondrial	MRPL47	RM47_HUMAN	29.5	100.0%	5	5	8	0.01%	17.2%	KFPHLAEAQK	99.5%	39.3	25	30	2	0	0	1168.65	237	246
39S ribosomal protein L47, mitochondrial	MRPL47	RM47_HUMAN	29.5	100.0%	5	5	8	0.01%	17.2%	NMLLTLEQEAK	99.6%	40.8	25	29.2	1	0	0	1289.68	110	120
39S ribosomal protein L47, mitochondrial	MRPL47	RM47_HUMAN	29.5	100.0%	5	5	8	0.01%	17.2%	NMLLTLEQEAKR	99.7%	56	25	43.9	2	0	0	1461.77	110	121
39S ribosomal protein L47, mitochondrial	MRPL47	RM47_HUMAN	29.5	100.0%	5	5	8	0.01%	17.2%	SGAAWTCQQLR	99.7%	54	25	45	2	0	0	1277.61	81	91
39S ribosomal protein L47, mitochondrial	MRPL47	RM47_HUMAN	29.5	100.0%	5	5	8	0.01%	17.2%	VVQEREDALR	99.5%	38.9	25	16.7	1	0	0	1214.65	145	154
39S ribosomal protein L48, mitochondrial	MRPL48	RM48_HUMAN	23.9	100.0%	4	5	9	0.01%	21.7%	ARPELEELLAK	99.7%	49.6	25	33.7	2	0	0	1268.72	200	210
39S ribosomal protein L48, mitochondrial	MRPL48	RM48_HUMAN	23.9	100.0%	4	5	9	0.01%	21.7%	MLLDSVLTTHER	99.7%	73.3	25	52.9	4	0	0	1414.74	144	155
39S ribosomal protein L48, mitochondrial	MRPL48	RM48_HUMAN	23.9	100.0%	4	5	9	0.01%	21.7%	TIEVLQLQDQGSK	99.7%	107	25	103	2	0	0	1458.78	131	143
39S ribosomal protein L48, mitochondrial	MRPL48	RM48_HUMAN	23.9	100.0%	4	5	9	0.01%	21.7%	VEESYAMPTK	99.7%	47.3	25	43.2	1	0	0	1170.53	121	130
39S ribosomal protein L49, mitochondrial	MRPL49	RM49_HUMAN	19.2	100.0%	4	4	7	0.01%	27.7%	FVESVDEYQFVER	99.7%	83.8	25	83.8	2	0	0	1646.77	38	50
39S ribosomal protein L49, mitochondrial	MRPL49	RM49_HUMAN	19.2	100.0%	4	4	7	0.01%	27.7%	GYFDQELK	95.4%	29	25	24.5	1	0	0	999.48	151	158
39S ribosomal protein L49, mitochondrial	MRPL49	RM49_HUMAN	19.2	100.0%	4	4	7	0.01%	27.7%	KVEGDIWALQK	99.7%	45.7	25	38.4	2	0	0	1286.71	112	122
39S ribosomal protein L49, mitochondrial	MRPL49	RM49_HUMAN	19.2	100.0%	4	4	7	0.01%	27.7%	TPVTQVNEVTGTLR	99.7%	90.3	25	90.3	2	0	0	1514.82	135	148

39S ribosomal protein L53, mitochondrial	MRPL53	RM53_HUMAN	12.1	99.9%	2	2	4	0.00%	20.5%	STNLNCSVIADVR	99.7%	64.6	25	56.8	2	0	0	1448.72	44	56
39S ribosomal protein L53, mitochondrial	MRPL53	RM53_HUMAN	12.1	99.9%	2	2	4	0.00%	20.5%	TFLQTVSSEK	99.7%	48.7	25	45.5	2	0	0	1139.59	32	41
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	7	7	11	0.01%	28.1%	ENLELILTQSVENVGVR	99.7%	55.8	25	55.8	4	0	0	1913.03	92	108
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	7	7	11	0.01%	28.1%	LLPQGLAVYASPENK	96.7%	30.2	25	29.4	2	0	0	1599.87	123	137
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	7	7	11	0.01%	28.1%	LLPQGLAVYASPENKK	99.7%	55.4	25	55.4	1	0	0	1727.97	123	138
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	7	7	11	0.01%	28.1%	LPEEPITR	98.4%	33.5	25	24.4	1	0	0	954.53	208	215
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	7	7	11	0.01%	28.1%	NLGVVVAPHTLK	97.3%	31.2	25	31.2	1	0	0	1247.75	196	207
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	7	7	11	0.01%	28.1%	VPMSVVNFEKPK	97.5%	31.4	25	29.4	1	0	0	1390.74	233	244
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	7	7	11	0.01%	28.1%	WELNPEIVAR	97.0%	30.7	25	21.9	1	0	0	1226.65	182	191
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	9	13	19	0.02%	55.6%	DLAPIGIR	98.2%	32.8	25	30.8	1	0	0	854.51	185	192
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	9	13	19	0.02%	55.6%	GGIVGMTLPIAR	99.7%	62.5	25	49.1	3	0	0	1200.68	173	184
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	9	13	19	0.02%	55.6%	GLVAVITGGASGLGLATAER	99.7%	137	25	137	1	2	0	1813.02	10	29
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	9	13	19	0.02%	55.6%	GQTHTLEDFQR	99.7%	58.1	25	58.1	2	1	0	1331.63	106	116
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	9	13	19	0.02%	55.6%	GVIINTASVAAFEGQVGQAAYSASK	99.7%	112	25	112	1	1	0	2439.25	148	172
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	9	13	19	0.02%	55.6%	LVAGEMGQNEPDQGGQR	99.7%	90	25	90	2	0	0	1785.82	131	147
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	9	13	19	0.02%	55.6%	LVGQGASAVLLDLPNSGGEAQAK	99.7%	105	25	105	1	0	0	2195.17	30	52
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	9	13	19	0.02%	55.6%	VDVAVNCAGIAVASK	99.7%	105	25	103	2	0	0	1473.77	85	99
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	9	13	19	0.02%	55.6%	VLDVNLMGTFNVIR	99.7%	82.3	25	74.2	2	0	0	1590.87	117	130
3-ketoacyl-CoA thiolase, mitochondrial	ACAA2	THIM_HUMAN	41.9	99.8%	2	2	4	0.00%	5.5%	DFTATDLSEFAAK	99.7%	95.8	25	95.3	2	0	0	1415.67	26	38
3-ketoacyl-CoA thiolase, mitochondrial	ACAA2	THIM_HUMAN	41.9	99.8%	2	2	4	0.00%	5.5%	ETPALTINR	99.7%	50.6	25	44.2	2	0	0	1014.56	82	90
3-keto-steroid reductase	HSD17B7	DHB7_HUMAN	38.2	99.8%	2	2	4	0.00%	6.2%	ALFFGLFSR	99.7%	44.3	25	36.8	2	0	0	1057.58	103	111
3-keto-steroid reductase	HSD17B7	DHB7_HUMAN	38.2	99.8%	2	2	4	0.00%	6.2%	YATDLLSVALNR	99.7%	59.3	25	59.3	2	0	0	1335.73	198	209
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	6	7	25	0.02%	35.2%	AEAGAGSATEFQFR	99.7%	102	25	94.4	5	0	0	1441.67	140	153
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	6	7	25	0.02%	35.2%	DYLHLPPEIVPATLR	97.6%	25.3	25	16.8	0	2	0	1733.96	81	95
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	6	7	25	0.02%	35.2%	GLEGERPAR	97.7%	31.8	25	21.6	1	0	0	984.52	108	116
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	6	7	25	0.02%	35.2%	GYVKEQFAWR	99.7%	51.2	25	49	4	0	0	1283.65	56	65
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	6	7	25	0.02%	35.2%	IAIYELLFK	99.7%	65.7	25	65.7	5	0	0	1109.66	9	17
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	6	7	25	0.02%	35.2%	KAEAGAGSATEFQFR	99.7%	121	25	118	4	4	0	1569.77	139	153
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	56	0.05%	53.8%	CPFTGNVSIR	99.7%	63.9	25	48.5	10	0	0	1150.57	60	69
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	56	0.05%	53.8%	DVQIGDIVTVGECRPLSK	99.7%	96.2	25	92.7	5	3	0	1986.03	119	136
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	56	0.05%	53.8%	DYLHYIR	96.3%	29.8	25	20.8	3	0	0	979.50	91	97
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	56	0.05%	53.8%	EAIEGTYIDK	99.7%	61.3	25	48.5	2	0	0	1138.56	49	58
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	56	0.05%	53.8%	EAIEGTYIDKK	99.7%	61.7	25	50.9	8	2	0	1266.66	49	59
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	56	0.05%	53.8%	ILSGVVTK	99.7%	51.3	25	25.1	3	0	0	816.52	72	79
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	56	0.05%	53.8%	KCPFTGNVSIR	99.7%	47.6	25	47.6	2	0	0	1278.66	59	69
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	56	0.05%	53.8%	NMSVHLSPCFR	99.7%	53.8	25	47.2	4	3	0	1347.63	108	118
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	56	0.05%	53.8%	QPTIFQNK	99.6%	40.2	25	34.7	3	0	0	975.53	13	20
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	56	0.05%	53.8%	RDYLHYIR	99.7%	49.8	25	19.1	2	0	0	1135.60	90	97
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	56	0.05%	53.8%	RVLLGETGK	98.9%	35.2	25	20.9	2	0	0	972.58	22	30
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	56	0.05%	53.8%	VLLGETGK	98.0%	32.4	25	19.7	2	0	0	816.48	23	30
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	56	0.05%	53.8%	VLLGETGKEK	99.7%	58.8	25	33.6	2	0	0	1073.62	23	32
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	7	10	39	0.04%	57.6%	ESQAKDVIEEYFK	99.7%	41.9	25	35.4	2	0	0	1585.77	117	129
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	7	10	39	0.04%	57.6%	KVVGCSCVVVK	99.7%	70.2	25	60.9	4	1	0	1234.66	102	112
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	7	10	39	0.04%	57.6%	LGEWVGLCK	99.7%	59.7	25	57.4	8	0	0	1061.55	85	93
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	7	10	39	0.04%	57.6%	LVEALCAEHQINLIK	99.7%	84.9	25	78.2	4	3	0	1750.95	64	78
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	7	10	39	0.04%	57.6%	QAHLCVLASNCDEPMYVK	99.7%	48.1	25	48.1	0	6	0	2150.97	46	63
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	7	10	39	0.04%	57.6%	TALIHDGLAR	99.7%	55.3	25	40.1	7	0	0	1066.60	24	33
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	7	10	39	0.04%	57.6%	VVGCSCVVVK	99.7%	61.3	25	52.1	4	0	0	1106.57	103	112
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	9	10	37	0.04%	54.3%	DSHGVAQVR	97.4%	31.4	25	21.1	1	0	0	968.49	56	64
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	9	10	37	0.04%	54.3%	GLAPDLPEDLYHLIK	99.7%	47.5	25	42.5	4	0	0	1693.92	79	93
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	9	10	37	0.04%	54.3%	GLTPSQIGVILR	99.7%	72.6	25	59.3	4	0	0	1253.76	44	55

40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	9	10	37	0.04%	54.3%	KGLTPSQIGVILR	99.7%	83.5	25	83.5	4	0	0	1381.85	43	55
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	9	10	37	0.04%	54.3%	LILIESR	99.7%	50.7	25	21.2	4	0	0	843.53	115	121
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	9	10	37	0.04%	54.3%	LTSDDVKEQIYK	99.7%	73.8	25	67	11	2	0	1438.74	28	39
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	9	10	37	0.04%	54.3%	RSVPTWLK	98.6%	34.1	25	13.7	2	0	0	986.58	20	27
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	9	10	37	0.04%	54.3%	VLPPNWKYESSTASALVA	99.7%	41.7	25	41.7	2	0	0	1933.01	134	151
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	9	10	37	0.04%	54.3%	YESSTASALVA	99.7%	42.2	25	42.2	3	0	0	1098.53	141	151
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	16	67	0.06%	41.7%	ADRDESSPYAAMLAAQDVAQR	99.7%	53.6	25	53.6	1	6	0	2281.05	64	84
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	16	67	0.06%	41.7%	CKELGITALHIK	99.7%	51.8	25	48.4	4	2	0	1382.78	85	96
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	16	67	0.06%	41.7%	DESSPYAAMLAAQDVAQR	99.7%	93.6	25	82.1	8	0	0	1922.89	67	84
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	16	67	0.06%	41.7%	ELGITALHIK	99.7%	53.5	25	45.9	4	0	0	1094.66	87	96
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	16	67	0.06%	41.7%	IEDVTPIPSDSTR	99.7%	75.3	25	65.7	6	0	0	1429.72	129	141
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	16	67	0.06%	41.7%	IEDVTPIPSDSTRR	99.7%	51.7	25	50.6	3	3	0	1585.82	129	142
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	16	67	0.06%	41.7%	IGRIEDVTPIPSDSTR	99.7%	58.1	25	58.1	3	3	0	1755.92	126	141
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	16	67	0.06%	41.7%	TKTPGPGAQSALR	99.7%	39.4	25	31.6	3	4	0	1283.71	105	117
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	16	67	0.06%	41.7%	TPGPGAQSALR	99.7%	73.3	25	73.1	17	0	0	1054.56	107	117
40S ribosomal protein S15	RPS15	RS15_HUMAN	17.0	100.0%	3	10	25	0.02%	22.1%	DMIILPEMVGSMVGVYNGK	99.7%	95.8	25	56.2	11	0	0	2085.01	82	100
40S ribosomal protein S15	RPS15	RS15_HUMAN	17.0	100.0%	3	10	25	0.02%	22.1%	EAPPMEKPEVVK	99.7%	48.1	25	38.3	4	3	0	1353.71	66	77
40S ribosomal protein S15	RPS15	RS15_HUMAN	17.0	100.0%	3	10	25	0.02%	22.1%	KEAPPMEKPEVVK	99.7%	47.8	25	47.8	3	4	0	1481.80	65	77
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	12	16	46	0.04%	76.2%	DLEKWQNNLLPSR	99.7%	50.7	25	33.8	2	0	0	1612.84	85	97
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	12	16	46	0.04%	76.2%	FDVQLKDLEK	99.7%	62.6	25	17.2	7	2	0	1234.67	79	88
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	12	16	46	0.04%	76.2%	FLTVMMK	99.4%	38.2	25	20.6	6	0	0	869.46	37	43
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	12	16	46	0.04%	76.2%	HGYIGEFEIIDDHR	99.7%	50.3	25	46.8	1	2	0	1700.80	44	57
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	12	16	46	0.04%	76.2%	IVVNLTGR	99.7%	49	25	30.2	4	0	0	871.54	61	68
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	12	16	46	0.04%	76.2%	LNKCGVISPR	99.7%	42.3	25	26.7	1	0	0	1143.63	69	78
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	12	16	46	0.04%	76.2%	MNVLADALK	99.7%	57.5	25	38	11	0	0	974.53	4	12
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	12	16	46	0.04%	76.2%	QFGFIVLTTSAGIMDHEEAR	99.7%	41.3	25	41.3	0	1	0	2238.09	98	117
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	12	16	46	0.04%	76.2%	QVLIRPCSK	95.3%	28.8	25	16.6	1	0	0	1100.62	24	32
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	12	16	46	0.04%	76.2%	RQVLIRPCSK	99.7%	33.8	25	33.8	0	2	0	1256.73	23	32
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	12	16	46	0.04%	76.2%	VRMNVLADALK	99.7%	39.5	25	32.5	0	2	0	1245.70	2	12
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	12	16	46	0.04%	76.2%	WQNNLLPSR	99.7%	43.9	25	37.8	4	0	0	1127.60	89	97
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	19	93	0.09%	54.8%	ALVAYYQK	99.7%	52.8	25	40.8	6	0	0	955.52	91	98
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	19	93	0.09%	54.8%	DILIQYDR	99.7%	51.1	25	33.7	2	0	0	1035.55	110	117
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	19	93	0.09%	54.8%	EIKDILIQYDR	99.7%	74.1	25	59.5	9	10	0	1405.77	107	117
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	19	93	0.09%	54.8%	GGGHVAQIYAIR	99.7%	58.9	25	58.9	8	1	0	1241.68	74	85
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	19	93	0.09%	54.8%	GPLQSVQVFGR	99.7%	82	25	66.6	5	0	0	1187.65	5	15
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	19	93	0.09%	54.8%	LLEPVLLLGK	99.7%	59.2	25	59.2	16	0	0	1094.72	51	60
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	19	93	0.09%	54.8%	LLEPVLLLGKER	99.7%	75.6	25	75.6	4	0	0	1379.86	51	62
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	19	93	0.09%	54.8%	PSKGPLQSVQVFGR	99.7%	61.6	25	61.6	4	4	0	1499.83	2	15
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	19	93	0.09%	54.8%	TLLVADPR	99.7%	49.5	25	23.3	4	0	0	884.52	118	125
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	19	93	0.09%	54.8%	TLLVADPRR	99.7%	50.5	25	39.3	4	0	0	1040.62	118	126
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	19	93	0.09%	54.8%	VKGGGHVAQIYAIR	99.7%	54.5	25	51.5	2	2	0	1468.84	72	85
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	19	93	0.09%	54.8%	VNGRPLEMIEPR	99.7%	34.6	25	34.6	4	8	0	1410.75	34	45
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	8	12	35	0.03%	40.7%	IAGYVTHLMK	99.7%	55.7	25	45.1	9	0	0	1132.62	50	59
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	8	12	35	0.03%	40.7%	IAGYVTHLMKR	99.7%	46.4	25	40.1	1	2	0	1304.71	50	60
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	8	12	35	0.03%	40.7%	LGNDFHTNK	99.7%	59.2	25	39	3	0	0	1045.51	24	32
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	8	12	35	0.03%	40.7%	LGNDFHTNKR	99.7%	69.2	25	59.2	3	4	0	1201.61	24	33
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	8	12	35	0.03%	40.7%	LLDFGSLSNLQVTQPTVGMNFK	99.7%	85.6	25	85.6	2	1	0	2425.24	108	129
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	8	12	35	0.03%	40.7%	RVCEEIAIIPSK	98.6%	34.2	25	26.7	2	0	0	1414.77	33	44
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	8	12	35	0.03%	40.7%	VCEEIAIIPSK	99.7%	66.9	25	36.7	4	0	0	1258.67	34	44
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	8	12	35	0.03%	40.7%	VCEEIAIIPSKK	99.7%	60.2	25	52	4	0	0	1386.77	34	45
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	17	21	75	0.07%	62.5%	ADIDLTKR	99.7%	58.9	25	35.2	2	0	0	931.52	48	55

40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	17	21	75	0.07%	62.5%	AGELTEDEVER	99.7%	85.1	25	78.8	7	0	0	1247.58	56	66
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	17	21	75	0.07%	62.5%	DGKYSQVLANGLDNK	99.7%	85.3	25	76.2	2	1	0	1621.82	92	106
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	17	21	75	0.07%	62.5%	FQHILR	95.7%	29.2	25	17.3	1	0	0	813.47	9	14
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	17	21	75	0.07%	62.5%	IAFAITAIK	99.7%	72.8	25	62.6	6	0	0	947.59	26	34
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	17	21	75	0.07%	62.5%	IPDWFLNR	99.7%	58.9	25	41.6	13	0	0	1060.56	79	86
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	17	21	75	0.07%	62.5%	KADIDLTK	99.7%	52.1	25	42.6	2	0	0	903.51	47	54
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	17	21	75	0.07%	62.5%	KIAFAITAIK	99.7%	53.5	25	49.5	2	0	0	1075.69	25	34
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	17	21	75	0.07%	62.5%	LREDLER	97.4%	31.3	25	11	2	0	0	930.50	107	113
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	17	21	75	0.07%	62.5%	QYKIPDWFLNR	95.0%	28.5	25	12.9	1	0	0	1479.77	76	86
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	17	21	75	0.07%	62.5%	RAGELTEDEVER	99.7%	61.4	25	50.4	4	2	0	1403.68	55	66
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	17	21	75	0.07%	62.5%	RYAHVVLR	97.5%	31.5	25	19.7	1	0	0	1013.60	39	46
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	17	21	75	0.07%	62.5%	VITIMQNPR	99.7%	60.8	25	54.3	12	0	0	1087.59	67	75
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	17	21	75	0.07%	62.5%	VLNTNIDGR	99.7%	62.7	25	53.8	9	0	0	1001.54	15	23
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	17	21	75	0.07%	62.5%	YAHVVLRK	96.7%	30.3	25	10.1	1	0	0	985.59	40	47
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	17	21	75	0.07%	62.5%	YSQVLANGLDNK	99.7%	84	25	76.4	3	0	0	1321.67	95	106
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	17	21	75	0.07%	62.5%	YSQVLANGLDNKLR	99.7%	68.9	25	54.7	2	2	0	1590.86	95	108
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	21	0.02%	53.1%	ALAAFLKK	95.2%	28.8	25	26.5	1	0	0	861.56	17	24
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	21	0.02%	53.1%	DVNQQEFVR	99.7%	61	25	46.6	4	0	0	1134.55	8	16
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	21	0.02%	53.1%	ELAPYDENWFYTR	99.7%	70.7	25	67.6	2	0	0	1703.77	44	56
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	21	0.02%	53.1%	IAGQVAAANK	99.7%	61.7	25	51.8	2	0	0	942.54	134	143
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	21	0.02%	53.1%	LKVPEWVDTVK	99.7%	58.2	25	42.1	2	2	0	1313.75	28	38
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	21	0.02%	53.1%	NGVMPSHFSR	97.5%	31.4	25	23.1	1	0	0	1147.53	85	94
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	21	0.02%	53.1%	PGVTVKDVNQQEFVR	99.7%	55.2	25	54.8	2	0	0	1715.91	2	16
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	21	0.02%	53.1%	RVLQALEGLK	97.0%	30.6	25	12.8	2	0	0	1126.69	102	111
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	21	0.02%	53.1%	VLQALEGLK	99.7%	55.7	25	45.5	2	0	0	970.59	103	111
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	21	0.02%	53.1%	VPEWVDTVK	98.6%	34	25	32.4	1	0	0	1072.57	30	38
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	22	83	0.08%	48.5%	AEDKEWMPVTK	99.7%	59.1	25	40.1	5	4	0	1333.65	55	65
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	22	83	0.08%	48.5%	AFVAIGDYNGHVGLGVK	99.7%	87.2	25	83	6	1	0	1716.91	126	142
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	22	83	0.08%	48.5%	ATFDAISK	99.7%	55.2	25	38.5	2	0	0	852.45	239	246
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	22	83	0.08%	48.5%	ESEIIDFFLGASLK	99.7%	69.3	25	59.2	1	0	0	1568.82	90	103
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	22	83	0.08%	48.5%	GCTATLGNFAK	99.7%	65.6	25	57.4	7	0	0	1139.55	228	238
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	22	83	0.08%	48.5%	GTGIVSAPVPK	99.7%	50.1	25	50.1	7	0	0	1025.60	201	211
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	22	83	0.08%	48.5%	IGKPHTVPCK	98.8%	34.7	25	20.2	2	0	0	1136.62	174	183
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	22	83	0.08%	48.5%	KLLMMAGIDDCYTSAR	99.7%	106	25	106	6	8	0	1844.87	212	227
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	22	83	0.08%	48.5%	LLMMAGIDDCYTSAR	99.7%	102	25	99.5	8	0	0	1716.78	213	227
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	22	83	0.08%	48.5%	LSIVPVRR	99.7%	45.1	25	25.6	4	0	0	939.61	160	167
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	22	83	0.08%	48.5%	SLEEIYLFSLPIK	99.7%	93.4	25	91.9	6	0	0	1551.87	77	89
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	22	83	0.08%	48.5%	SPYQEFTDHLVK	99.7%	58.6	25	58.6	6	4	0	1463.72	264	275
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	22	83	0.08%	48.5%	TYSYLTPDLWK	99.7%	65	25	58.7	6	0	0	1386.69	247	257
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	5	8	17	0.02%	29.4%	DTGKTPVEPEVAIHR	99.7%	50.2	25	50.2	2	2	0	1648.87	5	19
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	5	8	17	0.02%	29.4%	LIDLHSPSEIVK	99.7%	50.7	25	34.3	4	1	0	1350.76	88	99
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	5	8	17	0.02%	29.4%	RLIDLHSPSEIVK	99.7%	52.9	25	42.8	2	0	0	1506.86	87	99
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	5	8	17	0.02%	29.4%	TPVEPEVAIHR	99.7%	67.9	25	67.9	2	2	0	1247.67	9	19
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	5	8	17	0.02%	29.4%	VCADLIR	99.6%	40.8	25	25.3	2	0	0	846.45	35	41
40S ribosomal protein S21	RPS21	RS21_HUMAN	9.1	99.8%	2	3	6	0.01%	22.9%	MGESDDSILR	99.7%	65.9	25	58.3	3	0	0	1122.51	62	71
40S ribosomal protein S21	RPS21	RS21_HUMAN	9.1	99.8%	2	3	6	0.01%	22.9%	TYAICGAIR	99.5%	39.4	25	39.4	3	0	0	1024.52	52	60
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	5	6	24	0.02%	29.4%	AHLGTALK	98.4%	33.5	25	22.4	2	0	0	810.48	30	37
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	5	6	24	0.02%	29.4%	ANPFGGASHAK	99.6%	40	25	40	14	0	0	1056.52	38	48
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	5	6	24	0.02%	29.4%	GHAVGDIPGVR	99.4%	37.9	25	31.7	1	0	0	1077.58	109	119
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	5	6	24	0.02%	29.4%	KGHAVGDIPGVR	99.7%	54.4	25	41.6	2	2	0	1205.68	108	119
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	5	6	24	0.02%	29.4%	VANVSLLALYK	99.7%	91.9	25	91.9	3	0	0	1190.71	125	135

40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	10	52	0.05%	30.1%	KQMVIDVLHPGK	99.7%	61.6	25	51.1	2	4	0	1380.77	21	32
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	10	52	0.05%	30.1%	QMVIDVLHPGK	99.7%	62.3	25	48.4	6	2	0	1236.68	22	32
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	10	52	0.05%	30.1%	TTGFGMIYDSLDYAK	99.7%	92.6	25	92.6	21	0	0	1697.77	69	83
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	10	52	0.05%	30.1%	TTGFGMIYDSLDYAKK	99.7%	53.8	25	53.8	2	0	0	1809.87	69	84
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	10	52	0.05%	30.1%	TTPDVIFVFGFR	99.7%	65.3	25	65.3	15	0	0	1398.74	50	61
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	8	9	41	0.04%	47.2%	AALQELLSK	99.7%	68.5	25	55.2	11	0	0	972.57	86	94
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	8	9	41	0.04%	47.2%	AQVIYTR	99.4%	37.8	25	32.6	3	0	0	850.48	105	111
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	8	9	41	0.04%	47.2%	ATYDKLCK	99.6%	40.7	25	32.2	2	0	0	998.50	53	60
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	8	9	41	0.04%	47.2%	DKLNNLVLFDK	99.7%	59.5	25	48.4	6	2	0	1318.74	42	52
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	8	9	41	0.04%	47.2%	LITPAVVSER	99.7%	64.6	25	54.1	13	0	0	1084.64	67	76
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	8	9	41	0.04%	47.2%	LNNLVLFDK	99.7%	62.2	25	52.2	2	0	0	1075.61	44	52
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	8	9	41	0.04%	47.2%	LNNLVLFDKATYDK	99.7%	57.3	25	57.3	1	0	0	1653.88	44	57
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	8	9	41	0.04%	47.2%	NTKGGDAPAAGEDA	98.2%	33	25	32.5	1	0	0	1273.57	112	125
40S ribosomal protein S26	RPS26	RS26_HUMAN	13.0	100.0%	4	5	33	0.03%	44.3%	DISEASVFDAYVLPK	99.7%	98.4	25	84.3	15	0	0	1653.84	52	66
40S ribosomal protein S26	RPS26	RS26_HUMAN	13.0	100.0%	4	5	33	0.03%	44.3%	FRPAGAAPRPPPKPM	98.2%	26.4	25	22.7	0	1	0	1605.87	101	115
40S ribosomal protein S26	RPS26	RS26_HUMAN	13.0	100.0%	4	5	33	0.03%	44.3%	LHYCVSCAIHSK	99.7%	71.9	25	67.2	2	2	0	1474.69	71	82
40S ribosomal protein S26	RPS26	RS26_HUMAN	13.0	100.0%	4	5	33	0.03%	44.3%	NIVEAAAVR	99.7%	67.4	25	56.7	13	0	0	942.54	43	51
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	5	9	31	0.03%	40.5%	DLLHPSPEEEK	99.5%	31.8	25	27.7	2	1	0	1293.63	6	16
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	5	9	31	0.03%	40.5%	DLLHPSPEEEKR	99.7%	42.2	25	42.2	0	2	0	1449.73	6	17
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	5	9	31	0.03%	40.5%	LTEGCSFR	99.7%	54.5	25	54.1	7	0	0	969.45	73	80
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	5	9	31	0.03%	40.5%	LVQSPNSYFMDVK	99.7%	74.8	25	74.8	15	0	0	1527.75	24	36
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	5	9	31	0.03%	40.5%	RLVQSPNSYFMDVK	99.7%	41.8	25	41.8	2	2	0	1699.85	23	36
40S ribosomal protein S28	RPS28	RS28_HUMAN	7.8	99.8%	2	2	4	0.00%	30.4%	EGDVLTLLESER	99.7%	53.8	25	47.7	2	0	0	1360.70	52	63
40S ribosomal protein S28	RPS28	RS28_HUMAN	7.8	99.8%	2	2	4	0.00%	30.4%	VEFMDDTSR	99.7%	45.7	25	41.5	2	0	0	1115.47	32	40
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	27	123	0.12%	76.1%	ACYGVLR	99.7%	47	25	40.2	2	0	0	838.42	118	124
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	27	123	0.12%	76.1%	AELNEFLTR	99.7%	59.1	25	41.2	12	0	0	1092.57	19	27
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	27	123	0.12%	76.1%	DEILPTTPISEQK	99.7%	73.6	25	56.4	4	0	0	1470.77	215	227
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	27	123	0.12%	76.1%	ELAEDGYSGVEVR	99.7%	86.8	25	79.8	13	0	0	1423.67	28	40
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	27	123	0.12%	76.1%	ELTAVVQK	99.7%	47.8	25	30.7	2	0	0	887.52	68	75
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	27	123	0.12%	76.1%	FGFPEGSVELYAEK	99.7%	90	25	80.7	11	0	0	1572.76	77	90
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	27	123	0.12%	76.1%	FIMESGAK	99.7%	45.5	25	18.8	3	0	0	898.43	125	132
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	27	123	0.12%	76.1%	FVADGIFK	99.7%	42.5	25	38.9	2	0	0	896.49	11	18
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	27	123	0.12%	76.1%	FVDGLMIHSGDPVNYYVDTAVR	99.7%	93.3	25	93.3	4	4	0	2468.19	152	173
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	27	123	0.12%	76.1%	GCEVVVSGK	99.7%	51	25	42.5	4	0	0	934.47	133	141
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	27	123	0.12%	76.1%	GCEVVVSGKLR	99.7%	60.4	25	49.1	2	0	0	1203.65	133	143
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	27	123	0.12%	76.1%	GGKPEPPAMPQPVPTA	99.7%	55.9	25	46.7	11	0	0	1573.80	228	243
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	27	123	0.12%	76.1%	GLCAIAQAESLR	99.7%	86.4	25	73.4	12	0	0	1288.67	95	106
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	27	123	0.12%	76.1%	IMLPWDPTGK	99.7%	46	25	38.9	6	0	0	1173.60	188	197
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	27	123	0.12%	76.1%	IRELTAVVQK	99.7%	49.2	25	32.6	2	0	0	1156.70	66	75
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	27	123	0.12%	76.1%	KFVADGIFK	99.3%	37.5	25	20.6	3	0	0	1024.58	10	18
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	27	123	0.12%	76.1%	KPLPDHVSIVEPK	99.7%	45.9	25	43.8	2	2	0	1458.83	202	214
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	27	123	0.12%	76.1%	RACYGVLR	95.6%	29.1	25	13.2	1	0	0	994.53	117	124
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	27	123	0.12%	76.1%	TEIIILATR	99.7%	63.1	25	63.1	19	0	0	1029.63	46	54
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	27	123	0.12%	76.1%	TQNVLGEK	99.5%	39.5	25	25.9	2	0	0	888.48	55	62
40S ribosomal protein S30	FAU	RS30_HUMAN	6.6	100.0%	2	2	7	0.01%	18.6%	FVNVVPTFGK	99.7%	41.5	25	41.5	6	0	0	1107.62	42	51
40S ribosomal protein S30	FAU	RS30_HUMAN	6.6	100.0%	2	2	7	0.01%	18.6%	RFVNVVPTFGK	99.7%	41.7	25	38.2	1	0	0	1263.72	41	51
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	121	0.12%	65.5%	ACQSIYPLHDVFVR	99.7%	72.7	25	64.9	4	5	0	1704.85	200	213
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	121	0.12%	65.5%	ADGYEPPVQESV	99.7%	58.1	25	56.3	4	0	0	1290.58	253	264
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	121	0.12%	65.5%	APAMFNIR	99.7%	55.6	25	49.8	10	0	0	919.48	35	42
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	121	0.12%	65.5%	ATGDETGAKVER	99.7%	74.8	25	67	3	0	0	1233.61	241	252
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	121	0.12%	65.5%	DWYDVK	99.3%	37.5	25	16.4	2	0	0	825.38	29	34

40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	121	0.12%	65.5%	EVQTNDLK	99.7%	46.1	25	30	2	0	0	946.48	175	182
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	121	0.12%	65.5%	EVQTNDLKEVVNK	99.7%	79.9	25	73.3	7	2	0	1515.80	175	187
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	121	0.12%	65.5%	KMMEIMTR	99.0%	35.7	25	29.8	3	0	0	1039.51	167	174
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	121	0.12%	65.5%	KTSYAQHQQVR	99.7%	53.5	25	44.2	2	4	0	1345.70	152	162
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	121	0.12%	65.5%	LFCVGFTK	99.7%	51	25	40.2	6	0	0	971.50	137	144
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	121	0.12%	65.5%	LIPDSIGKDIEK	99.7%	55.2	25	44.4	4	0	0	1327.75	188	199
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	121	0.12%	65.5%	LITEDVQGK	99.7%	67.7	25	54.3	7	0	0	1002.55	86	94
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	121	0.12%	65.5%	LMELHGEGSSSGK	99.7%	81.7	25	73	8	4	0	1347.62	228	240
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	121	0.12%	65.5%	MMEIMTR	99.7%	45	25	12.3	9	0	0	927.41	168	174
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	121	0.12%	65.5%	NCLTNFHGMDLTR	99.7%	90.6	25	90.3	8	2	0	1594.71	95	107
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	121	0.12%	65.5%	TSYAQHQQVR	99.7%	77.3	25	68.7	4	1	0	1217.60	153	162
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	121	0.12%	65.5%	TTDGYLLR	99.7%	61.9	25	43.6	8	0	0	938.49	129	136
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	121	0.12%	65.5%	VFEVSLADLQNDEVAFR	99.7%	105	25	105	6	0	0	1951.98	66	82
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	121	0.12%	65.5%	VFEVSLADLQNDEVAFRK	99.7%	79.4	25	77.7	2	3	0	2080.07	66	83
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	33	121	0.12%	65.5%	VVDPFSKK	99.2%	36.5	25	25.2	1	0	0	919.52	21	28
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	129	0.12%	62.0%	DANGNSFATR	99.7%	68	25	61.6	4	0	0	1052.48	212	221
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	129	0.12%	62.0%	ECLPLIIFLR	99.7%	69.7	25	63.1	6	0	0	1273.73	40	49
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	129	0.12%	62.0%	ERHPGSFDVVHVK	99.7%	40.1	25	40.1	0	4	0	1506.78	199	211
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	129	0.12%	62.0%	FDTGNLCMVTGGANLGR	99.7%	111	25	104	12	1	0	1798.82	175	191
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	129	0.12%	62.0%	GIPHLVTHDAR	99.7%	53.6	25	45.4	4	5	0	1215.66	135	145
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	129	0.12%	62.0%	GNKPWISLPR	99.6%	40.1	25	33.3	6	0	0	1167.66	231	240
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	129	0.12%	62.0%	HPGSFDVVHVK	99.7%	61.5	25	60	3	3	0	1221.64	201	211
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	129	0.12%	62.0%	ITPEEAKYK	98.5%	33.7	25	16.3	2	0	0	1078.58	114	122
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	129	0.12%	62.0%	LRECLPLIIFLR	99.7%	51.5	25	51.5	4	4	0	1542.92	38	49
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	129	0.12%	62.0%	LSNIFVIGK	99.7%	63.7	25	58.2	20	0	0	990.60	222	230
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	129	0.12%	62.0%	LTGVFAPRPSTGPHK	99.7%	51	25	45	4	0	0	1564.86	23	37
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	129	0.12%	62.0%	LTIAEER	99.3%	37.5	25	11.6	6	0	0	831.46	246	252
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	129	0.12%	62.0%	TDITYPAGFMDVISIDK	99.7%	81.5	25	81.5	12	0	0	1885.93	78	94
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	129	0.12%	62.0%	TIRYPDPLIK	99.7%	37.4	25	25.9	1	4	0	1215.71	146	155
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	129	0.12%	62.0%	VNDTIQIDLETGK	99.7%	117	25	117	9	0	0	1445.75	156	168
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	129	0.12%	62.0%	YALTGDEVK	99.7%	51.2	25	42	5	0	0	995.50	54	62
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	129	0.12%	62.0%	YALTGDEVKK	99.7%	60.4	25	50.8	6	0	0	1123.60	54	63
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	18	25	129	0.12%	62.0%	YPDPLIK	99.2%	36.4	25	6.11	4	0	0	845.48	149	155
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	8	9	25	0.02%	32.8%	AQCPIVER	97.5%	31.5	25	21.1	2	0	0	972.49	64	71
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	8	9	25	0.02%	32.8%	GSSNSYAIKK	94.6%	28.3	25	28.3	1	0	0	1054.55	183	192
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	8	9	25	0.02%	32.8%	KAQCPIVER	99.7%	43.5	25	37.5	2	0	0	1100.59	63	71
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	8	9	25	0.02%	32.8%	LTNSMMMHGR	99.7%	50.1	25	45.2	4	0	0	1177.53	72	81
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	8	9	25	0.02%	32.8%	QAVDVSPLR	99.7%	69.2	25	52.6	3	0	0	984.55	137	145
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	8	9	25	0.02%	32.8%	QAVDVSPLRR	97.7%	31.9	25	25.8	2	0	0	1140.65	137	146
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	8	9	25	0.02%	32.8%	TIAECLADELINAAK	99.7%	93.2	25	91.2	8	0	0	1631.83	168	182
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	8	9	25	0.02%	32.8%	VNQAIWLLCTGAR	99.7%	97.6	25	93.1	3	0	0	1501.79	147	159
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	13	20	55	0.05%	40.2%	DIPGLTDTTVPR	99.7%	79.7	25	73	12	0	0	1284.68	120	131
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	13	20	55	0.05%	40.2%	GCIVDANLSVLNLVIVK	99.7%	122	25	111	5	0	0	1827.04	99	115
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	13	20	55	0.05%	40.2%	KLFNLSK	99.7%	46.6	25	34.7	2	0	0	849.52	143	149
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	13	20	55	0.05%	40.2%	LFNLSKEDDVR	99.7%	66.1	25	53.3	2	2	0	1335.69	144	154
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	13	20	55	0.05%	40.2%	LIEVDDER	99.7%	58	25	49.8	5	0	0	988.49	15	22
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	13	20	55	0.05%	40.2%	LIEVDDERK	99.7%	43.5	25	34.3	2	0	0	1116.59	15	23
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	13	20	55	0.05%	40.2%	LNISFPATGCQK	99.7%	61.5	25	59.5	2	0	0	1335.67	3	14
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	13	20	55	0.05%	40.2%	MATEVAADALGEEWK	99.7%	123	25	121	9	0	0	1620.76	32	46
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	13	20	55	0.05%	40.2%	MATEVAADALGEEWKGYVVR	99.7%	103	25	103	3	3	0	2211.08	32	51
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	13	20	55	0.05%	40.2%	MKLNISFPATGCQK	99.7%	77.9	25	66.1	2	2	0	1610.80	1	14

40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	13	20	55	0.05%	40.2%	NKEEAAEYAK	98.4%	33.5	25	22.7	1	0	0	1152.55	202	211
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	13	20	55	0.05%	40.2%	RMATEVAADALGEEWK	99.7%	35.9	25	30.4	0	2	0	1792.85	31	46
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	13	20	55	0.05%	40.2%	TFYEKR	96.3%	29.8	25	20	1	0	0	843.44	26	31
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	12	13	33	0.03%	52.1%	AIIIFVPVPQLK	99.7%	64.8	25	64.8	5	0	0	1337.86	59	70
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	12	13	33	0.03%	52.1%	AQQNNVEHKVETFSGVYK	99.7%	90.1	25	90.1	2	2	0	2078.03	161	178
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	12	13	33	0.03%	52.1%	DVNFEFPEFQL	99.7%	65.5	25	65.5	5	0	0	1384.64	184	194
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	12	13	33	0.03%	52.1%	EIEVGGGR	99.7%	48.3	25	40.7	2	0	0	816.42	50	57
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	12	13	33	0.03%	52.1%	ELNITAAK	99.7%	66.1	25	47.1	3	0	0	859.49	42	49
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	12	13	33	0.03%	52.1%	HVVFIAQR	96.7%	30.3	25	25.7	3	0	0	969.56	91	98
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	12	13	33	0.03%	52.1%	ILPKPTR	96.2%	29.7	25	10.3	2	0	0	824.54	100	106
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	12	13	33	0.03%	52.1%	KAIIIFVPVPQLK	99.7%	73.1	25	73.1	4	0	0	1465.95	58	70
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	12	13	33	0.03%	52.1%	TLTAVHDAILEDLVFPSEIVGK	99.7%	44.2	25	43	0	1	0	2367.28	121	142
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	12	13	33	0.03%	52.1%	VETFSGVYK	99.7%	46.9	25	19.9	2	0	0	1029.53	170	178
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	12	13	33	0.03%	52.1%	VETFSGVYKK	98.7%	34.3	25	26	1	0	0	1157.62	170	179
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	12	13	33	0.03%	52.1%	VHLDKAQQNNVEHK	97.3%	25	25	25	0	1	0	1659.86	156	169
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	17	64	0.06%	59.1%	ADGYVLEGK	99.7%	72.1	25	56.3	3	0	0	951.48	185	193
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	17	64	0.06%	59.1%	ADGYVLEGKELEFYLR	96.8%	24.3	25	24.3	0	2	0	1901.96	185	200
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	17	64	0.06%	59.1%	ELEFYLR	99.1%	36.3	25	26	2	0	0	969.50	194	200
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	17	64	0.06%	59.1%	ELEFYLRK	99.4%	38.1	25	26.6	1	0	0	1097.60	194	201
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	17	64	0.06%	59.1%	IIDVVYNASNNELVR	99.7%	111	25	103	14	2	0	1718.91	78	92
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	17	64	0.06%	59.1%	ISSLLEEQFQQGK	99.7%	65.4	25	42.7	11	0	0	1506.78	158	170
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	17	64	0.06%	59.1%	KYELGRPAANTK	99.7%	62.6	25	55.8	2	0	0	1347.74	26	37
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	17	64	0.06%	59.1%	LDVGNFSWGSECCTR	99.7%	89.6	25	89.6	3	0	0	1787.75	60	74
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	17	64	0.06%	59.1%	LDVGNFSWGSECCTRK	96.1%	23.6	25	23.6	0	1	0	1915.84	60	75
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	17	64	0.06%	59.1%	LLACIASRPGQCGR	99.7%	46.1	25	46.1	2	2	0	1558.79	171	184
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	17	64	0.06%	59.1%	LTPEEEEILNK	99.7%	68	25	60	5	0	0	1314.68	129	139
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	17	64	0.06%	59.1%	NCIVLIDSTPYR	99.7%	103	25	87.5	9	0	0	1450.74	99	110
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	17	64	0.06%	59.1%	QWYESHYALPLGR	99.7%	55.5	25	47.7	2	1	0	1619.80	111	123
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	17	64	0.06%	59.1%	YELGRPAANTK	99.7%	51.5	25	40.5	2	0	0	1219.64	27	37
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	22	79	0.08%	54.6%	ELLTLDEK	96.8%	30.4	25	24.7	1	0	0	960.53	59	66
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	22	79	0.08%	54.6%	ELLTLDEKDPR	98.0%	32.5	25	26.2	1	1	0	1328.71	59	69
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	22	79	0.08%	54.6%	HIDFSLR	99.3%	37	25	14.1	1	0	0	887.47	156	162
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	22	79	0.08%	54.6%	IEDFLER	99.7%	54.6	25	44.5	2	0	0	921.47	102	108
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	22	79	0.08%	54.6%	IEDFLERR	99.0%	35.6	25	19.5	1	0	0	1077.57	102	109
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	22	79	0.08%	54.6%	IGVLDEGK	99.7%	50.6	25	26.9	6	0	0	830.46	84	91
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	22	79	0.08%	54.6%	IGVLDEGKMK	99.7%	48.1	25	40.2	4	0	0	1089.60	84	93
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	22	79	0.08%	54.6%	KQVVNIPSFIVR	99.7%	65.9	25	65.9	3	2	0	1399.84	139	150
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	22	79	0.08%	54.6%	LFEGNALLR	99.7%	75.3	25	53.4	17	0	0	1032.58	71	79
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	22	79	0.08%	54.6%	LIGEYGLR	99.7%	61.1	25	39.8	2	0	0	920.52	31	38
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	22	79	0.08%	54.6%	LQTQVFK	99.7%	50.6	25	30.4	2	0	0	863.50	110	116
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	22	79	0.08%	54.6%	MKLDYILGLK	99.7%	56	25	38.9	4	0	0	1193.70	92	101
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	22	79	0.08%	54.6%	QVVNIPSFIVR	99.7%	51.5	25	36.8	12	0	0	1271.75	140	150
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	22	79	0.08%	54.6%	RLFEGNALLR	99.7%	53.4	25	31.4	2	0	0	1188.68	70	79
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	22	79	0.08%	54.6%	RLQTQVFK	99.2%	36.9	25	30	3	0	0	1019.60	109	116
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	22	79	0.08%	54.6%	SPYGGGRPGR	99.7%	41.8	25	15.9	8	0	0	1003.51	163	172
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	22	79	0.08%	54.6%	SRLDQELK	99.7%	42.6	25	15.9	5	0	0	988.54	23	30
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	18	22	79	0.08%	54.6%	VKFTLAK	99.5%	39.2	25	35.9	2	0	0	806.51	46	52
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	5	5	14	0.01%	21.7%	AIVAIENPADVSVISSR	99.7%	79.1	25	79.1	2	0	0	1740.95	64	80
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	5	5	14	0.01%	21.7%	FAAATGATPIAGR	99.7%	104	25	89.5	4	0	0	1203.65	90	102
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	5	5	14	0.01%	21.7%	FTPGTFTNQIQAAFR	99.7%	78.4	25	69.3	2	0	0	1698.86	103	117
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	5	5	14	0.01%	21.7%	KSDGIYIINLK	99.7%	50.5	25	28	2	0	0	1263.73	42	52

40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	5	5	14	0.01%	21.7%	LLVVTDPR	99.7%	49.2	25	41.3	4	0	0	912.55	121	128
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	9	9	15	0.01%	18.4%	ADLLLSTQPGREEGSPLELER	99.7%	45.1	25	45.1	0	1	0	2310.19	593	613
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	9	9	15	0.01%	18.4%	FTGLSKEELLK	98.9%	35.1	25	29.3	1	0	0	1264.71	161	171
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	9	9	15	0.01%	18.4%	GENSWFSTQVDTVATK	99.7%	94.9	25	94.9	1	0	0	1769.83	314	329
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	9	9	15	0.01%	18.4%	GLVLGPIHK	99.7%	49.8	25	36.6	2	0	0	933.59	258	266
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	9	9	15	0.01%	18.4%	GQSEDPGSLLSLFR	99.7%	61.1	25	52.6	2	0	0	1505.76	511	524
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	9	9	15	0.01%	18.4%	GRLDYLSSLK	99.3%	37.4	25	23	1	0	0	1151.64	246	255
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	9	9	15	0.01%	18.4%	LLTSFLPAQLLR	99.7%	56.2	25	56.2	2	0	0	1371.84	440	451
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	9	9	15	0.01%	18.4%	VAEDEAEAAAAAK	99.7%	91.8	25	83.3	2	0	0	1245.60	148	160
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	9	9	15	0.01%	18.4%	VILDLTPNYR	99.7%	56.6	25	49	3	0	0	1203.67	304	313
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	8	9	18	0.02%	12.2%	AALEEVYPDLTPEETRR	99.7%	47.2	25	46.9	0	1	0	1988.99	660	676
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	8	9	18	0.02%	12.2%	DQPAFTPSGILTPHALGSR	99.2%	29.7	25	28	0	1	0	1965.02	428	446
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	8	9	18	0.02%	12.2%	ELTMASLPFTFDVER	99.7%	57.1	25	56	5	0	0	1755.86	316	330
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	8	9	18	0.02%	12.2%	NLTVILSDASAPGEGEHK	99.5%	31.7	25	31.7	0	2	0	1837.93	190	207
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	8	9	18	0.02%	12.2%	NSLGGDVLFVGK	99.7%	62	25	55.4	2	0	0	1205.65	677	688
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	8	9	18	0.02%	12.2%	NSPGSQVASNPR	99.7%	76.5	25	69.8	5	0	0	1213.59	447	458
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	8	9	18	0.02%	12.2%	VREEILAK	98.7%	34.5	25	11.6	1	0	0	957.57	135	142
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	8	9	18	0.02%	12.2%	YAWQGVALLPFVDER	97.8%	32	25	27.9	1	0	0	1763.91	642	656
5'-AMP-activated protein kinase catalytic subunit alpha-2	PRKAA2	AAPK2_HUMAN	62.3	100.0%	3	3	6	0.01%	6.3%	IADFGLSNMMSDGEFLR	99.7%	52.3	25	52.3	2	0	0	1934.86	155	171
5'-AMP-activated protein kinase catalytic subunit alpha-2	PRKAA2	AAPK2_HUMAN	62.3	100.0%	3	3	6	0.01%	6.3%	MPPLIADSPK	97.5%	31.5	25	27.4	2	0	0	1084.57	370	379
5'-AMP-activated protein kinase catalytic subunit alpha-2	PRKAA2	AAPK2_HUMAN	62.3	100.0%	3	3	6	0.01%	6.3%	VVNAYHLR	99.7%	54.8	25	39.9	2	0	0	971.54	432	439
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	5	5	9	0.01%	15.1%	AFFALVTNGVR	99.7%	66.9	25	53.9	1	0	0	1194.66	60	70
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	5	5	9	0.01%	15.1%	FDVINLAAEK	99.7%	63.7	25	52	2	0	0	1119.60	244	253
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	5	5	9	0.01%	15.1%	LVEAEVHR	99.7%	55.5	25	50.8	2	0	0	952.52	292	299
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	5	5	9	0.01%	15.1%	LVVFDTSLQVK	99.7%	45.1	25	44.9	2	0	0	1248.72	48	58
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	5	5	9	0.01%	15.1%	VSALPVVDEK	99.7%	68.3	25	49.8	2	0	0	1056.59	225	234
5'-nucleotidase domain-containing protein 2	NT5DC2	NT5D2_HUMAN	60.7	100.0%	4	5	9	0.01%	8.1%	MQTYQDAESR	99.7%	61.5	25	53.8	4	0	0	1244.52	411	420
5'-nucleotidase domain-containing protein 2	NT5DC2	NT5D2_HUMAN	60.7	100.0%	4	5	9	0.01%	8.1%	QGNLFDFLR	99.7%	44.9	25	32	2	0	0	1109.57	336	344
5'-nucleotidase domain-containing protein 2	NT5DC2	NT5D2_HUMAN	60.7	100.0%	4	5	9	0.01%	8.1%	QLFLITNSPFSFVDK	99.7%	69.2	25	65.6	2	0	0	1755.93	263	277
5'-nucleotidase domain-containing protein 2	NT5DC2	NT5D2_HUMAN	60.7	100.0%	4	5	9	0.01%	8.1%	VDFTFYPR	99.7%	52.7	25	45.2	1	0	0	1044.51	481	488
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	55	0.05%	40.3%	AAVEEGIVLGGGCALLR	99.7%	70.3	25	65.6	2	2	0	1684.91	430	446
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	55	0.05%	40.3%	ALMLQGVDLLADAVAVTMGPK	99.7%	38.4	25	38.4	0	3	0	2129.13	38	58
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	55	0.05%	40.3%	APGFGDNRK	95.1%	28.6	25	13	1	0	0	961.49	302	310
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	55	0.05%	40.3%	CEFQDAYVLLSEK	99.7%	68.1	25	62	2	0	0	1601.75	237	249
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	55	0.05%	40.3%	CIPALDSLTPANEDQK	99.7%	76.4	25	76.4	2	0	0	1771.85	447	462
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	55	0.05%	40.3%	GANPVEIR	99.7%	50.2	25	15.5	2	0	0	855.47	134	141
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	55	0.05%	40.3%	GANPVEIRR	98.2%	33	25	27.7	1	0	0	1011.57	134	142
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	55	0.05%	40.3%	GYISPYFINTSK	99.7%	83.2	25	81.4	2	0	0	1389.70	222	233
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	55	0.05%	40.3%	IGIEIIKR	99.7%	60.7	25	31.1	2	0	0	941.61	463	470
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	55	0.05%	40.3%	ISSIQSIVPALEIANAHR	99.7%	43.7	25	43.7	1	2	0	1919.07	251	268
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	55	0.05%	40.3%	LVQDVANNTNEEAGDGTTTATVLAR	99.7%	148	25	147	2	2	0	2560.25	97	121
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	55	0.05%	40.3%	NAGVEGSLIVEK	99.7%	87.9	25	73.4	2	0	0	1215.66	482	493
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	55	0.05%	40.3%	TLNDELEIIEGMK	99.7%	94.1	25	91.1	2	0	0	1504.76	206	218
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	55	0.05%	40.3%	TVIIEQSWGSPK	99.7%	80.9	25	63.3	2	0	0	1344.72	61	72
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	55	0.05%	40.3%	VGEVIVTK	99.7%	70.5	25	49.3	3	0	0	844.51	345	352
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	55	0.05%	40.3%	VGEVIVTKDDAMLLK	99.7%	67.8	25	66	4	4	0	1630.91	345	359
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	55	0.05%	40.3%	VGGTSDVEVNEK	99.7%	92.5	25	85.7	4	0	0	1233.60	406	417
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	55	0.05%	40.3%	VGGTSDVEVNEKK	99.7%	69.3	25	61.5	2	2	0	1361.69	406	418
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	55	0.05%	40.3%	VGLQVVAVK	99.7%	72.6	25	69.1	2	0	0	912.59	293	301
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	20	27	55	0.05%	40.3%	VTDALNATR	99.7%	91.1	25	73.9	2	0	0	960.51	421	429
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	10	19	0.02%	20.8%	AIADWYNEK	99.6%	39.7	25	37	2	0	0	1109.53	151	159

60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	10	19	0.02%	20.8%	ALLQEMPLTALLR	99.7%	86.5	25	74.7	4	0	0	1468.86	271	283
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	10	19	0.02%	20.8%	EHLLTNHLK	95.8%	29.3	25	0	1	0	0	1104.62	256	264
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	10	19	0.02%	20.8%	FLCFGSEGGTYYIK	99.7%	78	25	78	2	0	0	1641.76	36	49
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	10	19	0.02%	20.8%	GGMALALAVTK	99.7%	70.1	25	55.8	2	0	0	1047.59	160	170
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	10	19	0.02%	20.8%	LGLENAEALIR	99.7%	77.6	25	68.5	2	0	0	1198.68	53	63
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	10	19	0.02%	20.8%	LSHLKPSSEGLAIVTK	99.7%	41.1	25	37.1	0	2	0	1679.97	185	200
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	10	19	0.02%	20.8%	MTANSVLEPGNSEVSLVCEK	99.7%	76.9	25	76.9	2	0	0	2180.02	288	307
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	10	19	0.02%	20.8%	WRPDEEILK	99.7%	56	25	46.6	2	0	0	1185.63	343	351
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	22	79	0.08%	55.8%	AFLADPSAFVAAAPVAAATTAAPAAAAAPAK	99.7%	104	25	104	2	7	0	2752.47	267	297
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	22	79	0.08%	55.8%	AGAIAPCEVTVPAQNTGLGPEK	99.7%	65.6	25	65.6	2	2	0	2180.10	113	134
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	22	79	0.08%	55.8%	CFIVGADNVGSK	97.8%	32	25	29.4	1	0	0	1266.61	27	38
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	22	79	0.08%	55.8%	DMLLANK	98.0%	32.5	25	21.3	2	0	0	804.43	100	106
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	22	79	0.08%	55.8%	DMLLANKVPAAAR	99.7%	65	25	54.6	2	0	0	1369.76	100	112
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	22	79	0.08%	55.8%	EDLTEIR	98.9%	35.3	25	17	2	0	0	875.45	93	99
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	22	79	0.08%	55.8%	EDLTEIRDMLLANK	99.7%	70	25	65.1	4	4	0	1660.86	93	106
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	22	79	0.08%	55.8%	GHLENNPALEK	99.7%	63.5	25	48.3	4	2	0	1221.62	67	77
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	22	79	0.08%	55.8%	GNVGFVFTK	99.7%	54	25	44.3	8	0	0	968.52	84	92
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	22	79	0.08%	55.8%	GNVGFVFTKEDLTEIR	99.7%	54.6	25	51.3	1	0	0	1824.95	84	99
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	22	79	0.08%	55.8%	GTIEILSDVQLIK	99.7%	90.9	25	80.3	9	0	0	1428.83	150	162
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	22	79	0.08%	55.8%	IIQLLDDYPK	99.7%	81.8	25	70.8	2	0	0	1217.68	17	26
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	22	79	0.08%	55.8%	TSFFQALGITTK	99.7%	99.9	25	99.9	16	0	0	1313.71	135	146
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	22	79	0.08%	55.8%	VEAKEESEESDEDMGFGLFD	99.7%	87.1	25	87.1	4	0	0	2262.92	298	317
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	22	79	0.08%	55.8%	VLALSVETDYTFPLAEK	99.7%	87.2	25	87	5	0	0	1896.00	248	264
60S acidic ribosomal protein P2	RPLP2	RLA2_HUMAN	11.7	100.0%	4	6	12	0.01%	69.6%	ILDSVGIEADDDRLNK	99.7%	95.4	25	90.6	2	2	0	1772.90	26	41
60S acidic ribosomal protein P2	RPLP2	RLA2_HUMAN	11.7	100.0%	4	6	12	0.01%	69.6%	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	99.7%	93.1	25	93.1	0	2	0	2774.43	62	94
60S acidic ribosomal protein P2	RPLP2	RLA2_HUMAN	11.7	100.0%	4	6	12	0.01%	69.6%	NIEDVIAQGIGK	99.7%	102	25	87.4	2	0	0	1256.68	50	61
60S acidic ribosomal protein P2	RPLP2	RLA2_HUMAN	11.7	100.0%	4	6	12	0.01%	69.6%	YVASYLLAALGGNSSPSAK	99.7%	98.6	25	91.7	2	2	0	1868.98	3	21
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	26	56	0.05%	59.3%	AKVDEFPLCGHMVSDEYEQLSSEALEAAR	99.7%	122	25	122	0	3	0	3281.51	41	69
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	26	56	0.05%	59.3%	EHVIEALR	98.3%	33.3	25	30.1	4	0	0	966.54	146	153
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	26	56	0.05%	59.3%	EHVIEALRR	99.5%	39.5	25	13.5	1	0	0	1122.64	146	154
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	26	56	0.05%	59.3%	FNADEFEDMVAEK	99.7%	95.2	25	95.2	2	0	0	1560.65	176	188
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	26	56	0.05%	59.3%	FNADEFEDMVAEKR	99.7%	100	25	90.8	2	4	0	1700.76	176	189
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	26	56	0.05%	59.3%	GAFGKPQGTVAR	99.7%	68.7	25	59	4	0	0	1188.65	117	128
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	26	56	0.05%	59.3%	ICANKYMVK	98.8%	34.7	25	34.7	2	0	0	1142.57	70	78
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	26	56	0.05%	59.3%	IFDLGRK	98.9%	35.3	25	0	2	0	0	848.50	33	39
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	26	56	0.05%	59.3%	LHPFHVIR	96.1%	29.6	25	29.6	1	0	0	1018.59	91	98
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	26	56	0.05%	59.3%	LQNKEHVIEALR	99.7%	59.4	25	55.4	2	2	0	1449.82	142	153
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	26	56	0.05%	59.3%	MLSCAGADR	99.7%	57.8	25	44.3	5	0	0	980.43	102	110
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	26	56	0.05%	59.3%	MLSCAGADRLQTGMR	99.7%	47.2	25	38.3	2	4	0	1666.78	102	116
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	26	56	0.05%	59.3%	RLIPDGCGVK	99.7%	47.1	25	35.6	2	0	0	1114.60	189	198
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	26	56	0.05%	59.3%	VDEFPLCGHMVSDEYEQLSSEALEAAR	99.7%	74.1	25	71.2	0	4	0	3098.37	43	69
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	26	56	0.05%	59.3%	VHIGQVIMSIR	99.7%	57	25	57	6	4	0	1252.72	129	139
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	19	44	0.04%	42.4%	AVDIPHMDIEALK	99.7%	49.5	25	42.3	4	0	0	1467.75	79	91
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	19	44	0.04%	42.4%	AVDIPHMDIEALKK	99.7%	59.7	25	44.2	3	3	0	1595.85	79	92
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	19	44	0.04%	42.4%	DTLYEAVR	99.7%	57.3	25	43.7	5	0	0	966.49	8	15
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	19	44	0.04%	42.4%	FPSLLTHNENMVAK	99.7%	55.8	25	54.3	5	3	0	1600.82	134	147
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	19	44	0.04%	42.4%	FSVCVLGDQQHCDEAK	99.7%	78.6	25	78.6	3	2	0	1892.83	63	78
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	19	44	0.04%	42.4%	ILGPGLNK	99.0%	35.7	25	23.1	2	0	0	811.50	123	130
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	19	44	0.04%	42.4%	KNWQNVR	97.5%	31.5	25	20.1	1	0	0	944.51	196	202
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	19	44	0.04%	42.4%	KYDAFLASESLIK	99.7%	76.4	25	72.9	5	2	0	1484.80	106	118
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	9	19	44	0.04%	42.4%	VLCLAVAVGHVK	99.7%	63	25	50.9	4	2	0	1265.74	162	173

60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	12	48	0.05%	39.3%	AEEILEK	97.8%	32.1	25	15.8	2	0	0	831.45	79	85
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	12	48	0.05%	39.3%	AEEILEKGLK	99.7%	41.5	25	31.9	1	0	0	1129.65	79	88
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	12	48	0.05%	39.3%	IAVHCTVR	99.7%	49.8	25	42.2	3	0	0	955.51	68	75
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	12	48	0.05%	39.3%	ISKEEAMR	99.7%	54.1	25	33.6	3	0	0	963.49	157	164
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	12	48	0.05%	39.3%	KLCLNICVGESGDR	99.7%	55.3	25	55.3	1	0	0	1620.78	19	32
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	12	48	0.05%	39.3%	LCLNICVGESGDR	99.5%	39.1	25	39.1	3	0	0	1492.69	20	32
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	12	48	0.05%	39.3%	VLEQLTGQTPVFSK	99.7%	93.5	25	87.4	17	0	0	1546.85	39	52
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	12	48	0.05%	39.3%	VLEQLTGQTPVFSKAR	99.7%	57.9	25	57.9	2	0	0	1773.99	39	54
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	12	48	0.05%	39.3%	WFQQKYDGIILPGK	99.7%	40.5	25	40.5	2	2	0	1692.91	165	178
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	12	48	0.05%	39.3%	YDGIILPGK	99.7%	63.3	25	58.6	12	0	0	975.55	170	178
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	6	8	33	0.03%	54.5%	CTGGEVGATSALAPK	99.7%	111	25	90.7	5	0	0	1418.69	17	31
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	6	8	33	0.03%	54.5%	EILGTAQSVGCNVDGR	99.7%	110	25	110	3	0	0	1675.81	131	146
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	6	8	33	0.03%	54.5%	HPHDIIDDINSGAVECPAS	99.7%	56	25	56	2	0	0	2046.92	147	165
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	6	8	33	0.03%	54.5%	HSGNITFDEIVNIAR	99.7%	101	25	101	2	4	0	1685.86	100	114
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	6	8	33	0.03%	54.5%	IGPLGLSPK	99.7%	57.3	25	39.6	8	0	0	881.55	32	40
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	6	8	33	0.03%	54.5%	QAQIEVVPSASALIIK	99.7%	95	25	95	7	2	0	1666.97	68	83
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	13	76	0.07%	38.9%	AKEAAEQDVEK	99.7%	76.9	25	69.1	2	1	0	1217.60	199	209
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	13	76	0.07%	38.9%	GFSLEELR	99.7%	53.7	25	39.7	15	0	0	950.49	75	82
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	13	76	0.07%	38.9%	LATQLTGPVMPVR	99.7%	73.3	25	72.4	11	0	0	1382.78	146	158
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	13	76	0.07%	38.9%	RVATWFNQPAR	99.7%	46.7	25	40.5	2	2	0	1345.71	21	31
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	13	76	0.07%	38.9%	SKLILFPR	99.7%	48.4	25	48.4	3	0	0	973.62	122	129
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	13	76	0.07%	38.9%	STESLQANVQR	99.7%	88.5	25	76.4	15	0	0	1232.62	106	116
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	13	76	0.07%	38.9%	TIGISVDPR	99.7%	59.1	25	47.4	10	0	0	957.54	93	101
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	13	76	0.07%	38.9%	VATWFNQPAR	99.7%	77.9	25	64.5	7	0	0	1189.61	22	31
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	13	76	0.07%	38.9%	VATWFNQPARK	99.7%	45.9	25	40.4	2	0	0	1317.71	22	32
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	13	76	0.07%	38.9%	VITEEEKNFK	99.7%	52	25	42.5	6	0	0	1236.65	168	177
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	8	11	22	0.02%	34.0%	CEGINISGNFYR	99.7%	65.5	25	62.6	1	0	0	1429.65	38	49
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	8	11	22	0.02%	34.0%	IDKYTEVLK	99.7%	55.8	25	33.7	2	0	0	1108.63	189	197
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	8	11	22	0.02%	34.0%	KFAYLGR	99.7%	46	25	31.4	2	0	0	854.49	134	140
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	8	11	22	0.02%	34.0%	LKYLAFLR	99.7%	48.3	25	40.7	2	0	0	1023.64	52	59
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	8	11	22	0.02%	34.0%	RMVVPAALK	99.7%	44.6	25	21.6	2	0	0	984.60	117	125
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	8	11	22	0.02%	34.0%	VFDGIPPPYDKK	99.7%	41.7	25	36.2	3	2	0	1375.73	104	115
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	8	11	22	0.02%	34.0%	YQAVTATLEEK	99.7%	51.2	25	44.5	6	0	0	1252.64	149	159
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	8	11	22	0.02%	34.0%	YQAVTATLEEKR	99.7%	68.2	25	68.2	1	1	0	1408.74	149	160
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	10	90	0.09%	27.9%	ALVDGPCTQVR	99.7%	87.9	25	82	6	0	0	1215.62	36	46
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	10	90	0.09%	27.9%	CMQLTDFILK	99.7%	53.4	25	36.4	13	0	0	1284.63	54	63
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	10	90	0.09%	27.9%	LVAIVDVIDQNR	99.7%	94.7	25	93.4	41	2	0	1354.77	24	35
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	10	90	0.09%	27.9%	MTDFDRFK	99.7%	44.9	25	44.9	9	0	0	1075.49	104	111
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	10	90	0.09%	27.9%	RFVEVGR	99.7%	48.1	25	37.2	4	0	0	862.49	5	11
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	10	90	0.09%	27.9%	VAYVSFGPHAGK	99.7%	63.8	25	52.3	14	1	0	1232.64	12	23
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	7	10	25	0.02%	32.8%	GATYGKPVHHGVNQLK	99.7%	68.6	25	60.6	2	2	0	1705.91	78	93
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	7	10	25	0.02%	32.8%	NPDTQWITKPVHK	99.7%	56.9	25	51.6	2	2	0	1563.83	145	157
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	7	10	25	0.02%	32.8%	NTLQLHR	99.7%	56.8	25	44.6	5	0	0	881.50	196	202
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	7	10	25	0.02%	32.8%	QLSALHR	99.7%	43.8	25	22.1	1	0	0	824.47	32	38
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	7	10	25	0.02%	32.8%	RNPDTQWITKPVHK	99.7%	45.3	25	44.2	2	2	0	1719.93	144	157
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	7	10	25	0.02%	32.8%	SLQSVAEER	99.7%	57.7	25	42	5	0	0	1018.52	97	105
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	7	10	25	0.02%	32.8%	VLNSYWVGEDSTYK	99.7%	93.2	25	88.8	2	0	0	1660.79	115	128
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	16	47	0.04%	46.7%	EQIVPKPEEEVAQK	99.7%	67	25	55.8	2	0	0	1623.86	154	167
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	16	47	0.04%	46.7%	EQIVPKPEEEVAQKK	99.7%	39.7	25	37.5	2	2	0	1751.95	154	168
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	16	47	0.04%	46.7%	ETAQAIKGMHIR	99.7%	41	25	39	0	2	0	1370.72	31	42
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	16	47	0.04%	46.7%	GLDVDSLVIEHIQVNK	99.7%	59.8	25	57.8	3	0	0	1778.96	106	121

60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	16	47	0.04%	46.7%	KSAEFLLHMLK	99.7%	45.1	25	41	4	2	0	1332.73	86	96
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	16	47	0.04%	46.7%	QWGWTQGR	99.7%	41.3	25	28.2	2	0	0	1018.49	75	82
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	16	47	0.04%	46.7%	QWGWTQGRWPK	99.6%	39.8	25	30	2	0	0	1429.71	75	85
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	16	47	0.04%	46.7%	SAEFLLHMLK	99.7%	67.8	25	59	6	1	0	1188.64	87	96
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	16	47	0.04%	46.7%	VRYSLDPENPTK	99.7%	53.4	25	51.3	2	0	0	1418.73	2	13
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	16	47	0.04%	46.7%	YLKDVTLQK	99.7%	46.7	25	39.4	8	0	0	1107.64	47	55
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	16	47	0.04%	46.7%	YSLDPENPTK	99.7%	62.7	25	62.2	9	0	0	1163.56	4	13
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	13	67	0.06%	46.3%	APGTPHSHTKPYVR	99.7%	36.9	25	36.9	2	2	0	1547.81	155	168
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	13	67	0.06%	46.3%	GCGTVLLSGPR	99.7%	84.1	25	74.3	8	0	0	1116.58	133	143
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	13	67	0.06%	46.3%	ILTFDQLALDSPK	99.7%	118	25	107	22	0	0	1460.80	120	132
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	13	67	0.06%	46.3%	LKVCALR	99.2%	36.4	25	28	2	0	0	859.52	98	104
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	13	67	0.06%	46.3%	RTNSTFNQVVLK	99.7%	53.9	25	18.4	3	0	0	1406.78	38	49
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	13	67	0.06%	46.3%	TAVVVGTITDDVR	99.7%	114	25	104	10	0	0	1345.73	79	91
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	13	67	0.06%	46.3%	TAVVVGTITDDVRVQEVPK	99.7%	45.6	25	44.5	2	2	0	2026.12	79	97
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	13	67	0.06%	46.3%	TNRPPLSLSR	99.3%	37.3	25	24.8	5	0	0	1140.65	56	65
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	13	67	0.06%	46.3%	TNSTFNQVVLK	99.7%	65.8	25	49.6	4	0	0	1250.67	39	49
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	13	67	0.06%	46.3%	TNSTFNQVVLKR	99.7%	55.6	25	49.3	4	1	0	1406.78	39	50
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	53	0.05%	56.8%	AHSIQIMK	99.7%	47.5	25	36.5	3	0	0	927.51	121	128
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	53	0.05%	56.8%	AHSIQIMKVEEIAASK	95.2%	22.8	25	22.8	0	1	0	1770.94	121	136
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	53	0.05%	56.8%	ASGTLREYK	97.4%	31.3	25	25.1	1	0	0	1024.54	3	11
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	53	0.05%	56.8%	DLTTAGAVTQCYR	99.7%	68.5	25	66.9	6	0	0	1455.69	99	111
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	53	0.05%	56.8%	DLTTAGAVTQCYRDMGAR	99.7%	53.8	25	53.8	0	2	0	2001.91	99	116
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	53	0.05%	56.8%	EYRDLTTAGAVTQCYR	99.7%	70.3	25	68.7	4	4	0	1903.90	96	111
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	53	0.05%	56.8%	FWYFVSQLKK	99.5%	38.6	25	34.7	1	0	0	1345.73	44	53
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	53	0.05%	56.8%	IFAPNHVVAK	99.5%	39.2	25	28.4	6	0	0	1095.63	32	41
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	53	0.05%	56.8%	IKFPLPHR	98.7%	34.5	25	29.1	2	0	0	1007.62	150	157
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	53	0.05%	56.8%	KSSGEIVYCGQVFEK	99.7%	68.4	25	68.4	2	2	0	1730.84	56	70
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	53	0.05%	56.8%	NFGIWLR	99.6%	40.5	25	24.7	4	0	0	905.50	77	83
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	53	0.05%	56.8%	SSGEIVYCGQVFEK	99.7%	100	25	96.2	9	0	0	1602.75	57	70
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	53	0.05%	56.8%	VEEIAASK	99.7%	49.9	25	32.9	2	0	0	846.46	129	136
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	53	0.05%	56.8%	VEEIAASKCR	98.4%	33.5	25	25.4	1	0	0	1162.59	129	138
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	53	0.05%	56.8%	VKNFGIWLR	99.7%	41.2	25	35.1	3	0	0	1132.66	75	83
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	8	9	25	0.02%	27.6%	HMYHSLYLK	99.1%	36.4	25	25.6	2	0	0	1191.60	118	126
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	8	9	25	0.02%	27.6%	ILMEHIHK	99.7%	50.4	25	39.9	6	0	0	1020.57	137	144
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	8	9	25	0.02%	27.6%	KLLADQAEAR	99.7%	78.5	25	69.8	2	0	0	1114.62	153	162
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	8	9	25	0.02%	27.6%	KVWLDPNETNEIANANSR	99.7%	51.8	25	51.8	0	2	0	2071.02	21	38
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	8	9	25	0.02%	27.6%	LLADQAEAR	99.7%	71.2	25	60	5	0	0	986.53	154	162
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	8	9	25	0.02%	27.6%	LLADQAEARR	99.6%	40.4	25	21.8	3	0	0	1142.63	154	163
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	8	9	25	0.02%	27.6%	RLASSVLR	97.7%	31.8	25	17.2	2	0	0	901.56	9	16
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	8	9	25	0.02%	27.6%	VWLDPNETNEIANANSR	99.7%	99	25	99	3	0	0	1942.93	22	38
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	9	14	38	0.04%	47.5%	EKGTWVQLK	96.7%	30.3	25	17.3	1	0	0	1088.61	121	129
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	9	14	38	0.04%	47.5%	GDIVDIKGMGTVQK	99.7%	49.9	25	47.5	3	0	0	1460.78	37	50
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	9	14	38	0.04%	47.5%	GTWVQLK	99.3%	37.2	25	22.5	2	0	0	831.47	123	129
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	9	14	38	0.04%	47.5%	GTWVQLKR	99.7%	45.5	25	29.5	4	0	0	987.57	123	130
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	9	14	38	0.04%	47.5%	HGVVPLATYMR	99.7%	61.5	25	61.5	4	1	0	1243.66	22	32
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	9	14	38	0.04%	47.5%	KGDIVDIK	99.4%	38	25	2.52	1	0	0	887.52	36	43
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	9	14	38	0.04%	47.5%	SRDSFLK	97.8%	32	25	13.8	1	0	0	852.46	101	107
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	9	14	38	0.04%	47.5%	TNGKEPELLEPIPYEFMA	99.2%	36.7	25	36.7	5	0	0	2094.01	143	160
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	9	14	38	0.04%	47.5%	VYNVTQHAVGIVVNK	99.7%	96.9	25	87.8	9	7	0	1640.91	64	78
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	7	32	0.03%	36.7%	AGNLGGGVVTIER	99.7%	98.2	25	90.6	7	0	0	1242.68	53	65
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	7	32	0.03%	36.7%	ITVTSEVPFSK	99.7%	74.4	25	70.3	9	0	0	1207.66	70	80

60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	7	32	0.03%	36.7%	ITVTSEVPFSKR	99.7%	73.8	25	68.1	4	2	0	1363.76	70	81
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	7	32	0.03%	36.7%	NNLRDWLR	98.2%	33	25	14.4	4	0	0	1086.58	94	101
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	7	32	0.03%	36.7%	SKITVTSEVPFSK	99.7%	92.9	25	90.1	4	0	0	1422.78	68	80
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	7	32	0.03%	36.7%	VVANSKESYELR	99.7%	50.4	25	45.2	2	0	0	1394.73	102	113
60S ribosomal protein L22-like 1	RPL22L1	RL22L_HUMAN	14.6	99.8%	2	3	6	0.01%	26.2%	NNLRDWLR	98.2%	33	25	14.4	4	0	0	1086.58	88	95
60S ribosomal protein L22-like 1	RPL22L1	RL22L_HUMAN	14.6	99.8%	2	3	6	0.01%	26.2%	TGNLGNVVHIER	99.7%	56	25	39.6	2	0	0	1308.70	48	59
60S ribosomal protein L22-like 1	RPL22L1	RL22L_HUMAN	14.6	99.8%	2	3	6	0.01%	26.2%	VVASDKETYELR	99.7%	83.4	25	83.4	2	2	0	1409.73	96	107
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	8	17	82	0.08%	52.9%	ECADLWPR	99.7%	58.9	25	27.8	6	0	0	1046.47	124	131
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	8	17	82	0.08%	52.9%	GSAITGPVAK	99.7%	62.2	25	50.3	9	0	0	900.52	114	123
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	8	17	82	0.08%	52.9%	ISLGLPVGAVINCADNTGAK	99.7%	92	25	88.9	11	2	0	1970.04	16	35
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	8	17	82	0.08%	52.9%	KVHPAVVIR	94.6%	28.3	25	28.3	1	0	0	1018.65	75	83
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	8	17	82	0.08%	52.9%	LNRLPAAGVGDMVMATVK	99.7%	67.6	25	67.6	6	10	0	1842.99	49	66
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	8	17	82	0.08%	52.9%	LPAAGVGDMVMATVK	99.7%	94.3	25	94.3	25	1	0	1459.76	52	66
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	8	17	82	0.08%	52.9%	LPAAGVGDMVMATVKK	99.7%	68.7	25	68.7	4	4	0	1587.86	52	67
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	8	17	82	0.08%	52.9%	NLYIISVK	99.7%	49.7	25	46.4	3	0	0	949.57	36	43
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	11	15	72	0.07%	51.3%	EAPAPPKAEAK	99.7%	59.3	25	57.7	5	0	0	1108.60	8	18
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	11	15	72	0.07%	51.3%	FPLTTESAMK	99.7%	56.6	25	48.8	8	0	0	1140.56	79	88
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	11	15	72	0.07%	51.3%	FPLTTESAMKK	95.2%	28.8	25	16.5	1	0	0	1268.66	79	89
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	11	15	72	0.07%	51.3%	KIEDNNTLVFIVDVK	99.2%	29.9	25	29.9	0	1	0	1746.96	89	103
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	11	15	72	0.07%	51.3%	KLYDIDVAK	99.7%	59.5	25	53.9	2	0	0	1064.60	115	123
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	11	15	72	0.07%	51.3%	LAPDYDALDVANK	99.7%	85.6	25	79.7	21	0	0	1404.70	140	152
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	11	15	72	0.07%	51.3%	LDHYAIIK	99.7%	52.8	25	17.5	3	0	0	972.55	71	78
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	11	15	72	0.07%	51.3%	LYDIDVAK	99.7%	51.1	25	41.7	5	0	0	936.50	116	123
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	11	15	72	0.07%	51.3%	NKLDHYAIIK	99.7%	48.6	25	16.6	2	2	0	1214.69	69	78
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	11	15	72	0.07%	51.3%	VNTLIRPDGEK	99.7%	60.8	25	50.5	14	2	0	1241.69	124	134
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	11	15	72	0.07%	51.3%	VNTLIRPDGEKK	99.7%	46.3	25	45.5	2	4	0	1369.78	124	135
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	13	99	0.09%	35.7%	AITGASLADIMAK	99.7%	106	25	98.2	43	0	0	1277.68	81	93
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	13	99	0.09%	35.7%	AITGASLADIMAKR	99.7%	47.5	25	47.5	2	0	0	1433.78	81	94
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	13	99	0.09%	35.7%	CESAFLSK	99.7%	52.3	25	44.1	8	0	0	941.44	36	43
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	13	99	0.09%	35.7%	CESAFLSKR	99.7%	52.9	25	38.4	2	0	0	1097.54	36	44
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	13	99	0.09%	35.7%	MKVELCSFSGYK	99.7%	76.7	25	68.3	9	2	0	1448.69	1	12
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	13	99	0.09%	35.7%	QINWTVLYR	99.7%	50.9	25	42.5	9	0	0	1192.65	48	56
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	13	99	0.09%	35.7%	TDGKVFQFLNAK	99.7%	40.5	25	39.5	0	4	0	1367.73	24	35
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	13	99	0.09%	35.7%	VELCSFSGYK	99.7%	57.6	25	48	2	0	0	1189.56	3	12
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	13	99	0.09%	35.7%	VFQFLNAK	99.7%	54.4	25	34	18	0	0	966.54	28	35
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	10	15	52	0.05%	40.7%	ANGTTVHVGIHPSK	99.7%	70.2	25	62	2	3	0	1417.75	90	103
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	10	15	52	0.05%	40.7%	DDEVQVVR	99.7%	54.1	25	34.7	6	0	0	959.48	52	59
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	10	15	52	0.05%	40.7%	FNPFVTSDR	99.7%	60	25	47.5	6	0	0	1082.53	3	11
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	10	15	52	0.05%	40.7%	IMSSPLSK	98.4%	33.5	25	21.6	3	0	0	878.47	29	36
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	10	15	52	0.05%	40.7%	KDDEVQVVR	99.7%	63.3	25	50.2	7	0	0	1087.57	51	59
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	10	15	52	0.05%	40.7%	KIMSSPLSK	98.8%	34.9	25	19.5	4	0	0	990.57	28	36
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	10	15	52	0.05%	40.7%	KYVIYIER	99.7%	48.2	25	44.7	4	0	0	1083.62	77	84
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	10	15	52	0.05%	40.7%	MKFNPFVTSDR	99.7%	67.5	25	61.4	6	1	0	1357.66	1	11
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	10	15	52	0.05%	40.7%	YKEETIEK	99.5%	38.8	25	31.3	2	0	0	1039.53	135	142
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	10	15	52	0.05%	40.7%	YVIYIER	99.7%	48.7	25	41.1	8	0	0	955.52	78	84
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	9	13	46	0.04%	55.9%	DVFRDPALK	98.0%	32.4	25	13.5	1	0	0	1060.58	99	107
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	9	13	46	0.04%	55.9%	NIDDGTSDRPYSHALVAGIDR	99.7%	50.4	25	50.4	0	2	0	2272.10	28	48
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	9	13	46	0.04%	55.9%	NKWFFQK	99.5%	39.3	25	18.7	2	0	0	997.53	127	133
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	9	13	46	0.04%	55.9%	TVVNKDVFR	99.6%	40.4	25	34.4	2	0	0	1077.61	94	102
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	9	13	46	0.04%	55.9%	VKFEER	94.5%	28.2	25	18	1	0	0	807.44	116	121
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	9	13	46	0.04%	55.9%	VVLVLAGR	99.7%	61.8	25	57.3	9	0	0	826.55	10	17

60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	9	13	46	0.04%	55.9%	VYNYNHLMPTR	99.7%	49.2	25	38	9	4	0	1407.68	74	84
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	9	13	46	0.04%	55.9%	YSVDIPLDK	99.7%	55.3	25	45.1	13	0	0	1049.55	85	93
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	9	13	46	0.04%	55.9%	YSVDIPLDKTVVNK	99.7%	63.7	25	62.9	2	1	0	1590.87	85	98
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	6	7	32	0.03%	40.5%	IKSVGGACVLVA	99.7%	41.8	25	41.8	1	0	0	1173.67	137	148
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	6	7	32	0.03%	40.5%	INFDKYHPGYFGK	99.7%	60.9	25	52.5	2	2	0	1585.78	43	55
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	6	7	32	0.03%	40.5%	LWTLVSEQTR	99.7%	51	25	38.8	4	0	0	1232.66	78	87
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	6	7	32	0.03%	40.5%	NKTGAAPIIDVVR	99.7%	43.4	25	39.6	0	2	0	1353.79	93	105
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	6	7	32	0.03%	40.5%	NQSFCPTVNLDK	99.7%	47.2	25	42.7	4	0	0	1422.67	66	77
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	6	7	32	0.03%	40.5%	TGAAPIIDVVR	99.7%	78.2	25	78.2	17	0	0	1111.65	95	105
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	43	0.04%	41.6%	GVVVVIKR	99.7%	48.7	25	39.8	2	0	0	869.59	59	66
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	43	0.04%	41.6%	KPATSYVR	99.7%	44.2	25	27	2	0	0	921.52	72	79
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	43	0.04%	41.6%	KTVGVEPAADGK	99.7%	46.5	25	36.2	7	0	0	1171.63	47	58
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	43	0.04%	41.6%	NCSSFLIK	99.3%	37.3	25	16	3	0	0	968.49	12	19
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	43	0.04%	41.6%	NCSSFLIKR	99.7%	48.8	25	42.1	2	0	0	1124.59	12	20
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	43	0.04%	41.6%	NKQTYSTEPNNLK	99.7%	69.5	25	48.5	7	1	0	1536.77	21	33
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	43	0.04%	41.6%	QTYSTEPNNLK	99.7%	59.3	25	49.9	8	0	0	1294.63	23	33
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	43	0.04%	41.6%	TVGVEPAADGK	99.7%	53.3	25	49.7	3	0	0	1043.54	48	58
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	43	0.04%	41.6%	TVGVEPAADGKGVVVVIK	99.7%	86.4	25	81.2	4	1	0	1738.01	48	65
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	43	0.04%	41.6%	YNGLIHR	99.6%	40.9	25	26.3	2	0	0	872.47	40	46
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	43	0.04%	41.6%	YNGLIHRK	95.9%	29.4	25	19.3	1	0	0	1000.57	40	47
60S ribosomal protein L29	RPL29	RL29_HUMAN	17.8	100.0%	4	5	28	0.03%	21.4%	AQAAAPASVPAQAPK	99.7%	85.4	25	84.7	16	0	0	1377.75	135	149
60S ribosomal protein L29	RPL29	RL29_HUMAN	17.8	100.0%	4	5	28	0.03%	21.4%	AQAAAPASVPAQAPKR	99.7%	61.5	25	61.5	2	2	0	1533.85	135	150
60S ribosomal protein L29	RPL29	RL29_HUMAN	17.8	100.0%	4	5	28	0.03%	21.4%	LAYIAHPK	98.9%	35.1	25	29.1	7	0	0	912.53	96	103
60S ribosomal protein L29	RPL29	RL29_HUMAN	17.8	100.0%	4	5	28	0.03%	21.4%	YESLKGVDPK	97.4%	31.4	25	17.6	1	0	0	1135.60	29	38
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	29	89	0.08%	45.4%	AFMGPLKK	97.8%	32.1	25	24	3	0	0	907.51	387	394
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	29	89	0.08%	45.4%	AGMTHIVR	99.7%	66.5	25	56.8	4	0	0	884.48	51	58
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	29	89	0.08%	45.4%	AHLMEIQVNGGTVAEK	99.7%	51.8	25	43	0	3	0	1712.86	178	193
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	29	89	0.08%	45.4%	DDPSKPVHLTAFLGYK	99.7%	49	25	49	2	2	0	1787.93	35	50
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	29	89	0.08%	45.4%	FQTMEEKK	95.7%	29.2	25	17.8	2	0	0	1040.51	379	386
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	29	89	0.08%	45.4%	HGSLGFLPR	99.7%	66.3	25	56	9	0	0	983.54	11	19
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	29	89	0.08%	45.4%	IGQGYLIK	99.7%	60.7	25	39.8	6	0	0	891.53	287	294
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	29	89	0.08%	45.4%	IGQGYLIKDGK	99.7%	59.7	25	53.8	2	0	0	1191.67	287	297
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	29	89	0.08%	45.4%	KAHLMEIQVNGGTVAEK	97.9%	25.9	25	25.9	0	1	0	1840.96	177	193
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	29	89	0.08%	45.4%	KSLLVQTK	98.9%	35.2	25	24.2	2	0	0	916.58	349	356
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	29	89	0.08%	45.4%	KVACIGAWHPAR	99.7%	51.4	25	51.4	1	2	0	1365.72	250	261
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	29	89	0.08%	45.4%	KYCQVIR	98.7%	34.5	25	21.9	1	0	0	966.52	155	161
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	29	89	0.08%	45.4%	LEQQVPVNQVFGQDEMIDVIGVTK	99.7%	64.6	25	64.6	3	2	0	2702.37	201	224
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	29	89	0.08%	45.4%	NNASTDYDLSDK	99.7%	73.7	25	73	14	0	0	1342.58	301	312
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	29	89	0.08%	45.4%	SINPLGGFVHYGEVTNDFVMLK	99.7%	48.7	25	48.7	0	4	0	2453.22	313	334
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	29	89	0.08%	45.4%	TVFAEHISDECK	99.7%	74.7	25	74.7	4	1	0	1435.65	104	115
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	29	89	0.08%	45.4%	TVFAEHISDECKR	99.7%	57.9	25	57.9	4	4	0	1591.75	104	116
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	29	89	0.08%	45.4%	VACIGAWHPAR	99.7%	71.9	25	67.5	4	2	0	1237.63	251	261
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	29	89	0.08%	45.4%	VIAHTQMR	99.7%	42.9	25	37.9	3	0	0	955.51	162	169
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	29	89	0.08%	45.4%	YCQVIR	99.0%	35.7	25	21.9	4	0	0	838.42	156	161
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	13	51	0.05%	59.1%	KSEIEYYAMLAK	99.7%	72.2	25	72.2	8	4	0	1461.73	57	68
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	13	51	0.05%	59.1%	KSLESINSR	99.7%	47.7	25	37.5	2	0	0	1033.56	9	17
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	13	51	0.05%	59.1%	LVILANNCPALR	99.7%	76.5	25	60.4	7	0	0	1353.77	45	56
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	13	51	0.05%	59.1%	LVILANNCPALRK	99.7%	49.8	25	43.5	2	0	0	1481.86	45	57
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	13	51	0.05%	59.1%	SEIEYYAMLAK	99.7%	85.1	25	73.8	10	0	0	1333.63	58	68
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	13	51	0.05%	59.1%	SLESINSR	99.6%	39.7	25	33.7	3	0	0	905.47	10	17
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	13	51	0.05%	59.1%	TGVHHYSGNNIELGTACGK	99.7%	64.8	25	60.7	2	6	0	2014.94	69	87

60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	13	51	0.05%	59.1%	VCTLAIIDPGDSDIIR	99.7%	94.9	25	87.4	7	0	0	1757.91	91	106
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	9	11	50	0.05%	56.8%	EMGTPDVR	99.7%	51.5	25	42.4	6	0	0	920.41	56	63
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	9	11	50	0.05%	56.8%	EYTINIHK	98.3%	33.2	25	20.3	1	0	0	1017.54	24	31
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	9	11	50	0.05%	56.8%	EYTINIHKR	99.7%	55.5	25	39.8	4	0	0	1173.64	24	32
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	9	11	50	0.05%	56.8%	FAMKEMGTPDVR	99.3%	37.7	25	21.7	3	3	0	1413.65	52	63
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	9	11	50	0.05%	56.8%	IHGVGFKK	98.3%	33.3	25	26.4	2	0	0	885.53	33	40
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	9	11	50	0.05%	56.8%	LYTLVTYVPVTTFK	99.7%	78.4	25	78.4	9	0	0	1644.92	102	115
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	9	11	50	0.05%	56.8%	NEDEDSPNKLYTLVTYVPVTTFK	95.2%	22.8	25	22.2	0	1	0	2673.33	93	115
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	9	11	50	0.05%	56.8%	NLQTVNVDEN	99.7%	72.5	25	68.9	4	0	0	1145.54	116	125
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	9	11	50	0.05%	56.8%	SAINEVVTR	99.7%	67.2	25	55	17	0	0	988.54	15	23
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	6	15	43	0.04%	37.0%	AALRPLVKPK	95.7%	29.2	25	26.6	1	0	0	1092.73	2	11
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	6	15	43	0.04%	37.0%	ELEVLLMCNK	99.7%	61.7	25	44.3	8	0	0	1264.63	84	93
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	6	15	43	0.04%	37.0%	FKGQILMPNIGYGSNK	99.7%	51.8	25	51.8	4	4	0	1782.92	49	64
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	6	15	43	0.04%	37.0%	GQILMPNIGYGSNK	99.7%	73.4	25	68.8	8	0	0	1491.76	51	64
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	6	15	43	0.04%	37.0%	GQILMPNIGYGSNKK	99.7%	52.5	25	47.4	4	3	0	1619.86	51	65
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	6	15	43	0.04%	37.0%	SYCAEIAHNVSSK	99.7%	87.4	25	84.6	9	2	0	1465.67	94	106
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	10	11	37	0.04%	43.6%	AFLIEEQK	99.7%	55.7	25	38.3	7	0	0	977.53	94	101
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	10	11	37	0.04%	43.6%	AFLIEEQKIVVK	99.7%	58.3	25	54.9	2	1	0	1416.85	94	105
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	10	11	37	0.04%	43.6%	AYGGSMCAK	99.7%	51.5	25	51.5	3	0	0	944.40	77	85
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	10	11	37	0.04%	43.6%	IVYLYTK	99.7%	45	25	29	3	0	0	899.52	30	36
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	10	11	37	0.04%	43.6%	IVYLYTKK	99.7%	52.5	25	38.8	2	0	0	1027.62	30	37
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	10	11	37	0.04%	43.6%	LSYNTASNK	99.7%	54.1	25	37	7	0	0	997.49	11	19
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	10	11	37	0.04%	43.6%	LSYNTASNKTR	99.4%	38.2	25	30.5	1	0	0	1254.64	11	21
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	10	11	37	0.04%	43.6%	RAFLIEEQK	98.0%	32.4	25	22.3	3	0	0	1133.63	93	101
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	10	11	37	0.04%	43.6%	RLSYNTASNK	99.7%	45.6	25	38.5	5	0	0	1153.60	10	19
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	10	11	37	0.04%	43.6%	SACGVCPGR	99.5%	38.7	25	34	3	0	0	963.41	44	52
60S ribosomal protein L35	RPL35	RL35_HUMAN	14.6	100.0%	4	6	21	0.02%	29.3%	QLDDLKVELSQLR	99.7%	80.4	25	64.6	3	2	0	1556.86	20	32
60S ribosomal protein L35	RPL35	RL35_HUMAN	14.6	100.0%	4	6	21	0.02%	29.3%	VLTVINQTQK	99.7%	66.4	25	59.7	11	0	0	1143.67	57	66
60S ribosomal protein L35	RPL35	RL35_HUMAN	14.6	100.0%	4	6	21	0.02%	29.3%	VLTVINQTQKENLR	99.7%	83.4	25	81.3	2	2	0	1655.94	57	70
60S ribosomal protein L35	RPL35	RL35_HUMAN	14.6	100.0%	4	6	21	0.02%	29.3%	YKPLDLRPK	99.3%	37.3	25	37.3	1	0	0	1129.67	78	86
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	31	0.03%	42.7%	AIFAGYKR	99.7%	43.6	25	33.8	2	0	0	925.53	9	16
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	31	0.03%	42.7%	AKNNTVTPGGKPNK	97.7%	25.6	25	25.6	0	2	0	1425.78	53	66
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	31	0.03%	42.7%	DETEFYLGK	99.7%	53.2	25	46.1	4	0	0	1101.51	37	45
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	31	0.03%	42.7%	DETEFYLGKR	99.7%	45.8	25	35.1	4	0	0	1257.61	37	46
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	31	0.03%	42.7%	IEGVYAR	99.7%	43.6	25	27.3	4	0	0	807.44	30	36
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	31	0.03%	42.7%	NNTVTPGGKPNK	99.6%	40.8	25	36.5	4	0	0	1226.65	55	66
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	31	0.03%	42.7%	VMLYPSR	94.6%	28.3	25	15.7	1	0	0	881.46	103	109
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	31	0.03%	42.7%	VMLYPSRI	99.7%	52.4	25	47.8	10	0	0	994.54	103	110
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	6	10	27	0.03%	33.3%	ALRYPMAVGLNK	99.7%	56.5	25	34.7	2	2	0	1348.74	2	13
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	6	10	27	0.03%	33.3%	EELSNVLAAMR	99.7%	99.4	25	92.5	5	0	0	1232.63	88	98
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	6	10	27	0.03%	33.3%	EELSNVLAAMRK	99.7%	44.1	25	42.8	2	0	0	1376.72	88	99
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	6	10	27	0.03%	33.3%	EVCGFAPYER	99.7%	52.8	25	52.8	6	0	0	1227.55	46	55
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	6	10	27	0.03%	33.3%	REELSNVLAAMR	99.7%	59.3	25	52.9	2	2	0	1388.73	87	98
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	6	10	27	0.03%	33.3%	YPMAVGLNK	99.7%	44.5	25	29.7	6	0	0	992.52	5	13
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	7	7	18	0.02%	45.3%	DSLYAQGR	99.7%	41.1	25	38	2	0	0	909.44	31	38
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	7	7	18	0.02%	45.3%	GKDSLYAQGR	99.7%	64.9	25	54.9	4	0	0	1094.56	29	38
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	7	7	18	0.02%	45.3%	HFELGGDK	97.0%	30.6	25	21	1	0	0	902.44	90	97
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	7	7	18	0.02%	45.3%	HFELGGDKK	99.5%	38.8	25	25.7	1	0	0	1030.53	90	98
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	7	7	18	0.02%	45.3%	KGQVIQF	95.6%	29.1	25	23.5	1	0	0	819.47	100	106
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	7	7	18	0.02%	45.3%	LECVEPNCR	99.7%	47.3	25	47.3	7	0	0	1176.51	70	78
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	7	7	18	0.02%	45.3%	QSGYGGQTKPIFR	99.7%	38.9	25	38.9	0	2	0	1438.74	45	57

60S ribosomal protein L37a	RPL37A	RL37A_HUMAN	10.3	100.0%	4	5	25	0.02%	51.1%	AVGIWHCGSCMK	99.7%	45.1	25	45.1	5	0	0	1405.62	51	62
60S ribosomal protein L37a	RPL37A	RL37A_HUMAN	10.3	100.0%	4	5	25	0.02%	51.1%	KIEISQHAK	99.7%	46.1	25	34.8	5	0	0	1053.61	28	36
60S ribosomal protein L37a	RPL37A	RL37A_HUMAN	10.3	100.0%	4	5	25	0.02%	51.1%	TVAGGAWTYNTTSAVTVK	99.7%	109	25	104	14	0	0	1826.93	63	80
60S ribosomal protein L37a	RPL37A	RL37A_HUMAN	10.3	100.0%	4	5	25	0.02%	51.1%	YTCSFCGK	97.6%	31.7	25	31.7	1	0	0	1022.41	37	44
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	5	7	29	0.03%	51.4%	IEEIKDFLLTAR	99.7%	54.2	25	54.2	3	2	0	1447.82	5	16
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	5	7	29	0.03%	51.4%	LKQSLPPGLAVK	99.7%	48.6	25	48.6	4	0	0	1250.78	56	67
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	5	7	29	0.03%	51.4%	QSLPPGLAVK	99.7%	81.7	25	76.8	8	0	0	1009.60	58	67
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	5	7	29	0.03%	51.4%	YLYTLVITDK	99.7%	56.1	25	46.6	2	0	0	1228.68	41	50
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	5	7	29	0.03%	51.4%	YLYTLVITDKEK	99.7%	68.1	25	62.6	6	4	0	1485.82	41	52
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	123	0.12%	46.1%	AAAAAAALQAK	99.7%	90.4	25	83.1	14	0	0	956.55	354	364
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	123	0.12%	46.1%	APIRPDIVNFVHTNLR	99.7%	62.3	25	62.3	0	6	0	1862.04	30	45
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	123	0.12%	46.1%	AWNDIKK	99.7%	43.8	25	24.5	1	0	0	874.48	176	182
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	123	0.12%	46.1%	EAVLLLKK	99.7%	52.4	25	32.4	2	0	0	913.61	166	173
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	123	0.12%	46.1%	FCIWTESAFR	99.7%	59	25	49.7	9	0	0	1316.61	249	258
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	123	0.12%	46.1%	GPCIIYNEDNGIIK	99.7%	64.3	25	64.3	2	0	0	1605.79	206	219
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	123	0.12%	46.1%	IEEVPELPLVVEDK	99.7%	69.4	25	69.4	2	0	0	1608.87	144	157
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	123	0.12%	46.1%	IEEVPELPLVVEDKVEGYK	99.7%	54.4	25	54.4	1	0	0	2185.16	144	162
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	123	0.12%	46.1%	KLDELYGTWR	99.7%	65.7	25	59.8	4	1	0	1280.66	259	268
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	123	0.12%	46.1%	LAPGGHVGR	99.7%	68.3	25	58.4	3	0	0	863.48	240	248
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	123	0.12%	46.1%	LDELYGTWR	99.7%	75.8	25	72.2	2	0	0	1152.57	260	268
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	123	0.12%	46.1%	MINTDLSR	99.7%	63.7	25	53.9	11	0	0	949.48	284	291
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	123	0.12%	46.1%	NIPGITLLNVSK	99.7%	80.2	25	75.7	16	0	0	1268.76	223	234
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	123	0.12%	46.1%	NVTLPAVFK	99.7%	40.9	25	27.2	4	0	0	988.58	21	29
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	123	0.12%	46.1%	QPYAVSELAGHQTSAESWGTGR	99.7%	104	25	104	2	2	0	2332.10	50	71
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	123	0.12%	46.1%	RGPCIIYNEDNGIIK	99.7%	58.2	25	42.8	2	3	0	1761.90	205	219
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	123	0.12%	46.1%	SGQGAFGNMCR	99.7%	69.8	25	69.8	8	0	0	1184.49	87	97
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	123	0.12%	46.1%	SNYNLPMHK	99.7%	43.8	25	42.9	10	0	0	1119.53	275	283
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	123	0.12%	46.1%	TKEAVLLLK	99.7%	41.2	25	34	3	0	0	1014.66	164	172
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	20	29	123	0.12%	46.1%	YAICSALAASALPALVMSK	99.7%	98	25	98	8	7	0	1937.02	122	140
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	16	31	78	0.07%	42.8%	DIICQIAYAR	99.7%	64.8	25	50.5	2	0	0	1222.63	59	68
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	16	31	78	0.07%	42.8%	EFNAEVHR	99.7%	46.3	25	35	2	0	0	1001.48	189	196
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	16	31	78	0.07%	42.8%	EFNAEVHRK	99.1%	35.9	25	22.9	2	0	0	1129.57	189	197
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	16	31	78	0.07%	42.8%	ENPVYEK	97.7%	31.8	25	12.3	2	0	0	878.43	249	255
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	16	31	78	0.07%	42.8%	FPGYDSESK	99.7%	50.1	25	48.1	2	0	0	1029.45	180	188
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	16	31	78	0.07%	42.8%	GAVDGGLSIPHSTK	99.7%	80.2	25	73.9	4	3	0	1338.70	165	178
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	16	31	78	0.07%	42.8%	GAVDGGLSIPHSTKR	99.7%	55.7	25	55.7	1	2	0	1494.80	165	179
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	16	31	78	0.07%	42.8%	HIMGQNVADYMR	99.7%	62	25	49.3	8	5	0	1434.66	198	209
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	16	31	78	0.07%	42.8%	IEGDMIVCAAYAHELPK	99.7%	81.8	25	77.6	4	4	0	1916.92	69	85
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	16	31	78	0.07%	42.8%	KHIMGQNVADYMR	99.0%	28.8	25	28.8	0	2	0	1578.75	197	209
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	16	31	78	0.07%	42.8%	NSVTPDMMEEMYK	99.7%	78.1	25	78.1	7	0	0	1574.65	229	241
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	16	31	78	0.07%	42.8%	NSVTPDMMEEMYKK	99.7%	81.3	25	81.3	7	2	0	1702.75	229	242
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	16	31	78	0.07%	42.8%	RFPGYDSESK	99.6%	40.9	25	29.5	3	0	0	1185.55	179	188
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	16	31	78	0.07%	42.8%	VGLTNYAAAYCTGLLLAR	99.7%	104	25	104	4	2	0	1927.01	90	107
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	16	31	78	0.07%	42.8%	VTNRDIICQIAYAR	99.7%	57.7	25	53.4	0	2	0	1692.89	55	68
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	16	31	78	0.07%	42.8%	YLMEEDEDAYKK	99.7%	73.6	25	63.3	4	4	0	1533.68	210	221
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	17	24	88	0.08%	50.0%	AGEKVEKPDTK	99.7%	56.9	25	50.6	2	2	0	1201.64	2	12
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	17	24	88	0.08%	50.0%	AIPQLQGYLR	99.7%	65	25	60.1	7	0	0	1158.66	263	272
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	17	24	88	0.08%	50.0%	ASITPGTILIILTGR	99.7%	126	25	126	14	3	0	1525.93	142	156
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	17	24	88	0.08%	50.0%	AVDSQILPK	99.7%	68.7	25	41.7	2	0	0	970.56	252	260
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	17	24	88	0.08%	50.0%	EKYEITEQR	99.7%	43.4	25	34.7	2	0	0	1195.60	238	246
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	17	24	88	0.08%	50.0%	FVIATSTK	99.6%	40.9	25	32.9	2	0	0	866.50	193	200

60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	17	24	88	0.08%	50.0%	HLTDAYFKK	99.7%	42.4	25	33.1	2	0	0	1122.59	211	219
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	17	24	88	0.08%	50.0%	HQEGEIFDTEK	99.7%	74.1	25	74.1	3	0	0	1332.61	227	237
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	17	24	88	0.08%	50.0%	HQEGEIFDTEKEK	99.7%	60.1	25	58.4	2	2	0	1589.74	227	239
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	17	24	88	0.08%	50.0%	KPFSQHVR	97.4%	31.4	25	14.3	1	0	0	998.55	131	138
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	17	24	88	0.08%	50.0%	QLASGLLLVTGPLVLNR	99.7%	126	25	126	10	3	0	1764.07	167	183
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	17	24	88	0.08%	50.0%	SVFALTNGIYPHK	99.7%	61.3	25	57.1	5	1	0	1446.77	273	285
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	17	24	88	0.08%	50.0%	VLATVTKPVGGDK	99.7%	61.2	25	61.2	10	3	0	1284.75	88	100
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	17	24	88	0.08%	50.0%	YEITEQR	99.7%	44.9	25	38.5	4	0	0	938.46	240	246
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	17	24	88	0.08%	50.0%	YEITEQRK	98.2%	33	25	27	1	0	0	1066.55	240	247
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	17	24	88	0.08%	50.0%	YYPTEDVPR	99.7%	52.1	25	52.1	3	0	0	1139.54	115	123
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	17	24	88	0.08%	50.0%	YYPTEDVPRK	98.5%	33.7	25	21.2	2	2	0	1267.63	115	124
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	20	56	0.05%	55.2%	AGNFYVPAEPK	99.7%	42.8	25	37.1	2	0	0	1192.60	78	88
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	20	56	0.05%	55.2%	ASINMLR	99.7%	67.6	25	50.1	6	0	0	804.44	128	134
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	20	56	0.05%	55.2%	EANNFLWPFK	99.7%	49.7	25	40.7	5	0	0	1265.63	203	212
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	20	56	0.05%	55.2%	EVPAVPETLKK	98.9%	35.3	25	35.3	2	0	0	1210.70	10	20
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	20	56	0.05%	55.2%	FKEANNFLWPFK	99.7%	71.6	25	66.2	2	0	0	1540.79	201	212
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	20	56	0.05%	55.2%	IALTDNALIAR	99.7%	101	25	83.7	7	0	0	1170.68	167	177
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	20	56	0.05%	55.2%	IVEPYIAWGYPNLK	99.7%	76.6	25	48.2	8	0	0	1662.89	135	148
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	20	56	0.05%	55.2%	KAGNFYVPAEPK	99.7%	55.6	25	55.2	4	2	0	1320.69	77	88
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	20	56	0.05%	55.2%	KVLQLLR	99.3%	37.7	25	27.1	1	0	0	869.59	107	113
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	20	56	0.05%	55.2%	QIFNGTFVK	99.5%	38.8	25	31.9	1	0	0	1053.57	116	124
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	20	56	0.05%	55.2%	RIALTDNALIAR	99.7%	76.3	25	60.7	2	1	0	1326.79	166	177
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	20	56	0.05%	55.2%	RNFAELK	95.5%	29	25	0.64	1	0	0	877.49	23	29
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	20	56	0.05%	55.2%	SVNELIYK	99.7%	59.9	25	44.6	2	0	0	965.53	149	156
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	20	56	0.05%	55.2%	SVNELIYKR	99.7%	53.1	25	41.3	4	0	0	1121.63	149	157
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	20	56	0.05%	55.2%	TTHFVEGGDAGNREDQINR	99.7%	74.1	25	74.1	2	2	0	2115.98	224	242
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	20	56	0.05%	55.2%	YGIICMEDLIHEIYTVGK	98.9%	35.2	25	35.2	2	0	0	2170.06	182	199
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	22	58	0.06%	45.1%	AGVNTVTTLVENK	99.7%	97.1	25	91.9	10	0	0	1345.73	138	150
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	22	58	0.06%	45.1%	AGVNTVTTLVENKK	99.7%	84.8	25	84.8	2	2	0	1473.83	138	151
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	22	58	0.06%	45.1%	HWGGNVLGPK	99.7%	42.7	25	38.9	2	0	0	1064.56	236	245
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	22	58	0.06%	45.1%	KMGVPYCIIK	99.7%	53.8	25	44.8	3	4	0	1224.65	176	185
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	22	58	0.06%	45.1%	KVAPAPAVVK	99.7%	44.6	25	43.5	2	0	0	979.63	11	20
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	22	58	0.06%	45.1%	KVVNPLFEK	99.6%	39.6	25	24.9	2	0	0	1073.64	26	34
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	22	58	0.06%	45.1%	LKVPPAINQFTQALDR	99.7%	80.8	25	77.6	3	4	0	1811.02	74	89
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	22	58	0.06%	45.1%	MGVPYCIIK	99.7%	42.1	25	34.9	2	0	0	1080.56	177	185
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	22	58	0.06%	45.1%	NFGIGQDIQPK	99.7%	73.2	25	62.3	3	0	0	1216.63	38	48
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	22	58	0.06%	45.1%	QTATQLLK	99.7%	47.4	25	27.7	3	0	0	902.53	90	97
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	22	58	0.06%	45.1%	RHWGGNVLGPK	99.7%	38.9	25	35.3	0	2	0	1220.66	235	245
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	22	58	0.06%	45.1%	TCTTVAFTQVNSEDK	99.7%	114	25	109	2	0	0	1700.78	198	212
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	22	58	0.06%	45.1%	TCTTVAFTQVNSEDKGALAK	99.7%	95.6	25	95.3	2	2	0	2141.05	198	217
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	22	58	0.06%	45.1%	TNYNDRYDEIR	98.4%	33.3	25	28.3	2	0	0	1458.66	224	234
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	15	22	58	0.06%	45.1%	VPPAINQFTQALDR	99.7%	103	25	97.2	4	2	0	1569.84	76	89
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	8	10	29	0.03%	24.1%	ASGNYATVISHNPETK	99.7%	87.8	25	82.9	6	3	0	1688.82	129	144
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	8	10	29	0.03%	24.1%	ASGNYATVISHNPETKK	99.7%	73.1	25	72.1	2	2	0	1816.92	129	145
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	8	10	29	0.03%	24.1%	AVDFAER	99.7%	51.5	25	40.7	2	0	0	807.40	31	37
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	8	10	29	0.03%	24.1%	AVVGVVAGGGR	99.7%	96.2	25	81.1	7	0	0	941.55	164	174
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	8	10	29	0.03%	24.1%	DIIHDPGR	99.3%	37.6	25	27.9	2	0	0	922.47	47	54
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	8	10	29	0.03%	24.1%	GIVKDIIHDPGR	99.2%	30	25	29.5	0	2	0	1319.74	43	54
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	8	10	29	0.03%	24.1%	IDKPILK	97.7%	31.9	25	5.52	2	0	0	826.54	175	181
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	8	10	29	0.03%	24.1%	KVGLIAAR	97.2%	31	25	21.3	1	0	0	827.55	234	241
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	8	14	35	0.03%	34.9%	DFNHINVELSLLGK	99.7%	66.1	25	57.2	3	2	0	1598.85	37	50

60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	8	14	35	0.03%	34.9%	DFNHINVELSLLGKK	99.7%	41.3	25	41.3	0	2	0	1726.95	37	51
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	8	14	35	0.03%	34.9%	FLDGIYVSEK	99.7%	70.9	25	59.6	11	0	0	1170.60	175	184
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	8	14	35	0.03%	34.9%	FLDGIYVSEKGTVQQADE	95.8%	29.2	25	29.2	1	0	0	1998.97	175	192
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	8	14	35	0.03%	34.9%	KFLDGIYVSEK	99.7%	71.9	25	62.3	2	1	0	1298.70	174	184
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	8	14	35	0.03%	34.9%	MRPGVACSVSQAQK	99.7%	51.8	25	47	2	4	0	1518.75	128	141
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	8	14	35	0.03%	34.9%	TICSHVQNMIK	99.7%	75.6	25	68.5	5	1	0	1330.66	72	82
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	8	14	35	0.03%	34.9%	TVIVKGPR	95.5%	29	25	29	1	0	0	869.56	24	31
60S ribosome subunit biogenesis protein NIP7 homolog	NIP7	NIP7_HUMAN	20.5	100.0%	3	4	6	0.01%	23.9%	LAANISGDKLVSLGTCFGK	96.3%	29.8	25	29.8	1	0	0	1951.03	54	72
60S ribosome subunit biogenesis protein NIP7 homolog	NIP7	NIP7_HUMAN	20.5	100.0%	3	4	6	0.01%	23.9%	LHVTALDYLAPYAK	99.6%	40.8	25	40.8	2	0	0	1574.86	81	94
60S ribosome subunit biogenesis protein NIP7 homolog	NIP7	NIP7_HUMAN	20.5	100.0%	3	4	6	0.01%	23.9%	MRPLTEEETR	99.5%	38.9	25	22.7	3	0	0	1277.62	1	10
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	PFKFB3	F263_HUMAN	59.6	100.0%	3	3	4	0.00%	5.4%	IGGDSGLSSR	99.7%	44.9	25	38.7	2	0	0	948.47	265	274
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	PFKFB3	F263_HUMAN	59.6	100.0%	3	3	4	0.00%	5.4%	STIQTAEALR	99.7%	53	25	31.9	1	0	0	1089.59	303	312
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	PFKFB3	F263_HUMAN	59.6	100.0%	3	3	4	0.00%	5.4%	VFNVGEYR	97.8%	32	25	28.1	1	0	0	983.49	68	75
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	7	7	12	0.01%	13.1%	AIGVLTSGGDAQGMNAAVR	99.7%	123	25	123	4	0	0	1787.91	26	44
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	7	7	12	0.01%	13.1%	EWSGLLEELAR	99.7%	44.6	25	23.9	2	0	0	1302.67	140	150
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	7	7	12	0.01%	13.1%	GITNLCVIGGDGSLTGANLFR	99.7%	80.4	25	80.4	1	0	0	2135.09	118	138
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	7	7	12	0.01%	13.1%	NGQIDKEAVQK	99.7%	41.3	25	29.9	2	0	0	1229.65	151	161
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	7	7	12	0.01%	13.1%	NVIFQPVAELK	99.6%	40.6	25	35.1	2	0	0	1257.72	726	736
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	7	7	12	0.01%	13.1%	NVIFQPVAELKK	99.3%	37.2	25	37.2	1	0	0	1385.82	726	737
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	7	7	12	0.01%	13.1%	SFAGNLNTYK	99.7%	49.5	25	41.5	2	0	0	1114.55	386	395
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	7	7	12	0.01%	13.1%	TFVLEVMGR	99.7%	68.5	25	61.9	2	0	0	1051.56	211	219
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	7	7	12	0.01%	13.1%	YLEEIATQMR	99.7%	64.8	25	55.3	2	0	0	1253.62	487	496
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	10	11	21	0.02%	16.9%	AIGVLTSGGDAQGMNAAVR	99.7%	123	25	123	4	0	0	1787.91	17	35
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	10	11	21	0.02%	16.9%	AVAFSPVTELKK	99.1%	35.9	25	29.5	2	0	0	1289.75	716	727
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	10	11	21	0.02%	16.9%	GQLESIVENIR	99.7%	66.9	25	57.1	2	0	0	1257.68	475	485
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	10	11	21	0.02%	16.9%	IMEVIDAITTTAQSHQR	99.7%	54.6	25	12.9	0	2	0	1913.98	185	201
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	10	11	21	0.02%	16.9%	LLAHQKPPK	95.7%	29.2	25	26.4	1	0	0	1031.64	387	395
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	10	11	21	0.02%	16.9%	LNIIIIAEGAIDR	99.7%	64.9	25	64.9	1	0	0	1410.83	257	269
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	10	11	21	0.02%	16.9%	TFVLEVMGR	99.7%	68.5	25	61.9	2	0	0	1051.56	202	210
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	10	11	21	0.02%	16.9%	TNVLGHLQQGGAPTPFDR	99.7%	63.8	25	56.4	0	2	0	1907.97	655	672
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	10	11	21	0.02%	16.9%	VFANAPDSACVIGLK	99.7%	82.7	25	79.4	3	0	0	1561.80	699	713
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	10	11	21	0.02%	16.9%	VTVLGHVQR	99.7%	72.6	25	72.6	2	0	0	1008.59	293	301
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	6	6	9	0.01%	12.7%	DLQANVEHLVQK	99.7%	59	25	53	2	0	0	1393.74	604	615
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	6	6	9	0.01%	12.7%	GITNLCVIGGDGSLTGADTFR	99.7%	116	25	116	2	0	0	2124.04	109	129
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	6	6	9	0.01%	12.7%	IFANTPDSGCVLGMR	99.7%	70.9	25	65.9	2	0	0	1637.78	700	714
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	6	6	9	0.01%	12.7%	SEWSDLLSDLQK	99.3%	37.3	25	25.1	1	0	0	1420.70	130	141
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	6	6	9	0.01%	12.7%	TFVLEVMGR	99.7%	68.5	25	61.9	2	0	0	1051.56	202	210
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	6	6	9	0.01%	12.7%	VGIFTGAR	99.7%	52.9	25	40.2	1	0	0	820.47	40	47
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	6	6	9	0.01%	12.7%	VLVVHDGFEGLAK	99.7%	51.2	25	44.7	1	0	0	1383.76	433	445
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	6	6	9	0.01%	12.7%	VTVLGHVQR	99.7%	72.6	25	72.6	2	0	0	1008.59	293	301
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	8	10	17	0.02%	20.9%	AGQAVDDFIEK	99.7%	52.5	25	28.8	2	0	0	1192.58	77	87
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	8	10	17	0.02%	20.9%	CLSSLKDER	99.2%	36.8	25	11.1	2	0	0	1107.55	289	297
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	8	10	17	0.02%	20.9%	FQDTDGKHLLPK	96.3%	23.8	25	22	0	1	0	1398.74	242	253
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	8	10	17	0.02%	20.9%	GILFVGSGVSGGEEGAR	99.7%	110	25	104	2	0	0	1591.81	120	136
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	8	10	17	0.02%	20.9%	IISYAQGFMLLR	99.7%	74	25	66.3	4	0	0	1427.77	332	343
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	8	10	17	0.02%	20.9%	LVPLLDTGDIIIDGGNSEYR	99.7%	84.7	25	84.7	2	0	0	2160.12	88	107
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	8	10	17	0.02%	20.9%	TIFQGIAAK	96.1%	29.6	25	26.9	1	0	0	948.55	155	163
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	8	10	17	0.02%	20.9%	YGPSLMPGGNK	99.7%	51.6	25	41.5	3	0	0	1136.54	137	147
6-phosphogluconolactonase	PGLS	6PGL_HUMAN	27.5	99.8%	2	2	2	0.00%	8.9%	TVIFVATGEGK	99.7%	49.6	25	37	1	0	0	1121.62	198	208
6-phosphogluconolactonase	PGLS	6PGL_HUMAN	27.5	99.8%	2	2	2	0.00%	8.9%	VTLTLPVLNAAR	99.7%	44.5	25	39.9	1	0	0	1267.77	186	197
6-pyruvoyl tetrahydrobiopterin synthase	PTS	PTPS_HUMAN	16.4	100.0%	4	4	5	0.00%	31.0%	FLSDEENLK	99.6%	39.8	25	1.28	1	0	0	1094.54	30	38

6-pyruvoyl tetrahydrobiopterin synthase	PTS	PTPS_HUMAN	16.4	100.0%	4	4	5	0.00%	31.0%	VLPVGVLYK	94.6%	28.3	25	23.6	1	0	0	987.62	121	129
6-pyruvoyl tetrahydrobiopterin synthase	PTS	PTPS_HUMAN	16.4	100.0%	4	4	5	0.00%	31.0%	VYETDNNIVVYKGE	99.7%	58.2	25	55.9	2	0	0	1642.80	132	145
6-pyruvoyl tetrahydrobiopterin synthase	PTS	PTPS_HUMAN	16.4	100.0%	4	4	5	0.00%	31.0%	YMEEAIMQPLDHK	95.0%	28.5	25	28.5	1	0	0	1604.74	79	91
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	17	20	34	0.03%	36.2%	DAGTIAGLNVMR	99.7%	78.3	25	67.6	2	0	0	1217.63	186	197
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	17	20	34	0.03%	36.2%	ELEEIVQPIISK	99.7%	55.8	25	43.6	2	0	0	1397.79	622	633
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	17	20	34	0.03%	36.2%	IINEPTAAAIAYGLDK	99.7%	103	25	101	2	0	0	1659.90	198	213
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	17	20	34	0.03%	36.2%	IINEPTAAAIAYGLDKR	99.6%	33.2	25	33.2	0	2	0	1816.00	198	214
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	17	20	34	0.03%	36.2%	ITITNDQNR	98.4%	33.4	25	28.6	2	0	0	1074.55	524	532
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	17	20	34	0.03%	36.2%	ITPSYVAFTPEGER	99.7%	49.2	25	44.8	2	0	0	1566.78	61	74
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	17	20	34	0.03%	36.2%	LYGSAGPPPTGEEDTAEKDEL	99.7%	99.4	25	99.4	2	0	0	2175.99	634	654
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	17	20	34	0.03%	36.2%	MKETAEAYLGK	99.7%	45.9	25	40.2	2	0	0	1256.62	153	163
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	17	20	34	0.03%	36.2%	NQLTSNPENTVFDAK	99.7%	99	25	91	2	0	0	1677.81	82	96
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	17	20	34	0.03%	36.2%	SDIDEIVLVGGSTR	99.7%	69.5	25	67.7	2	0	0	1460.76	354	367
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	17	20	34	0.03%	36.2%	SQIFSTASDNQPTVTIK	99.7%	116	25	98.5	2	0	0	1836.93	448	464
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	17	20	34	0.03%	36.2%	TFAPEEISAMVLTK	99.7%	109	25	97	3	0	0	1536.80	139	152
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	17	20	34	0.03%	36.2%	TKPYIQVDIGGGQTK	99.7%	57.8	25	57.8	1	0	0	1604.86	124	138
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	17	20	34	0.03%	36.2%	TWNDPSVQQDIK	99.7%	49.1	25	42.6	2	0	0	1430.69	102	113
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	17	20	34	0.03%	36.2%	VEIIANDQGNR	99.7%	76.2	25	0	2	0	0	1228.63	50	60
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	17	20	34	0.03%	36.2%	VLEDSDLKK	99.7%	49.5	25	29.1	2	0	0	1046.57	345	353
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	17	20	34	0.03%	36.2%	VMEHFIK	99.2%	36.7	25	27.2	2	0	0	903.48	262	268
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	17	20	34	0.03%	36.2%	VTHAVVTVPAYFNDAQR	99.7%	38.3	25	31.5	0	2	0	1887.97	165	181
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	17	20	34	0.03%	36.2%	VYEGERPLTK	99.7%	50.2	25	43.4	2	0	0	1191.64	465	474
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	4	5	18	0.02%	11.6%	FLPGYVGGIQEGAVTPAGVVNK	99.7%	94.7	25	94.7	4	2	0	2173.17	121	142
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	4	5	18	0.02%	11.6%	LLVSGFWGVAR	99.7%	83.3	25	83.3	5	0	0	1204.68	394	404
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	4	5	18	0.02%	11.6%	SLDGVTNDR	99.0%	35.4	25	28.1	3	0	0	976.47	14	22
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	4	5	18	0.02%	11.6%	VIECSYTSADGQR	99.7%	80.3	25	80.3	4	0	0	1485.66	377	389
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	15	18	50	0.05%	43.8%	DGLTDVYNK	99.7%	44.3	25	36.6	3	0	0	1024.49	182	190
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	15	18	50	0.05%	43.8%	EAYMGNVLQGGEGQAPTR	99.7%	101	25	101	8	0	0	1877.88	88	105
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	15	18	50	0.05%	43.8%	ENGTVTAANASTLNDGAAALVLMTADAAK	99.7%	44.2	25	43.7	0	2	0	2761.37	274	302
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	15	18	50	0.05%	43.8%	EVVIVSATR	99.7%	69.3	25	65.8	4	0	0	973.57	41	49
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	15	18	50	0.05%	43.8%	IHMGSCAENTAK	99.7%	61.3	25	61.3	2	2	0	1318.59	191	202
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	15	18	50	0.05%	43.8%	IVGHLTHALK	99.7%	51.3	25	40.3	4	0	0	1088.66	394	403
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	15	18	50	0.05%	43.8%	LEDLIVK	96.5%	30.1	25	17.9	1	0	0	829.50	175	181
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	15	18	50	0.05%	43.8%	LKTVFQK	96.5%	30.1	25	11.9	1	0	0	863.54	267	273
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	15	18	50	0.05%	43.8%	LNVTPLAR	99.7%	44.2	25	37.7	4	0	0	883.54	304	311
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	15	18	50	0.05%	43.8%	MLEIDPQK	99.0%	35.5	25	21.6	1	0	0	989.50	366	373
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	15	18	50	0.05%	43.8%	NEQDAYAINSYTR	99.7%	112	25	112	4	0	0	1544.70	209	221
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	15	18	50	0.05%	43.8%	QAVLGAGLPISTPCTTINK	99.7%	101	25	98.5	4	0	0	1941.05	106	124
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	15	18	50	0.05%	43.8%	RLNVTPLAR	99.6%	39.8	25	38.3	4	0	0	1039.64	303	311
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	15	18	50	0.05%	43.8%	TPIGSFLGSLSLLPATK	99.7%	92.8	25	92.8	4	0	0	1701.98	50	66
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	15	18	50	0.05%	43.8%	VNINGGAVSLGHPIGMSGAR	99.7%	35	25	34.9	0	2	0	1922.99	374	393
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	12	12	18	0.02%	6.1%	AIGIGAYLVR	99.7%	51.6	25	42.1	2	0	0	1032.62	1824	1833
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	12	12	18	0.02%	6.1%	DEPIHILNVAIK	99.7%	58.6	25	57.9	1	0	0	1361.78	1283	1294
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	12	12	18	0.02%	6.1%	DFTVASPAEFVTR	99.7%	45.4	25	36.3	1	0	0	1439.72	99	111
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	12	12	18	0.02%	6.1%	FVVMVTPEDLK	99.7%	50.6	25	40.7	2	0	0	1277.68	153	163
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	12	12	18	0.02%	6.1%	IGLAEEIR	99.7%	56.1	25	48.1	2	0	0	900.52	1724	1731
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	12	12	18	0.02%	6.1%	IGSFGPQEDLLFLR	99.7%	56	25	55.5	2	0	0	1591.85	1688	1701
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	12	12	18	0.02%	6.1%	IIQQAGQVWFPDSAFK	99.7%	53.4	25	48.8	1	0	0	1834.95	2010	2025
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	12	12	18	0.02%	6.1%	ILNVPQELYEK	99.6%	40.2	25	40.2	2	0	0	1345.74	278	288
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	12	12	18	0.02%	6.1%	ITDIIGKEEGIGPENLR	99.7%	38	25	37	0	2	0	1854.00	1782	1798
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	12	12	18	0.02%	6.1%	LPELLLK	96.5%	30	25	12.2	1	0	0	825.54	218	224

Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	12	12	18	0.02%	6.1%	VEVGTEVTDYR	99.7%	63.2	25	61.8	1	0	0	1267.62	1410	1420
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	12	12	18	0.02%	6.1%	VQQAELHTGSLPR	99.7%	83	25	76.8	1	0	0	1435.77	826	838
Acidic fibroblast growth factor intracellular-binding protein	FIBP	FIBP_HUMAN	41.9	99.8%	2	2	3	0.00%	6.0%	DYAAIVFFANNR	98.3%	33.3	25	33.3	1	0	0	1400.70	172	183
Acidic fibroblast growth factor intracellular-binding protein	FIBP	FIBP_HUMAN	41.9	99.8%	2	2	3	0.00%	6.0%	YYAFDEAFVR	99.7%	65.4	25	65.4	2	0	0	1280.59	96	105
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.9%	2	4	7	0.01%	34.5%	AGFAGDDAPR	99.7%	67.4	25	53.8	23	0	0	976.45	21	30
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.9%	2	4	7	0.01%	34.5%	AVFPSIVGRPR	99.7%	58.7	25	58.1	4	0	0	1198.71	31	41
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.9%	2	4	7	0.01%	34.5%	DLTDYLMK	99.7%	53.8	25	41.7	9	0	0	1014.48	186	193
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.9%	2	4	7	0.01%	34.5%	DSYVGDEAQSK	99.7%	71.3	25	66.2	15	0	0	1198.52	53	63
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.9%	2	4	7	0.01%	34.5%	DSYVGDEAQSKR	99.7%	70.1	25	70.1	12	2	0	1354.62	53	64
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.9%	2	4	7	0.01%	34.5%	EITALAPSTMK	99.7%	71.3	25	49.8	37	0	0	1161.62	318	328
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.9%	2	4	7	0.01%	34.5%	GYSFVTTAER	99.7%	41.4	25	26.3	1	0	0	1130.55	199	208
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.9%	2	4	7	0.01%	34.5%	HQGVMVGMGQK	99.7%	64.8	25	64.8	16	3	0	1171.57	42	52
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.9%	2	4	7	0.01%	34.5%	IIAPPERK	99.7%	46.3	25	38.4	2	0	0	923.57	331	338
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.9%	2	4	7	0.01%	34.5%	IWHHTFYNELR	99.7%	58.7	25	55	2	5	0	1515.75	87	97
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.9%	2	4	7	0.01%	34.5%	LDLAGRDLTDYLMK	99.7%	38.8	25	30.7	4	2	0	1639.84	180	193
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.9%	2	4	7	0.01%	34.5%	SYELPDGQVITIGNER	99.7%	121	25	112	19	0	0	1790.89	241	256
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.9%	2	4	7	0.01%	34.5%	YPIEHGIITNWDDMEK	99.7%	44.8	25	14.3	3	3	0	1960.91	71	86
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	40	287	0.27%	68.0%	AGFAGDDAPR	99.7%	67.4	25	53.8	23	0	0	976.45	19	28
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	40	287	0.27%	68.0%	AVFPSIVGRPR	99.7%	58.7	25	58.1	4	0	0	1198.71	29	39
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	40	287	0.27%	68.0%	CDVDIRK	99.2%	37	25	13	2	0	0	905.45	285	291
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	40	287	0.27%	68.0%	CPEALFQPSFLGMESCGIHETTFNSIMK	99.2%	30	25	11.9	0	2	0	3247.46	257	284
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	40	287	0.27%	68.0%	DLTDYLMK	99.7%	53.8	25	41.7	9	0	0	1014.48	184	191
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	40	287	0.27%	68.0%	DLYANTVLSGGTTMYPGIADR	99.7%	121	25	121	25	3	0	2215.07	292	312
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	40	287	0.27%	68.0%	DSYVGDEAQSK	99.7%	71.3	25	66.2	15	0	0	1198.52	51	61
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	40	287	0.27%	68.0%	DSYVGDEAQSKR	99.7%	70.1	25	70.1	12	2	0	1354.62	51	62
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	40	287	0.27%	68.0%	EITALAPSTMK	99.7%	71.3	25	49.8	37	0	0	1161.62	316	326
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	40	287	0.27%	68.0%	GYSFTTTAER	99.7%	79.1	25	72.3	24	0	0	1132.53	197	206
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	40	287	0.27%	68.0%	HQGVMVGMGQK	99.7%	64.8	25	64.8	16	3	0	1171.57	40	50
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	40	287	0.27%	68.0%	IIAPPERK	99.7%	46.3	25	38.4	2	0	0	923.57	329	336
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	40	287	0.27%	68.0%	IWHHTFYNELR	99.7%	58.7	25	55	2	5	0	1515.75	85	95
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	40	287	0.27%	68.0%	KDLYANTVLSGGTTMYPGIADR	99.7%	75.9	25	75.9	0	3	0	2359.16	291	312
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	40	287	0.27%	68.0%	LCYVALDFEQEMATAASSSSLEK	99.7%	164	25	164	11	11	0	2566.17	216	238
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	40	287	0.27%	68.0%	LDLAGRDLTDYLMK	99.7%	38.8	25	30.7	4	2	0	1639.84	178	191
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	40	287	0.27%	68.0%	QEYDESGPSIVHR	99.7%	58.1	25	58.1	5	9	0	1516.70	360	372
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	40	287	0.27%	68.0%	QEYDESGPSIVHRK	98.9%	28.5	25	28.1	1	2	0	1644.80	360	373
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	40	287	0.27%	68.0%	SYELPDGQVITIGNER	99.7%	121	25	112	19	0	0	1790.89	239	254
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	40	287	0.27%	68.0%	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	99.7%	76.7	25	76.7	0	8	0	3183.61	148	177
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	21	40	287	0.27%	68.0%	VAPEEHPVLLTEAPLNPK	99.7%	83.6	25	49	13	13	0	1954.06	96	113
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	6	8	11	0.01%	17.5%	DLMVGDEASELR	99.7%	56.2	25	48.5	2	0	0	1350.62	54	65
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	6	8	11	0.01%	17.5%	GYAFNHSADFETVR	99.7%	70.9	25	57.4	2	1	0	1613.73	201	214
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	6	8	11	0.01%	17.5%	HLWDYTFGPEK	98.5%	33.8	25	28.3	1	0	0	1392.66	87	97
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	6	8	11	0.01%	17.5%	ILLTEPPMNPTK	99.7%	46.9	25	38.8	2	0	0	1353.74	107	118
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	6	8	11	0.01%	17.5%	LCYVGYNIEQEQK	99.7%	86.2	25	79.6	2	0	0	1643.77	220	232
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	6	8	11	0.01%	17.5%	RLDIAGR	96.6%	30.1	25	3.78	1	0	0	800.47	181	187
Actin-related protein 2/3 complex subunit 2	ARPC2	ARPC2_HUMAN	34.3	100.0%	3	3	4	0.00%	11.0%	ASHTAPQVLFSHR	99.7%	42.5	25	38.8	0	1	0	1450.75	191	203
Actin-related protein 2/3 complex subunit 2	ARPC2	ARPC2_HUMAN	34.3	100.0%	3	3	4	0.00%	11.0%	DNTINLIHTFR	99.7%	60.4	25	54.7	2	0	0	1343.71	238	248
Actin-related protein 2/3 complex subunit 2	ARPC2	ARPC2_HUMAN	34.3	100.0%	3	3	4	0.00%	11.0%	MILLEVNNR	99.7%	41	25	36.4	1	0	0	1101.61	1	9
Actin-related protein 2/3 complex subunit 3	ARPC3	ARPC3_HUMAN	20.5	100.0%	4	5	9	0.01%	27.0%	DTDIVDEAIYYFK	99.7%	61.8	25	61.8	2	0	0	1591.75	38	50
Actin-related protein 2/3 complex subunit 3	ARPC3	ARPC3_HUMAN	20.5	100.0%	4	5	9	0.01%	27.0%	LIGNMALLPIR	99.5%	39.2	25	36.3	4	0	0	1210.73	15	25
Actin-related protein 2/3 complex subunit 3	ARPC3	ARPC3_HUMAN	20.5	100.0%	4	5	9	0.01%	27.0%	PAYHSSLMDPDTK	98.1%	26.4	25	26.4	0	1	0	1477.66	2	14
Actin-related protein 2/3 complex subunit 3	ARPC3	ARPC3_HUMAN	20.5	100.0%	4	5	9	0.01%	27.0%	VFDPQNDKPSK	99.7%	52.8	25	40.2	2	0	0	1274.64	148	158

Actin-related protein 2/3 complex subunit 4	ARPC4	ARPC4_HUMAN	19.7	100.0%	3	3	7	0.01%	17.3%	AENFFILR	99.7%	49.4	25	33.6	2	0	0	1009.55	98	105
Actin-related protein 2/3 complex subunit 4	ARPC4	ARPC4_HUMAN	19.7	100.0%	3	3	7	0.01%	17.3%	ELLLQPVTISR	99.7%	61.2	25	61.2	3	0	0	1268.76	45	55
Actin-related protein 2/3 complex subunit 4	ARPC4	ARPC4_HUMAN	19.7	100.0%	3	3	7	0.01%	17.3%	IVAEEFLKNF	95.7%	29.1	25	23.3	2	0	0	1209.65	159	168
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	6	7	12	0.01%	16.7%	DITYFIQQLLR	99.7%	56.1	25	41.7	2	0	0	1409.78	199	209
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	6	7	12	0.01%	16.7%	FMEQVIFK	96.9%	30.5	25	28.3	1	0	0	1041.54	92	99
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	6	7	12	0.01%	16.7%	LGYAGNTEPQFIIPSCIAIK	99.7%	59.8	25	59.8	2	0	0	2192.14	19	38
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	6	7	12	0.01%	16.7%	LSEELSGGR	99.7%	56.8	25	44.2	2	0	0	947.48	349	357
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	6	7	12	0.01%	16.7%	NIVLSGGSTMFR	99.7%	65.7	25	65	3	0	0	1281.66	318	329
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	6	7	12	0.01%	16.7%	YSYVCPDLVK	99.0%	35.6	25	33.2	2	0	0	1243.60	231	240
Activated RNA polymerase II transcriptional coactivator p15	SUB1	TCP4_HUMAN	14.4	100.0%	4	5	9	0.01%	40.9%	DDNMFQIGK	99.7%	52.3	25	52	2	0	0	1083.48	60	68
Activated RNA polymerase II transcriptional coactivator p15	SUB1	TCP4_HUMAN	14.4	100.0%	4	5	9	0.01%	40.9%	ELVSSSSSGSDSDSEVDKK	99.7%	94.9	25	94.9	2	1	0	1942.87	6	24
Activated RNA polymerase II transcriptional coactivator p15	SUB1	TCP4_HUMAN	14.4	100.0%	4	5	9	0.01%	40.9%	EQISDIDDAVR	99.7%	50.4	25	43.9	1	0	0	1260.61	115	125
Activated RNA polymerase II transcriptional coactivator p15	SUB1	TCP4_HUMAN	14.4	100.0%	4	5	9	0.01%	40.9%	GISLNPEQWSQLK	99.7%	41.4	25	41.4	3	0	0	1499.79	102	114
Activating signal cointegrator 1 complex subunit 1	ASCC1	ASCC1_HUMAN	45.5	99.8%	2	2	3	0.00%	4.3%	FQEEVLAK	99.5%	38.8	25	19	2	0	0	963.51	181	188
Activating signal cointegrator 1 complex subunit 1	ASCC1	ASCC1_HUMAN	45.5	99.8%	2	2	3	0.00%	4.3%	YNLYTAEGK	99.7%	48	25	42.5	1	0	0	1058.52	323	331
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	6	6	9	0.01%	2.9%	ALAAEMTDYFSR	96.4%	29.9	25	24.2	1	0	0	1374.64	541	552
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	6	6	9	0.01%	2.9%	DLADWLNIK	99.7%	48.9	25	36.3	2	0	0	1087.58	1498	1506
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	6	6	9	0.01%	2.9%	SVGDVALSQIVR	99.3%	37.3	25	27.2	1	0	0	1243.70	595	606
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	6	6	9	0.01%	2.9%	TGYFSSTDLGR	99.7%	69.6	25	60.6	2	0	0	1203.56	973	983
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	6	6	9	0.01%	2.9%	TVAAELAIFR	99.7%	59.9	25	56.2	2	0	0	1090.63	1356	1365
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	6	6	9	0.01%	2.9%	VFNKYPTSK	97.1%	30.8	25	26.9	1	0	0	1083.58	1366	1374
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	7	8	15	0.01%	22.8%	ADATNVNNWHWTER	97.8%	32	25	29.5	1	0	0	1713.77	17	30
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	7	8	15	0.01%	22.8%	DASNWSTDKLK	99.7%	42.3	25	30.2	2	0	0	1264.62	31	41
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	7	8	15	0.01%	22.8%	EAMGIYISTLK	99.7%	56.4	25	46.2	4	0	0	1241.64	146	156
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	7	8	15	0.01%	22.8%	ETFLTSPEELYR	99.7%	47.7	25	43.1	2	0	0	1484.73	213	224
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	7	8	15	0.01%	22.8%	GIPAPEEERTR	99.7%	49.6	25	49.6	2	0	0	1254.64	306	316
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	7	8	15	0.01%	22.8%	LDGEASINNR	99.7%	72.2	25	56.5	2	0	0	1088.53	64	73
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	7	8	15	0.01%	22.8%	QTFGYGAR	99.7%	44.1	25	38.7	2	0	0	899.44	329	336
Active regulator of SIRT1	RPS19BP1	AROS_HUMAN	15.4	99.8%	2	2	3	0.00%	25.0%	GLELLAASEAPRDPPGQAKPR	99.7%	51	25	51	0	1	0	2173.17	9	29
Active regulator of SIRT1	RPS19BP1	AROS_HUMAN	15.4	99.8%	2	2	3	0.00%	25.0%	STVAESVSQQILR	99.7%	67.6	25	53.4	2	0	0	1417.76	84	96
Acyl-CoA dehydrogenase family member 11	ACAD11	ACD11_HUMAN	87.3	99.8%	2	2	2	0.00%	2.8%	EATLTIAQYR	99.7%	45.5	25	31.9	1	0	0	1165.62	41	50
Acyl-CoA dehydrogenase family member 11	ACAD11	ACD11_HUMAN	87.3	99.8%	2	2	2	0.00%	2.8%	VPATNLILGEGR	99.7%	92.8	25	89.7	1	0	0	1239.71	608	619
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	20	23	43	0.04%	34.1%	FFTEEVDSR	99.7%	58	25	46.3	2	0	0	1129.52	77	85
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	20	23	43	0.04%	34.1%	FSMGSVVAGLLK	99.7%	53.8	25	53.1	4	0	0	1224.67	305	316
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	20	23	43	0.04%	34.1%	GIILAGTEEQK	99.7%	49.6	25	40.4	2	0	0	1158.64	152	162
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	20	23	43	0.04%	34.1%	GSNTCEVHFENTK	99.7%	45.5	25	45.5	1	0	0	1522.66	267	279
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	20	23	43	0.04%	34.1%	ILLIFEGTNEILR	99.7%	69.2	25	63.4	2	0	0	1530.89	421	433
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	20	23	43	0.04%	34.1%	IPVENILGEVGDGFK	99.7%	79.8	25	78.5	2	0	0	1586.84	280	294
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	20	23	43	0.04%	34.1%	ITAFIVER	99.7%	51.8	25	43.3	2	0	0	948.55	242	249
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	20	23	43	0.04%	34.1%	LASGEHIAAFCLTEPASGSDAASIR	99.7%	49.6	25	43.8	0	2	0	2531.22	169	193
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	20	23	43	0.04%	34.1%	LIEMTAEYACTR	99.7%	76.5	25	76.5	4	0	0	1457.68	318	329
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	20	23	43	0.04%	34.1%	LSEFGLIQEK	99.7%	70.8	25	56.7	1	0	0	1163.63	336	345
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	20	23	43	0.04%	34.1%	MYIALTGLQHAGR	99.1%	29.4	25	21.9	0	2	0	1430.76	434	446
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	20	23	43	0.04%	34.1%	TEVVDSDGSVK	98.0%	32.5	25	31.4	1	0	0	1135.55	229	239
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	20	23	43	0.04%	34.1%	TEVVDSDGSVKDK	99.7%	55.6	25	48.5	2	0	0	1378.67	229	241
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	20	23	43	0.04%	34.1%	TIMEEQLVLK	99.6%	40.2	25	26.9	2	0	0	1203.67	522	531
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	20	23	43	0.04%	34.1%	TVETLLLR	99.7%	49.4	25	29.1	2	0	0	944.58	511	518
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	20	23	43	0.04%	34.1%	VAMNILNSGR	99.7%	78.4	25	68.9	2	0	0	1090.57	295	304
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	20	23	43	0.04%	34.1%	VSQQILEK	99.7%	43.9	25	25.6	2	0	0	944.54	601	608
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	20	23	43	0.04%	34.1%	VSTVMDTVGR	99.7%	76.2	25	67.5	4	0	0	1064.54	460	469
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	20	23	43	0.04%	34.1%	YAPENLDEQIK	99.7%	57.1	25	45.3	2	0	0	1319.65	589	599

Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	20	23	43	0.04%	34.1%	YAPENLDEQIKK	98.7%	34.3	25	27.6	2	0	0	1447.74	589	600
Acyl-coenzyme A thioesterase 1	ACOT1	ACOT1_HUMAN	46.3	100.0%	3	3	4	0.00%	7.4%	AATLILEPAGR	99.7%	42.8	25	37.2	1	0	0	1111.65	2	12
Acyl-coenzyme A thioesterase 1	ACOT1	ACOT1_HUMAN	46.3	100.0%	3	3	4	0.00%	7.4%	GALFQAHAR	99.7%	51.5	25	37.9	1	0	0	970.52	43	51
Acyl-coenzyme A thioesterase 1	ACOT1	ACOT1_HUMAN	46.3	100.0%	3	3	4	0.00%	7.4%	GLAPEQPVTLR	99.7%	48.2	25	39.7	2	0	0	1180.67	25	35
Acyl-coenzyme A thioesterase 13	ACOT13	ACO13_HUMAN	15.0	100.0%	3	3	6	0.01%	25.0%	ITLVSAAPGK	99.7%	52.1	25	45.4	2	0	0	956.58	28	37
Acyl-coenzyme A thioesterase 13	ACOT13	ACO13_HUMAN	15.0	100.0%	3	3	6	0.01%	25.0%	LGEDIVITAHVLK	99.7%	59.3	25	58.9	1	0	0	1407.82	96	108
Acyl-coenzyme A thioesterase 13	ACOT13	ACO13_HUMAN	15.0	100.0%	3	3	6	0.01%	25.0%	TLAFTSVDLTNK	99.7%	82.4	25	76.7	3	0	0	1309.70	112	123
Acyl-coenzyme A thioesterase 8	ACOT8	ACOT8_HUMAN	35.9	100.0%	3	3	5	0.00%	15.0%	IAAQEVPIEIKPVNPSPLSQLQR	99.2%	30	25	30	0	1	0	2527.42	178	200
Acyl-coenzyme A thioesterase 8	ACOT8	ACOT8_HUMAN	35.9	100.0%	3	3	5	0.00%	15.0%	LFGGQIVGQALVAAAK	99.7%	84.3	25	79.6	2	0	0	1542.90	54	69
Acyl-coenzyme A thioesterase 8	ACOT8	ACOT8_HUMAN	35.9	100.0%	3	3	5	0.00%	15.0%	LPVLYQVER	99.7%	61.3	25	55.6	2	0	0	1116.64	92	100
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	ACOT9_HUMAN	49.9	100.0%	4	4	5	0.00%	8.7%	EIVGASTNWR	99.4%	38	25	34.3	1	0	0	1132.57	46	55
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	ACOT9_HUMAN	49.9	100.0%	4	4	5	0.00%	8.7%	IAFSSTSLLK	98.9%	35.3	25	35.3	1	0	0	1066.61	241	250
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	ACOT9_HUMAN	49.9	100.0%	4	4	5	0.00%	8.7%	IFGGFLMR	99.7%	56.2	25	49.6	2	0	0	940.51	310	317
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	ACOT9_HUMAN	49.9	100.0%	4	4	5	0.00%	8.7%	SLEICHPQER	98.5%	33.7	25	33.7	1	0	0	1268.61	295	304
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	5	6	10	0.01%	13.3%	ATVFLNPAACK	99.7%	60.2	25	54.4	2	0	0	1191.62	63	73
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	5	6	10	0.01%	13.3%	EQPVFAMTGLR	99.7%	43.7	25	35.9	3	0	0	1264.64	200	210
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	5	6	10	0.01%	13.3%	GDFITIGSR	99.7%	71.9	25	58.8	2	0	0	965.51	343	351
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	5	6	10	0.01%	13.3%	GETVPLDVLQIK	99.7%	61.5	25	60.3	2	0	0	1311.75	185	196
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	5	6	10	0.01%	13.3%	VQHITDATLAIVK	99.7%	36.3	25	36.3	0	1	0	1408.82	172	184
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	5	7	17	0.02%	35.6%	AELEIQKDALEPGQR	99.7%	63.1	25	63.1	2	2	0	1696.89	108	122
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	5	7	17	0.02%	35.6%	DISPVLKDPASFR	99.4%	37.8	25	36.6	2	2	0	1444.78	28	40
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	5	7	17	0.02%	35.6%	IDYIAGLDSR	99.7%	64.7	25	58.3	4	0	0	1122.58	58	67
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	5	7	17	0.02%	35.6%	LAPVPFFSLLQYE	99.6%	39.8	25	39	2	0	0	1523.81	168	180
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	5	7	17	0.02%	35.6%	SFPDFPTPGVVFR	99.5%	38.9	25	36.5	3	0	0	1465.75	15	27
Adenosylhomocysteinase	AHCY	SAHH_HUMAN	47.7	99.8%	2	2	3	0.00%	6.3%	GISEETTTGVHNLYK	99.7%	74.7	25	73.9	1	0	0	1648.82	152	166
Adenosylhomocysteinase	AHCY	SAHH_HUMAN	47.7	99.8%	2	2	3	0.00%	6.3%	VPAINVNDSVTK	99.7%	60	25	60	2	0	0	1256.68	175	186
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	10	17	0.02%	34.5%	ASTEVGEMAK	99.7%	44.8	25	32.5	2	0	0	1022.48	46	55
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	10	17	0.02%	34.5%	AVILGPPGSGK	99.7%	48.8	25	32.4	2	0	0	995.59	8	18
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	10	17	0.02%	34.5%	DVAKPVIELYK	99.0%	35.8	25	29.8	2	1	0	1274.74	176	186
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	10	17	0.02%	34.5%	GVLHQFSGTETNK	99.7%	58.5	25	56.4	2	1	0	1417.71	189	201
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	10	17	0.02%	34.5%	IWPYVYTLFSNK	99.6%	40.7	25	38.4	1	0	0	1530.80	202	213
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	10	17	0.02%	34.5%	LMMSELENR	99.7%	61.3	25	46.3	4	0	0	1122.53	72	80
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	10	17	0.02%	34.5%	SLLVPDHVITR	99.7%	47.3	25	45.4	2	0	0	1249.73	61	71
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	7	7	12	0.01%	16.9%	AFIITGQTYTR	98.9%	35.1	25	33.5	1	0	0	1270.68	235	245
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	7	7	12	0.01%	16.9%	FLEEEVYPLLKPYESVMK	96.1%	23.5	25	23.5	0	1	0	2214.14	460	477
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	7	7	12	0.01%	16.9%	NALDLLLPK	99.7%	50.2	25	35.1	2	0	0	996.61	126	134
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	7	7	12	0.01%	16.9%	QEGGDNDLIER	99.7%	55.2	25	41.4	2	0	0	1245.57	416	426
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	7	7	12	0.01%	16.9%	SNLENIDFK	99.7%	56.8	25	52	2	0	0	1079.54	67	75
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	7	7	12	0.01%	16.9%	VLSQQAASVVK	99.7%	81.5	25	65.4	2	0	0	1129.66	405	415
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	7	7	12	0.01%	16.9%	YASPEMCFVFSDR	99.7%	61.9	25	61.9	2	0	0	1608.68	21	33
Adenylosuccinate synthetase isozyme 2	ADSS	PURA2_HUMAN	50.1	100.0%	5	5	8	0.01%	12.5%	ELPVNAQNYVR	95.9%	29.4	25	26.4	1	0	0	1302.68	420	430
Adenylosuccinate synthetase isozyme 2	ADSS	PURA2_HUMAN	50.1	100.0%	5	5	8	0.01%	12.5%	FIEDELQIPVK	99.7%	41.3	25	29.7	2	0	0	1330.73	431	441
Adenylosuccinate synthetase isozyme 2	ADSS	PURA2_HUMAN	50.1	100.0%	5	5	8	0.01%	12.5%	GREFGVTTGR	99.7%	42.2	25	36.9	2	0	0	1079.56	325	334
Adenylosuccinate synthetase isozyme 2	ADSS	PURA2_HUMAN	50.1	100.0%	5	5	8	0.01%	12.5%	LDILDMFTEIK	99.7%	71.8	25	65.3	1	0	0	1337.70	363	373
Adenylosuccinate synthetase isozyme 2	ADSS	PURA2_HUMAN	50.1	100.0%	5	5	8	0.01%	12.5%	VVDLLAQDADIVCR	99.7%	98	25	95.8	2	0	0	1586.82	46	59
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	8	0.01%	46.6%	AAYFGVYDTAK	99.7%	74.6	25	74.6	9	0	0	1205.58	189	199
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	8	0.01%	46.6%	DFLAGGVAAAVSK	99.7%	88.7	25	79.5	2	0	0	1205.65	11	23
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	8	0.01%	46.6%	EFHGLGDCIIK	99.7%	48.8	25	37	2	0	0	1288.64	153	163
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	8	0.01%	46.6%	EQGFLSFWR	98.4%	33.4	25	33.4	2	0	0	1169.57	64	72
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	8	0.01%	46.6%	GADIMYTGTVDCWR	99.7%	89.2	25	78.7	4	0	0	1644.71	246	259
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	8	0.01%	46.6%	GAWSNVLR	99.7%	58.6	25	37.4	9	0	0	902.48	273	280

ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	8	0.01%	46.6%	GMGGAFVLVLYDEIK	99.7%	56.4	25	0	2	0	0	1627.84	281	295
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	8	0.01%	46.6%	GNLANVIR	99.4%	37.8	25	23.5	2	0	0	856.50	73	80
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	8	0.01%	46.6%	KGADIMYTGTVDCWR	99.7%	35.6	25	35.6	1	1	0	1788.80	245	259
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	8	0.01%	46.6%	LLLQVQHASK	99.7%	43.7	25	33.1	18	0	0	1136.68	34	43
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	8	0.01%	46.6%	MMMQSGR	99.3%	37.2	25	37.2	2	0	0	840.35	238	244
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	8	0.01%	46.6%	QLFLGGVDR	99.7%	47.5	25	32.2	2	0	0	1004.55	97	105
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	8	0.01%	46.6%	RMMMQSGR	99.7%	51.9	25	49.6	2	0	0	996.45	237	244
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	8	0.01%	46.6%	TAVAPIER	99.7%	42.1	25	30.5	8	0	0	856.49	24	31
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	8	0.01%	46.6%	YFPTQALNFAFK	99.7%	91.2	25	76.8	36	0	0	1446.74	81	92
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	8	0.01%	46.6%	YFPTQALNFAFKDK	99.7%	66.7	25	62.3	4	0	0	1689.86	81	94
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	149	0.14%	46.0%	AAYFGIYDTAK	99.7%	74.4	25	59.1	6	0	0	1219.60	189	199
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	149	0.14%	46.0%	DFLAGGVAAAISK	99.7%	101	25	87.5	8	0	0	1219.67	11	23
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	149	0.14%	46.0%	EQGVLSFWR	99.7%	64.2	25	60.6	22	0	0	1121.57	64	72
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	149	0.14%	46.0%	GAWSNVLR	99.7%	58.6	25	37.4	9	0	0	902.48	273	280
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	149	0.14%	46.0%	GLGDCLVK	99.7%	44.2	25	30.3	5	0	0	861.45	156	163
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	149	0.14%	46.0%	GMGGAFVLVLYDEIK	99.7%	56.4	25	0	2	0	0	1627.84	281	295
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	149	0.14%	46.0%	GNLANVIR	99.4%	37.8	25	23.5	2	0	0	856.50	73	80
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	149	0.14%	46.0%	GTDIMYTGTLDCWR	99.7%	74.7	25	69.1	4	0	0	1704.74	246	259
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	149	0.14%	46.0%	KGTDIMYTGTLDCWR	99.7%	71.5	25	71.5	4	2	0	1832.83	245	259
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	149	0.14%	46.0%	LLLQVQHASK	99.7%	43.7	25	33.1	18	0	0	1136.68	34	43
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	149	0.14%	46.0%	MMMQSGR	99.3%	37.2	25	37.2	2	0	0	840.35	238	244
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	149	0.14%	46.0%	QIFLGGVDK	99.7%	58.8	25	41.4	6	0	0	976.55	97	105
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	149	0.14%	46.0%	QIFLGGVDKR	99.7%	53.4	25	39.4	9	0	0	1132.65	97	106
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	149	0.14%	46.0%	RMMMQSGR	99.7%	51.9	25	49.6	2	0	0	996.45	237	244
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	149	0.14%	46.0%	TAVAPIER	99.7%	42.1	25	30.5	8	0	0	856.49	24	31
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	149	0.14%	46.0%	YFPTQALNFAFK	99.7%	91.2	25	76.8	36	0	0	1446.74	81	92
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	17	20	149	0.14%	46.0%	YFPTQALNFAFKDK	99.7%	66.7	25	62.3	4	0	0	1689.86	81	94
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	6	38	0.04%	45.6%	AAYFGVYDTAK	99.7%	74.6	25	74.6	9	0	0	1205.58	189	199
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	6	38	0.04%	45.6%	DFLAGGIAAAISK	99.7%	113	25	106	23	0	0	1233.68	11	23
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	6	38	0.04%	45.6%	EQGVLSFWR	99.7%	64.2	25	60.6	22	0	0	1121.57	64	72
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	6	38	0.04%	45.6%	GADIMYTGTVDCWR	99.7%	89.2	25	78.7	4	0	0	1644.71	246	259
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	6	38	0.04%	45.6%	GAWSNVLR	99.7%	58.6	25	37.4	9	0	0	902.48	273	280
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	6	38	0.04%	45.6%	GLGDCLVK	99.7%	44.2	25	30.3	5	0	0	861.45	156	163
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	6	38	0.04%	45.6%	GMGGAFVLVLYDELK	99.7%	56.4	25	0	2	0	0	1627.84	281	295
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	6	38	0.04%	45.6%	GNLANVIR	99.4%	37.8	25	23.5	2	0	0	856.50	73	80
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	6	38	0.04%	45.6%	KGADIMYTGTVDCWR	99.7%	35.6	25	35.6	1	1	0	1788.80	245	259
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	6	38	0.04%	45.6%	LLLQVQHASK	99.7%	43.7	25	33.1	18	0	0	1136.68	34	43
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	6	38	0.04%	45.6%	MMMQSGR	99.3%	37.2	25	37.2	2	0	0	840.35	238	244
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	6	38	0.04%	45.6%	QIFLGGVDK	99.7%	58.8	25	41.4	6	0	0	976.55	97	105
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	6	38	0.04%	45.6%	RMMMQSGR	99.7%	51.9	25	49.6	2	0	0	996.45	237	244
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	6	38	0.04%	45.6%	TAVAPIER	99.7%	42.1	25	30.5	8	0	0	856.49	24	31
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	6	38	0.04%	45.6%	YFPTQALNFAFK	99.7%	91.2	25	76.8	36	0	0	1446.74	81	92
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	6	38	0.04%	45.6%	YFPTQALNFAFKDK	99.7%	66.7	25	62.3	4	0	0	1689.86	81	94
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN	20.6	100.0%	3	6	11	0.01%	33.1%	DAVLLVFANK	99.7%	80.3	25	72.6	4	0	0	1089.63	118	127
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN	20.6	100.0%	3	6	11	0.01%	33.1%	ILMVGLDAAGK	99.7%	76.8	25	60.8	13	0	0	1087.62	20	30
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN	20.6	100.0%	3	6	11	0.01%	33.1%	NISFTVWDVGGQDK	99.7%	125	25	115	4	0	0	1565.76	60	73
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN	20.6	100.0%	3	6	11	0.01%	33.1%	QDLPNAMNAAEITDK	99.7%	62.6	25	58.5	3	0	0	1646.77	128	142
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN	20.6	100.0%	3	6	11	0.01%	33.1%	VNEAREELMR	99.0%	35.6	25	29.8	3	1	0	1246.62	100	109
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	6	7	22	0.02%	37.8%	DAVLLLFANK	99.7%	46.6	25	38	1	0	0	1103.65	118	127
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	6	7	22	0.02%	37.8%	ILMVGLDAAGK	99.7%	76.8	25	60.8	13	0	0	1087.62	20	30
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	6	7	22	0.02%	37.8%	IQEVADELQK	99.7%	61.3	25	45.6	3	0	0	1172.62	100	109

ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	6	7	22	0.02%	37.8%	MLLVDELR	98.3%	33.2	25	22.8	1	0	0	988.55	110	117
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	6	7	22	0.02%	37.8%	NICFTVWDVGGQDR	99.7%	92.5	25	92.5	3	0	0	1666.76	60	73
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	6	7	22	0.02%	37.8%	QDLPNAMAISEMTDK	99.7%	60.9	25	56.1	1	0	0	1695.76	128	142
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	100.0%	4	4	10	0.01%	33.3%	DAVLLVFANK	99.7%	80.3	25	72.6	4	0	0	1089.63	118	127
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	100.0%	4	4	10	0.01%	33.3%	ILMVGLDAAGK	99.7%	76.8	25	60.8	13	0	0	1087.62	20	30
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	100.0%	4	4	10	0.01%	33.3%	NICFTVWDVGGQDK	99.7%	109	25	107	2	0	0	1638.76	60	73
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	100.0%	4	4	10	0.01%	33.3%	QDMPNAMPVSELTDK	99.3%	37.3	25	36.6	2	0	0	1675.77	128	142
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	100.0%	4	4	10	0.01%	33.3%	VQESADELQK	99.7%	61	25	56.6	2	0	0	1146.56	100	109
ADP-ribosylation factor 6	ARF6	ARF6_HUMAN	20.1	100.0%	4	6	13	0.01%	30.3%	DAIILIFANK	99.7%	67.6	25	0	3	0	0	1117.66	114	123
ADP-ribosylation factor 6	ARF6	ARF6_HUMAN	20.1	100.0%	4	6	13	0.01%	30.3%	FNVWDVGGQDK	99.7%	79.4	25	66.1	2	0	0	1264.60	59	69
ADP-ribosylation factor 6	ARF6	ARF6_HUMAN	20.1	100.0%	4	6	13	0.01%	30.3%	ILMLGLDAAGK	99.7%	75.9	25	65.9	4	0	0	1101.63	16	26
ADP-ribosylation factor 6	ARF6	ARF6_HUMAN	20.1	100.0%	4	6	13	0.01%	30.3%	LGQSVTTIPTVGFNVETVTYK	99.7%	51.4	25	51.4	2	2	0	2254.20	35	55
ADP-ribosylation factor-like protein 1	ARL1	ARL1_HUMAN	20.4	100.0%	4	5	7	0.01%	22.1%	AILVVFANK	99.7%	64.5	25	64.5	2	0	0	974.60	119	127
ADP-ribosylation factor-like protein 1	ARL1	ARL1_HUMAN	20.4	100.0%	4	5	7	0.01%	22.1%	ILILGLDGAGK	99.7%	81.8	25	81.2	1	0	0	1069.66	20	30
ADP-ribosylation factor-like protein 1	ARL1	ARL1_HUMAN	20.4	100.0%	4	5	7	0.01%	22.1%	KWQIFK	99.7%	46.5	25	20.1	1	0	0	849.50	152	157
ADP-ribosylation factor-like protein 1	ARL1	ARL1_HUMAN	20.4	100.0%	4	5	7	0.01%	22.1%	SELVAMLEEEELRK	99.7%	52.4	25	48.9	3	0	0	1691.85	105	118
ADP-ribosylation factor-like protein 2	ARL2	ARL2_HUMAN	20.9	100.0%	5	6	13	0.01%	30.4%	ELQSLLVEER	99.7%	87.6	25	73.1	2	0	0	1215.66	105	114
ADP-ribosylation factor-like protein 2	ARL2	ARL2_HUMAN	20.9	100.0%	5	6	13	0.01%	30.4%	LAGATLLIFANK	99.7%	88	25	88	3	0	0	1231.74	115	126
ADP-ribosylation factor-like protein 2	ARL2	ARL2_HUMAN	20.9	100.0%	5	6	13	0.01%	30.4%	LLMLGLDNAGK	99.7%	74.9	25	64.2	4	0	0	1160.63	19	29
ADP-ribosylation factor-like protein 2	ARL2	ARL2_HUMAN	20.9	100.0%	5	6	13	0.01%	30.4%	LNIWDVGGQK	99.7%	58.3	25	54.1	2	0	0	1129.60	62	71
ADP-ribosylation factor-like protein 2	ARL2	ARL2_HUMAN	20.9	100.0%	5	6	13	0.01%	30.4%	QDLPGALSSNAIR	99.7%	75.5	25	66.9	2	0	0	1341.71	127	139
ADP-ribosylation factor-like protein 6	ARL6	ARL6_HUMAN	21.1	99.8%	2	2	2	0.00%	12.9%	LSVLLGLK	96.7%	30.2	25	30.2	1	0	0	842.57	7	14
ADP-ribosylation factor-like protein 6	ARL6	ARL6_HUMAN	21.1	99.8%	2	2	2	0.00%	12.9%	SSSLSFTVFDMSGQGR	99.5%	39.4	25	37	1	0	0	1721.78	60	75
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	8	8	11	0.01%	10.5%	GAILTGPPGTGK	97.4%	31.2	25	30.8	1	0	0	1068.61	343	354
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	8	8	11	0.01%	10.5%	GLGYAQYLPK	97.4%	31.4	25	24.7	1	0	0	1109.60	602	611
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	8	8	11	0.01%	10.5%	ILINDAYKR	99.7%	41.3	25	32.4	1	0	0	1105.64	703	711
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	8	8	11	0.01%	10.5%	NLETLQQELGIEGENR	99.7%	90.1	25	87.2	1	0	0	1842.92	225	240
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	8	8	11	0.01%	10.5%	QIFIGPPDIK	97.8%	32	25	16.4	1	0	0	1127.65	472	481
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	8	8	11	0.01%	10.5%	VALLLLEK	99.7%	45	25	45	2	0	0	898.60	726	733
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	8	8	11	0.01%	10.5%	VGQISFDLPR	99.7%	73.9	25	54.7	2	0	0	1131.62	670	679
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	8	8	11	0.01%	10.5%	VSEEIFFGR	99.7%	65.6	25	48.5	2	0	0	1083.55	633	641
A-kinase anchor protein 8-like	AKAP8L	AKP8L_HUMAN	71.6	100.0%	2	2	3	0.00%	3.7%	QTADFLQEYVTNK	99.7%	88.5	25	87	2	0	0	1556.76	427	439
A-kinase anchor protein 8-like	AKAP8L	AKP8L_HUMAN	71.6	100.0%	2	2	3	0.00%	3.7%	SGRPMASGYGR	99.2%	36.8	25	26.8	1	0	0	1154.54	189	199
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	5	5	7	0.01%	10.6%	FAVALLDDSVR	99.7%	68.6	25	43.8	1	0	0	1205.65	166	176
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	5	5	7	0.01%	10.6%	GALLSVGWSTGR	99.7%	66.9	25	63.4	1	0	0	1203.65	467	478
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	5	5	7	0.01%	10.6%	GQWINLPVLQLTK	99.1%	36.1	25	27.1	2	0	0	1509.88	40	52
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	5	5	7	0.01%	10.6%	ILATTPSAVFR	99.7%	70.2	25	58.6	2	0	0	1175.68	302	312
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	5	5	7	0.01%	10.6%	TASGWALALCR	98.9%	35.3	25	35.3	1	0	0	1205.61	109	119
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	22	0.02%	17.2%	AAFLNFFR	99.7%	54.5	25	43.3	2	0	0	985.53	44	51
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	22	0.02%	17.2%	AGLDPDLETR	99.7%	47.2	25	39.1	2	0	0	1086.54	178	187
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	22	0.02%	17.2%	AGQEDVLFPVAR	99.7%	44.9	25	41.1	1	0	0	1301.68	581	592
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	22	0.02%	17.2%	EADGSLQPLPQR	97.4%	31.4	25	24	1	0	0	1310.67	251	262
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	22	0.02%	17.2%	ELGQSLAQEVK	99.7%	56.9	25	51.1	2	0	0	1201.64	791	801
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	22	0.02%	17.2%	GPLIVDTVSAESLSVLVK	99.7%	60.9	25	50.4	1	0	0	1827.05	881	898
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	22	0.02%	17.2%	GVQLDSAGLER	99.7%	64.9	25	53	2	0	0	1144.60	461	471
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	22	0.02%	17.2%	LDVTTQTPLTPEQLR	99.7%	56.8	25	46.7	2	0	0	1711.92	664	678
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	22	0.02%	17.2%	LLAVTGEQAQQAR	99.7%	76.9	25	64.6	2	0	0	1384.75	778	790
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	22	0.02%	17.2%	LVPSASVRPR	97.8%	32	25	28.5	1	0	0	1081.65	58	67
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	22	0.02%	17.2%	LWISYFDGDPK	99.7%	49	25	36.7	2	0	0	1340.65	167	177
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	22	0.02%	17.2%	SLDEVYPDPVR	99.6%	40.1	25	39.8	2	0	0	1289.64	712	722
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	22	0.02%	17.2%	TGAVGDLVIIGDR	99.7%	75.1	25	67.1	1	0	0	1285.71	757	769

Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	22	0.02%	17.2%	TNFYAEQGGQASDR	99.7%	85.2	25	80.5	1	0	0	1543.68	562	575
Alcohol dehydrogenase class-3	ADH5	ADHX_HUMAN	39.7	100.0%	5	5	8	0.01%	16.3%	AFELMHSGK	99.7%	46.7	25	35.9	1	0	0	1019.50	358	366
Alcohol dehydrogenase class-3	ADH5	ADHX_HUMAN	39.7	100.0%	5	5	8	0.01%	16.3%	AGDTVIPLYIPQCGECK	99.7%	60.4	25	58	2	0	0	1920.92	85	101
Alcohol dehydrogenase class-3	ADH5	ADHX_HUMAN	39.7	100.0%	5	5	8	0.01%	16.3%	IDPLAPLDK	98.8%	34.6	25	34.6	1	0	0	981.56	160	168
Alcohol dehydrogenase class-3	ADH5	ADHX_HUMAN	39.7	100.0%	5	5	8	0.01%	16.3%	IIGVDINKDK	99.7%	47.4	25	17.5	2	0	0	1114.65	219	228
Alcohol dehydrogenase class-3	ADH5	ADHX_HUMAN	39.7	100.0%	5	5	8	0.01%	16.3%	VDEFVTHNLSFDEINK	99.6%	33	25	33	0	2	0	1906.92	342	357
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	9	9	19	0.02%	22.8%	EEIFGPVQPLFK	99.7%	50.6	25	16.6	1	0	0	1403.76	415	426
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	9	9	19	0.02%	22.8%	KIEEVVER	99.7%	63.9	25	46.2	2	0	0	1001.56	429	436
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	9	9	19	0.02%	22.8%	LAPALATGNTVVMK	99.7%	81.7	25	72.8	2	0	0	1385.78	196	209
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	9	9	19	0.02%	22.8%	LLNLLADLVER	99.7%	61.3	25	56.3	1	0	0	1268.76	104	114
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	9	9	19	0.02%	22.8%	TFVEESIYNEFLER	99.7%	93	25	86.9	3	0	0	1775.85	325	338
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	9	9	19	0.02%	22.8%	VAEQTPLSALYLASLIK	99.7%	96.8	25	96.8	4	0	0	1817.04	210	226
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	9	9	19	0.02%	22.8%	VGNPFELDTQQGPQVDKEQFER	99.7%	60.9	25	60.9	0	2	0	2561.23	348	369
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	9	9	19	0.02%	22.8%	VLGYIQLGQK	99.7%	61.6	25	45.8	2	0	0	1118.66	370	379
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	9	9	19	0.02%	22.8%	YGLAAAVFTR	99.7%	99.2	25	95.2	2	0	0	1068.58	442	451
Aldehyde dehydrogenase, mitochondrial	ALDH2	ALDH2_HUMAN	56.4	100.0%	3	3	4	0.00%	6.2%	LLCGGGIAADR	99.7%	69.7	25	57	2	0	0	1102.57	384	394
Aldehyde dehydrogenase, mitochondrial	ALDH2	ALDH2_HUMAN	56.4	100.0%	3	3	4	0.00%	6.2%	TIEEVVGR	98.9%	35.1	25	22.3	1	0	0	902.49	429	436
Aldehyde dehydrogenase, mitochondrial	ALDH2	ALDH2_HUMAN	56.4	100.0%	3	3	4	0.00%	6.2%	VIQVAAGSSNLKR	99.7%	42	25	42	1	0	0	1342.78	269	281
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	99.9%	2	2	4	0.00%	4.3%	GISDPLTVFEQTEAAAR	99.7%	96.8	25	93.6	2	0	0	1804.91	587	603
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	99.9%	2	2	4	0.00%	4.3%	GVQFAPFSTCR	99.6%	39.7	25	38.6	2	0	0	1269.60	556	566
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	7	7	9	0.01%	17.6%	DLPLAQGIK	99.0%	35.4	25	25.9	1	0	0	954.56	529	537
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	7	7	9	0.01%	17.6%	GAPTTSLISVAVTK	99.7%	91.8	25	77.3	1	0	0	1344.77	219	232
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	7	7	9	0.01%	17.6%	GEVITTYCPANNEPIAR	99.5%	38.9	25	38.9	1	0	0	1904.92	63	79
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	7	7	9	0.01%	17.6%	MIGGPILPSER	99.7%	41.5	25	26.6	1	0	0	1169.63	163	173
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	7	7	9	0.01%	17.6%	QASVADYEETVKK	99.7%	56.6	25	49.7	1	0	0	1467.73	82	94
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	7	7	9	0.01%	17.6%	VGNPWDPNVLYGPLHTK	99.1%	29.3	25	27.9	0	2	0	1906.98	359	375
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	7	7	9	0.01%	17.6%	VNLLSFTGSTQVGK	99.7%	96.4	25	96.4	2	0	0	1450.79	267	280
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	12	17	33	0.03%	44.4%	ACYLSINPQKDETLETEK	99.7%	77.8	25	69	2	2	0	2139.03	221	238
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	12	17	33	0.03%	44.4%	AGFAGDQIPK	99.7%	72.7	25	52.4	2	0	0	1003.52	23	32
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	12	17	33	0.03%	44.4%	AQYYLPDGSTIEIGPSR	99.7%	141	25	141	2	0	0	1866.92	239	255
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	12	17	33	0.03%	44.4%	DQLQTFSEEHPVLLTEAPLNPR	99.7%	65.3	25	54.2	0	2	0	2534.29	97	118
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	12	17	33	0.03%	44.4%	EGYDFHSSSEFEIVK	99.7%	69.3	25	66.6	2	1	0	1773.80	201	215
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	12	17	33	0.03%	44.4%	IWQYVYSK	99.7%	44.2	25	32.5	2	0	0	1086.56	89	96
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	12	17	33	0.03%	44.4%	LLSEVKK	99.7%	44.2	25	21.8	2	0	0	816.52	314	320
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	12	17	33	0.03%	44.4%	LYSTWIGGSILASLDTFKK	99.7%	54.8	25	54.8	2	0	0	2100.14	337	355
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	12	17	33	0.03%	44.4%	TLFSNIVLSGGSTLFK	99.7%	128	25	128	4	2	0	1683.93	293	308
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	12	17	33	0.03%	44.4%	VMAGALEGDIFIGPK	99.7%	96.2	25	0	4	0	0	1517.80	47	61
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	12	17	33	0.03%	44.4%	YCFPNYVGRPK	99.7%	56.3	25	55.3	2	1	0	1400.68	33	43
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	12	17	33	0.03%	44.4%	YPMEHGIVK	96.4%	29.9	25	22.9	1	0	0	1089.54	73	81
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	13	32	0.03%	31.1%	AAVPSGASTGIYEALELR	99.7%	120	25	118	2	0	0	1804.94	33	50
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	13	32	0.03%	31.1%	DATNVGDEGGFAPNILENK	99.7%	47.4	25	13.9	1	0	0	1960.92	203	221
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	13	32	0.03%	31.1%	DATNVGDEGGFAPNILENKEGLELLK	99.7%	52.5	25	52.5	0	2	0	2743.38	203	228
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	13	32	0.03%	31.1%	IGAEVYHNLK	99.7%	59	25	50.5	6	0	0	1143.62	184	193
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	13	32	0.03%	31.1%	KLNVTEQEK	99.7%	47.5	25	23.6	2	0	0	1088.59	81	89
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	13	32	0.03%	31.1%	LAMQEFMILPVGAANFR	99.7%	81.2	25	81.2	6	1	0	1939.98	163	179
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	13	32	0.03%	31.1%	SCNCLLLK	98.3%	33.2	25	24.3	2	0	0	1007.50	336	343
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	13	32	0.03%	31.1%	VNQIGSVTESLQACK	99.7%	102	25	0	5	0	0	1633.82	344	358
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	13	32	0.03%	31.1%	VVIGMDVAASEFFR	99.7%	51.7	25	51.7	1	0	0	1556.78	240	253
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	13	32	0.03%	31.1%	YISPDQLADLYK	99.7%	52.9	25	52.9	2	0	0	1425.73	270	281
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	13	32	0.03%	31.1%	YNQLLR	97.6%	31.6	25	24.3	2	0	0	806.45	407	412
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	9	9	17	0.02%	20.0%	ALEAELAALR	99.7%	61.5	25	49.6	2	0	0	1056.60	121	130

Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	9	9	17	0.02%	20.0%	AQLEEASSAR	99.7%	70.4	25	61	4	0	0	1061.52	152	161
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	9	9	17	0.02%	20.0%	EYQDLLNVK	99.7%	58.5	25	57	6	0	0	1121.58	378	386
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	9	9	17	0.02%	20.0%	FANLNEQAAR	99.7%	70	25	36.5	2	0	0	1133.57	291	300
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	9	9	17	0.02%	20.0%	LSGAGGAGGFR	99.7%	58.5	25	45.5	2	0	0	949.49	29	39
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	9	9	17	0.02%	20.0%	NLQSAEEWYK	99.7%	42.3	25	32.9	1	0	0	1267.60	279	288
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	9	9	17	0.02%	20.0%	SNIEETTISSQK	99.7%	50.1	25	44.7	1	0	0	1336.66	487	498
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	9	9	17	0.02%	20.0%	TIEIEGLR	98.9%	35.3	25	24.4	1	0	0	930.53	323	330
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	9	9	17	0.02%	20.0%	TNEKEQLQGLNDR	99.7%	52.7	25	48.3	2	0	0	1544.77	92	104
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	9	9	17	0.02%	20.0%	VGELFQR	99.7%	67.5	25	48.5	2	0	0	848.46	139	145
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	12	15	30	0.03%	44.2%	AILQATLR	99.7%	52.4	25	43.8	1	0	0	885.55	36	43
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	12	15	30	0.03%	44.2%	AILQATLREEK	99.5%	38.7	25	34.1	2	0	0	1271.73	36	46
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	12	15	30	0.03%	44.2%	GAEADQIIEYLK	99.7%	74.5	25	67.7	4	0	0	1349.69	15	26
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	12	15	30	0.03%	44.2%	IEILAPPNGSVPGDR	99.7%	43	25	36.8	2	0	0	1534.82	236	250
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	12	15	30	0.03%	44.2%	IGCIITAR	99.7%	71.8	25	52	2	0	0	903.51	159	166
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	12	15	30	0.03%	44.2%	ITFDAFPGEPDKELNPK	99.7%	67.6	25	67.6	2	2	0	1917.96	251	267
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	12	15	30	0.03%	44.2%	IWEQIQPDLHTNDECVATYK	97.9%	25.9	25	25.9	0	1	0	2460.15	270	289
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	12	15	30	0.03%	44.2%	KQQSIAGSADSKPIDVSR	99.7%	49.2	25	49.2	0	2	0	1886.99	137	154
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	12	15	30	0.03%	44.2%	MVILLCNLKPAK	99.7%	44.3	25	44.3	2	0	0	1399.82	206	217
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	12	15	30	0.03%	44.2%	QQSIAGSADSKPIDVSR	99.7%	55.4	25	55.4	2	2	0	1758.90	138	154
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	12	15	30	0.03%	44.2%	QQVSLLK	99.7%	47.1	25	14.9	2	0	0	815.50	27	33
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	12	15	30	0.03%	44.2%	TVVSGLVNHVPLEQMQNR	99.7%	57.9	25	57.9	0	4	0	2021.06	188	205
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	6	7	16	0.02%	25.9%	FLFSLFGQK	99.7%	44	25	34.3	3	0	0	1086.60	216	224
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	6	7	16	0.02%	25.9%	FSIQTMCPIEGEGNIAR	99.7%	117	25	116	4	0	0	1938.91	199	215
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	6	7	16	0.02%	25.9%	LLCEHFR	99.4%	37.9	25	23.8	1	0	0	974.49	141	147
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	6	7	16	0.02%	25.9%	SCENLAPFNTALK	99.7%	71.2	25	65.7	2	0	0	1464.72	305	317
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	6	7	16	0.02%	25.9%	SYGPAPGAGHVQEESNLSLQALESR	99.7%	45.9	25	45.9	0	1	0	2597.26	34	58
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	6	7	16	0.02%	25.9%	VLSTVHTHSSVK	99.7%	55	25	53.7	5	0	0	1294.71	148	159
Anaphase-promoting complex subunit 1	ANAPC1	APC1_HUMAN	216.5	100.0%	5	5	6	0.01%	2.9%	DLETLPFGIALPIR	98.7%	34.5	25	34.3	1	0	0	1554.89	943	956
Anaphase-promoting complex subunit 1	ANAPC1	APC1_HUMAN	216.5	100.0%	5	5	6	0.01%	2.9%	FNISSHNQSPK	99.7%	48.3	25	42.7	1	0	0	1258.62	369	379
Anaphase-promoting complex subunit 1	ANAPC1	APC1_HUMAN	216.5	100.0%	5	5	6	0.01%	2.9%	HSTSVSSLAER	95.5%	29	25	28.2	1	0	0	1173.59	919	929
Anaphase-promoting complex subunit 1	ANAPC1	APC1_HUMAN	216.5	100.0%	5	5	6	0.01%	2.9%	LQVEQEENR	99.7%	42	25	41.6	2	0	0	1144.56	906	914
Anaphase-promoting complex subunit 1	ANAPC1	APC1_HUMAN	216.5	100.0%	5	5	6	0.01%	2.9%	SPSISNMAALSR	98.5%	33.6	25	17.9	1	0	0	1233.63	341	352
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	13	15	25	0.02%	26.2%	AGQERPSVTSYK	99.7%	52.9	25	48.4	2	0	0	1322.67	182	193
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	13	15	25	0.02%	26.2%	AIQLNSNSVQALLLK	99.7%	87	25	73.5	2	0	0	1611.94	365	379
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	13	15	25	0.02%	26.2%	AYAFVHTGDNSR	99.7%	50	25	50	2	0	0	1337.62	242	253
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	13	15	25	0.02%	26.2%	DMAAAGLHSNVR	99.7%	69.8	25	66.9	4	0	0	1241.61	43	54
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	13	15	25	0.02%	26.2%	DNVDLLGSLADLYFR	99.7%	76.7	25	76.7	2	0	0	1710.87	269	283
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	13	15	25	0.02%	26.2%	FEQAQMLDPYLIK	99.7%	72.5	25	65.4	1	0	0	1595.81	294	306
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	13	15	25	0.02%	26.2%	GMDVYGYLLAR	99.7%	52.3	25	52.3	2	0	0	1257.63	307	317
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	13	15	25	0.02%	26.2%	KAELLSR	96.6%	30.2	25	7.91	1	0	0	816.49	482	488
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	13	15	25	0.02%	26.2%	LEDVENLGCR	99.7%	66.4	25	59.8	2	0	0	1204.56	321	330
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	13	15	25	0.02%	26.2%	VQEAIIHFR	99.7%	42.8	25	34	1	0	0	1112.62	389	397
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	13	15	25	0.02%	26.2%	VRPSTGNSASTPQSQCLPSEIEVK	99.7%	41.8	25	41.8	0	1	0	2572.27	116	139
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	13	15	25	0.02%	26.2%	YEDGIALLR	99.7%	52.3	25	46	2	0	0	1049.56	492	500
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	13	15	25	0.02%	26.2%	YTMALQQK	99.6%	40.2	25	23.6	3	0	0	998.50	100	107
Ancient ubiquitous protein 1	AUP1	AUP1_HUMAN	53.0	100.0%	3	3	6	0.01%	8.8%	GTQSLPTASASK	99.7%	41.2	25	30.9	3	0	0	1147.60	414	425
Ancient ubiquitous protein 1	AUP1	AUP1_HUMAN	53.0	100.0%	3	3	6	0.01%	8.8%	LPPTPLLLFPEEEATNGR	99.7%	56.7	25	56.7	2	0	0	1994.06	217	234
Ancient ubiquitous protein 1	AUP1	AUP1_HUMAN	53.0	100.0%	3	3	6	0.01%	8.8%	QLGEANEEFALR	99.7%	57.7	25	50	1	0	0	1376.68	298	309
Angio-associated migratory cell protein	AAMP	AAMP_HUMAN	46.7	100.0%	3	3	5	0.00%	8.5%	AVVGYEDGTIR	99.7%	54	25	49.5	2	0	0	1179.60	230	240
Angio-associated migratory cell protein	AAMP	AAMP_HUMAN	46.7	100.0%	3	3	5	0.00%	8.5%	DASLVVTTSGDHK	99.7%	53.4	25	46	2	0	0	1329.66	411	423
Angio-associated migratory cell protein	AAMP	AAMP_HUMAN	46.7	100.0%	3	3	5	0.00%	8.5%	TFQGPNCPATCGR	99.7%	58.5	25	58.5	1	0	0	1465.63	210	222

Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	ANFY1_HUMAN	128.4	99.8%	2	2	2	0.00%	2.1%	GDLFAATFLIK	99.7%	56.6	25	43.3	1	0	0	1195.67	300	310
Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	ANFY1_HUMAN	128.4	99.8%	2	2	2	0.00%	2.1%	TQDGETALQLAIR	99.7%	72.6	25	59.5	1	0	0	1415.75	652	664
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.8%	AAMIWIVGEYAER	99.7%	81.3	25	70.2	2	0	0	1508.76	446	458
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.8%	CVSTLLDLIQTK	99.7%	78.1	25	56.5	2	0	0	1390.76	391	402
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.8%	DCPLNAEAASSK	99.7%	60.7	25	55.1	2	0	0	1262.57	865	876
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.8%	DLDYYGTLLK	99.7%	81.5	25	67.2	2	0	0	1200.61	273	282
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.8%	EYATEVDVDFVR	99.7%	81	25	81	2	0	0	1442.68	360	371
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.8%	GLEISGTFTR	99.7%	53.2	25	51.5	2	0	0	1080.57	731	740
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.8%	ITEYLCEPLRK	99.5%	39.3	25	25.5	1	0	0	1421.75	118	128
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.8%	KGEIFELK	99.7%	41.1	25	17.6	2	0	0	963.55	12	19
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.8%	LASQANIAQVLAELK	99.7%	117	25	112	2	0	0	1568.90	345	359
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.8%	LQSSNIFTVAK	99.7%	49.2	25	38.2	2	0	0	1207.67	877	887
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.8%	LSHANSAVVLSAVK	99.7%	80.2	25	79.6	2	2	0	1395.80	248	261
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.8%	MEPLNNLQVAVK	99.5%	39.5	25	30.2	2	0	0	1371.73	806	817
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.8%	NINLIVQK	98.0%	32.4	25	29.1	2	0	0	941.58	305	312
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.8%	VNYVVQEAIVVIK	98.9%	35.2	25	30.8	1	0	0	1473.87	403	415
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.8%	YNDPIYVK	99.7%	43.4	25	32.1	2	0	0	1011.51	328	335
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	14	14	26	0.02%	17.4%	AALCAVHVIR	99.7%	79.4	25	78.3	2	0	0	1109.62	157	166
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	14	14	26	0.02%	17.4%	ADCASGIFLAAEK	99.7%	74.1	25	67.8	2	0	0	1352.65	398	410
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	14	14	26	0.02%	17.4%	AVEYNALFK	99.6%	40.1	25	38.4	2	0	0	1054.56	563	571
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	14	14	26	0.02%	17.4%	ELLYFLDSCEPEFK	99.7%	70.2	25	62	2	0	0	1789.84	384	397
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	14	14	26	0.02%	17.4%	FTCTVNR	99.7%	41.7	25	30.2	2	0	0	897.42	537	543
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	14	14	26	0.02%	17.4%	IEFTFER	99.6%	39.9	25	35.4	2	0	0	941.47	717	723
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	14	14	26	0.02%	17.4%	IGYLGAMLLLDER	99.7%	50.1	25	45.3	1	0	0	1463.79	84	96
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	14	14	26	0.02%	17.4%	SPDMLAHFR	99.5%	39.4	25	28.7	1	0	0	1089.51	205	213
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	14	14	26	0.02%	17.4%	SSFREEDNTYR	99.7%	35.4	25	29.3	0	2	0	1403.62	36	46
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	14	14	26	0.02%	17.4%	TQAEEREMIQK	98.1%	32.6	25	29.2	1	0	0	1378.66	19	29
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	14	14	26	0.02%	17.4%	TVQTDHNAVQR	98.7%	27.7	25	25.2	0	1	0	1268.63	335	345
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	14	14	26	0.02%	17.4%	VLAINILGR	99.7%	74.1	25	62.7	4	0	0	968.63	307	315
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	14	14	26	0.02%	17.4%	VLTTAGSYVR	99.7%	80.2	25	72.7	2	0	0	1066.59	425	434
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	14	14	26	0.02%	17.4%	YVALTSLLK	99.7%	45.7	25	45.7	2	0	0	1007.61	326	334
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	12	20	0.02%	32.2%	FEIPYFTTSGIQVR	99.7%	115	25	112	2	0	0	1657.86	380	393
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	12	20	0.02%	32.2%	HNNLYLVATSK	99.7%	61.4	25	48.1	2	0	0	1259.67	62	72
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	12	20	0.02%	32.2%	ILQEYITQEGHK	99.7%	76.9	25	60.7	2	0	0	1458.76	130	141
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	12	20	0.02%	32.2%	LETGAPRPPATVTNAVSWR	99.7%	42.7	25	42.7	0	2	0	2023.07	142	160
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	12	20	0.02%	32.2%	SGYQALPWVR	99.7%	41.3	25	38.9	2	0	0	1176.62	401	410
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	12	20	0.02%	32.2%	SVELEDVKFHQCVR	97.3%	24.9	25	20.5	0	1	0	1745.86	230	243
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	12	20	0.02%	32.2%	TISFIPPDGEFELMSYR	94.5%	28.2	25	28.2	1	0	0	2017.96	252	268
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	12	20	0.02%	32.2%	VFLSGMPELR	99.7%	57.8	25	50	4	0	0	1148.61	202	211
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	12	20	0.02%	32.2%	VLFDNTGR	99.3%	37.6	25	27.1	1	0	0	921.48	218	225
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	12	20	0.02%	32.2%	VVQVFSEYFK	99.7%	47	25	40.6	1	0	0	1245.65	87	96
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	11	12	20	0.02%	32.2%	YITQNGDYQLR	99.7%	48.8	25	48.7	2	0	0	1370.67	411	421
AP-1 complex subunit sigma-1A	AP1S1	AP1S1_HUMAN	18.7	100.0%	3	4	13	0.01%	20.9%	AIEQADLLQEEDESPR	99.7%	116	25	116	4	0	0	1842.87	134	149
AP-1 complex subunit sigma-1A	AP1S1	AP1S1_HUMAN	18.7	100.0%	3	4	13	0.01%	20.9%	ELMQVVLAR	99.7%	64.4	25	48.8	4	0	0	1058.60	34	42
AP-1 complex subunit sigma-1A	AP1S1	AP1S1_HUMAN	18.7	100.0%	3	4	13	0.01%	20.9%	MCSFLEWR	99.7%	43.6	25	43.6	5	0	0	1128.50	46	53
AP-1 complex subunit sigma-2	AP1S2	AP1S2_HUMAN	18.6	100.0%	2	2	8	0.01%	21.0%	AIEQADLLQEEAETPR	99.7%	97.2	25	92.3	2	0	0	1812.90	133	148
AP-1 complex subunit sigma-2	AP1S2	AP1S2_HUMAN	18.6	100.0%	2	2	8	0.01%	21.0%	ELVQTVLAR	99.7%	55.4	25	39	6	0	0	1028.61	33	41
AP-1 complex subunit sigma-2	AP1S2	AP1S2_HUMAN	18.6	100.0%	2	2	8	0.01%	21.0%	MCSFLEWR	99.7%	43.6	25	43.6	5	0	0	1128.50	45	52
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	13	13	23	0.02%	15.4%	ACNQLGQFLQHR	99.0%	29	25	17.6	0	2	0	1471.72	330	341
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	13	13	23	0.02%	15.4%	ALLLSTYIK	99.7%	59.2	25	59.2	2	0	0	1021.63	539	547
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	13	13	23	0.02%	15.4%	EMGEAFAADIPR	99.7%	57.5	25	57.5	2	0	0	1306.61	142	153

AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	13	13	23	0.02%	15.4%	FFQPTEMAAQDFFQR	99.7%	67.7	25	67.7	2	0	0	1862.85	864	878
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	13	13	23	0.02%	15.4%	FINLFPETK	98.5%	33.7	25	32.5	2	0	0	1108.60	548	556
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	13	13	23	0.02%	15.4%	GLAVFISDIR	99.7%	80.7	25	72	2	0	0	1090.63	12	21
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	13	13	23	0.02%	15.4%	IAGDYVSEEVWYR	99.7%	79.6	25	73.4	1	0	0	1586.75	452	464
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	13	13	23	0.02%	15.4%	ILVAGDSMDSVK	99.7%	48.3	25	40.2	2	0	0	1234.63	154	165
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	13	13	23	0.02%	15.4%	NADVELQQR	99.5%	39	25	33.8	2	0	0	1072.54	571	579
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	13	13	23	0.02%	15.4%	QLSLPQQEAQK	97.3%	31.2	25	29	1	0	0	1269.68	881	891
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	13	13	23	0.02%	15.4%	TCVSLAVSR	99.7%	43.2	25	22.7	2	0	0	992.52	224	232
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	13	13	23	0.02%	15.4%	THIDTVINALK	96.4%	29.9	25	29.9	1	0	0	1224.69	368	378
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	13	13	23	0.02%	15.4%	VGGYILGEFGNLIAGDPR	99.7%	97.9	25	92.9	2	0	0	1847.97	499	516
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	12	20	0.02%	23.4%	ACNQLGQFLQHR	99.0%	29	25	17.6	0	2	0	1471.72	329	340
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	12	20	0.02%	23.4%	ALLLSTYIK	99.7%	59.2	25	59.2	2	0	0	1021.63	538	546
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	12	20	0.02%	23.4%	AVDLLYAMCDR	99.7%	64.7	25	63.1	1	0	0	1326.62	388	398
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	12	20	0.02%	23.4%	EMAEAFAGEIPK	99.7%	70	25	58.7	2	0	0	1292.62	142	153
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	12	20	0.02%	23.4%	FFQPTEMASQDFFQR	99.7%	71.8	25	25.7	2	0	0	1878.85	826	840
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	12	20	0.02%	23.4%	FVNLFPEVKPTIQDVLR	99.7%	37.5	25	37.5	0	1	0	2015.13	547	563
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	12	20	0.02%	23.4%	GLAVFISDIR	99.7%	80.7	25	72	2	0	0	1090.63	12	21
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	12	20	0.02%	23.4%	IAGDYVSEEVWYR	99.7%	79.6	25	73.4	1	0	0	1586.75	451	463
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	12	20	0.02%	23.4%	LTECLETILNK	99.7%	72.6	25	66.5	2	0	0	1333.70	279	289
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	12	20	0.02%	23.4%	NADVELQQR	99.5%	39	25	33.8	2	0	0	1072.54	570	578
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	12	20	0.02%	23.4%	NNGVLFENQLLQIGLK	99.7%	56.2	25	56.2	1	0	0	1800.00	713	728
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	12	20	0.02%	23.4%	THIETVINALK	99.7%	48.1	25	42.4	2	0	0	1238.71	367	377
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	12	20	0.02%	23.4%	TTQIGCLLR	99.7%	47.2	25	29.7	2	0	0	1061.58	898	906
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	12	20	0.02%	23.4%	TVFEALQAPACHENLVK	98.8%	34.6	25	34.6	1	0	0	1926.97	481	497
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	12	20	0.02%	23.4%	VGGYILGEFGNLIAGDPR	99.7%	97.9	25	92.9	2	0	0	1847.97	498	515
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	12	20	0.02%	23.4%	VLVAGDTMDSVK	99.7%	48.1	25	28.5	4	0	0	1250.63	154	165
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	12	20	0.02%	23.4%	YGGTFQNVSVQLPITLNK	99.7%	78.9	25	78.9	2	0	0	1979.06	808	825
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	13	13	23	0.02%	30.8%	ASENAIVWK	99.7%	45.6	25	33.5	2	0	0	1017.54	346	354
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	13	13	23	0.02%	30.8%	IPTPLNTSGVQVICMK	99.7%	47.3	25	47.3	1	0	0	1757.93	324	339
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	13	13	23	0.02%	30.8%	LNYSDHDVIK	99.7%	68	25	61.4	2	0	0	1203.60	411	420
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	13	13	23	0.02%	30.8%	MCDVMAAYFGK	99.7%	65.5	25	64.2	2	0	0	1292.55	85	95
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	13	13	23	0.02%	30.8%	MIGGLFIYNHK	98.2%	33	25	28.9	1	0	0	1292.68	1	11
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	13	13	23	0.02%	30.8%	SGIYETR	97.3%	31.1	25	22.3	2	0	0	825.41	428	434
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	13	13	23	0.02%	30.8%	SISFIPPDGEFELMR	99.7%	42.1	25	30.2	2	0	0	1737.85	262	276
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	13	13	23	0.02%	30.8%	SNFKPSLLAQK	99.7%	50.2	25	40.6	2	0	0	1232.70	309	319
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	13	13	23	0.02%	30.8%	SNIWLAAVTK	99.7%	45.9	25	35.4	2	0	0	1102.63	61	70
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	13	13	23	0.02%	30.8%	SPVTNIAR	97.6%	31.7	25	23	2	0	0	857.48	45	52
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	13	13	23	0.02%	30.8%	SYLSGMPECK	98.4%	33.4	25	27.9	1	0	0	1171.51	204	213
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	13	13	23	0.02%	30.8%	TFITQQGIK	99.7%	44.6	25	35.1	2	0	0	1035.58	131	139
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	13	13	23	0.02%	30.8%	VNVIHAR	99.7%	49.9	25	45.8	2	0	0	808.48	34	40
AP-2 complex subunit sigma	AP2S1	AP2S1_HUMAN	17.0	100.0%	3	3	5	0.00%	16.9%	FILIQNR	99.7%	44.8	25	12.4	2	0	0	903.54	4	10
AP-2 complex subunit sigma	AP2S1	AP2S1_HUMAN	17.0	100.0%	3	3	5	0.00%	16.9%	HTNFVEFR	97.8%	32	25	25.1	1	0	0	1049.52	46	53
AP-2 complex subunit sigma	AP2S1	AP2S1_HUMAN	17.0	100.0%	3	3	5	0.00%	16.9%	QLLMLQSLE	99.3%	37.6	25	32.2	2	0	0	1090.58	134	142
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	24	0.02%	11.2%	ASILWLIGENCER	99.7%	69.7	25	65.4	1	0	0	1560.78	497	509
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	24	0.02%	11.2%	EGSTAQLIINTEK	99.7%	78.8	25	71.5	2	0	0	1403.74	1064	1076
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	24	0.02%	11.2%	KIENIHIGEK	99.7%	45	25	39.7	1	0	0	1180.67	913	922
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	24	0.02%	11.2%	LLTQYILNLGK	99.7%	80	25	70.2	6	0	0	1275.77	553	563
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	24	0.02%	11.2%	LQILNLGAK	99.7%	52.7	25	37.1	2	0	0	969.61	534	542
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	24	0.02%	11.2%	LYSLDPEQK	99.7%	40.9	25	35.2	2	0	0	1092.56	177	185
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	24	0.02%	11.2%	NASELFPAVVK	99.7%	58.2	25	43.2	2	0	0	1174.65	75	85
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	24	0.02%	11.2%	NTKPLLQSR	96.8%	30.4	25	22.4	1	0	0	1056.62	303	311

AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	24	0.02%	11.2%	NVEVIELAK	98.4%	33.4	25	31.9	1	0	0	1014.58	650	658
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	24	0.02%	11.2%	QFAAATIQTIGR	99.7%	81.1	25	72.5	2	0	0	1276.70	419	430
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	24	0.02%	11.2%	TVIGSVLLR	99.7%	45.8	25	33.9	2	0	0	957.61	1077	1085
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	24	0.02%	11.2%	YDQNYDIR	99.7%	59.5	25	47.2	2	0	0	1086.49	564	571
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	7	7	12	0.01%	6.3%	ALDLLYGMVSK	99.7%	75.9	25	72.6	2	0	0	1209.65	360	370
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	7	7	12	0.01%	6.3%	AVFHEEEQR	99.7%	43.7	25	38.1	2	0	0	1144.54	643	651
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	7	7	12	0.01%	6.3%	ILIEDSDQNLK	99.7%	55.3	25	50.3	2	0	0	1287.68	310	320
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	7	7	12	0.01%	6.3%	KGENSVSVDGK	96.0%	29.5	25	23.8	1	0	0	1119.56	1122	1132
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	7	7	12	0.01%	6.3%	LFGALTPLEPR	99.7%	42.4	25	34	2	0	0	1213.69	244	254
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	7	7	12	0.01%	6.3%	NYLSLAPLFFK	99.5%	39.2	25	39.2	2	0	0	1312.73	217	227
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	7	7	12	0.01%	6.3%	YLGLLAMSK	99.1%	36.3	25	32.3	1	0	0	995.56	321	329
AP-3 complex subunit sigma-1	AP3S1	AP3S1_HUMAN	21.7	100.0%	5	6	9	0.01%	27.5%	ETFHLVSK	98.6%	34.1	25	21.8	1	0	0	960.51	34	41
AP-3 complex subunit sigma-1	AP3S1	AP3S1_HUMAN	21.7	100.0%	5	6	9	0.01%	27.5%	FYQPYSEDTQQQIIR	99.7%	74.5	25	62.9	2	0	0	1915.92	19	33
AP-3 complex subunit sigma-1	AP3S1	AP3S1_HUMAN	21.7	100.0%	5	6	9	0.01%	27.5%	NINIGDISIK	97.9%	32.1	25	16.1	1	0	0	1086.62	176	185
AP-3 complex subunit sigma-1	AP3S1	AP3S1_HUMAN	21.7	100.0%	5	6	9	0.01%	27.5%	NMNLPEIPR	99.2%	36.5	25	24	2	0	0	1099.56	167	175
AP-3 complex subunit sigma-1	AP3S1	AP3S1_HUMAN	21.7	100.0%	5	6	9	0.01%	27.5%	SEAGLAGAPAR	99.7%	63.2	25	49	3	0	0	999.52	150	160
AP-3 complex subunit sigma-2	AP3S2	AP3S2_HUMAN	22.0	100.0%	2	2	5	0.00%	11.4%	FPEEIQQQIVR	97.3%	31.1	25	26.8	1	0	0	1386.74	23	33
AP-3 complex subunit sigma-2	AP3S2	AP3S2_HUMAN	22.0	100.0%	2	2	5	0.00%	11.4%	SEGGLSAAPAR	99.7%	49.8	25	37.7	4	0	0	1015.52	150	160
Apolipoprotein O-like	APOOL	APOOL_HUMAN	29.2	99.8%	2	2	2	0.00%	9.3%	HSVPLPTELSSEAK	98.2%	32.9	25	30.3	1	0	0	1494.78	219	232
Apolipoprotein O-like	APOOL	APOOL_HUMAN	29.2	99.8%	2	2	2	0.00%	9.3%	SSKEESLPKPK	97.2%	24.8	25	18.6	0	1	0	1229.67	186	196
Apoptosis regulator BAX	BAX	BAX_HUMAN	21.2	100.0%	2	2	3	0.00%	10.4%	KLSECLK	95.1%	28.6	25	3.64	1	0	0	877.48	58	64
Apoptosis regulator BAX	BAX	BAX_HUMAN	21.2	100.0%	2	2	3	0.00%	10.4%	TGALLLQGFIQDR	99.7%	50.4	25	50.4	2	0	0	1431.80	22	34
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	22	47	0.04%	35.4%	AALSASEGEEVPQDK	99.7%	78.1	25	71.4	2	0	0	1530.73	113	127
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	22	47	0.04%	35.4%	ALGTEVIQLFPEK	99.7%	97	25	90.7	4	0	0	1444.80	325	337
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	22	47	0.04%	35.4%	CLIATGGTPR	99.7%	47.6	25	24.7	2	0	0	1045.55	256	265
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	22	47	0.04%	35.4%	DGEQHEDLNEVAK	99.7%	66.2	25	59.5	2	2	0	1483.67	594	606
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	22	47	0.04%	35.4%	ELWFSDDPNVTK	99.7%	45	25	39	2	0	0	1450.69	178	189
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	22	47	0.04%	35.4%	ILPEYLSNWTMEK	99.7%	63.3	25	57.8	3	0	0	1623.81	343	355
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	22	47	0.04%	35.4%	ISGLGLTPEQK	99.7%	53	25	45.1	4	0	0	1142.64	99	109
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	22	47	0.04%	35.4%	KVVQLDVR	99.6%	40.2	25	23.5	2	0	0	956.59	232	239
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	22	47	0.04%	35.4%	LFNIHED	98.9%	35	25	35	2	0	0	887.43	607	613
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	22	47	0.04%	35.4%	LNDGSQITYEK	99.7%	67.6	25	59.9	3	0	0	1267.62	245	255
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	22	47	0.04%	35.4%	SATEQSGTGIR	99.7%	91.1	25	71.7	2	0	0	1106.54	519	529
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	22	47	0.04%	35.4%	SNIWVAGDAACFYDIK	99.7%	77.9	25	77.9	2	0	0	1829.85	431	446
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	22	47	0.04%	35.4%	TGGLEIDSDFGGFR	99.7%	82.7	25	82.7	2	0	0	1470.69	409	422
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	22	47	0.04%	35.4%	VETDHIVAAVGLEPNVELAK	99.7%	39.7	25	39.7	0	2	0	2104.13	389	408
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	22	47	0.04%	35.4%	VLIVSEDPELPYMRPPLSK	99.7%	41.4	25	41.4	0	4	0	2183.18	159	177
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	22	47	0.04%	35.4%	VMPNAIVQSVGVSSGK	99.7%	98.6	25	92.6	4	0	0	1572.84	363	378
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	22	47	0.04%	35.4%	VNAELQAR	99.7%	41.3	25	24.6	1	0	0	900.49	423	430
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	22	47	0.04%	35.4%	VVQLDVR	99.7%	48.8	25	39.7	2	0	0	828.49	233	239
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	10	10	25	0.02%	9.0%	AAPCIYWLPLTDSQIVQK	98.5%	33.9	25	29.9	1	0	0	2103.09	1220	1237
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	10	10	25	0.02%	9.0%	GLLVDRPSETK	98.4%	33.4	25	21.7	3	0	0	1214.67	1097	1107
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	10	10	25	0.02%	9.0%	GVPAGNSDTEGGQPGR	99.7%	87.4	25	87.4	4	0	0	1498.69	832	847
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	10	10	25	0.02%	9.0%	KPSISITTESLK	99.7%	45.7	25	43.5	2	0	0	1303.75	861	872
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	10	10	25	0.02%	9.0%	RLSQPESAEK	98.6%	34.2	25	29.2	1	0	0	1144.60	708	717
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	10	10	25	0.02%	9.0%	SGVSITIDDPVR	99.7%	62.4	25	46.7	1	0	0	1258.66	987	998
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	10	10	25	0.02%	9.0%	SQEQEVLER	99.7%	51.5	25	39.4	2	0	0	1117.55	328	336
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	10	10	25	0.02%	9.0%	TGTLVEEAFWIDK	99.7%	64.5	25	56.4	2	0	0	1508.76	1035	1047
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	10	10	25	0.02%	9.0%	VTLGDTLTR	99.7%	50	25	41	4	0	0	975.55	971	979
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	10	10	25	0.02%	9.0%	WGASTATTQK	99.7%	43.8	25	36.6	5	0	0	1050.52	851	860
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	37.1%	AAYPDLENPPLLVTPSQQAK	99.7%	76.1	25	70.2	3	0	0	2152.13	90	109

Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	37.1%	AYQCVVLLQGK	99.7%	71.6	25	51.5	2	0	0	1278.69	290	300
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	37.1%	EIAENITK	99.7%	45.2	25	30.8	1	0	0	917.49	136	143
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	37.1%	GESFYQDR	99.4%	38	25	36.7	2	0	0	1001.43	334	341
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	37.1%	GFDILGIKPVQR	99.7%	54.7	25	54.7	3	1	0	1342.78	648	659
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	37.1%	GFVQVDDGRK	99.7%	43.5	25	35.7	4	0	0	1120.57	353	362
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	37.1%	IVFVPGCSIPLTIVK	99.7%	67.9	25	59.1	4	0	0	1642.96	363	377
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	37.1%	IYDALDVSLIER	99.7%	71.8	25	65.9	2	0	0	1406.75	322	333
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	37.1%	LANIDEEMLQK	99.7%	68.9	25	55.9	4	0	0	1303.66	547	557
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	37.1%	LFEFAGYDVLR	99.7%	68.6	25	61	4	0	0	1329.68	224	234
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	37.1%	LLQQEEEIK	99.7%	45.3	25	28.1	2	0	0	1129.61	12	20
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	37.1%	LMDLLGEGLKR	99.2%	36.7	25	28.5	2	0	0	1244.70	462	472
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	37.1%	LNDYIFSFDK	99.7%	74.4	25	69.9	4	0	0	1261.61	513	522
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	37.1%	MLLCEAVAAVMAK	99.7%	78.1	25	59	4	0	0	1406.72	635	647
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	37.1%	NCGCLGASPNLEQLQEENLK	99.7%	59.7	25	59.7	1	0	0	2274.05	31	50
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	37.1%	NMINIISR	99.7%	42.6	25	25.7	2	0	0	960.53	72	79
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	37.1%	SDGGYTYDTSDLAAIK	99.7%	98.6	25	87.8	4	0	0	1676.77	378	393
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	37.1%	SLTAEIDR	99.7%	42.3	25	29.6	2	0	0	904.47	21	28
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	37.1%	STIIGESISR	99.7%	93.6	25	75.8	5	0	0	1062.58	214	223
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	37.1%	VEIAGPGFINVHLR	99.7%	60.5	25	55.5	2	2	0	1521.85	154	167
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	37.1%	YADLSHNR	99.7%	59	25	51.5	5	0	0	975.46	505	512
Argininosuccinate synthase	ASS1	ASSY_HUMAN	46.5	100.0%	4	4	8	0.01%	8.7%	FELSCYSLAPQIK	99.7%	61.6	25	57.2	2	0	0	1555.78	128	140
Argininosuccinate synthase	ASS1	ASSY_HUMAN	46.5	100.0%	4	4	8	0.01%	8.7%	GQVYILGR	99.6%	40.3	25	19.4	2	0	0	905.52	356	363
Argininosuccinate synthase	ASS1	ASSY_HUMAN	46.5	100.0%	4	4	8	0.01%	8.7%	MPEFYNR	99.2%	36.6	25	33	2	0	0	956.43	147	153
Argininosuccinate synthase	ASS1	ASSY_HUMAN	46.5	100.0%	4	4	8	0.01%	8.7%	VFIEDVSR	99.7%	59.2	25	42.1	2	0	0	964.51	59	66
Armadillo repeat-containing protein 6	ARMC6	ARMC6_HUMAN	54.1	100.0%	6	6	9	0.01%	13.8%	AIAGNDDVKDAIVR	99.7%	68.9	25	68.9	1	0	0	1456.78	353	366
Armadillo repeat-containing protein 6	ARMC6	ARMC6_HUMAN	54.1	100.0%	6	6	9	0.01%	13.8%	DQSGVQELVK	99.1%	36.4	25	17.4	1	0	0	1102.57	336	345
Armadillo repeat-containing protein 6	ARMC6	ARMC6_HUMAN	54.1	100.0%	6	6	9	0.01%	13.8%	GAYPIIFTAWK	99.7%	54.2	25	45.9	2	0	0	1266.69	135	145
Armadillo repeat-containing protein 6	ARMC6	ARMC6_HUMAN	54.1	100.0%	6	6	9	0.01%	13.8%	IAQETFDAAVR	99.7%	67.3	25	59.9	2	0	0	1220.63	31	41
Armadillo repeat-containing protein 6	ARMC6	ARMC6_HUMAN	54.1	100.0%	6	6	9	0.01%	13.8%	IIVEGGGAVAALQAMK	99.7%	64.3	25	62.6	2	0	0	1527.86	407	422
Armadillo repeat-containing protein 6	ARMC6	ARMC6_HUMAN	54.1	100.0%	6	6	9	0.01%	13.8%	QVLSTLR	97.7%	31.9	25	13.4	1	0	0	816.49	346	352
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	19	33	0.03%	36.5%	ADWLSHYWMPK	96.6%	30.1	25	25.4	1	0	0	1449.66	530	540
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	19	33	0.03%	36.5%	AMTEDGFLAVCSEAK	99.7%	93.7	25	93.7	4	0	0	1644.72	148	162
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	19	33	0.03%	36.5%	APSPEKAEEESER	99.7%	75.3	25	75.3	2	0	0	1458.67	380	392
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	19	33	0.03%	36.5%	ASVGMYLISK	98.9%	35.3	25	24	2	0	0	1084.57	341	350
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	19	33	0.03%	36.5%	DVPLHALYDNVEK	99.7%	70.7	25	67	2	0	0	1512.77	209	221
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	19	33	0.03%	36.5%	EAFSDGITSVK	99.7%	67.6	25	62.3	3	0	0	1153.57	468	478
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	19	33	0.03%	36.5%	ELYLFDVLR	99.7%	63.9	25	53.6	2	0	0	1167.64	396	404
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	19	33	0.03%	36.5%	ETFEDSNLIPK	99.7%	52.2	25	42.3	1	0	0	1292.64	450	460
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	19	33	0.03%	36.5%	FSSYYLSLPPEMR	99.7%	53	25	53	1	0	0	1589.77	425	437
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	19	33	0.03%	36.5%	IGCLLSGGLDSSLVAATLLK	99.7%	76.6	25	76.6	2	0	0	1988.11	253	272
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	19	33	0.03%	36.5%	ILFNNAVK	94.5%	28.2	25	5.68	1	0	0	918.54	237	244
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	19	33	0.03%	36.5%	ILQEYVEHQVDDAMMANAAQK	99.7%	49.4	25	47.1	0	1	0	2436.12	484	504
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	19	33	0.03%	36.5%	LAVVDPLFGMQPIR	99.7%	69.1	25	65.2	4	0	0	1571.86	50	63
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	19	33	0.03%	36.5%	LFPGFEIETVK	99.2%	36.9	25	21.4	1	0	0	1279.69	222	232
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	19	33	0.03%	36.5%	VASVEMVK	97.1%	30.8	25	15.9	2	0	0	878.47	196	203
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	19	33	0.03%	36.5%	VPFLDHR	99.7%	42.6	25	34.8	2	0	0	883.48	418	424
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	17	19	33	0.03%	36.5%	WINATDPSAR	99.7%	43.2	25	37.3	2	0	0	1130.56	541	550
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	5	5	9	0.01%	11.9%	ASAELALGENSEVLK	99.7%	91.7	25	87	2	0	0	1530.80	108	122
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	5	5	9	0.01%	11.9%	FVTVQTISGTGALR	99.7%	101	25	95.3	2	0	0	1449.81	126	139
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	5	5	9	0.01%	11.9%	IAAAILNTPDLR	99.7%	66.5	25	53.7	1	0	0	1267.74	326	337
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	5	5	9	0.01%	11.9%	IAAAILNTPDLRK	99.7%	55.5	25	55.5	2	0	0	1395.83	326	338

Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	5	5	9	0.01%	11.9%	VGAFTMVCK	99.6%	40.1	25	31.3	2	0	0	1012.50	288	296
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	26	35	61	0.06%	58.9%	ADEVVWVR	99.7%	72	25	61.2	2	0	0	973.51	56	63
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	26	35	61	0.06%	58.9%	ALHHGIDLEK	98.8%	34.6	25	24.8	2	0	0	1132.61	442	451
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	26	35	61	0.06%	58.9%	EAGVEMGDEDDLSTPNEK	99.7%	104	25	104	3	0	0	1935.81	357	374
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	26	35	61	0.06%	58.9%	EIMDAAEDYAK	99.7%	50.3	25	48.3	2	0	0	1271.55	16	26
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	26	35	61	0.06%	58.9%	ESIVDVEGVVR	99.7%	76.6	25	69.3	2	0	0	1201.64	111	121
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	26	35	61	0.06%	58.9%	FGAPPHAGGGIGLER	99.7%	77.2	25	65.1	2	2	0	1435.74	461	475
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	26	35	61	0.06%	58.9%	FLEPTLR	99.2%	36.4	25	21.5	2	0	0	875.50	339	345
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	26	35	61	0.06%	58.9%	FQTEIQTVNK	99.7%	60.2	25	46	2	0	0	1207.63	321	330
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	26	35	61	0.06%	58.9%	GEEILSGAQR	99.7%	90.6	25	56.2	2	0	0	1059.54	422	431
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	26	35	61	0.06%	58.9%	GFVEIQTPK	99.7%	50.2	25	36.2	2	0	0	1018.56	214	222
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	26	35	61	0.06%	58.9%	IGSCTQQDVELHVQK	99.7%	72.2	25	72.1	2	1	0	1741.85	127	141
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	26	35	61	0.06%	58.9%	IHDPQLLTER	99.7%	34.7	25	23.2	1	2	0	1221.66	432	441
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	26	35	61	0.06%	58.9%	IYVISLAEPR	99.7%	42.2	25	40.2	2	0	0	1160.67	142	151
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	26	35	61	0.06%	58.9%	LEYCEALAMLR	99.7%	64.6	25	55	2	0	0	1368.67	346	356
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	26	35	61	0.06%	58.9%	LPLQLDDAVRPEAEGEEEGR	99.7%	44.6	25	44.6	2	2	0	2223.09	152	171
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	26	35	61	0.06%	58.9%	LQSGICHLFR	99.7%	64.2	25	54	2	1	0	1230.64	198	207
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	26	35	61	0.06%	58.9%	NNAYLAQSPQLYK	99.7%	88.5	25	80.3	2	0	0	1509.77	242	254
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	26	35	61	0.06%	58.9%	QCFLVLR	99.3%	37.6	25	16.8	2	0	0	935.51	75	81
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	26	35	61	0.06%	58.9%	QMCICADFEK	99.7%	43.2	25	43.2	2	0	0	1317.53	255	264
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	26	35	61	0.06%	58.9%	QQQFNVQALVAVGDHASK	99.5%	31.9	25	31.9	0	1	0	1940.00	82	99
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	26	35	61	0.06%	58.9%	QSNSYDMFMR	99.7%	61.2	25	61.2	2	0	0	1278.52	412	421
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	26	35	61	0.06%	58.9%	QTSMFPR	99.7%	43.8	25	39.3	1	0	0	882.41	488	494
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	26	35	61	0.06%	58.9%	TSTSQAVFR	99.7%	76	25	68.1	2	0	0	996.51	189	197
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	26	35	61	0.06%	58.9%	VFSIGPVFR	99.7%	58	25	53.1	2	0	0	1021.58	265	273
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	26	35	61	0.06%	58.9%	VTMLFLGLHNVR	99.7%	65.7	25	58.7	4	0	0	1399.79	476	487
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	26	35	61	0.06%	58.9%	YGISSMIQSQEKPDR	99.7%	67.6	25	59.7	1	2	0	1754.84	29	43
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	12	13	23	0.02%	33.3%	AEGDISNVANGFK	99.7%	75.7	25	66.8	2	0	0	1321.64	359	371
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	12	13	23	0.02%	33.3%	CGLQFLGNIASR	99.7%	69.9	25	63.1	2	0	0	1335.68	134	145
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	12	13	23	0.02%	33.3%	ETTNIFSNCGCVR	99.7%	72.3	25	72.3	2	0	0	1557.68	346	358
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	12	13	23	0.02%	33.3%	ITSDEPLTKDDIPVFLR	99.7%	41.7	25	38.5	0	2	0	1959.04	254	270
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	12	13	23	0.02%	33.3%	LASEEPPDDEEALATIR	99.7%	97.6	25	92.5	1	0	0	1855.89	289	305
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	12	13	23	0.02%	33.3%	LIGNLCYK	98.5%	33.8	25	24.6	1	0	0	980.52	377	384
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	12	13	23	0.02%	33.3%	LSGVMVPAPIQDLEALR	99.7%	56.2	25	54	2	0	0	1824.99	11	27
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	12	13	23	0.02%	33.3%	NACIECSVNQNSIR	99.7%	83.4	25	77.1	2	0	0	1664.75	90	103
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	12	13	23	0.02%	33.3%	NLTEDNSQNQDLIAK	99.7%	90	25	90	1	0	0	1702.82	424	438
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	12	13	23	0.02%	33.3%	SPELVQAMFPK	99.7%	62.1	25	62.1	2	0	0	1262.65	227	237
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	12	13	23	0.02%	33.3%	VEQESLLTAFR	99.7%	75.3	25	66.5	2	0	0	1292.68	123	133
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	12	13	23	0.02%	33.3%	VTLLDLMIAK	99.7%	69	25	59	4	0	0	1116.67	244	253
Ataxin-2-like protein	ATXN2L	ATX2L_HUMAN	113.4	99.8%	2	2	2	0.00%	1.9%	ISLAPTDVK	95.8%	29.3	25	15.6	1	0	0	943.55	499	507
Ataxin-2-like protein	ATXN2L	ATX2L_HUMAN	113.4	99.8%	2	2	2	0.00%	1.9%	STSTPTSPGPR	96.2%	29.7	25	17.6	1	0	0	1087.54	678	688
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	10	14	26	0.02%	47.3%	HVVQSISTQQEK	99.7%	68.4	25	63.4	1	0	0	1383.72	222	233
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	10	14	26	0.02%	47.3%	HVVQSISTQQEKETIAK	99.7%	56	25	53.4	0	2	0	1926.03	222	238
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	10	14	26	0.02%	47.3%	HYLFDVQR	96.7%	30.3	25	23.6	1	0	0	1077.55	164	171
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	10	14	26	0.02%	47.3%	LAQLEEAK	99.7%	45.8	25	29.1	1	0	0	901.50	132	139
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	10	14	26	0.02%	47.3%	NRLDYHISVQNMMR	99.4%	30.9	25	27.1	0	2	0	1776.86	195	208
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	10	14	26	0.02%	47.3%	QASIQHIQNAIDTEK	99.7%	66.1	25	62.5	2	1	0	1695.87	140	154
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	10	14	26	0.02%	47.3%	QASIQHIQNAIDTEKSQQALVQK	99.1%	29.5	25	29.5	0	2	0	2578.36	140	162
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	10	14	26	0.02%	47.3%	TGVTGPYVLGTGLILYALSK	99.7%	87.3	25	87.3	2	2	0	2023.15	71	90
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	10	14	26	0.02%	47.3%	YGLIPEEFFQFLYPK	99.7%	43.1	25	43.1	6	0	0	1890.97	56	70
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	10	14	26	0.02%	47.3%	YGPFVADFADKLNEQK	99.7%	64.5	25	64.5	2	2	0	1841.91	116	131

ATP synthase mitochondrial F1 complex assembly factor 2	ATPAF2	ATPF2_HUMAN	32.8	99.8%	2	2	2	0.00%	10.0%	LTVEQAVLLSR	99.7%	68.1	25	49.7	1	0	0	1228.73	228	238
ATP synthase mitochondrial F1 complex assembly factor 2	ATPAF2	ATPF2_HUMAN	32.8	99.8%	2	2	2	0.00%	10.0%	TAAGTLFIHLCSESTTVK	98.4%	27	25	27	0	1	0	1935.98	266	283
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	AVDSLVPIGR	99.7%	78.9	25	72.8	10	0	0	1026.59	195	204
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	EAYPGDVFYLHSR	99.7%	88.9	25	83.8	9	2	0	1553.74	335	347
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	EIVTNFLAGFEA	99.7%	86.7	25	82.2	6	0	0	1310.66	542	553
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	ELIIGDR	99.7%	42.4	25	19.4	5	0	0	815.46	208	214
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	EPMQTGIK	99.7%	45.1	25	28.7	2	0	0	903.46	187	194
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	EVAAFAQFGSDLDAATQQLLSR	99.7%	136	25	136	4	3	0	2338.17	442	463
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	FENAFLSHVVSQHQALLGTIR	99.7%	70.3	25	70.3	0	2	0	2367.26	507	527
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	GIRPAINVGLSVSR	99.7%	53.5	25	53.5	2	2	0	1438.85	403	416
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	GMSLNLEPDNVGVVVFGNDK	99.7%	106	25	97.8	17	0	0	2104.04	104	123
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	GYLDKLEPSK	99.7%	50.1	25	39.3	6	0	0	1149.62	494	503
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	HALIIYDDLSK	99.7%	78.2	25	73.4	8	0	0	1287.69	306	316
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	ILGADTSVDLEETGR	99.7%	135	25	131	12	0	0	1575.79	59	73
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	ISVREPMQTGIK	99.7%	54.2	25	41.6	2	2	0	1358.75	183	194
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	LELAQYR	99.5%	38.7	25	22.5	2	0	0	892.49	435	441
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	LKEIVTNFLAGFEA	99.7%	69.8	25	69.8	5	0	0	1551.84	540	553
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	LTDADAMK	97.2%	30.9	25	19.2	2	0	0	864.41	263	270
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	LYCIYVAIGQK	99.7%	73.7	25	65.7	2	0	0	1327.71	242	252
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	NVQAEEMVEFSSGLK	99.7%	109	25	104	9	0	0	1667.79	89	103
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	QGQYSPMAIEEQVAVIYAGVR	99.7%	79.9	25	74	1	0	0	2325.15	473	493
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	QMSLLLR	99.7%	49.6	25	30.2	4	0	0	860.50	323	329
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	RLTDADAMK	99.7%	47.7	25	33.3	2	0	0	1020.51	262	270
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	RSTVAQLVK	99.3%	37	25	26.6	1	0	0	1001.61	253	261
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	RTGAIVDVPVGEELLGR	99.7%	59.9	25	53.7	0	2	0	1780.99	133	149
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	STVAQLVK	99.7%	67.5	25	42.8	8	0	0	845.51	254	261
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	TGAIVDVPVGEELLGR	99.7%	93.6	25	92	13	0	0	1624.89	134	149
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	TGTAEMSSILEER	99.7%	117	25	104	5	0	0	1423.67	46	58
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	TSIAIDTIINQK	99.7%	78.9	25	62	8	0	0	1316.74	219	230
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	VLSIGDGIAR	99.7%	68.2	25	52.7	15	0	0	1000.58	74	83
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	VVDALGNAIDGK	99.7%	83.6	25	75.4	7	0	0	1171.63	150	161
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	30	39	189	0.18%	57.5%	VVDALGNAIDGKGPIGSK	99.7%	78.5	25	78.5	5	4	0	1710.94	150	167
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	40	217	0.21%	49.1%	AHGGYSVFAGVGER	99.7%	96.3	25	94.1	7	5	0	1406.68	226	239
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	40	217	0.21%	49.1%	AIAELGIYPAVDPLDSTSR	99.7%	103	25	102	9	0	0	1988.03	388	406
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	40	217	0.21%	49.1%	DQEGQDVLLFIDNIFR	99.7%	55.5	25	55.5	1	0	0	1921.97	295	310
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	40	217	0.21%	49.1%	EGNDLYHEMIESGVINLK	99.7%	75.9	25	67.2	2	3	0	2061.00	242	259
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	40	217	0.21%	49.1%	FLSQPFQVAEVFTGHMGK	99.7%	76.5	25	76.3	6	7	0	2023.01	463	480
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	40	217	0.21%	49.1%	FTQAGSEVSALLGR	99.7%	112	25	98.1	11	0	0	1435.75	311	324
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	40	217	0.21%	49.1%	IGLFGGAGVGK	99.7%	59	25	53.9	8	0	0	975.56	202	212
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	40	217	0.21%	49.1%	IMDPNIVGSEHYDVAR	99.7%	96.5	25	96.4	10	10	0	1815.87	407	422
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	40	217	0.21%	49.1%	IMNVIGEPIDER	99.7%	66	25	56.8	14	0	0	1385.71	144	155
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	40	217	0.21%	49.1%	IMNVIGEPIDERGPIK	99.7%	63.4	25	59.3	4	2	0	1780.96	144	159
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	40	217	0.21%	49.1%	IPSAVGYQPTLATDMGTMQER	99.7%	116	25	116	13	5	0	2266.08	325	345
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	40	217	0.21%	49.1%	IPVGPETLGR	99.7%	56.5	25	50.7	7	0	0	1038.59	134	143
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	40	217	0.21%	49.1%	LVLEVAQHLGESTVR	99.7%	103	25	103	6	4	0	1650.92	95	109
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	40	217	0.21%	49.1%	TIAMDGTEGLVR	99.7%	75.3	25	62.5	13	0	0	1262.64	110	121
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	40	217	0.21%	49.1%	TVLIMELINNVAK	99.7%	99.4	25	76.2	22	0	0	1457.84	213	225
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	40	217	0.21%	49.1%	VALTGLTVAEYFR	99.7%	97.4	25	85.2	10	0	0	1439.79	282	294
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	40	217	0.21%	49.1%	VALVYGQMNEPPGAR	99.7%	102	25	90.5	14	0	0	1601.81	265	279
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	40	217	0.21%	49.1%	VLDSGAPIK	99.7%	64.2	25	49.8	7	0	0	899.52	125	133
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	40	217	0.21%	49.1%	VLDSGAPIKIPVGPETLGR	99.7%	87.5	25	87.5	4	6	0	1919.10	125	143

ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	40	217	0.21%	49.1%	VVDLLAPYAK	99.7%	51.3	25	51.3	7	0	0	1088.64	189	198
ATP synthase subunit delta, mitochondrial	ATP5D	ATPD_HUMAN	17.5	99.8%	2	2	3	0.00%	13.7%	AQAELVGTADEATR	99.7%	116	25	111	2	0	0	1431.71	137	150
ATP synthase subunit delta, mitochondrial	ATP5D	ATPD_HUMAN	17.5	99.8%	2	2	3	0.00%	13.7%	IEANEALVK	99.7%	55.2	25	40.4	1	0	0	986.55	157	165
ATP synthase subunit e, mitochondrial	ATP5I	ATP5I_HUMAN	7.9	100.0%	4	4	6	0.01%	60.9%	ELAEDDSILK	99.4%	38.5	25	32	2	0	0	1132.57	60	69
ATP synthase subunit e, mitochondrial	ATP5I	ATP5I_HUMAN	7.9	100.0%	4	4	6	0.01%	60.9%	VPPVQVSPLIK	99.7%	45.5	25	42.6	1	0	0	1176.74	2	12
ATP synthase subunit e, mitochondrial	ATP5I	ATP5I_HUMAN	7.9	100.0%	4	4	6	0.01%	60.9%	YNYLKPR	97.9%	32.3	25	20.6	1	0	0	953.52	30	36
ATP synthase subunit e, mitochondrial	ATP5I	ATP5I_HUMAN	7.9	100.0%	4	4	6	0.01%	60.9%	YSALFLGVAYGATR	99.7%	77.2	25	70.8	2	0	0	1488.78	16	29
ATP synthase subunit f, mitochondrial	ATP5J2	ATPK_HUMAN	10.9	99.8%	2	3	9	0.01%	25.5%	DFSPSGIFGAFQR	99.7%	59.4	25	58.4	6	0	0	1428.69	34	46
ATP synthase subunit f, mitochondrial	ATP5J2	ATPK_HUMAN	10.9	99.8%	2	3	9	0.01%	25.5%	LGELPSWILMR	99.7%	55.3	25	47.2	3	0	0	1330.72	23	33
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	32	0.03%	47.6%	IVNSAQTGSFK	99.7%	74.6	25	63.3	4	0	0	1151.61	56	66
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	32	0.03%	47.6%	KIVNSAQTGSFK	99.7%	55.7	25	50.9	4	0	0	1279.70	55	66
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	32	0.03%	47.6%	LATFWYYAK	99.7%	42.1	25	38.8	4	0	0	1162.59	27	35
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	32	0.03%	47.6%	TPALVNAAVTYSKPR	99.7%	61.9	25	61.9	7	7	0	1587.89	12	26
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	32	0.03%	47.6%	VELVPPTPAEIPR	99.7%	46.8	25	36.4	6	0	0	1417.81	36	48
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	34	0.03%	32.2%	ELIEIISGAAALD	99.7%	67.8	25	61.1	3	0	0	1314.72	286	298
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	34	0.03%	32.2%	EVMLVGIGDK	99.7%	45.8	25	30.1	4	0	0	1060.57	127	136
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	34	0.03%	32.2%	EVMLVGIGDKIR	99.7%	79.2	25	61.7	4	0	0	1329.76	127	138
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	34	0.03%	32.2%	GLCGAIHSSIAK	99.7%	67.1	25	63.4	2	0	0	1213.64	101	112
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	34	0.03%	32.2%	HLLIGVSSDR	99.7%	58.9	25	40.8	3	0	0	1096.61	91	100
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	34	0.03%	32.2%	IYGLGSLALYEK	99.7%	88.8	25	82.3	2	0	0	1326.73	68	79
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	34	0.03%	32.2%	LTLTFNR	98.1%	32.7	25	14.1	1	0	0	864.49	271	277
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	34	0.03%	32.2%	NASEMIDKLTLTFNR	99.7%	80	25	80	4	4	0	1752.90	263	277
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	34	0.03%	32.2%	SEVATLTAAGK	99.7%	75.2	25	58.3	2	0	0	1047.57	116	126
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	34	0.03%	32.2%	THSDQFLVAFK	99.7%	73.7	25	62.9	3	2	0	1292.66	144	154
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	7	9	22	0.02%	36.2%	LVRPPVQVYGIEGR	99.7%	44.2	25	44.2	1	2	0	1582.91	27	40
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	7	9	22	0.02%	36.2%	SFLSQGQVLK	98.0%	32.4	25	26.1	2	0	0	1106.62	163	172
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	7	9	22	0.02%	36.2%	SLNDITAKER	99.7%	42.5	25	33.7	1	0	0	1146.61	91	100
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	7	9	22	0.02%	36.2%	TDPSILGGMIVR	99.7%	62	25	55.2	6	0	0	1274.68	177	188
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	7	9	22	0.02%	36.2%	VAASVLNPYVK	99.7%	75.4	25	71	4	0	0	1160.67	74	84
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	7	9	22	0.02%	36.2%	VAQILKEPK	99.7%	44.9	25	29.3	2	0	0	1025.64	65	73
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	7	9	22	0.02%	36.2%	YATALYSAASK	99.7%	100	25	90.6	4	0	0	1145.58	41	51
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	20	23	48	0.05%	34.9%	AEGPGRGDEPSPS	99.7%	44.3	25	38.3	2	0	0	1255.56	622	634
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	20	23	48	0.05%	34.9%	AERENADIIR	95.7%	29.2	25	11.9	1	0	0	1186.62	247	256
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	20	23	48	0.05%	34.9%	ATLNAFLYR	99.7%	71.9	25	60.8	2	0	0	1068.58	479	487
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	20	23	48	0.05%	34.9%	DALNLAQMQEQTLQLEQQSK	99.7%	80.2	25	80.2	2	1	0	2332.15	73	92
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	20	23	48	0.05%	34.9%	GEGAGPPPPLPPAQPGAEGGGDR	99.7%	112	25	112	2	0	0	2081.01	13	35
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	20	23	48	0.05%	34.9%	GLGDRPAPK	99.7%	43.7	25	34.8	2	0	0	910.51	36	44
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	20	23	48	0.05%	34.9%	INEMVHFDLPGQEER	99.7%	49.2	25	49.2	0	2	0	1813.85	515	529
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	20	23	48	0.05%	34.9%	ITVLEALR	99.7%	55.3	25	38	4	0	0	914.57	339	346
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	20	23	48	0.05%	34.9%	LAQFDYGR	99.7%	48.3	25	23.9	3	0	0	969.48	554	561
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	20	23	48	0.05%	34.9%	LAQFDYGRK	99.5%	38.6	25	38.6	2	0	0	1097.57	554	562
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	20	23	48	0.05%	34.9%	LFDWANTSR	99.7%	57.1	25	39.5	2	0	0	1109.54	443	451
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	20	23	48	0.05%	34.9%	LGKPSLVR	99.0%	35.8	25	18.4	2	0	0	869.56	327	334
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	20	23	48	0.05%	34.9%	LLSRPQDALEGVVLSPSLEAR	99.7%	49.9	25	49.3	0	2	0	2250.25	355	375
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	20	23	48	0.05%	34.9%	LTEGMSGR	99.7%	52.3	25	47.6	2	0	0	850.41	569	576
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	20	23	48	0.05%	34.9%	NILMYGPPGTGK	99.7%	64.2	25	55	4	0	0	1263.64	395	406
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	20	23	48	0.05%	34.9%	QQQLLNEENLR	99.7%	69.2	25	56.9	3	0	0	1384.72	195	205
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	20	23	48	0.05%	34.9%	QRYEDQLK	98.9%	35.1	25	22.6	2	0	0	1079.55	187	194
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	20	23	48	0.05%	34.9%	QTVLESIR	99.5%	38.9	25	22.1	2	0	0	945.54	268	275
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	20	23	48	0.05%	34.9%	TAGTLFGEGFR	99.7%	78.7	25	74.9	4	0	0	1155.58	276	286
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	20	23	48	0.05%	34.9%	VRDIAIATR	99.5%	38.7	25	34.2	2	0	0	1014.61	376	384

ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	3	4	9	0.01%	27.0%	AERENADIIR	95.7%	29.2	25	11.9	1	0	0	1186.62	199	208
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	3	4	9	0.01%	27.0%	EALNLAQMQEQTLQLEQQSK	99.7%	68.4	25	68.4	2	0	0	2330.17	73	92
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	3	4	9	0.01%	27.0%	GEGAGPPPPLPPAQPGAEGGGDR	99.7%	112	25	112	2	0	0	2081.01	13	35
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	3	4	9	0.01%	27.0%	GLGDRPAPK	99.7%	43.7	25	34.8	2	0	0	910.51	36	44
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	3	4	9	0.01%	27.0%	HILLYGPPGTGK	99.7%	46.1	25	31.9	2	0	0	1252.71	347	358
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	3	4	9	0.01%	27.0%	ITVLEALR	99.7%	55.3	25	38	4	0	0	914.57	291	298
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	3	4	9	0.01%	27.0%	LAQFDYGR	99.7%	48.3	25	23.9	3	0	0	969.48	506	513
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	3	4	9	0.01%	27.0%	LAQFDYGRK	99.5%	38.6	25	38.6	2	0	0	1097.57	506	514
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	3	4	9	0.01%	27.0%	LFDWANTSR	99.7%	57.1	25	39.5	2	0	0	1109.54	395	403
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	3	4	9	0.01%	27.0%	LGKPSLVR	99.0%	35.8	25	18.4	2	0	0	869.56	279	286
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	3	4	9	0.01%	27.0%	LKEYEAAVEQLK	99.7%	75.1	25	68.2	4	1	0	1420.77	93	104
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	3	4	9	0.01%	27.0%	LTEGMSGR	99.7%	52.3	25	47.6	2	0	0	850.41	521	528
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	3	4	9	0.01%	27.0%	QQQLLNEENLR	99.7%	69.2	25	56.9	3	0	0	1384.72	147	157
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	3	4	9	0.01%	27.0%	QRYEDQLK	98.9%	35.1	25	22.6	2	0	0	1079.55	139	146
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	3	4	9	0.01%	27.0%	QTVLESIR	99.5%	38.9	25	22.1	2	0	0	945.54	220	227
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	3	4	9	0.01%	27.0%	TAGTLFGEGFR	99.7%	78.7	25	74.9	4	0	0	1155.58	228	238
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	3	4	9	0.01%	27.0%	VRDIAIATR	99.5%	38.7	25	34.2	2	0	0	1014.61	328	336
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	3	3	5	0.00%	4.5%	STVLSLLLR	99.7%	63.1	25	25.6	2	0	0	1001.64	534	542
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	3	3	5	0.00%	4.5%	TVLVIAHR	99.3%	37	25	32.6	2	0	0	908.57	684	691
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	3	3	5	0.00%	4.5%	VTQDSLAQATQLAEER	99.7%	86.3	25	79.8	1	0	0	1759.88	342	357
ATP-binding cassette sub-family B member 7, mitochondrial	ABCB7	ABCB7_HUMAN	82.6	100.0%	2	2	6	0.01%	2.9%	AGAAFFNEVR	99.7%	53	25	39.6	2	0	0	1081.54	201	210
ATP-binding cassette sub-family B member 7, mitochondrial	ABCB7	ABCB7_HUMAN	82.6	100.0%	2	2	6	0.01%	2.9%	VAISLGFLGGAK	99.7%	55.1	25	52.5	4	0	0	1132.67	140	151
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	5	6	10	0.01%	9.1%	DQVIYPDGREDQK	99.6%	40	25	26.2	1	0	0	1562.74	521	533
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	5	6	10	0.01%	9.1%	FSMGFIDSIIAK	99.6%	40.5	25	33.2	3	0	0	1344.69	311	322
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	5	6	10	0.01%	9.1%	IANPDQLLTQDVEK	99.7%	98.5	25	98.4	3	0	0	1583.83	182	195
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	5	6	10	0.01%	9.1%	ITELMQVLK	99.7%	45.5	25	17.6	1	0	0	1090.62	391	399
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	5	6	10	0.01%	9.1%	VLGELWPLFGGR	99.7%	48.8	25	44.2	2	0	0	1343.75	485	496
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	7	13	0.01%	12.2%	ADIFMFDEPSSYLDVK	99.7%	64.2	25	64.2	3	0	0	1876.87	235	250
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	7	13	0.01%	12.2%	AIIKPQYVDQIPK	94.6%	22.4	25	22.4	0	1	0	1512.88	166	178
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	7	13	0.01%	12.2%	GSELQNYFTK	99.7%	55.4	25	47.4	2	0	0	1186.57	149	158
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	7	13	0.01%	12.2%	NVEDLSGGELQR	99.7%	57.5	25	48.4	2	0	0	1316.64	213	224
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	7	13	0.01%	12.2%	VAETANEEEVKK	99.7%	61.9	25	54	4	0	0	1346.68	333	344
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	7	13	0.01%	12.2%	VIVFDGVPSK	99.7%	46.5	25	35.6	1	0	0	1060.60	532	541
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	7	7	15	0.01%	9.0%	ADDPYAHLSK	99.7%	41.3	25	27.4	1	0	0	1116.53	246	255
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	7	7	15	0.01%	9.0%	AVSEEQQPALK	99.7%	67.3	25	58	3	0	0	1199.63	164	174
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	7	7	15	0.01%	9.0%	GAVIVVSHDAR	99.7%	54.2	25	38.1	3	0	0	1123.62	790	800
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	7	7	15	0.01%	9.0%	GFNLPYQDAR	99.7%	42.3	25	26.5	3	0	0	1180.57	714	723
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	7	7	15	0.01%	9.0%	LQGQLEQGDDTAAER	99.7%	82.4	25	80.2	2	0	0	1630.77	397	411
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	7	7	15	0.01%	9.0%	STLLLLLTGK	99.7%	52.9	25	52.9	2	0	0	1058.68	665	674
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	7	7	15	0.01%	9.0%	VVFAELACR	98.8%	34.8	25	8.99	1	0	0	1064.56	751	759
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	12	17	30	0.03%	21.2%	ETTEVDLLTK	99.7%	42.5	25	27.1	2	0	0	1148.60	49	58
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	12	17	30	0.03%	21.2%	ILHGLGFTPAMQR	98.3%	33.2	25	25.2	1	0	0	1456.77	211	223
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	12	17	30	0.03%	21.2%	IPPPVIMVQNVSFK	99.7%	79.1	25	75.8	2	2	0	1568.89	391	404
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	12	17	30	0.03%	21.2%	LAHEDAECEK	99.4%	37.9	25	36.7	1	0	0	1201.52	179	188
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	12	17	30	0.03%	21.2%	LEELDADKAEMR	99.7%	73.7	25	61.9	3	1	0	1419.68	196	207
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	12	17	30	0.03%	21.2%	LLTGELLPTDGMIR	99.7%	75.5	25	75.5	4	0	0	1544.84	442	455
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	12	17	30	0.03%	21.2%	LVDEEPQLTK	99.7%	43	25	27.8	2	0	0	1171.62	609	618
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	12	17	30	0.03%	21.2%	MMASGLTER	99.6%	40.2	25	34	4	0	0	995.46	366	374
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	12	17	30	0.03%	21.2%	SMLLSAIGK	99.3%	37.6	25	14.4	2	0	0	935.52	125	133
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	12	17	30	0.03%	21.2%	TRLELEENQMK	99.0%	35.6	25	30.1	2	0	0	1390.70	316	326
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	12	17	30	0.03%	21.2%	WPGDILAYK	99.6%	39.8	25	34.4	2	0	0	1062.56	594	602

ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	12	17	30	0.03%	21.2%	YYTGNYDQYVK	99.7%	62.6	25	53.8	2	0	0	1413.63	305	315
ATP-binding cassette sub-family F member 3	ABCF3	ABCF3_HUMAN	79.7	99.8%	2	2	3	0.00%	3.4%	ASVILAGLGFTPK	99.7%	42	25	41.7	2	0	0	1273.75	307	319
ATP-binding cassette sub-family F member 3	ABCF3	ABCF3_HUMAN	79.7	99.8%	2	2	3	0.00%	3.4%	GGVILVSHDER	98.0%	32.4	25	29.7	1	0	0	1181.63	658	668
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	AFDSGIIPMEFVNK	99.7%	86.6	25	75.5	8	0	0	1567.78	949	962
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	AIVWGMQTR	99.7%	53.5	25	37.5	3	0	0	1061.56	499	507
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	AKPAMPQDSVPSPR	99.7%	43.9	25	43.9	2	0	0	1480.76	470	483
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	AVQGMLDFDYVCSR	99.7%	104	25	104	4	0	0	1676.74	508	521
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	DEPSVAAMVYPFTGDHK	99.7%	89.4	25	89.4	4	0	0	1879.85	522	538
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	DGVYVLDLAAK	99.7%	76	25	68.8	5	0	0	1163.63	210	220
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	DLVSSLTSGLLTIGDR	99.7%	108	25	107	9	0	0	1646.90	919	934
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	EAYPEEAYIADLDAK	99.7%	90	25	90	4	0	0	1697.79	245	259
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	EGDYVLFHHEGGVDVGDVDAK	99.7%	53.1	25	53.1	0	2	0	2258.04	128	148
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	EILIPVFK	97.8%	32.1	25	17.5	1	0	0	958.60	547	554
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	FGGALDAAAK	99.7%	76.6	25	58.7	2	0	0	920.48	935	944
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	FICTTSAIQNR	99.7%	68.5	25	64.3	3	0	0	1310.65	18	28
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	GGPNYQEGLR	99.7%	41.8	25	3.48	1	0	0	1090.53	380	389
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	GQELIYAGMPITEVFK	99.7%	79.3	25	74.3	4	0	0	1795.93	849	864
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	GVTIIGPATVGGIKPGCFK	99.7%	62.6	25	62.6	2	1	0	1872.04	617	635
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	IGNTGGMLDNILASK	99.7%	99	25	91.6	6	0	0	1503.78	636	650
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	KPASFMTSICDER	99.7%	70	25	60.2	2	3	0	1541.71	836	848
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	LGLVGVNLTLDGVK	99.7%	72.7	25	71	5	0	0	1397.84	69	82
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	LGQEATVGK	99.7%	63	25	47.9	4	0	0	902.49	89	97
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	LIMGIGHR	98.7%	34.3	25	25.2	2	0	0	912.51	969	976
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	LLVGVDEK	99.7%	46.9	25	26.1	1	0	0	872.51	152	159
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	LNPEDIKK	97.5%	31.4	25	19.2	2	0	0	956.54	160	167
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	LYRPGSVAYVSR	99.7%	45.6	25	38.8	2	4	0	1367.74	651	662
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	MIVVLGEIGGTEEYK	99.7%	129	25	129	6	0	0	1637.85	712	726
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	RGGPNYQEGLR	99.7%	48.4	25	41	2	0	0	1246.63	379	389
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	SAYDSTMETMNYAQIR	99.7%	95.7	25	95.7	5	0	0	1880.82	577	592
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	SGGMSNELNNIISR	99.7%	80.8	25	71.8	7	0	0	1507.72	663	676
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	SINNPDMR	96.9%	30.5	25	18.7	2	0	0	946.44	979	986
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	SMGFIGHYLDQK	99.7%	53.3	25	45.4	4	0	0	1395.67	1066	1077
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	STTLFSR	99.1%	36	25	18.9	1	0	0	811.43	489	495
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	TASFSESR	99.4%	38.4	25	26.8	2	0	0	884.41	453	460
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	TIAIIAEGIPEALTR	99.7%	134	25	127	10	1	0	1567.91	593	607
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	TILSLMTR	99.7%	49.6	25	36.9	6	0	0	934.54	322	329
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	TTDGVYEGVAIGGDR	99.7%	101	25	88.7	2	0	0	1509.72	677	691
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	VDATADYICK	99.7%	59.9	25	59.9	4	0	0	1155.54	221	230
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	VTPDTDWAR	99.4%	37.8	25	35.1	3	0	0	1060.51	34	42
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	WGDIEFPPPFGR	99.7%	43.1	25	42.6	4	0	0	1417.69	233	244
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	38	54	146	0.14%	40.9%	YQDTPGVK	99.7%	43	25	32.2	1	0	0	907.45	704	711
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	9	9	17	0.02%	17.5%	AAAAADLANR	99.7%	57.4	25	53.2	1	0	0	943.50	453	462
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	9	9	17	0.02%	17.5%	DLIEFGMIPEFVGR	99.7%	47.9	25	41.4	1	0	0	1638.82	486	499
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	9	9	17	0.02%	17.5%	DVGGEGVQQGLLK	99.7%	89.3	25	87.6	2	0	0	1299.69	374	386
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	9	9	17	0.02%	17.5%	LLQDANYNVEK	99.7%	60.5	25	45.5	2	0	0	1306.66	339	349
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	9	9	17	0.02%	17.5%	SGESNTHQDIEEKDR	99.7%	47.6	25	47.6	0	3	0	1744.77	463	477
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	9	9	17	0.02%	17.5%	SIIKEPESAAEAVK	99.7%	54.9	25	33	2	0	0	1471.80	145	158
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	9	9	17	0.02%	17.5%	SNILLLGPTGSGK	99.7%	77.9	25	76.6	2	0	0	1256.72	287	299
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	9	9	17	0.02%	17.5%	TLLAQTLAK	99.5%	38.9	25	26.7	2	0	0	958.59	300	308
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	9	9	17	0.02%	17.5%	YLGFGTPSNLGK	99.7%	58.3	25	54.4	2	0	0	1253.65	438	449
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	AAECNIVVTQPR	99.7%	80.1	25	71.2	6	0	0	1357.69	435	446

ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	AAMEALVVEVTK	99.7%	92.3	25	82.8	12	0	0	1276.68	1105	1116
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	AENNSEVGASGYGVPGPTWDR	99.7%	88.4	25	88.4	4	0	0	2162.97	121	141
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	AIEPPPLDAVIEAEHTLR	99.7%	87.6	25	87.6	3	2	0	1971.05	820	837
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	DFVNYLVR	99.7%	58.6	25	46.4	10	0	0	1025.54	64	71
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	DINTDFLLVVLR	99.7%	91.5	25	82.6	9	0	0	1417.81	517	528
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	DVVQAYPEVR	99.7%	67.1	25	59.9	8	0	0	1175.61	529	538
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	ELDALDANDELTPLGR	99.7%	117	25	105	9	0	0	1741.86	838	853
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	ETPFELIEALLK	99.7%	52.6	25	50.5	1	0	0	1402.78	631	642
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	FESEILEAISQNSVVIIR	99.7%	76.6	25	76.6	1	0	0	2047.11	393	410
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	GANLKDYYSR	99.7%	65.1	25	56.2	4	0	0	1186.59	142	151
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	GISHVIVDEIHER	99.7%	62.5	25	62.5	2	2	0	1503.79	504	516
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	GMTLVTPLQLLLFASK	99.7%	96.3	25	96.3	15	0	0	1748.00	1058	1073
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	ISAVSVAER	99.7%	78.3	25	62.9	5	0	0	931.52	448	456
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	KILTTEGR	98.3%	33.2	25	16.5	1	0	0	917.54	1011	1018
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	KMTPSYEIR	99.7%	53.7	25	42.1	3	0	0	1124.58	16	24
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	KVFDPVPVGVTK	99.7%	77	25	75.3	6	0	0	1285.75	697	708
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	LAAQSCALSLVR	99.7%	81.8	25	75.9	9	0	0	1288.70	237	248
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	LAQFEPSQR	99.7%	53.8	25	48.8	7	0	0	1075.55	315	323
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	LETHMTPEMFR	99.7%	45.8	25	44.2	6	6	0	1391.64	785	795
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	LFTAHNNMTNYATVWASK	99.7%	37.2	25	35.2	0	2	0	2084.99	738	755
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	LGGIGQFLAK	99.7%	81.2	25	75.9	12	0	0	1003.59	810	819
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	LNMATLR	99.7%	60	25	42.3	4	0	0	818.46	945	951
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	LNQYFQK	99.7%	48.4	25	36.9	7	0	0	940.49	185	191
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	LQISHEAAACITGLR	99.7%	102	25	102	2	2	0	1639.86	1090	1104
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	LSMSQLNEK	99.7%	62.6	25	52.4	14	0	0	1049.53	622	630
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	MGGEEAEIR	99.7%	86.3	25	73.2	11	0	0	991.45	930	938
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	MTPSYEIR	98.8%	34.9	25	26	2	0	0	1012.48	17	24
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	NFLYAWCGK	99.7%	48.2	25	28.8	4	0	0	1158.54	6	14
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	QLYHLGVVEAYSGLTK	98.6%	33.9	25	32.7	1	0	0	1777.95	249	264
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	QPAIISQLDPVNER	99.7%	91.2	25	90.5	4	1	0	1579.84	1117	1130
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	RISAVSVAER	99.7%	56.5	25	43.2	8	0	0	1087.62	447	456
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	RLNMATLR	97.0%	30.7	25	17.6	2	0	0	974.56	944	951
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	SCGYSVR	94.9%	28.5	25	28.5	1	0	0	828.37	468	474
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	SFIAEMTIYIK	99.7%	61.8	25	53.3	2	0	0	1331.69	210	220
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	SSVNCPFSSQDMK	99.7%	67.3	25	67.3	4	0	0	1502.63	1025	1037
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	TPLHEIALSIK	99.7%	67.8	25	63	2	5	0	1221.72	796	806
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	TTQVPQFILDDFIQNDR	99.7%	67.9	25	60.9	7	0	0	2050.02	418	434
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	VFDPVPVGVTK	99.7%	51.9	25	50.5	8	0	0	1157.66	698	708
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	VQSDGQIVLVDDWIK	99.7%	85.9	25	81.5	4	0	0	1714.90	1075	1089
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	VRPGFCFHLCSR	99.7%	41	25	41	0	2	0	1535.74	768	779
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	YGDGPRPPK	99.7%	45.2	25	45.2	10	0	0	986.51	1155	1163
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	YPSPFFVFGEK	99.7%	48.3	25	40.5	9	0	0	1317.65	1038	1048
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	YQILPLHSQIPR	99.7%	46.5	25	42.1	4	4	0	1464.83	681	692
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	279	0.27%	38.7%	YTQVGPDHNR	99.7%	54.4	25	41.2	10	0	0	1186.56	200	209
ATP-dependent RNA helicase DDX1	DDX1	DDX1_HUMAN	82.4	100.0%	5	5	8	0.01%	6.1%	ALIVEPSR	99.0%	35.8	25	29.5	1	0	0	884.52	289	296
ATP-dependent RNA helicase DDX1	DDX1	DDX1_HUMAN	82.4	100.0%	5	5	8	0.01%	6.1%	ELLIIGGVAAR	99.7%	86	25	78.3	2	0	0	1111.68	320	330
ATP-dependent RNA helicase DDX1	DDX1	DDX1_HUMAN	82.4	100.0%	5	5	8	0.01%	6.1%	FLICTDVAAR	99.7%	50.7	25	44.2	2	0	0	1165.60	568	577
ATP-dependent RNA helicase DDX1	DDX1	DDX1_HUMAN	82.4	100.0%	5	5	8	0.01%	6.1%	LDDLVSTGK	96.6%	30.2	25	25.5	1	0	0	947.50	350	358
ATP-dependent RNA helicase DDX1	DDX1	DDX1_HUMAN	82.4	100.0%	5	5	8	0.01%	6.1%	LNLSQVR	99.7%	46.5	25	23.3	2	0	0	829.49	359	365
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	7	8	15	0.01%	11.9%	ELAMQTFGVLK	99.7%	79	25	71.9	3	0	0	1236.67	262	272
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	7	8	15	0.01%	11.9%	ISDIQSQLEK	99.7%	43.5	25	7.24	1	0	0	1160.62	558	567

ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	7	8	15	0.01%	11.9%	LGNGINIIVATPGR	99.7%	48.6	25	48.6	2	0	0	1394.81	298	311
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	7	8	15	0.01%	11.9%	MVNDAEPDTKK	99.7%	41.8	25	34.9	2	0	0	1247.59	117	127
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	7	8	15	0.01%	11.9%	QTMLFSATQTR	99.7%	74.9	25	56.2	2	0	0	1283.64	359	369
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	7	8	15	0.01%	11.9%	SIRPLLEGR	98.4%	33.3	25	25	2	0	0	1040.62	209	217
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	7	8	15	0.01%	11.9%	TLAFLIPAVELIVK	99.7%	56.1	25	56.1	3	0	0	1526.96	230	243
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	12	13	32	0.03%	28.7%	DPNSPLYSVK	99.7%	42.2	25	33.3	4	0	0	1119.57	82	91
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	12	13	32	0.03%	28.7%	GLAVNMVDSK	99.7%	60.4	25	54.7	2	0	0	1049.53	436	445
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	12	13	32	0.03%	28.7%	HSMNILNR	99.7%	49.7	25	37.1	2	0	0	984.50	446	453
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	12	13	32	0.03%	28.7%	IQEHFNK	98.6%	34	25	22	3	0	0	915.47	454	460
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	12	13	32	0.03%	28.7%	LDTDDLDEIEK	99.7%	79.8	25	72.2	3	0	0	1305.61	465	475
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	12	13	32	0.03%	28.7%	QYYVLCSSR	99.7%	49	25	46.1	1	0	0	1175.55	308	316
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	12	13	32	0.03%	28.7%	REEETLDTIK	99.7%	49.9	25	33.8	1	0	0	1233.63	298	307
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	12	13	32	0.03%	28.7%	SMTNLQIKEEK	99.7%	52.8	25	29.5	2	0	0	1336.68	19	29
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	12	13	32	0.03%	28.7%	SNLVDNTNQVEVLQR	99.7%	107	25	95.2	4	0	0	1728.89	67	81
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	12	13	32	0.03%	28.7%	TAAFVLAMLSR	99.7%	76.5	25	67.6	5	0	0	1179.66	144	154
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	12	13	32	0.03%	28.7%	VEPSDRYPQCLCLSPTYELALQTGK	99.7%	37.1	25	37.1	0	1	0	2925.41	155	179
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	12	13	32	0.03%	28.7%	VLVTTNVCAR	99.7%	58.4	25	53.3	4	0	0	1132.61	385	394
ATP-dependent RNA helicase DDX24	DDX24	DDX24_HUMAN	96.3	100.0%	4	4	4	0.00%	7.3%	DKLDILGAAETGSGK	99.7%	54.3	25	54.3	1	0	0	1474.78	229	243
ATP-dependent RNA helicase DDX24	DDX24	DDX24_HUMAN	96.3	100.0%	4	4	4	0.00%	7.3%	GLEPSQSTAAK	99.6%	39.9	25	28.8	1	0	0	1088.56	162	172
ATP-dependent RNA helicase DDX24	DDX24	DDX24_HUMAN	96.3	100.0%	4	4	4	0.00%	7.3%	RPEIVVATPGR	98.8%	34.7	25	22.9	1	0	0	1194.70	437	447
ATP-dependent RNA helicase DDX24	DDX24	DDX24_HUMAN	96.3	100.0%	4	4	4	0.00%	7.3%	TGGTVSDQALLFGDDDAGEGPSSLIR	99.7%	68.5	25	68.5	1	0	0	2578.23	321	346
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	8	9	21	0.02%	19.2%	DVQEIFR	98.4%	33.3	25	14.2	2	0	0	906.47	209	215
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	8	9	21	0.02%	19.2%	ELAFQISK	99.6%	40.2	25	31.8	2	0	0	935.52	123	130
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	8	9	21	0.02%	19.2%	GLAITFVSDENDAK	99.7%	73.5	25	64.9	2	0	0	1479.73	384	397
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	8	9	21	0.02%	19.2%	GSYVSIHSSGFR	99.7%	71.8	25	70.4	2	0	0	1296.63	36	47
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	8	9	21	0.02%	19.2%	ILNDVQDR	99.7%	55.1	25	44.5	2	0	0	972.51	398	405
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	8	9	21	0.02%	19.2%	ILVATNLFGR	99.7%	73.9	25	56.8	5	0	0	1103.66	339	348
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	8	9	21	0.02%	19.2%	NCPHVVVGTPGR	99.7%	78.5	25	64.9	2	2	0	1292.65	163	174
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	8	9	21	0.02%	19.2%	VSVFFGGLSIK	99.7%	58.8	25	52.5	2	0	0	1153.66	144	154
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	18	20	37	0.04%	33.2%	DKDAYSSFGSR	99.7%	65.8	25	57.1	2	0	0	1232.55	65	75
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	18	20	37	0.04%	33.2%	DLLDLLVEAK	99.7%	76.1	25	65.6	3	0	0	1128.65	555	564
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	18	20	37	0.04%	33.2%	DLMACAQTGSGK	99.7%	63.9	25	51.9	3	0	0	1238.55	219	230
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	18	20	37	0.04%	33.2%	DREEALHQFR	99.2%	29.5	25	29.5	1	1	0	1300.64	479	488
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	18	20	37	0.04%	33.2%	ELAVQIYEEAR	99.7%	57.1	25	52.1	2	0	0	1320.68	277	287
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	18	20	37	0.04%	33.2%	GCHLLVATPGR	99.7%	46.3	25	45.2	1	0	0	1180.63	316	326
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	18	20	37	0.04%	33.2%	IGLDFCK	99.7%	43.4	25	37.9	2	0	0	852.43	336	342
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	18	20	37	0.04%	33.2%	IVEQDTMPPK	99.7%	53.3	25	52.5	2	0	0	1173.58	364	373
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	18	20	37	0.04%	33.2%	LEQELFSGGNTGINFEK	99.7%	95.4	25	91.4	2	0	0	1882.92	146	162
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	18	20	37	0.04%	33.2%	MLDMGFEPQIR	99.7%	74.2	25	43.5	6	0	0	1352.63	352	362
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	18	20	37	0.04%	33.2%	QSSGASSSSFSSSR	99.7%	97.4	25	85.8	2	0	0	1361.59	604	617
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	18	20	37	0.04%	33.2%	QYPISLVLAPTR	99.7%	46.1	25	40.3	2	0	0	1357.78	265	276
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	18	20	37	0.04%	33.2%	SDYDGIGSR	99.7%	49.1	25	49.1	2	0	0	969.43	102	110
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	18	20	37	0.04%	33.2%	SFLLDLLNATGK	99.7%	98.9	25	84.7	2	0	0	1291.73	429	440
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	18	20	37	0.04%	33.2%	SPILVATAVAAR	99.7%	93.1	25	84.7	2	0	0	1168.70	492	503
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	18	20	37	0.04%	33.2%	VGNLGLATSFFNER	99.7%	64.4	25	64.4	2	0	0	1524.78	535	548
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	18	20	37	0.04%	33.2%	VGSTSENITQK	99.7%	67.9	25	52.6	2	0	0	1163.59	408	418
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	18	20	37	0.04%	33.2%	VRPCVVYGGADIGQQIR	99.7%	61.9	25	48.8	0	2	0	1887.99	295	311
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	18	20	37	0.04%	33.2%	YLVLDEADR	99.7%	58	25	39.8	2	0	0	1093.55	343	351
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	7	7	10	0.01%	14.7%	EGAFSNFPISEETIK	99.7%	67.1	25	67.1	6	0	0	1668.81	136	150
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	7	7	10	0.01%	14.7%	GVTYLFPIQVK	99.7%	79.1	25	60.7	2	0	0	1264.73	156	166
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	7	7	10	0.01%	14.7%	KLSSNAVSQITR	99.7%	46.4	25	30.4	1	0	0	1303.73	611	622

ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	7	7	10	0.01%	14.7%	NGIDILVGTPGR	99.7%	77.3	25	64	3	0	0	1211.67	258	269
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	7	7	10	0.01%	14.7%	QNAQCLHGDIAQSQR	99.5%	32	25	32	0	1	0	1725.81	413	427
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	7	7	10	0.01%	14.7%	SRYEQVDLVGK	99.6%	40.2	25	12.2	1	0	0	1293.68	343	353
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	7	7	10	0.01%	14.7%	TFSFAIPLIER	99.7%	58.8	25	56.9	2	0	0	1293.72	188	198
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	7	7	10	0.01%	14.7%	VGVPSTMDLVK	99.1%	36.2	25	33.3	1	0	0	1145.62	514	524
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	7	7	10	0.01%	14.7%	VLVATNVAAR	99.7%	84.2	25	78.9	2	0	0	1013.61	441	450
ATP-dependent RNA helicase DDX54	DDX54	DDX54_HUMAN	98.6	100.0%	3	3	4	0.00%	4.4%	FEEEELQR	97.7%	31.8	25	19.6	1	0	0	1079.50	552	559
ATP-dependent RNA helicase DDX54	DDX54	DDX54_HUMAN	98.6	100.0%	3	3	4	0.00%	4.4%	QEQQEGPVGPAPSRPALQEK	99.7%	42.2	25	42.2	0	1	0	2146.09	612	631
ATP-dependent RNA helicase DDX54	DDX54	DDX54_HUMAN	98.6	100.0%	3	3	4	0.00%	4.4%	VADNAQQQYVR	99.7%	60.3	25	52.2	2	0	0	1291.64	511	521
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	9	9	16	0.02%	9.1%	AICSGFFR	99.4%	38.2	25	35.7	2	0	0	957.46	1106	1113
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	9	9	16	0.02%	9.1%	EEFPDFDEETGILPK	99.7%	43	25	43	2	0	0	1765.82	414	428
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	9	9	16	0.02%	9.1%	FEDCTSPETVIK	99.7%	48.9	25	47.4	2	0	0	1425.66	648	659
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	9	9	16	0.02%	9.1%	FSQYFYEAPIFTIPGR	99.5%	38.7	25	38.7	2	0	0	1935.96	725	740
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	9	9	16	0.02%	9.1%	IFDPAPPGSR	99.7%	47.5	25	41.6	2	0	0	1056.55	824	833
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	9	9	16	0.02%	9.1%	LIVTSATLDAVK	99.7%	79.1	25	75.4	2	0	0	1230.73	713	724
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	9	9	16	0.02%	9.1%	TQMSILEQR	99.2%	36.9	25	18.7	1	0	0	1105.57	554	562
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	9	9	16	0.02%	9.1%	TYPVEILYTK	97.8%	32	25	31.1	1	0	0	1226.67	741	750
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	9	9	16	0.02%	9.1%	VANVADVVSK	99.7%	57.9	25	52.7	2	0	0	1001.56	306	315
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	9	9	16	0.02%	9.1%	YMTDGMLLR	99.7%	52.5	25	47.2	1	0	0	1099.53	660	668
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L1_HUMAN	86.5	99.9%	2	2	3	0.00%	3.0%	LSPETQSAIEQEIR	99.7%	51.2	25	34.3	2	0	0	1600.82	709	722
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L1_HUMAN	86.5	99.9%	2	2	3	0.00%	3.0%	TGFAEGFLK	99.7%	43.3	25	40.3	1	0	0	969.50	270	278
Basic leucine zipper and W2 domain-containing protein 1	BZW1	BZW1_HUMAN	48.0	100.0%	4	4	7	0.01%	8.4%	AEVLSEEPILK	99.7%	69.4	25	58.5	2	0	0	1227.68	369	379
Basic leucine zipper and W2 domain-containing protein 1	BZW1	BZW1_HUMAN	48.0	100.0%	4	4	7	0.01%	8.4%	ELSEYVR	97.7%	31.8	25	27.1	1	0	0	895.45	240	246
Basic leucine zipper and W2 domain-containing protein 1	BZW1	BZW1_HUMAN	48.0	100.0%	4	4	7	0.01%	8.4%	GFEDEVKK	99.4%	38.3	25	28.5	2	0	0	951.48	127	134
Basic leucine zipper and W2 domain-containing protein 1	BZW1	BZW1_HUMAN	48.0	100.0%	4	4	7	0.01%	8.4%	LMELFPANK	99.7%	60	25	48.3	2	0	0	1062.57	215	223
Basic leucine zipper and W2 domain-containing protein 2	BZW2	BZW2_HUMAN	48.2	99.8%	2	2	3	0.00%	4.5%	EGIAASFAVK	98.5%	33.9	25	19.6	1	0	0	992.54	180	189
Basic leucine zipper and W2 domain-containing protein 2	BZW2	BZW2_HUMAN	48.2	99.8%	2	2	3	0.00%	4.5%	LLELFPVNR	99.7%	45.7	25	37.8	2	0	0	1100.65	216	224
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	7	7	16	0.02%	9.0%	ETGYVVERPSTTK	99.7%	43.2	25	38.8	1	0	0	1466.75	463	475
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	7	7	16	0.02%	9.0%	LLASTLVHSVK	99.7%	60.3	25	50.6	4	0	0	1167.71	570	580
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	7	7	16	0.02%	9.0%	MAPVPLDDSNRPASLTK	98.9%	35.1	25	35.1	1	0	0	1827.93	551	567
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	7	7	16	0.02%	9.0%	NTEEEGLKYK	99.4%	38.3	25	23.1	3	0	0	1210.60	430	439
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	7	7	16	0.02%	9.0%	SAAMTLNER	97.0%	30.7	25	18.4	2	0	0	1008.48	623	631
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	7	7	16	0.02%	9.0%	SSFYPDGGDQETAK	99.7%	71.6	25	59.2	2	0	0	1501.64	319	332
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	7	7	16	0.02%	9.0%	TIAPQNAPR	99.7%	54.3	25	42.2	3	0	0	967.53	304	312
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	8	8	16	0.02%	14.6%	AGATLDLLVENMGR	99.7%	66.5	25	57.8	2	0	0	1459.76	469	482
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	8	8	16	0.02%	14.6%	AYVAVDGIPQGVLER	99.7%	76	25	76	2	0	0	1586.85	443	457
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	8	8	16	0.02%	14.6%	MFEIDYSR	99.7%	42.1	25	42.1	2	0	0	1060.48	31	38
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	8	8	16	0.02%	14.6%	SLYPLTFIQVK	99.7%	51.6	25	51.6	2	0	0	1308.76	400	410
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	8	8	16	0.02%	14.6%	TEAVASSLYDILAR	99.7%	92.4	25	68.7	2	0	0	1508.80	286	299
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	8	8	16	0.02%	14.6%	TVGAALDILCPSGPIK	99.7%	81.3	25	81.3	2	0	0	1611.88	384	399
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	8	8	16	0.02%	14.6%	VNYGAYINDFK	99.7%	59.6	25	50.6	2	0	0	1303.63	483	493
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	8	8	16	0.02%	14.6%	YISGSIHYSR	99.7%	60.7	25	60.7	2	0	0	1182.59	50	59
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	6	6	11	0.01%	15.5%	AVAQAGTVGTLLIVK	99.7%	81.7	25	72.5	2	0	0	1440.88	95	109
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	6	6	11	0.01%	15.5%	LEQPDPGAVAAAAILR	99.7%	66.6	25	62.2	2	0	0	1591.88	552	567
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	6	6	11	0.01%	15.5%	LSVLLLEK	99.7%	43.6	25	43.6	2	0	0	914.59	435	442
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	6	6	11	0.01%	15.5%	SPGADLLQVLTK	99.7%	81.5	25	75.9	2	0	0	1241.71	511	522
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	6	6	11	0.01%	15.5%	VAGALAEAGVGLEEIAK	99.7%	90.7	25	81.6	1	0	0	1597.88	163	179
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	6	6	11	0.01%	15.5%	VAPAEPQEAPDSTAAGGSASK	99.7%	83.4	25	83.4	2	0	0	1940.92	352	372
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	AALLNQHYQVNFK	99.7%	41.9	25	41.9	2	0	0	1545.82	217	229
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	AIQGGTSHHLGQNFSK	98.6%	27.4	25	26.4	0	1	0	1681.84	1235	1250
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	AYVDDTPAEQMK	99.7%	70.7	25	63.5	3	0	0	1383.61	289	300

Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	DQDLEPGAPSMGAK	99.7%	70.4	25	49	4	0	0	1431.64	1464	1477
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	DQVDIAVQELLQLK	99.7%	97.8	25	79.3	4	0	0	1611.90	926	939
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	EYIPGQPPLSQSSDSSPTR	99.7%	86.8	25	82.9	4	0	0	2045.98	871	889
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	FVELPGAEMGK	99.7%	47.6	25	39.4	2	0	0	1177.59	187	197
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	GDIIQLQR	99.7%	53.5	25	28.2	2	0	0	942.54	667	674
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	GNAAWQEQLK	99.7%	46	25	33.2	2	0	0	1144.57	130	139
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	GSQFGQSCCLR	99.7%	47.3	25	47.3	3	0	0	1299.56	329	339
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	INEAVECLLSLK	99.7%	84.7	25	70.2	6	0	0	1388.75	850	861
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	KPYIWEYSR	99.6%	40.2	25	29.3	2	0	0	1241.63	417	425
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	KVIDPVAPR	98.4%	33.5	25	22.4	2	0	0	994.60	498	506
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	LGVENCYFPMFVSQSALEK	98.4%	33.5	25	33.5	3	0	0	2235.05	1071	1089
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	LLSVNIR	95.8%	29.2	25	14.6	1	0	0	814.51	1334	1340
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	LNLNNTVLSK	99.7%	63.5	25	50.3	4	0	0	1115.64	426	435
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	LNQWCNVVR	99.7%	56.5	25	45.1	2	0	0	1188.59	1144	1152
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	LQAILEDIQVTLFTR	99.7%	44.1	25	44.1	1	0	0	1760.00	1401	1415
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	LTVAENEAETK	99.7%	79.8	25	79.2	6	0	0	1204.61	1390	1400
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	NPEVGLKPVWYSPK	99.7%	50.8	25	48.7	2	0	0	1613.87	536	549
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	NQGGGLSSSGAGEGQGPK	99.7%	101	25	101	5	0	0	1587.74	992	1009
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	NSEPAGLETPEAK	99.7%	65.4	25	51.7	4	0	0	1342.65	890	902
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	SCQFVAVR	99.7%	48.9	25	40.8	3	0	0	966.48	1376	1383
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	SLYDEVAAQGEVVR	99.7%	107	25	105	4	0	0	1535.77	825	838
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	TELAEPIAIRPTSETVMYPAYAK	99.7%	38.1	25	37.7	0	1	0	2551.31	1110	1132
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	TGQEYKPGNPPAEIGQNISSNSSASILESK	99.7%	60.7	25	60.7	0	2	0	3103.52	795	824
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	VASQGEVVR	99.7%	49	25	36.6	4	0	0	944.52	908	916
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	VAVQGDVVR	99.7%	54.1	25	41.1	4	0	0	942.54	757	765
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	VIDPVAPR	99.7%	51	25	51	4	0	0	866.51	499	506
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	30	33	88	0.08%	25.4%	WFGFLEAQQAFQSVGTK	99.7%	64	25	61.1	1	0	0	1943.97	150	166
Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	MTHFD2	MTDC_HUMAN	37.9	99.8%	2	2	4	0.00%	6.6%	EGAAVIDVGINR	99.7%	75.5	25	58.8	2	0	0	1213.65	267	278
Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	MTHFD2	MTDC_HUMAN	37.9	99.8%	2	2	4	0.00%	6.6%	LVGDVDFEGVR	99.7%	56.4	25	46.3	2	0	0	1205.62	289	299
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	17	0.02%	11.6%	ANSSVVSVNCK	99.7%	60.7	25	60	2	0	0	1164.57	587	597
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	17	0.02%	11.6%	EIPVESIEEVSK	99.7%	50.1	25	41.7	2	0	0	1358.71	258	269
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	17	0.02%	11.6%	ESQATLEER	99.7%	47.4	25	36.8	2	0	0	1062.51	5	13
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	17	0.02%	11.6%	GGLAGEFQR	99.4%	37.9	25	30.2	2	0	0	934.47	683	691
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	17	0.02%	11.6%	LGCFEIAK	99.6%	40	25	31.2	2	0	0	937.48	894	901
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	17	0.02%	11.6%	LLPGIEVLWTGPK	99.7%	42.9	25	42.9	1	0	0	1422.84	241	253
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	17	0.02%	11.6%	LLPIDGANDLFFQPPPLTPTSK	99.7%	69	25	69	2	0	0	2381.28	692	713
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	17	0.02%	11.6%	SMMACLLSSLK	99.3%	37.4	25	29.9	2	0	0	1240.61	859	869
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	9	9	17	0.02%	11.6%	WELNTYLYAPK	99.7%	85.9	25	84.7	2	0	0	1397.71	88	98
Bifunctional purine biosynthesis protein PURH	ATIC	PUR9_HUMAN	64.6	100.0%	2	2	3	0.00%	3.4%	SLFSNVVTK	99.6%	40.4	25	34.1	2	0	0	994.56	398	406
Bifunctional purine biosynthesis protein PURH	ATIC	PUR9_HUMAN	64.6	100.0%	2	2	3	0.00%	3.4%	YTQSNSVCYAK	99.7%	46	25	46	1	0	0	1320.59	427	437
Biliverdin reductase A	BLVRA	BIEA_HUMAN	33.4	99.8%	2	2	3	0.00%	8.1%	FGVVVVGVGR	99.7%	51.2	25	48.9	1	0	0	988.59	9	18
Biliverdin reductase A	BLVRA	BIEA_HUMAN	33.4	99.8%	2	2	3	0.00%	8.1%	SGSLENVPNVGVNK	99.7%	65.3	25	64.9	2	0	0	1413.73	235	248
BolA-like protein 2	BOLA2	BOLA2_HUMAN	10.1	100.0%	2	3	5	0.00%	29.1%	DLEAEHVEVEDTTLNR	99.7%	107	25	107	2	2	0	1869.88	15	30
BolA-like protein 2	BOLA2	BOLA2_HUMAN	10.1	100.0%	2	3	5	0.00%	29.1%	FEGKPLLQR	98.7%	34.4	25	29.9	1	0	0	1087.63	44	52
Bystin	BYSL	BYST_HUMAN	49.6	100.0%	4	4	6	0.01%	9.6%	EAIIVGSIITK	99.7%	54.4	25	48.7	2	0	0	1143.70	304	314
Bystin	BYSL	BYST_HUMAN	49.6	100.0%	4	4	6	0.01%	9.6%	FYNLVLLPR	99.7%	45.9	25	25.3	2	0	0	1134.67	249	257
Bystin	BYSL	BYST_HUMAN	49.6	100.0%	4	4	6	0.01%	9.6%	GTGEAEEEYVGPR	99.7%	70.4	25	52.9	1	0	0	1393.62	41	53
Bystin	BYSL	BYST_HUMAN	49.6	100.0%	4	4	6	0.01%	9.6%	VRDDVAEYK	98.1%	32.6	25	24	1	0	0	1094.55	258	266
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	AAEEIGIK	99.7%	53	25	30	2	0	0	830.46	59	66
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	AAQAPSSFQLLYDLK	99.7%	96.5	25	94.8	3	0	0	1651.87	805	819
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	APAEILNGK	99.7%	42.7	25	36.8	2	0	0	912.52	2	10

C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	AYIQENLELVEK	99.7%	51.3	25	43.9	2	0	0	1448.76	722	733
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	DDSNLYINVK	99.7%	65.9	25	58.8	2	0	0	1180.58	47	56
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	EIGLLSEEVELYGETK	99.7%	102	25	102	4	0	0	1808.92	337	352
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	EISAQIR	99.4%	38	25	0.15	2	0	0	816.46	11	17
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	EQVPGFTPR	98.7%	34.4	25	28.2	1	0	0	1030.53	29	37
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	ETGVPIAGR	99.7%	56.3	25	46.1	2	0	0	899.49	158	166
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	FSDIQIR	99.7%	47	25	13.1	3	0	0	878.47	489	495
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	GALALAQAVQR	99.7%	74.4	25	69.3	4	0	0	1097.64	794	804
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	GCLELIK	96.8%	30.4	25	13.4	2	0	0	832.46	151	157
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	GDLNDCFIPCTPK	99.7%	41.8	25	41.8	2	0	0	1536.68	138	150
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	GVPTGFILPIR	99.7%	72.1	25	66.5	5	0	0	1169.70	879	889
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	IFHELTQTDK	99.7%	61	25	45.1	2	2	0	1231.63	464	473
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	ITIGQAPTEK	97.2%	31	25	28.3	1	0	0	1057.59	544	553
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	IYGADDIELLPEAQHK	99.7%	89.1	25	81.7	2	2	0	1811.92	833	848
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	KGEPVSAEDLGVSGALTVLMK	99.7%	33.7	25	33.2	0	1	0	2117.12	596	616
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	KITIGQAPTEK	99.7%	60.5	25	43.6	3	0	0	1185.68	543	553
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	KVVGDVAYDEAK	99.7%	78.8	25	73.6	2	0	0	1293.67	251	262
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	LAILQVGNR	99.7%	75.9	25	67.1	2	0	0	983.60	38	46
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	LDIDPETITWQR	99.7%	63.5	25	58.7	2	0	0	1486.75	521	532
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	LVGPEGFVVTEAGFGADIGMEK	99.7%	66.3	25	60.9	2	2	0	2239.10	658	679
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	MFGIPVVVAVNAFK	99.7%	73.3	25	63.1	7	0	0	1491.84	747	760
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	MHGGGPTVTAGLPLPK	99.7%	56.4	25	56.3	1	1	0	1532.83	706	721
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	QGFGNLPICMAK	96.1%	29.6	25	29.1	1	0	0	1335.66	855	866
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	QPSQGPTFGIK	99.2%	36.6	25	31	2	0	0	1159.61	411	421
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	TDPTTLTDEEINR	99.7%	75.2	25	65.2	2	0	0	1504.71	505	517
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	TDTESELDLISR	99.7%	94.7	25	89.2	2	0	0	1378.67	761	772
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	THLSLSHNPEQK	99.7%	70.4	25	65.2	2	2	0	1390.71	867	878
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	TPVPSDIDISR	99.7%	65.1	25	61	2	0	0	1199.63	314	324
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	VLLSALER	99.7%	59.1	25	42.5	4	0	0	900.55	355	362
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	VVGDVAYDEAK	99.7%	70.4	25	67	2	0	0	1165.57	252	262
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	VVGDVAYDEAKER	99.7%	69.1	25	65.9	2	0	0	1450.72	252	264
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	WMIQYNNLNLK	99.7%	54.7	25	40.3	3	0	0	1436.74	303	313
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	YSGLCPHVVVLVATVR	99.7%	59.7	25	59.7	0	2	0	1769.97	687	702
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	96	0.09%	44.0%	YVVVTGITPTPLGEGK	99.7%	114	25	114	2	0	0	1630.91	371	386
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	AAFALGGLGSGFASNR	99.7%	136	25	133	2	0	0	1495.77	556	571
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	ASDPGLPAEEPK	99.7%	44.8	25	43.6	2	0	0	1210.60	1858	1869
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	ATGYPLAYVAAK	99.7%	52.4	25	51.5	2	0	0	1224.66	697	708
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	EATAGNPGGQTVR	99.7%	57.8	25	56.7	2	0	0	1257.62	359	371
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	ELSDLESAR	99.7%	45.3	25	39.7	2	0	0	1019.50	1067	1075
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	FLSSAAAVSK	99.4%	38.3	25	25.4	2	0	0	980.54	1110	1119
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	GEVAYIDGQVLVPPGYGQDVR	98.3%	33.2	25	29.6	1	0	0	2232.13	1790	1810
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	GEVRPELGSR	99.7%	43	25	33.6	2	0	0	1099.59	1658	1667
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	GHNQPCLLVGSGR	98.9%	35.2	25	29.8	1	0	0	1394.70	275	287
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	HPQPGAVELAAK	97.8%	32	25	18.1	1	0	0	1217.66	2025	2036
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	IIAHAQLLEQHR	98.9%	28.5	25	27.3	0	2	0	1428.81	843	854
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	ILALDCGLK	99.6%	40.9	25	20.5	2	0	0	1002.57	178	186
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	LALGIPLPELR	99.7%	44.9	25	44.9	1	0	0	1191.75	709	719
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	LFVEALGQIGPAPPLK	99.7%	79.7	25	79.7	2	0	0	1649.96	1435	1450
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	LGGAVLSFSEATSSVQK	99.7%	115	25	115	2	0	0	1680.88	1987	2003
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	LGYPVLVR	99.7%	43	25	36	2	0	0	916.56	548	555
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	LLDTIGISQPQWR	99.7%	62.8	25	62.8	2	0	0	1526.83	1054	1066

CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	LYLNETFSELR	99.7%	48.8	25	40	1	0	0	1384.71	1557	1567
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	MAEIGEHVAPSEAANSLEQAQAAAER	99.7%	40.5	25	40.5	0	1	0	2680.26	522	547
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	MALLATVLGRF	99.7%	56.7	25	52	2	0	0	1207.69	2215	2225
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	NILLTIGSYK	99.7%	43.8	25	34.3	2	0	0	1121.66	1314	1323
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	NKSELLPTVR	98.7%	34.4	25	28.9	1	0	0	1156.67	1324	1333
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	NSVTGGTAAFEPSVDYCVVK	99.7%	105	25	104	2	0	0	2100.99	720	739
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	QELGICPAVK	99.7%	41.1	25	18	1	0	0	1114.59	892	901
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	SELLPTVR	96.7%	30.3	25	30.3	1	0	0	914.53	1326	1333
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	SFEEAFQK	98.9%	35.3	25	23.3	2	0	0	985.46	771	778
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	SILEQLAEK	99.7%	51.7	25	39	2	0	0	1030.58	1379	1387
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	SVGEVMGIGR	99.7%	58.5	25	50.2	4	0	0	1020.51	761	770
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	SVHICHVAR	98.7%	34.4	25	31.1	2	0	0	1078.56	1609	1617
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	TLGVDLVALATR	99.7%	68.2	25	54.7	2	0	0	1228.73	1229	1240
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	TPHVLVLGSGVYR	99.7%	42.4	25	41.2	1	2	0	1397.79	932	944
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	TSSSFAAAMAR	99.7%	86.9	25	71.5	4	0	0	1099.52	1976	1986
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	VFNTGGAPR	99.7%	52.6	25	38.3	2	0	0	918.48	169	177
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	VHVDCMTSQK	99.2%	36.7	25	29.8	2	0	0	1204.55	1451	1460
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	VIMGEEVEPVGLMTGSGVVGVK	99.7%	95.8	25	95.8	4	0	0	2187.14	1241	1262
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	VLGTPVETIELTEDR	99.0%	35.5	25	32	1	0	0	1671.88	501	515
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	VLGTSPEAIDSAENR	99.7%	116	25	114	2	0	0	1558.77	1034	1048
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	VNEISVEVDSDPR	99.7%	97.2	25	85.3	2	0	0	1458.71	2188	2200
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	75	0.07%	21.4%	VPQFSFSR	99.7%	46.1	25	38.6	2	0	0	967.50	1263	1270
Calcium uniporter protein, mitochondrial	MCU	MCU_HUMAN	39.9	99.8%	2	2	2	0.00%	6.6%	LEDLKEQLAPLEK	99.7%	52.2	25	45.3	1	0	0	1525.85	207	219
Calcium uniporter protein, mitochondrial	MCU	MCU_HUMAN	39.9	99.8%	2	2	2	0.00%	6.6%	VAIYSPDGVR	96.7%	30.2	25	23	1	0	0	1076.57	125	134
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	AGQTTYSGVIDCFR	99.7%	89.1	25	89.1	2	0	0	1574.73	552	565
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	AGQTTYSGVIDCFRK	99.7%	78.9	25	78.9	2	0	0	1702.82	552	566
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	DLGIFGLYK	98.9%	35.2	25	35.2	1	0	0	1025.57	474	482
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	GLIPQLIGVAPEK	99.7%	69.7	25	0	3	0	0	1334.80	391	403
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	IVQLLAGVADQTK	99.7%	63.7	25	57.6	2	0	0	1355.79	56	68
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	KIYSTLAGTR	99.7%	61.3	25	50.3	2	0	0	1109.63	234	243
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	LATATFAGIENK	99.7%	73.3	25	60.4	2	0	0	1235.66	641	652
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	LQVAGEITTGPR	99.7%	59	25	40.2	2	0	0	1241.69	454	465
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	LTVNDFVR	99.7%	55.6	25	52	2	0	0	963.53	407	414
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	NIFLQYASTEVDGER	99.7%	89.3	25	89.3	2	0	0	1741.84	18	32
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	VSALNVLR	99.7%	44	25	24.5	2	0	0	871.54	466	473
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	YEGFFGLYR	99.7%	58.8	25	56.6	2	0	0	1151.55	382	390
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	22	23	44	0.04%	40.1%	AGQTTYSGVIDCFR	99.7%	89.1	25	89.1	2	0	0	1574.73	554	567
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	22	23	44	0.04%	40.1%	AGQTTYSGVIDCFRK	99.7%	78.9	25	78.9	2	0	0	1702.82	554	568
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	22	23	44	0.04%	40.1%	ASGDSARPVLLQVAESAYR	99.7%	46.2	25	46.2	0	2	0	1990.04	313	331
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	22	23	44	0.04%	40.1%	DIPFSAIYFPCYAHVK	99.7%	68.1	25	18.3	2	0	0	1927.94	493	508
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	22	23	44	0.04%	40.1%	DLGFFGIYK	99.7%	50.7	25	49.6	2	0	0	1059.55	476	484
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	22	23	44	0.04%	40.1%	FGLGSVAGAVGATAVYPIDLVK	99.7%	87.2	25	87.2	2	0	0	2105.16	332	353
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	22	23	44	0.04%	40.1%	GLLPQLLGVAPEK	99.7%	69.7	25	0	3	0	0	1334.80	393	405
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	22	23	44	0.04%	40.1%	IAPLEEGTLPFNLAEAQR	99.7%	76.3	25	76.3	2	2	0	1969.04	293	310
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	22	23	44	0.04%	40.1%	ILREEGPK	98.8%	34.6	25	22.8	2	0	0	941.54	569	576
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	22	23	44	0.04%	40.1%	INLPAPNPDHVGGYK	99.7%	76.8	25	69	1	0	0	1591.82	627	641
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	22	23	44	0.04%	40.1%	KIYSTLAGTR	99.7%	61.3	25	50.3	2	0	0	1109.63	235	244
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	22	23	44	0.04%	40.1%	LAVATFAGIENK	99.7%	93.2	25	83.6	2	0	0	1233.68	642	653
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	22	23	44	0.04%	40.1%	LQVAGEITTGPR	99.7%	59	25	40.2	2	0	0	1241.69	456	467
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	22	23	44	0.04%	40.1%	LTVNDFVR	99.7%	55.6	25	52	2	0	0	963.53	409	416
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	22	23	44	0.04%	40.1%	MTLADIER	99.7%	46.4	25	29.3	2	0	0	948.48	285	292

Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	22	23	44	0.04%	40.1%	NGEFFMSPNDFVTR	99.7%	59.9	25	59.9	2	0	0	1676.74	30	43
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	22	23	44	0.04%	40.1%	SSPQFGVTLLTYELLQR	99.7%	71.5	25	71.5	1	0	0	1952.05	589	605
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	22	23	44	0.04%	40.1%	STGSFVGELMYK	99.7%	50.3	25	44.5	2	0	0	1318.63	361	372
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	22	23	44	0.04%	40.1%	TVELLSGVVDQTK	99.7%	110	25	99.3	2	0	0	1388.76	57	69
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	22	23	44	0.04%	40.1%	VSALSVVR	99.7%	54.8	25	46.5	2	0	0	830.51	468	475
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	22	23	44	0.04%	40.1%	YEGFFGLYR	99.7%	58.8	25	56.6	2	0	0	1151.55	384	392
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	22	23	44	0.04%	40.1%	YLNIFGESQPNPK	99.7%	75.7	25	75.7	1	0	0	1506.76	44	56
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	12	12	22	0.02%	29.4%	FISGSMAGATAQTFIYPMEVMK	99.7%	64.9	25	62.8	2	0	0	2380.14	292	313
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	12	12	22	0.02%	29.4%	FWAYEQYKK	98.8%	34.6	25	31.5	2	0	0	1262.62	269	277
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	12	12	22	0.02%	29.4%	HEGLGAFYK	99.5%	38.8	25	38.8	2	0	0	1021.51	337	345
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	12	12	22	0.02%	29.4%	IMMQVHGSK	97.9%	32.3	25	32.3	1	0	0	1030.52	220	228
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	12	12	22	0.02%	29.4%	MNIFGGFR	99.7%	45.1	25	35.7	2	0	0	941.47	232	239
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	12	12	22	0.02%	29.4%	NGDGVVDIGELQEGLR	99.7%	91.3	25	85.5	2	0	0	1670.83	34	49
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	12	12	22	0.02%	29.4%	NLGIPLGQDAEEK	99.7%	49.8	25	48.8	2	0	0	1383.71	50	62
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	12	12	22	0.02%	29.4%	QLLAGGIAGAVSR	99.7%	110	25	101	2	0	0	1212.71	197	209
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	12	12	22	0.02%	29.4%	SDKMNIFGGFR	97.5%	31.5	25	31.5	1	0	0	1287.62	229	239
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	12	12	22	0.02%	29.4%	TGQYSGIYDCAK	99.7%	66.4	25	66.4	2	0	0	1362.60	321	332
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	12	12	22	0.02%	29.4%	VLPAVGISYVVYENMK	99.7%	58.1	25	58.1	2	0	0	1781.95	454	469
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	12	12	22	0.02%	29.4%	YETLFQALDR	99.7%	52.3	25	42.6	2	0	0	1255.63	24	33
Calmodulin-like protein 5	CALML5	CALL5_HUMAN	15.9	99.8%	2	2	2	0.00%	21.2%	AFSAVDTDGNGTINAQELGAALK	99.7%	91.4	25	86.3	1	0	0	2263.12	16	38
Calmodulin-like protein 5	CALML5	CALL5_HUMAN	15.9	99.8%	2	2	2	0.00%	21.2%	NLSEAQLR	99.6%	40.8	25	26.4	1	0	0	930.50	43	50
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	4	4	5	0.00%	3.5%	APAEEEVGPR	99.7%	56.2	25	51.6	1	0	0	1054.52	964	973
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	4	4	5	0.00%	3.5%	AVASSPAATNSEVK	99.7%	64.1	25	59.5	2	0	0	1331.68	550	563
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	4	4	5	0.00%	3.5%	SLDQYDFSR	99.5%	39	25	38.3	1	0	0	1130.51	23	31
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	4	4	5	0.00%	3.5%	SPGPGPSQSPR	99.2%	36.8	25	33.2	1	0	0	1066.53	769	779
Calpain-2 catalytic subunit	CAPN2	CAN2_HUMAN	80.0	100.0%	3	3	5	0.00%	4.3%	MPCQLHQVIVAR	99.3%	30.4	25	22.1	0	1	0	1451.76	638	649
Calpain-2 catalytic subunit	CAPN2	CAN2_HUMAN	80.0	100.0%	3	3	5	0.00%	4.3%	SDGFSIETCK	98.7%	34.2	25	34.2	2	0	0	1143.50	569	578
Calpain-2 catalytic subunit	CAPN2	CAN2_HUMAN	80.0	100.0%	3	3	5	0.00%	4.3%	SDTFINLR	99.7%	55.1	25	19.7	2	0	0	965.51	462	469
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	8	8	11	0.01%	23.1%	AKEDFLK	98.8%	34.7	25	15.3	1	0	0	850.47	23	29
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	8	8	11	0.01%	23.1%	ATEQYYAMK	96.9%	30.6	25	23.6	1	0	0	1120.50	65	73
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	8	8	11	0.01%	23.1%	FSEPHAR	95.5%	29	25	26	1	0	0	843.41	139	145
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	8	8	11	0.01%	23.1%	ILQAVNFPFLVR	99.7%	65.2	25	65.2	2	0	0	1416.84	95	106
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	8	8	11	0.01%	23.1%	KVEAPFIPK	99.6%	40.2	25	32.2	1	0	0	1028.61	310	318
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	8	8	11	0.01%	23.1%	NLLQVDLTK	97.9%	32.3	25	20.7	2	0	0	1043.61	272	280
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	8	8	11	0.01%	23.1%	TLGTGSFGR	99.7%	44.9	25	39.3	2	0	0	895.46	49	57
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	8	8	11	0.01%	23.1%	TWTLCGTPEYLAPEIILSK	99.7%	49.5	25	49.5	1	0	0	2192.13	196	214
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	6	7	15	0.01%	36.3%	GKPLALVEEIR	99.7%	50.5	25	50	2	2	0	1224.73	149	159
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	6	7	15	0.01%	36.3%	HVFLTGPPGVGK	99.7%	64	25	64	2	0	0	1208.68	4	15
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	6	7	15	0.01%	36.3%	IGFDVVTLSGTR	99.7%	79.7	25	73.9	2	0	0	1264.69	48	59
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	6	7	15	0.01%	36.3%	QTLSTPGTIILGTIPVPK	99.7%	73.8	25	73.8	2	0	0	1836.08	131	148
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	6	7	15	0.01%	36.3%	RIGFDVVTLSGTR	99.3%	37.3	25	35.8	2	0	0	1420.79	47	59
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	6	7	15	0.01%	36.3%	SSGVPVDGFYTEEVR	99.7%	97.2	25	90.2	3	0	0	1641.78	28	42
Carbonyl reductase [NADPH] 1	CBR1	CBR1_HUMAN	30.4	99.8%	2	2	3	0.00%	11.9%	EYGGLDVLVNNAGIAFK	99.7%	91.8	25	91.2	2	0	0	1779.93	80	96
Carbonyl reductase [NADPH] 1	CBR1	CBR1_HUMAN	30.4	99.8%	2	2	3	0.00%	11.9%	GQAAVQQLQAEGLSPR	99.7%	90.9	25	85.8	1	0	0	1652.87	43	58
Carboxymethylenebutenolidase homolog	CMBL	CMBL_HUMAN	28.0	100.0%	4	4	5	0.00%	14.3%	AGVSVYGIVK	99.7%	49.8	25	44.1	2	0	0	992.58	150	159
Carboxymethylenebutenolidase homolog	CMBL	CMBL_HUMAN	28.0	100.0%	4	4	5	0.00%	14.3%	DSEDIYNLK	99.7%	46.4	25	36	1	0	0	1096.52	160	168
Carboxymethylenebutenolidase homolog	CMBL	CMBL_HUMAN	28.0	100.0%	4	4	5	0.00%	14.3%	EVQVEHIK	99.0%	35.7	25	24.1	1	0	0	981.54	24	31
Carboxymethylenebutenolidase homolog	CMBL	CMBL_HUMAN	28.0	100.0%	4	4	5	0.00%	14.3%	LEYGGLGR	98.8%	34.8	25	22.9	1	0	0	864.46	16	23
Cartilage-associated protein	CRTAP	CRTAP_HUMAN	46.6	100.0%	3	3	4	0.00%	9.5%	FLQFAYFK	98.5%	33.7	25	18.3	1	0	0	1063.56	150	157
Cartilage-associated protein	CRTAP	CRTAP_HUMAN	46.6	100.0%	3	3	4	0.00%	9.5%	SLPGAEDYIKDLETK	99.7%	57.9	25	55.9	1	0	0	1678.85	190	204
Cartilage-associated protein	CRTAP	CRTAP_HUMAN	46.6	100.0%	3	3	4	0.00%	9.5%	TSITDMELALPDFFK	99.7%	78.3	25	78.3	2	0	0	1727.86	224	238

Casein kinase I isoform epsilon	CSNK1E	KC1E_HUMAN	47.3	99.8%	2	2	3	0.00%	5.3%	NPEDVDRER	97.7%	31.9	25	24.7	1	0	0	1129.52	300	308
Casein kinase I isoform epsilon	CSNK1E	KC1E_HUMAN	47.3	99.8%	2	2	3	0.00%	5.3%	SAAEPVASTPASR	99.7%	44	25	35.8	2	0	0	1243.63	343	355
Casein kinase II subunit alpha'	CSNK2A2	CSK22_HUMAN	41.2	99.9%	2	2	3	0.00%	6.0%	VLGTEELYGYLK	99.1%	36	25	35.1	1	0	0	1384.74	249	260
Casein kinase II subunit alpha'	CSNK2A2	CSK22_HUMAN	41.2	99.9%	2	2	3	0.00%	6.0%	VYAEVNSLR	99.7%	61.5	25	49.1	2	0	0	1050.56	12	20
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	11	23	0.02%	28.8%	ATHDGAPELGAGGTR	99.7%	65	25	63.7	2	2	0	1409.68	332	346
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	11	23	0.02%	28.8%	IEGVLLLGEPVR	99.7%	50.8	25	50.8	1	0	0	1294.77	189	200
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	11	23	0.02%	28.8%	LFSEYHEK	98.9%	35	25	24	2	0	0	1052.50	125	132
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	11	23	0.02%	28.8%	LVNSQGQLR	99.7%	54.3	25	42.4	2	0	0	1014.57	74	82
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	11	23	0.02%	28.8%	MAFPLLDMVDLER	99.7%	56.8	25	52.5	6	0	0	1549.78	162	174
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	11	23	0.02%	28.8%	MLVSGQGPVMENAQGLGFR	99.7%	86.8	25	82.5	2	0	0	2022.97	134	152
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	11	23	0.02%	28.8%	NPQSTEPVLGGGEPPFHGHR	99.7%	40.4	25	38.9	0	2	0	2113.02	370	389
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	11	23	0.02%	28.8%	NVVTVDELR	99.7%	53.2	25	33.3	2	0	0	1044.57	153	161
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	11	23	0.02%	28.8%	VPVVFVTNAGNILQHSK	99.7%	85.6	25	85.6	2	0	0	1823.02	83	99
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	10	17	0.02%	12.3%	ALSAIADLLTNEHER	99.7%	101	25	94.3	1	1	0	1652.86	711	725
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	10	17	0.02%	12.3%	GIPVLVGLLDHPK	99.7%	58.2	25	58.2	2	0	0	1357.82	409	421
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	10	17	0.02%	12.3%	GSLASLDSLRK	99.7%	44.8	25	38.2	1	0	0	1146.65	345	355
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	10	17	0.02%	12.3%	GYELLFQPEVVR	99.7%	60.2	25	39.8	4	0	0	1449.77	655	666
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	10	17	0.02%	12.3%	QDVYGPQPQVR	99.5%	39.3	25	27.4	2	0	0	1286.65	254	264
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	10	17	0.02%	12.3%	SDFQVNLNNASR	99.7%	66.5	25	60.3	1	0	0	1364.66	847	858
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	10	17	0.02%	12.3%	SLDNNYSTPNER	99.7%	44.4	25	43.9	2	0	0	1409.63	899	910
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	10	17	0.02%	12.3%	VGGSSVDLHR	99.7%	58.5	25	45	2	0	0	1026.53	265	274
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	10	17	0.02%	12.3%	YQEAAPNVANNTGPHAASCFGAK	99.7%	34.5	25	34.5	0	1	0	2375.08	600	622
CCAAT/enhancer-binding protein zeta	CEBPZ	CEBPZ_HUMAN	121.0	100.0%	2	2	3	0.00%	2.0%	ALLVQVVNK	99.7%	46.8	25	40	2	0	0	983.62	382	390
CCAAT/enhancer-binding protein zeta	CEBPZ	CEBPZ_HUMAN	121.0	100.0%	2	2	3	0.00%	2.0%	FTDADKETEIVK	99.7%	60.9	25	53.7	1	0	0	1395.70	647	658
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	19	0.02%	6.9%	AVEGLLDATSGADADLLLR	99.7%	79.2	25	74.4	1	0	0	1900.00	1665	1683
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	19	0.02%	6.9%	EPLLMSISTNLK	98.7%	34.5	25	34.5	1	0	0	1345.74	1459	1470
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	19	0.02%	6.9%	EVTAAQVAR	99.7%	46	25	38.9	2	0	0	944.52	284	292
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	19	0.02%	6.9%	GNAPEGLPQLMEVVR	98.7%	34.6	25	34.2	1	0	0	1609.84	1800	1814
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	19	0.02%	6.9%	GQQELLYVVPFVAK	99.7%	62.7	25	57.8	1	0	0	1590.89	1228	1241
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	19	0.02%	6.9%	IVEPPENIQEK	98.8%	34.8	25	31.6	1	0	0	1295.68	1088	1098
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	19	0.02%	6.9%	NLDEQLSAPK	99.7%	47.2	25	31.3	2	0	0	1114.57	1311	1320
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	19	0.02%	6.9%	NLILSAFPR	99.7%	52.5	25	30.4	2	0	0	1030.60	2130	2138
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	19	0.02%	6.9%	SLLEVVVLSR	99.7%	54.3	25	23.6	2	0	0	1114.68	1641	1650
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	19	0.02%	6.9%	SNLQVSNEPGNR	99.6%	40.2	25	32.8	1	0	0	1314.64	2198	2209
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	19	0.02%	6.9%	SNYEAMIDR	97.9%	32.3	25	25.7	1	0	0	1114.48	1815	1823
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	19	0.02%	6.9%	SPVTFLSDLR	99.7%	62.9	25	46.8	2	0	0	1134.62	2188	2197
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	19	0.02%	6.9%	TVTVTRPTGVSFK	99.7%	48.8	25	42.1	1	0	0	1392.78	1051	1063
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	14	14	19	0.02%	6.9%	VDMLSEINIAPR	97.4%	31.3	25	23.8	1	0	0	1357.71	2152	2163
CCR4-NOT transcription complex subunit 2	CNOT2	CNOT2_HUMAN	59.7	99.8%	2	2	3	0.00%	5.6%	EGSGNPTPLINPLAGR	99.7%	60.4	25	60.4	2	0	0	1592.84	240	255
CCR4-NOT transcription complex subunit 2	CNOT2	CNOT2_HUMAN	59.7	99.8%	2	2	3	0.00%	5.6%	TNSMSSSGLGSPNR	99.7%	52.9	25	52.9	1	0	0	1410.63	155	168
CCR4-NOT transcription complex subunit 8	CNOT8	CNOT8_HUMAN	33.5	99.8%	2	2	2	0.00%	8.6%	GGLQEVADQLDLQR	99.7%	53.9	25	50.7	1	0	0	1541.79	207	220
CCR4-NOT transcription complex subunit 8	CNOT8	CNOT8_HUMAN	33.5	99.8%	2	2	2	0.00%	8.6%	LYGLGTGVAQK	95.7%	29.2	25	22.3	1	0	0	1106.62	259	269
CDP-diacylglycerol--inositol 3-phosphatidyltransferase	CDIPT	CDIPT_HUMAN	23.5	100.0%	3	6	15	0.01%	16.0%	MGLWVTAPIALLK	98.9%	35.2	25	30	2	0	0	1428.83	174	186
CDP-diacylglycerol--inositol 3-phosphatidyltransferase	CDIPT	CDIPT_HUMAN	23.5	100.0%	3	6	15	0.01%	16.0%	MIDLSGNPVLR	99.7%	70.6	25	67.6	10	0	0	1214.66	122	132
CDP-diacylglycerol--inositol 3-phosphatidyltransferase	CDIPT	CDIPT_HUMAN	23.5	100.0%	3	6	15	0.01%	16.0%	NMAALDAADR	99.7%	53.3	25	42.1	3	0	0	1063.48	200	209
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	5	5	8	0.01%	6.3%	FAEFQYLQPGPPR	99.7%	52.6	25	44.8	2	0	0	1549.78	405	417
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	5	5	8	0.01%	6.3%	LAEAEETAR	99.7%	50.2	25	46.5	3	0	0	989.49	868	876
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	5	5	8	0.01%	6.3%	SPAPPLLHVAALGQK	95.5%	23	25	23	0	1	0	1498.87	124	138
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	5	5	8	0.01%	6.3%	VQTLSNQPLLK	99.7%	41.9	25	34.1	1	0	0	1240.73	113	123
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	5	5	8	0.01%	6.3%	VVTQNICQYR	99.7%	44.8	25	42.6	1	0	0	1280.64	748	757
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	4	4	7	0.01%	15.4%	IYQWINELSSPETR	99.7%	74.5	25	63.8	1	0	0	1735.87	22	35

Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	4	4	7	0.01%	15.4%	LTSLGVIGALVK	99.7%	89.9	25	82.9	2	0	0	1170.75	137	148
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	4	4	7	0.01%	15.4%	NLQEGQVTDPR	99.7%	50.6	25	44.5	2	0	0	1256.62	282	292
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	4	4	7	0.01%	15.4%	TVATFILQK	99.7%	64.6	25	46.7	2	0	0	1020.61	180	188
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	4	4	8	0.01%	7.4%	EFYEVVQSQR	99.7%	49.5	25	42.2	2	0	0	1284.62	9	18
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	4	4	8	0.01%	7.4%	EMIEESANK	96.7%	30.2	25	30.2	2	0	0	1050.48	342	350
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	4	4	8	0.01%	7.4%	LQEFLADMGLPLK	99.7%	53.8	25	48.9	2	0	0	1490.79	311	323
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	4	4	8	0.01%	7.4%	YVTDVGVLQR	99.7%	53.7	25	37.8	2	0	0	1149.63	238	247
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	17	18	37	0.04%	28.8%	AAGIEIQK	99.5%	38.8	25	29.2	2	0	0	829.48	193	200
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	17	18	37	0.04%	28.8%	DNEEETTDDPRK	98.3%	33	25	29.2	2	0	0	1448.61	111	122
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	17	18	37	0.04%	28.8%	EIDDTYIEDAADVDAR	99.7%	89.3	25	89.3	1	0	0	1810.80	506	521
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	17	18	37	0.04%	28.8%	ESDLPSAILQTSGVSEFTK	99.7%	136	25	136	3	0	0	2009.01	272	290
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	17	18	37	0.04%	28.8%	GGLNTPLHESDFSGVTPQR	99.7%	38.6	25	37.9	0	1	0	2011.98	381	399
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	17	18	37	0.04%	28.8%	GVDYNAEIPFEK	99.7%	55.3	25	55.3	2	0	0	1381.66	207	218
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	17	18	37	0.04%	28.8%	ILLGGYQSR	99.7%	53.6	25	37	3	0	0	1006.57	719	727
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	17	18	37	0.04%	28.8%	ILQEAQNLMALTNVDTPLK	99.7%	112	25	112	4	0	0	2112.14	362	380
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	17	18	37	0.04%	28.8%	LGLLGLPAPK	99.7%	83.1	25	83.1	4	0	0	978.63	478	487
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	17	18	37	0.04%	28.8%	LVLPAPQISDAELQEVVK	99.7%	88	25	87.3	2	0	0	1949.10	295	312
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	17	18	37	0.04%	28.8%	NTEDEILK	96.1%	29.6	25	15.1	1	0	0	961.48	13	20
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	17	18	37	0.04%	28.8%	QVVQTPNTVLSTPFR	99.7%	80.4	25	78.8	2	0	0	1686.92	400	414
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	17	18	37	0.04%	28.8%	SGTTPKPVINSTPGR	99.7%	60.5	25	56.3	1	0	0	1511.82	427	441
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	17	18	37	0.04%	28.8%	TPSNGAEGLTPR	99.7%	103	25	95.6	1	0	0	1199.60	415	426
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	17	18	37	0.04%	28.8%	TVGFGTNNSEHITYLEHNPYEK	99.7%	41	25	41	0	2	0	2550.19	602	623
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	17	18	37	0.04%	28.8%	VGQASEIAR	99.7%	68.8	25	54.4	4	0	0	930.50	313	321
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	17	18	37	0.04%	28.8%	YADLLLEK	99.7%	48.4	25	47.1	2	0	0	964.54	788	795
Cell division cycle protein 16 homolog	CDC16	CDC16_HUMAN	71.7	99.8%	2	2	3	0.00%	2.9%	IYDALDNR	99.7%	42.3	25	25.1	2	0	0	979.48	139	146
Cell division cycle protein 16 homolog	CDC16	CDC16_HUMAN	71.7	99.8%	2	2	3	0.00%	2.9%	LCNEEQELLR	95.6%	29.1	25	20.7	1	0	0	1303.63	193	202
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	5	5	8	0.01%	9.7%	AWYGLGQTYEILK	99.7%	71.4	25	63.7	2	0	0	1541.80	401	413
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	5	5	8	0.01%	9.7%	AYAVGDVEK	97.2%	31	25	27.2	1	0	0	951.48	459	467
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	5	5	8	0.01%	9.7%	IENMDTFSNLLYVR	99.7%	48.8	25	41	2	0	0	1714.85	297	310
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	5	5	8	0.01%	9.7%	MLVALGECYEK	99.3%	37.3	25	31.4	2	0	0	1328.62	435	445
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	5	5	8	0.01%	9.7%	YQNLIDVGFSK	99.7%	50.4	25	50.4	1	0	0	1283.66	251	261
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	8	8	11	0.01%	24.5%	DAVEQQGEVKK	97.1%	30.9	25	25.5	1	0	0	1230.63	176	186
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	8	8	11	0.01%	24.5%	EQDQRPLHPVANPHAEISTK	99.7%	43.8	25	43.8	0	2	0	2267.15	149	168
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	8	8	11	0.01%	24.5%	MKLPEHPEGGEPEDDEAPAK	99.7%	46.1	25	46	0	1	0	2191.98	287	306
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	8	8	11	0.01%	24.5%	QAPDNEITIK	98.9%	35	25	26.4	1	0	0	1128.59	321	330
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	8	8	11	0.01%	24.5%	VFFTCNACGESVK	99.7%	74.5	25	74.5	1	0	0	1518.67	2	14
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	8	8	11	0.01%	24.5%	VFFTCNACGESVKK	99.7%	54.8	25	50.1	2	0	0	1646.77	2	15
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	8	8	11	0.01%	24.5%	VKDAVEQQGEVK	99.7%	65.8	25	45.8	1	0	0	1329.70	174	185
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	8	8	11	0.01%	24.5%	VRELLEQISAFDNVPR	99.7%	51.3	25	48.8	0	2	0	1886.01	94	109
Cellular nucleic acid-binding protein	CNBP	CNBP_HUMAN	19.5	99.8%	2	2	4	0.00%	11.9%	CGETGHVAINCSK	99.7%	63.1	25	50.2	2	0	0	1432.63	140	152
Cellular nucleic acid-binding protein	CNBP	CNBP_HUMAN	19.5	99.8%	2	2	4	0.00%	11.9%	TSEVNCYR	99.1%	36.1	25	32.7	2	0	0	1028.45	153	160
Cellular tumor antigen p53	TP53	P53_HUMAN	43.7	100.0%	3	3	8	0.01%	8.7%	ALPNNTSSSPQPK	99.7%	62.4	25	59.1	4	0	0	1340.68	307	319
Cellular tumor antigen p53	TP53	P53_HUMAN	43.7	100.0%	3	3	8	0.01%	8.7%	SVTCTYSPALNK	99.7%	42.3	25	42.3	1	0	0	1340.65	121	132
Cellular tumor antigen p53	TP53	P53_HUMAN	43.7	100.0%	3	3	8	0.01%	8.7%	TYQGSYGFR	99.0%	35.5	25	35.5	3	0	0	1078.50	102	110
Centrin-2	CETN2	CETN2_HUMAN	19.7	99.8%	2	3	4	0.00%	16.9%	EAFDLFDADGTGTIDVK	99.3%	37.5	25	37.5	1	0	0	1813.85	35	51
Centrin-2	CETN2	CETN2_HUMAN	19.7	99.8%	2	3	4	0.00%	16.9%	MISEIDKEGTGK	99.7%	44.2	25	40.5	3	0	0	1307.65	72	83
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	6	9	16	0.02%	35.3%	GAEHITTYTFNTHK	99.7%	60.1	25	55.1	1	2	0	1619.78	197	210
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	6	9	16	0.02%	35.3%	LLLDTFEYQGLVK	99.7%	93.1	25	79.4	2	0	0	1538.85	135	147
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	6	9	16	0.02%	35.3%	SGASGASAAPAASAAAALAPSATR	99.7%	99.5	25	99.5	2	0	0	1985.00	18	41
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	6	9	16	0.02%	35.3%	SMVTEEFNGSDWEK	99.7%	76.7	25	76.7	4	0	0	1658.70	248	261
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	6	9	16	0.02%	35.3%	SNPGGFGIAPHCLDEGTVR	99.7%	42.9	25	41.8	1	2	0	1983.93	229	247

Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	6	9	16	0.02%	35.3%	SQAVEKPPSEKPR	98.2%	26.5	25	25.3	0	2	0	1452.78	53	65
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	4	5	8	0.01%	6.7%	AMGTLLNTAISEVIGK	99.3%	37.2	25	36.3	2	0	0	1633.88	652	667
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	4	5	8	0.01%	6.7%	LEKEDLGTR	97.0%	30.6	25	13.7	1	0	0	1060.56	15	23
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	4	5	8	0.01%	6.7%	NLMTSEIHNTVK	99.7%	76.2	25	71.6	3	0	0	1402.70	413	424
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	4	5	8	0.01%	6.7%	QLLDLPLDTDLENEK	99.7%	58.4	25	58.4	2	0	0	1755.90	306	320
Chitobiosyldiphosphodolichol beta-mannosyltransferase	ALG1	ALG1_HUMAN	52.5	99.8%	2	2	3	0.00%	5.6%	ETPLDLQHR	97.5%	31.5	25	22.7	1	0	0	1108.57	224	232
Chitobiosyldiphosphodolichol beta-mannosyltransferase	ALG1	ALG1_HUMAN	52.5	99.8%	2	2	3	0.00%	5.6%	IQIVGLTELQSLAVGPR	99.7%	65.3	25	65.3	2	0	0	1794.05	83	99
Chloride channel CLIC-like protein 1	CLCC1	CLCC1_HUMAN	62.0	99.8%	2	2	3	0.00%	4.0%	AFDVPDAEAR	98.3%	33.1	25	25.4	2	0	0	1090.52	444	453
Chloride channel CLIC-like protein 1	CLCC1	CLCC1_HUMAN	62.0	99.8%	2	2	3	0.00%	4.0%	ETGGILGEGTPK	95.9%	29.3	25	14.7	1	0	0	1158.60	473	484
Chromatin target of PRMT1 protein	CHTOP	CHTOP_HUMAN	26.4	100.0%	5	9	26	0.02%	28.2%	ASMQQQQQLASAR	99.7%	83.5	25	73.3	13	0	0	1462.71	39	51
Chromatin target of PRMT1 protein	CHTOP	CHTOP_HUMAN	26.4	100.0%	5	9	26	0.02%	28.2%	EQLDNQLDAYMSK	99.7%	92.4	25	92.4	4	0	0	1570.71	214	226
Chromatin target of PRMT1 protein	CHTOP	CHTOP_HUMAN	26.4	100.0%	5	9	26	0.02%	28.2%	GHLDAELDAYMAQTDPETND	99.7%	94.5	25	94.5	2	0	0	2221.92	229	248
Chromatin target of PRMT1 protein	CHTOP	CHTOP_HUMAN	26.4	100.0%	5	9	26	0.02%	28.2%	LAQQMENRPSVQAALK	99.7%	62.7	25	37.9	4	2	0	1783.95	55	70
Chromatin target of PRMT1 protein	CHTOP	CHTOP_HUMAN	26.4	100.0%	5	9	26	0.02%	28.2%	QPTPVNIR	96.9%	30.6	25	18	1	0	0	924.53	31	38
Chromobox protein homolog 3	CBX3	CBX3_HUMAN	20.8	99.8%	2	2	4	0.00%	14.8%	KVEEAEPEEFVVEK	99.7%	53.3	25	50.8	2	0	0	1661.83	21	34
Chromobox protein homolog 3	CBX3	CBX3_HUMAN	20.8	99.8%	2	2	4	0.00%	14.8%	WKDSDEADLVLAK	99.7%	47.1	25	40.8	2	0	0	1489.75	142	154
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	5	5	8	0.01%	6.2%	GIPTYIYYFPR	99.7%	62.1	25	58.5	2	0	0	1389.72	867	877
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	5	5	8	0.01%	6.2%	GSVLIPGLVEGSTK	99.7%	54.4	25	46.2	2	0	0	1356.77	617	630
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	5	5	8	0.01%	6.2%	LLQPFLLR	99.7%	46.8	25	35.5	1	0	0	999.64	253	260
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	5	5	8	0.01%	6.2%	SFEQLVNLQK	99.7%	51.2	25	42.2	2	0	0	1205.65	591	600
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	5	5	8	0.01%	6.2%	SYQLEGVNWLAQR	96.5%	30.1	25	25.2	1	0	0	1563.79	48	60
Chromodomain-helicase-DNA-binding protein 4	CHD4	CHD4_HUMAN	218.0	100.0%	6	6	7	0.01%	3.4%	APEPTPQQVAQQQ	99.7%	40.9	25	26	1	0	0	1421.70	1900	1912
Chromodomain-helicase-DNA-binding protein 4	CHD4	CHD4_HUMAN	218.0	100.0%	6	6	7	0.01%	3.4%	AYVSLFMR	99.2%	36.4	25	32.9	1	0	0	1002.51	1458	1465
Chromodomain-helicase-DNA-binding protein 4	CHD4	CHD4_HUMAN	218.0	100.0%	6	6	7	0.01%	3.4%	GAADVEKVEEK	99.7%	51.3	25	25	2	0	0	1174.60	1637	1647
Chromodomain-helicase-DNA-binding protein 4	CHD4	CHD4_HUMAN	218.0	100.0%	6	6	7	0.01%	3.4%	IDGGITGNMR	99.7%	45.2	25	34.9	1	0	0	1049.50	1096	1105
Chromodomain-helicase-DNA-binding protein 4	CHD4	CHD4_HUMAN	218.0	100.0%	6	6	7	0.01%	3.4%	VGGNIEVLGFNAR	99.7%	44.5	25	44.5	1	0	0	1345.72	1407	1419
Chromodomain-helicase-DNA-binding protein 4	CHD4	CHD4_HUMAN	218.0	100.0%	6	6	7	0.01%	3.4%	VLIFSQMTK	98.2%	33	25	24.3	1	0	0	1082.59	1069	1077
Chromosome transmission fidelity protein 18 homolog	CHTF18	CTF18_HUMAN	107.4	100.0%	2	2	4	0.00%	2.7%	NLIQTLVSGIAPATR	99.7%	47.9	25	47.9	2	0	0	1553.90	735	749
Chromosome transmission fidelity protein 18 homolog	CHTF18	CTF18_HUMAN	107.4	100.0%	2	2	4	0.00%	2.7%	VVQGLFDNFLR	99.7%	50.6	25	39	2	0	0	1307.71	648	658
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	25	27	69	0.07%	17.1%	DAMQYASESK	99.6%	40.5	25	40.5	1	0	0	1129.48	1536	1545
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	25	27	69	0.07%	17.1%	ENPYYDSR	96.2%	29.7	25	23.3	3	0	0	1043.44	896	903
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	25	27	69	0.07%	17.1%	ESNCYDPER	98.8%	34.9	25	34.9	1	0	0	1169.45	750	758
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	25	27	69	0.07%	17.1%	ESYVETELIFALAK	99.7%	58.6	25	57	3	0	0	1612.85	1166	1179
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	25	27	69	0.07%	17.1%	EVCFACVDGK	99.7%	43	25	43	4	0	0	1184.51	1255	1264
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	25	27	69	0.07%	17.1%	GQFSTDELVAEVEK	99.7%	59.8	25	59.8	2	0	0	1551.75	838	851
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	25	27	69	0.07%	17.1%	HELIEFR	99.3%	37.1	25	36.5	2	0	0	943.50	1502	1508
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	25	27	69	0.07%	17.1%	IHEGCEEPATHNALAK	99.7%	41	25	41	0	2	0	1776.83	866	881
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	25	27	69	0.07%	17.1%	ISGETIFVTAPHEATAGIIGVNR	99.6%	33.3	25	33.3	0	1	0	2353.25	298	320
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	25	27	69	0.07%	17.1%	IVLDNSVFSEHR	99.7%	73.7	25	73.7	4	1	0	1415.73	1011	1022
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	25	27	69	0.07%	17.1%	IYIDSNNNPER	99.7%	70.9	25	61.4	4	0	0	1334.63	882	892
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	25	27	69	0.07%	17.1%	LLLPWLEAR	95.5%	29	25	17	1	0	0	1110.67	857	865
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	25	27	69	0.07%	17.1%	LLYNNVSNFGR	99.7%	54.4	25	54.4	4	0	0	1296.67	1216	1226
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	25	27	69	0.07%	17.1%	NLQNLLILTAIK	99.7%	70.1	25	68.7	2	0	0	1353.85	1023	1034
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	25	27	69	0.07%	17.1%	NNLAGAEELFAR	99.7%	85.4	25	82.3	4	0	0	1304.66	355	366
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	25	27	69	0.07%	17.1%	SVDPTLALSVYLR	99.7%	89.9	25	89.9	4	0	0	1433.80	469	481
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	25	27	69	0.07%	17.1%	TLQIFNIEMK	99.7%	45.7	25	40.8	5	0	0	1252.66	87	96
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	25	27	69	0.07%	17.1%	VANVELYYR	99.7%	75	25	71.5	4	0	0	1126.59	1398	1406
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	25	27	69	0.07%	17.1%	VDKLDASESLR	99.7%	44.4	25	36.8	2	0	0	1232.65	1610	1620
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	25	27	69	0.07%	17.1%	VGYTPDWIFLLR	99.7%	59.1	25	59.1	1	0	0	1479.80	508	519
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	25	27	69	0.07%	17.1%	VIQCFAETGQVQK	99.7%	93.1	25	84.3	5	0	0	1507.76	488	500
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	25	27	69	0.07%	17.1%	VMEYINR	98.7%	34.3	25	27.5	2	0	0	940.46	1040	1046

Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	25	27	69	0.07%	17.1%	VVGAMQLYSVDR	99.7%	50.3	25	45.9	2	0	0	1337.69	177	188
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	25	27	69	0.07%	17.1%	WLLLTGISAQQNR	99.7%	86.9	25	81.4	4	0	0	1499.83	164	176
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	25	27	69	0.07%	17.1%	YIEIYVQK	99.7%	41.1	25	37.9	1	0	0	1055.58	799	806
Clathrin light chain A	CLTA	CLCA_HUMAN	27.1	100.0%	3	3	4	0.00%	7.7%	LEALDANSR	99.7%	51	25	40.7	1	0	0	988.51	121	129
Clathrin light chain A	CLTA	CLCA_HUMAN	27.1	100.0%	3	3	4	0.00%	7.7%	LQSEPESIR	95.0%	28.5	25	15.8	1	0	0	1058.55	103	111
Clathrin light chain A	CLTA	CLCA_HUMAN	27.1	100.0%	3	3	4	0.00%	7.7%	LQSEPESIRK	98.0%	32.4	25	20.9	2	0	0	1186.64	103	112
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	14	15	26	0.02%	10.5%	DALLLSFK	97.4%	31.3	25	21.8	1	0	0	906.53	92	99
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	14	15	26	0.02%	10.5%	DGFVQNVHTPR	99.7%	41.5	25	36.3	2	0	0	1269.63	130	140
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	14	15	26	0.02%	10.5%	DLSGMFTTESR	99.7%	58.3	25	49.5	2	0	0	1243.56	703	713
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	14	15	26	0.02%	10.5%	EVLLVALGSR	99.7%	81.4	25	69.2	2	0	0	1056.64	848	857
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	14	15	26	0.02%	10.5%	HGFLILSR	97.6%	31.7	25	18.8	1	0	0	942.55	572	579
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	14	15	26	0.02%	10.5%	LGNSLLLK	98.4%	33.4	25	17.8	2	0	0	857.55	388	395
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	14	15	26	0.02%	10.5%	LSVVEYDPGTHDLK	99.7%	41.5	25	38.4	2	1	0	1572.79	103	116
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	14	15	26	0.02%	10.5%	NVLDGELLNR	99.7%	68.5	25	52.5	2	0	0	1142.62	1397	1406
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	14	15	26	0.02%	10.5%	QGELPLVK	99.2%	36.9	25	25.7	1	0	0	883.52	840	847
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	14	15	26	0.02%	10.5%	SSFLPSYIIDVR	99.7%	77.5	25	64.3	2	0	0	1396.75	183	194
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	14	15	26	0.02%	10.5%	VLVDSSFGQPTTQGEAR	99.7%	104	25	103	2	0	0	1791.89	817	833
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	14	15	26	0.02%	10.5%	VYAVATSTNTPCAR	99.7%	98.7	25	92	2	0	0	1510.73	1033	1046
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	14	15	26	0.02%	10.5%	YIVQVSPLGIR	99.7%	47.3	25	27.1	2	0	0	1244.74	617	627
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	14	15	26	0.02%	10.5%	YLYLSTMER	99.5%	38.8	25	32.2	2	0	0	1175.58	1407	1415
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	7	7	14	0.01%	10.2%	DLFIQWCQDPK	99.7%	64.3	25	61.6	2	0	0	1449.68	340	350
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	7	7	14	0.01%	10.2%	FLIDNPSEK	95.5%	29	25	7.25	2	0	0	1062.55	367	375
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	7	7	14	0.01%	10.2%	FSQIVNLK	98.7%	34.4	25	21.5	2	0	0	948.55	131	138
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	7	7	14	0.01%	10.2%	IRDLLYEQYAIV	99.7%	42.7	25	42.7	2	0	0	1495.82	771	782
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	7	7	14	0.01%	10.2%	LHETVDATSETHIYQVR	99.7%	41.5	25	41.5	0	2	0	1998.99	593	609
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	7	7	14	0.01%	10.2%	NSIILTYR	99.7%	51.5	25	39.6	2	0	0	979.56	351	358
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	7	7	14	0.01%	10.2%	VVLASQPDLECGFSR	99.7%	77.6	25	76.6	2	0	0	1677.83	325	339
Cleavage and polyadenylation specificity factor subunit 4	CPSF4	CPSF4_HUMAN	30.3	100.0%	3	3	6	0.01%	14.1%	MPECYFYSK	99.7%	55	25	45.9	2	0	0	1240.50	93	101
Cleavage and polyadenylation specificity factor subunit 4	CPSF4	CPSF4_HUMAN	30.3	100.0%	3	3	6	0.01%	14.1%	SGAAVCEFFLK	99.7%	56.2	25	56.2	3	0	0	1228.60	36	46
Cleavage and polyadenylation specificity factor subunit 4	CPSF4	CPSF4_HUMAN	30.3	100.0%	3	3	6	0.01%	14.1%	TPQVIGVMQSQNSSAGNR	99.7%	75.9	25	67.8	1	0	0	1889.91	218	235
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	6	8	12	0.01%	24.7%	GVTQFGNK	99.7%	53.5	25	31	2	0	0	850.44	16	23
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	6	8	12	0.01%	24.7%	KLFLVQLQEK	99.7%	63.5	25	63.5	1	0	0	1245.76	173	182
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	6	8	12	0.01%	24.7%	LFLVQLQEK	99.7%	63.4	25	42.3	2	0	0	1117.66	174	182
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	6	8	12	0.01%	24.7%	LMTEILGR	99.7%	51.3	25	42.1	2	0	0	948.52	124	131
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	6	8	12	0.01%	24.7%	LPGGELNPGEDEVEGLKR	99.7%	78	25	78	1	2	0	1908.97	106	123
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	6	8	12	0.01%	24.7%	YIQQTKPLTLER	99.7%	44.7	25	34.4	2	0	0	1489.84	24	35
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	6	7	12	0.01%	13.2%	AISSSAISR	99.7%	48.8	25	36.9	2	0	0	891.49	423	431
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	6	7	12	0.01%	13.2%	GAAPNVVYTYTGK	99.7%	87.1	25	83.5	2	0	0	1340.68	67	79
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	6	7	12	0.01%	13.2%	GDYGPPGR	96.0%	29.5	25	22.8	1	0	0	818.38	393	400
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	6	7	12	0.01%	13.2%	GFALVGVGSEASSK	99.7%	99	25	90.5	2	0	0	1308.68	125	138
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	6	7	12	0.01%	13.2%	RELHGQNPVVTPCNK	99.7%	33.6	25	26	0	1	0	1748.89	147	161
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	6	7	12	0.01%	13.2%	TPLSEAEFEEIMNR	99.7%	107	25	107	4	0	0	1681.77	407	420
Cleavage and polyadenylation specificity factor subunit 7	CPSF7	CPSF7_HUMAN	52.1	100.0%	6	6	9	0.01%	14.2%	ATPSENLVPSSAR	99.7%	47.6	25	42.1	1	0	0	1328.68	202	214
Cleavage and polyadenylation specificity factor subunit 7	CPSF7	CPSF7_HUMAN	52.1	100.0%	6	6	9	0.01%	14.2%	LLELLPGK	99.0%	35.7	25	30.6	1	0	0	882.57	141	148
Cleavage and polyadenylation specificity factor subunit 7	CPSF7	CPSF7_HUMAN	52.1	100.0%	6	6	9	0.01%	14.2%	QNLSQFEAQAR	99.7%	76.6	25	66.4	1	0	0	1291.64	163	173
Cleavage and polyadenylation specificity factor subunit 7	CPSF7	CPSF7_HUMAN	52.1	100.0%	6	6	9	0.01%	14.2%	SSSTEPPPPVR	99.7%	42.4	25	31.3	2	0	0	1153.58	46	56
Cleavage and polyadenylation specificity factor subunit 7	CPSF7	CPSF7_HUMAN	52.1	100.0%	6	6	9	0.01%	14.2%	SYSVGASGSSSR	99.7%	75.5	25	75.5	2	0	0	1144.52	407	418
Cleavage and polyadenylation specificity factor subunit 7	CPSF7	CPSF7_HUMAN	52.1	100.0%	6	6	9	0.01%	14.2%	TPAILYTYSGLR	99.7%	69.6	25	65.3	2	0	0	1354.74	67	78
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	27	73	0.07%	22.8%	ASNLENSTYDLYTIPK	99.7%	96.9	25	94.7	4	0	0	1828.90	383	398
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	27	73	0.07%	22.8%	CPLSGACYSPEFK	99.7%	53.7	25	53.7	2	0	0	1515.66	1185	1197
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	27	73	0.07%	22.8%	DADSITLFDVQQK	99.7%	68.5	25	56.6	1	0	0	1479.73	468	480

Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	27	73	0.07%	22.8%	DADSQNPDAPEGK	99.7%	45.8	25	45.8	2	0	0	1343.57	399	411
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	27	73	0.07%	22.8%	DADSQNPDAPEGKR	99.7%	47.6	25	44.9	3	0	0	1499.67	399	412
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	27	73	0.07%	22.8%	DVAVMQLR	99.7%	44.1	25	34.2	8	0	0	931.50	351	358
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	27	73	0.07%	22.8%	GFFEGTIASK	99.7%	68.5	25	66.6	4	0	0	1056.54	816	825
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	27	73	0.07%	22.8%	GHYNNVSCAVFHPR	99.7%	38.6	25	38.6	0	1	0	1657.77	247	260
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	27	73	0.07%	22.8%	GITGVDLFGTTDAVVK	99.7%	94.3	25	90.8	3	0	0	1592.85	183	198
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	27	73	0.07%	22.8%	KLDALCNIHENIR	99.7%	34.2	25	32	0	2	0	1595.83	517	529
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	27	73	0.07%	22.8%	LLELGPKPEVAQQTR	99.7%	48.8	25	48.8	0	2	0	1678.95	1128	1142
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	27	73	0.07%	22.8%	LNDLIQR	99.7%	51.1	25	39	4	0	0	871.50	1003	1009
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	27	73	0.07%	22.8%	LSFLYLITGNLEK	99.7%	71.3	25	71.3	2	0	0	1510.85	703	715
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	27	73	0.07%	22.8%	LVGQSIIAYLQK	99.7%	95.8	25	95.8	4	0	0	1332.79	620	631
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	27	73	0.07%	22.8%	NLSPGAVESDVR	99.7%	57.1	25	46	4	0	0	1243.63	171	182
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	27	73	0.07%	22.8%	QELILSNSEDK	96.4%	29.9	25	8.95	1	0	0	1275.64	261	271
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	27	73	0.07%	22.8%	QLFLQTYAR	99.7%	53	25	38.7	4	0	0	1139.62	957	965
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	27	73	0.07%	22.8%	QQPLFVSGGDDYK	99.3%	37.4	25	37.4	1	0	0	1453.70	62	74
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	27	73	0.07%	22.8%	SILLSVPLLVVDNK	99.7%	81.9	25	81.9	5	0	0	1509.93	1031	1044
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	27	73	0.07%	22.8%	SSGLTAVWVAR	99.7%	74.5	25	48.5	2	0	0	1146.63	413	423
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	27	73	0.07%	22.8%	TALNLFFK	99.7%	60.2	25	50.4	4	0	0	953.55	1107	1114
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	27	73	0.07%	22.8%	TGVQTFR	97.6%	31.6	25	24.7	2	0	0	808.43	282	288
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	27	73	0.07%	22.8%	TLDLPIYVTR	99.7%	63.9	25	55.7	4	0	0	1190.68	563	572
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	27	73	0.07%	22.8%	VWDISGLR	99.7%	45.6	25	26.9	1	0	0	945.52	161	168
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	27	73	0.07%	22.8%	YAVTTGDHGIIR	99.7%	57.7	25	46.9	2	1	0	1302.68	551	562
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	AAAQCYIDLIIK	99.7%	60.8	25	54.2	4	0	0	1378.74	280	291
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	ALSGYCGFMAANLYAR	99.7%	76.4	25	73.1	1	0	0	1764.82	883	898
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	CIYNLLQSSSPAVK	99.7%	84.9	25	80.8	2	0	0	1579.81	248	261
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	DLQHPNEFIR	98.7%	34.2	25	24.3	2	0	0	1268.64	108	117
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	EAELLEPLMPAIR	99.7%	53	25	42.7	2	0	0	1481.80	129	141
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	EAGELKPEEEITVGPVQK	99.7%	78.5	25	75.8	2	0	0	1953.02	496	513
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	EDIQSVMTEIR	99.7%	59.9	25	57.1	1	0	0	1320.65	470	480
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	FVLPLQDHTIK	99.4%	38.5	25	22.8	1	1	0	1310.75	65	75
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	GALWILGEYCSTK	99.7%	60.8	25	60	3	0	0	1497.74	457	469
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	KPITDDDVDR	99.7%	54.6	25	33.6	2	0	0	1173.57	603	612
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	LLLVFWEIVPK	99.7%	79	25	62.5	2	0	0	1356.83	77	87
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	LPGLLMTIIR	99.7%	60.4	25	50.4	4	0	0	1126.70	55	64
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	LVEKPSPLTLAPHDFANIK	99.7%	51.4	25	51.4	0	2	0	2090.16	768	786
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	LVTEMGTYATQSALSSSRPTK	99.7%	46.2	25	43.3	0	4	0	2228.12	514	534
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	MLEVFHAIK	99.4%	37.9	25	26.9	3	0	0	1087.60	442	450
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	NAVLAIYTIYR	99.7%	82.9	25	82.9	4	0	0	1296.73	154	164
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	NVEELVIVLK	99.5%	38.8	25	34.1	2	0	0	1155.70	352	361
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	NVTVQPDDPISFMQLTAK	99.7%	81.5	25	77	2	0	0	2004.01	662	679
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	SLGEIPIVESEIKK	99.7%	55.4	25	55.4	2	0	0	1541.88	482	495
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	SQGMALSLGDK	99.7%	55.6	25	45.4	2	0	0	1106.55	933	943
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	TLQLALDLVSSR	99.7%	78.8	25	78.8	3	0	0	1315.76	340	351
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	TNNVSEHEDTDKYR	99.7%	62.5	25	62.5	0	2	0	1707.76	367	380
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	VASTENGIIFGNIVYDVSGAASDR	99.7%	70.9	25	70.9	1	2	0	2455.21	791	814
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	VIIMILNGEK	99.7%	56	25	51.4	3	0	0	1145.66	45	54
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	VLQDLVMDILR	99.7%	74.8	25	66.5	6	0	0	1314.75	317	327
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	VLSECSPLMNDIFNK	99.7%	80.4	25	72.4	2	0	0	1766.85	619	633
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	VLSTPDLEVR	99.5%	39.5	25	30.8	1	0	0	1128.63	328	337
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	28	35	70	0.07%	38.4%	YVALVQEK	99.1%	35.9	25	24.3	2	0	0	949.54	568	575
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	3	3	9	0.01%	4.2%	AAESLADPTEYENLFPGLK	99.7%	71.8	25	71.8	2	0	0	2065.01	784	802

Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	3	3	9	0.01%	4.2%	HSEVQQANLK	99.7%	60.2	25	47.2	3	0	0	1153.60	319	328
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	3	3	9	0.01%	4.2%	LPEAAFLAR	99.7%	67	25	55.3	4	0	0	987.56	751	759
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	33	0.03%	35.2%	ENVNLAQIR	99.7%	73.5	25	60.8	3	0	0	1056.58	123	131
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	33	0.03%	35.2%	GKEVDNFVDK	99.7%	47.8	25	44.7	2	0	0	1150.57	232	241
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	33	0.03%	35.2%	GVQLQTHPNVDKK	99.7%	48.4	25	48.3	1	0	0	1463.80	324	336
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	33	0.03%	35.2%	IEGLLAAFPK	99.7%	50.8	25	32.5	2	0	0	1058.62	29	38
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	33	0.03%	35.2%	KNYCNIQVTK	99.7%	61.5	25	54.7	2	0	0	1267.65	476	485
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	33	0.03%	35.2%	LFTAESLIGLK	99.7%	82.8	25	70.1	2	0	0	1191.70	337	347
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	33	0.03%	35.2%	LYMVLITTK	99.7%	58.4	25	58.4	2	0	0	1081.63	64	72
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	33	0.03%	35.2%	NSNILEDLETLR	99.7%	98.8	25	89.5	2	0	0	1416.73	73	84
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	33	0.03%	35.2%	NTLEWCLPVIDAK	99.7%	78.5	25	66.5	2	0	0	1558.79	436	448
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	33	0.03%	35.2%	NYCNIQVTK	98.4%	33.4	25	27.7	1	0	0	1139.55	477	485
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	33	0.03%	35.2%	QHTFVETESVR	99.7%	51.4	25	40.7	1	0	0	1332.65	45	55
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	33	0.03%	35.2%	SEGETIMSSSMGK	99.7%	55.1	25	46.5	3	0	0	1375.57	244	256
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	33	0.03%	35.2%	SFPVNSDVGVLK	99.7%	43.3	25	36.9	2	0	0	1261.68	352	363
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	33	0.03%	35.2%	TFTEMDSHEEK	99.7%	56.4	25	49.4	2	0	0	1353.56	132	142
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	33	0.03%	35.2%	TRIEGLLAAFPK	98.9%	35	25	30.4	1	0	0	1315.77	27	38
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	33	0.03%	35.2%	VAPAPARPSGPSK	99.7%	44.7	25	27.2	1	0	0	1234.69	212	224
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	33	0.03%	35.2%	VLLAAAVCTK	99.7%	54.7	25	49.1	2	0	0	1045.61	2	11
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	18	18	33	0.03%	35.2%	VTQVDGNSPVR	99.7%	53.8	25	42.5	2	0	0	1171.61	486	496
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	11	14	24	0.02%	43.8%	APPAPGPASGGSGEVDELFDVK	99.7%	99.6	25	99.6	2	0	0	2097.01	2	23
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	11	14	24	0.02%	43.8%	DSIVAELDR	99.7%	57.6	25	41.7	1	0	0	1017.52	98	106
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	11	14	24	0.02%	43.8%	DSIVAELDREMSR	99.2%	36.9	25	34.6	2	0	0	1536.73	98	110
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	11	14	24	0.02%	43.8%	ENDFDRLVLQYAPSA	98.3%	33	25	21.8	2	0	0	1737.84	294	308
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	11	14	24	0.02%	43.8%	FGVVLDEIKPSSAPELQAVR	99.7%	64.7	25	64.7	0	2	0	2155.18	66	85
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	11	14	24	0.02%	43.8%	LDRLDLAR	96.5%	30.1	25	25.7	1	0	0	971.56	159	166
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	11	14	24	0.02%	43.8%	LQDAYYIFQEMADK	99.7%	93.4	25	93.4	3	0	0	1750.80	198	211
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	11	14	24	0.02%	43.8%	MFADYLAHESR	99.7%	91.9	25	85	4	0	0	1339.61	86	96
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	11	14	24	0.02%	43.8%	MFADYLAHESRR	99.3%	30.2	25	26.1	0	3	0	1495.71	86	97
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	11	14	24	0.02%	43.8%	NAFYIGSYQQCINEAQR	99.7%	93	25	93	2	0	0	2061.94	24	40
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	11	14	24	0.02%	43.8%	WEAAEGLLQEALDK	99.7%	66.2	25	60.3	2	0	0	1572.79	232	245
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	20	22	51	0.05%	30.7%	ALCQITDSTMLQAIER	99.7%	95.2	25	95.2	1	0	0	1849.91	127	142
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	20	22	51	0.05%	30.7%	ALQQYTLEPSEKPFDLK	98.9%	28.6	25	28.6	0	2	0	2007.04	561	577
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	20	22	51	0.05%	30.7%	ATFYLNVLEQK	99.7%	65.5	25	50	2	0	0	1325.71	528	538
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	20	22	51	0.05%	30.7%	DSPLFDFIESCLR	99.7%	46.3	25	43.1	1	0	0	1598.75	248	260
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	20	22	51	0.05%	30.7%	ELAPAVSVLQLFCSSPK	99.7%	95.9	25	95.9	7	0	0	1845.98	284	300
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	20	22	51	0.05%	30.7%	EMSCIAEDVIIVTSSLTK	99.7%	67.2	25	67.2	1	0	0	1996.00	94	111
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	20	22	51	0.05%	30.7%	FGAQNEEMLPSILVLLK	99.7%	53.3	25	53.2	2	0	0	1902.04	498	514
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	20	22	51	0.05%	30.7%	GGHDILVR	99.4%	38	25	11.3	2	0	0	866.48	836	843
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	20	22	51	0.05%	30.7%	ILHLLGQEGPK	99.7%	56	25	55.9	2	2	0	1204.71	455	465
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	20	22	51	0.05%	30.7%	LFQSNDPTLR	99.7%	62.2	25	48.3	2	0	0	1190.62	76	85
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	20	22	51	0.05%	30.7%	LLLLDTVTMQVTAR	99.7%	88	25	88	2	0	0	1589.89	846	859
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	20	22	51	0.05%	30.7%	QEIFQEQLAAVPEFR	99.7%	64	25	59.8	2	0	0	1804.92	610	624
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	20	22	51	0.05%	30.7%	SAVLQEAR	99.5%	39.1	25	14	2	0	0	873.48	25	32
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	20	22	51	0.05%	30.7%	SIATLAITTLLK	99.7%	98.9	25	98.9	8	0	0	1244.78	339	350
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	20	22	51	0.05%	30.7%	SLPYNQPGTCYTLVALPK	99.7%	63.2	25	61.5	2	0	0	2022.04	697	714
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	20	22	51	0.05%	30.7%	SSPEPVALTESETEYVIR	99.7%	109	25	107	2	0	0	2006.99	632	649
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	20	22	51	0.05%	30.7%	SVPLATAPMAEQR	99.7%	42.2	25	38	1	0	0	1386.70	578	590
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	20	22	51	0.05%	30.7%	VFNETPINPR	99.7%	41.5	25	36.9	2	0	0	1186.62	33	42
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	20	22	51	0.05%	30.7%	VVLEHEEVR	99.7%	54.2	25	48.7	4	0	0	1109.59	480	488
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	20	22	51	0.05%	30.7%	VVVVQAISALCQK	99.7%	60.2	25	60.2	2	0	0	1414.81	377	389

Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	9	10	20	0.02%	17.1%	AIVDCIISIVEENPESK	99.7%	100	25	100	2	0	0	1915.97	416	432
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	9	10	20	0.02%	17.1%	ATFYLNVLQQR	99.7%	66.5	25	64.9	2	0	0	1352.73	528	538
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	9	10	20	0.02%	17.1%	EMATISEDVIIVTSSLTK	99.7%	68	25	66.4	2	0	0	1937.01	94	111
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	9	10	20	0.02%	17.1%	IFNETPINPR	99.7%	46.6	25	32.6	4	0	0	1200.64	33	42
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	9	10	20	0.02%	17.1%	LFQSNDQTLR	99.7%	59.7	25	49.9	2	0	0	1221.62	76	85
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	9	10	20	0.02%	17.1%	LPDDDPTAVAGSFSCTMK	99.7%	72.6	25	72.6	1	0	0	1911.85	709	726
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	9	10	20	0.02%	17.1%	SAVLQEAR	99.5%	39.1	25	14	2	0	0	873.48	25	32
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	9	10	20	0.02%	17.1%	SIATLAITTLLK	99.7%	98.9	25	98.9	8	0	0	1244.78	339	350
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	9	10	20	0.02%	17.1%	SIPLAMAPVFEQK	99.7%	62.9	25	61.7	3	0	0	1430.77	578	590
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	9	10	20	0.02%	17.1%	SQFAYCMLIR	99.7%	52.8	25	39.3	1	0	0	1288.62	225	234
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	9	10	20	0.02%	17.1%	VVLENEAVR	99.7%	54.4	25	53.6	3	0	0	1028.57	480	488
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	9	10	20	0.02%	17.1%	VVVVQAISALCQK	99.7%	60.2	25	60.2	2	0	0	1414.81	377	389
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	6	6	14	0.01%	47.0%	AVLFCLSEDKK	99.7%	58.1	25	56	2	0	0	1309.68	35	45
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	6	6	14	0.01%	47.0%	EILVGDVGQTVDDPYATFVK	99.7%	70.9	25	70.9	1	0	0	2166.10	54	73
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	6	6	14	0.01%	47.0%	HELQANCYEEVKDR	99.7%	46.9	25	46.9	0	2	0	1790.81	133	146
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	6	6	14	0.01%	47.0%	LGGSAVISLEGKPL	99.7%	86	25	81	4	0	0	1340.78	153	166
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	6	6	14	0.01%	47.0%	VFNDMKVR	98.5%	33.6	25	18.5	1	0	0	1024.52	14	21
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	6	6	14	0.01%	47.0%	YALYDATYETK	99.7%	69.7	25	62.8	4	0	0	1337.63	82	92
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	3	3	5	0.00%	2.9%	FALTFGLDQLK	99.7%	60.1	25	0	2	0	0	1252.69	955	965
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	3	3	5	0.00%	2.9%	ITELFAVALPQLLAK	99.7%	49.2	25	49.2	1	0	0	1626.98	563	577
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	3	3	5	0.00%	2.9%	YYNDYGDIIK	99.7%	46.2	25	40.3	2	0	0	1263.59	892	901
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	12	21	0.02%	24.8%	ARVEENFLK	99.7%	46.6	25	28.5	2	0	0	1105.60	411	419
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	12	21	0.02%	24.8%	ELLESNFTLVGDDGTNK	99.7%	80.8	25	80.8	2	0	0	1851.90	173	189
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	12	21	0.02%	24.8%	ELLESNFTLVGDDGTNKEATSTGK	99.7%	40	25	40	0	2	0	2526.22	173	196
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	12	21	0.02%	24.8%	IMNEEDPEKQR	99.7%	57.5	25	56.6	3	2	0	1388.65	444	454
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	12	21	0.02%	24.8%	LAQAWFNTHR	99.4%	30.9	25	23.9	0	1	0	1243.63	163	172
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	12	21	0.02%	24.8%	LNQENEHIYNLWCSGR	99.7%	34.3	25	34.3	0	2	0	2032.93	197	212
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	12	21	0.02%	24.8%	MMRPVSDQVQIK	98.3%	26.7	25	19.8	0	2	0	1463.73	237	248
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	12	21	0.02%	24.8%	RQDLLNVLAR	99.7%	41	25	41	2	0	0	1197.71	227	236
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	12	21	0.02%	24.8%	TLLFTFNVPGSGNTYPK	99.7%	50.6	25	48.1	1	0	0	1855.96	358	374
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	10	12	21	0.02%	24.8%	VCCEGMLIQLR	99.7%	82.7	25	78.7	2	0	0	1378.66	213	223
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	9	9	15	0.01%	39.2%	AAANEQLTR	99.7%	64.1	25	51.2	2	0	0	973.51	96	104
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	9	9	15	0.01%	39.2%	ERICSEEER	98.5%	33.8	25	20	1	0	0	1207.54	109	117
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	9	9	15	0.01%	39.2%	LSENVIDR	99.7%	55.9	25	49.2	2	0	0	945.50	28	35
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	9	9	15	0.01%	39.2%	VAEELALEQAK	99.7%	87.8	25	79.4	2	0	0	1200.65	66	76
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	9	9	15	0.01%	39.2%	VTFEADENENITVVK	98.8%	34.7	25	33.3	1	0	0	1707.84	10	24
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	9	9	15	0.01%	39.2%	VTTEQYQK	99.7%	51.1	25	41.2	2	0	0	996.50	158	165
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	9	9	15	0.01%	39.2%	YESHPVCADLQAK	99.6%	40.2	25	35.7	2	0	0	1517.71	177	189
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	9	9	15	0.01%	39.2%	YSGAYGASVSDEELK	99.7%	97.5	25	97.5	2	0	0	1575.72	49	63
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	9	9	15	0.01%	39.2%	YSGAYGASVSDEELKR	98.7%	27.7	25	27.5	0	1	0	1731.82	49	64
Coiled-coil-helix-coiled-coil-helix domain-containing protein 6, mitochondrial	CHCHD6	CHCH6_HUMAN	26.5	99.8%	2	2	4	0.00%	11.9%	ASLPTGEGSISHEEQK	99.7%	64.4	25	60.5	2	0	0	1669.80	118	133
Coiled-coil-helix-coiled-coil-helix domain-containing protein 6, mitochondrial	CHCHD6	CHCH6_HUMAN	26.5	99.8%	2	2	4	0.00%	11.9%	LSSEQFHEAASK	99.7%	52.9	25	52.9	2	0	0	1333.64	172	183
Coilin	COIL	COIL_HUMAN	62.6	99.8%	2	2	3	0.00%	4.2%	NSSTIIQNPVETPK	99.7%	65.3	25	65.3	1	0	0	1527.80	445	458
Coilin	COIL	COIL_HUMAN	62.6	99.8%	2	2	3	0.00%	4.2%	VVTDLISLIR	99.7%	84.2	25	69.8	2	0	0	1128.70	37	46
Cold-inducible RNA-binding protein	CIRBP	CIRBP_HUMAN	18.6	99.8%	2	2	4	0.00%	14.0%	DSYDSYATHNE	99.7%	90.1	25	89.8	2	0	0	1301.49	162	172
Cold-inducible RNA-binding protein	CIRBP	CIRBP_HUMAN	18.6	99.8%	2	2	4	0.00%	14.0%	YGQISEVVVVKDR	99.7%	76.6	25	67.9	2	0	0	1491.82	29	41
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	C1QBP_HUMAN	31.4	100.0%	4	7	12	0.01%	22.0%	AFVDFLSDEIKEER	99.7%	79.8	25	76.5	2	2	0	1697.84	81	94
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	C1QBP_HUMAN	31.4	100.0%	4	7	12	0.01%	22.0%	EVSFQSTGESEWK	99.7%	85.7	25	75.9	2	0	0	1513.68	208	220
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	C1QBP_HUMAN	31.4	100.0%	4	7	12	0.01%	22.0%	MSGGWELELNGTEAK	99.7%	97.2	25	90.8	3	0	0	1621.75	105	119
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	C1QBP_HUMAN	31.4	100.0%	4	7	12	0.01%	22.0%	VEEQEPELTSTPNFVVEVIK	99.7%	76.2	25	76.2	2	1	0	2287.17	155	174
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	13	13	22	0.02%	10.3%	AIIDEFEQK	99.5%	39.5	25	31	2	0	0	1092.56	1280	1288

Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	13	13	22	0.02%	10.3%	DLAYCVSQLPLTER	99.7%	70.4	25	66	2	0	0	1664.83	1225	1238
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	13	13	22	0.02%	10.3%	EAITHLLGVALTR	99.7%	43.2	25	43.1	1	0	0	1393.82	221	233
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	13	13	22	0.02%	10.3%	EAVLNAYR	99.7%	58.9	25	49.1	2	0	0	935.49	691	698
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	13	13	22	0.02%	10.3%	ELEIGQAGSQR	99.7%	71.5	25	64.2	2	0	0	1187.60	1302	1312
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	13	13	22	0.02%	10.3%	GFAAFLTELAER	99.7%	42.7	25	25.7	1	0	0	1324.69	299	310
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	13	13	22	0.02%	10.3%	IYQLLAK	95.9%	29.4	25	17.2	1	0	0	848.52	520	526
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	13	13	22	0.02%	10.3%	KITEAIGIISK	99.7%	41.6	25	38.9	2	0	0	1172.73	633	643
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	13	13	22	0.02%	10.3%	LLENPTINHQK	99.7%	46	25	31.8	2	0	0	1306.71	205	215
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	13	13	22	0.02%	10.3%	LSDADLAGPLQK	99.7%	64.3	25	57.8	2	0	0	1227.66	441	452
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	13	13	22	0.02%	10.3%	QTLAAFVPLLLK	99.7%	50.3	25	47.2	2	0	0	1313.82	1009	1020
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	13	13	22	0.02%	10.3%	SGGVNQYVVQEVLSIK	99.7%	87.3	25	82.8	2	0	0	1719.93	20	35
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	13	13	22	0.02%	10.3%	VACCPLER	99.7%	48.7	25	40.6	1	0	0	1004.47	764	771
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	6	6	11	0.01%	8.4%	APLQQCAEDR	99.7%	74.3	25	71.5	2	0	0	1187.55	304	313
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	6	6	11	0.01%	8.4%	EAALAEVADEK	99.7%	53.2	25	42.2	2	0	0	1145.57	675	685
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	6	6	11	0.01%	8.4%	LLASPSSR	99.3%	37.5	25	28.3	1	0	0	830.47	84	91
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	6	6	11	0.01%	8.4%	VAAGTLDASTK	99.7%	47.9	25	42.1	2	0	0	1033.55	153	163
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	6	6	11	0.01%	8.4%	VDAVHADVYR	99.7%	46.6	25	38.3	2	0	0	1144.57	169	178
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	6	6	11	0.01%	8.4%	VFDLQFSTDSPR	99.7%	96.7	25	92.2	2	0	0	1411.69	72	83
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	7	7	19	0.02%	8.5%	APIVTVGVNNDPADVR	99.7%	91.1	25	91.1	3	0	0	1636.87	471	486
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	7	7	19	0.02%	8.5%	EFIGQQLILIIK	99.7%	58	25	58	2	0	0	1414.87	399	410
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	7	7	19	0.02%	8.5%	IQAVLALSR	95.0%	28.6	25	26.6	1	0	0	970.60	160	168
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	7	7	19	0.02%	8.5%	LLSDFLDSEVSELR	99.7%	94.9	25	89.3	4	0	0	1622.83	695	708
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	7	7	19	0.02%	8.5%	LMFSGLLVSSR	99.7%	59.7	25	51	4	0	0	1209.67	718	728
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	7	7	19	0.02%	8.5%	LNLAQFLNEDLS	99.4%	37.9	25	37.9	1	0	0	1376.71	1004	1015
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	7	7	19	0.02%	8.5%	TQIVTEIISEIR	99.7%	71.2	25	63.2	4	0	0	1401.79	459	470
Condensin-2 complex subunit D3	NCAPD3	CNDD3_HUMAN	168.9	100.0%	3	3	4	0.00%	2.3%	FLVQEIMFDR	99.7%	43.2	25	43.2	1	0	0	1297.66	443	452
Condensin-2 complex subunit D3	NCAPD3	CNDD3_HUMAN	168.9	100.0%	3	3	4	0.00%	2.3%	SALQVLVSILK	99.7%	64.3	25	61.3	1	0	0	1170.75	560	570
Condensin-2 complex subunit D3	NCAPD3	CNDD3_HUMAN	168.9	100.0%	3	3	4	0.00%	2.3%	TFAAQSLVQLLSK	99.7%	81.4	25	81.4	2	0	0	1405.81	372	384
Condensin-2 complex subunit G2	NCAPG2	CNDG2_HUMAN	131.0	100.0%	3	3	3	0.00%	2.5%	GFSEAAAPR	99.7%	45.6	25	39.2	1	0	0	905.45	812	820
Condensin-2 complex subunit G2	NCAPG2	CNDG2_HUMAN	131.0	100.0%	3	3	3	0.00%	2.5%	LETDSRPVSR	97.2%	31	25	17.2	1	0	0	1159.61	507	516
Condensin-2 complex subunit G2	NCAPG2	CNDG2_HUMAN	131.0	100.0%	3	3	3	0.00%	2.5%	YSLHDNSEK	97.6%	31.6	25	26.5	1	0	0	1092.50	466	474
Conserved oligomeric Golgi complex subunit 1	COG1	COG1_HUMAN	109.0	100.0%	3	3	6	0.01%	3.2%	ALQLLYDLR	99.7%	52.8	25	48.1	2	0	0	1104.64	806	814
Conserved oligomeric Golgi complex subunit 1	COG1	COG1_HUMAN	109.0	100.0%	3	3	6	0.01%	3.2%	FGLLPLSMTSTR	99.2%	36.6	25	31.1	2	0	0	1322.71	911	922
Conserved oligomeric Golgi complex subunit 1	COG1	COG1_HUMAN	109.0	100.0%	3	3	6	0.01%	3.2%	QALTDFLLAR	99.7%	61.7	25	51.3	2	0	0	1147.65	225	234
Conserved oligomeric Golgi complex subunit 2	COG2	COG2_HUMAN	83.2	99.8%	2	2	3	0.00%	4.3%	ETSALEASSPLLTGQILER	99.7%	72.3	25	68.1	1	0	0	2015.07	154	172
Conserved oligomeric Golgi complex subunit 2	COG2	COG2_HUMAN	83.2	99.8%	2	2	3	0.00%	4.3%	SFSALAELVAAAK	99.7%	89.1	25	87.6	2	0	0	1277.71	718	730
Conserved oligomeric Golgi complex subunit 4	COG4	COG4_HUMAN	89.1	99.8%	2	2	3	0.00%	2.6%	LLQEAEQR	99.7%	52.8	25	40.3	2	0	0	986.53	187	194
Conserved oligomeric Golgi complex subunit 4	COG4	COG4_HUMAN	89.1	99.8%	2	2	3	0.00%	2.6%	LSQMATILNLER	99.7%	55.1	25	41	1	0	0	1388.76	730	741
Conserved oligomeric Golgi complex subunit 5	COG5	COG5_HUMAN	92.7	99.8%	2	2	2	0.00%	2.9%	IGALQGAVDR	99.7%	62	25	42.5	1	0	0	999.56	138	147
Conserved oligomeric Golgi complex subunit 5	COG5	COG5_HUMAN	92.7	99.8%	2	2	2	0.00%	2.9%	LFDPINLVFPPGGR	99.7%	43.7	25	38.7	1	0	0	1541.85	493	506
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	8	8	13	0.01%	9.8%	AEGSSTASSGSQLAEGK	99.7%	84.4	25	83.8	2	0	0	1566.72	503	519
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	8	8	13	0.01%	9.8%	APSHSESALNNDSK	99.4%	31.4	25	26.7	0	2	0	1456.67	1073	1086
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	8	8	13	0.01%	9.8%	GVISTPVIR	99.5%	38.8	25	25.8	2	0	0	941.58	987	995
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	8	8	13	0.01%	9.8%	LYEPDQLQELK	99.4%	38.2	25	29.7	1	0	0	1375.71	748	758
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	8	8	13	0.01%	9.8%	NIQDTSDLDAIAK	99.7%	83.9	25	75.6	2	0	0	1403.70	292	304
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	8	8	13	0.01%	9.8%	SPQTPELVEALAFR	99.7%	59.9	25	59.9	2	0	0	1557.83	652	665
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	8	8	13	0.01%	9.8%	SQGGVQPIPSQGGK	99.7%	47.4	25	45.3	1	0	0	1339.70	933	946
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	8	8	13	0.01%	9.8%	VAAASGHCGAFSGSDSSR	99.7%	54.7	25	51.3	0	1	0	1723.75	912	929
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	5	5	10	0.01%	10.4%	AESTPEIAEQR	99.7%	50.2	25	42.9	2	0	0	1230.60	225	235
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	5	5	10	0.01%	10.4%	DSQTQAILTK	99.7%	51.5	25	37.7	2	0	0	1104.59	239	248
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	5	5	10	0.01%	10.4%	EGSQGELTPANSQSR	99.7%	67.6	25	67.1	4	0	0	1560.72	472	486

COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	5	5	10	0.01%	10.4%	MALSFVQR	99.7%	45.5	25	38	1	0	0	951.51	77	84
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	5	5	10	0.01%	10.4%	TLYTQIR	95.8%	29.3	25	24.1	1	0	0	894.50	364	370
COP9 signalosome complex subunit 7a	COPS7A	CSN7A_HUMAN	30.3	99.9%	2	2	3	0.00%	7.6%	ELAESDFASTFR	99.7%	52.1	25	52.1	2	0	0	1372.64	54	65
COP9 signalosome complex subunit 7a	COPS7A	CSN7A_HUMAN	30.3	99.9%	2	2	3	0.00%	7.6%	LEVDYSIGR	99.7%	48.8	25	35.9	1	0	0	1051.54	152	160
COP9 signalosome complex subunit 8	COPS8	CSN8_HUMAN	23.2	99.8%	2	2	2	0.00%	13.9%	GILEQGWQADSTTR	99.6%	39.8	25	26.3	1	0	0	1561.76	147	160
COP9 signalosome complex subunit 8	COPS8	CSN8_HUMAN	23.2	99.8%	2	2	2	0.00%	13.9%	SANSELGGIWSVGQR	99.7%	74.8	25	68.8	1	0	0	1560.78	66	80
Coronin-1C	CORO1C	COR1C_HUMAN	53.3	99.8%	2	2	3	0.00%	2.7%	KTTDTASVQNEAK	99.7%	88.6	25	74.3	2	0	0	1392.70	428	440
Coronin-1C	CORO1C	COR1C_HUMAN	53.3	99.8%	2	2	3	0.00%	2.7%	TTDTASVQNEAK	99.7%	44.6	25	39.9	1	0	0	1264.60	429	440
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	5	6	10	0.01%	16.8%	FCTGLTQIETLFK	99.7%	74.4	25	66.9	2	0	0	1557.80	253	265
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	5	6	10	0.01%	16.8%	FSEVLKR	99.7%	42.1	25	22.7	2	0	0	878.51	308	314
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	5	6	10	0.01%	16.8%	LAVEALSSLDGDLAGR	99.7%	104	25	104	2	0	0	1586.84	157	172
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	5	6	10	0.01%	16.8%	LGFSEVELVQMVVDGVK	99.6%	39.8	25	39.8	2	0	0	1864.97	342	358
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	5	6	10	0.01%	16.8%	VLTPELYAELR	99.7%	46.9	25	36.6	2	0	0	1303.73	33	43
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	12	13	24	0.02%	15.7%	AIANVPPIQEK	99.7%	53.7	25	51.3	2	0	0	1179.67	517	527
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	12	13	24	0.02%	15.7%	AIYELAISQPR	99.7%	44.3	25	37	2	0	0	1260.69	661	671
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	12	13	24	0.02%	15.7%	ALDVDYR	97.9%	32.1	25	28.2	1	0	0	851.43	268	274
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	12	13	24	0.02%	15.7%	APAEVQITAEQLLR	99.7%	63.5	25	57.1	2	0	0	1538.85	183	196
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	12	13	24	0.02%	15.7%	FAELETILGDIDR	99.7%	112	25	105	2	0	0	1491.77	646	658
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	12	13	24	0.02%	15.7%	FEENQKEFER	99.7%	44.7	25	34.1	2	1	0	1355.62	422	431
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	12	13	24	0.02%	15.7%	FVLVHPDVK	99.5%	39.3	25	32.2	2	0	0	1053.61	369	377
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	12	13	24	0.02%	15.7%	GIEDIIVSK	99.7%	57.4	25	47.3	2	0	0	973.56	467	475
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	12	13	24	0.02%	15.7%	LMLLESWR	99.7%	49.8	25	45.6	2	0	0	1047.57	752	759
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	12	13	24	0.02%	15.7%	LVESDAEAEAVR	99.7%	96.7	25	87.8	2	0	0	1288.64	500	511
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	12	13	24	0.02%	15.7%	SFEEEFGTASDKER	99.7%	85.7	25	85.7	2	0	0	1631.72	760	773
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	12	13	24	0.02%	15.7%	YTYMEEMLGNVAGAR	99.7%	72.7	25	72.7	2	0	0	1704.77	316	330
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	4	4	7	0.01%	11.4%	IGSGFDNIDIK	99.7%	56.5	25	44.5	2	0	0	1178.61	98	108
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	4	4	7	0.01%	11.4%	IRGETLGIIGLGR	99.4%	31.4	25	27.5	0	1	0	1354.82	172	184
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	4	4	7	0.01%	11.4%	QGAFLVNTAR	99.7%	45.3	25	37.2	2	0	0	1076.58	257	266
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	4	4	7	0.01%	11.4%	VGQAVALR	99.7%	70.1	25	54.8	2	0	0	813.49	185	192
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	4	4	7	0.01%	11.4%	VQSVEQIR	99.7%	47.3	25	26.8	2	0	0	958.53	156	163
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	4	4	6	0.01%	11.0%	GAALDVHESEPFSFAQGPLK	99.7%	37.8	25	35.7	0	1	0	2100.04	292	311
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	4	4	6	0.01%	11.0%	IGSGYDNVDIK	99.7%	48.6	25	41.8	2	0	0	1180.58	104	114
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	4	4	6	0.01%	11.0%	QGAFLVNAAR	99.7%	51.5	25	46.7	1	0	0	1046.57	263	272
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	4	4	6	0.01%	11.0%	VQSVEQIR	99.7%	47.3	25	26.8	2	0	0	958.53	162	169
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	39	0.04%	33.8%	ALEHSALAINHK	99.7%	50.4	25	50.4	2	2	0	1303.71	320	331
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	39	0.04%	33.8%	CSNPLDTSVK	99.7%	45.8	25	42.8	1	0	0	1120.53	218	227
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	39	0.04%	33.8%	ENFCNIHVSLVPQPSSTGEQK	99.7%	36.9	25	35.6	0	2	0	2371.13	173	193
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	39	0.04%	33.8%	FSDSYASVIK	99.7%	70.4	25	48.5	2	0	0	1116.56	310	319
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	39	0.04%	33.8%	FVGQDVEGER	99.7%	67	25	56.6	2	0	0	1135.54	499	508
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	39	0.04%	33.8%	GIIASSVGTILK	99.7%	63.3	25	60.2	2	0	0	1158.71	17	28
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	39	0.04%	33.8%	GLGLSPDLVVCR	99.3%	37.4	25	36.6	1	0	0	1285.69	206	217
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	39	0.04%	33.8%	IQAIAWAR	99.7%	62.3	25	43.2	2	0	0	928.54	382	389
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	39	0.04%	33.8%	IYQYVINK	99.5%	39.2	25	23.5	2	0	0	1040.58	93	100
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	39	0.04%	33.8%	KLYGDADYLEER	99.7%	76.9	25	70.9	2	2	0	1471.71	466	477
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	39	0.04%	33.8%	LCSAHGVLVPGGFGVR	99.7%	75.8	25	70.2	2	2	0	1625.86	361	376
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	39	0.04%	33.8%	LLETCSIALVGK	99.7%	95.5	25	88.2	2	0	0	1303.73	295	306
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	39	0.04%	33.8%	LSHYLQK	99.7%	46	25	28.1	1	0	0	888.49	551	557
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	39	0.04%	33.8%	LYGDADYLEER	99.7%	73.8	25	65.1	2	0	0	1343.61	467	477
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	39	0.04%	33.8%	RLDLPIER	99.7%	41.9	25	28.3	2	0	0	1011.59	269	276
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	39	0.04%	33.8%	SCGLHVTSIK	99.7%	47.9	25	31.5	2	0	0	1101.57	29	38
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	39	0.04%	33.8%	YIDSADLEPITSQEEPVR	99.7%	113	25	102	2	0	0	2062.00	336	353

CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	18	21	39	0.04%	33.8%	YILVTGGVISGIGK	99.7%	108	25	105	2	0	0	1376.82	3	16
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	2	2	4	0.00%	8.5%	ALEHSALAINHK	99.7%	50.4	25	50.4	2	2	0	1303.71	320	331
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	2	2	4	0.00%	8.5%	GIIASSIGTILK	99.7%	48.3	25	25.7	2	0	0	1172.73	17	28
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	2	2	4	0.00%	8.5%	VPVLLEEQSIVK	99.7%	72.2	25	72.2	2	0	0	1353.80	253	264
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	2	2	4	0.00%	8.5%	YILVTGGVISGIGK	99.7%	108	25	105	2	0	0	1376.82	3	16
Cullin-1	CUL1	CUL1_HUMAN	89.7	100.0%	2	2	3	0.00%	2.2%	LLIQAAIVR	99.7%	55.7	25	46.7	1	0	0	996.66	709	717
Cullin-1	CUL1	CUL1_HUMAN	89.7	100.0%	2	2	3	0.00%	2.2%	QVTNAVLK	99.4%	38.3	25	10.2	2	0	0	872.52	178	185
Cullin-4B	CUL4B	CUL4B_HUMAN	104.0	100.0%	5	5	7	0.01%	5.7%	ETVEEQASTTER	99.7%	76.6	25	76.6	1	0	0	1379.63	830	841
Cullin-4B	CUL4B	CUL4B_HUMAN	104.0	100.0%	5	5	7	0.01%	5.7%	QYQIDAAIVR	99.7%	46.6	25	41.3	1	0	0	1176.64	847	856
Cullin-4B	CUL4B	CUL4B_HUMAN	104.0	100.0%	5	5	7	0.01%	5.7%	RPNKPAELIAK	99.3%	30.6	25	24.7	0	2	0	1236.74	555	565
Cullin-4B	CUL4B	CUL4B_HUMAN	104.0	100.0%	5	5	7	0.01%	5.7%	SIFLFLDR	95.6%	29.1	25	26.1	1	0	0	1010.57	305	312
Cullin-4B	CUL4B	CUL4B_HUMAN	104.0	100.0%	5	5	7	0.01%	5.7%	TIDGILLLIER	99.7%	64.4	25	57.9	2	0	0	1255.76	346	356
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	AADIDQEVK	99.7%	51.3	25	36.5	2	0	0	988.49	578	586
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	AADIDQEVKER	99.7%	61.6	25	55	3	0	0	1273.64	578	588
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	ALTLIAGSPLK	99.7%	77.1	25	75.8	6	0	0	1083.68	631	641
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	AVAALLTIPEAEK	99.7%	77.3	25	60.7	4	0	0	1325.77	1179	1191
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	DLFTCTIK	96.3%	29.9	25	23.5	1	0	0	997.50	567	574
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	DLLDTVLPHLYNETK	99.7%	64.3	25	62.1	2	0	0	1770.93	1043	1057
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	DSIKLDDDSER	98.9%	35.3	25	17.7	2	0	0	1292.60	37	47
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	DSSSTNLESMDTS	99.7%	55.6	25	55.6	2	0	0	1389.53	1218	1230
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	EGPAVVGQFIQDVK	99.7%	60.8	25	52.8	6	0	0	1486.79	813	826
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	FMATNDLMTELQK	99.7%	91.8	25	86.6	5	0	0	1541.73	24	36
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	FTISDHPQPIDPLLK	99.7%	37.9	25	33.2	2	4	0	1720.93	991	1005
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	GYLISGSSYAR	99.7%	55.4	25	41.3	4	0	0	1173.59	972	982
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	HEMLPEFYK	94.9%	28.5	25	28.5	1	0	0	1193.57	365	373
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	HTVDDGLDIR	99.7%	47.6	25	33.5	2	0	0	1140.56	1073	1082
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	IGEYLEK	99.6%	40.3	25	32	2	0	0	851.45	249	255
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	ISGSILNELIGLVR	99.7%	63.3	25	60.2	1	0	0	1483.88	730	743
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	ITSEALLVTQQLVK	99.7%	92.9	25	81.2	4	1	0	1542.91	535	548
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	LGTLSALDILIK	99.7%	73.1	25	64.5	4	0	0	1256.78	668	679
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	LSTLCPSAVLQR	99.7%	53.6	25	43.8	2	0	0	1344.73	1130	1141
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	LTLIDPETLLPR	99.7%	64.3	25	64.3	7	0	0	1380.81	958	969
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	MLTFLMLVR	99.7%	60.8	25	15.9	5	0	0	1139.63	1121	1129
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	MLTGPVYSQSTALTHK	99.7%	93.7	25	90.3	4	3	0	1733.89	778	793
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	MTSSDKDFR	99.7%	47.7	25	40	2	0	0	1086.49	15	23
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	NCIGDFLK	97.2%	30.9	25	21.6	1	0	0	966.47	1006	1013
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	NVVAECLGK	98.7%	34.4	25	29.3	1	0	0	989.51	949	957
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	SVILEAFSSPSEEVK	99.7%	100	25	94.9	6	0	0	1621.83	859	873
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	TLEDPDLNVR	99.7%	70.5	25	57.4	2	0	0	1171.60	1014	1023
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	TVIGELPPASSGSALAANVCK	99.7%	110	25	110	2	0	0	2042.06	112	132
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	TVSPALISR	98.0%	32.4	25	15.9	2	0	0	943.56	374	382
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	TYIQCIAAISR	99.7%	83	25	74.3	2	0	0	1295.68	233	243
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	31	39	101	0.10%	29.3%	VIRPLDQPSSFDATPYIK	99.7%	64.8	25	64.8	1	3	0	2047.09	549	566
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	46	0.04%	52.2%	ALGTPNNEVWPEVESLQDYK	99.7%	76.3	25	76.3	2	0	0	2289.10	219	238
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	46	0.04%	52.2%	DLKPQNLLIDDKGTIK	99.7%	61.3	25	61.3	2	2	0	1811.03	128	143
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	46	0.04%	52.2%	IGEGTYGVVYK	99.7%	95.7	25	47.9	4	0	0	1185.62	10	20
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	46	0.04%	52.2%	IRLESEEEGVPSTAIR	99.7%	94.3	25	88.7	2	0	0	1785.93	35	50
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	46	0.04%	52.2%	LADFGLAR	99.7%	44.3	25	0	4	0	0	862.48	144	151
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	46	0.04%	52.2%	LESEEEGVPSTAIR	99.7%	66.5	25	57.6	3	0	0	1516.75	37	50
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	46	0.04%	52.2%	MALNHPYFNDLDNQIK	99.7%	59	25	56.8	4	4	0	1948.92	280	295
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	46	0.04%	52.2%	MLIYDPAK	99.7%	42.5	25	40.9	3	0	0	950.50	267	274

Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	46	0.04%	52.2%	MLIYDPAKR	99.7%	46.1	25	40.4	4	0	0	1122.60	267	275
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	46	0.04%	52.2%	NLDENGLDLLSK	99.7%	77.4	25	58.5	2	0	0	1330.69	255	266
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	46	0.04%	52.2%	SPEVLLGSAR	99.7%	66.9	25	58.7	2	0	0	1028.57	171	180
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	46	0.04%	52.2%	TTGQVVAMK	99.7%	59.9	25	44.5	2	0	0	934.50	25	33
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	46	0.04%	52.2%	WKPGSLASHVK	99.7%	43.1	25	43.1	0	2	0	1209.67	244	254
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	46	0.04%	52.2%	YLDSIPPGQYMDSSLVK	99.7%	64.7	25	63.1	4	0	0	1912.94	90	106
Cyclin-dependent kinase 11B	CDK11B	CD11B_HUMAN	92.7	100.0%	4	4	7	0.01%	5.4%	APELLLGAK	99.7%	43.4	25	31	2	0	0	911.56	605	613
Cyclin-dependent kinase 11B	CDK11B	CD11B_HUMAN	92.7	100.0%	4	4	7	0.01%	5.4%	FGALLSDQGFDLMNK	99.1%	36.2	25	36.2	1	0	0	1671.81	688	702
Cyclin-dependent kinase 11B	CDK11B	CD11B_HUMAN	92.7	100.0%	4	4	7	0.01%	5.4%	IEEGTYGVVYR	99.7%	76.6	25	76.6	2	0	0	1285.64	444	454
Cyclin-dependent kinase 11B	CDK11B	CD11B_HUMAN	92.7	100.0%	4	4	7	0.01%	5.4%	TLMIQLLR	99.5%	38.8	25	23.9	2	0	0	987.60	541	548
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	6	8	16	0.02%	33.6%	ALFPGDSEIDQLFR	99.7%	84.1	25	78.9	2	0	0	1607.81	201	214
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	6	8	16	0.02%	33.6%	APEILLGCK	99.7%	55.2	25	52.7	2	0	0	1000.55	170	178
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	6	8	16	0.02%	33.6%	DLKPQNLLINTEGAIK	99.7%	70.9	25	70.9	2	2	0	1767.00	127	142
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	6	8	16	0.02%	33.6%	FMDASALTGIPLPLIK	99.7%	119	25	119	4	0	0	1686.95	90	105
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	6	8	16	0.02%	33.6%	IGEGTYGVVYK	99.7%	95.7	25	47.9	4	0	0	1185.62	10	20
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	6	8	16	0.02%	33.6%	IRLDTETEGVPSTAIR	99.5%	31.4	25	23.3	0	2	0	1757.94	35	50
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	6	8	16	0.02%	33.6%	LADFGLAR	99.7%	44.3	25	0	4	0	0	862.48	143	150
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	6	8	16	0.02%	33.6%	LTGEVVALKK	99.7%	43.6	25	35.3	2	0	0	1057.66	25	34
Cyclin-dependent kinase 5	CDK5	CDK5_HUMAN	33.3	100.0%	3	3	3	0.00%	16.8%	DLKPQNLLINR	99.7%	43.3	25	41.7	1	0	0	1323.77	126	136
Cyclin-dependent kinase 5	CDK5	CDK5_HUMAN	33.3	100.0%	3	3	3	0.00%	16.8%	LADFGLAR	99.7%	44.3	25	0	4	0	0	862.48	142	149
Cyclin-dependent kinase 5	CDK5	CDK5_HUMAN	33.3	100.0%	3	3	3	0.00%	16.8%	LPDYKPYPMYPATTSLVNVVPK	99.5%	31.9	25	31.9	0	1	0	2509.31	233	254
Cyclin-dependent kinase 5	CDK5	CDK5_HUMAN	33.3	100.0%	3	3	3	0.00%	16.8%	SFLFQLLK	95.0%	28.5	25	12.9	1	0	0	995.59	105	112
Cyclin-dependent kinase 9	CDK9	CDK9_HUMAN	42.8	100.0%	3	3	6	0.01%	11.3%	GSQITQQSTNQSR	99.7%	92.6	25	80.4	2	0	0	1434.69	346	358
Cyclin-dependent kinase 9	CDK9	CDK9_HUMAN	42.8	100.0%	3	3	6	0.01%	11.3%	LADFGLAR	99.7%	44.3	25	0	4	0	0	862.48	165	172
Cyclin-dependent kinase 9	CDK9	CDK9_HUMAN	42.8	100.0%	3	3	6	0.01%	11.3%	LLVLDPAQR	99.7%	51.4	25	45.7	2	0	0	1024.62	295	303
Cyclin-dependent kinase 9	CDK9	CDK9_HUMAN	42.8	100.0%	3	3	6	0.01%	11.3%	NPATTNQTEFER	99.7%	71.5	25	66.1	2	0	0	1407.65	359	370
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	6	6	9	0.01%	10.9%	AAQELQEGQR	99.7%	64.9	25	51.8	2	0	0	1129.56	360	369
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	6	6	9	0.01%	10.9%	FDSPESHVGVAWR	97.5%	25.3	25	23.4	0	1	0	1486.71	197	209
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	6	6	9	0.01%	10.9%	IGDTPMVR	99.7%	44.1	25	33.9	2	0	0	904.46	84	91
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	6	6	9	0.01%	10.9%	KIGDTPMVR	98.8%	34.7	25	25.4	1	0	0	1032.55	83	91
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	6	6	9	0.01%	10.9%	PSETPQAEVGPTGCPHR	99.7%	58.2	25	49.8	0	1	0	1819.84	2	18
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	6	6	9	0.01%	10.9%	SNDEEAFTFAR	99.7%	74.4	25	74.3	2	0	0	1286.56	326	336
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	7	7	8	0.01%	17.5%	AIGTDEDLAHSSIR	99.7%	61.2	25	57.2	1	0	0	1484.73	394	407
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	7	7	8	0.01%	17.5%	GVGAIYIR	98.8%	35	25	23	2	0	0	848.50	264	271
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	7	7	8	0.01%	17.5%	IPLDVNDMK	98.3%	33.2	25	28.4	1	0	0	1044.54	240	248
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	7	7	8	0.01%	17.5%	KVYFHTDAAQAVGK	95.1%	22.7	25	18.7	0	1	0	1534.80	226	239
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	7	7	8	0.01%	17.5%	LIQNIMK	95.0%	28.6	25	21	1	0	0	875.50	329	335
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	7	7	8	0.01%	17.5%	QQVASLIGADPR	99.7%	43.4	25	35.6	1	0	0	1254.68	108	119
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	7	7	8	0.01%	17.5%	SLEAEGFQVTYLPVQK	99.7%	45	25	42.2	1	0	0	1808.94	165	180
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	6	6	9	0.01%	15.6%	FTGSEIR	99.3%	37.2	25	32.2	2	0	0	809.42	270	276
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	6	6	9	0.01%	15.6%	IAEVDASVVR	99.7%	75.6	25	43.7	2	0	0	1058.58	433	442
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	6	6	9	0.01%	15.6%	LCTSATESEVAR	99.7%	104	25	94.4	2	0	0	1323.62	379	390
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	6	6	9	0.01%	15.6%	MVLAAAGGVEHQQLLDLAQK	99.6%	33.2	25	33.2	0	1	0	2092.12	229	248
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	6	6	9	0.01%	15.6%	NALVSHLDGTTPVCEDIGR	99.7%	36.5	25	36.5	0	1	0	2054.00	397	415
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	6	6	9	0.01%	15.6%	SLLTYGR	96.0%	29.5	25	22.3	1	0	0	809.45	416	422
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	21	42	0.04%	45.3%	ATAAPAGAPPQPQDLEFTK	99.7%	86.3	25	82.3	2	0	0	1909.97	24	42
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	21	42	0.04%	45.3%	AVAFQNPQTHVIENLHAAAYR	99.7%	56.7	25	56.7	0	2	0	2350.21	163	183
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	21	42	0.04%	45.3%	ENMAYTVECLR	99.7%	77.2	25	66.9	4	0	0	1401.61	117	127
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	21	42	0.04%	45.3%	GSNTTSHLHQAVAK	99.7%	55.6	25	46.8	2	0	0	1450.74	302	315
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	21	42	0.04%	45.3%	LPNGLVIASLENYSPVSR	99.7%	97	25	97	2	2	0	1929.04	43	60
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	21	42	0.04%	45.3%	LTSSLTTK	97.9%	32.2	25	31.6	1	0	0	850.49	85	92

Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	21	42	0.04%	45.3%	MALIGLGVSHPVLK	99.7%	68.4	25	68.4	2	2	0	1450.85	218	231
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	21	42	0.04%	45.3%	NALANPLYCPDYR	99.7%	63.2	25	54.3	2	0	0	1566.74	184	196
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	21	42	0.04%	45.3%	QVAEQFLNMR	99.7%	74.8	25	65.4	4	0	0	1251.62	232	241
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	21	42	0.04%	45.3%	RWEVADLQPQLK	99.7%	65.9	25	59.1	2	2	0	1482.81	148	159
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	21	42	0.04%	45.3%	SMAASGNLGHTPFVDEL	99.7%	71.8	25	70.8	4	0	0	1761.81	437	453
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	21	42	0.04%	45.3%	TIAQGNLSNTDVQAAK	99.7%	98.8	25	94.7	3	0	0	1630.84	360	375
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	21	42	0.04%	45.3%	VTSEELHYFVQNHFTSAR	99.7%	39.5	25	39.5	0	2	0	2165.04	200	217
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	21	42	0.04%	45.3%	WEVADLQPQLK	99.7%	60.5	25	48.4	2	0	0	1326.71	149	159
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	15	21	42	0.04%	45.3%	YEDFSNLGTTHLLR	99.7%	89.5	25	89.5	2	0	0	1665.82	71	84
Cytochrome b-c1 complex subunit 8	UQCRQ	QCR8_HUMAN	9.9	100.0%	3	4	7	0.01%	37.8%	GREFGNLTR	98.4%	33.4	25	6.03	2	0	0	1049.55	2	10
Cytochrome b-c1 complex subunit 8	UQCRQ	QCR8_HUMAN	9.9	100.0%	3	4	7	0.01%	37.8%	HVISYSLSPFEQR	99.7%	62.4	25	62.4	2	2	0	1562.80	13	25
Cytochrome b-c1 complex subunit 8	UQCRQ	QCR8_HUMAN	9.9	100.0%	3	4	7	0.01%	37.8%	NPAAYENDK	98.9%	35	25	35	1	0	0	1021.46	74	82
Cytochrome b-c1 complex subunit 9	UQCR10	QCR9_HUMAN	7.3	99.8%	2	2	3	0.00%	38.1%	AFDQGADAIYDHINEGK	99.7%	51.9	25	51.9	2	0	0	1863.85	35	51
Cytochrome b-c1 complex subunit 9	UQCR10	QCR9_HUMAN	7.3	99.8%	2	2	3	0.00%	38.1%	LYSLLFR	98.5%	33.7	25	27.1	1	0	0	911.53	10	16
Cytochrome b-c1 complex subunit Rieske, mitochondrial	UQCRFS1	UCRI_HUMAN	29.7	100.0%	3	3	6	0.01%	19.0%	EIEQEAAVELSQLRDPQHDLDR	99.6%	32.4	25	32.4	0	1	0	2591.27	183	204
Cytochrome b-c1 complex subunit Rieske, mitochondrial	UQCRFS1	UCRI_HUMAN	29.7	100.0%	3	3	6	0.01%	19.0%	NAVTQFVSSMSASADVLALAK	99.7%	53.8	25	51.6	1	0	0	2110.08	131	151
Cytochrome b-c1 complex subunit Rieske, mitochondrial	UQCRFS1	UCRI_HUMAN	29.7	100.0%	3	3	6	0.01%	19.0%	RLEVLDSTK	99.7%	45.1	25	35.9	4	0	0	1060.60	93	101
Cytochrome c oxidase assembly factor 3 homolog, mitochondrial	COA3	COA3_HUMAN	11.7	99.8%	2	2	3	0.00%	17.9%	FLDELEDEAK	99.3%	37.1	25	28	2	0	0	1208.57	84	93
Cytochrome c oxidase assembly factor 3 homolog, mitochondrial	COA3	COA3_HUMAN	11.7	99.8%	2	2	3	0.00%	17.9%	RGEAPFAQR	96.1%	29.6	25	13.9	1	0	0	1031.54	14	22
Cytochrome c oxidase assembly protein COX15 homolog	COX15	COX15_HUMAN	46.0	99.8%	2	2	3	0.00%	4.6%	LPETHQLLQLR	99.7%	34.5	25	34.3	0	2	0	1347.77	251	261
Cytochrome c oxidase assembly protein COX15 homolog	COX15	COX15_HUMAN	46.0	99.8%	2	2	3	0.00%	4.6%	YQQFPEFK	95.5%	29	25	26	1	0	0	1086.53	124	131
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	5	7	18	0.02%	18.9%	IFEMGPVFTL	97.2%	31	25	23	2	0	0	1169.59	218	227
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	5	7	18	0.02%	18.9%	ILYMTDEVNDPSLTIK	99.7%	103	25	91.5	8	0	0	1851.94	83	98
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	5	7	18	0.02%	18.9%	LLDVDNR	99.7%	50.6	25	29.3	2	0	0	844.45	135	141
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	5	7	18	0.02%	18.9%	LLDVDNRVVLPIEAPIR	99.7%	40.6	25	38.3	0	2	0	1932.13	135	151
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	5	7	18	0.02%	18.9%	VVLPIEAPIR	99.7%	49.2	25	49.2	4	0	0	1106.69	142	151
Cytochrome c oxidase subunit 7A2, mitochondrial	COX7A2	CX7A2_HUMAN	9.4	99.8%	2	2	4	0.00%	27.7%	GGVADALLYR	99.7%	82.4	25	63.9	2	0	0	1034.56	47	56
Cytochrome c oxidase subunit 7A2, mitochondrial	COX7A2	CX7A2_HUMAN	9.4	99.8%	2	2	4	0.00%	27.7%	LFQEDDEIPLYLK	99.7%	65.3	25	54.6	2	0	0	1622.83	34	46
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	5	5	8	0.01%	7.1%	FVEFFGPGVAQLSIADR	99.7%	97.7	25	95.9	2	0	0	1852.96	277	293
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	5	5	8	0.01%	7.1%	GPFLLGIK	99.6%	40.1	25	33.8	2	0	0	844.53	786	793
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	5	5	8	0.01%	7.1%	SPPFFENLTLDLQPPK	99.4%	38.5	25	30.4	1	0	0	1842.96	645	660
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	5	5	8	0.01%	7.1%	VLLEAAIR	99.7%	47.9	25	38.5	1	0	0	884.56	41	48
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	5	5	8	0.01%	7.1%	YQQAGLPLIVLAGK	99.7%	74.4	25	74.4	2	0	0	1470.87	759	772
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	AATSPALFNR	99.7%	51.2	25	36.9	2	0	0	1047.56	3079	3088
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	AERPDVDEKR	99.7%	42.2	25	38.8	1	2	0	1214.61	3719	3728
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	AISKDHLYGTLDPNTR	97.3%	25	25	25	0	1	0	1800.92	2258	2273
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	ALGEYLER	99.7%	48.2	25	41.8	2	0	0	950.49	1614	1621
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	ALGHQLGR	98.7%	34.4	25	25.8	1	0	0	851.48	1918	1925
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	ANEVEQMIR	99.7%	54.1	25	43.8	2	0	0	1089.54	3430	3438
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	ASLACGPMVK	99.0%	35.7	25	30.3	2	0	0	1033.52	3385	3394
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	ASVVTLPVYLNFTR	99.6%	40.6	25	40.6	2	0	0	1579.88	4602	4615
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	CYLTMTQALEAR	99.7%	77.5	25	76.8	2	0	0	1456.69	1888	1899
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	DAATIMQPYFTSNGLVTK	99.7%	60.4	25	59.2	1	0	0	1972.97	2418	2435
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	DLFQVAFNR	99.7%	59.1	25	51.8	6	0	0	1109.57	3862	3870
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	DLPPVSGSIIWAK	99.7%	62.7	25	58.8	2	0	0	1382.77	640	652
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	DSAIQQQVANLQMK	99.7%	91.3	25	79.6	4	0	0	1573.80	1229	1242
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	DYIPVDQEELRDYVK	99.7%	48.3	25	41	2	0	0	1881.92	2880	2894
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	EAIVNSCVFVHQTLHQANAR	98.3%	26.6	25	26.6	0	1	0	2294.15	3141	3160
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	EALELTDTGLLSGSEER	99.7%	126	25	116	2	0	0	1819.89	1302	1318
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	EFGPVVIDYGK	99.3%	37.4	25	37.4	2	0	0	1223.63	1101	1111
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	EGLMLDSHEELYK	99.7%	47.3	25	42.9	1	0	0	1563.74	3040	3052

Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	EHINSVSAMK	99.7%	50.4	25	43.5	4	0	0	1115.55	1499	1508
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	EQPWVSVQPR	94.8%	28.4	25	24.6	1	0	0	1225.63	1348	1357
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	ESPEVLLTLDILK	99.7%	78.2	25	66.9	1	0	0	1469.85	293	305
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	EYQTQLIQR	99.0%	35.8	25	22.4	2	0	0	1178.62	603	611
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	FNYGFEYLGVQDK	99.7%	88.6	25	88.6	2	0	0	1579.74	1866	1878
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	FQSISTEFLALMK	99.7%	82.1	25	77.9	2	0	0	1530.79	1568	1580
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	FTQDTQPHYIYSPR	99.7%	74.9	25	74.9	2	1	0	1752.83	2784	2797
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	GTFDNAETKK	99.1%	36.4	25	31.8	2	0	0	1110.54	1091	1100
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	GWDDLFNK	95.9%	29.4	25	16.7	1	0	0	994.46	1489	1496
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	GWENHVEGQK	99.7%	43.5	25	33.7	1	0	0	1183.55	672	681
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	HLLPVETQR	99.4%	38	25	36.3	1	0	0	1092.62	1559	1567
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	IAFIMDESNVLDSGFLER	99.4%	38.4	25	37.9	1	0	0	2072.00	2990	3007
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	IFTIESTR	99.7%	58.1	25	40.7	2	0	0	966.53	717	724
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	IFVFEPPPGVK	99.7%	45.9	25	35.2	4	0	0	1229.69	4144	4154
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	IMFEVQDLK	99.7%	47.4	25	41.6	2	0	0	1138.58	2341	2349
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	INEWLTLVEK	99.7%	65.7	25	56.1	2	0	0	1244.69	1698	1707
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	INMLVIELK	99.7%	67.8	25	54	2	0	0	1088.64	1396	1404
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	IQFVGACNPPTDPGR	99.7%	106	25	101	2	0	0	1628.79	2706	2720
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	IQGLTVEQAEAVVR	99.7%	99.5	25	94.1	2	0	0	1512.84	3924	3937
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	ITNQVIYLNPPIEECR	99.7%	70.9	25	70.9	2	0	0	1959.00	964	979
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	IWAHEALR	99.4%	38.1	25	20.5	1	0	0	995.54	2824	2831
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	KIIDSVR	98.9%	35.2	25	16.7	1	0	0	830.51	2286	2292
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	KYEFGESDLR	99.7%	47.9	25	31.5	2	0	0	1243.60	4204	4213
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	LEGVEGVAHIIDPK	97.1%	24.7	25	22.6	0	1	0	1476.81	2244	2257
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	LFLTMEINPK	99.7%	50.9	25	43.9	3	0	0	1205.66	4124	4133
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	LGGSPFGPAGTGK	99.7%	71.6	25	69.7	2	0	0	1145.60	1900	1912
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	LKQDGDSFR	99.7%	57.1	25	54.3	2	0	0	1065.53	682	690
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	LLAESVTEVEIFGK	99.7%	49.4	25	49.4	1	0	0	1534.84	1716	1729
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	LLNTFLER	99.7%	52.8	25	41.2	2	0	0	1005.57	4264	4271
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	LNTQEIFDDWAR	99.7%	74.9	25	67.5	1	0	0	1507.72	693	704
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	LQGEFQLR	99.7%	49.9	25	37.5	2	0	0	990.54	3734	3741
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	LRDQLGTAK	99.7%	48.2	25	37.5	2	0	0	1001.57	568	576
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	LSCLPAFK	99.3%	37	25	28.8	2	0	0	935.50	3938	3945
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	LSLSNAISTALPLTQLR	99.7%	57.3	25	56.9	2	0	0	1798.04	4575	4591
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	LVQTPLTDR	99.7%	47.8	25	43.1	2	0	0	1042.59	1879	1887
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	MLSAVSQQVQCIQEALR	99.7%	71.6	25	64.1	1	0	0	1960.99	1967	1983
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	MVVLSLPR	99.7%	51.5	25	49.8	4	0	0	914.55	991	998
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	NANEMFR	98.9%	35.3	25	30.8	1	0	0	881.39	577	583
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	NTISLLVAGLK	99.7%	75.9	25	49	2	0	0	1128.70	799	809
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	NVVHELR	94.8%	28.4	25	16.3	1	0	0	866.48	957	963
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	NYMSNPSYNYEIVNR	99.7%	99.2	25	99.2	4	0	0	1879.83	3370	3384
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	QALETVNDYNPLMK	99.7%	57.6	25	57.6	1	0	0	1635.80	324	337
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	QLQNISLAAASGGAK	99.7%	56	25	44.5	1	0	0	1428.78	4488	4502
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	QLTAYMK	99.6%	40.1	25	30.6	1	0	0	854.44	657	663
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	QNLDALLNQLK	99.7%	62.8	25	46.9	2	0	0	1269.72	1361	1371
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	QTDVLQQLSIQMANAK	99.7%	74.9	25	74.9	2	0	0	1787.93	1850	1865
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	QYASYEFVQR	99.7%	52.9	25	45.2	2	0	0	1290.61	1379	1388
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	SFEWLSQMR	98.5%	33.8	25	29.7	1	0	0	1199.55	1835	1843
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	SIPLDEGEDEAQR	99.7%	58.5	25	54.9	2	0	0	1458.67	2384	2396
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	SIPLDEGEDEAQRR	97.5%	31.5	25	31.5	1	0	0	1614.77	2384	2397
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	SLETCMYDHK	99.7%	50.5	25	50.5	2	0	0	1283.54	863	872

Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	SLLQALNEVK	99.7%	73.1	25	61	4	0	0	1114.65	3748	3757
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	SMANPPAAVK	99.3%	37.5	25	31.2	3	0	0	985.51	3309	3318
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	SNSLAFIK	99.7%	67.2	25	54.4	2	0	0	879.49	113	120
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	SPLVMDVLNIQGVQR	99.7%	96.6	25	89.2	4	0	0	1684.91	1585	1599
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	SSLQSQCLNEVLK	99.7%	71.5	25	60.9	2	0	0	1505.76	3706	3718
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	SVLVSAGNVK	97.8%	32	25	22.8	2	0	0	973.57	2095	2104
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	SVLVSAGNVKR	99.7%	46.3	25	35.9	2	0	0	1129.67	2095	2105
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	TEYLSNADER	99.7%	41.2	25	36.3	3	0	0	1197.54	3550	3559
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	TFSEILNR	99.7%	47.9	25	39	2	0	0	979.52	873	880
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	TFSSIPVSR	99.6%	40.1	25	33.5	3	0	0	993.54	4160	4168
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	TLINELVK	96.8%	30.4	25	2.76	1	0	0	929.57	4450	4457
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	TLMAQSIYGGR	99.7%	57.8	25	51.6	1	0	0	1196.61	4245	4255
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	TMTLFSALR	99.7%	48.3	25	40.1	2	0	0	1055.56	2602	2610
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	TPNGVVLAPVQLGK	99.7%	64.4	25	64.4	2	0	0	1392.82	2644	2657
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	TPVIDADKPVSSQLR	99.7%	63.7	25	59.1	1	2	0	1625.89	122	136
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	TPVSITEHPK	99.7%	56	25	49.1	2	0	0	1108.60	1688	1697
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	TSAPITCELLNK	99.7%	61.6	25	49.5	2	0	0	1346.70	1993	2004
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	TSFLDDAFRK	99.7%	61.5	25	53.4	2	0	0	1199.61	3612	3621
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	TTDLLTDWEK	99.7%	45.1	25	42.6	2	0	0	1221.60	1254	1263
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	TVENIKDPLFR	98.9%	35	25	25.2	2	0	0	1331.73	4401	4411
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	VAAPDVVVPTLDTVR	99.7%	57.9	25	57.9	2	0	0	1551.87	2562	2576
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	VDNEFDQR	99.7%	53.6	25	45	2	0	0	1022.45	4256	4263
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	VEPLRNELQK	98.2%	33	25	17.1	1	0	0	1225.69	3409	3418
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	VLLTTQGVDMISK	99.7%	104	25	99.7	5	0	0	1404.78	4330	4342
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	VLRPQVTAVAQQNQGEVPEPQDMK	99.7%	52.2	25	51	0	2	0	2662.36	483	506
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	VMSQEIQEQLHK	99.7%	48.7	25	37.9	2	0	0	1469.74	3255	3266
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	VNFLPEIITLSK	99.7%	50.3	25	43.1	2	0	0	1373.80	737	748
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	VPLAIVNK	99.7%	51.5	25	51.5	2	0	0	853.55	760	767
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	VPQIEVETHK	99.7%	52.2	25	39.6	2	0	0	1179.64	2552	2561
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	VPVNLLR	99.0%	35.6	25	25	2	0	0	810.52	4134	4140
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	VQVALEELQDLK	99.7%	60.7	25	46.8	1	0	0	1384.77	1319	1330
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	VQYPQSQACK	99.4%	38.4	25	26.5	2	0	0	1208.57	625	634
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	VTFVNFTVTR	99.7%	75.8	25	69.3	2	0	0	1183.65	3696	3705
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	WQALLVQIR	99.1%	36.4	25	36.4	2	0	0	1126.67	1079	1087
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	WTDENIDTVALK	99.7%	73.5	25	69.5	2	0	0	1404.70	2845	2856
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	105	116	210	0.20%	25.1%	YATLATVSR	99.7%	55.9	25	46.6	2	0	0	981.54	2350	2358
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	6	7	9	0.01%	16.4%	IGILHENFQTLK	99.7%	44.7	25	40.7	1	2	0	1412.79	333	344
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	6	7	9	0.01%	16.4%	IPAVVVEK	99.7%	43.6	25	27.2	2	0	0	854.53	311	318
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	6	7	9	0.01%	16.4%	KPVTVSPTTPTSPTEGEAS	99.7%	52.7	25	52.7	1	0	0	1885.94	505	523
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	6	7	9	0.01%	16.4%	QPPTAAGRPVDASPR	95.2%	22.8	25	22.2	0	1	0	1519.80	386	400
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	6	7	9	0.01%	16.4%	SGQKPVLDVHAELDR	99.7%	45	25	36.1	0	1	0	1663.88	487	501
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	6	7	9	0.01%	16.4%	SVSSNVASVSPIPAGSK	99.7%	70.8	25	66.7	1	0	0	1586.84	412	428
Cytoplasmic dynein 2 heavy chain 1	DYNC2H1	DYHC2_HUMAN	492.6	100.0%	3	3	4	0.00%	0.9%	TVAGGGLETISNLK	99.7%	57.1	25	36	1	0	0	1359.75	999	1012
Cytoplasmic dynein 2 heavy chain 1	DYNC2H1	DYHC2_HUMAN	492.6	100.0%	3	3	4	0.00%	0.9%	VLSFPGGSLLLAGR	99.7%	52.9	25	52.9	2	0	0	1386.81	2643	2656
Cytoplasmic dynein 2 heavy chain 1	DYNC2H1	DYHC2_HUMAN	492.6	100.0%	3	3	4	0.00%	0.9%	VTTLTTHAGIR	99.2%	36.5	25	29.5	1	0	0	1169.66	1388	1398
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	11	13	20	0.02%	10.5%	ALNLAYSSIYGSYR	99.7%	62.5	25	39.2	1	0	0	1577.80	893	906
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	11	13	20	0.02%	10.5%	AVGPSSTQLYMVR	99.7%	81.9	25	81.9	4	0	0	1408.73	551	563
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	11	13	20	0.02%	10.5%	EANHNVSAPYGR	99.7%	44.8	25	44.8	1	2	0	1314.62	827	838
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	11	13	20	0.02%	10.5%	EFFLELTMGR	97.7%	31.9	25	31.9	1	0	0	1258.61	625	634
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	11	13	20	0.02%	10.5%	LGTPQQIAIAR	99.7%	72.4	25	61.4	2	0	0	1167.68	1066	1076
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	11	13	20	0.02%	10.5%	NVIQSVLQAIR	99.7%	69.7	25	46.9	2	0	0	1240.74	505	515

Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	11	13	20	0.02%	10.5%	SGDGEGTPVEHVR	99.3%	37.6	25	35.5	1	0	0	1339.62	1228	1240
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	11	13	20	0.02%	10.5%	SLLQGTILQYVK	99.7%	50.9	25	50.9	1	0	0	1362.80	939	950
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	11	13	20	0.02%	10.5%	SSLEGPTILDIEK	99.7%	87.9	25	76.2	2	0	0	1401.75	582	594
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	11	13	20	0.02%	10.5%	TVEVLEPEVTK	99.7%	45.8	25	35	1	0	0	1243.68	111	121
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	11	13	20	0.02%	10.5%	YSNSEVVTGSGR	99.7%	95.8	25	86.3	2	0	0	1255.59	366	377
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	8	8	13	0.01%	4.7%	EGLDEVAGIINDAK	99.7%	83.5	25	79.3	2	0	0	1443.73	879	892
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	8	8	13	0.01%	4.7%	HCTASTLPK	97.0%	30.8	25	30.8	1	0	0	1014.50	426	434
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	8	8	13	0.01%	4.7%	HINDSAPEVR	95.5%	29	25	19.4	2	0	0	1137.56	447	456
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	8	8	13	0.01%	4.7%	LDDIFEPVLIPEPK	99.7%	49.6	25	41.9	2	0	0	1624.88	1510	1523
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	8	8	13	0.01%	4.7%	NLGIPIITVLGDSK	97.7%	31.8	25	31.8	2	0	0	1439.85	941	954
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	8	8	13	0.01%	4.7%	NSSQFFQSYVER	99.7%	64.4	25	64.4	1	0	0	1491.69	1871	1882
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	8	8	13	0.01%	4.7%	TALAATNPAVR	99.7%	47.2	25	36.1	1	0	0	1084.61	762	772
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	8	8	13	0.01%	4.7%	TTGEVVSGVVSK	99.7%	61.5	25	51.2	2	0	0	1162.63	85	96
Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	NUBP2_HUMAN	28.8	99.8%	2	2	4	0.00%	10.0%	STISTELALALR	99.7%	49.6	25	40.7	2	0	0	1274.73	29	40
Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	NUBP2_HUMAN	28.8	99.8%	2	2	4	0.00%	10.0%	VGILDVDLCGPSIPR	99.7%	83.2	25	73.6	2	0	0	1610.86	46	60
Cytosolic non-specific dipeptidase	CNDP2	CNDP2_HUMAN	52.9	100.0%	4	4	6	0.01%	10.1%	EGGSIPVTLTFQEATGK	98.7%	34.2	25	34.2	1	0	0	1734.89	414	430
Cytosolic non-specific dipeptidase	CNDP2	CNDP2_HUMAN	52.9	100.0%	4	4	6	0.01%	10.1%	QLGGSVELVDIGK	98.1%	32.7	25	6.68	1	0	0	1314.73	54	66
Cytosolic non-specific dipeptidase	CNDP2	CNDP2_HUMAN	52.9	100.0%	4	4	6	0.01%	10.1%	TGQEIPVNVR	99.7%	46.5	25	33.8	2	0	0	1112.61	150	159
Cytosolic non-specific dipeptidase	CNDP2	CNDP2_HUMAN	52.9	100.0%	4	4	6	0.01%	10.1%	YNYIEGTK	99.7%	46.7	25	39.2	2	0	0	987.48	454	461
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	113	0.11%	44.8%	AGTGVDNVDLEAATR	99.7%	107	25	93.3	8	0	0	1488.73	76	90
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	113	0.11%	44.8%	ALQSGQCAGAALDVFTEEPPRDR	99.7%	74.1	25	74.1	0	2	0	2488.19	248	270
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	113	0.11%	44.8%	ALVDHENVISCPHLGASTK	99.7%	102	25	95.9	2	2	0	2048.02	271	289
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	113	0.11%	44.8%	CGEEIAVQFVDMVK	99.7%	106	25	106	6	0	0	1624.77	295	308
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	113	0.11%	44.8%	DLPLLLFR	99.7%	58.9	25	51.1	18	0	0	986.60	462	469
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	113	0.11%	44.8%	EELIAELQDCEGLIVR	99.7%	67.5	25	64.9	2	0	0	1886.95	39	54
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	113	0.11%	44.8%	FMGTELNGK	99.7%	52.9	25	40	4	0	0	996.48	138	146
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	113	0.11%	44.8%	GGIVDEGALLR	99.7%	93.8	25	63.2	6	0	0	1099.61	237	247
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	113	0.11%	44.8%	GTIQVITQGTSLK	99.7%	87.7	25	79.8	7	0	0	1345.77	352	364
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	113	0.11%	44.8%	ILQDGGLQVVEK	99.7%	84.2	25	75.3	5	0	0	1298.73	22	33
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	113	0.11%	44.8%	KFMGTELNGK	99.5%	38.9	25	34.6	1	0	0	1140.57	137	146
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	113	0.11%	44.8%	MQSFGMK	98.2%	32.8	25	26.1	2	0	0	828.37	164	170
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	113	0.11%	44.8%	NAGNCLSPAVIVGLLK	99.7%	67.6	25	61	8	0	0	1625.90	365	380
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	113	0.11%	44.8%	QADVNLVNAK	99.7%	56.3	25	49	2	0	0	1071.58	385	394
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	113	0.11%	44.8%	QIPQATASMK	99.7%	41.7	25	35.8	3	0	0	1090.56	120	129
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	113	0.11%	44.8%	TLGILGLGR	99.7%	70.6	25	56.8	10	0	0	899.57	147	155
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	113	0.11%	44.8%	TQTSDPAMLPTMIGLLAEAGVR	99.7%	115	25	107	7	6	0	2272.17	470	491
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	113	0.11%	44.8%	VLISDSLDPCCR	99.7%	73.2	25	70.4	2	0	0	1434.67	9	20
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	113	0.11%	44.8%	VLISDSLDPCCRK	99.2%	36.4	25	20.6	2	0	0	1562.77	9	21
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	113	0.11%	44.8%	VTADVINAAEK	99.7%	91.9	25	76.8	8	0	0	1130.61	59	69
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	9	10	17	0.02%	19.1%	ESVLTATSILNNPIVK	99.7%	114	25	104	3	0	0	1698.96	444	459
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	9	10	17	0.02%	19.1%	FGGSYGGR	99.7%	48.3	25	34.9	1	0	0	800.37	103	110
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	9	10	17	0.02%	19.1%	FGPYESYDSR	99.7%	53	25	53	2	0	0	1220.52	71	80
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	9	10	17	0.02%	19.1%	MAFTCSFCK	99.5%	39.2	25	38	3	0	0	1151.47	310	318
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	9	10	17	0.02%	19.1%	NQGGSSWEAPYSR	99.7%	47.2	25	44.6	2	0	0	1438.63	126	138
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	9	10	17	0.02%	19.1%	NSLDSFGGR	99.7%	55.8	25	45.2	2	0	0	952.45	117	125
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	9	10	17	0.02%	19.1%	QQTNNQTEVVK	99.7%	44.4	25	37.3	1	0	0	1288.65	373	383
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	9	10	17	0.02%	19.1%	SGYGFNEPEQSR	99.7%	49.5	25	49.5	2	0	0	1370.60	91	102
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	9	10	17	0.02%	19.1%	SMDSYLNQSYGMDNHSGGGGGSR	99.7%	37.6	25	37.6	0	1	0	2408.95	48	70
DDB1- and CUL4-associated factor 7	DCAF7	DCAF7_HUMAN	38.9	100.0%	4	4	8	0.01%	14.0%	GVYPDLLATSGDYLR	99.7%	117	25	113	2	0	0	1639.83	82	96
DDB1- and CUL4-associated factor 7	DCAF7	DCAF7_HUMAN	38.9	100.0%	4	4	8	0.01%	14.0%	LALGSFVEEYNNK	99.7%	65.4	25	61.5	2	0	0	1483.74	34	46
DDB1- and CUL4-associated factor 7	DCAF7	DCAF7_HUMAN	38.9	100.0%	4	4	8	0.01%	14.0%	NTFDHPYPTTK	98.8%	34.7	25	34	2	0	0	1320.62	63	73

DDB1- and CUL4-associated factor 7	DCAF7	DCAF7_HUMAN	38.9	100.0%	4	4	8	0.01%	14.0%	VNLVSGHVK	99.7%	41	25	32.7	2	0	0	952.56	159	167
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	3	3	3	0.00%	1.9%	ESGVSLIATVTR	99.7%	44.5	25	31.3	1	0	0	1232.68	1146	1157
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	3	3	3	0.00%	1.9%	IGCTVSLLNFYK	99.7%	53.6	25	53.6	1	0	0	1414.74	1179	1190
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	3	3	3	0.00%	1.9%	TVESQLYTNPDSR	99.7%	64.3	25	57.6	1	0	0	1509.72	815	827
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	8	13	22	0.02%	32.9%	GTIMDTTVDVDKR	99.3%	37.5	25	31.6	2	0	0	1450.72	149	161
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	8	13	22	0.02%	32.9%	HATQAFFDCLR	99.7%	61.2	25	59.8	2	0	0	1365.64	212	222
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	8	13	22	0.02%	32.9%	NAVVVITGATSGLGK	99.7%	100	25	91	2	0	0	1386.80	52	66
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	8	13	22	0.02%	32.9%	QGHIVAISSIQGK	99.7%	46.6	25	37.2	1	1	0	1337.75	186	198
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	8	13	22	0.02%	32.9%	SPVEVAQDVLAAVGK	99.7%	105	25	100	2	0	0	1482.82	268	282
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	8	13	22	0.02%	32.9%	TLAPGLFFSLMASR	99.7%	69.1	25	69.1	4	0	0	1510.81	302	315
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	8	13	22	0.02%	32.9%	VMETNYFGPVALTK	99.7%	96.8	25	72.1	4	0	0	1569.80	162	175
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	8	13	22	0.02%	32.9%	YGVMDTTTAQGR	99.7%	92.5	25	92.5	4	0	0	1299.60	256	267
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	5	5	9	0.01%	11.9%	NAAGNFYINDK	99.2%	36.8	25	36.8	1	0	0	1226.58	499	509
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	5	5	9	0.01%	11.9%	SADVESVVSGTLR	99.7%	92.7	25	88.6	2	0	0	1319.68	326	338
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	5	5	9	0.01%	11.9%	SSPSLTILAGGK	99.7%	59.2	25	49.9	2	0	0	1130.64	409	420
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	5	5	9	0.01%	11.9%	STGSIVGQQPFGGAR	99.7%	66.3	25	62	2	0	0	1461.74	510	524
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	5	5	9	0.01%	11.9%	VANEPVLAFTQGSPER	99.7%	84.5	25	82.9	2	0	0	1714.88	32	47
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	26	30	68	0.06%	34.5%	DLEEAEGR	99.3%	37	25	25.6	2	0	0	918.42	410	417
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	26	30	68	0.06%	34.5%	EAVQLVNTR	99.7%	59.1	25	46.8	3	0	0	1029.57	531	539
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	26	30	68	0.06%	34.5%	EAVQLVNTREEVEDLCR	99.7%	34.7	25	34.7	0	1	0	2060.01	531	547
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	26	30	68	0.06%	34.5%	EEVEDLCR	99.1%	36	25	35	1	0	0	1049.46	540	547
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	26	30	68	0.06%	34.5%	EMAIPVLEAR	99.7%	41.4	25	37.7	2	0	0	1144.60	150	159
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	26	30	68	0.06%	34.5%	EMMLVTSGAVAFGK	99.7%	71.1	25	14.1	2	0	0	1456.72	111	124
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	26	30	68	0.06%	34.5%	FASYLTFSPSEVK	99.7%	83.8	25	82.9	2	0	0	1475.74	650	662
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	26	30	68	0.06%	34.5%	GKDHVVSDFSEHGSLK	99.7%	57.1	25	57.1	0	2	0	1741.85	766	781
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	26	30	68	0.06%	34.5%	GPVGLEGLLTTK	99.7%	73.5	25	73.5	2	0	0	1184.69	750	761
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	26	30	68	0.06%	34.5%	HEILLSQSVR	99.7%	61.4	25	50.7	2	0	0	1181.66	129	138
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	26	30	68	0.06%	34.5%	LASIVEQVSVLQNQGR	99.7%	84.6	25	72.8	4	0	0	1740.96	95	110
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	26	30	68	0.06%	34.5%	LGSAVVTR	99.7%	69.8	25	47.8	4	0	0	802.48	77	84
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	26	30	68	0.06%	34.5%	LIDIFYPGDQQSVTFGTK	99.7%	107	25	105	5	0	0	2029.03	283	300
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	26	30	68	0.06%	34.5%	LNSLAIGLR	99.7%	84.8	25	67.4	2	0	0	956.59	433	441
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	26	30	68	0.06%	34.5%	LRHEILLSQSVR	99.2%	29.6	25	29.6	0	2	0	1450.85	127	138
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	26	30	68	0.06%	34.5%	MIDLIIPR	99.7%	65.3	25	47	6	0	0	970.58	551	558
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	26	30	68	0.06%	34.5%	MLATLEPEQR	99.7%	60.8	25	43.3	4	0	0	1203.60	376	385
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	26	30	68	0.06%	34.5%	NLNGTLHELLR	99.7%	52.8	25	45.7	2	0	0	1279.71	202	212
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	26	30	68	0.06%	34.5%	QALHSGQNQLK	99.7%	36.1	25	27.2	0	2	0	1223.65	139	149
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	26	30	68	0.06%	34.5%	QIAASSQDSVGR	99.7%	86	25	83.5	2	0	0	1218.61	442	453
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	26	30	68	0.06%	34.5%	TPLFDQIIDMLR	99.7%	72.3	25	66.6	2	0	0	1477.77	627	638
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	26	30	68	0.06%	34.5%	VGMGGMEAK	99.7%	48.7	25	41.4	2	0	0	879.41	303	311
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	26	30	68	0.06%	34.5%	VGTFFSEVKPAGPTVEQQGEMAR	99.7%	94.3	25	94.3	0	4	0	2465.21	349	371
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	26	30	68	0.06%	34.5%	VSGHVITDIVEGK	99.7%	52.2	25	49.7	2	0	0	1353.74	335	347
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	26	30	68	0.06%	34.5%	VSGHVITDIVEGKK	99.7%	55.5	25	55.5	0	2	0	1481.83	335	348
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	26	30	68	0.06%	34.5%	YLHENLPIPQR	99.1%	36.2	25	36.2	2	2	0	1379.74	782	792
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	8	8	10	0.01%	14.7%	FENLGVSSLGER	99.7%	67.7	25	63.2	2	0	0	1307.66	86	97
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	8	8	10	0.01%	14.7%	FIPLARPEVK	97.8%	32	25	23.2	1	0	0	1169.70	221	230
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	8	8	10	0.01%	14.7%	GGFEEPVLLK	99.7%	49.5	25	27.7	1	0	0	1088.60	57	66
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	8	8	10	0.01%	14.7%	IIDTPQFQR	99.7%	44.3	25	35.2	2	0	0	1117.60	135	143
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	8	8	10	0.01%	14.7%	ISTAIDDMEAYTK	99.7%	90.7	25	83.1	1	0	0	1457.68	409	421
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	8	8	10	0.01%	14.7%	SFLYEIVSNKR	99.7%	64.7	25	64.3	1	0	0	1355.73	295	305
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	8	8	10	0.01%	14.7%	VGNIIDTMITDAFLK	99.7%	51.9	25	51.9	1	0	0	1650.88	378	392
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	8	8	10	0.01%	14.7%	YVGETQPTGQIK	99.7%	41.7	25	34.7	1	0	0	1320.68	456	467

Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial	DUT	DUT_HUMAN	26.6	99.8%	2	2	3	0.00%	7.1%	IAQLICER	99.7%	55	25	45.6	2	0	0	1002.54	217	224
Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial	DUT	DUT_HUMAN	26.6	99.8%	2	2	3	0.00%	7.1%	LSEHATAPTR	99.4%	38.4	25	31.2	1	0	0	1082.56	119	128
Dephospho-CoA kinase domain-containing protein	DCAKD	DCAKD_HUMAN	26.6	100.0%	4	4	7	0.01%	19.9%	HVVQPGYPAHR	99.0%	35.6	25	35.6	1	0	0	1260.66	37	47
Dephospho-CoA kinase domain-containing protein	DCAKD	DCAKD_HUMAN	26.6	100.0%	4	4	7	0.01%	19.9%	INAQLPLTDK	99.7%	53	25	39.1	2	0	0	1112.63	159	168
Dephospho-CoA kinase domain-containing protein	DCAKD	DCAKD_HUMAN	26.6	100.0%	4	4	7	0.01%	19.9%	MFLVGLTGGIASGK	99.7%	98.9	25	98.9	2	0	0	1350.75	1	14
Dephospho-CoA kinase domain-containing protein	DCAKD	DCAKD_HUMAN	26.6	100.0%	4	4	7	0.01%	19.9%	QVILLHTELER	96.9%	30.6	25	21.7	2	0	0	1350.77	188	198
Dermcidin	DCD	DCD_HUMAN	11.3	100.0%	3	4	59	0.06%	22.7%	DAVEDLESVGK	99.7%	70.9	25	66.3	16	0	0	1161.56	86	96
Dermcidin	DCD	DCD_HUMAN	11.3	100.0%	3	4	59	0.06%	22.7%	ENAGEDPGLAR	99.7%	80.6	25	75.9	36	0	0	1128.53	43	53
Dermcidin	DCD	DCD_HUMAN	11.3	100.0%	3	4	59	0.06%	22.7%	LGKDAVEDLESVGK	99.7%	80.1	25	74.5	5	2	0	1459.76	83	96
Desmoglein-4	DSG4	DSG4_HUMAN	113.8	100.0%	3	3	3	0.00%	2.5%	EITPLFLIYCR	99.7%	47.2	25	46.8	1	0	0	1424.76	118	128
Desmoglein-4	DSG4	DSG4_HUMAN	113.8	100.0%	3	3	3	0.00%	2.5%	IQVVDVR	99.0%	35.4	25	17.9	1	0	0	828.49	374	380
Desmoglein-4	DSG4	DSG4_HUMAN	113.8	100.0%	3	3	3	0.00%	2.5%	TGEIQFSR	99.7%	52.5	25	34.5	1	0	0	937.47	443	450
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	11	11	14	0.01%	4.2%	AELIVQPELK	99.7%	43.2	25	34.9	3	0	0	1139.67	85	94
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	11	11	14	0.01%	4.2%	AITGFDDPFSGK	99.1%	35.9	25	29.9	1	0	0	1254.60	2092	2103
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	11	11	14	0.01%	4.2%	ALLQAILQTEDMLK	99.7%	63.5	25	59.5	2	0	0	1602.88	772	785
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	11	11	14	0.01%	4.2%	IEVLEEELR	99.7%	48.6	25	40.2	1	0	0	1129.61	1034	1042
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	11	11	14	0.01%	4.2%	LASLEELKR	98.7%	34.2	25	19.1	1	0	0	1058.62	1076	1084
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	11	11	14	0.01%	4.2%	LLEAQIATGGIIDPK	99.7%	64.1	25	57.7	1	0	0	1538.88	2367	2381
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	11	11	14	0.01%	4.2%	NQCTQVVQER	99.2%	36.4	25	23.8	1	0	0	1261.60	1803	1812
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	11	11	14	0.01%	4.2%	QLQNIIQATSR	99.7%	44.7	25	43.8	1	0	0	1271.71	271	281
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	11	11	14	0.01%	4.2%	RVEEDIQQQK	94.8%	28.4	25	20.7	1	0	0	1272.65	1425	1434
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	11	11	14	0.01%	4.2%	SQLQISNNR	99.7%	47.5	25	31.2	1	0	0	1059.55	1754	1762
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	11	11	14	0.01%	4.2%	YEVTSGGGGTSR	99.6%	39.8	25	30.3	1	0	0	1170.54	28	39
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	3	3	6	0.01%	21.9%	INLVLSR	99.7%	47.9	25	28.9	2	0	0	814.51	72	78
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	3	3	6	0.01%	21.9%	LLPEYPGVLSDVQEEK	99.7%	92	25	88.8	2	0	0	1815.94	159	174
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	3	3	6	0.01%	21.9%	VGSLNCIVAVSQNMGIGK	99.7%	83.3	25	80.5	2	0	0	1862.95	2	19
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	12	14	26	0.02%	28.9%	ADGGTQVIDTK	99.7%	81.5	25	68.1	2	0	0	1104.55	167	177
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	12	14	26	0.02%	28.9%	ALLNNSHYYHMAHGK	96.2%	23.6	25	23.6	0	1	0	1755.84	90	104
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	12	14	26	0.02%	28.9%	ALTGGIAHLFK	99.7%	55.1	25	45.7	2	0	0	1127.66	133	143
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	12	14	26	0.02%	28.9%	FPFAANSR	99.4%	38.5	25	26.4	2	0	0	909.46	421	428
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	12	14	26	0.02%	28.9%	GIEMSEVR	99.4%	38	25	33.3	2	0	0	936.45	110	117
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	12	14	26	0.02%	28.9%	GRIPVNTR	96.7%	30.3	25	16.2	2	0	0	912.54	335	342
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	12	14	26	0.02%	28.9%	IPNIYAIGDVVAGPMLAHK	99.7%	78.8	25	77.8	0	3	0	1979.08	347	365
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	12	14	26	0.02%	28.9%	NETLGGTCLNVGCIPSK	99.7%	119	25	113	2	0	0	1819.87	73	89
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	12	14	26	0.02%	28.9%	NLGLEELGIELDPR	99.7%	68.8	25	64.8	2	0	0	1567.83	321	334
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	12	14	26	0.02%	28.9%	SEEQLKEEGIEYK	99.7%	65.7	25	65.7	2	2	0	1581.76	405	417
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	12	14	26	0.02%	28.9%	TNADTDGMVK	99.7%	44.6	25	43.4	2	0	0	1051.47	431	440
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	12	14	26	0.02%	28.9%	VCHAHPTLSEAFR	99.7%	38.4	25	30.2	0	2	0	1524.74	483	495
Dihydrolipoyl lysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	5	6	10	0.01%	9.9%	DVPLGTPLCIIVEK	99.7%	67.2	25	67.2	2	0	0	1553.86	283	296
Dihydrolipoyl lysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	5	6	10	0.01%	9.9%	GVETIANDVVSLATK	99.7%	71.8	25	60.8	2	0	0	1516.82	533	547
Dihydrolipoyl lysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	5	6	10	0.01%	9.9%	ILVAEGTR	97.2%	31	25	16.3	1	0	0	858.50	148	155
Dihydrolipoyl lysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	5	6	10	0.01%	9.9%	VPLPSLSPTMQAGTIAR	99.7%	72.2	25	72.2	4	0	0	1738.95	94	110
Dihydrolipoyl lysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	5	6	10	0.01%	9.9%	YLEKPITMLL	99.3%	37.6	25	31	1	0	0	1236.69	638	647
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	7	8	11	0.01%	14.2%	GMYDGPVYEVPATPK	99.7%	82	25	82	1	0	0	1639.77	497	511
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	7	8	11	0.01%	14.2%	INCPVYITK	94.9%	28.5	25	20.2	1	0	0	1107.59	246	254
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	7	8	11	0.01%	14.2%	MDENQFVAVTSTNAAK	99.7%	44.7	25	44.7	2	0	0	1741.81	375	390
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	7	8	11	0.01%	14.2%	QIGENLIVPGGVK	98.1%	32.6	25	26.2	2	0	0	1323.76	44	56
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	7	8	11	0.01%	14.2%	SAADIIALAR	99.7%	72.3	25	61	2	0	0	1000.58	259	268
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	7	8	11	0.01%	14.2%	SIPHITSDR	96.5%	30	25	22.9	1	0	0	1025.54	8	16
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	7	8	11	0.01%	14.2%	VFGLQGVSR	99.7%	49.2	25	31.2	2	0	0	962.54	488	496
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	4	4	6	0.01%	8.9%	GAPAVVISQGR	99.7%	69	25	69	2	0	0	1054.60	441	451

Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	4	4	6	0.01%	8.9%	IFNFYPR	99.0%	35.5	25	11	2	0	0	956.50	391	397
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	4	4	6	0.01%	8.9%	NLHQSGFSLSGSQADDHIAR	99.7%	52.3	25	52.3	0	1	0	2140.02	533	552
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	4	4	6	0.01%	8.9%	QIGENLIVPGGIK	95.1%	28.7	25	28.7	1	0	0	1337.78	44	56
Dihydropyrimidinase-related protein 5	DPYSL5	DPYL5_HUMAN	61.4	100.0%	4	4	5	0.00%	9.6%	FVAVTSSNAAK	99.7%	54.1	25	54.1	2	0	0	1094.58	373	383
Dihydropyrimidinase-related protein 5	DPYSL5	DPYL5_HUMAN	61.4	100.0%	4	4	5	0.00%	9.6%	IIPGADADVVVWDPEATK	99.7%	56.3	25	54.8	1	0	0	1895.98	394	411
Dihydropyrimidinase-related protein 5	DPYSL5	DPYL5_HUMAN	61.4	100.0%	4	4	5	0.00%	9.6%	IPHGVSGVQDR	96.5%	30	25	19.1	1	0	0	1164.61	344	354
Dihydropyrimidinase-related protein 5	DPYSL5	DPYL5_HUMAN	61.4	100.0%	4	4	5	0.00%	9.6%	VHAENGELVAEGAK	99.7%	64.8	25	64.8	1	0	0	1423.72	190	203
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	5	6	8	0.01%	16.8%	FIPGLQMLSDAAPGK	99.7%	46	25	41.8	3	0	0	1560.81	90	104
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	5	6	8	0.01%	16.8%	LLELADIDPTLRPR	96.9%	30.5	25	30.5	1	0	0	1621.93	280	293
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	5	6	8	0.01%	16.8%	QLSQNFLLDLR	99.7%	49.4	25	25.6	1	0	0	1346.74	32	42
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	5	6	8	0.01%	16.8%	TQMTLTFQK	98.2%	32.8	25	23	1	0	0	1113.56	170	178
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	5	6	8	0.01%	16.8%	VVQNVFQFR	99.7%	52.3	25	39.5	2	0	0	1136.62	248	256
Dimethyladenosine transferase 2, mitochondrial	TFB2M	TFB2M_HUMAN	45.4	100.0%	2	2	4	0.00%	6.3%	NLGIEAVPWTADIPLK	99.7%	47.8	25	46.2	2	0	0	1736.96	175	190
Dimethyladenosine transferase 2, mitochondrial	TFB2M	TFB2M_HUMAN	45.4	100.0%	2	2	4	0.00%	6.3%	SATVIDHLR	99.7%	44.3	25	26.7	2	0	0	1011.56	332	340
Diphosphoinositol polyphosphate phosphohydrolase 3-beta	NUDT11	NUD11_HUMAN	18.6	100.0%	3	3	3	0.00%	12.8%	EVYEEAGVK	98.6%	34	25	19.1	1	0	0	1023.50	65	73
Diphosphoinositol polyphosphate phosphohydrolase 3-beta	NUDT11	NUD11_HUMAN	18.6	100.0%	3	3	3	0.00%	12.8%	LLGVFEQNQDR	98.0%	32.5	25	21.5	1	0	0	1318.68	79	89
Diphosphoinositol polyphosphate phosphohydrolase 3-beta	NUDT11	NUD11_HUMAN	18.6	100.0%	3	3	3	0.00%	12.8%	LLGVFEQNQDRK	95.0%	28.5	25	28.5	1	0	0	1446.77	79	90
DNA ligase 3	LIG3	DNLI3_HUMAN	112.9	100.0%	4	4	6	0.01%	4.6%	DLEQGDVSETIR	99.7%	66.7	25	63	1	0	0	1361.65	344	355
DNA ligase 3	LIG3	DNLI3_HUMAN	112.9	100.0%	4	4	6	0.01%	4.6%	SEAHTADGISIR	96.9%	30.6	25	21.2	1	0	0	1256.62	792	803
DNA ligase 3	LIG3	DNLI3_HUMAN	112.9	100.0%	4	4	6	0.01%	4.6%	VIQEGLEGLVLK	99.7%	88	25	81.8	2	0	0	1297.77	649	660
DNA ligase 3	LIG3	DNLI3_HUMAN	112.9	100.0%	4	4	6	0.01%	4.6%	VLLDIFTGVR	99.7%	75.2	25	75.2	2	0	0	1132.67	933	942
DNA methyltransferase 1-associated protein 1	DMAP1	DMAP1_HUMAN	53.0	99.8%	2	2	3	0.00%	6.0%	DTIIDVVGAPLTPNSR	97.2%	31	25	30.1	1	0	0	1667.90	434	449
DNA methyltransferase 1-associated protein 1	DMAP1	DMAP1_HUMAN	53.0	99.8%	2	2	3	0.00%	6.0%	LITAADTTAEQR	99.7%	80.3	25	64	2	0	0	1289.67	271	282
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	13	13	24	0.02%	16.0%	DIYQDLNR	95.5%	29	25	12.2	2	0	0	1036.51	236	243
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	13	13	24	0.02%	16.0%	DSLIIIDELGR	99.7%	79.6	25	68.6	2	0	0	1243.69	742	752
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	13	13	24	0.02%	16.0%	LDSSAQFGYYFR	99.7%	78.8	25	76	2	0	0	1453.67	513	524
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	13	13	24	0.02%	16.0%	LLLAVFVTPLTDLR	99.7%	61.3	25	61.3	2	0	0	1570.96	431	444
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	13	13	24	0.02%	16.0%	LNLVEAFVEDAELR	99.7%	124	25	119	3	0	0	1617.85	360	373
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	13	13	24	0.02%	16.0%	LTSLNEEYTK	99.7%	52.8	25	52.8	2	0	0	1197.60	556	565
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	13	13	24	0.02%	16.0%	LYQGINQLPNVIQALEK	99.7%	64.6	25	64.6	2	0	0	1941.08	407	423
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	13	13	24	0.02%	16.0%	NLQSVVLSK	99.7%	51.1	25	36.3	2	0	0	987.58	74	82
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	13	13	24	0.02%	16.0%	NNSFVNEIISR	99.7%	57.7	25	45	2	0	0	1292.66	919	929
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	13	13	24	0.02%	16.0%	QAANLQDCYR	99.3%	37.7	25	37.1	1	0	0	1238.56	397	406
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	13	13	24	0.02%	16.0%	QTLQEDLLR	99.7%	54.4	25	42.7	1	0	0	1115.61	374	382
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	13	13	24	0.02%	16.0%	QVGVGYVDSIQR	99.7%	61.2	25	56.5	2	0	0	1320.69	160	171
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	13	13	24	0.02%	16.0%	TEYEEAQDAIVK	99.7%	44.4	25	37.1	1	0	0	1395.66	568	579
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	16	17	30	0.03%	13.1%	AIMYEETTYSK	99.7%	49.8	25	49.8	1	0	0	1335.61	842	852
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	16	17	30	0.03%	13.1%	AYGVCFVDTSLGK	99.7%	88.3	25	88.3	2	0	0	1416.68	555	567
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	16	17	30	0.03%	13.1%	EVCLASER	99.3%	37.2	25	29.8	2	0	0	963.46	1335	1342
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	16	17	30	0.03%	13.1%	GTQTYSVLEGDPSENYSK	99.7%	84.8	25	84.8	2	0	0	1974.89	520	537
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	16	17	30	0.03%	13.1%	IIDFLSALEGFK	99.7%	51.2	25	40.5	2	0	0	1352.75	855	866
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	16	17	30	0.03%	13.1%	IIGIMEEVADGFK	99.7%	50	25	50	2	0	0	1421.73	871	883
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	16	17	30	0.03%	13.1%	KLPDLER	97.7%	31.8	25	0	1	0	0	870.50	814	820
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	16	17	30	0.03%	13.1%	LANLINAEER	99.7%	52.2	25	44.5	2	0	0	1142.62	1015	1024
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	16	17	30	0.03%	13.1%	LANLPEEVIQK	99.7%	64.3	25	48.8	2	0	0	1253.71	1305	1315
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	16	17	30	0.03%	13.1%	LSDGIGVMLPQVLK	99.7%	62.8	25	58.7	3	0	0	1485.83	647	660
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	16	17	30	0.03%	13.1%	QVISLQTK	97.3%	31.2	25	23.1	2	0	0	916.55	889	896
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	16	17	30	0.03%	13.1%	STVDAEAVHK	99.5%	38.7	25	37.3	2	0	0	1056.53	1343	1352
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	16	17	30	0.03%	13.1%	TLLEEEYFR	99.7%	41.7	25	35.1	2	0	0	1199.59	636	644
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	16	17	30	0.03%	13.1%	VDTCHTPFGK	96.9%	30.5	25	25.4	1	0	0	1161.54	762	771
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	16	17	30	0.03%	13.1%	VHVQFFDDSPTR	99.7%	44.3	25	44.3	2	0	0	1447.70	129	140

DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	16	17	30	0.03%	13.1%	YQLEIPENFTTR	99.7%	41.5	25	32.2	2	0	0	1510.75	977	988
DNA polymerase alpha catalytic subunit	POLA1	DPOLA_HUMAN	165.9	100.0%	3	3	3	0.00%	2.5%	AAYAGGLVLDPK	99.5%	38.6	25	31.9	1	0	0	1174.65	837	848
DNA polymerase alpha catalytic subunit	POLA1	DPOLA_HUMAN	165.9	100.0%	3	3	3	0.00%	2.5%	DTGNFVIGQILSDQSR	99.7%	94.4	25	86.5	1	0	0	1749.88	1090	1105
DNA polymerase alpha catalytic subunit	POLA1	DPOLA_HUMAN	165.9	100.0%	3	3	3	0.00%	2.5%	VEVAATER	98.6%	34.1	25	18.3	1	0	0	874.46	609	616
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	17	25	0.02%	18.4%	DLEDQEQLLR	99.7%	59.1	25	43.9	1	0	0	1258.63	1088	1097
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	17	25	0.02%	18.4%	DNCPLVANLVTASLR	99.7%	76.2	25	76.2	2	0	0	1642.86	835	849
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	17	25	0.02%	18.4%	ELNLAISR	99.7%	51.2	25	36.6	2	0	0	915.53	167	174
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	17	25	0.02%	18.4%	FGVSSVAEAMALGR	99.7%	102	25	102	2	0	0	1394.71	763	776
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	17	25	0.02%	18.4%	IDISQLVITK	99.7%	81.3	25	53.7	2	0	0	1129.68	876	885
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	17	25	0.02%	18.4%	IFEPILGEGR	99.7%	53.2	25	47.1	2	0	0	1130.62	969	978
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	17	25	0.02%	18.4%	LLEQGIR	96.6%	30.1	25	0	2	0	0	828.49	226	232
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	17	25	0.02%	18.4%	LPCLEISQSVTGFGR	99.7%	73.5	25	73.5	1	0	0	1663.85	711	725
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	17	25	0.02%	18.4%	TPTGDEFVK	98.9%	35.2	25	22.9	1	0	0	993.49	640	648
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	17	25	0.02%	18.4%	TVLSHQGAVCEFCQPR	99.7%	41.4	25	41.4	0	1	0	1888.88	1017	1032
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	17	25	0.02%	18.4%	VGGLLAFAK	99.3%	37.3	25	37.3	2	0	0	875.54	999	1007
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	17	25	0.02%	18.4%	VLSFDIECAGR	99.3%	37.2	25	37.2	1	0	0	1266.61	312	322
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	17	25	0.02%	18.4%	VQMDMLQVLLR	99.7%	66.2	25	50.6	1	0	0	1345.73	455	465
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	17	25	0.02%	18.4%	VSANSVYGFTGAQVGK	99.7%	77.2	25	70.4	2	0	0	1584.80	695	710
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	17	25	0.02%	18.4%	VTGVPLSYLLSR	99.7%	45.3	25	22.3	2	0	0	1304.76	538	549
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	17	25	0.02%	18.4%	VYFPYLLISK	99.4%	37.7	25	36.8	1	0	0	1242.71	797	806
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	17	25	0.02%	18.4%	WGEPEPFLR	97.5%	31.5	25	8.7	1	0	0	1130.56	344	352
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	17	17	25	0.02%	18.4%	YTVENGYSTSAK	99.7%	49.2	25	49.2	1	0	0	1319.61	739	750
DNA polymerase delta subunit 2	POLD2	DPOD2_HUMAN	51.3	99.8%	2	2	4	0.00%	6.0%	FLGTSGQNVSDIFR	99.7%	79.8	25	75.3	2	0	0	1540.78	341	354
DNA polymerase delta subunit 2	POLD2	DPOD2_HUMAN	51.3	99.8%	2	2	4	0.00%	6.0%	LVTGTVLAVFGSVR	99.7%	45.2	25	45.2	2	0	0	1418.84	153	166
DNA polymerase delta subunit 3	POLD3	DPOD3_HUMAN	51.4	100.0%	2	2	3	0.00%	5.8%	DSGPLFNTDYDILK	99.7%	70.6	25	52.5	2	0	0	1597.77	110	123
DNA polymerase delta subunit 3	POLD3	DPOD3_HUMAN	51.4	100.0%	2	2	3	0.00%	5.8%	IVEQPTVSVTEPK	99.6%	40.4	25	39.4	1	0	0	1426.78	262	274
DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	5	5	7	0.01%	2.8%	AIPLAIFQAEPTVR	99.7%	45.3	25	39.6	2	0	0	1525.87	1093	1106
DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	5	5	7	0.01%	2.8%	GSTLEEVYGSVAK	99.7%	61.2	25	45.6	1	0	0	1339.67	996	1008
DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	5	5	7	0.01%	2.8%	IITIPAALQQVK	97.7%	31.8	25	31.8	2	0	0	1294.81	1144	1155
DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	5	5	7	0.01%	2.8%	SLAQFSYLEPGSIR	99.7%	58.2	25	50.8	1	0	0	1567.81	1472	1485
DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	5	5	7	0.01%	2.8%	SSSLQDFDIR	99.7%	54.8	25	23.8	1	0	0	1167.56	1116	1125
DNA primase large subunit	PRIM2	PRI2_HUMAN	58.8	100.0%	3	3	4	0.00%	7.5%	IPFADALDLFR	99.7%	67.5	25	54.3	2	0	0	1277.69	186	196
DNA primase large subunit	PRIM2	PRI2_HUMAN	58.8	100.0%	3	3	4	0.00%	7.5%	KEPIQPETPQPKPSVQK	99.3%	30.4	25	30.4	0	1	0	1931.06	463	479
DNA primase large subunit	PRIM2	PRI2_HUMAN	58.8	100.0%	3	3	4	0.00%	7.5%	SLPAVQSDER	99.1%	36.2	25	32.5	1	0	0	1101.55	236	245
DNA primase small subunit	PRIM1	PRI1_HUMAN	49.9	100.0%	3	3	3	0.00%	8.1%	LGAFQAQEK	99.7%	49.4	25	35	1	0	0	991.52	96	104
DNA primase small subunit	PRIM1	PRI1_HUMAN	49.9	100.0%	3	3	3	0.00%	8.1%	SPFSVHPK	97.9%	32.2	25	28.6	1	0	0	898.48	319	326
DNA primase small subunit	PRIM1	PRI1_HUMAN	49.9	100.0%	3	3	3	0.00%	8.1%	VDQFDPFTVPTISFICR	99.7%	68.4	25	67	1	0	0	2042.01	339	355
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	14	27	0.03%	10.7%	DVNGELIAVQR	99.7%	63.7	25	48.2	2	0	0	1213.65	88	98
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	14	27	0.03%	10.7%	EQVSPLETTLEK	99.7%	51.6	25	44.6	2	0	0	1373.72	910	921
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	14	27	0.03%	10.7%	GQDIEYIEIR	99.7%	81.4	25	73	2	0	0	1235.63	1157	1166
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	14	27	0.03%	10.7%	LEENIDNIKR	99.7%	73.5	25	65.8	2	0	0	1243.66	1060	1069
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	14	27	0.03%	10.7%	LKEIEHNLSK	99.2%	36.8	25	30.9	2	0	0	1210.68	255	264
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	14	27	0.03%	10.7%	LQGIDLDR	99.7%	49.9	25	36.5	2	0	0	929.51	816	823
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	14	27	0.03%	10.7%	MEVISLQNEK	99.7%	47.4	25	27.1	1	0	0	1190.61	502	511
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	14	27	0.03%	10.7%	NIDQCSEIVK	99.7%	43.8	25	27.2	2	0	0	1205.58	1292	1301
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	14	27	0.03%	10.7%	SDADENVSASDK	99.7%	80.8	25	79.8	2	0	0	1237.52	1167	1178
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	14	27	0.03%	10.7%	SELLVEQGR	99.7%	58.2	25	41.5	2	0	0	1030.55	344	352
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	14	27	0.03%	10.7%	VIAQLSECEK	99.7%	51.1	25	51.1	2	0	0	1176.59	983	992
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	14	27	0.03%	10.7%	VLASLIIR	99.7%	66.9	25	49	2	0	0	884.59	1207	1214
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	14	27	0.03%	10.7%	WLQDNLTLR	99.7%	48.8	25	35.9	2	0	0	1158.63	1017	1025
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	14	27	0.03%	10.7%	YELQQLEGSSDR	99.7%	78.7	25	75.3	2	0	0	1424.67	462	473

DNA replication licensing factor MCM2	MCM2	MCM2_HUMAN	101.9	99.8%	2	2	2	0.00%	2.4%	AGIVTSLQAR	99.2%	36.8	25	32.1	1	0	0	1015.59	614	623
DNA replication licensing factor MCM2	MCM2	MCM2_HUMAN	101.9	99.8%	2	2	2	0.00%	2.4%	GLALALFGGEPK	99.7%	54.4	25	43.4	1	0	0	1172.67	494	505
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	52	0.05%	34.4%	AILCLLLGGVER	99.7%	82.1	25	72.4	2	0	0	1313.76	316	327
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	52	0.05%	34.4%	APAGQLPR	99.7%	48.1	25	26.3	3	0	0	809.46	208	215
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	52	0.05%	34.4%	DAQPSFSAEDIAK	99.7%	70.9	25	67	2	0	0	1378.65	271	283
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	52	0.05%	34.4%	DLENGSHIR	99.6%	40	25	29.1	2	0	0	1040.51	328	336
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	52	0.05%	34.4%	DSEEPFSSVEIQAALSK	99.7%	117	25	102	2	0	0	1836.89	775	791
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	52	0.05%	34.4%	DYLDFLDDEEDQGIYQSK	99.7%	104	25	104	2	0	0	2192.95	18	35
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	52	0.05%	34.4%	EAHAQSIGMNR	99.7%	76.3	25	66.9	3	1	0	1213.57	757	767
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	52	0.05%	34.4%	ELISDNQYR	99.7%	64.5	25	60.7	2	0	0	1137.55	38	46
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	52	0.05%	34.4%	ESQKVELSESR	99.7%	41.8	25	29.9	2	0	0	1291.65	733	743
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	52	0.05%	34.4%	GDINILLIGDPSVAK	99.7%	54.9	25	54.9	2	0	0	1524.86	337	351
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	52	0.05%	34.4%	GGYTSGTFR	99.7%	44.1	25	40.8	2	0	0	945.44	249	257
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	52	0.05%	34.4%	GSSGVGLTAAVTTDQETGER	99.7%	113	25	112	2	0	0	1935.93	372	391
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	52	0.05%	34.4%	LIVNVNDLR	99.7%	67.7	25	52.2	2	0	0	1055.62	47	55
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	52	0.05%	34.4%	LLNNAFEELVAFQR	99.7%	60.2	25	59.2	2	0	0	1663.88	65	78
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	52	0.05%	34.4%	SKDIFDQLAK	99.7%	55.7	25	46.5	1	0	0	1164.63	292	301
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	52	0.05%	34.4%	SLAPSIHGHDYVK	99.7%	53.9	25	52	1	0	0	1423.73	302	314
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	52	0.05%	34.4%	SVDVILDDDLVDK	99.7%	59.2	25	46.5	2	0	0	1445.74	216	228
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	52	0.05%	34.4%	SVHYCPATK	99.7%	45.6	25	27.8	2	0	0	1062.50	144	152
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	52	0.05%	34.4%	TAIHEVMEQGR	99.6%	40.6	25	40	3	0	0	1286.62	420	430
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	52	0.05%	34.4%	TLETLIR	99.2%	36.5	25	8.02	2	0	0	845.51	617	623
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	52	0.05%	34.4%	TPMENIGLQDSLLSR	99.7%	74.2	25	74.2	4	0	0	1689.85	464	478
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	52	0.05%	34.4%	TVLIACNVK	96.2%	29.7	25	14.9	2	0	0	1017.58	258	266
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	52	0.05%	34.4%	VALLDVFR	99.7%	55.9	25	47.1	2	0	0	932.56	749	756
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	52	0.05%	34.4%	YVLCTAPR	99.7%	49.4	25	36.9	2	0	0	979.50	357	364
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	10	11	22	0.02%	14.8%	ALADDDFLTVTGK	99.7%	110	25	110	2	0	0	1365.69	846	858
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	10	11	22	0.02%	14.8%	GILLQLFGGTR	99.7%	69.6	25	61.1	4	0	0	1174.69	479	489
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	10	11	22	0.02%	14.8%	IAEPSVCGR	99.7%	46.8	25	27.1	2	0	0	988.49	322	330
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	10	11	22	0.02%	14.8%	LASALAPSIYEHEDIKK	99.3%	30.5	25	30.5	0	1	0	1885.01	462	478
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	10	11	22	0.02%	14.8%	LVIWGTDVNVAACK	99.7%	89.5	25	89.5	2	0	0	1545.81	150	163
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	10	11	22	0.02%	14.8%	QRPDLGSAQK	99.7%	44.9	25	32.4	2	0	0	1099.59	114	123
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	10	11	22	0.02%	14.8%	RLHGLDEEAEQK	99.7%	48.5	25	46.3	0	2	0	1424.71	428	439
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	10	11	22	0.02%	14.8%	TGIVDISILTTGMSATSR	99.7%	83.7	25	83.7	2	0	0	1822.96	778	795
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	10	11	22	0.02%	14.8%	TTIENIQLPHTLLSR	99.7%	80.9	25	69.9	1	2	0	1735.97	629	643
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	10	11	22	0.02%	14.8%	YQQLFEDIR	99.7%	59.7	25	29.5	2	0	0	1211.61	820	828
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	17	30	0.03%	24.8%	AGITTTLNSR	99.7%	74.2	25	54.8	2	0	0	1033.56	472	481
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	17	30	0.03%	24.8%	AIACLLFGGSR	99.7%	80.1	25	79.4	2	0	0	1164.62	352	362
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	17	30	0.03%	24.8%	CSVLAAANSVFGR	99.7%	70.2	25	70.2	2	0	0	1351.68	482	494
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	17	30	0.03%	24.8%	FAIGSQVSEHSIIK	99.7%	65.5	25	53.7	1	0	0	1515.82	683	696
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	17	30	0.03%	24.8%	GSSAAGLTASVMR	99.7%	85.5	25	68.6	2	0	0	1207.61	408	420
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	17	30	0.03%	24.8%	HMQLYCDR	99.7%	47.5	25	41.3	4	0	0	1138.48	244	251
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	17	30	0.03%	24.8%	IPGIIIAASAVR	99.7%	87.7	25	87.7	2	0	0	1180.74	151	162
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	17	30	0.03%	24.8%	LAALPNVYEVISK	99.7%	77.4	25	77.4	2	0	0	1416.81	325	337
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	17	30	0.03%	24.8%	LQELPDAVPHGEMPR	96.7%	24.2	25	20.5	0	1	0	1704.84	229	243
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	17	30	0.03%	24.8%	LQPFATEADVEEALR	99.7%	94.5	25	87.9	2	0	0	1688.85	628	642
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	17	30	0.03%	24.8%	QPAEHLQLLEEAAK	99.6%	32.5	25	26.5	0	1	0	1576.83	91	104
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	17	30	0.03%	24.8%	SIAPSIFGGTDMK	99.7%	58.5	25	57	2	0	0	1323.66	338	350
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	17	30	0.03%	24.8%	SIAPSIFGGTDMKK	99.6%	39.8	25	38.6	1	0	0	1467.75	338	351
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	17	30	0.03%	24.8%	VLGIQVDTDGSGR	99.7%	73.7	25	73.7	2	0	0	1316.68	296	308
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	17	30	0.03%	24.8%	VLQLMLR	99.7%	46.5	25	21.5	2	0	0	872.54	711	717

DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	16	17	30	0.03%	24.8%	VTIMGIYSIK	99.7%	52.6	25	42.2	2	0	0	1124.64	263	272
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	21	38	0.04%	25.5%	AEAVESAQAGDK	99.7%	55.7	25	51.5	2	0	0	1175.55	230	241
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	21	38	0.04%	25.5%	DFYVAFQDLPTR	99.7%	74.8	25	63.5	2	0	0	1471.72	109	120
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	21	38	0.04%	25.5%	EIESEIDSEEELINK	99.7%	111	25	95.8	2	0	0	1776.84	755	769
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	21	38	0.04%	25.5%	ELRDEEQTAESIK	99.7%	54.1	25	43.5	2	0	0	1547.75	314	326
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	21	38	0.04%	25.5%	ESEDFIVEQYK	99.5%	39.5	25	37.1	1	0	0	1386.64	589	599
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	21	38	0.04%	25.5%	GDINVCIVGDPSTAK	99.7%	61.5	25	50.8	2	0	0	1545.76	388	402
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	21	38	0.04%	25.5%	GVLLMLFGGVPK	99.7%	68.2	25	48.8	4	0	0	1230.73	367	378
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	21	38	0.04%	25.5%	HVEEFSPR	97.6%	31.7	25	31.7	2	0	0	1000.48	408	415
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	21	38	0.04%	25.5%	IQETQAELPR	99.7%	77.4	25	62.1	2	0	0	1184.63	208	217
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	21	38	0.04%	25.5%	ISNLIVLHLR	99.7%	51.6	25	38.4	2	0	0	1177.74	723	732
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	21	38	0.04%	25.5%	LGFSEYCR	99.7%	43	25	43	2	0	0	1031.46	715	722
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	21	38	0.04%	25.5%	LVFLACCVAPTNPR	99.7%	72.7	25	72.3	2	0	0	1617.82	296	309
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	21	38	0.04%	25.5%	MHCCDEVQPK	98.4%	33.4	25	33.4	1	0	0	1319.52	634	643
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	21	38	0.04%	25.5%	SELVNWYLK	99.7%	49	25	40.8	2	0	0	1151.61	746	754
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	21	38	0.04%	25.5%	TSILAAANPISGHYDR	99.7%	85.4	25	85.4	2	1	0	1685.86	497	512
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	21	38	0.04%	25.5%	VSGVDGYETEGIR	99.7%	91.1	25	81.6	2	0	0	1381.66	270	282
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	21	38	0.04%	25.5%	YLQLAEELIRPER	99.3%	30.1	25	27	2	1	0	1629.90	46	58
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	18	21	38	0.04%	25.5%	YTQPNICR	99.2%	36.8	25	24.4	2	0	0	1051.50	174	181
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	17	20	37	0.04%	28.8%	AGILTTLNAR	99.7%	66	25	53	2	0	0	1029.61	472	481
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	17	20	37	0.04%	28.8%	ALLLLLVGGVDQSPR	99.7%	79.2	25	79.2	2	0	0	1550.93	353	367
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	17	20	37	0.04%	28.8%	CSILAAANPAYGR	99.7%	75.8	25	68.9	2	0	0	1363.68	482	494
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	17	20	37	0.04%	28.8%	FLQEFYQDDELGKK	96.9%	24.4	25	19	0	1	0	1759.85	16	29
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	17	20	37	0.04%	28.8%	GNINICLMGDPGVAK	99.7%	57.7	25	57.7	2	0	0	1558.77	373	387
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	17	20	37	0.04%	28.8%	GSSGVGLTAAVLR	99.7%	75.7	25	52.9	2	0	0	1187.67	408	420
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	17	20	37	0.04%	28.8%	LFADAVQELLPQYK	99.7%	93.1	25	77.3	4	0	0	1634.88	76	89
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	17	20	37	0.04%	28.8%	MQEHSDQVPVGNIPR	98.0%	26.2	25	7.51	0	1	0	1722.82	237	251
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	17	20	37	0.04%	28.8%	QIAEEDFYEK	99.3%	37.4	25	37.4	2	0	0	1271.58	326	335
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	17	20	37	0.04%	28.8%	SEDDESGAGELTR	99.7%	60.8	25	60.8	2	0	0	1365.58	309	321
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	17	20	37	0.04%	28.8%	SITVLVEGENTR	99.7%	81.5	25	69	1	0	0	1317.70	252	263
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	17	20	37	0.04%	28.8%	SLEQNIQLPAALLSR	99.7%	92.8	25	92.8	2	0	0	1652.93	500	514
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	17	20	37	0.04%	28.8%	SPQNQYPAELMR	99.7%	55.5	25	55.5	3	0	0	1449.68	121	132
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	17	20	37	0.04%	28.8%	SQLLSYIDR	99.7%	54.3	25	28.3	3	0	0	1094.58	388	396
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	17	20	37	0.04%	28.8%	TLLAILR	99.3%	37.6	25	11.9	2	0	0	799.54	605	611
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	17	20	37	0.04%	28.8%	TQRPADVIFATVR	99.7%	43.2	25	39.3	2	2	0	1473.82	654	666
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	17	20	37	0.04%	28.8%	YGNQLVR	99.7%	55.2	25	41.8	2	0	0	849.46	33	39
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	20	23	51	0.05%	26.7%	AEEVATFFAK	99.7%	72.9	25	65.2	5	0	0	1112.56	253	262
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	20	23	51	0.05%	26.7%	AVAILCNHQR	99.7%	61.7	25	44	2	0	0	1181.62	625	634
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	20	23	51	0.05%	26.7%	AVALYFIDK	99.7%	45.8	25	29.8	2	0	0	1039.58	476	484
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	20	23	51	0.05%	26.7%	CDFTQMSQYFK	99.7%	56.9	25	56.9	2	0	0	1454.61	300	310
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	20	23	51	0.05%	26.7%	DEDDADYKPK	99.7%	46.5	25	41.2	2	0	0	1195.51	141	150
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	20	23	51	0.05%	26.7%	ELTAPDENIPAK	99.7%	45	25	42.5	2	0	0	1297.66	604	615
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	20	23	51	0.05%	26.7%	GPVFAPPYEPLPENVK	99.7%	77.3	25	74.7	6	0	0	1753.92	224	239
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	20	23	51	0.05%	26.7%	HLQDLMEGLTAK	99.7%	68.9	25	34.1	4	0	0	1355.70	576	587
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	20	23	51	0.05%	26.7%	IMPEDIIINCSK	99.4%	38.2	25	38.2	1	0	0	1432.72	377	388
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	20	23	51	0.05%	26.7%	ITVAWCK	99.6%	40.5	25	18.5	2	0	0	877.46	728	734
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	20	23	51	0.05%	26.7%	LEEEEDGKLK	97.0%	30.7	25	21.5	1	0	0	1189.59	165	174
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	20	23	51	0.05%	26.7%	LEVQATDREENK	99.7%	56.9	25	52.7	3	0	0	1431.71	701	712
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	20	23	51	0.05%	26.7%	LNTGILNK	99.7%	51	25	26.9	1	0	0	872.52	568	575
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	20	23	51	0.05%	26.7%	MLDHEYTTK	99.7%	58	25	51.8	4	0	0	1137.52	263	271
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	20	23	51	0.05%	26.7%	NLQLFMENK	99.7%	47.6	25	37.5	2	0	0	1136.58	550	558

DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	20	23	51	0.05%	26.7%	QIALGTSK	97.9%	32.1	25	9.81	1	0	0	817.48	713	720
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	20	23	51	0.05%	26.7%	SMMNLQTK	99.7%	41.5	25	35.3	2	0	0	952.46	643	650
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	20	23	51	0.05%	26.7%	TYNASITLQQQLK	99.7%	96.5	25	87.6	3	0	0	1507.81	591	603
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	20	23	51	0.05%	26.7%	VPSPPPGHK	99.6%	40.6	25	27.3	2	0	0	915.50	392	400
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	20	23	51	0.05%	26.7%	YIMLNPSSR	99.3%	37.3	25	28.1	4	0	0	1096.55	426	434
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	22	23	43	0.04%	16.3%	DKYGVFPLR	99.6%	40.9	25	34	1	0	0	1094.60	479	487
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	22	23	43	0.04%	16.3%	EKQDEQVGLPGK	99.7%	55.5	25	42.2	2	0	0	1327.69	1185	1196
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	22	23	43	0.04%	16.3%	ELILFSNSDNER	99.7%	73	25	68.2	2	0	0	1436.70	702	713
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	22	23	43	0.04%	16.3%	EVTFVPGLYK	98.8%	34.8	25	32	1	0	0	1152.63	74	83
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	22	23	43	0.04%	16.3%	FLEEFITPIVK	99.7%	47.7	25	44.3	4	0	0	1335.76	569	579
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	22	23	43	0.04%	16.3%	FTVETASR	99.7%	52.8	25	41.4	2	0	0	910.46	177	184
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	22	23	43	0.04%	16.3%	GFQQISFVNSIATSK	99.7%	75.3	25	75.3	2	0	0	1626.85	307	321
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	22	23	43	0.04%	16.3%	HVDYVADQIVTK	99.7%	74.4	25	74.4	3	0	0	1387.72	325	336
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	22	23	43	0.04%	16.3%	IFDEILVNAADNK	99.7%	98.4	25	96.4	5	0	0	1461.76	84	96
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	22	23	43	0.04%	16.3%	IIIENKPK	99.6%	40.7	25	28.1	2	0	0	954.60	1063	1070
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	22	23	43	0.04%	16.3%	KPSTSDDSDSNFEK	98.1%	32.8	25	32.6	1	0	0	1556.67	1467	1480
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	22	23	43	0.04%	16.3%	KYDTVLDILR	98.5%	33.8	25	27.9	2	0	0	1235.70	1011	1020
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	22	23	43	0.04%	16.3%	LCNIFSTK	98.6%	34.1	25	26.9	1	0	0	982.50	169	176
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	22	23	43	0.04%	16.3%	NSTECTLILTEGDSAK	99.7%	103	25	89.2	2	0	0	1738.82	451	466
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	22	23	43	0.04%	16.3%	QIMENAEINNIIK	99.7%	81.4	25	70.4	1	0	0	1529.80	500	512
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	22	23	43	0.04%	16.3%	SFGSTCQLSEK	99.7%	61.9	25	51.8	2	0	0	1243.56	387	397
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	22	23	43	0.04%	16.3%	SVVSDLEADDVK	99.7%	87.6	25	78.2	2	0	0	1276.63	1374	1385
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	22	23	43	0.04%	16.3%	TLAVSGLGVVGR	99.7%	87.5	25	73.4	2	0	0	1128.67	467	478
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	22	23	43	0.04%	16.3%	TQMAEVLPSPR	99.7%	42.7	25	38.8	3	0	0	1228.64	1205	1215
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	22	23	43	0.04%	16.3%	VTIDPENNLISIWNNGK	98.0%	32.4	25	32.4	1	0	0	1926.99	107	123
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	22	23	43	0.04%	16.3%	YDTVLDILR	99.3%	37.7	25	27.9	1	0	0	1107.60	1012	1020
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	22	23	43	0.04%	16.3%	YSGPEDDAAISLAFSK	99.7%	64.1	25	53.6	1	0	0	1670.79	640	655
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	10	10	22	0.02%	10.8%	DKLDETGVALK	99.7%	46.4	25	35.2	1	0	0	1188.65	298	308
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	10	10	22	0.02%	10.8%	DLIQMLVQR	99.7%	54.2	25	43.8	4	0	0	1115.62	1093	1101
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	10	10	22	0.02%	10.8%	ELILFSNSDNER	99.7%	73	25	68.2	2	0	0	1436.70	723	734
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	10	10	22	0.02%	10.8%	EVTFVPGLYK	98.8%	34.8	25	32	1	0	0	1152.63	95	104
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	10	10	22	0.02%	10.8%	GFQQISFVNSIATTK	99.7%	67.2	25	51.6	1	0	0	1640.86	328	342
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	10	10	22	0.02%	10.8%	HVDYVVDQVVGK	99.7%	57.8	25	50.8	1	0	0	1357.71	346	357
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	10	10	22	0.02%	10.8%	IFDEILVNAADNK	99.7%	98.4	25	96.4	5	0	0	1461.76	105	117
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	10	10	22	0.02%	10.8%	LAQAEAAGLHK	99.7%	61.2	25	48.3	4	0	0	1108.61	998	1008
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	10	10	22	0.02%	10.8%	LCNIFSTK	98.6%	34.1	25	26.9	1	0	0	982.50	190	197
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	10	10	22	0.02%	10.8%	LLFPAVDDNLLK	99.7%	58	25	46.1	4	0	0	1357.77	837	848
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	10	10	22	0.02%	10.8%	LPNYDAR	96.7%	30.3	25	10.6	1	0	0	848.43	885	891
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	10	10	22	0.02%	10.8%	NTVEITELPVR	99.7%	43.1	25	38	2	0	0	1270.70	940	950
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	10	10	22	0.02%	10.8%	QIMENAEINNIIK	99.7%	81.4	25	70.4	1	0	0	1529.80	521	533
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	10	10	22	0.02%	10.8%	SQDFGNLFSFPSYSQK	99.7%	70.9	25	70.9	2	0	0	1851.85	1441	1456
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	10	10	22	0.02%	10.8%	YAGPEDDAAITLAFSK	99.7%	105	25	105	2	0	0	1668.81	661	676
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	AALSALESFLK	99.7%	83.6	25	61.9	2	0	0	1149.65	311	321
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	AAYLSDPR	98.9%	35	25	25.7	2	0	0	892.45	3826	3833
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	AQEPESGLSEETQVK	99.7%	89.8	25	76.2	2	0	0	1631.78	4091	4105
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	ATQMPEGGQGAPPMYQLYK	99.7%	59.2	25	53.5	2	0	0	2082.96	945	963
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	ATQQQHDFTLTQTADGR	99.7%	98	25	93.2	2	2	0	1917.91	2637	2653
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	AYVPALQMAFK	99.4%	38	25	38	2	0	0	1238.66	747	757
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	CFGTGAAGNR	99.7%	60.8	25	50.1	2	0	0	1010.45	1312	1321
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	CGAALAGHQLIR	99.7%	65.1	25	62.9	2	1	0	1266.67	25	36
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	CLMDQATDPNILGR	99.7%	89.2	25	89.2	2	0	0	1603.76	4106	4119

DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	DCLSIPYR	99.7%	42.3	25	30.9	2	0	0	1023.49	2247	2254
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	DFGLLVFVR	99.7%	66.2	25	55.9	2	0	0	1065.61	62	70
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	DFSAFINLVEFCR	99.7%	64.2	25	57.4	2	0	0	1617.77	619	631
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	DILETHLR	99.7%	43.6	25	29.2	2	0	0	996.55	1413	1420
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	DILPCLDGYLK	99.7%	41.3	25	20.5	2	0	0	1306.67	791	801
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	DLCNTHLMR	99.6%	40.5	25	32.8	2	0	0	1175.53	1362	1370
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	DLLLNTMSQEEK	99.7%	80.5	25	68.3	2	0	0	1436.69	3814	3825
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	DQNILLGTTYR	99.7%	83.1	25	79.7	4	0	0	1293.68	3325	3335
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	DVDFMYVELIQR	99.7%	84.2	25	76.6	4	0	0	1543.75	380	391
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	DVLIQGLIDENPGLQLIIR	94.8%	28.4	25	28.4	1	0	0	2119.21	2504	2522
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	ECREEILK	97.9%	32.2	25	14.7	1	0	0	1076.54	80	87
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	EIFNFVLK	98.9%	35.1	25	17.8	2	0	0	1009.57	247	254
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	ELLNPVVEFVSHPSTTCR	99.7%	75.1	25	75.1	2	2	0	2085.04	2453	2470
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	EQQHVMEELFQSSFR	99.7%	40.5	25	31.1	0	2	0	1910.87	1769	1783
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	FMNAVFFLLPK	99.7%	63.2	25	58.3	4	0	0	1342.72	2378	2388
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	FNNYVDCMK	99.0%	35.8	25	29.1	2	0	0	1190.50	1736	1744
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	FNNYVDCMKK	97.0%	30.7	25	24.1	1	0	0	1334.59	1736	1745
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	FYGELALK	98.9%	35.1	25	26	2	0	0	940.51	156	163
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	FYGELALKK	99.7%	46.8	25	41.3	1	0	0	1068.61	156	164
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	FYQGFLFSEKPEK	99.7%	43.3	25	36.9	2	0	0	1619.81	1961	1973
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	GFPPSASLCLLDLVK	96.0%	29.5	25	27.9	2	0	0	1616.87	1156	1170
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	GGSWIQEINVAEK	99.7%	56.1	25	51.1	2	0	0	1430.73	4024	4036
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	GIAPGDER	97.8%	32	25	23.2	1	0	0	814.41	1490	1497
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	GIFTSEIGTK	99.7%	68.4	25	62.4	3	0	0	1052.56	2941	2950
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	GLSSLLCNFTK	99.7%	70.2	25	56.7	2	0	0	1239.64	226	236
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	GPESESEDHRASGEVR	99.0%	29	25	29	0	2	0	1741.77	500	515
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	GYGLFAGPCK	99.6%	40.6	25	33.6	2	0	0	1069.51	365	374
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	HGDLPDIQIK	99.7%	54.2	25	44.8	4	0	0	1135.61	2777	2786
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	HNLEIIK	99.7%	42.9	25	13.5	2	0	0	866.51	2233	2239
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	HSSLITPLQAVAQR	99.7%	57.7	25	45.8	2	2	0	1520.85	2787	2800
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	IAPYSVEIK	99.7%	43.3	25	29.9	2	0	0	1019.58	100	108
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	ICSKPVVLPK	98.2%	33	25	23	2	0	0	1140.68	490	499
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	ILDVMYSR	99.7%	51.1	25	43.6	4	0	0	1012.51	1876	1883
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	ILELSGSSSEDSEK	99.7%	113	25	104	3	0	0	1480.70	3359	3372
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	IMEFTTTLLNTSPEGWK	99.7%	96.8	25	90	4	0	0	1983.97	1341	1357
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	INQVFHGSCITEGNELTK	99.7%	57.7	25	57.7	2	2	0	2046.99	1896	1913
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	IPALDLLIK	97.1%	30.8	25	29.1	2	0	0	995.65	125	133
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	KNILEESLCELVAK	99.7%	67.3	25	62	2	0	0	1645.88	2334	2347
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	KQNNFSLAMK	99.7%	61.1	25	51.5	3	0	0	1180.61	3248	3257
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LAAVVSACK	99.7%	60.5	25	49.7	2	0	0	918.51	1448	1456
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LACDVDQVTR	99.7%	60.6	25	40.7	2	0	0	1176.57	972	981
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LATTILQHWK	99.7%	55.1	25	54.9	2	0	0	1210.69	1618	1627
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LCYDAFTENMAGENQLLER	99.7%	125	25	118	2	0	0	2290.01	1918	1936
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LGASLAFNNIYR	99.7%	66.1	25	40.8	4	0	0	1338.72	1076	1087
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LGLPGDEVDNK	99.3%	37.2	25	36.2	2	0	0	1156.58	2705	2715
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LGLPGDEVDNKVK	99.7%	51.9	25	49.8	2	0	0	1383.75	2705	2717
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LGNPIVPLNIR	99.7%	42.6	25	42.6	2	0	0	1205.74	2133	2143
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LLEEALLR	99.7%	66.4	25	62.1	4	0	0	956.58	2892	2899
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LLLQGEADQSLLTFIDK	99.7%	105	25	103	4	0	0	1904.04	3051	3067
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LLNFLMK	99.0%	35.5	25	24.5	4	0	0	894.51	2215	2221
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LLNTWTNR	99.7%	46.6	25	40.2	2	0	0	1017.55	3160	3167

DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LLPAELPAKR	99.0%	35.7	25	35.7	2	0	0	1107.69	2900	2909
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LLQDFNR	99.7%	44.2	25	22.3	2	0	0	905.48	2836	2842
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LLQIIER	99.7%	47.1	25	31.8	4	0	0	884.56	3468	3474
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LLSITVR	99.5%	39.3	25	14.9	2	0	0	801.52	669	675
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LNESTFDTQITK	99.7%	83	25	73.2	2	0	0	1396.70	1858	1869
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LNESTFDTQITKK	99.7%	68.9	25	68.9	2	0	0	1524.79	1858	1870
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LPKDDVHAK	99.7%	48.5	25	36	2	0	0	1022.56	1884	1892
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LPPDVLR	99.0%	35.5	25	35.5	2	0	0	809.49	2916	2922
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LPSNTLDR	99.7%	44.3	25	35.7	2	0	0	915.49	2531	2538
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LPVLAGCLK	99.7%	46.9	25	46.9	2	0	0	970.58	217	225
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LQETLSAADR	99.7%	88.4	25	66.8	4	0	0	1103.57	15	24
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LSDFNDITNMLLLK	99.7%	70.8	25	70.8	5	0	0	1636.86	3656	3669
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LSFAVPFR	99.7%	51.7	25	45.4	4	0	0	936.53	892	899
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LSLMYAR	99.7%	48.8	25	26.5	4	0	0	869.46	2739	2745
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LVINTEEVFRPYAK	99.7%	57.4	25	57.4	2	0	0	1678.92	2149	2162
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	LYSLALHPNAFK	99.7%	48	25	43.6	2	1	0	1373.76	1063	1074
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	MAVLALLAK	99.7%	66.1	25	54.2	4	0	0	929.59	1643	1651
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	MDPMNIWDDIITNR	99.7%	72.2	25	72.2	2	0	0	1765.79	3173	3186
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	MEVQEQEEDISSLIR	99.7%	80.3	25	63.4	2	0	0	1805.86	3218	3232
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	MKQDAQVVLYR	99.7%	78.7	25	70.7	2	1	0	1350.72	2763	2773
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	MQLVCCR	99.0%	35.7	25	21.6	2	0	0	966.43	453	459
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	MSPYKDILETHLR	99.7%	38.1	25	38.1	0	2	0	1618.83	1408	1420
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	MSTSPEAFLALR	99.7%	81.3	25	69.7	8	0	0	1322.68	3890	3901
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	MVSAVLNGMLDQSFR	99.7%	94.2	25	73	3	0	0	1683.82	1592	1606
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	MYAALGDPK	99.7%	61.3	25	55.6	5	0	0	965.48	3613	3621
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	NCISTVVHQGLIR	99.7%	70.5	25	60.9	2	2	0	1496.80	477	489
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	NFWSHETR	98.5%	33.6	25	28.5	1	0	0	1076.49	2523	2530
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	NLDLAVLELMQSSVDNTK	99.7%	108	25	108	4	0	0	2006.01	1574	1591
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	NLLIFENLIDLK	99.7%	74.7	25	65.8	1	0	0	1444.84	1974	1985
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	NLLTVTSSDEMMK	99.7%	97.5	25	83.3	6	0	0	1500.69	869	881
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	NLSSNEAISLEEIR	99.7%	102	25	74.6	2	0	0	1574.80	839	852
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	NNWEVSALSR	99.7%	66.7	25	58.8	2	0	0	1175.58	811	820
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	NVDSNNKELSIAIR	99.7%	82.4	25	82.3	2	2	0	1572.83	351	364
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	QCLPSLDLSCK	99.7%	59.6	25	55.8	2	0	0	1320.63	1498	1508
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	QDAQVVLYR	99.7%	63.3	25	48.4	2	0	0	1091.58	2765	2773
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	QFINLMLPMK	99.7%	45.2	25	28.4	3	0	0	1266.66	3966	3975
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	QGNLSSQVPLKR	99.3%	30.4	25	27	1	2	0	1326.75	3148	3159
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	QITPQQQEK	95.5%	29	25	22.2	1	0	0	1099.57	1043	1051
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	QITQSALLAEAR	99.7%	88	25	72.5	4	0	0	1300.72	2951	2962
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	QLFSSLFSGILK	99.7%	68.6	25	57.5	2	0	0	1339.76	2807	2818
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	QMFLTQTDTGDDR	99.7%	81.3	25	66.7	3	0	0	1543.67	394	406
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	QVSNMVAK	99.1%	36.3	25	23.7	2	0	0	876.46	322	329
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	RLSFAVPFR	97.9%	32.2	25	21.2	1	0	0	1092.63	891	899
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	SDPGLLTNTMDVFVK	99.7%	88.7	25	83.2	6	0	0	1636.83	3993	4007
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	SIELFYK	97.8%	31.9	25	15.7	1	0	0	899.49	1187	1193
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	SKDFVQVMR	99.7%	54.8	25	41.8	2	0	0	1109.58	2417	2425
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	SLEYCSTASIDSENPPDLNK	99.7%	86.3	25	86.3	2	0	0	2240.00	3010	3029
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	SLGPPQGEEDSVPR	99.7%	75.4	25	74.9	2	0	0	1467.71	2107	2120
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	SLGTIQQCCDAIDHLCR	99.7%	35.4	25	35.4	0	2	0	2046.92	1120	1136
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	SLNSIEFR	99.7%	47.9	25	38.4	2	0	0	965.51	72	79
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	SMEEDPQTSR	99.7%	42.2	25	34.4	2	0	0	1179.49	237	246

DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	SPNLWLK	96.6%	30.2	25	21.8	1	0	0	857.49	1203	1209
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	SQGCSEQVLTVLK	99.7%	87.2	25	81.6	3	0	0	1448.74	3290	3302
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	STVLTPMFVETQASQGTLQTR	99.7%	110	25	110	4	2	0	2295.17	2599	2619
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	SVGPDFGK	96.8%	30.4	25	22.8	1	0	0	806.40	2695	2702
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	TETVTSFR	99.7%	42.2	25	35.5	3	0	0	940.47	3865	3872
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	TSALSDETKNNWEVSALSR	99.7%	42.3	25	42.3	0	2	0	2108.03	802	820
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	TVGALQVLGTEAQSSLLK	99.7%	116	25	116	4	0	0	1815.02	1275	1292
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	TVSLLDENNVSSYLSK	99.7%	121	25	114	4	0	0	1768.90	3303	3318
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	TYSVVPMTSR	99.7%	41.8	25	30.2	2	0	0	1140.57	3790	3799
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	VCLDIIYK	99.7%	41.3	25	21.8	1	0	0	1023.55	2434	2441
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	VEGMTELYFQLK	99.7%	51.6	25	40.2	2	0	0	1457.73	2405	2416
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	VFLALAAK	95.9%	29.4	25	15	1	0	0	832.53	464	471
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	VIAGLYQR	99.7%	54.5	25	48.2	1	0	0	919.54	3373	3380
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	VLEQLIVAHFPMQSR	98.4%	33.5	25	33.5	1	0	0	1783.95	1713	1727
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	VTELALTASDR	99.7%	99.6	25	77.4	3	0	0	1175.63	914	924
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	VTVMASLR	99.7%	51	25	33.7	2	0	0	876.50	3726	3733
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	VVQMLGSLGGQINK	99.7%	84.6	25	64.8	4	0	0	1459.79	855	868
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	WPVAGQIR	99.7%	40.9	25	35	2	0	0	926.52	2629	2636
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	YAVPSAGLR	99.7%	50.7	25	40.9	1	0	0	933.52	265	273
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	YFEGVSPK	99.6%	40.6	25	28.5	1	0	0	926.46	682	689
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	YNFPVEVEVPMER	99.7%	61.7	25	60.2	4	0	0	1608.77	1988	2000
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	YPEETLSLMTK	99.7%	49.5	25	38	4	0	0	1311.65	3475	3485
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	134	167	343	0.33%	35.1%	YSCFALFVK	99.7%	45	25	38.7	2	0	0	1134.57	701	709
DNA-directed RNA polymerase I subunit RPA49	POLR1E	RPA49_HUMAN	54.0	100.0%	2	2	3	0.00%	5.0%	CIWFLDTLIK	99.6%	40.1	25	30	2	0	0	1308.70	338	347
DNA-directed RNA polymerase I subunit RPA49	POLR1E	RPA49_HUMAN	54.0	100.0%	2	2	3	0.00%	5.0%	LSYVGNNFGTGALK	95.0%	28.5	25	28.5	1	0	0	1440.75	129	142
DNA-directed RNA polymerase II subunit RPB1	POLR2A	RPB1_HUMAN	217.2	99.9%	2	2	3	0.00%	1.4%	TPSLTVFLLGQSAR	99.7%	71	25	65.9	2	0	0	1489.84	1136	1149
DNA-directed RNA polymerase II subunit RPB1	POLR2A	RPB1_HUMAN	217.2	99.9%	2	2	3	0.00%	1.4%	YSPTSPTYSPTSPK	99.7%	46.6	25	44.7	1	0	0	1512.72	1909	1922
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	6	6	9	0.01%	5.8%	EGEEQLQTQHQK	99.0%	35.7	25	29.1	2	0	0	1454.69	135	146
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	6	6	9	0.01%	5.8%	GPIQILNR	99.7%	54	25	44.8	2	0	0	910.55	1065	1072
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	6	6	9	0.01%	5.8%	KGFDQEEVFEKPTR	94.5%	22.4	25	22.4	0	1	0	1709.85	821	834
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	6	6	9	0.01%	5.8%	NLTYSAPLYVDITK	99.7%	53.4	25	53.3	2	0	0	1597.85	117	130
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	6	6	9	0.01%	5.8%	QEVPIIIVFR	98.8%	34.8	25	26.1	1	0	0	1213.73	265	274
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	6	6	9	0.01%	5.8%	VSGDDVIIGK	99.7%	41	25	23.1	1	0	0	1002.55	860	869
DNA-directed RNA polymerase II subunit RPB3	POLR2C	RPB3_HUMAN	31.4	100.0%	3	3	5	0.00%	13.8%	FIIENTDLAVANSIR	99.7%	98.6	25	91.8	2	0	0	1675.90	21	35
DNA-directed RNA polymerase II subunit RPB3	POLR2C	RPB3_HUMAN	31.4	100.0%	3	3	5	0.00%	13.8%	LGLIPLISDDIVDK	99.7%	46.3	25	40.5	2	0	0	1510.87	68	81
DNA-directed RNA polymerase II subunit RPB3	POLR2C	RPB3_HUMAN	31.4	100.0%	3	3	5	0.00%	13.8%	PYANQPTVR	96.9%	30.5	25	30.5	1	0	0	1045.54	2	10
DNA-directed RNA polymerase II subunit RPB7	POLR2G	RPB7_HUMAN	19.3	99.8%	2	2	2	0.00%	13.4%	LFTEVEGTCTGK	99.1%	36.1	25	29.4	1	0	0	1341.64	30	41
DNA-directed RNA polymerase II subunit RPB7	POLR2G	RPB7_HUMAN	19.3	99.8%	2	2	2	0.00%	13.4%	YFGPNLLNTVK	95.2%	28.7	25	23.2	1	0	0	1265.69	17	27
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	6	6	10	0.01%	4.8%	GFSIGIGDVTPGQGLLK	99.7%	46	25	46	3	0	0	1658.91	695	711
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	6	6	10	0.01%	4.8%	IDEVAVPVHVAK	99.7%	62.6	25	51.5	2	0	0	1276.73	377	388
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	6	6	10	0.01%	4.8%	LAPVYLSNR	98.6%	34	25	28.6	1	0	0	1032.58	686	694
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	6	6	10	0.01%	4.8%	LEVNAETVR	99.7%	49.7	25	33.1	1	0	0	1030.55	1142	1150
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	6	6	10	0.01%	4.8%	LLVEGDNLR	99.6%	40.8	25	32.8	1	0	0	1028.57	1225	1233
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	6	6	10	0.01%	4.8%	VVVQGIPEVSR	99.7%	66.7	25	66.7	2	0	0	1182.68	1199	1209
DNA-directed RNA polymerase III subunit RPC10	POLR3K	RPC10_HUMAN	12.3	99.8%	2	2	3	0.00%	18.5%	AYFMQLQTR	99.6%	40	25	34.6	2	0	0	1173.57	77	85
DNA-directed RNA polymerase III subunit RPC10	POLR3K	RPC10_HUMAN	12.3	99.8%	2	2	3	0.00%	18.5%	SADEPMTTFYK	96.2%	29.7	25	29.7	1	0	0	1305.57	86	96
DNA-directed RNA polymerase III subunit RPC2	POLR3B	RPC2_HUMAN	127.8	100.0%	3	3	3	0.00%	3.4%	GAVGASVTSSTHEK	99.7%	50.8	25	47.2	1	0	0	1330.66	197	210
DNA-directed RNA polymerase III subunit RPC2	POLR3B	RPC2_HUMAN	127.8	100.0%	3	3	3	0.00%	3.4%	LNECPLDPGGYFIVK	99.7%	48.4	25	48.4	1	0	0	1721.86	158	172
DNA-directed RNA polymerase III subunit RPC2	POLR3B	RPC2_HUMAN	127.8	100.0%	3	3	3	0.00%	3.4%	VILIQEQLSK	99.7%	61.5	25	45.4	1	0	0	1170.71	177	186
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	5	5	9	0.01%	5.1%	LLQEAPGK	99.2%	36.6	25	21.8	1	0	0	855.49	194	201
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	5	5	9	0.01%	5.1%	LSLAQHLR	99.7%	50.8	25	43.7	2	0	0	937.56	783	790

DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	5	5	9	0.01%	5.1%	LSLDVEQAPSGQHSQAQLSGQQQR	99.7%	53.5	25	53.5	0	2	0	2592.28	202	225
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	5	5	9	0.01%	5.1%	VAQVLEGFITR	99.7%	71.8	25	61.8	2	0	0	1232.70	977	987
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	5	5	9	0.01%	5.1%	VLDLVLQLFQAK	99.7%	71.5	25	58.2	2	0	0	1386.84	713	724
DNA-directed RNA polymerases I, II, and III subunit RPABC1	POLR2E	RPAB1_HUMAN	24.6	100.0%	4	4	6	0.01%	20.0%	ALIVVQQGMTPSAK	99.7%	78.7	25	75.8	2	0	0	1442.80	102	115
DNA-directed RNA polymerases I, II, and III subunit RPABC1	POLR2E	RPAB1_HUMAN	24.6	100.0%	4	4	6	0.01%	20.0%	EEVTELLAR	99.7%	43	25	29.3	1	0	0	1059.57	154	162
DNA-directed RNA polymerases I, II, and III subunit RPABC1	POLR2E	RPAB1_HUMAN	24.6	100.0%	4	4	6	0.01%	20.0%	IIRPSETAGR	99.3%	37	25	23	2	0	0	1099.62	193	202
DNA-directed RNA polymerases I, II, and III subunit RPABC1	POLR2E	RPAB1_HUMAN	24.6	100.0%	4	4	6	0.01%	20.0%	IQAGDPVAR	97.5%	31.4	25	30.3	1	0	0	926.51	173	181
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	6	8	15	0.01%	43.3%	ADQFEYVMYGK	99.7%	61.5	25	60.1	2	0	0	1350.60	85	95
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	6	8	15	0.01%	43.3%	IEGDETSTEAATR	99.7%	61.1	25	60.8	2	0	0	1379.63	99	111
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	6	8	15	0.01%	43.3%	LHCESESFK	95.8%	29.2	25	29.2	2	0	0	1136.50	28	36
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	6	8	15	0.01%	43.3%	LQGDANNLHGFEVDSR	99.7%	55.3	25	55.3	2	1	0	1771.84	125	140
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	6	8	15	0.01%	43.3%	LSAYVSYGGLLMR	99.7%	78.3	25	70.5	4	0	0	1445.75	112	124
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	6	8	15	0.01%	43.3%	VYRIEGDETSTEAATR	99.7%	70.3	25	70.3	2	0	0	1797.86	96	111
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	7	8	13	0.01%	17.1%	CVLNEGMPIYR	99.5%	39.2	25	39.2	2	0	0	1367.64	302	312
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	7	8	13	0.01%	17.1%	ELYDKGGEQAIK	99.7%	56.8	25	35.2	2	0	0	1350.69	62	73
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	7	8	13	0.01%	17.1%	ILEVHIDK	99.7%	43.3	25	13.5	2	0	0	966.56	207	214
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	7	8	13	0.01%	17.1%	KILEVHIDK	99.7%	42.4	25	12.3	1	0	0	1094.66	206	214
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	7	8	13	0.01%	17.1%	NVICDKCEGR	99.4%	38.5	25	38.4	1	0	0	1250.56	131	140
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	7	8	13	0.01%	17.1%	QISQAYEVLSDAK	99.7%	123	25	120	2	0	0	1451.74	47	59
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	7	8	13	0.01%	17.1%	TIVITSHPGQIVK	99.7%	61.1	25	61.1	2	1	0	1392.82	284	296
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	11	11	21	0.02%	27.2%	DGNDLHMTYK	99.7%	48.9	25	46.9	2	0	0	1193.53	263	272
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	11	11	21	0.02%	27.2%	EISFAYEVLSNPEK	99.7%	64.6	25	55.7	2	0	0	1625.81	49	62
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	11	11	21	0.02%	27.2%	EISFAYEVLSNPEKR	99.7%	70.4	25	70.4	2	0	0	1781.91	49	63
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	11	11	21	0.02%	27.2%	GEGMPQYR	95.6%	29.1	25	16.8	1	0	0	937.42	314	321
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	11	11	21	0.02%	27.2%	IGLVEALCGFQFTFK	99.7%	103	25	101	2	0	0	1729.90	273	287
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	11	11	21	0.02%	27.2%	ILEVHVDK	99.7%	47.7	25	28	2	0	0	952.55	216	223
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	11	11	21	0.02%	27.2%	LYDILGVPPGASENELKK	99.7%	36	25	32.9	0	2	0	1943.05	9	26
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	11	11	21	0.02%	27.2%	NVLCSACSGQGGK	99.7%	86.1	25	86.1	2	0	0	1337.59	140	152
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	11	11	21	0.02%	27.2%	VIEPGCVR	99.7%	41.5	25	39.2	2	0	0	929.49	303	310
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	11	11	21	0.02%	27.2%	VSLEDLYNGK	99.7%	65.6	25	56.9	2	0	0	1137.58	122	131
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	11	11	21	0.02%	27.2%	YGEQGLR	99.7%	53.3	25	32.3	2	0	0	822.41	69	75
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	5	6	13	0.01%	14.2%	EFTVNIMDTCER	99.7%	69.8	25	69.8	1	0	0	1530.66	227	238
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	5	6	13	0.01%	14.2%	FSQLAEAYEVLSDEVK	99.7%	46.8	25	46.6	2	0	0	1827.90	135	150
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	5	6	13	0.01%	14.2%	GGPTVDPEELFR	99.7%	57.8	25	56.8	2	0	0	1316.65	176	187
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	5	6	13	0.01%	14.2%	GSIIISPCVVCR	99.7%	58.6	25	44.7	4	0	0	1360.71	282	293
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	5	6	13	0.01%	14.2%	VMIPVPAGVEDGQTVR	99.7%	73.6	25	69.4	4	0	0	1683.87	304	319
DnaJ homolog subfamily B member 11	DNAJB11	DJB11_HUMAN	40.5	100.0%	3	3	5	0.00%	11.5%	FQDLGAAYEVLSDSEK	99.7%	124	25	118	2	0	0	1771.84	67	82
DnaJ homolog subfamily B member 11	DNAJB11	DJB11_HUMAN	40.5	100.0%	3	3	5	0.00%	11.5%	KGEGLPNFDNNNIK	99.7%	43.6	25	39.9	1	0	0	1559.78	302	315
DnaJ homolog subfamily B member 11	DNAJB11	DJB11_HUMAN	40.5	100.0%	3	3	5	0.00%	11.5%	TLEVEIEPGVR	99.7%	63	25	53.1	2	0	0	1241.67	207	217
DnaJ homolog subfamily B member 12	DNAJB12	DJB12_HUMAN	41.8	100.0%	3	3	6	0.01%	9.6%	AIGTAYAVLSNPEK	99.7%	84.8	25	79.4	2	0	0	1433.76	153	166
DnaJ homolog subfamily B member 12	DNAJB12	DJB12_HUMAN	41.8	100.0%	3	3	6	0.01%	9.6%	GYTAEQVAAVK	99.7%	55.5	25	53.5	2	0	0	1136.59	93	103
DnaJ homolog subfamily B member 12	DNAJB12	DJB12_HUMAN	41.8	100.0%	3	3	6	0.01%	9.6%	NVEDDYIANLR	99.7%	50.9	25	50.9	2	0	0	1321.64	316	326
DnaJ homolog subfamily B member 6	DNAJB6	DNJB6_HUMAN	36.1	100.0%	5	5	11	0.01%	20.2%	APGPWDPLASAAGLK	99.7%	46.6	25	46.6	2	0	0	1450.77	288	302
DnaJ homolog subfamily B member 6	DNAJB6	DNJB6_HUMAN	36.1	100.0%	5	5	11	0.01%	20.2%	QVAEAYEVLSDAK	99.7%	76.9	25	71.4	3	0	0	1422.71	48	60
DnaJ homolog subfamily B member 6	DNAJB6	DNJB6_HUMAN	36.1	100.0%	5	5	11	0.01%	20.2%	SLTINGVADDDALAEER	99.7%	75.9	25	74.7	1	0	0	1788.86	226	242
DnaJ homolog subfamily B member 6	DNAJB6	DNJB6_HUMAN	36.1	100.0%	5	5	11	0.01%	20.2%	VDYYEVLGVQR	99.7%	82.4	25	62.7	3	0	0	1340.68	2	12
DnaJ homolog subfamily B member 6	DNAJB6	DNJB6_HUMAN	36.1	100.0%	5	5	11	0.01%	20.2%	VEVEEDGQLK	98.7%	34.3	25	28.2	2	0	0	1145.57	216	225
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	5	5	11	0.01%	6.8%	ASNLLYGQLK	99.7%	51.9	25	43.8	2	0	0	1106.62	493	502
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	5	5	11	0.01%	6.8%	GVNSYPSLFIFR	99.7%	43.1	25	43.1	2	0	0	1399.74	197	208
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	5	5	11	0.01%	6.8%	ILYDILAFAK	99.7%	48.7	25	44.5	3	0	0	1166.68	439	448
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	5	5	11	0.01%	6.8%	NFQEEQINTR	99.7%	58.8	25	34.2	2	0	0	1278.61	757	766

DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	5	5	11	0.01%	6.8%	NSILFLNSLDAK	99.7%	60.5	25	60.5	2	0	0	1334.73	326	337
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	5	5	8	0.01%	11.1%	AGFFGTVVEYGAER	99.7%	87.9	25	78.5	2	0	0	1502.73	328	341
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	5	5	8	0.01%	11.1%	AGLPGFYDPCVGEEK	99.7%	66.6	25	65.1	2	0	0	1638.75	509	523
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	5	5	8	0.01%	11.1%	GIRPGLTTVLAR	98.8%	34.7	25	20.2	2	0	0	1253.77	249	260
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	5	5	8	0.01%	11.1%	IIEAEESR	97.1%	30.8	25	22	1	0	0	946.48	452	459
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	5	5	8	0.01%	11.1%	VIDVTVPLQCLVK	99.7%	66.1	25	56.9	1	0	0	1483.86	485	497
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	6	6	9	0.01%	3.3%	DSLLASLLDGVR	99.7%	73	25	64.2	2	0	0	1258.70	312	323
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	6	6	9	0.01%	3.3%	ENGLEVLQEAFSR	99.7%	74	25	65.3	1	0	0	1491.74	1443	1455
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	6	6	9	0.01%	3.3%	IFIAQPAWVLR	99.7%	61.8	25	51.9	2	0	0	1313.77	1987	1997
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	6	6	9	0.01%	3.3%	IVDGPDPENIILILK	99.7%	70.4	25	61.4	2	0	0	1648.95	1360	1374
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	6	6	9	0.01%	3.3%	TELLTEALR	97.2%	31	25	14.5	1	0	0	1045.59	91	99
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	6	6	9	0.01%	3.3%	VYNEVPTFQLEVPK	95.8%	29.3	25	22.2	1	0	0	1662.87	1695	1708
DnaJ homolog subfamily C member 7	DNAJC7	DNJC7_HUMAN	56.4	100.0%	3	3	5	0.00%	6.9%	AVQFFVQALR	99.7%	51.6	25	42.2	2	0	0	1178.67	229	238
DnaJ homolog subfamily C member 7	DNAJC7	DNJC7_HUMAN	56.4	100.0%	3	3	5	0.00%	6.9%	EALGDAQQSVR	99.7%	48.8	25	40.9	1	0	0	1173.59	80	90
DnaJ homolog subfamily C member 7	DNAJC7	DNJC7_HUMAN	56.4	100.0%	3	3	5	0.00%	6.9%	YPEAQSVASDILR	99.6%	40.8	25	39	2	0	0	1448.74	192	204
DnaJ homolog subfamily C member 9	DNAJC9	DNJC9_HUMAN	29.9	100.0%	4	4	6	0.01%	20.0%	ELGLDEGVDSLK	99.7%	60.7	25	60.7	1	0	0	1274.65	206	217
DnaJ homolog subfamily C member 9	DNAJC9	DNJC9_HUMAN	29.9	100.0%	4	4	6	0.01%	20.0%	ISLEDIQAFEK	99.7%	65.1	25	56.9	1	0	0	1292.67	108	118
DnaJ homolog subfamily C member 9	DNAJC9	DNJC9_HUMAN	29.9	100.0%	4	4	6	0.01%	20.0%	NIIQQAIDAGEVPSYNAFVK	99.7%	53.3	25	52.7	2	0	0	2177.12	161	180
DnaJ homolog subfamily C member 9	DNAJC9	DNJC9_HUMAN	29.9	100.0%	4	4	6	0.01%	20.0%	VSLQVHPDR	99.6%	39.6	25	30.5	2	0	0	1050.57	38	46
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	9	16	0.02%	31.5%	DVAEQLEK	99.6%	40.7	25	21.4	2	0	0	931.47	73	80
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	9	16	0.02%	31.5%	EGNFDIVSGTR	99.7%	81.7	25	76.1	2	0	0	1194.58	137	147
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	9	16	0.02%	31.5%	GYVFQMEMIVR	99.7%	56	25	53.8	2	0	0	1404.67	206	216
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	9	16	0.02%	31.5%	LGGNEIVSFLK	99.7%	56.5	25	54.1	2	0	0	1176.66	241	251
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	9	16	0.02%	31.5%	LGLGTAYIHGMK	99.4%	38.4	25	35.6	3	0	0	1260.68	96	107
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	9	16	0.02%	31.5%	QKEGNFDIVSGTR	98.0%	26.1	25	17.2	0	1	0	1450.73	135	147
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	9	16	0.02%	31.5%	QLNYTIGEVPISFVDR	99.7%	68.6	25	68.6	2	0	0	1850.96	219	234
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	9	16	0.02%	31.5%	YSVLLPTYNER	99.7%	47	25	47	2	0	0	1354.70	27	37
Dolichol-phosphate mannosyltransferase subunit 3	DPM3	DPM3_HUMAN	10.1	99.8%	2	2	6	0.01%	23.9%	ELQSQIQEAR	99.7%	72.6	25	57.1	4	0	0	1201.62	73	82
Dolichol-phosphate mannosyltransferase subunit 3	DPM3	DPM3_HUMAN	10.1	99.8%	2	2	6	0.01%	23.9%	VATFHDCEDAAR	99.7%	56.9	25	50.1	2	0	0	1391.60	61	72
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	10	10	18	0.02%	24.3%	ELGSECGIEFDEEK	99.7%	85.7	25	79.3	2	0	0	1641.70	140	153
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	10	10	18	0.02%	24.3%	ETHSLFFR	99.3%	37.2	25	25.1	1	0	0	1036.52	58	65
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	10	10	18	0.02%	24.3%	GFELTFK	96.0%	29.4	25	25.8	1	0	0	841.45	71	77
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	10	10	18	0.02%	24.3%	LPDVYGVFQFK	99.7%	58	25	49.1	2	0	0	1312.69	381	391
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	10	10	18	0.02%	24.3%	NTLLIAGLQAR	99.7%	96.1	25	73.8	2	0	0	1169.70	240	250
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	10	10	18	0.02%	24.3%	SSLNPILFR	99.7%	58.1	25	36.2	3	0	0	1046.60	190	198
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	10	10	18	0.02%	24.3%	TLVLLDNLNVR	99.7%	75	25	62.3	2	0	0	1269.75	47	57
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	10	10	18	0.02%	24.3%	WVFKEEGVLR	99.7%	51.1	25	40.8	2	0	0	1262.69	298	307
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	10	10	18	0.02%	24.3%	WVPFDGDDIQLEFVR	99.7%	52.2	25	51	1	0	0	1835.90	345	359
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	10	10	18	0.02%	24.3%	YSQTGNYELAVALSR	99.7%	104	25	97.8	2	0	0	1671.83	283	297
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	13	15	26	0.02%	25.4%	ALTSEIALLQSR	99.7%	84.8	25	71.8	2	0	0	1301.74	525	536
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	13	15	26	0.02%	25.4%	ATSFLLALEPELEAR	99.7%	68.8	25	64.5	3	0	0	1659.90	66	80
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	13	15	26	0.02%	25.4%	DVPAYSQDTFK	99.5%	39	25	34.2	2	0	0	1270.60	205	215
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	13	15	26	0.02%	25.4%	GEDEEENNLEVR	99.7%	70	25	60.7	2	0	0	1432.62	90	101
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	13	15	26	0.02%	25.4%	HFDETVNR	99.1%	36.1	25	21	1	0	0	1017.47	495	502
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	13	15	26	0.02%	25.4%	IDHILDAL	99.6%	40.4	25	38.9	2	0	0	909.50	600	607
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	13	15	26	0.02%	25.4%	LKTEGSDLCDR	99.7%	54.6	25	40.3	2	1	0	1293.61	537	547
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	13	15	26	0.02%	25.4%	LPVALDPGAK	99.5%	38.8	25	38.8	2	0	0	980.58	117	126
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	13	15	26	0.02%	25.4%	NIEIDSPYEISR	99.7%	78.4	25	68.5	2	0	0	1435.71	380	391
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	13	15	26	0.02%	25.4%	QPDSGISSIR	99.4%	38.5	25	25	1	0	0	1059.54	269	278
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	13	15	26	0.02%	25.4%	SEDLLDYGPFR	99.7%	69.1	25	62.2	2	0	0	1311.62	194	204
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	13	15	26	0.02%	25.4%	VHYENNSPFLTITSMTR	99.2%	29.6	25	29.6	0	1	0	2009.97	216	232

Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	13	15	26	0.02%	25.4%	VTAEVVLAHLGGGSTSR	99.7%	104	25	104	2	1	0	1653.89	49	65
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	8	9	19	0.02%	18.5%	FELDTSER	99.4%	38	25	24.5	3	0	0	996.46	461	468
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	8	9	19	0.02%	18.5%	FPEEEAPSTVLSQNLFTPK	99.7%	67.8	25	66.5	1	0	0	2134.07	505	523
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	8	9	19	0.02%	18.5%	ISTEVGITNVDLSTVDKDQSIAPK	99.7%	51.8	25	51.8	0	2	0	2530.33	369	392
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	8	9	19	0.02%	18.5%	LQVTNVLSQPLTQATVK	99.7%	117	25	107	4	0	0	1840.05	290	306
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	8	9	19	0.02%	18.5%	MLAQQAVK	99.7%	42.5	25	24.4	2	0	0	904.49	620	627
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	8	9	19	0.02%	18.5%	TGQEVVFVAEPDNK	99.7%	81.3	25	72.2	2	0	0	1532.76	443	456
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	8	9	19	0.02%	18.5%	TSFTPVGDVFELNFMNVK	99.7%	67.1	25	67.1	3	0	0	2045.00	323	340
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	8	9	19	0.02%	18.5%	YIANTVELR	99.7%	44.5	25	38.6	2	0	0	1078.59	358	366
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	DAD1	DAD1_HUMAN	12.5	100.0%	3	3	8	0.01%	28.3%	ADFQGISPER	99.3%	37.2	25	28.8	3	0	0	1119.54	83	92
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	DAD1	DAD1_HUMAN	12.5	100.0%	3	3	8	0.01%	28.3%	FLEEYLSSTPQR	99.7%	47.6	25	46.7	1	0	0	1469.73	12	23
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	DAD1	DAD1_HUMAN	12.5	100.0%	3	3	8	0.01%	28.3%	SASVVSVISR	99.7%	50.9	25	44.9	4	0	0	1004.57	2	11
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	6	6	12	0.01%	9.2%	EGSPVLLNCLMYK	99.7%	47.8	25	47.8	2	0	0	1523.76	629	641
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	6	6	12	0.01%	9.2%	ENDYYTPTGEFR	99.7%	58.5	25	49	2	0	0	1491.64	614	625
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	6	6	12	0.01%	9.2%	FGQVYTEAK	99.7%	60	25	51	2	0	0	1042.52	647	655
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	6	6	12	0.01%	9.2%	FLAEEGFYK	99.7%	42.1	25	30.6	2	0	0	1103.54	59	67
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	6	6	12	0.01%	9.2%	FYSLLDPSYAK	99.7%	44.6	25	41.3	3	0	0	1303.66	330	340
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	6	6	12	0.01%	9.2%	VGQAMASTEEK	99.7%	45.3	25	39.2	1	0	0	1150.54	555	565
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	STT3B	STT3B_HUMAN	93.7	100.0%	6	6	10	0.01%	8.1%	ESDYFTPQGEFR	99.7%	48.2	25	48.2	2	0	0	1475.64	692	703
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	STT3B	STT3B_HUMAN	93.7	100.0%	6	6	10	0.01%	8.1%	FGEMQLDFR	99.3%	37.2	25	31.1	1	0	0	1142.53	725	733
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	STT3B	STT3B_HUMAN	93.7	100.0%	6	6	10	0.01%	8.1%	FYSLWDTGYAK	99.7%	57.7	25	56.9	2	0	0	1350.64	384	394
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	STT3B	STT3B_HUMAN	93.7	100.0%	6	6	10	0.01%	8.1%	SSLNSSPWSGLMALGNSR	99.7%	41.8	25	41.8	1	0	0	1863.90	13	30
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	STT3B	STT3B_HUMAN	93.7	100.0%	6	6	10	0.01%	8.1%	TEEGLGPNIK	99.1%	36.1	25	36.1	2	0	0	1057.55	527	536
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	STT3B	STT3B_HUMAN	93.7	100.0%	6	6	10	0.01%	8.1%	VTNIFPK	98.4%	33.5	25	24.3	2	0	0	818.48	787	793
Dolichyl-phosphate beta-glucosyltransferase	ALG5	ALG5_HUMAN	36.9	99.8%	2	2	4	0.00%	7.7%	ETLPSIWDSPTK	99.7%	55.6	25	47.7	2	0	0	1373.69	54	65
Dolichyl-phosphate beta-glucosyltransferase	ALG5	ALG5_HUMAN	36.9	99.8%	2	2	4	0.00%	7.7%	QLSVVVPSYNEEK	99.7%	42.4	25	36.7	2	0	0	1491.77	66	78
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	11	12	35	0.03%	23.6%	ATVTAMIAR	99.7%	48.5	25	33.6	1	0	0	933.52	449	457
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	11	12	35	0.03%	23.6%	EFVMQVK	98.0%	32.4	25	16.8	2	0	0	880.46	318	324
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	11	12	35	0.03%	23.6%	ELLYGGTSPTAETILK	99.7%	90.6	25	86.2	4	0	0	1692.91	458	473
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	11	12	35	0.03%	23.6%	LAQIQQAK	99.7%	56.5	25	45.3	4	0	0	899.53	291	298
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	11	12	35	0.03%	23.6%	LLSELDQQSTEMPR	99.7%	79.2	25	79.2	1	0	0	1646.81	552	565
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	11	12	35	0.03%	23.6%	NAAENMLEILGFK	99.7%	82.2	25	80.6	7	0	0	1449.74	343	355
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	11	12	35	0.03%	23.6%	NAAIAVLEELKK	99.7%	58	25	50	3	0	0	1298.77	240	251
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	11	12	35	0.03%	23.6%	NLPVNFEVAR	99.4%	38.1	25	33.3	2	0	0	1158.63	197	206
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	11	12	35	0.03%	23.6%	TKPIVKPQTSPEYGQGINPISR	97.1%	24.6	25	24.6	0	1	0	2410.31	269	290
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	11	12	35	0.03%	23.6%	VPQAQPTKPALK	99.7%	55.6	25	46.2	6	0	0	1277.76	356	367
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	11	12	35	0.03%	23.6%	VSVGEFVGEGEGK	99.7%	104	25	95.7	4	0	0	1293.63	220	232
Double-stranded RNA-binding protein Staufen homolog 2	STAU2	STAU2_HUMAN	62.6	100.0%	7	8	18	0.02%	17.0%	ALQALQNEPIPER	99.7%	48.5	25	44.9	4	0	0	1478.80	175	187
Double-stranded RNA-binding protein Staufen homolog 2	STAU2	STAU2_HUMAN	62.6	100.0%	7	8	18	0.02%	17.0%	ALTESTLPKPVQKPPK	95.6%	23.1	25	23.1	0	1	0	1734.02	69	84
Double-stranded RNA-binding protein Staufen homolog 2	STAU2	STAU2_HUMAN	62.6	100.0%	7	8	18	0.02%	17.0%	ASTNLQDQLEK	99.7%	43.4	25	24.6	4	0	0	1246.63	377	387
Double-stranded RNA-binding protein Staufen homolog 2	STAU2	STAU2_HUMAN	62.6	100.0%	7	8	18	0.02%	17.0%	EFVMQVK	98.0%	32.4	25	16.8	2	0	0	880.46	339	345
Double-stranded RNA-binding protein Staufen homolog 2	STAU2	STAU2_HUMAN	62.6	100.0%	7	8	18	0.02%	17.0%	GSSPTPPCSPVQPSK	96.1%	29.6	25	29.2	1	0	0	1525.73	484	498
Double-stranded RNA-binding protein Staufen homolog 2	STAU2	STAU2_HUMAN	62.6	100.0%	7	8	18	0.02%	17.0%	LAQIQQAK	99.7%	56.5	25	45.3	4	0	0	899.53	312	319
Double-stranded RNA-binding protein Staufen homolog 2	STAU2	STAU2_HUMAN	62.6	100.0%	7	8	18	0.02%	17.0%	VGNEVATGTGPNK	99.7%	52.5	25	41.3	2	0	0	1243.63	346	358
Double-stranded RNA-binding protein Staufen homolog 2	STAU2	STAU2_HUMAN	62.6	100.0%	7	8	18	0.02%	17.0%	VGNEVATGTGPNKK	99.5%	31.7	25	28.9	1	1	0	1371.72	346	359
Double-stranded RNA-binding protein Staufen homolog 2	STAU2	STAU2_HUMAN	62.6	100.0%	7	8	18	0.02%	17.0%	VISGTTLGYLSPK	99.7%	56.6	25	43.4	4	0	0	1335.75	430	442
Double-stranded RNA-specific adenosine deaminase	ADAR	DSRAD_HUMAN	136.1	100.0%	3	5	9	0.01%	3.0%	AMTILLEEAK	99.7%	64	25	53.1	3	0	0	1118.61	565	574
Double-stranded RNA-specific adenosine deaminase	ADAR	DSRAD_HUMAN	136.1	100.0%	3	5	9	0.01%	3.0%	LVDQSGPPHEPK	99.7%	58.8	25	52.2	3	1	0	1303.66	746	757
Double-stranded RNA-specific adenosine deaminase	ADAR	DSRAD_HUMAN	136.1	100.0%	3	5	9	0.01%	3.0%	YLNTNPVGGLLEYAR	99.7%	81.4	25	75.1	2	0	0	1679.88	722	736
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	18	0.02%	25.2%	DVKPSNILVNSR	99.7%	54	25	52.5	2	0	0	1341.75	194	205
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	18	0.02%	25.2%	ISELGAGNGGVVTK	99.7%	84.6	25	78.4	2	0	0	1301.71	75	88

Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	18	0.02%	25.2%	LNQPGTPTR	99.7%	45	25	40.1	1	0	0	983.53	389	397
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	18	0.02%	25.2%	LPNGVFTPDFQEFVNK	99.7%	48.6	25	46.9	2	0	0	1851.93	333	348
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	18	0.02%	25.2%	RIPEEILGK	98.3%	33	25	31.6	2	0	0	1054.63	164	172
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	18	0.02%	25.2%	RLEAFLTQK	99.3%	37.3	25	24.8	2	0	0	1105.64	53	61
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	18	0.02%	25.2%	VGELKDDDFER	99.7%	60	25	52.2	2	2	0	1322.62	64	74
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	18	0.02%	25.2%	VQHRPSGLIMAR	98.8%	28.3	25	27.1	0	2	0	1364.76	89	100
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	18	0.02%	25.2%	YPIPPPDAK	98.9%	35	25	17.3	1	0	0	997.54	265	273
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	8	11	18	0.02%	30.5%	DVKPSNVLINK	99.1%	36.3	25	27.8	2	0	0	1226.71	190	200
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	8	11	18	0.02%	30.5%	FPYESWGTPFQQLK	99.0%	35.5	25	35.5	1	0	0	1727.84	266	279
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	8	11	18	0.02%	30.5%	FSPEFVDFTAQCLR	99.7%	88.7	25	88.7	2	0	0	1716.81	294	307
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	8	11	18	0.02%	30.5%	HAQSGTIMAVK	99.7%	41.7	25	29.8	4	0	0	1142.60	83	93
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	8	11	18	0.02%	30.5%	ISCMSKPPAPNPTPPR	99.7%	35.5	25	35.5	0	3	0	1765.87	27	42
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	8	11	18	0.02%	30.5%	LLMDLDINMR	96.2%	29.7	25	29.7	1	0	0	1265.62	107	116
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	8	11	18	0.02%	30.5%	MCDFGISGYLVDSVAK	99.7%	88.7	25	88.2	3	0	0	1777.81	206	221
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	8	11	18	0.02%	30.5%	QVVEEPSPQLPADR	99.7%	61.5	25	57.9	2	0	0	1564.80	280	293
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	51	0.05%	23.6%	AEITDAEGLGLK	99.7%	80.5	25	72.8	2	0	0	1216.64	933	944
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	51	0.05%	23.6%	AESLQQEVEALK	99.7%	76	25	67.3	2	0	0	1344.70	318	329
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	51	0.05%	23.6%	AFLQGGQEATDIALLLR	99.7%	77.7	25	68.5	2	0	0	1816.00	769	785
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	51	0.05%	23.6%	ASEQIYGTPSSSPYECLR	99.7%	65	25	63.2	1	0	0	2044.93	873	890
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	51	0.05%	23.6%	ASLASLPPLHVAK	99.7%	47.8	25	47.8	2	0	0	1303.77	1121	1133
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	51	0.05%	23.6%	DLEEKLETLR	99.7%	53.3	25	35.5	2	0	0	1245.67	226	235
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	51	0.05%	23.6%	DLETSCSDIR	99.7%	73.5	25	62.5	2	0	0	1195.53	786	795
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	51	0.05%	23.6%	DQLDETVNVEPLTK	99.7%	73.7	25	60.7	1	0	0	1600.81	709	722
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	51	0.05%	23.6%	DSPLLLQQISAMR	99.7%	76.1	25	76.1	4	0	0	1471.79	1089	1101
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	51	0.05%	23.6%	ELTNQQEASVER	99.7%	79.4	25	72	2	0	0	1403.68	533	544
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	51	0.05%	23.6%	FTQSALDCMSVEVGR	99.7%	68.7	25	68.7	2	0	0	1699.78	752	766
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	51	0.05%	23.6%	GSDGAASSYQLK	99.7%	61.8	25	51.8	2	0	0	1183.56	350	361
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	51	0.05%	23.6%	GTVAYVGATLFATGK	99.4%	37.9	25	37.9	1	0	0	1455.78	42	56
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	51	0.05%	23.6%	IKGEELSEANVR	99.7%	58	25	58	2	1	0	1344.71	961	972
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	51	0.05%	23.6%	KNQELEVVR	98.9%	35.3	25	20.2	1	0	0	1114.62	398	406
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	51	0.05%	23.6%	LEDRETVIK	95.3%	28.9	25	16.9	2	0	0	1102.61	945	953
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	51	0.05%	23.6%	LSHEGPGSELPAGALYR	99.7%	46.6	25	45.1	0	2	0	1753.89	1134	1150
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	51	0.05%	23.6%	MQEQQADLQR	99.7%	76.4	25	61.2	4	0	0	1246.58	265	274
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	51	0.05%	23.6%	NQELEVVR	99.4%	37.8	25	22	1	0	0	986.53	399	406
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	51	0.05%	23.6%	QLTAHLQDVNR	98.4%	33.4	25	18.4	1	0	0	1294.69	522	532
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	51	0.05%	23.6%	SPSAQLMEQVAQLK	99.7%	95.9	25	89.3	4	0	0	1529.80	1180	1193
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	51	0.05%	23.6%	VDELTTDLEILK	99.7%	90.4	25	69.4	2	0	0	1388.75	332	343
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	51	0.05%	23.6%	VGSLYPEMSAHER	99.6%	40.5	25	37.4	1	1	0	1475.69	685	697
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	51	0.05%	23.6%	VTFSCAAGFGQR	99.7%	88.3	25	81.2	2	0	0	1300.61	1248	1259
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	25	30	51	0.05%	23.6%	WVGVILDEAK	99.7%	46.9	25	37.8	2	0	0	1129.63	57	66
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	4	5	7	0.01%	6.8%	FATEYCNTIEGTAK	99.7%	86.4	25	76.6	2	0	0	1604.73	340	353
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	4	5	7	0.01%	6.8%	IFSPNVVNLTLVDLPGMTK	99.7%	43.6	25	43.6	2	0	0	2058.13	134	152
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	4	5	7	0.01%	6.8%	LGIIGVVNR	99.7%	78.6	25	62.6	2	0	0	940.59	239	247
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	4	5	7	0.01%	6.8%	RLEEPSLR	99.7%	43.7	25	35.5	1	0	0	999.56	423	430
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	35	0.03%	27.1%	AIPNQGEILVIR	95.2%	28.7	25	25.1	1	0	0	1322.78	511	522
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	35	0.03%	27.1%	ALLQMVQQFGVDFEK	99.7%	58.7	25	53.7	1	0	0	1752.90	328	342
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	35	0.03%	27.1%	DMILQFISR	99.7%	52.4	25	28.5	2	0	0	1122.60	158	166
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	35	0.03%	27.1%	ESSLILAVTPANMDLANSDALK	99.7%	80.3	25	75.7	3	0	0	2273.17	167	188
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	35	0.03%	27.1%	EVDPQGLR	99.7%	51.3	25	35.6	2	0	0	913.47	192	199
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	35	0.03%	27.1%	FPFELVK	99.7%	48.6	25	0	2	0	0	879.50	370	376
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	35	0.03%	27.1%	GISPVPINLR	95.9%	29.4	25	29.4	1	0	0	1065.64	114	123

Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	35	0.03%	27.1%	GMEELIPLVNK	99.7%	42.7	25	32.9	2	0	0	1242.68	5	15
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	35	0.03%	27.1%	GYIGVVNR	99.5%	39.4	25	29.9	2	0	0	877.49	230	237
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	35	0.03%	27.1%	IEGSGDQVDTLELSGGAR	99.7%	127	25	127	1	0	0	1803.87	344	361
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	35	0.03%	27.1%	IVTTYIR	99.5%	39.4	25	29.8	1	0	0	865.51	459	465
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	35	0.03%	27.1%	LQSQLLSLEK	99.7%	70.9	25	0	2	0	0	1158.67	300	309
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	35	0.03%	27.1%	MGTPHLQK	98.5%	33.8	25	22.5	2	0	0	911.48	272	279
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	35	0.03%	27.1%	NLVDSYVAIINK	99.7%	81.5	25	69.8	2	0	0	1348.75	658	669
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	35	0.03%	27.1%	SSVLENFVGR	99.7%	50.1	25	38.6	2	0	0	1107.58	45	54
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	35	0.03%	27.1%	TGLFTPDLAFEAIVK	99.7%	79.9	25	74.2	2	0	0	1621.88	400	414
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	35	0.03%	27.1%	TLNQQLTNHIR	99.7%	61	25	55.1	2	1	0	1337.73	280	290
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	35	0.03%	27.1%	VPVGDQPPDIEYQIK	99.7%	84.5	25	74.6	2	0	0	1697.87	143	157
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	35	0.03%	27.1%	VYSPHVLNLTLIDLPGITK	99.6%	33.1	25	33.1	0	1	0	2093.20	124	142
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	35	0.03%	27.1%	YMLPLDNLK	95.2%	28.8	25	8.98	1	0	0	1106.59	563	571
Dynein light chain 1, cytoplasmic	DYNLL1	DYL1_HUMAN	10.4	100.0%	4	5	13	0.01%	58.4%	DIAAHIKK	97.4%	31.3	25	12.4	1	0	0	895.54	37	44
Dynein light chain 1, cytoplasmic	DYNLL1	DYL1_HUMAN	10.4	100.0%	4	5	13	0.01%	58.4%	NADMSEEMQQDSVECATQALEK	99.7%	44.8	25	44.6	1	4	0	2546.03	10	31
Dynein light chain 1, cytoplasmic	DYNLL1	DYL1_HUMAN	10.4	100.0%	4	5	13	0.01%	58.4%	NFGSYVTHETK	99.7%	63.7	25	53.5	4	0	0	1282.61	61	71
Dynein light chain 1, cytoplasmic	DYNLL1	DYL1_HUMAN	10.4	100.0%	4	5	13	0.01%	58.4%	YNPTWHCIVGR	99.7%	52.1	25	52.1	3	0	0	1402.67	50	60
Dynein light chain Tctex-type 1	DYNLT1	DYLT1_HUMAN	12.5	99.8%	2	4	7	0.01%	23.0%	EAIESAIGGNAYQHSK	99.7%	71.4	25	71.4	2	1	0	1674.81	23	38
Dynein light chain Tctex-type 1	DYNLT1	DYLT1_HUMAN	12.5	99.8%	2	4	7	0.01%	23.0%	YIVTCVIMQK	99.7%	46.4	25	40.8	4	0	0	1254.66	63	72
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	10	10	14	0.01%	4.1%	APGTNVAMASNQAVR	98.5%	33.6	25	33.6	1	0	0	1486.74	1307	1321
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	10	10	14	0.01%	4.1%	EGQWDCSVCLVR	99.7%	64.6	25	62.2	2	0	0	1508.66	1607	1618
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	10	10	14	0.01%	4.1%	ELLQSFDSALQSVK	99.7%	81.1	25	76	2	0	0	1564.82	257	270
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	10	10	14	0.01%	4.1%	ELVGPPLAETVFTPK	99.7%	124	25	119	2	0	0	1597.88	1384	1398
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	10	10	14	0.01%	4.1%	FGISEPGNQEK	96.6%	30.2	25	24.1	1	0	0	1205.58	1900	1910
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	10	10	14	0.01%	4.1%	IAVAVLEETTR	99.7%	111	25	104	1	0	0	1201.68	2467	2477
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	10	10	14	0.01%	4.1%	IIDDSDSNLSVVK	99.7%	86.9	25	0	1	0	0	1404.72	721	733
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	10	10	14	0.01%	4.1%	SGSSFVHQASFK	99.7%	50.1	25	39.3	1	0	0	1281.62	1447	1458
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	10	10	14	0.01%	4.1%	SNNSETSSVAQSGSESK	99.7%	62.8	25	62.8	1	0	0	1698.74	2555	2571
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	10	10	14	0.01%	4.1%	YIASVQGSTPSPR	99.7%	60.7	25	59.5	2	0	0	1362.70	11	23
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	AALPLTTSDTK	99.5%	39.5	25	38.8	2	0	0	1117.61	1498	1508
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	ADGTATAPPPR	99.7%	41.8	25	41.8	2	0	0	1053.53	707	717
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	AGSSTPGDAPPAVAEVQGR	99.7%	70.3	25	66.2	2	0	0	1766.87	2885	2903
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	AIQDPAFSDGIR	99.7%	62.4	25	61.7	2	0	0	1289.65	518	529
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	ALAELFGLLVK	99.7%	71.1	25	45.8	2	0	0	1173.72	1062	1072
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	DGGSGNSTIIVSR	99.7%	59.2	25	43.8	1	0	0	1262.63	2359	2371
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	DSAVAISGADSR	99.7%	66	25	56.9	2	0	0	1148.55	2930	2941
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	EVLGSLPNVFSALCLNAR	99.7%	43.4	25	43.4	1	0	0	1960.03	599	616
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	EYNLEQQR	99.7%	51.8	25	41.9	1	0	0	1079.51	3647	3654
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	FLQFVTGTSK	99.7%	58.8	25	49.1	2	0	0	1127.61	4296	4305
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	GLQSFVQCQPFER	99.7%	63.9	25	62.9	2	0	0	1595.76	617	629
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	GNDTPLALESTNTEKETSLEETK	95.7%	23.2	25	23.2	0	1	0	2507.20	1719	1741
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	HADHSSLTLGSGSSTTR	99.7%	66.8	25	60.7	0	2	0	1713.82	2522	2538
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	LGSSGLGSASSIQAAVR	99.7%	110	25	103	2	0	0	1560.83	3750	3766
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	LLECYFTR	99.7%	63	25	46.2	2	0	0	1101.54	4123	4130
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	LLSLISIALPENK	99.7%	42.1	25	40	2	0	0	1410.86	3456	3468
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	LPGGVQNFPQFSALR	99.7%	75	25	75	2	0	0	1630.87	1226	1240
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	NLCYHAQTR	99.7%	41.6	25	35.9	2	0	0	1162.54	3211	3219
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	NPDIFTEVANCCIR	99.7%	68.9	25	68.9	2	0	0	1708.78	1881	1894
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	QIGTLLAELR	97.7%	31.8	25	24.8	1	0	0	1113.66	3637	3646
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	SAATSGAGSTTSGVVSGSLGSR	99.7%	102	25	94.8	1	0	0	1896.93	1844	1865
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	SILTLSHEPK	99.4%	38.5	25	28.2	1	0	0	1124.63	830	839

E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	SLLSILQR	99.7%	61.9	25	40.7	1	0	0	929.58	3225	3232
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	SSESELCIETPK	96.1%	29.6	25	25.8	1	0	0	1379.64	3233	3244
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	TLTSIVHLER	99.7%	54.8	25	48.9	2	0	0	1168.67	330	339
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	TPTEAPADCR	95.8%	29.3	25	29.3	1	0	0	1117.49	11	20
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	VLLSPDYLPAMR	99.3%	37.2	25	32.9	1	0	0	1390.74	633	644
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	28	45	0.04%	8.2%	VSDGGSSSTDFK	99.7%	53	25	53	2	0	0	1186.52	3559	3570
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	13	13	23	0.02%	26.3%	ALCWVCAQSR	99.7%	51.4	25	46.6	2	0	0	1250.58	109	118
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	13	13	23	0.02%	26.3%	DHAMVPLEEAAQEYQEK	99.7%	85.8	25	83.5	1	0	0	1987.91	122	138
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	13	13	23	0.02%	26.3%	DLDITSPELR	99.7%	56.1	25	46.8	2	0	0	1158.60	261	270
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	13	13	23	0.02%	26.3%	EAWDLGVCR	99.7%	57.2	25	56.5	2	0	0	1105.51	352	360
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	13	13	23	0.02%	26.3%	GGGSVCPVCR	96.8%	30.4	25	30.4	2	0	0	1048.47	46	55
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	13	13	23	0.02%	26.3%	IHAEFVQQK	99.7%	51.8	25	37.7	2	0	0	1099.59	178	186
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	13	13	23	0.02%	26.3%	LGDTQQSIPGNEER	99.7%	64.5	25	62.1	2	0	0	1543.73	311	324
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	13	13	23	0.02%	26.3%	LQVALGELR	99.7%	58.3	25	28.8	2	0	0	998.60	139	147
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	13	13	23	0.02%	26.3%	LQVALGELRR	97.8%	32	25	26.1	1	0	0	1154.70	139	148
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	13	13	23	0.02%	26.3%	NFLVEEEQR	99.7%	52.3	25	28.8	2	0	0	1163.57	187	195
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	13	13	23	0.02%	26.3%	SESWNLKDLDITSPELR	99.6%	32.6	25	28.8	0	2	0	2003.01	254	270
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	13	13	23	0.02%	26.3%	SGFWTIWLWNK	99.7%	52.6	25	46.8	2	0	0	1437.73	375	385
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	13	13	23	0.02%	26.3%	SVCHVPGLK	95.1%	28.7	25	21.9	1	0	0	996.53	271	279
E3 ubiquitin-protein ligase TRIP12	TRIP12	TRIPC_HUMAN	220.4	99.9%	2	2	3	0.00%	1.4%	IDPLALVQAIER	99.7%	79.1	25	74.3	1	0	0	1337.78	1289	1300
E3 ubiquitin-protein ligase TRIP12	TRIP12	TRIPC_HUMAN	220.4	99.9%	2	2	3	0.00%	1.4%	SSAVVVDAIPVFLEK	99.7%	54.8	25	49.7	2	0	0	1573.88	515	529
E3 ubiquitin-protein ligase UBR4	UBR4	UBR4_HUMAN	573.8	100.0%	2	2	2	0.00%	0.5%	IISLDLPVAEVYK	99.2%	36.5	25	22.4	1	0	0	1459.84	4414	4426
E3 ubiquitin-protein ligase UBR4	UBR4	UBR4_HUMAN	573.8	100.0%	2	2	2	0.00%	0.5%	ILGPAESDEFLAR	99.7%	78.8	25	73.5	1	0	0	1417.73	1337	1349
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	12	12	21	0.02%	16.1%	AQFAEATQR	99.7%	56.3	25	51.3	2	0	0	1021.51	18	26
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	12	12	21	0.02%	16.1%	AVFVPDIYSR	97.1%	30.8	25	29	1	0	0	1166.62	242	251
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	12	12	21	0.02%	16.1%	CVPQIIAFLNSK	99.7%	57.7	25	41.4	1	0	0	1389.76	708	719
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	12	12	21	0.02%	16.1%	FFADDTQAALTK	99.7%	87.2	25	81.5	2	0	0	1327.65	560	571
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	12	12	21	0.02%	16.1%	FINDCTELFR	99.7%	49.3	25	47.4	2	0	0	1314.61	368	377
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	12	12	21	0.02%	16.1%	GVIFTEAFVAR	99.7%	73.5	25	67.2	2	0	0	1209.66	175	185
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	12	12	21	0.02%	16.1%	IISGHIDLDNR	99.7%	50.2	25	43.9	2	0	0	1252.66	164	174
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	12	12	21	0.02%	16.1%	LAADFQR	99.7%	42	25	31.8	2	0	0	820.43	11	17
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	12	12	21	0.02%	16.1%	LGIPDAVSYIK	99.4%	38.5	25	30	2	0	0	1175.67	275	285
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	12	12	21	0.02%	16.1%	TQSTWVDSFFR	99.7%	51.4	25	47.7	2	0	0	1373.65	252	262
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	12	12	21	0.02%	16.1%	TTQLLFLK	99.7%	44.5	25	32.7	1	0	0	963.59	290	297
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	12	12	21	0.02%	16.1%	TYDLPGNFLTQALTQR	99.7%	80.8	25	56.4	2	0	0	1837.94	145	160
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	9	15	0.01%	18.5%	ADQIETQQLMR	99.7%	44.8	25	31.2	2	0	0	1348.65	221	231
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	9	15	0.01%	18.5%	EHQISPGDFPSLR	99.7%	44	25	37.3	0	2	0	1482.73	345	357
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	9	15	0.01%	18.5%	ELVNNLGEIYQK	99.7%	73.1	25	72.9	2	0	0	1419.75	330	341
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	9	15	0.01%	18.5%	IINTPEVVR	98.7%	34.2	25	27.2	1	0	0	1040.61	243	251
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	9	15	0.01%	18.5%	KLNDLIK	99.2%	36.8	25	7.25	2	0	0	843.53	293	299
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	9	15	0.01%	18.5%	LLDTVDDMLANDIAR	99.7%	71.5	25	71.5	1	0	0	1674.84	378	392
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	9	15	0.01%	18.5%	LNAFGNAFLNR	99.7%	61.9	25	53.9	2	0	0	1236.65	125	135
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	9	15	0.01%	18.5%	SKLPNTVLGK	95.2%	28.7	25	27.9	1	0	0	1056.64	474	483
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	9	15	0.01%	18.5%	VYGALMWSLGK	99.7%	58.7	25	57.4	2	0	0	1240.64	232	242
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	3	3	5	0.00%	9.4%	AGGADAVQTVTGGLR	99.7%	74.9	25	67.3	2	0	0	1372.72	15	29
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	3	3	5	0.00%	9.4%	FGNAFLNR	99.7%	63.9	25	52	2	0	0	938.48	131	138
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	3	3	5	0.00%	9.4%	KLNDLIK	99.2%	36.8	25	7.25	2	0	0	843.53	296	302
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	3	3	5	0.00%	9.4%	LPEIYIQLQR	99.5%	39	25	28.5	1	0	0	1272.73	338	347
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	3	3	5	0.00%	9.4%	VYGALMWSLGK	99.7%	58.7	25	57.4	2	0	0	1240.64	235	245
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	21	67	0.06%	52.8%	AINTLNGLR	99.7%	72.9	25	55.8	7	0	0	971.56	77	85
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	21	67	0.06%	52.8%	DANLYISGLPR	99.7%	71	25	65.1	2	0	0	1218.65	105	115

ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	21	67	0.06%	52.8%	DKVAGHSLGYGFVNYVTAK	99.7%	81.9	25	81.9	0	2	0	2026.04	54	72
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	21	67	0.06%	52.8%	DVEDMFSR	99.7%	49.9	25	41.4	4	0	0	998.42	121	128
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	21	67	0.06%	52.8%	FAANPNQNK	99.7%	50.6	25	39.9	4	0	0	1003.50	183	191
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	21	67	0.06%	52.8%	FGGPVHHQAQR	99.7%	56.9	25	47.8	2	4	0	1233.62	207	217
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	21	67	0.06%	52.8%	ILQVSFK	99.7%	48.8	25	0	4	0	0	834.51	314	320
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	21	67	0.06%	52.8%	NVALLSQLYHSPAR	99.7%	71.1	25	55.7	4	2	0	1568.85	192	205
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	21	67	0.06%	52.8%	SEAEEAITSFNGHKPPGSSEPITVK	99.7%	70.1	25	70.1	0	2	0	2612.28	158	182
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	21	67	0.06%	52.8%	SLFSSIGEVESAK	99.7%	85.1	25	76.3	5	0	0	1353.69	38	50
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	21	67	0.06%	52.8%	TMTQKDVEDMFSR	99.7%	42.8	25	42.8	0	2	0	1619.70	116	128
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	21	67	0.06%	52.8%	TNLIVNYLPQNMTQDELR	99.7%	96.7	25	93.4	8	4	0	2162.09	20	37
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	21	67	0.06%	52.8%	VAGHSLGYGFVNYVTAK	99.7%	47	25	47	0	2	0	1782.92	56	72
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	21	67	0.06%	52.8%	VLVDQTTGLSR	99.7%	89.2	25	62.8	5	0	0	1188.66	137	147
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	21	67	0.06%	52.8%	VSYARPSSEVIK	99.7%	45	25	31.6	4	0	0	1335.73	93	104
ELAV-like protein 2	ELAVL2	ELAV2_HUMAN	39.5	100.0%	8	8	23	0.02%	29.0%	AINTLNGLR	99.7%	72.9	25	55.8	7	0	0	971.56	96	104
ELAV-like protein 2	ELAVL2	ELAV2_HUMAN	39.5	100.0%	8	8	23	0.02%	29.0%	DANLYVSGLPK	99.7%	84	25	69.5	2	0	0	1176.63	124	134
ELAV-like protein 2	ELAVL2	ELAV2_HUMAN	39.5	100.0%	8	8	23	0.02%	29.0%	ELEQLFSQYGR	99.7%	56.3	25	56.3	4	0	0	1369.67	140	150
ELAV-like protein 2	ELAVL2	ELAV2_HUMAN	39.5	100.0%	8	8	23	0.02%	29.0%	ILVDQVTGISR	99.7%	91.3	25	76.6	4	0	0	1200.69	156	166
ELAV-like protein 2	ELAVL2	ELAV2_HUMAN	39.5	100.0%	8	8	23	0.02%	29.0%	RIEAEEAIK	97.8%	32	25	6.67	1	0	0	1058.58	176	184
ELAV-like protein 2	ELAVL2	ELAV2_HUMAN	39.5	100.0%	8	8	23	0.02%	29.0%	SLFGSIGEIESCK	99.7%	80.6	25	80.6	4	0	0	1426.69	57	69
ELAV-like protein 2	ELAVL2	ELAV2_HUMAN	39.5	100.0%	8	8	23	0.02%	29.0%	TNLIVNYLPQNMTQEELK	99.7%	45.1	25	45.1	2	0	0	2148.10	39	56
ELAV-like protein 2	ELAVL2	ELAV2_HUMAN	39.5	100.0%	8	8	23	0.02%	29.0%	TNQAILSQLYQSPNR	99.7%	90.5	25	79.7	4	0	0	1732.90	210	224
ELAV-like protein 2	ELAVL2	ELAV2_HUMAN	39.5	100.0%	8	8	23	0.02%	29.0%	VLQVSFK	98.3%	33	25	27	2	0	0	820.49	346	352
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	11	13	32	0.03%	46.5%	AAVDAGFVPNDMQVGQTGK	99.7%	105	25	104	4	0	0	1920.91	250	268
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	11	13	32	0.03%	46.5%	ASSTSPVEISEWLDQK	99.7%	99.7	25	97.8	2	0	0	1776.87	188	203
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	11	13	32	0.03%	46.5%	GLLPEELTPLILATQK	99.7%	114	25	114	2	2	0	1736.02	86	101
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	11	13	32	0.03%	46.5%	GTSFDAAATSGGSASSEK	99.7%	126	25	121	2	0	0	1630.72	170	187
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	11	13	32	0.03%	46.5%	LEVAPISDIIAIK	99.7%	83.7	25	69.4	6	0	0	1381.83	127	139
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	11	13	32	0.03%	46.5%	LGGEVSCLVAGTK	99.7%	85.2	25	84.6	2	0	0	1290.67	47	59
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	11	13	32	0.03%	46.5%	LLYDLADQLHAAVGASR	99.7%	63.7	25	57.1	0	2	0	1812.96	233	249
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	11	13	32	0.03%	46.5%	QFNYTHICAGASAFGK	99.7%	42.4	25	42.4	0	2	0	1771.82	102	117
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	11	13	32	0.03%	46.5%	SDRPELTGAK	99.7%	47.7	25	39.3	2	0	0	1073.56	207	216
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	11	13	32	0.03%	46.5%	SPDTFVR	99.7%	44.6	25	26.8	2	0	0	821.42	140	146
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	11	13	32	0.03%	46.5%	VLVAQHDVYK	99.7%	61.8	25	53	4	0	0	1171.65	76	85
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	9	9	16	0.02%	39.6%	EIDGGLETLR	99.7%	71.1	25	66.3	2	0	0	1102.57	165	174
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	9	9	16	0.02%	39.6%	EVIAVSCGPAQCQETIR	99.7%	102	25	102	2	0	0	1917.92	60	76
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	9	9	16	0.02%	39.6%	IEVIKPGDLGVDLTSK	99.7%	74.7	25	74.7	1	0	0	1683.95	206	221
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	9	9	16	0.02%	39.6%	LGPLQVAR	99.7%	67.8	25	59	2	0	0	853.53	99	106
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	9	9	16	0.02%	39.6%	LPAVVTADLR	99.6%	40.2	25	36.1	2	0	0	1054.63	177	186
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	9	9	16	0.02%	39.6%	LSVISVEDPPQR	99.7%	73.1	25	72.2	2	0	0	1339.72	222	233
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	9	9	16	0.02%	39.6%	TALAMGADR	99.7%	43.1	25	30.5	2	0	0	905.45	77	85
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	9	9	16	0.02%	39.6%	TGVVTDGVK	99.6%	40.5	25	27.6	1	0	0	875.48	27	35
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	9	9	16	0.02%	39.6%	VETTEDLVAK	99.7%	71.5	25	60.6	2	0	0	1104.58	239	248
ELMO domain-containing protein 2	ELMOD2	ELMD2_HUMAN	35.0	100.0%	3	4	7	0.01%	9.9%	IENSLTYSK	99.7%	41	25	36.4	2	0	0	1054.54	47	55
ELMO domain-containing protein 2	ELMOD2	ELMD2_HUMAN	35.0	100.0%	3	4	7	0.01%	9.9%	IFDTYVGAQR	99.7%	84.6	25	75.8	2	0	0	1169.60	34	43
ELMO domain-containing protein 2	ELMOD2	ELMD2_HUMAN	35.0	100.0%	3	4	7	0.01%	9.9%	MCLLQITGYK	98.0%	32.5	25	26.5	3	0	0	1242.62	97	106
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	20	30	225	0.21%	56.3%	DGNASGTTLLEALDCILPPTRPTDKPLR	99.7%	80.5	25	80.5	0	2	0	3021.57	220	247
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	20	30	225	0.21%	56.3%	EHALLAYTLGVK	99.7%	88.6	25	77.6	21	6	0	1314.74	135	146
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	20	30	225	0.21%	56.3%	EVSTYIK	96.8%	30.5	25	0.46	3	0	0	839.45	173	179
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	20	30	225	0.21%	56.3%	EVSTYIKK	99.7%	44.1	25	36.5	6	0	0	967.55	173	180
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	20	30	225	0.21%	56.3%	FEKEAAEMGK	99.7%	54.7	25	42.9	4	0	0	1139.54	42	51
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	20	30	225	0.21%	56.3%	IGGIGTVPVGR	99.7%	94.8	25	89.2	22	0	0	1025.61	256	266

Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	20	30	225	0.21%	56.3%	LPLQDVYK	99.7%	57.7	25	47	13	0	0	975.55	248	255
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	20	30	225	0.21%	56.3%	MDSTEPPYSQK	99.7%	59	25	59	4	0	0	1282.56	155	165
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	20	30	225	0.21%	56.3%	NMITGTSQADCAVLIVAAGVGEFEAGISK	99.7%	54	25	54	0	1	0	2925.43	101	129
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	20	30	225	0.21%	56.3%	QLIVGVNK	99.7%	43.3	25	31.4	11	0	0	870.54	147	154
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	20	30	225	0.21%	56.3%	QTVAVGVIK	99.7%	69.4	25	46.7	10	0	0	914.57	431	439
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	20	30	225	0.21%	56.3%	SGDAAIVDMVPGKPMCVESFSDYPPLGR	99.7%	74.8	25	74.8	0	6	0	3027.39	396	423
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	20	30	225	0.21%	56.3%	STTTGHLIYK	99.7%	51.8	25	40	34	0	0	1120.60	21	30
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	20	30	225	0.21%	56.3%	SVEMHHEALSEALPGDNVGFNVK	99.7%	56.5	25	53	0	1	0	2480.19	291	313
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	20	30	225	0.21%	56.3%	THINIVVIGHVDSGK	99.7%	114	25	108	7	13	0	1588.88	6	20
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	20	30	225	0.21%	56.3%	TIEKFEK	98.8%	34.8	25	28	5	0	0	894.49	38	44
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	20	30	225	0.21%	56.3%	VETGVLKPGMVVTFAPVNVTTEVK	99.7%	55.4	25	55.4	4	19	0	2531.38	267	290
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	20	30	225	0.21%	56.3%	YEEIVKEVSTYIK	99.7%	67.3	25	67	1	0	0	1600.85	167	179
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	20	30	225	0.21%	56.3%	YYVTIIDAPGHR	99.7%	68.5	25	66.1	20	8	0	1404.73	85	96
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	20	30	225	0.21%	56.3%	YYVTIIDAPGHRDFIK	99.7%	64	25	64	2	2	0	1908.00	85	100
Elongation factor 1-beta	EEF1B2	EF1B_HUMAN	24.8	100.0%	2	2	4	0.00%	12.4%	SIQADGLVWGSSK	99.7%	82.6	25	77.9	2	0	0	1347.69	164	176
Elongation factor 1-beta	EEF1B2	EF1B_HUMAN	24.8	100.0%	2	2	4	0.00%	12.4%	SPAGLQVLNDYLADK	99.7%	99.2	25	99.2	2	0	0	1603.83	8	22
Elongation factor 1-delta	EEF1D	EF1D_HUMAN	31.1	100.0%	3	3	5	0.00%	12.1%	IASLEVENQSLR	99.7%	99.7	25	87	2	0	0	1358.73	84	95
Elongation factor 1-delta	EEF1D	EF1D_HUMAN	31.1	100.0%	3	3	5	0.00%	12.1%	LVPVGYGIR	96.1%	29.6	25	23.9	1	0	0	973.58	233	241
Elongation factor 1-delta	EEF1D	EF1D_HUMAN	31.1	100.0%	3	3	5	0.00%	12.1%	SIQLDGLVWGASK	99.7%	81.8	25	77.7	2	0	0	1373.74	220	232
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	34	0.03%	30.0%	AKDPFAHLPK	99.3%	37.5	25	23.2	1	0	0	1123.63	276	285
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	34	0.03%	30.0%	ALIAAQYSGAQVR	99.7%	90.6	25	90.3	6	0	0	1347.74	18	30
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	34	0.03%	30.0%	EYFSWEGAFQHVGK	99.2%	30	25	28	0	2	0	1684.78	415	428
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	34	0.03%	30.0%	FAETQPK	98.2%	33	25	18.8	2	0	0	820.42	221	227
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	34	0.03%	30.0%	ILGLLDAYLK	99.7%	60.8	25	53.2	5	0	0	1118.68	138	147
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	34	0.03%	30.0%	KLDPGSEETQTLVR	99.7%	89.4	25	81.7	2	2	0	1572.82	401	414
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	34	0.03%	30.0%	QAFPNTNR	99.6%	39.8	25	33.2	2	0	0	947.47	182	189
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	34	0.03%	30.0%	QATENAKEEVR	99.7%	44.7	25	31.6	1	0	0	1274.63	126	136
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	34	0.03%	30.0%	STFVLDEFKR	99.7%	48	25	45.5	2	2	0	1241.65	286	295
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	34	0.03%	30.0%	TFLVGER	99.7%	42.8	25	32.9	2	0	0	821.45	150	156
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	34	0.03%	30.0%	VLSAPPHFHFGQTNR	99.1%	29.3	25	27.8	0	2	0	1707.87	31	45
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	34	0.03%	30.0%	WFLTCINQPQFR	99.7%	62.6	25	46.6	3	0	0	1609.79	190	201
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	23	27	52	0.05%	30.8%	ARPFPDGLAEDIDKGEVSAR	99.7%	64.2	25	63.6	0	2	0	2143.08	606	625
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	23	27	52	0.05%	30.8%	AYLPVNESFGFTADLR	99.7%	92.5	25	91.7	2	0	0	1799.90	786	801
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	23	27	52	0.05%	30.8%	CLYASVLTAQPR	99.7%	70.7	25	62	2	0	0	1378.71	728	739
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	23	27	52	0.05%	30.8%	EGALCEENMR	99.7%	70.1	25	59.6	3	0	0	1208.50	689	698
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	23	27	52	0.05%	30.8%	EGIPALDNFLDKL	99.7%	75.1	25	68.8	2	0	0	1444.77	846	858
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	23	27	52	0.05%	30.8%	ETVSEESNVLCLSK	99.7%	96.1	25	86.9	2	0	0	1594.76	581	594
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	23	27	52	0.05%	30.8%	GEGQLGPAER	99.7%	42.6	25	32	3	0	0	1013.50	240	249
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	23	27	52	0.05%	30.8%	GGGQIIPTAR	99.0%	35.7	25	22.6	4	0	0	969.55	717	726
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	23	27	52	0.05%	30.8%	GHVFEESQVAGTPMFVVK	96.7%	24.2	25	24.2	0	1	0	1961.98	768	785
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	23	27	52	0.05%	30.8%	GPLMMYISK	99.7%	46.7	25	2.87	3	0	0	1055.53	392	400
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	23	27	52	0.05%	30.8%	IMGPNYTPGK	99.7%	54.3	25	49.9	2	0	0	1077.54	429	438
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	23	27	52	0.05%	30.8%	IMGPNYTPGKK	98.6%	33.9	25	27.4	1	0	0	1205.63	429	439
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	23	27	52	0.05%	30.8%	KEDLYLKPIQR	99.7%	44	25	40.6	0	2	0	1402.81	439	449
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	23	27	52	0.05%	30.8%	NMSVIAHVDHGK	99.7%	68.7	25	58	1	0	0	1307.65	21	32
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	23	27	52	0.05%	30.8%	QFAEMYVAK	94.5%	28.2	25	25.1	1	0	0	1086.53	227	235
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	23	27	52	0.05%	30.8%	SDPVVSYR	99.7%	48.8	25	38.3	2	0	0	922.46	573	580
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	23	27	52	0.05%	30.8%	STLTDSLVCK	99.7%	62.5	25	54.8	2	0	0	1123.57	33	42
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	23	27	52	0.05%	30.8%	TFCQLILDPIFK	99.7%	65.3	25	63.6	2	0	0	1494.80	288	299
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	23	27	52	0.05%	30.8%	TGTITTFEHAHNMR	99.1%	29.3	25	29.3	0	2	0	1615.76	482	495
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	23	27	52	0.05%	30.8%	VFDAIMNFK	99.7%	63.3	25	60.8	4	0	0	1084.55	300	308

Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	23	27	52	0.05%	30.8%	VFSGLVSTGLK	99.7%	81.8	25	67.8	4	0	0	1107.64	416	426
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	23	27	52	0.05%	30.8%	VNFTVDQIR	99.7%	84	25	63.5	6	0	0	1091.58	2	10
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	23	27	52	0.05%	30.8%	YEWDVAEAR	99.7%	63.9	25	57.3	2	0	0	1138.52	639	647
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	23	27	52	0.05%	30.8%	YFDPANGK	98.0%	32.4	25	29.7	1	0	0	911.43	265	272
Elongation factor Ts, mitochondrial	TSFM	EFTS_HUMAN	35.4	100.0%	3	3	5	0.00%	11.7%	GFLNSSELSGLPAGPDR	99.7%	56	25	56	2	0	0	1716.86	162	178
Elongation factor Ts, mitochondrial	TSFM	EFTS_HUMAN	35.4	100.0%	3	3	5	0.00%	11.7%	TNLEDVGR	98.5%	33.9	25	20.2	1	0	0	903.45	247	254
Elongation factor Ts, mitochondrial	TSFM	EFTS_HUMAN	35.4	100.0%	3	3	5	0.00%	11.7%	YGALVICETSEQK	99.7%	71.9	25	69.2	2	0	0	1497.73	234	246
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	32	108	0.10%	60.4%	ADAVQDSEMVELVELEIR	99.7%	98.8	25	98.2	1	0	0	2062.00	183	200
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	32	108	0.10%	60.4%	AEAGDNLGALVR	99.7%	103	25	84.8	7	0	0	1185.62	316	327
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	32	108	0.10%	60.4%	DLEKPFLLPVEAVYSVPGR	99.7%	72	25	72	7	2	0	2129.16	253	271
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	32	108	0.10%	60.4%	EHLLLAR	98.6%	34	25	30.5	3	0	0	851.51	163	169
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	32	108	0.10%	60.4%	ELAMPGEDLK	98.5%	33.9	25	28.1	3	0	0	1102.55	396	405
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	32	108	0.10%	60.4%	ELLTEFGYK	99.7%	41.4	25	36	2	0	0	1099.57	201	209
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	32	108	0.10%	60.4%	GDECELLGHSK	99.7%	54.2	25	54.2	2	0	0	1244.56	287	297
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	32	108	0.10%	60.4%	GITINAAHVEYSTAAR	99.7%	85	25	75.2	6	6	0	1673.86	105	120
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	32	108	0.10%	60.4%	GLVMVKPGSIKPHQK	99.2%	29.8	25	29.8	0	1	0	1634.94	337	351
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	32	108	0.10%	60.4%	GTVVTGTLER	99.7%	68.9	25	49.1	8	0	0	1032.57	272	281
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	32	108	0.10%	60.4%	HYAHTDCPGHADYVK	99.7%	48	25	44.9	0	2	0	1770.77	121	135
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	32	108	0.10%	60.4%	IILPPEKELAMPGEDLK	99.7%	34.7	25	33.8	0	3	0	1909.04	389	405
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	32	108	0.10%	60.4%	KGDECELLGHSK	99.7%	68.9	25	59.4	2	5	0	1372.65	286	297
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	32	108	0.10%	60.4%	LLDAVDTYIPVPAR	99.7%	91.6	25	88.1	10	0	0	1542.85	239	252
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	32	108	0.10%	60.4%	NMITGTAPLDGCILVVAANDGPMPQTR	95.8%	23.3	25	23.3	0	1	0	2844.37	136	162
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	32	108	0.10%	60.4%	QIGVEHVVVYVNK	99.7%	70.3	25	57	2	1	0	1483.83	170	182
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	32	108	0.10%	60.4%	QPMILEK	98.0%	32.5	25	11	2	0	0	858.48	412	418
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	32	108	0.10%	60.4%	TIGTGLVTNTLAMTEEEK	99.7%	127	25	120	10	0	0	1907.96	430	447
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	32	108	0.10%	60.4%	TIGTGLVTNTLAMTEEEKNIK	98.6%	27.6	25	27.6	0	2	0	2263.19	430	450
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	32	108	0.10%	60.4%	TTLTAAITK	99.7%	57.2	25	46.8	2	0	0	919.55	71	79
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	32	108	0.10%	60.4%	TVVTGIEMFHK	99.7%	49.5	25	31.6	6	2	0	1261.66	301	311
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	32	108	0.10%	60.4%	VEAQVYILSK	99.7%	85.4	25	78.5	8	0	0	1149.65	352	361
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	23	32	108	0.10%	60.4%	YEEIDNAPEER	99.7%	66.5	25	62.4	2	0	0	1364.60	92	102
Elongator complex protein 1	IKBKAP	ELP1_HUMAN	150.3	100.0%	3	3	5	0.00%	2.6%	IVTVVPQDTK	94.9%	28.5	25	14.8	1	0	0	1099.64	697	706
Elongator complex protein 1	IKBKAP	ELP1_HUMAN	150.3	100.0%	3	3	5	0.00%	2.6%	SVVLQLADGQIFK	99.7%	55.8	25	46.5	2	0	0	1417.81	568	580
Elongator complex protein 1	IKBKAP	ELP1_HUMAN	150.3	100.0%	3	3	5	0.00%	2.6%	VFLGNVETFIK	99.7%	48	25	43.3	2	0	0	1266.71	762	772
Emerin	EMD	EMD_HUMAN	29.0	100.0%	7	8	17	0.02%	38.6%	DSAYQSITHYRPVSASR	99.7%	36	25	31.2	0	3	0	1937.95	158	174
Emerin	EMD	EMD_HUMAN	29.0	100.0%	7	8	17	0.02%	38.6%	GDADMYDLPK	99.7%	47.3	25	38.9	1	0	0	1140.49	69	78
Emerin	EMD	EMD_HUMAN	29.0	100.0%	7	8	17	0.02%	38.6%	GYNDDYYEESYFTTR	99.7%	70.9	25	70.9	1	0	0	1922.77	89	103
Emerin	EMD	EMD_HUMAN	29.0	100.0%	7	8	17	0.02%	38.6%	KEDALLYQSK	99.7%	52.4	25	39.8	2	0	0	1194.64	79	88
Emerin	EMD	EMD_HUMAN	29.0	100.0%	7	8	17	0.02%	38.6%	LSPPSSSAASSYSFSDLNSTR	99.7%	106	25	103	2	0	0	2161.00	48	68
Emerin	EMD	EMD_HUMAN	29.0	100.0%	7	8	17	0.02%	38.6%	TYGEPESAGPSR	99.7%	60.8	25	48.7	4	0	0	1250.56	104	115
Emerin	EMD	EMD_HUMAN	29.0	100.0%	7	8	17	0.02%	38.6%	YNIPHGPVVGSTR	99.7%	52.7	25	45.4	2	2	0	1396.73	19	31
Endonuclease III-like protein 1	NTHL1	NTH_HUMAN	34.4	100.0%	2	2	4	0.00%	8.7%	DQVTAGAMQR	99.7%	43.8	25	34.2	2	0	0	1092.51	144	153
Endonuclease III-like protein 1	NTHL1	NTH_HUMAN	34.4	100.0%	2	2	4	0.00%	8.7%	GLTVDSILQTDDATLGK	99.7%	105	25	97.5	2	0	0	1746.91	158	174
Endoplasmic reticulum-Golgi intermediate compartment protein 1	ERGIC1	ERGI1_HUMAN	32.6	99.9%	2	2	4	0.00%	6.9%	EYVAYSHTGR	99.7%	44	25	37.8	1	0	0	1182.55	215	224
Endoplasmic reticulum-Golgi intermediate compartment protein 1	ERGIC1	ERGI1_HUMAN	32.6	99.9%	2	2	4	0.00%	6.9%	YSYQYTVANK	99.7%	60.6	25	53.5	3	0	0	1236.59	205	214
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	5	5	6	0.01%	8.0%	DISTNYYASQK	97.4%	31.2	25	31.2	1	0	0	1289.60	672	682
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	5	5	6	0.01%	8.0%	ELISNASDALDK	99.7%	84	25	75.5	8	0	0	1275.64	103	114
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	5	5	6	0.01%	8.0%	ELISNASDALDKIR	99.7%	111	25	88.2	10	2	0	1544.83	103	116
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	5	5	6	0.01%	8.0%	FAFQAEVNR	99.7%	56.7	25	41.8	2	0	0	1081.54	76	84
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	5	5	6	0.01%	8.0%	GVVDSDDLPLNVSR	99.7%	62.8	25	56.5	1	0	0	1485.75	435	448
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	5	5	6	0.01%	8.0%	SGYLLPDTK	95.3%	28.9	25	23.1	1	0	0	993.53	725	733
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	5	5	6	0.01%	8.0%	TFEINPR	99.1%	36.2	25	23.3	1	0	0	876.46	684	690

Enhancer of mRNA-decapping protein 3	EDC3	EDC3_HUMAN	56.1	100.0%	3	3	6	0.01%	7.1%	AGDITELK	99.7%	50.8	25	18	2	0	0	846.46	56	63
Enhancer of mRNA-decapping protein 3	EDC3	EDC3_HUMAN	56.1	100.0%	3	3	6	0.01%	7.1%	KPASSSSAPQNIPK	99.7%	48	25	47	2	0	0	1411.75	106	119
Enhancer of mRNA-decapping protein 3	EDC3	EDC3_HUMAN	56.1	100.0%	3	3	6	0.01%	7.1%	MLESITNELSLFSK	99.7%	68.6	25	59.8	2	0	0	1627.82	374	387
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	6	9	16	0.02%	45.2%	ADTQTYQPYNK	99.7%	46.2	25	43	2	0	0	1328.61	74	84
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	6	9	16	0.02%	45.2%	ADTQTYQPYNKDWIK	99.7%	46.4	25	44.1	2	1	0	1870.90	74	88
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	6	9	16	0.02%	45.2%	IYVLLRR	97.8%	32	25	14	2	0	0	932.60	91	97
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	6	9	16	0.02%	45.2%	MYEEHLK	97.5%	31.5	25	13.5	1	0	0	949.44	35	41
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	6	9	16	0.02%	45.2%	MYEEHLKR	99.7%	44	25	37.3	4	0	0	1105.55	35	42
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	6	9	16	0.02%	45.2%	TYADYESVNECMEGVCK	99.7%	96.1	25	96.1	4	0	0	2054.81	18	34
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	5	7	17	0.02%	22.1%	AFAAGADIK	99.7%	54.9	25	40.1	2	0	0	863.46	93	101
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	5	7	17	0.02%	22.1%	AQFAQPEILIGTIPGAGGTQR	99.7%	97.3	25	95.3	2	2	0	2125.14	158	178
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	5	7	17	0.02%	22.1%	EGMTAFVEK	97.5%	31.4	25	27.3	2	0	0	1011.48	274	282
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	5	7	17	0.02%	22.1%	NNTVGLIQLNRPK	99.7%	74.5	25	74.5	2	0	0	1466.84	44	56
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	5	7	17	0.02%	22.1%	SLAMEMVLTGDR	99.7%	78.7	25	29.4	7	0	0	1338.64	186	197
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	5	5	8	0.01%	6.5%	FASLEFSPGSK	99.7%	60.8	25	55.9	2	0	0	1169.58	42	52
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	5	5	8	0.01%	6.5%	FNVEDGEIVQQVR	99.7%	88.2	25	80.1	2	0	0	1532.77	202	214
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	5	5	8	0.01%	6.5%	NFPQTALVSFATTGEK	99.7%	48.6	25	48.6	1	0	0	1710.87	315	330
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	5	5	8	0.01%	6.5%	TFIGIFLIDGVTGR	99.7%	56.4	25	51.6	2	0	0	1508.85	755	768
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	5	5	8	0.01%	6.5%	WSQVAPPVLK	99.6%	39.8	25	39.8	1	0	0	1124.65	611	620
ER membrane protein complex subunit 3	EMC3	EMC3_HUMAN	30.0	100.0%	4	4	7	0.01%	19.5%	AGPELLLDSNIR	99.7%	62.7	25	53.8	1	0	0	1297.71	2	13
ER membrane protein complex subunit 3	EMC3	EMC3_HUMAN	30.0	100.0%	4	4	7	0.01%	19.5%	LTQEQVSDSQVLIR	99.7%	86.3	25	63.4	2	0	0	1615.87	44	57
ER membrane protein complex subunit 3	EMC3	EMC3_HUMAN	30.0	100.0%	4	4	7	0.01%	19.5%	SIYSLILGQDNAADQSR	99.7%	114	25	112	2	0	0	1850.92	181	197
ER membrane protein complex subunit 3	EMC3	EMC3_HUMAN	30.0	100.0%	4	4	7	0.01%	19.5%	VPFPLTLR	98.2%	32.9	25	17.5	2	0	0	942.58	140	147
ER membrane protein complex subunit 4	EMC4	EMC4_HUMAN	20.1	100.0%	4	4	9	0.01%	27.9%	CWDIALGPLK	99.7%	46.3	25	45.4	1	0	0	1172.61	69	78
ER membrane protein complex subunit 4	EMC4	EMC4_HUMAN	20.1	100.0%	4	4	9	0.01%	27.9%	GSGQGDSLYPVGYLDK	99.7%	69.8	25	69.8	4	0	0	1655.79	35	50
ER membrane protein complex subunit 4	EMC4	EMC4_HUMAN	20.1	100.0%	4	4	9	0.01%	27.9%	QVPDTSVQETDR	98.9%	35.1	25	34.2	1	0	0	1374.65	51	62
ER membrane protein complex subunit 4	EMC4	EMC4_HUMAN	20.1	100.0%	4	4	9	0.01%	27.9%	WAIELSGPGGGSR	99.7%	88.9	25	81.3	3	0	0	1286.65	17	29
ER membrane protein complex subunit 6	EMC6	EMC6_HUMAN	12.0	99.8%	2	2	4	0.00%	20.0%	EGPPFISEAAVR	98.3%	33	25	33	2	0	0	1272.66	9	20
ER membrane protein complex subunit 6	EMC6	EMC6_HUMAN	12.0	99.8%	2	2	4	0.00%	20.0%	GNAAVLDYCR	99.7%	63.8	25	56	2	0	0	1138.53	21	30
ER membrane protein complex subunit 7	EMC7	EMC7_HUMAN	26.5	100.0%	2	2	3	0.00%	9.5%	SSGPPSYFIK	97.2%	30.9	25	18.9	1	0	0	1082.55	142	151
ER membrane protein complex subunit 7	EMC7	EMC7_HUMAN	26.5	100.0%	2	2	3	0.00%	9.5%	VLVDGEEHVGFLK	99.7%	62.5	25	62.5	2	0	0	1441.77	67	79
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	6	8	14	0.01%	31.2%	ADAEYYAAHK	99.7%	56.1	25	53.8	2	0	0	1138.52	258	267
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	6	8	14	0.01%	31.2%	DLNLMAPGLTIQAVR	99.7%	65	25	62.3	2	0	0	1611.89	155	169
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	6	8	14	0.01%	31.2%	EALEPSGENVIQNK	99.7%	76.6	25	74.6	2	0	0	1527.77	329	342
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	6	8	14	0.01%	31.2%	IPEAIRR	98.0%	32.4	25	15	1	0	0	854.52	175	181
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	6	8	14	0.01%	31.2%	ISEIEDAAFLAR	99.7%	89.9	25	74.4	3	0	0	1334.70	242	253
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	6	8	14	0.01%	31.2%	IYFGSNIPNMFVDSSCALK	99.7%	100	25	100	4	0	0	2179.02	295	313
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	6	8	14	0.01%	31.2%	NFELMEAEK	99.1%	36	25	16.9	3	0	0	1126.51	182	190
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	6	8	14	0.01%	31.2%	SVQTTLQTDEVK	99.7%	81.7	25	64.9	4	0	0	1348.70	61	72
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	6	8	14	0.01%	31.2%	VVEKEAETER	99.7%	54.7	25	52.4	2	0	0	1189.61	202	211
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	30	0.03%	51.3%	ADAECYTAMK	99.7%	57.3	25	53.6	2	0	0	1159.48	258	267
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	30	0.03%	51.3%	DIPNMFMDSAGSVSK	99.7%	108	25	97.7	5	0	0	1598.72	300	314
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	30	0.03%	51.3%	GGALLTSTSGPGFHLMLPFITSYK	98.1%	26.3	25	26.3	0	1	0	2511.30	37	60
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	30	0.03%	51.3%	IEEGHIGVYYR	99.7%	58.9	25	42.3	1	0	0	1335.67	26	36
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	30	0.03%	51.3%	IEVVNFLVPNAVYDIVK	99.7%	57.7	25	57.7	1	0	0	1932.08	89	105
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	30	0.03%	51.3%	ISEIEDAAFLAR	99.7%	89.9	25	74.4	3	0	0	1334.70	242	253
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	30	0.03%	51.3%	KISEIEDAAFLAR	99.7%	98.7	25	93.5	2	0	0	1462.79	241	253
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	30	0.03%	51.3%	LALQQDLTSMAPGLVIQAVR	99.7%	53.2	25	53.2	1	0	0	2124.18	150	169
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	30	0.03%	51.3%	LTPEYLQLMK	99.5%	38.8	25	32.4	2	0	0	1251.67	276	285
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	30	0.03%	51.3%	NYELMESEK	98.0%	32.5	25	25.9	2	0	0	1142.50	182	190
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	30	0.03%	51.3%	SVQTTLQTDEVK	99.7%	81.7	25	64.9	4	0	0	1348.70	61	72

Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	30	0.03%	51.3%	VAQVAEITYGQK	99.7%	82.5	25	79.7	2	0	0	1306.70	221	232
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	30	0.03%	51.3%	VTKPNIPEAIR	97.4%	31.3	25	24.4	2	0	0	1237.73	170	180
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	30	0.03%	51.3%	VVEKEAETER	99.7%	54.7	25	52.4	2	0	0	1189.61	202	211
Estradiol 17-beta-dehydrogenase 11	HSD17B11	DHB11_HUMAN	32.9	99.8%	2	2	4	0.00%	7.7%	FAAVGFHK	99.7%	44.8	25	8.88	2	0	0	876.47	190	197
Estradiol 17-beta-dehydrogenase 11	HSD17B11	DHB11_HUMAN	32.9	99.8%	2	2	4	0.00%	7.7%	TLTDELAALQITGVK	99.7%	76.6	25	74.5	2	0	0	1572.88	198	212
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	10	14	30	0.03%	45.2%	GVFVQSVLPYFVATK	99.7%	65.9	25	64.5	3	0	0	1654.92	224	238
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	10	14	30	0.03%	45.2%	ISYSLFTALR	99.7%	101	25	86.7	2	0	0	1170.65	26	35
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	10	14	30	0.03%	45.2%	KPTLDKPSPETFVK	99.7%	58.8	25	55.5	1	2	0	1586.88	244	257
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	10	14	30	0.03%	45.2%	LDQVSSEIKEK	99.7%	64	25	49.5	2	0	0	1275.68	87	97
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	10	14	30	0.03%	45.2%	MININILSVCK	99.7%	97.5	25	92.9	4	0	0	1304.71	157	167
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	10	14	30	0.03%	45.2%	MTQLVLPGMVER	99.7%	77.4	25	65.6	8	0	0	1389.72	168	179
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	10	14	30	0.03%	45.2%	SYAEELAK	95.2%	28.8	25	15	1	0	0	910.45	65	72
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	10	14	30	0.03%	45.2%	TFVDFFSQCLHEEYR	99.7%	62.6	25	62.6	2	2	0	1977.88	207	221
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	10	14	30	0.03%	45.2%	TIAVDFASEDIYDKIK	99.7%	98.1	25	91.8	2	0	0	1827.94	104	119
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	10	14	30	0.03%	45.2%	VWGVGNEAGVGPGLGEWAVVTGSTDGIGK	97.7%	25.6	25	25	0	1	0	2769.38	36	64
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	6	6	15	0.01%	22.8%	DLLGTVWGGPANLEAIAK	99.7%	77	25	77	3	0	0	1824.99	284	301
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	6	6	15	0.01%	22.8%	ELYLEEALQNER	99.7%	53.8	25	53.8	2	0	0	1506.74	272	283
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	6	6	15	0.01%	22.8%	LVEIIGSR	99.7%	51.1	25	49.5	2	0	0	886.54	199	206
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	6	6	15	0.01%	22.8%	QFIQGPPEVIR	99.7%	48.7	25	29.2	2	0	0	1283.71	251	261
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	6	6	15	0.01%	22.8%	SLEEAQEWLK	99.7%	65.5	25	51.3	4	0	0	1232.62	241	250
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	6	6	15	0.01%	22.8%	VIELENWTEGK	99.7%	73.7	25	73.7	2	0	0	1317.67	90	100
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	16	23	46	0.04%	49.3%	ATQALVLAPTR	99.7%	69	25	61.6	2	0	0	1140.67	100	110
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	16	23	46	0.04%	49.3%	DFTVSAMHGDMDQKER	99.7%	39.4	25	39.4	0	4	0	1866.81	296	311
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	16	23	46	0.04%	49.3%	EELTLEGIR	98.4%	33.5	25	21.4	1	0	0	1059.57	239	247
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	16	23	46	0.04%	49.3%	ELAQQIQK	99.7%	44.9	25	26.9	2	0	0	957.54	111	118
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	16	23	46	0.04%	49.3%	GFKDQIYDIFQK	99.7%	67.8	25	61.9	2	2	0	1501.77	191	202
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	16	23	46	0.04%	49.3%	GIYAYGFEKPSAIQQR	99.7%	98.9	25	94.7	2	0	0	1827.94	46	61
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	16	23	46	0.04%	49.3%	GVAINMVTEEDKR	99.7%	58.6	25	58.6	2	0	0	1461.74	370	382
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	16	23	46	0.04%	49.3%	GYDVIAQAQSGTGK	99.7%	128	25	120	2	0	0	1394.69	69	82
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	16	23	46	0.04%	49.3%	KEELTLEGIR	99.7%	53.6	25	39.4	2	0	0	1187.66	238	247
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	16	23	46	0.04%	49.3%	KVDWLTEK	98.6%	33.9	25	16.5	2	0	0	1018.56	284	291
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	16	23	46	0.04%	49.3%	LNSNTQVVLLSATMPSDVLEVTK	99.7%	60.8	25	60.8	3	0	0	2475.30	203	225
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	16	23	46	0.04%	49.3%	LQMEAPHIIVGTPGR	99.7%	56.7	25	53.6	4	4	0	1618.87	147	161
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	16	23	46	0.04%	49.3%	MFVLDEADEMLSR	99.7%	117	25	111	7	0	0	1555.71	178	190
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	16	23	46	0.04%	49.3%	QFYINVER	99.7%	51.3	25	38.1	2	0	0	1068.55	248	255
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	16	23	46	0.04%	49.3%	VLITTDLLAR	99.7%	73.1	25	69.4	2	0	0	1114.68	325	334
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	16	23	46	0.04%	49.3%	VVMALGDYMGASCHACIGGTNVR	99.7%	43.4	25	43.4	0	1	0	2471.09	119	141
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	28	0.03%	32.4%	DVIAQSQSGTGK	99.7%	69.7	25	65	1	0	0	1190.60	77	88
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	28	0.03%	32.4%	ELAVQIQK	99.7%	44.6	25	35.6	2	0	0	928.55	117	124
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	28	0.03%	32.4%	ETQALILAPTR	99.7%	72.1	25	55.7	2	0	0	1212.69	106	116
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	28	0.03%	32.4%	GFKEQIYDVYR	99.7%	51	25	42.1	2	0	0	1417.71	196	206
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	28	0.03%	32.4%	GIYAYGFEKPSAIQQR	99.7%	98.9	25	94.7	2	0	0	1827.94	52	67
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	28	0.03%	32.4%	GRDVIAQSQSGTGK	99.7%	99.3	25	94.7	2	2	0	1403.72	75	88
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	28	0.03%	32.4%	KGVAINFVK	99.7%	49.7	25	41.4	2	0	0	975.60	374	382
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	28	0.03%	32.4%	KLDYGQHVVAGTPGR	99.7%	44.4	25	30.6	0	2	0	1597.84	152	166
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	28	0.03%	32.4%	KVDWLTEK	98.6%	33.9	25	16.5	2	0	0	1018.56	289	296
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	28	0.03%	32.4%	LDYGQHVVAGTPGR	99.7%	69	25	62.3	2	2	0	1469.75	153	166
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	28	0.03%	32.4%	MLVLDEADEMLNK	99.7%	91.3	25	86.7	3	0	0	1536.73	183	195
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	28	0.03%	32.4%	QFFVAVER	99.7%	56.8	25	39.7	2	0	0	995.53	253	260
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	28	0.03%	32.4%	RDELTLEGIK	98.7%	34.5	25	13.7	2	0	0	1173.65	243	252
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	28	0.03%	32.4%	VLISTDVWAR	99.7%	54.2	25	48.1	2	0	0	1159.65	330	339

Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	5	6	13	0.01%	25.9%	AIVQQWLEYR	99.7%	56.8	25	49.2	4	0	0	1305.70	69	78
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	5	6	13	0.01%	25.9%	EYLLGSTAEEK	99.7%	53.7	25	44.7	2	0	0	1239.61	58	68
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	5	6	13	0.01%	25.9%	FIVDLTVQEKEK	99.7%	74	25	63.7	2	0	0	1448.80	127	138
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	5	6	13	0.01%	25.9%	NDIHTLLK	97.5%	31.5	25	20.4	1	0	0	953.54	89	96
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	5	6	13	0.01%	25.9%	QANKEYLLGSTAEEK	99.7%	66.8	25	63.2	2	2	0	1680.84	54	68
Eukaryotic translation initiation factor 1A, X-chromosomal	EIF1AX	IF1AX_HUMAN	16.5	99.8%	2	2	4	0.00%	15.3%	AYGELPEHAK	99.7%	52.3	25	40	2	0	0	1114.55	105	114
Eukaryotic translation initiation factor 1A, X-chromosomal	EIF1AX	IF1AX_HUMAN	16.5	99.8%	2	2	4	0.00%	15.3%	DYQDNKADVILK	99.2%	36.5	25	29.5	2	0	0	1421.73	83	94
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	10	11	21	0.02%	33.0%	AGLNCSTENMPIK	99.7%	56.5	25	56.5	2	0	0	1434.67	214	226
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	10	11	21	0.02%	33.0%	GVFNVQMEPK	99.7%	51.3	25	16.5	4	0	0	1164.57	267	276
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	10	11	21	0.02%	33.0%	INLIAPPR	99.5%	39.4	25	37.8	2	0	0	893.56	227	234
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	10	11	21	0.02%	33.0%	NECVVVIR	99.7%	55.1	25	37.8	2	0	0	988.52	68	75
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	10	11	21	0.02%	33.0%	RPGYGAYDAFK	94.8%	28.4	25	8.73	1	0	0	1244.61	144	154
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	10	11	21	0.02%	33.0%	TAWVFDDKYK	98.3%	33	25	30.4	1	0	0	1272.63	134	143
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	10	11	21	0.02%	33.0%	TEGLSVLSQAMAVIK	99.7%	62.2	25	54.3	1	0	0	1562.85	245	259
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	10	11	21	0.02%	33.0%	TVYSILR	99.7%	40.9	25	25.8	1	0	0	851.50	107	113
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	10	11	21	0.02%	33.0%	VVTDTDETELAR	99.7%	96.3	25	81.9	5	0	0	1348.66	277	288
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	10	11	21	0.02%	33.0%	YVMTTTTLER	99.7%	51.2	25	40.4	2	0	0	1230.60	235	244
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	IF2G_HUMAN	51.1	100.0%	7	8	11	0.01%	16.3%	AISGVHTVR	99.4%	38	25	33.8	1	0	0	939.54	60	68
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	IF2G_HUMAN	51.1	100.0%	7	8	11	0.01%	16.3%	GVTIKPTVDDD	99.7%	58.8	25	52.3	1	0	0	1159.58	462	472
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	IF2G_HUMAN	51.1	100.0%	7	8	11	0.01%	16.3%	IVLTNPVCTEVGEK	99.7%	61	25	60.1	1	0	0	1558.81	427	440
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	IF2G_HUMAN	51.1	100.0%	7	8	11	0.01%	16.3%	LIGWGQIR	97.7%	31.9	25	19.4	1	0	0	942.55	453	460
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	IF2G_HUMAN	51.1	100.0%	7	8	11	0.01%	16.3%	LTPLSHEVISR	99.7%	51.7	25	51.7	3	0	0	1251.71	28	38
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	IF2G_HUMAN	51.1	100.0%	7	8	11	0.01%	16.3%	QDLTTLDVTK	99.7%	52.3	25	45.3	2	0	0	1133.61	18	27
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	IF2G_HUMAN	51.1	100.0%	7	8	11	0.01%	16.3%	VGQEIEVRPGIVSK	99.7%	45.6	25	41.2	1	1	0	1510.86	290	303
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	ANEFLEVGK	99.6%	40.5	25	29.6	2	0	0	1006.52	15	23
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	ANEFLEVGKK	99.6%	40.6	25	21.8	2	0	0	1134.62	15	24
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	AVEDIHGLFSLSK	99.7%	95.8	25	92.1	3	0	0	1415.75	252	264
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	EDAPIGPHLQSMPSEQIR	99.7%	49.5	25	49.5	0	8	0	2020.98	503	520
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	EEELREYQER	98.7%	34.4	25	25.1	2	0	0	1380.64	838	847
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	ELEIEERER	99.7%	47.3	25	1.03	2	0	0	1202.60	862	870
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	FCLQYTR	99.7%	43.6	25	38.2	5	0	0	987.47	184	190
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	FLWESYR	99.4%	38	25	29	2	0	0	1000.49	152	158
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	FNVLQYVVPEVK	99.7%	76.6	25	64.2	6	0	0	1434.80	377	388
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	GLDEDRGSWR	98.4%	33.3	25	26.3	1	0	0	1190.56	1021	1030
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	IGLINDMVR	99.7%	55.6	25	43.4	9	0	0	1046.57	368	376
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	ILQEHEQIK	99.7%	41.5	25	32.4	5	0	0	1137.63	624	632
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	ILQEHEQIKK	99.3%	30.1	25	18.8	0	1	0	1265.72	624	633
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	ITTMQLER	99.7%	58.5	25	39.7	5	0	0	991.52	733	740
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	KGPEADSEWR	98.4%	33.3	25	29.3	1	0	0	1174.55	901	910
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	KIDYFER	98.9%	35.1	25	20	3	0	0	970.50	694	700
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	KLCDNLR	96.5%	30	25	15	1	0	0	918.48	196	202
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	LATLLGLQAPPTR	99.7%	50	25	47.6	3	0	0	1350.81	355	367
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	LEEIPLIK	96.3%	29.8	25	16.1	3	0	0	954.59	704	711
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	LESLNIQR	99.7%	59.5	25	28.3	4	0	0	972.55	582	589
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	LGDSSLSR	99.7%	59.7	25	40.8	2	0	0	834.43	878	885
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	LKQFEER	99.7%	40.9	25	0	2	0	0	949.51	776	782
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	LLDMDGIIVEK	99.7%	78.4	25	72.1	8	0	0	1245.68	341	351
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	LLLTPWVK	97.8%	32	25	9.89	2	0	0	969.61	144	151
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	LLQQVSQIYQSIEFSR	99.7%	72.9	25	72	4	0	0	1939.03	439	454
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	LTSLVPFVDAFQLER	99.7%	106	25	106	5	0	0	1734.94	455	469
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	LYHDIAQQAFK	99.7%	65	25	51.7	3	0	0	1333.69	173	183

Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	MHLSQIQR	99.3%	37	25	30.4	5	0	0	1028.53	203	210
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	NADDDRIPR	98.1%	32.7	25	16.6	2	0	0	1071.52	1122	1130
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	NICQQVNIK	99.7%	47	25	29.9	4	0	0	1116.58	76	84
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	NLTQDEMQR	99.7%	43.4	25	41.7	4	0	0	1150.52	309	317
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	NMDDDRLSR	99.5%	38.8	25	29.4	2	0	0	1121.50	1142	1150
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	NQLTAMSSVLAK	99.7%	93.1	25	78.6	11	0	0	1262.68	521	532
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	QCLDLLR	99.7%	44.4	25	3.88	2	0	0	917.49	159	165
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	QPALDVLYDVMK	99.7%	46.8	25	44.9	2	0	0	1391.72	25	36
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	RGPAEESSSWR	99.7%	45.5	25	44.3	2	0	0	1261.59	1250	1260
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	RLEEIPLIK	99.6%	39.7	25	38.4	2	0	0	1110.69	703	711
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	RLGDSSLSR	99.5%	38.8	25	26.4	2	0	0	990.53	877	885
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	SGNALFHASTLHR	99.7%	54.2	25	50.7	0	6	0	1410.72	286	298
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	SLEDVVR	99.1%	36.3	25	13.9	2	0	0	817.44	85	91
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	TLSFGSDLNYATR	99.7%	88.4	25	81.7	5	0	0	1444.71	490	502
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	42	49	151	0.14%	28.0%	VLLATLSIPITPER	99.7%	61.1	25	61.1	6	0	0	1522.92	322	335
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	28	70	0.07%	32.8%	AQAVSEDAGGNEGR	99.7%	98.7	25	98.7	5	0	0	1360.61	121	134
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	28	70	0.07%	32.8%	DQYSVIFESGDR	99.7%	94.4	25	93.7	2	0	0	1415.64	304	315
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	28	70	0.07%	32.8%	ETIIAFAWEPNGSK	99.7%	66.5	25	63	2	0	0	1562.79	563	576
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	28	70	0.07%	32.8%	FAVLHGEAPR	99.7%	51	25	45.8	3	0	0	1096.59	577	586
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	28	70	0.07%	32.8%	FSHQGVQLIDFSPCER	99.7%	41.3	25	41.3	0	2	0	1919.91	371	386
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	28	70	0.07%	32.8%	GIALWGGEK	99.6%	40.8	25	31.1	2	0	0	930.50	356	364
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	28	70	0.07%	32.8%	GTQGVVTNFEIFR	99.7%	69.4	25	69.4	6	0	0	1467.76	536	548
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	28	70	0.07%	32.8%	GTYLATFHQR	99.7%	64	25	56.3	4	0	0	1193.61	346	355
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	28	70	0.07%	32.8%	GYIFLEYASPAHAVDAVK	99.7%	82.1	25	82.1	2	2	0	1951.00	231	248
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	28	70	0.07%	32.8%	ISVSFYHVK	99.3%	37.7	25	24.7	2	0	0	1079.59	587	595
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	28	70	0.07%	32.8%	ITNDFYPEEDGK	99.7%	59.7	25	59.7	2	0	0	1427.63	217	228
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	28	70	0.07%	32.8%	ITNDFYPEEDGKTK	99.7%	59.2	25	59.2	2	2	0	1656.78	217	230
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	28	70	0.07%	32.8%	MAQELYMEQK	99.7%	65.6	25	49.2	7	0	0	1270.58	763	772
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	28	70	0.07%	32.8%	MTLDTLSIYETPSMGLLDK	99.7%	78.3	25	68.2	2	0	0	2128.06	441	459
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	28	70	0.07%	32.8%	NGDYLCVK	99.7%	46.9	25	37	1	0	0	968.45	522	529
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	28	70	0.07%	32.8%	NLFNVVDCK	99.7%	54.9	25	42	3	0	0	1108.55	508	516
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	28	70	0.07%	32.8%	QVPVDVVEMK	98.3%	33.1	25	28.5	2	0	0	1143.61	553	562
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	28	70	0.07%	32.8%	TMMEDFRK	96.3%	29.8	25	24.6	2	0	0	1057.48	752	759
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	28	70	0.07%	32.8%	TSIFWNDVKDPVSIEER	99.7%	46.9	25	46.9	0	2	0	2035.01	316	332
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	28	70	0.07%	32.8%	VDNAYWLWTFQGR	99.7%	75.8	25	75.7	2	0	0	1655.80	677	689
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	28	70	0.07%	32.8%	VNLFTDFDK	99.7%	49.4	25	48.5	2	0	0	1098.55	263	271
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	28	70	0.07%	32.8%	VTLMQLPTR	99.7%	62.7	25	45.1	6	0	0	1058.60	493	501
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	28	70	0.07%	32.8%	WTETYVR	95.1%	28.6	25	14.7	2	0	0	954.47	335	341
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	28	70	0.07%	32.8%	YWLEEAECR	99.4%	38.4	25	38.4	1	0	0	1255.54	295	303
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	12	12	22	0.02%	12.2%	DFESHITSYK	98.6%	34	25	27.7	2	0	0	1226.57	151	160
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	12	12	22	0.02%	12.2%	ELLGQGLLLR	99.7%	70.3	25	54.2	2	0	0	1111.68	644	653
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	12	12	22	0.02%	12.2%	FEELTNLIR	99.7%	61.6	25	38.6	2	0	0	1134.62	57	65
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	12	12	22	0.02%	12.2%	GCILTLVER	99.7%	67.8	25	53.7	2	0	0	1060.58	442	450
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	12	12	22	0.02%	12.2%	GTEITHAVVIK	99.7%	52	25	40.9	2	0	0	1167.67	321	331
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	12	12	22	0.02%	12.2%	KIQEESLR	94.9%	28.5	25	16.2	1	0	0	1002.56	782	789
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	12	12	22	0.02%	12.2%	KLNEILQAR	99.2%	36.5	25	15	2	0	0	1084.65	332	340
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	12	12	22	0.02%	12.2%	LGSLVENNER	99.7%	64.7	25	43.8	2	0	0	1130.58	863	872
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	12	12	22	0.02%	12.2%	LNEILQAR	99.7%	56.4	25	46.8	2	0	0	956.55	333	340
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	12	12	22	0.02%	12.2%	QGTYGGYFR	99.4%	37.7	25	28.7	1	0	0	1048.48	878	886
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	12	12	22	0.02%	12.2%	SIVDKEGVPR	99.7%	47.1	25	35.6	2	0	0	1099.61	95	104
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	12	12	22	0.02%	12.2%	TEPTAQQNLALQLAEK	99.7%	105	25	103	2	0	0	1754.93	847	862

Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	8	9	22	0.02%	15.7%	GAVIATELK	99.7%	48.8	25	34.9	2	0	0	901.54	418	426
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	8	9	22	0.02%	15.7%	IFHTVTTTDDPVIR	99.7%	82.3	25	74.4	2	2	0	1614.85	223	236
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	8	9	22	0.02%	15.7%	LFFDKR	99.6%	39.7	25	16.4	1	0	0	825.46	276	281
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	8	9	22	0.02%	15.7%	LGDDIDLIVR	99.7%	89.5	25	66.7	4	0	0	1128.63	365	374
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	8	9	22	0.02%	15.7%	SVYSWDIVVQR	99.7%	69.9	25	67.5	2	0	0	1351.70	261	271
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	8	9	22	0.02%	15.7%	VADWTGATYQDKR	99.7%	55.3	25	52	4	0	0	1510.73	42	54
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	8	9	22	0.02%	15.7%	WTCCALLAGSEYLK	99.7%	73.6	25	73.6	3	0	0	1671.79	435	448
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	8	9	22	0.02%	15.7%	YLILKDPNK	99.4%	38.5	25	29.7	2	0	0	1103.65	506	514
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	52.8%	EIYNEKELLQGK	99.7%	64	25	42.3	2	0	0	1463.77	30	41
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	52.8%	ETIDNNSVSSPLQSLQQR	99.7%	95.3	25	87.5	2	0	0	2016.00	194	211
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	52.8%	IAHFLDR	99.7%	46.2	25	31.4	2	0	0	871.48	10	16
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	52.8%	LASEILMQNWDAAMEDLTR	99.7%	76.6	25	76.6	2	0	0	2207.05	173	191
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	52.8%	LDLLSDTNMVDFAMDVYK	99.7%	97.3	25	69.4	3	0	0	2105.98	42	59
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	52.8%	LFIFETFCR	99.7%	73.6	25	63.7	7	0	0	1232.61	338	346
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	52.8%	LGHVVMGNNAVSPYQQVIEK	99.7%	53.6	25	50.8	0	4	0	2199.12	388	407
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	52.8%	LKETIDNNSVSSPLQSLQQR	99.7%	47.1	25	45.7	0	2	0	2257.18	192	211
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	52.8%	LNMTPEEAER	98.6%	34.2	25	29.5	2	0	0	1189.55	360	369
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	52.8%	MFEDPETTR	99.7%	45.8	25	31.6	4	0	0	1125.49	94	102
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	52.8%	MLFDYLADK	99.7%	66.9	25	51.2	4	0	0	1115.54	112	120
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	52.8%	NALSSLWGK	99.7%	49.5	25	41.6	2	0	0	975.53	164	172
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	52.8%	NLYSDDIPHALR	99.7%	57.8	25	51.1	2	2	0	1413.71	60	71
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	52.8%	QEYLDTLYR	99.7%	49.5	25	37.9	2	0	0	1200.59	125	133
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	52.8%	QLQAETEPIVK	99.7%	57.4	25	31.5	2	0	0	1255.69	83	93
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	52.8%	RTTVVAQLK	99.7%	41.6	25	34.5	2	0	0	1015.63	74	82
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	52.8%	SEAPNWATQDSGFY	99.7%	80.4	25	80.4	2	0	0	1572.66	432	445
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	52.8%	SQMLAMNIEK	99.7%	71.1	25	56	4	0	0	1164.58	415	424
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	52.8%	TTVVAQLK	98.2%	32.9	25	17	2	0	0	859.52	75	82
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	52.8%	VLVPATDR	99.7%	41.8	25	34.8	2	0	0	870.50	156	163
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	52.8%	WIVNLIR	99.6%	39.6	25	12.8	2	0	0	913.56	370	376
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	52.8%	YLTTAVITNK	99.7%	59.7	25	53.3	2	0	0	1123.64	256	265
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	23	30	62	0.06%	52.8%	YLTTAVITNKDVR	99.7%	64	25	55.2	2	0	0	1493.83	256	268
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	6	9	15	0.01%	19.9%	AYVSTLMGVPGR	99.7%	57.5	25	50.4	4	0	0	1250.66	215	226
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	6	9	15	0.01%	19.9%	FLMSLVNQVPK	99.7%	85.3	25	70.7	3	0	0	1275.71	307	317
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	6	9	15	0.01%	19.9%	TMGVMFTPLTVK	99.7%	42.2	25	37.9	2	0	0	1356.69	227	238
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	6	9	15	0.01%	19.9%	VIGLSSDLQQVGGASAR	99.7%	133	25	131	2	0	0	1657.89	262	278
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	6	9	15	0.01%	19.9%	VIGTLLGTVDK	99.7%	57.5	25	48.8	2	0	0	1115.67	116	126
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	6	9	15	0.01%	19.9%	YAYYDTER	99.5%	38.6	25	35.9	2	0	0	1080.46	239	246
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	7	7	13	0.01%	23.4%	CPYKDTLGPMQK	97.3%	25	25	25	0	1	0	1437.69	169	180
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	7	7	13	0.01%	23.4%	EKLPGELEPVQATQNK	99.7%	43.8	25	42.8	0	2	0	1780.94	194	209
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	7	7	13	0.01%	23.4%	ELAEQLGLSTGEK	99.7%	60.7	25	54.7	2	0	0	1374.71	181	193
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	7	7	13	0.01%	23.4%	ETDLQELFRPFGSISR	99.2%	30	25	30	0	2	0	1894.97	252	267
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	7	7	13	0.01%	23.4%	GFAFISFHR	99.7%	45	25	30.5	2	0	0	1081.56	281	289
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	7	7	13	0.01%	23.4%	LPGELEPVQATQNK	99.7%	67.4	25	67.4	2	0	0	1523.81	196	209
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	7	7	13	0.01%	23.4%	VTNLSEDTR	99.7%	44.9	25	27.6	2	0	0	1034.51	243	251
Eukaryotic translation initiation factor 3 subunit H	EIF3H	EIF3H_HUMAN	39.9	100.0%	2	2	3	0.00%	8.8%	EGTGSTATSSSSTAGAAGK	99.7%	73.5	25	65.6	2	0	0	1627.74	6	24
Eukaryotic translation initiation factor 3 subunit H	EIF3H	EIF3H_HUMAN	39.9	100.0%	2	2	3	0.00%	8.8%	LFMAQALQEYNN	99.7%	61.3	25	61.3	1	0	0	1441.68	341	352
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	12	16	41	0.04%	44.0%	DMTMFVTASK	99.7%	67.6	25	59.3	5	0	0	1130.52	199	208
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	12	16	41	0.04%	44.0%	DPIVNVWYSVNGER	99.7%	72.7	25	72.7	2	0	0	1647.81	31	44
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	12	16	41	0.04%	44.0%	DPSQIDNNEPYMK	99.7%	53.9	25	49	2	0	0	1566.67	129	141
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	12	16	41	0.04%	44.0%	EGDLLFTVAK	99.7%	58.2	25	50.5	4	0	0	1092.59	21	30
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	12	16	41	0.04%	44.0%	GHFGPINSVAFHPDGK	99.7%	41.2	25	40.5	0	2	0	1679.83	283	298

Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	12	16	41	0.04%	44.0%	HVLTGSADNSCR	99.7%	71	25	71	4	2	0	1316.60	66	77
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	12	16	41	0.04%	44.0%	LFDSTTLEHQK	99.7%	62.1	25	46.9	4	2	0	1318.66	214	224
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	12	16	41	0.04%	44.0%	LWDCETGK	94.6%	28.3	25	28.3	1	0	0	1008.45	78	85
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	12	16	41	0.04%	44.0%	MKPILLQGHER	99.7%	40.3	25	35.9	0	4	0	1337.74	1	11
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	12	16	41	0.04%	44.0%	SGEVLVNVK	99.7%	65.3	25	57.5	2	0	0	944.54	177	185
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	12	16	41	0.04%	44.0%	SYSSGGEDGYVR	99.7%	77	25	73.2	5	0	0	1276.54	299	310
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	12	16	41	0.04%	44.0%	TCGFDFGGNIIMFSTDK	99.7%	81.6	25	81.6	2	0	0	1909.85	98	114
Eukaryotic translation initiation factor 3 subunit K	EIF3K	EIF3K_HUMAN	25.1	100.0%	4	5	9	0.01%	19.7%	CMIDQAHQEERPIR	99.7%	52.4	25	52.4	0	2	0	1782.84	87	100
Eukaryotic translation initiation factor 3 subunit K	EIF3K	EIF3K_HUMAN	25.1	100.0%	4	5	9	0.01%	19.7%	ENAYDLEANLAVLK	99.7%	58.2	25	48.7	1	0	0	1562.81	39	52
Eukaryotic translation initiation factor 3 subunit K	EIF3K	EIF3K_HUMAN	25.1	100.0%	4	5	9	0.01%	19.7%	GIDRYNPENLATLER	99.7%	88.7	25	88.7	2	2	0	1760.89	17	31
Eukaryotic translation initiation factor 3 subunit K	EIF3K	EIF3K_HUMAN	25.1	100.0%	4	5	9	0.01%	19.7%	YNPENLATLER	99.7%	55.2	25	44.5	2	0	0	1319.66	21	31
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	52	0.05%	35.6%	EPFLQQLK	99.5%	39.1	25	21	2	0	0	1002.56	438	445
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	52	0.05%	35.6%	IDESIHLQLR	99.7%	54.1	25	45	2	2	0	1223.67	382	391
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	52	0.05%	35.6%	KSEEEIDFLR	99.7%	57.1	25	52	2	0	0	1265.64	207	216
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	52	0.05%	35.6%	LAGFLDLTEQEFR	99.7%	94.3	25	88.1	5	0	0	1538.79	475	487
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	52	0.05%	35.6%	LHSLLGDYYQAIK	99.7%	51.8	25	43	2	2	0	1520.81	280	292
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	52	0.05%	35.6%	LYTTMPVAK	99.7%	60.4	25	46.2	2	0	0	1039.55	466	474
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	52	0.05%	35.6%	MLGYFSLVGLLR	99.7%	78.4	25	72.2	2	0	0	1384.77	268	279
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	52	0.05%	35.6%	QDLAYER	99.7%	46.6	25	28.9	2	0	0	894.43	32	38
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	52	0.05%	35.6%	QLEVYTSGGDPESVAGEYGR	99.7%	114	25	114	2	0	0	2113.97	243	262
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	52	0.05%	35.6%	QYEQQTYQVIPEVIK	99.7%	61.2	25	59.7	2	0	0	1865.96	39	53
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	52	0.05%	35.6%	RYGDFFIR	98.4%	33.5	25	25.5	1	0	0	1073.55	538	545
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	52	0.05%	35.6%	SEEEIDFLR	99.7%	61.2	25	49.3	2	0	0	1137.54	208	216
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	52	0.05%	35.6%	TVSDLIDQK	99.5%	38.7	25	26.1	1	0	0	1018.54	62	70
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	52	0.05%	35.6%	VFSDEVQQQAQLSTIR	99.7%	96.9	25	96.9	5	0	0	1848.95	446	461
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	52	0.05%	35.6%	VLENIELNKK	99.7%	55.2	25	41.3	2	0	0	1199.70	293	302
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	52	0.05%	35.6%	VSGGPSLEQR	99.7%	81	25	64.8	2	0	0	1029.53	144	153
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	52	0.05%	35.6%	VSSDVIDQK	99.7%	64.7	25	50.4	4	0	0	990.51	79	87
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	52	0.05%	35.6%	VYEIQDIYENSWTK	99.7%	79.6	25	79.6	2	0	0	1787.85	88	101
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	52	0.05%	35.6%	VYELQASR	99.7%	57.6	25	46.9	4	0	0	965.51	71	78
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	52	0.05%	35.6%	YGDFFIR	99.7%	46.9	25	30	2	0	0	917.45	539	545
Eukaryotic translation initiation factor 3 subunit M	EIF3M	EIF3M_HUMAN	42.5	99.8%	2	3	6	0.01%	5.6%	LLTFMGMAVENK	99.7%	57.6	25	42.2	4	0	0	1353.69	279	290
Eukaryotic translation initiation factor 3 subunit M	EIF3M	EIF3M_HUMAN	42.5	99.8%	2	3	6	0.01%	5.6%	YTVYCSLIK	99.7%	42.4	25	37.8	2	0	0	1146.59	121	129
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	12	0.01%	10.1%	EDITQEFPGK	99.1%	36.4	25	33.3	1	0	0	1163.56	871	880
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	12	0.01%	10.1%	FLLQDTVELR	99.7%	55.2	25	40.5	1	0	0	1233.68	296	305
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	12	0.01%	10.1%	GLSFLFPLLK	99.7%	61.5	25	61.2	2	0	0	1134.69	723	732
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	12	0.01%	10.1%	GVILLIVDK	99.7%	56.8	25	43.2	1	0	0	969.63	113	121
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	12	0.01%	10.1%	LEVDIPLVK	99.6%	40.5	25	30.2	1	0	0	1025.62	632	640
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	12	0.01%	10.1%	SYLAQFAAR	99.7%	55.3	25	48	2	0	0	1026.54	641	649
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	12	0.01%	10.1%	TNPPLIQEKPAK	99.7%	48.9	25	46.7	2	0	0	1335.76	521	532
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	12	0.01%	10.1%	TQTPPLGQTPQLGLK	98.6%	34	25	29.3	1	0	0	1578.89	506	520
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	12	0.01%	10.1%	VIILSLDR	98.1%	32.7	25	27.4	1	0	0	928.58	585	592
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	7	8	34	0.03%	15.5%	AASIFGGAKPVDTAAR	99.7%	61.9	25	61.2	4	4	0	1531.82	357	372
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	7	8	34	0.03%	15.5%	GLNISAVR	99.7%	56.2	25	32.8	4	0	0	829.49	118	125
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	7	8	34	0.03%	15.5%	SILPTAPR	99.2%	36.6	25	26.1	3	0	0	854.51	71	78
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	7	8	34	0.03%	15.5%	SQSSDTEQQSPTSGGGK	99.7%	102	25	102	4	0	0	1680.73	495	511
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	7	8	34	0.03%	15.5%	STPKEDDSSASTSQSTR	99.7%	69	25	69	4	0	0	1783.79	340	356
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	7	8	34	0.03%	15.5%	TGSESSQTGTSTTSSR	99.7%	82.8	25	79.9	4	0	0	1573.69	420	435
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	7	8	34	0.03%	15.5%	VAPAQPSEEGPGR	99.7%	63.8	25	63.8	7	0	0	1294.64	512	524
Eukaryotic translation initiation factor 5B	EIF5B	IF2P_HUMAN	138.8	100.0%	2	2	2	0.00%	1.9%	HFEATDILVSK	95.5%	29	25	29	1	0	0	1259.66	1175	1185
Eukaryotic translation initiation factor 5B	EIF5B	IF2P_HUMAN	138.8	100.0%	2	2	2	0.00%	1.9%	LLQAQGVEVPSK	99.7%	41	25	41	1	0	0	1268.72	425	436

Eukaryotic translation initiation factor 6	EIF6	IF6_HUMAN	26.6	100.0%	2	2	2	0.00%	13.1%	HGLLVPNNTTDQELQHIR	99.7%	50.6	25	50.6	0	1	0	2085.08	68	85
Eukaryotic translation initiation factor 6	EIF6	IF6_HUMAN	26.6	100.0%	2	2	2	0.00%	13.1%	LNEAQPSTIATSMR	99.7%	73	25	71.3	1	0	0	1534.75	224	237
Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	ECSIT	ECSIT_HUMAN	49.1	100.0%	3	3	6	0.01%	10.7%	ALVPFEDLFGQAPGGER	99.7%	48.1	25	46.7	2	0	0	1802.91	68	84
Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	ECSIT	ECSIT_HUMAN	49.1	100.0%	3	3	6	0.01%	10.7%	DLAVYNQLLNIFPK	99.7%	58	25	58	2	0	0	1647.91	125	138
Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	ECSIT	ECSIT_HUMAN	49.1	100.0%	3	3	6	0.01%	10.7%	DLPQDPVELAMFGLR	99.7%	77.8	25	74.6	2	0	0	1700.87	218	232
Exocyst complex component 2	EXOC2	EXOC2_HUMAN	104.1	100.0%	4	4	7	0.01%	5.0%	ASNTADTLFQEVLGR	99.7%	94.7	25	83.1	2	0	0	1621.82	249	263
Exocyst complex component 2	EXOC2	EXOC2_HUMAN	104.1	100.0%	4	4	7	0.01%	5.0%	FLFNLPLNIER	99.6%	40.8	25	32.8	2	0	0	1375.77	282	292
Exocyst complex component 2	EXOC2	EXOC2_HUMAN	104.1	100.0%	4	4	7	0.01%	5.0%	GALLPLSIR	96.8%	30.5	25	27.3	1	0	0	939.60	519	527
Exocyst complex component 2	EXOC2	EXOC2_HUMAN	104.1	100.0%	4	4	7	0.01%	5.0%	VIEAVSEELSR	99.7%	59.9	25	45.3	2	0	0	1231.65	828	838
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	4	4	6	0.01%	6.1%	DASVPLIDVTNLPTPR	99.7%	96.4	25	82.5	2	0	0	1707.93	224	239
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	4	4	6	0.01%	6.1%	ESEVLIGNLGDK	99.7%	61.9	25	56.3	1	0	0	1273.66	682	693
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	4	4	6	0.01%	6.1%	SGELQGGPDDNLIEGGGTK	99.7%	106	25	106	1	0	0	1843.87	468	486
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	4	4	6	0.01%	6.1%	STTQVADSGYQR	99.7%	63.1	25	58.4	2	0	0	1312.61	314	325
Exocyst complex component 5	EXOC5	EXOC5_HUMAN	81.9	99.8%	2	2	2	0.00%	3.3%	NVDTVLMELGVR	96.8%	30.4	25	30.4	1	0	0	1345.71	598	609
Exocyst complex component 5	EXOC5	EXOC5_HUMAN	81.9	99.8%	2	2	2	0.00%	3.3%	SIGTGGIQDLK	99.7%	41	25	26.1	1	0	0	1088.59	378	388
Exosome complex component CSL4	EXOSC1	EXOS1_HUMAN	21.5	100.0%	4	4	8	0.01%	29.7%	ETESQLLPDVGAIVTCK	99.7%	54.2	25	54.2	2	0	0	1859.94	58	74
Exosome complex component CSL4	EXOSC1	EXOS1_HUMAN	21.5	100.0%	4	4	8	0.01%	29.7%	LCNLEEGSPGSGTYTR	99.7%	79.4	25	79.4	2	0	0	1740.79	14	29
Exosome complex component CSL4	EXOSC1	EXOS1_HUMAN	21.5	100.0%	4	4	8	0.01%	29.7%	SFRPGDIVLAK	99.7%	41.6	25	22.6	2	0	0	1202.69	121	131
Exosome complex component CSL4	EXOSC1	EXOS1_HUMAN	21.5	100.0%	4	4	8	0.01%	29.7%	SSENGALPVVSVVR	99.7%	69.2	25	66.7	2	0	0	1413.77	44	57
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	5	5	9	0.01%	20.2%	GGGPAGAGGEAPAALR	99.7%	65.1	25	65.1	2	0	0	1308.67	78	93
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	5	5	9	0.01%	20.2%	GSAYLEAGGTK	99.7%	65.4	25	59.8	2	0	0	1053.52	51	61
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	5	5	9	0.01%	20.2%	LGLEGCQR	99.7%	40.9	25	33.8	1	0	0	932.46	243	250
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	5	5	9	0.01%	20.2%	LYPVLQQSLVR	99.7%	71.1	25	64.8	2	0	0	1315.77	251	261
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	5	5	9	0.01%	20.2%	VLCAVSGPR	99.7%	66.1	25	54.8	2	0	0	958.51	62	70
Exosome complex component RRP4	EXOSC2	EXOS2_HUMAN	32.8	100.0%	4	4	8	0.01%	16.4%	LGQGVLVQVSPSLVK	99.7%	77	25	65.9	2	0	0	1523.92	166	180
Exosome complex component RRP4	EXOSC2	EXOS2_HUMAN	32.8	100.0%	4	4	8	0.01%	16.4%	LIASVAGSVER	99.7%	68.6	25	59.6	2	0	0	1101.63	52	62
Exosome complex component RRP4	EXOSC2	EXOS2_HUMAN	32.8	100.0%	4	4	8	0.01%	16.4%	NCIISLVTQR	99.7%	70.8	25	62.8	2	0	0	1203.65	239	248
Exosome complex component RRP4	EXOSC2	EXOS2_HUMAN	32.8	100.0%	4	4	8	0.01%	16.4%	YIGEVGDIVVGR	99.7%	54.3	25	48.5	2	0	0	1276.69	76	87
Exosome complex component RRP41	EXOSC4	EXOS4_HUMAN	26.4	100.0%	2	2	4	0.00%	9.0%	ALAVVYGPHEIR	99.7%	43.6	25	43.6	2	0	0	1324.74	48	59
Exosome complex component RRP41	EXOSC4	EXOS4_HUMAN	26.4	100.0%	2	2	4	0.00%	9.0%	VLEAAAQAAR	99.7%	91.9	25	77.9	2	0	0	999.56	213	222
Exosome complex component RRP46	EXOSC5	EXOS5_HUMAN	25.2	99.9%	2	2	3	0.00%	11.1%	AVLTFALDSVER	99.7%	84.9	25	55.5	2	0	0	1320.72	179	190
Exosome complex component RRP46	EXOSC5	EXOS5_HUMAN	25.2	99.9%	2	2	3	0.00%	11.1%	NTCEAVVLGTLHPR	99.7%	82.5	25	79.9	1	0	0	1566.81	100	113
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	12	12	23	0.02%	15.1%	ASLTYAEAQLR	99.7%	42.8	25	32.8	2	0	0	1222.64	586	596
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	12	12	23	0.02%	15.1%	AVHEDIVAVELLPK	99.7%	67.6	25	66.9	1	0	0	1532.87	286	299
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	12	12	23	0.02%	15.1%	IEDTVFHVFDK	99.7%	49.6	25	44.7	2	0	0	1349.67	896	906
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	12	12	23	0.02%	15.1%	IIFSEHLPLSK	99.7%	64.1	25	58.3	2	0	0	1283.74	226	236
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	12	12	23	0.02%	15.1%	IMLDSSNLQHQK	99.7%	57.1	25	49.7	1	0	0	1413.72	911	922
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	12	12	23	0.02%	15.1%	LACLSEEGNEIESGK	99.7%	103	25	103	1	0	0	1635.75	211	225
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	12	12	23	0.02%	15.1%	LLAVAIGADCTYPELTDK	99.7%	70.4	25	63.3	2	0	0	1949.99	790	807
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	12	12	23	0.02%	15.1%	NAIVVLIPK	99.7%	51.5	25	51.5	2	0	0	966.63	858	866
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	12	12	23	0.02%	15.1%	NVIVLQTVLQEVR	99.7%	87.7	25	86.7	4	0	0	1510.90	87	99
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	12	12	23	0.02%	15.1%	SLTANPELIDR	99.7%	44.8	25	35.4	2	0	0	1228.65	200	210
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	12	12	23	0.02%	15.1%	YADVIVHR	99.7%	42.8	25	29.4	2	0	0	972.53	782	789
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	12	12	23	0.02%	15.1%	YGLEGTVFFEEK	99.7%	76.1	25	68.1	2	0	0	1418.68	867	878
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	6	6	10	0.01%	7.5%	AAAEQAISVR	99.7%	64.4	25	39.9	2	0	0	1015.55	759	768
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	6	6	10	0.01%	7.5%	ASGGLPQFGDEYDFYR	99.7%	61.7	25	61.7	1	0	0	1821.81	49	64
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	6	6	10	0.01%	7.5%	FALGSVVAVTK	99.7%	81.3	25	76.8	1	0	0	1091.65	38	48
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	6	6	10	0.01%	7.5%	LAQVQVQK	99.5%	39.2	25	21.8	2	0	0	913.55	726	733
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	6	6	10	0.01%	7.5%	LYCNVDSNK	99.4%	38.4	25	29.9	2	0	0	1112.50	409	417
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	6	6	10	0.01%	7.5%	TEDFIIDTLELR	99.7%	88	25	76.2	2	0	0	1464.76	335	346
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	AIIASNIMYIVGQYPR	99.7%	89.9	25	81.1	4	2	0	1824.97	538	553

Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	AVGHPFVIQLGR	99.7%	54.1	25	47.4	2	2	0	1293.74	701	712
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	DFEEYPEHR	98.7%	34.5	25	34.5	2	0	0	1221.52	837	845
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	DTDSINLYK	98.8%	34.8	25	33.7	1	0	0	1068.52	447	455
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	EFAGEDTSDLFLEER	99.7%	93.7	25	79.1	2	0	0	1757.79	1024	1038
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	EFMKDTDSINLYK	99.6%	40.5	25	36.3	1	0	0	1619.76	443	455
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	EPEVLSTMAIIVNK	99.7%	86.8	25	86.8	4	0	0	1559.84	797	810
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	ESPFSTSASPLLSGSQHFDVPPR	98.3%	26.8	25	26.8	0	1	0	2443.19	383	405
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	ETLVYLTHLDYVDTER	99.7%	79.7	25	79.7	2	2	0	1966.98	459	474
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	FLNVPMFR	95.8%	29.3	25	19.4	1	0	0	1023.54	254	261
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	FLVTVIK	99.7%	45.3	25	11.7	2	0	0	819.53	516	522
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	HWPTFISDIVGASR	99.3%	30.5	25	20.3	0	2	0	1585.81	145	158
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	IYLDMLNVYK	99.7%	57	25	53.9	5	0	0	1271.67	713	722
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	LDINLLDNVVNCLYHGEGAQQR	99.7%	46.2	25	40.6	0	1	0	2541.25	23	44
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	LISGWVSR	99.7%	55.4	25	35.9	2	0	0	917.52	758	765
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	LISTLIYK	99.7%	47.9	25	43.2	2	0	0	950.59	246	253
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	LLSEEVFDFSSGQITQVK	99.7%	129	25	129	5	1	0	2027.03	173	190
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	LNMILVQILK	99.7%	58.1	25	37	1	0	0	1200.74	130	139
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	LVLDSIIWAFK	99.7%	83	25	83	3	0	0	1304.76	873	883
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	MAKPEEVLVVENDQGEVVR	99.7%	74.3	25	73	0	4	0	2157.09	424	442
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	MAQEVLTHLK	99.7%	59.2	25	50.9	4	0	0	1185.63	45	54
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	NVDILKDPETVK	99.7%	58.1	25	49.6	2	1	0	1370.75	675	686
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	QLLDFSQK	99.7%	47.7	25	37	2	0	0	978.53	15	22
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	QMLPLNTNIR	99.7%	58.4	25	45.8	4	0	0	1199.66	296	305
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	SAFPHLQDAQVK	99.7%	58.5	25	49.3	2	0	0	1340.70	984	995
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	TSESLCQNNMVILK	99.7%	90.7	25	79.8	4	0	0	1636.80	159	172
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	TSSDPTCVEK	99.7%	51.3	25	32.2	2	0	0	1123.49	113	122
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	TSSDPTCVEKEK	99.7%	63.1	25	50.9	2	0	0	1380.63	113	124
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	VDTILEFSQNMNTK	99.7%	103	25	103	4	0	0	1655.79	63	76
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	YMLLPNQVWDSIIQQATK	99.0%	35.7	25	29.8	1	0	0	2148.12	657	674
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	YVVGLIIK	99.7%	44.3	25	31.9	2	0	0	904.59	105	112
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	45	86	0.08%	35.8%	YYGLQILENVIK	99.7%	82.2	25	82.2	2	0	0	1452.81	77	88
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	AACDLVR	99.7%	43.3	25	28	2	0	0	804.40	385	391
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	AADEEAFEDNSEEYIR	99.7%	102	25	102	2	0	0	1887.79	356	371
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	AADEEAFEDNSEEYIRR	99.7%	41	25	41	0	2	0	2043.89	356	372
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	ALTLPGSSENEYIMK	99.7%	94.3	25	80.9	4	0	0	1668.82	560	574
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	ANIVHLMLSSPEQIQK	99.7%	85.3	25	83.2	2	4	0	1807.97	94	109
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	ATIELCSTHANDASALR	99.7%	125	25	120	2	2	0	1829.88	190	206
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	DAAIYLVTSLASK	99.7%	101	25	89.1	2	0	0	1351.75	428	440
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	DLEGSDIDTR	99.7%	43.7	25	36.8	1	0	0	1120.51	373	382
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	DLEGSDIDTRR	99.6%	40.5	25	25	2	0	0	1276.61	373	383
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	EHDPVGQMVNNPK	99.7%	67.4	25	65.3	2	1	0	1480.69	913	925
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	FQSGDFHVINGVLR	99.0%	28.8	25	23.3	0	2	0	1588.82	138	151
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	GSNTIASAAADK	99.7%	47.5	25	36.9	1	0	0	1105.55	715	726
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	GSNTIASAAADKIPGLLGVFQK	99.7%	55.3	25	51.8	0	2	0	2158.19	715	736
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	ICAVGITK	98.4%	33.5	25	19.2	2	0	0	861.49	841	848
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	IHLAQSLHK	99.7%	47.5	25	44.6	2	0	0	1046.61	926	934
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	IIIPEIQK	98.6%	33.9	25	0	1	0	0	953.60	825	832
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	ILFSSLILISK	99.7%	86.3	25	86.3	2	0	0	1233.78	207	217
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	IVEDEPNKICEADR	99.7%	86.8	25	86.8	2	2	0	1687.80	76	89
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	KICAVGITK	99.7%	48.8	25	41.7	2	0	0	989.58	840	848
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	LLQAFLER	99.7%	62	25	45.8	6	0	0	989.58	707	714

Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	LLQTDDEEEAGLLELLK	99.7%	107	25	100	3	0	0	1929.01	252	268
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	LLTECPPMMDTEYTK	99.7%	59.6	25	59.6	4	0	0	1828.82	849	863
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	LSTACPGR	97.8%	32	25	21.6	1	0	0	861.42	935	942
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	LVLDAFALPLTNLFK	99.7%	64	25	64	2	0	0	1674.98	175	189
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	NLFEDQNTLTSICEK	99.7%	96.6	25	91.2	2	0	0	1811.85	332	346
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	QIFILLFQR	99.7%	58.7	25	57.9	4	0	0	1177.71	769	777
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	QLSDAISIIGR	99.7%	79.3	25	54.8	2	0	0	1172.66	110	120
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	SANVNEFPVLK	99.7%	57	25	43.5	2	0	0	1217.65	471	481
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	SNELWTEIK	99.7%	57.7	25	41.5	2	0	0	1119.57	166	174
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	SQICDNAALYAQK	99.7%	88.1	25	79.5	2	0	0	1481.71	269	281
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	TGNIPALVR	99.7%	61	25	50.5	4	0	0	940.56	698	706
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	TLDPDPAIR	99.5%	39.3	25	31.6	1	0	0	997.53	18	26
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	VCASVTFK	94.6%	28.3	25	23.5	1	0	0	911.47	60	67
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	VIVPNMEFR	95.7%	29.2	25	24.5	1	0	0	1104.59	347	355
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	WPDLLTEMVNR	99.7%	53.7	25	53.1	2	0	0	1373.69	127	137
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	YDEEFQR	99.7%	46.5	25	46.2	3	0	0	986.42	282	288
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	YGALALQEIFDGIQPK	99.7%	101	25	101	4	0	0	1762.94	801	816
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	45	93	0.09%	41.4%	YIMIFR	95.2%	28.8	25	8.91	1	0	0	842.46	487	492
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	14	16	31	0.03%	15.0%	AGGFVVGYTSSGNPIFR	99.7%	106	25	104	2	0	0	1728.87	746	762
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	14	16	31	0.03%	15.0%	ALDMLDAEK	99.6%	39.6	25	37.7	1	0	0	1021.49	802	810
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	14	16	31	0.03%	15.0%	AVMEQIPEIQK	99.7%	70.8	25	65.9	2	0	0	1285.68	1113	1123
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	14	16	31	0.03%	15.0%	AVTVMMDPNSTQR	99.7%	84.3	25	82.9	3	0	0	1481.67	16	28
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	14	16	31	0.03%	15.0%	DIQQTLTQNMER	99.7%	49.3	25	45	2	0	0	1476.71	177	188
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	14	16	31	0.03%	15.0%	DPLLLAIIPK	99.7%	52.2	25	52.2	4	0	0	1092.70	387	396
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	14	16	31	0.03%	15.0%	IFSFLLNTLQENVNK	99.7%	87.7	25	72.8	2	0	0	1779.96	189	203
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	14	16	31	0.03%	15.0%	LFSSVTFETVEESK	99.7%	93.5	25	93.5	2	0	0	1602.79	577	590
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	14	16	31	0.03%	15.0%	LLDNLLALIR	99.7%	85.2	25	65.3	3	0	0	1153.73	772	781
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	14	16	31	0.03%	15.0%	NPCTEQILK	99.7%	44.2	25	37.6	2	0	0	1102.56	763	771
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	14	16	31	0.03%	15.0%	QLLSNELLLTQMEK	99.7%	110	25	99.3	2	0	0	1659.90	632	645
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	14	16	31	0.03%	15.0%	SAILGLPQPLLELNDSPVFK	99.7%	79.7	25	79.7	2	0	0	2151.21	811	830
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	14	16	31	0.03%	15.0%	TDSPSCEYSR	99.7%	56	25	56	2	0	0	1201.48	414	423
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	14	16	31	0.03%	15.0%	VLSDVDAFIAYVGTDQK	99.7%	91.9	25	89.9	2	0	0	1840.93	688	704
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	5	5	7	0.01%	4.4%	AELFELLFR	99.6%	39.6	25	39.6	1	0	0	1137.63	936	944
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	5	5	7	0.01%	4.4%	DLSSLLQAVGR	99.7%	49.4	25	37.1	2	0	0	1158.65	556	566
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	5	5	7	0.01%	4.4%	FNDALTVVER	99.7%	55	25	48.6	1	0	0	1163.61	580	589
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	5	5	7	0.01%	4.4%	NLKPSAVAPQR	97.7%	31.8	25	26.4	1	0	0	1180.68	764	774
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	5	5	7	0.01%	4.4%	STVLASVQR	99.7%	78.7	25	53.7	2	0	0	960.55	956	964
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	18	18	31	0.03%	20.3%	AALSGSYVNFGVFR	99.7%	77.7	25	73.9	2	0	0	1487.76	841	854
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	18	18	31	0.03%	20.3%	ALVEFTNSPDCLSK	99.7%	53.6	25	43.8	2	0	0	1580.76	33	46
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	18	18	31	0.03%	20.3%	DSSLFDIFTLSCNLLK	99.7%	64.3	25	63.8	1	0	0	1872.94	183	198
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	18	18	31	0.03%	20.3%	GIAFAFNAK	99.7%	45.7	25	35.9	2	0	0	938.51	728	736
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	18	18	31	0.03%	20.3%	GSSSYSQLLAATCLTK	99.7%	60.9	25	60.9	2	0	0	1686.84	54	69
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	18	18	31	0.03%	20.3%	IYIGDQVQK	99.4%	37.8	25	23.5	1	0	0	1063.58	560	568
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	18	18	31	0.03%	20.3%	LATFVTQALIQLYAR	99.7%	42.8	25	42.8	1	0	0	1707.98	100	114
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	18	18	31	0.03%	20.3%	LESVHIILR	99.7%	56.3	25	56.3	2	0	0	1079.66	418	426
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	18	18	31	0.03%	20.3%	LMAELVHNR	99.6%	40.4	25	35.7	2	0	0	1082.58	774	782
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	18	18	31	0.03%	20.3%	LQFDVSSPNGILLFR	99.7%	65.7	25	58.3	2	0	0	1705.93	786	800
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	18	18	31	0.03%	20.3%	LYGDDALDNALQTFIK	99.7%	101	25	101	2	0	0	1796.91	855	870
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	18	18	31	0.03%	20.3%	NSIVNSQPPEK	99.7%	60.2	25	47.5	2	0	0	1212.62	1021	1031
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	18	18	31	0.03%	20.3%	NYVLNYLATRPK	99.7%	63.7	25	63.7	2	0	0	1451.80	88	99
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	18	18	31	0.03%	20.3%	SNYQLGELVK	99.7%	45.8	25	37.7	1	0	0	1150.61	339	348

Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	18	18	31	0.03%	20.3%	TLQLLNDLSIGYSSVR	99.7%	46.6	25	28.3	2	0	0	1778.96	613	628
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	18	18	31	0.03%	20.3%	TNNPLPLEQR	99.7%	56	25	46	2	0	0	1181.63	74	83
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	18	18	31	0.03%	20.3%	VENYPEVIR	98.6%	34.2	25	25.9	2	0	0	1118.58	349	357
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	18	18	31	0.03%	20.3%	VLQLMNLTDSR	99.7%	49.7	25	43.4	1	0	0	1289.69	527	537
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.1%	ALAYFEQLK	99.7%	46.8	25	46.8	3	0	0	1082.59	21	29
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.1%	ANVEAIMLAVMK	99.7%	90	25	84	2	0	0	1289.70	370	381
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.1%	ASALQDMMR	99.2%	36.8	25	36.8	1	0	0	1054.47	475	483
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.1%	DGPVGFADFVYK	99.7%	66.1	25	66.1	2	0	0	1314.64	860	871
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.1%	DLQEFIPLINQITAK	99.7%	76.3	25	67.8	2	0	0	1742.97	738	752
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.1%	DVVHTSEEAR	99.6%	40.2	25	35.1	2	0	0	1142.54	157	166
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.1%	EEACDCLFEVVNK	99.7%	77.6	25	75.5	1	0	0	1612.70	241	253
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.1%	FFCFQVLEHQVK	99.7%	64.9	25	64.9	2	2	0	1581.79	54	65
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.1%	FMEVEVAIR	99.7%	67.2	25	57.4	1	0	0	1109.57	443	451
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.1%	GVDLYLR	99.7%	41.4	25	34.8	2	0	0	835.47	138	144
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.1%	ISPDAWQVCAEALAQR	99.7%	83.4	25	83.4	1	0	0	1814.89	30	45
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.1%	LAQVSPELLLASVR	99.7%	66.3	25	62.8	5	0	0	1495.88	415	428
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.1%	LMLAQDEER	99.5%	39	25	23.5	3	0	0	1104.54	635	643
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.1%	NAQEALQAIETK	99.7%	76.8	25	67.6	2	0	0	1315.69	317	328
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.1%	QASLADCLNHAVGFASR	99.4%	30.8	25	30.8	0	2	0	1816.88	644	660
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.1%	QMNPFIEDILNR	99.7%	50	25	49.7	2	0	0	1489.75	558	569
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.1%	TCFIILSK	99.7%	51.5	25	42.4	2	0	0	981.54	844	851
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.1%	VFSSTLQNWQTTR	99.7%	91.6	25	82.3	2	0	0	1567.79	430	442
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.1%	VLVTVIQGAVEYPDPIAQK	99.7%	111	25	111	2	2	0	2040.14	825	843
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.1%	YSELTTVQQQLIR	99.7%	75.2	25	72.1	2	0	0	1578.85	68	80
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	6	6	9	0.01%	7.6%	ITVPLVSEVQIAQLR	99.7%	72.6	25	72.6	2	0	0	1665.99	365	379
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	6	6	9	0.01%	7.6%	LLDEWFTLDEVPK	99.7%	64.8	25	60.6	2	0	0	1604.82	484	496
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	6	6	9	0.01%	7.6%	SSSSLLASPGHISVK	98.8%	34.8	25	27.8	1	0	0	1469.80	736	750
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	6	6	9	0.01%	7.6%	VDVGQQPLR	99.7%	44.8	25	27.3	1	0	0	1011.56	240	248
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	6	6	9	0.01%	7.6%	VGNQIFQSR	99.1%	36.2	25	34.5	1	0	0	1048.55	420	428
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	6	6	9	0.01%	7.6%	VYTENVDKR	99.6%	40.7	25	26.2	2	0	0	1123.57	254	262
FACT complex subunit SPT16	SUPT16H	SP16H_HUMAN	119.9	100.0%	6	6	10	0.01%	7.7%	AASITSEVFNK	99.7%	42.8	25	38.1	1	0	0	1166.61	186	196
FACT complex subunit SPT16	SUPT16H	SP16H_HUMAN	119.9	100.0%	6	6	10	0.01%	7.7%	APGEQTVPALNLQNAFR	99.7%	67.2	25	67.2	2	0	0	1825.96	607	623
FACT complex subunit SPT16	SUPT16H	SP16H_HUMAN	119.9	100.0%	6	6	10	0.01%	7.7%	GNENANGAPAITLLIR	99.7%	60.6	25	58.7	1	0	0	1623.88	93	108
FACT complex subunit SPT16	SUPT16H	SP16H_HUMAN	119.9	100.0%	6	6	10	0.01%	7.7%	INFYCPGSALGR	99.7%	48.2	25	44.3	1	0	0	1354.66	570	581
FACT complex subunit SPT16	SUPT16H	SP16H_HUMAN	119.9	100.0%	6	6	10	0.01%	7.7%	NEGNIFPNPEATFVK	99.7%	53.7	25	31.1	4	0	0	1676.83	582	596
FACT complex subunit SPT16	SUPT16H	SP16H_HUMAN	119.9	100.0%	6	6	10	0.01%	7.7%	QDSLVINLNR	99.4%	38.3	25	35.8	1	0	0	1171.64	648	657
FACT complex subunit SSRP1	SSRP1	SSRP1_HUMAN	81.1	100.0%	3	3	6	0.01%	4.9%	ADVIQATGDAICIFR	99.7%	74.1	25	69.2	2	0	0	1649.83	189	203
FACT complex subunit SSRP1	SSRP1	SSRP1_HUMAN	81.1	100.0%	3	3	6	0.01%	4.9%	FDEISFVNFAR	99.7%	71.3	25	65.4	2	0	0	1344.66	371	381
FACT complex subunit SSRP1	SSRP1	SSRP1_HUMAN	81.1	100.0%	3	3	6	0.01%	4.9%	SFDFEIETK	98.7%	34.5	25	22.4	2	0	0	1115.53	388	396
F-actin-capping protein subunit alpha-1	CAPZA1	CAZA1_HUMAN	32.9	99.8%	2	2	4	0.00%	8.7%	FTITPPTAQVVGVLK	99.7%	45.5	25	45.5	2	0	0	1570.92	179	193
F-actin-capping protein subunit alpha-1	CAPZA1	CAZA1_HUMAN	32.9	99.8%	2	2	4	0.00%	8.7%	LLLNNDNLLR	99.7%	66.1	25	43.1	2	0	0	1197.70	38	47
FAD-dependent oxidoreductase domain-containing protein 1	FOXRED1	FXRD1_HUMAN	53.8	99.8%	2	2	2	0.00%	4.9%	EGLGSNYLGGR	97.0%	30.7	25	26.2	1	0	0	1122.55	353	363
FAD-dependent oxidoreductase domain-containing protein 1	FOXRED1	FXRD1_HUMAN	53.8	99.8%	2	2	2	0.00%	4.9%	FQTIDLSPFLFTR	99.7%	58.5	25	53.5	1	0	0	1584.84	461	473
Fanconi anemia group D2 protein	FANCD2	FACD2_HUMAN	166.5	100.0%	5	5	6	0.01%	5.0%	AIEEIAGVGVPELINSPK	99.7%	51.8	25	51.8	1	0	0	1836.01	1199	1216
Fanconi anemia group D2 protein	FANCD2	FACD2_HUMAN	166.5	100.0%	5	5	6	0.01%	5.0%	DGGPVTSQESGQK	96.6%	30.2	25	30.2	2	0	0	1289.60	711	723
Fanconi anemia group D2 protein	FANCD2	FACD2_HUMAN	166.5	100.0%	5	5	6	0.01%	5.0%	GILDYLDNISPQQIR	99.7%	54	25	51.1	1	0	0	1744.92	516	530
Fanconi anemia group D2 protein	FANCD2	FACD2_HUMAN	166.5	100.0%	5	5	6	0.01%	5.0%	KIEPGTAADSQQIHEEK	99.5%	32.1	25	25	0	1	0	1880.94	1248	1264
Fanconi anemia group D2 protein	FANCD2	FACD2_HUMAN	166.5	100.0%	5	5	6	0.01%	5.0%	SESPSLTQER	99.7%	53.2	25	42.6	1	0	0	1133.54	590	599
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	20	20	33	0.03%	17.5%	CLSQQADVR	99.6%	40.4	25	30	2	0	0	1076.52	594	602
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	20	20	33	0.03%	17.5%	DLQLLQGSK	99.2%	37	25	25.7	2	0	0	1001.56	340	348
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	20	20	33	0.03%	17.5%	DVPLTAEEVEFVVEK	99.7%	106	25	97	2	0	0	1703.87	183	197

Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	20	20	33	0.03%	17.5%	EALLLVTVLTSLSK	99.7%	48	25	48	1	0	0	1486.91	981	994
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	20	20	33	0.03%	17.5%	EGDLTNLLQNQAVK	99.7%	74.8	25	68.6	2	0	0	1542.81	26	39
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	20	20	33	0.03%	17.5%	ETGHVSGPDGQNPEK	99.7%	60.5	25	49.6	2	0	0	1551.70	855	869
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	20	20	33	0.03%	17.5%	FVSSLLTALFR	99.7%	76.1	25	76.1	2	0	0	1253.73	809	819
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	20	20	33	0.03%	17.5%	GSPCSEEAGTLR	99.7%	71.7	25	71.7	1	0	0	1263.56	53	64
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	20	20	33	0.03%	17.5%	IFQNLCDITR	99.7%	61.5	25	43.8	1	0	0	1279.65	870	879
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	20	20	33	0.03%	17.5%	IFSAVQQFYQPK	99.7%	65.5	25	44.4	2	0	0	1455.76	915	926
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	20	20	33	0.03%	17.5%	IQQFLR	95.8%	29.3	25	0	1	0	0	804.47	927	932
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	20	20	33	0.03%	17.5%	LEACILTQGDK	97.7%	31.8	25	26	1	0	0	1247.63	647	657
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	20	20	33	0.03%	17.5%	LSDILNEK	98.2%	32.9	25	23.3	1	0	0	931.51	781	788
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	20	20	33	0.03%	17.5%	SADFSQSTSIGIK	99.7%	67.4	25	57.3	2	0	0	1340.67	726	738
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	20	20	33	0.03%	17.5%	SAVAGFLLLLK	99.7%	57.8	25	50.8	2	0	0	1131.71	535	545
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	20	20	33	0.03%	17.5%	SISLLCLEGLQK	99.7%	63.7	25	35.7	2	0	0	1360.75	903	914
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	20	20	33	0.03%	17.5%	SLLNLLSSQEEDFNSK	99.7%	71.4	25	71.4	2	0	0	1823.90	965	980
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	20	20	33	0.03%	17.5%	TAAPTVCLLVLSQAEK	99.7%	78.7	25	70.7	2	0	0	1700.93	1079	1094
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	20	20	33	0.03%	17.5%	TIETSPSLSR	96.6%	30.1	25	25	1	0	0	1090.57	403	412
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	20	20	33	0.03%	17.5%	YAVNVALQK	99.3%	37.7	25	33.5	2	0	0	1005.57	841	849
Far upstream element-binding protein 2	KHSRP	FUBP2_HUMAN	73.1	99.8%	2	2	4	0.00%	3.4%	IGGGIDVPVPR	99.7%	77.9	25	69	2	0	0	1079.62	321	331
Far upstream element-binding protein 2	KHSRP	FUBP2_HUMAN	73.1	99.8%	2	2	4	0.00%	3.4%	VQISPDSGGLPER	99.7%	51.6	25	49.6	2	0	0	1354.70	178	190
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	34	0.03%	34.1%	AAQVMGPPDR	99.7%	67.1	25	66.9	2	0	0	1057.51	300	309
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	34	0.03%	34.1%	AEGFVDALHR	99.7%	49	25	43.2	2	0	0	1114.56	16	25
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	34	0.03%	34.1%	DGFGGLAAAR	99.7%	62.3	25	33.6	2	0	0	934.47	328	337
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	34	0.03%	34.1%	EMVLEIIR	99.6%	40.3	25	0	2	0	0	1002.57	226	233
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	34	0.03%	34.1%	FAVGIVIGR	99.7%	64.8	25	52.9	2	0	0	931.57	263	271
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	34	0.03%	34.1%	GDWSVGAPGGVQEITYTVPADK	99.7%	71.7	25	70.5	1	0	0	2247.09	344	365
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	34	0.03%	34.1%	GVPQQIEVAR	99.7%	49.2	25	38.1	2	0	0	1096.61	409	418
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	34	0.03%	34.1%	IDSIPHLNNSTPLVDPSVYGYGVQK	99.7%	37.5	25	37.5	0	1	0	2713.38	33	57
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	34	0.03%	34.1%	IQFKPDDGISPER	99.7%	48.7	25	40.7	2	2	0	1501.76	287	299
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	34	0.03%	34.1%	LLGQIVDR	99.7%	56.2	25	42.8	3	0	0	913.55	140	147
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	34	0.03%	34.1%	MGGGSIEVSVPR	99.7%	94.7	25	86.1	4	0	0	1204.60	251	262
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	34	0.03%	34.1%	MVGFIIGR	99.4%	38	25	32	2	0	0	908.50	88	95
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	34	0.03%	34.1%	MVMIQDGPLPTGADKPLR	99.7%	45.4	25	45.4	0	3	0	1971.00	196	213
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	34	0.03%	34.1%	RPLDDGVGNQLGALVHQR	99.7%	48.3	25	48.3	0	2	0	1945.04	58	75
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	34	0.03%	34.1%	SINQQSGAHVELQR	99.7%	61.1	25	52.1	2	0	0	1566.80	379	392
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	6	11	20	0.02%	17.4%	ATPEQYQILK	99.7%	48.1	25	35.8	2	0	0	1190.64	344	353
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	6	11	20	0.02%	17.4%	CSWLVVQCLQR	99.7%	60.3	25	52.5	2	0	0	1448.71	333	343
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	6	11	20	0.02%	17.4%	IGTDIQDNK	99.7%	48.2	25	33	2	0	0	1003.51	324	332
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	6	11	20	0.02%	17.4%	LKEVLEYNAIGGK	99.7%	75.2	25	63.1	2	2	0	1433.80	111	123
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	6	11	20	0.02%	17.4%	QDFVQHFSQIVR	99.7%	36.4	25	28.5	1	1	0	1503.77	81	92
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	6	11	20	0.02%	17.4%	VLTEDEMGHPEIGDAIAR	99.7%	66	25	66	4	4	0	1952.94	93	110
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	6	6	9	0.01%	16.4%	DLTQEQTEK	99.7%	42.1	25	33	2	0	0	1091.52	8	16
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	6	6	9	0.01%	16.4%	ENTYPFLAMIMLK	99.5%	39	25	38	2	0	0	1570.80	227	239
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	6	6	9	0.01%	16.4%	FQIEANFPR	96.5%	30.1	25	12.9	1	0	0	1121.57	401	409
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	6	6	9	0.01%	16.4%	IYSYVVSRPQPR	98.7%	34.3	25	29.3	1	0	0	1464.80	78	89
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	6	6	9	0.01%	16.4%	QQQDEAYLASLR	99.7%	73.9	25	63.9	2	0	0	1421.70	291	302
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	6	6	9	0.01%	16.4%	VTDPVGDIVSFMHSFEEK	99.7%	75.6	25	75.6	1	0	0	2036.96	129	146
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	6	6	9	0.01%	10.6%	DIISELLTSDDMK	99.7%	57.1	25	52.1	2	0	0	1495.72	523	535
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	6	6	9	0.01%	10.6%	ILVDQQVWK	96.8%	30.4	25	26.9	1	0	0	1128.64	295	303
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	6	6	9	0.01%	10.6%	LDDTVYLR	99.7%	60.1	25	52.1	1	0	0	994.52	549	556
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	6	6	9	0.01%	10.6%	LGIPQNTILVQTLLR	99.7%	54.7	25	54.7	1	0	0	1679.02	242	256
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	6	6	9	0.01%	10.6%	NQVLPLSDVDTTSATDIQR	99.7%	130	25	130	2	0	0	2073.05	615	633

FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	6	6	9	0.01%	10.6%	SAYCLGSSHPR	99.7%	64.6	25	64.6	2	0	0	1234.56	642	652
FAST kinase domain-containing protein 5	FASTKD5	FAKD5_HUMAN	86.6	99.9%	2	2	3	0.00%	3.0%	AAVPLGGFLCNVADK	99.7%	46.6	25	44.6	2	0	0	1531.79	661	675
FAST kinase domain-containing protein 5	FASTKD5	FAKD5_HUMAN	86.6	99.9%	2	2	3	0.00%	3.0%	LAVQFTNR	99.7%	46.5	25	13.6	1	0	0	948.53	697	704
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	36	0.03%	8.7%	AALQEELQLCK	99.5%	39.2	25	26.5	1	0	0	1302.67	1132	1142
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	36	0.03%	8.7%	ADEASELACPTPK	99.7%	51.4	25	51.4	1	0	0	1388.64	2194	2206
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	36	0.03%	8.7%	AQVADVVVSR	99.7%	68	25	50.6	2	0	0	1043.58	1073	1082
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	36	0.03%	8.7%	DGAWGAFR	98.3%	33.1	25	17.2	1	0	0	879.41	1508	1515
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	36	0.03%	8.7%	DNLEFFLAGIGR	99.7%	69.1	25	44.7	2	0	0	1351.70	791	802
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	36	0.03%	8.7%	EDGLAQQQTQLNLR	99.7%	75.4	25	67.1	2	0	0	1613.82	2207	2220
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	36	0.03%	8.7%	FDASFFGVHPK	99.7%	48.8	25	32.6	1	0	0	1251.62	60	70
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	36	0.03%	8.7%	FPQLDSTSFANSR	99.7%	82.1	25	72.3	2	0	0	1469.70	1712	1724
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	36	0.03%	8.7%	GLVQALQTK	99.7%	53.3	25	34.3	2	0	0	957.57	1143	1151
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	36	0.03%	8.7%	HGLYLPTR	98.5%	33.8	25	28.9	2	0	0	956.53	1044	1051
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	36	0.03%	8.7%	LLEQGLR	96.6%	30.1	25	0	2	0	0	828.49	437	443
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	36	0.03%	8.7%	LPEDPLLSGLLDSPALK	99.7%	85.5	25	83.4	3	0	0	1778.00	1209	1225
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	36	0.03%	8.7%	LQVVDQPLPVR	99.7%	54	25	54	2	0	0	1263.74	374	384
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	36	0.03%	8.7%	QEPLLIGSTK	95.7%	29.2	25	25.8	1	0	0	1085.62	317	326
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	36	0.03%	8.7%	SEGVVAVLLTK	99.7%	54.3	25	49.2	2	0	0	1115.67	225	235
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	36	0.03%	8.7%	SFYGSTLFLCR	99.7%	57.4	25	43.5	2	0	0	1350.65	1394	1404
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	36	0.03%	8.7%	TGTVSLEVR	99.7%	57.7	25	50.3	2	0	0	961.53	928	936
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	36	0.03%	8.7%	VLEALLPLK	99.7%	48.4	25	48.4	1	0	0	995.65	2383	2391
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	36	0.03%	8.7%	VVVQVLAEEPEAVLK	99.7%	81.9	25	72.8	4	0	0	1622.94	1852	1866
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	36	0.03%	8.7%	VYQWDDPDPR	98.5%	33.7	25	32.4	1	0	0	1290.58	958	967
Fatty acyl-CoA reductase 1	FAR1	FACR1_HUMAN	59.4	100.0%	3	3	4	0.00%	7.4%	ALAEYVVQQEGAK	99.7%	89.5	25	76.4	1	0	0	1405.73	209	221
Fatty acyl-CoA reductase 1	FAR1	FACR1_HUMAN	59.4	100.0%	3	3	4	0.00%	7.4%	IIAINSELTQPK	99.7%	88.3	25	88.3	1	0	0	1326.76	79	90
Fatty acyl-CoA reductase 1	FAR1	FACR1_HUMAN	59.4	100.0%	3	3	4	0.00%	7.4%	NVLLTGATGFLGK	99.7%	82.9	25	81	2	0	0	1290.74	12	24
Fermitin family homolog 2	FERMT2	FERM2_HUMAN	77.9	99.9%	2	2	3	0.00%	3.5%	GCEVTPDVNISGQK	99.2%	36.6	25	32.8	1	0	0	1503.71	425	438
Fermitin family homolog 2	FERMT2	FERM2_HUMAN	77.9	99.9%	2	2	3	0.00%	3.5%	YYSFFDLNPK	99.7%	41.7	25	41.3	2	0	0	1293.62	276	285
Filaggrin-2	FLG2	FILA2_HUMAN	248.1	99.8%	2	2	9	0.01%	1.0%	FSNSSSSNEFSK	99.7%	60.8	25	60	4	0	0	1320.57	404	415
Filaggrin-2	FLG2	FILA2_HUMAN	248.1	99.8%	2	2	9	0.01%	1.0%	SVVTVIDVFYK	99.7%	53.1	25	51.6	5	0	0	1269.71	7	17
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	20	20	27	0.03%	10.0%	AFGPGLQGGSAGSPAR	99.7%	65.3	25	60.9	1	0	0	1429.72	1072	1087
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	20	20	27	0.03%	10.0%	AGVAPLQVK	99.6%	39.7	25	33.1	2	0	0	882.54	1478	1486
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	20	20	27	0.03%	10.0%	ALTQTGGPHVK	99.1%	36	25	32.8	1	0	0	1108.61	1284	1294
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	20	20	27	0.03%	10.0%	ANLPQSFQVDTSK	99.7%	41.4	25	41.3	2	0	0	1434.72	1465	1477
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	20	20	27	0.03%	10.0%	AWGPGLEGGVVGK	99.4%	38.3	25	38.3	2	0	0	1226.65	581	593
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	20	20	27	0.03%	10.0%	EATTEFSVDAR	99.7%	50.5	25	46.5	1	0	0	1225.57	1273	1283
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	20	20	27	0.03%	10.0%	IVGPSGAAVPCK	99.7%	41.5	25	41.5	1	0	0	1155.62	1008	1019
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	20	20	27	0.03%	10.0%	LYSVSYLLK	99.2%	36.7	25	11.2	1	0	0	1085.62	2613	2621
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	20	20	27	0.03%	10.0%	SPFSVAVSPSLDLSK	99.7%	60.2	25	52.6	2	0	0	1533.82	959	973
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	20	20	27	0.03%	10.0%	SPYTVTVGQACNPSACR	99.7%	78.2	25	78.2	1	0	0	1867.84	468	484
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	20	20	27	0.03%	10.0%	TGVAVNKPAEFTVDAK	99.0%	28.7	25	28.7	0	1	0	1646.87	685	700
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	20	20	27	0.03%	10.0%	TGVELGKPTHFTVNAK	98.3%	26.6	25	26.6	0	1	0	1698.92	885	900
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	20	20	27	0.03%	10.0%	TPCEEILVK	99.1%	35.9	25	21.8	1	0	0	1088.57	2599	2607
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	20	20	27	0.03%	10.0%	VEPGLGADNSVVR	98.9%	35	25	31.8	1	0	0	1312.69	1020	1032
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	20	20	27	0.03%	10.0%	VNVGAGSHPNK	99.7%	61.3	25	57.1	2	0	0	1079.56	761	771
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	20	20	27	0.03%	10.0%	VPVHDVTDASK	99.7%	48.1	25	36.2	1	0	0	1167.60	1440	1450
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	20	20	27	0.03%	10.0%	VTAQGPGLEPSGNIANK	99.7%	85.2	25	82.3	2	0	0	1652.86	384	400
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	20	20	27	0.03%	10.0%	VTVLFAGQHIAK	99.7%	41.7	25	38.3	1	0	0	1283.75	356	367
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	20	20	27	0.03%	10.0%	YGGDEIPFSPYR	99.7%	53.1	25	28.2	2	0	0	1400.65	1622	1633
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	20	20	27	0.03%	10.0%	YTPVQQGPVGVNVTYGGDPIPK	99.7%	58.5	25	58.5	1	0	0	2286.18	937	958
Flap endonuclease 1	FEN1	FEN1_HUMAN	42.6	100.0%	4	5	7	0.01%	15.3%	EAHQLFLEPEVLDPESVELK	99.5%	32.1	25	32.1	0	1	0	2322.19	278	297

Flap endonuclease 1	FEN1	FEN1_HUMAN	42.6	100.0%	4	5	7	0.01%	15.3%	KLPIQEFHLSR	99.5%	32.1	25	30.5	0	2	0	1367.78	201	211
Flap endonuclease 1	FEN1	FEN1_HUMAN	42.6	100.0%	4	5	7	0.01%	15.3%	LIADVAPSAIR	99.7%	62.7	25	43.7	2	0	0	1125.66	9	19
Flap endonuclease 1	FEN1	FEN1_HUMAN	42.6	100.0%	4	5	7	0.01%	15.3%	QLQQAQAAGAEQEVEK	99.7%	112	25	101	1	1	0	1727.86	110	125
Fragile X mental retardation protein 1	FMR1	FMR1_HUMAN	71.2	100.0%	5	5	7	0.01%	12.7%	EDLMGLAIGTHGANIQQAR	99.7%	46.2	25	42.2	0	2	0	1995.01	227	245
Fragile X mental retardation protein 1	FMR1	FMR1_HUMAN	71.2	100.0%	5	5	7	0.01%	12.7%	ENSTHFSQPNSTK	99.4%	38.5	25	27.8	1	0	0	1476.67	360	372
Fragile X mental retardation protein 1	FMR1	FMR1_HUMAN	71.2	100.0%	5	5	7	0.01%	12.7%	LIQEIVDK	99.5%	38.7	25	18.9	2	0	0	957.56	303	310
Fragile X mental retardation protein 1	FMR1	FMR1_HUMAN	71.2	100.0%	5	5	7	0.01%	12.7%	LQIDEQLR	99.7%	53.4	25	40.3	2	0	0	1014.56	435	442
Fragile X mental retardation protein 1	FMR1	FMR1_HUMAN	71.2	100.0%	5	5	7	0.01%	12.7%	SFLEFAEDVIQVPR	99.7%	42.3	25	39.5	1	0	0	1649.85	277	290
Fragile X mental retardation protein 1	FMR1	FMR1_HUMAN	71.2	100.0%	5	5	7	0.01%	12.7%	TTDGSLQIR	99.0%	35.5	25	26.8	1	0	0	990.52	573	581
Fragile X mental retardation protein 1	FMR1	FMR1_HUMAN	71.2	100.0%	5	5	7	0.01%	12.7%	VRIEAENEK	99.7%	46.8	25	36.2	2	0	0	1087.57	316	324
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	10	12	20	0.02%	20.2%	AGYSTDESSSSSLHATR	99.7%	96.5	25	86.7	2	1	0	1755.78	407	423
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	10	12	20	0.02%	20.2%	EDLMGLAIGTHGANIQQAR	99.7%	46.2	25	42.2	0	2	0	1995.01	237	255
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	10	12	20	0.02%	20.2%	EEGMVPFIFVGTR	99.7%	45.8	25	45.8	2	0	0	1497.74	339	351
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	10	12	20	0.02%	20.2%	IYGETPEACR	99.7%	49	25	37.4	2	0	0	1195.54	274	283
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	10	12	20	0.02%	20.2%	LQIDEQLR	99.7%	53.4	25	40.3	2	0	0	1014.56	379	386
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	10	12	20	0.02%	20.2%	LRPVNPNPLATK	99.7%	43.8	25	41.5	2	0	0	1319.78	122	133
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	10	12	20	0.02%	20.2%	SYLEFSEDSVQVPR	99.7%	59.1	25	56.8	2	0	0	1655.79	287	300
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	10	12	20	0.02%	20.2%	TGGPAYGPSSDVSTASETESEKR	99.7%	34.1	25	34.1	0	2	0	2313.05	438	460
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	10	12	20	0.02%	20.2%	TKPSEDSLSGQK	99.2%	36.6	25	26.6	1	0	0	1276.64	631	642
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	10	12	20	0.02%	20.2%	VIQEIVDK	98.6%	34	25	22	2	0	0	943.55	313	320
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	7	7	12	0.01%	20.3%	AAQEEYVKR	99.7%	70	25	62.3	2	0	0	1093.56	323	331
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	7	7	12	0.01%	20.3%	ADDGRPFPQVIK	99.3%	37.4	25	28.6	1	0	0	1342.71	88	99
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	7	7	12	0.01%	20.3%	ALANSLACQGK	99.7%	57.3	25	45.9	1	0	0	1132.58	332	342
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	7	7	12	0.01%	20.3%	ALQASALK	99.1%	36.3	25	12.5	2	0	0	801.48	305	312
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	7	7	12	0.01%	20.3%	ELSDIAHR	97.5%	31.5	25	24.3	2	0	0	940.48	15	22
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	7	7	12	0.01%	20.3%	GILAADESTGSIAK	99.7%	85.5	25	77.1	2	0	0	1332.70	29	42
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	7	7	12	0.01%	20.3%	PYQYPALTPEQK	99.7%	61.8	25	51	2	0	0	1434.73	2	13
Fumarylacetoacetate hydrolase domain-containing protein 2A	FAHD2A	FAH2A_HUMAN	34.6	99.8%	2	2	4	0.00%	8.0%	DSVADPHNLK	99.7%	55.8	25	52.2	2	0	0	1095.54	225	234
Fumarylacetoacetate hydrolase domain-containing protein 2A	FAHD2A	FAH2A_HUMAN	34.6	99.8%	2	2	4	0.00%	8.0%	TFDTFCPLGPALVTK	99.7%	62.5	25	52.8	2	0	0	1666.85	210	224
G2/mitotic-specific cyclin-B1	CCNB1	CCNB1_HUMAN	48.3	99.8%	2	2	2	0.00%	4.4%	QLEEEQAVRPK	99.7%	55.2	25	46.8	1	0	0	1326.70	180	190
G2/mitotic-specific cyclin-B1	CCNB1	CCNB1_HUMAN	48.3	99.8%	2	2	2	0.00%	4.4%	VSEQLQAK	98.3%	33.2	25	11.9	1	0	0	902.49	52	59
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	14	14	23	0.02%	35.2%	AFREEFGAEPELAVSAPGR	98.5%	27.3	25	27.3	0	1	0	2033.01	19	37
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	14	14	23	0.02%	35.2%	DGLVSLLTTSEGADEPQR	99.7%	66.4	25	48.9	1	0	0	1887.93	70	87
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	14	14	23	0.02%	35.2%	EEFGAEPELAVSAPGR	99.7%	49.2	25	49.2	1	0	0	1658.80	22	37
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	14	14	23	0.02%	35.2%	EVQLEELEAAR	99.7%	91.2	25	76.5	2	0	0	1286.66	257	267
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	14	14	23	0.02%	35.2%	GHALLIDCR	99.7%	48.8	25	46.8	2	0	0	1054.55	196	204
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	14	14	23	0.02%	35.2%	HSLASSEYPVR	99.7%	60.7	25	51.7	2	0	0	1245.62	229	239
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	14	14	23	0.02%	35.2%	HVVGEIR	98.7%	34.5	25	19.7	1	0	0	809.46	280	286
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	14	14	23	0.02%	35.2%	KDGLVSLLTTSEGADEPQR	99.7%	91	25	82.4	2	0	0	2016.02	69	87
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	14	14	23	0.02%	35.2%	LAVLITNSNVR	99.6%	40.1	25	30.8	2	0	0	1199.71	218	228
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	14	14	23	0.02%	35.2%	LMVESHR	99.3%	37.2	25	11.8	2	0	0	871.45	306	312
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	14	14	23	0.02%	35.2%	LQFPLPTAQR	97.9%	32.2	25	13.5	1	0	0	1170.66	88	97
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	14	14	23	0.02%	35.2%	QPQVAELLAEAR	99.7%	68.3	25	65	2	0	0	1324.72	6	17
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	14	14	23	0.02%	35.2%	SLETSLVPLSDPK	99.7%	55	25	46.2	2	0	0	1385.75	205	217
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	14	14	23	0.02%	35.2%	TAQAAAALR	99.7%	51.5	25	38.2	2	0	0	872.49	288	296
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	6	6	10	0.01%	7.7%	AASAPYFEVLEK	98.2%	32.9	25	26.6	1	0	0	1324.68	382	393
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	6	6	10	0.01%	7.7%	NLDPLVYLLSK	99.7%	44.1	25	43.2	2	0	0	1274.74	77	87
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	6	6	10	0.01%	7.7%	TFLVDPNLDLSIR	99.7%	58.4	25	43.7	2	0	0	1502.82	245	257
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	6	6	10	0.01%	7.7%	VLLDFLMEEK	99.7%	45	25	34.3	2	0	0	1236.65	498	507
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	6	6	10	0.01%	7.7%	WPLSLIINR	99.7%	42.7	25	42.7	1	0	0	1111.66	624	632
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	6	6	10	0.01%	7.7%	YTIVQQQIPSFLQK	99.7%	95.5	25	94.5	2	0	0	1692.93	432	445

GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	5	5	11	0.01%	13.7%	FYQASTSELYGK	99.7%	74.8	25	64.2	3	0	0	1393.66	150	161
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	5	5	11	0.01%	13.7%	GYEVHGIVR	99.7%	41.2	25	41.2	2	0	0	1029.55	47	55
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	5	5	11	0.01%	13.7%	LHYGDLTDSTCLVK	99.7%	41.9	25	41.9	2	0	0	1621.79	82	95
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	5	5	11	0.01%	13.7%	VAFDELVR	99.7%	41.4	25	26.6	3	0	0	948.51	349	356
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	5	5	11	0.01%	13.7%	VHVTVDLK	99.7%	42	25	31	1	0	0	910.54	315	322
Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	4	4	5	0.00%	4.7%	ALEDITASIAMAVIQQK	99.7%	44	25	36.4	2	0	0	1817.97	398	414
Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	4	4	5	0.00%	4.7%	EWGEELQAVLR	99.7%	42.9	25	33	1	0	0	1329.68	326	336
Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	4	4	5	0.00%	4.7%	SIAEGIGPEER	99.7%	57.3	25	57.3	1	0	0	1157.58	1037	1047
Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	4	4	5	0.00%	4.7%	SSQGTSYDSYR	98.8%	34.6	25	29.4	1	0	0	1250.53	337	347
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	8	8	11	0.01%	6.3%	GVLQTAAER	99.7%	64.5	25	37.4	3	0	0	944.52	934	942
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	8	8	11	0.01%	6.3%	LSGEAFDINK	99.7%	49.6	25	40	1	0	0	1093.55	515	524
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	8	8	11	0.01%	6.3%	SIFSLDTPEQYQEAFQK	99.7%	54.8	25	54.8	1	0	0	2030.97	1166	1182
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	8	8	11	0.01%	6.3%	SLEAFFLYGR	99.7%	48.8	25	43.4	2	0	0	1202.62	1275	1284
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	8	8	11	0.01%	6.3%	TVAEVQETLAEMIR	98.7%	34.4	25	34.4	1	0	0	1589.82	1373	1386
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	8	8	11	0.01%	6.3%	VGPGAGESPGTPPFR	99.5%	38.6	25	38.6	1	0	0	1425.71	41	55
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	8	8	11	0.01%	6.3%	VIGELVGHTER	99.7%	46.1	25	46.1	1	0	0	1209.66	56	66
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	8	8	11	0.01%	6.3%	VYEAVELLK	98.9%	35.3	25	23.8	1	0	0	1063.60	991	999
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	8	8	10	0.01%	3.8%	DMLTQTYDLIER	99.7%	77.6	25	69.9	1	0	0	1497.73	367	378
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	8	8	10	0.01%	3.8%	GISQAEIR	97.4%	31.3	25	13.9	1	0	0	873.48	383	390
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	8	8	10	0.01%	3.8%	IASNVLNTK	98.4%	33.4	25	24.1	2	0	0	959.55	1278	1286
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	8	8	10	0.01%	3.8%	NLIIEAVTNLR	99.7%	55.5	25	50	2	0	0	1255.74	619	629
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	8	8	10	0.01%	3.8%	NLSEEGLLR	98.2%	32.9	25	23.2	1	0	0	1030.55	665	673
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	8	8	10	0.01%	3.8%	NPQAYLNYK	98.3%	33.3	25	29.9	1	0	0	1110.56	1326	1334
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	8	8	10	0.01%	3.8%	VCLAEVYQDK	99.3%	37.4	25	29.6	1	0	0	1224.59	1335	1344
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	8	8	10	0.01%	3.8%	VLAIGDEKDQTR	98.9%	35.4	25	26.9	1	0	0	1344.71	1402	1413
General transcription factor 3C polypeptide 2	GTF3C2	TF3C2_HUMAN	100.7	99.8%	2	2	3	0.00%	2.1%	DLDRPESQSPK	99.0%	35.4	25	31.3	1	0	0	1271.62	159	169
General transcription factor 3C polypeptide 2	GTF3C2	TF3C2_HUMAN	100.7	99.8%	2	2	3	0.00%	2.1%	SPLFSVQR	99.7%	56.2	25	38.5	2	0	0	933.52	355	362
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	5	5	6	0.01%	6.7%	AIFAVLTSVLTK	99.7%	92.3	25	92.3	2	0	0	1262.77	611	622
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	5	5	6	0.01%	6.7%	ELEYFGLSAAILDK	99.7%	57.7	25	39.4	1	0	0	1568.82	667	680
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	5	5	6	0.01%	6.7%	ILNLLSPSDGER	96.2%	29.7	25	29	1	0	0	1313.71	277	288
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	5	5	6	0.01%	6.7%	VVDLAPLHLDAR	96.1%	23.5	25	23.5	0	1	0	1318.75	482	493
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	5	5	6	0.01%	6.7%	YNLAVVWLR	99.6%	40	25	27.6	1	0	0	1133.65	453	461
General transcription factor 3C polypeptide 4	GTF3C4	TF3C4_HUMAN	92.0	100.0%	3	3	4	0.00%	4.6%	NEAPEGNLGDFAEFQR	99.7%	76.1	25	76.1	1	0	0	1793.81	226	241
General transcription factor 3C polypeptide 4	GTF3C4	TF3C4_HUMAN	92.0	100.0%	3	3	4	0.00%	4.6%	NYQVQFVTLK	99.7%	56.5	25	55.4	2	0	0	1239.67	507	516
General transcription factor 3C polypeptide 4	GTF3C4	TF3C4_HUMAN	92.0	100.0%	3	3	4	0.00%	4.6%	QLIPIFTDVALK	98.9%	35.1	25	19.6	1	0	0	1357.81	449	460
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	8	8	16	0.02%	18.1%	DPYCHPVCANR	98.0%	32.4	25	30.3	2	0	0	1388.58	68	78
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	8	8	16	0.02%	18.1%	EGYNNPPISGENLIGLSR	99.7%	59.8	25	59.8	2	0	0	1929.97	192	209
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	8	8	16	0.02%	18.1%	FSTSSLLLR	99.7%	59.6	25	44.1	2	0	0	1023.58	79	87
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	8	8	16	0.02%	18.1%	HGYAPSDLPVK	99.7%	52.8	25	52.8	2	0	0	1183.61	329	339
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	8	8	16	0.02%	18.1%	IYQVLDFR	99.7%	62.4	25	50.1	2	0	0	1053.57	315	322
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	8	8	16	0.02%	18.1%	MLPTLGGEEGVSR	99.7%	58.3	25	52.6	2	0	0	1361.67	39	51
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	8	8	16	0.02%	18.1%	QGLGPSGTSGAR	99.7%	51.2	25	36.5	2	0	0	1087.55	368	379
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	8	8	16	0.02%	18.1%	STYNYSLPITVK	99.7%	54.9	25	54.9	2	0	0	1385.73	343	354
General transcription factor II-I	GTF2I	GTF2I_HUMAN	112.4	100.0%	2	2	3	0.00%	2.1%	EQVNDLFSR	99.7%	46.3	25	36.2	1	0	0	1107.54	870	878
General transcription factor II-I	GTF2I	GTF2I_HUMAN	112.4	100.0%	2	2	3	0.00%	2.1%	FAQALGLTEAVK	99.7%	74	25	57.3	2	0	0	1247.70	583	594
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	10	11	21	0.02%	14.0%	EQDDLLVLLADQDQK	99.7%	99.2	25	80.3	2	0	0	1742.88	905	919
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	10	11	21	0.02%	14.0%	GVMGGQSAGPQHTEAETIQK	99.6%	32.8	25	32.8	0	2	0	2041.96	6	25
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	10	11	21	0.02%	14.0%	IVAFENAFER	99.7%	60.8	25	60.2	2	0	0	1195.61	203	212
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	10	11	21	0.02%	14.0%	LMDLLADSR	99.7%	68.7	25	55.5	4	0	0	1033.53	171	179
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	10	11	21	0.02%	14.0%	LSALLQETK	99.7%	51.7	25	41.7	2	0	0	1002.58	850	858
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	10	11	21	0.02%	14.0%	NDGVLLLQALTR	99.7%	92.7	25	82.9	2	0	0	1312.76	184	195

General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	10	11	21	0.02%	14.0%	QSEDLGSQFTEIFIK	99.7%	103	25	99.7	2	0	0	1741.86	105	119
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	10	11	21	0.02%	14.0%	SQLNSQSVEITK	99.7%	65.1	25	59.1	2	0	0	1333.70	799	810
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	10	11	21	0.02%	14.0%	SSQTSGTNEQSSAIVSAR	99.7%	147	25	133	2	0	0	1809.86	765	782
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	10	11	21	0.02%	14.0%	SVEVQGETETIIATK	99.7%	77.7	25	66.8	1	0	0	1604.84	828	842
Geranylgeranyl transferase type-2 subunit alpha	RABGGTA	PGTA_HUMAN	65.1	99.9%	2	2	2	0.00%	4.1%	AELGFLESCLR	99.6%	40.7	25	36.7	1	0	0	1294.65	91	101
Geranylgeranyl transferase type-2 subunit alpha	RABGGTA	PGTA_HUMAN	65.1	99.9%	2	2	2	0.00%	4.1%	LYQSATQAVFQK	99.7%	46.2	25	39.4	1	0	0	1383.73	27	38
Glomulin	GLMN	GLMN_HUMAN	68.2	100.0%	3	3	4	0.00%	5.6%	GLELLENSLLR	99.7%	57.3	25	44	2	0	0	1256.72	335	345
Glomulin	GLMN	GLMN_HUMAN	68.2	100.0%	3	3	4	0.00%	5.6%	IMASLNLLR	97.4%	31.3	25	18.1	1	0	0	1030.61	471	479
Glomulin	GLMN	GLMN_HUMAN	68.2	100.0%	3	3	4	0.00%	5.6%	TWNYLEFEEEENK	99.7%	59.9	25	54.2	1	0	0	1730.75	268	280
Glucose-6-phosphate 1-dehydrogenase	G6PD	G6PD_HUMAN	59.3	100.0%	2	2	2	0.00%	5.2%	DNIACVILTFK	99.5%	39.3	25	39.3	1	0	0	1293.69	228	238
Glucose-6-phosphate 1-dehydrogenase	G6PD	G6PD_HUMAN	59.3	100.0%	2	2	2	0.00%	5.2%	LFYLALPPTVYEAVTK	99.7%	48	25	48	1	0	0	1825.01	137	152
Glucose-6-phosphate isomerase	GPI	G6PI_HUMAN	63.1	100.0%	3	3	3	0.00%	7.0%	SPEDLER	99.7%	45.5	25	35.3	1	0	0	845.40	455	461
Glucose-6-phosphate isomerase	GPI	G6PI_HUMAN	63.1	100.0%	3	3	3	0.00%	7.0%	TFTTQETITNAETAK	99.7%	95.4	25	95.4	1	0	0	1655.81	212	226
Glucose-6-phosphate isomerase	GPI	G6PI_HUMAN	63.1	100.0%	3	3	3	0.00%	7.0%	TLAQLNPESSLFIIASK	99.7%	52.1	25	52.1	1	0	0	1832.02	195	211
Glutamate--cysteine ligase regulatory subunit	GCLM	GSH0_HUMAN	30.7	99.8%	2	2	3	0.00%	8.4%	INPDEREEMK	98.1%	32.8	25	32	2	0	0	1260.59	81	90
Glutamate--cysteine ligase regulatory subunit	GCLM	GSH0_HUMAN	30.7	99.8%	2	2	3	0.00%	8.4%	LFIVESNSSSSTR	99.7%	60.6	25	60.6	1	0	0	1426.72	95	107
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	7	7	12	0.01%	15.9%	AQTGAPCLSFDIVR	99.7%	58.6	25	55.5	2	0	0	1534.77	60	73
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	7	7	12	0.01%	15.9%	EPFLLSGGDDGALK	99.7%	47	25	46	2	0	0	1418.72	320	333
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	7	7	12	0.01%	15.9%	GQVEVFALR	99.7%	55.4	25	43.4	2	0	0	1018.57	173	181
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	7	7	12	0.01%	15.9%	LLQVVEEPQALAAFLR	99.7%	94.2	25	88.9	2	0	0	1797.03	183	198
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	7	7	12	0.01%	15.9%	LLTGDCQK	98.9%	35.3	25	30.7	1	0	0	934.47	230	237
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	7	7	12	0.01%	15.9%	REPFLLSGGDDGALK	99.7%	46.6	25	46.6	0	2	0	1574.82	319	333
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	7	7	12	0.01%	15.9%	SGSPVATFK	95.7%	29.1	25	20.8	1	0	0	893.47	342	350
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	6	6	10	0.01%	10.0%	AVQTLQMELQQIMK	99.6%	39.6	25	38.2	1	0	0	1660.88	323	336
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	6	6	10	0.01%	10.0%	EILETLIK	98.0%	32.4	25	13.3	1	0	0	958.58	18	25
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	6	6	10	0.01%	10.0%	GSPLLIGVR	99.7%	46.5	25	36.1	2	0	0	911.57	204	212
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	6	6	10	0.01%	10.0%	GYDFESETDTETIAK	99.7%	97.7	25	97.7	2	0	0	1705.74	140	154
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	6	6	10	0.01%	10.0%	GYDVDFPR	99.6%	40.3	25	37.4	2	0	0	968.45	683	690
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	6	6	10	0.01%	10.0%	VIFLEDDDVAAVVDGR	99.7%	80.5	25	78.1	2	0	0	1732.88	291	306
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	19	30	0.03%	26.3%	AINFNFGYAK	99.7%	46.3	25	31.4	2	0	0	1144.58	283	292
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	19	30	0.03%	26.3%	AMAVLESLR	99.7%	64.4	25	32.6	1	0	0	989.54	568	576
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	19	30	0.03%	26.3%	ANNGICFLR	99.7%	64.4	25	51.9	1	0	0	1064.53	293	301
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	19	30	0.03%	26.3%	DVLNDTAPR	99.7%	41.2	25	32.9	1	0	0	1000.51	559	567
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	19	30	0.03%	26.3%	EAATQAQQTLGSTIDK	99.7%	107	25	104	2	0	0	1661.83	35	50
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	19	30	0.03%	26.3%	FDDTNPEKEEAK	99.7%	67.1	25	61.3	2	0	0	1422.64	302	313
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	19	30	0.03%	26.3%	FSEGEATLR	99.7%	53.9	25	40.7	2	0	0	1009.49	395	403
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	19	30	0.03%	26.3%	GFHQVPFAPIVFIER	99.0%	28.8	25	28.8	0	2	0	1756.95	602	616
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	19	30	0.03%	26.3%	GLAYVCHQR	99.7%	53	25	31.6	2	0	0	1103.54	353	361
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	19	30	0.03%	26.3%	GPSGCVESLEVTCR	99.7%	87	25	87	1	0	0	1550.69	653	666
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	19	30	0.03%	26.3%	HTGYVIELQHVVK	99.7%	40.3	25	40.3	0	2	0	1522.84	640	652
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	19	30	0.03%	26.3%	ILQLVATGAVR	99.7%	78.9	25	74.8	2	0	0	1140.71	499	509
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	19	30	0.03%	26.3%	LAWGQPVGLR	99.7%	58.2	25	47.7	2	0	0	1096.63	630	639
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	19	30	0.03%	26.3%	LGYFSVDPDSHQGK	99.7%	47.6	25	47.6	1	1	0	1549.73	746	759
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	19	30	0.03%	26.3%	LSFLVSYIASK	99.7%	71.4	25	71.4	2	0	0	1227.70	69	79
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	19	30	0.03%	26.3%	NSALSAQLR	99.7%	76.3	25	65	2	0	0	959.53	26	34
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	19	30	0.03%	26.3%	SHPLDPIDTVDFER	99.7%	51.8	25	51.3	1	0	0	1640.79	96	109
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	19	30	0.03%	26.3%	VIITNFPAAK	99.5%	38.9	25	16.5	1	0	0	1073.64	577	586
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	8	9	20	0.02%	20.2%	FLEATLR	99.5%	39.3	25	21.8	2	0	0	849.48	118	124
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	8	9	20	0.02%	20.2%	GLMEPLLPPK	99.3%	37.7	25	25.1	3	0	0	1110.62	17	26
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	8	9	20	0.02%	20.2%	HLAQLMESIPHSPGPTR	99.7%	36.8	25	36.8	0	2	0	1886.95	242	258
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	8	9	20	0.02%	20.2%	HLTLACHYDSK	99.7%	54.8	25	49.8	2	1	0	1344.64	162	172

Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	8	9	20	0.02%	20.2%	KFLEATLR	98.9%	35.3	25	14.9	2	0	0	977.58	117	124
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	8	9	20	0.02%	20.2%	TPGSPGNLQVR	99.7%	73.3	25	62.5	4	0	0	1125.60	106	116
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	8	9	20	0.02%	20.2%	VPLIGSLPEAR	99.7%	54.7	25	53	2	0	0	1151.68	70	80
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	8	9	20	0.02%	20.2%	VVGQLDPQR	98.7%	34.3	25	32.2	2	0	0	1011.56	84	92
Glutathione S-transferase kappa 1	GSTK1	GSTK1_HUMAN	25.5	100.0%	4	4	5	0.00%	22.6%	AGMSAEQAQGLLEK	99.7%	80.6	25	75.9	2	0	0	1432.71	145	158
Glutathione S-transferase kappa 1	GSTK1	GSTK1_HUMAN	25.5	100.0%	4	4	5	0.00%	22.6%	DFLSVMLEK	99.0%	35.5	25	22	1	0	0	1081.56	86	94
Glutathione S-transferase kappa 1	GSTK1	GSTK1_HUMAN	25.5	100.0%	4	4	5	0.00%	22.6%	DSGNKPPGLLPR	97.7%	31.9	25	31.8	1	0	0	1250.69	50	61
Glutathione S-transferase kappa 1	GSTK1	GSTK1_HUMAN	25.5	100.0%	4	4	5	0.00%	22.6%	NEDITEPQSILAAAEK	99.7%	117	25	115	1	0	0	1728.87	129	144
Glutathione S-transferase P	GSTP1	GSTP1_HUMAN	23.4	100.0%	2	2	2	0.00%	12.9%	FQDGDLTLYQSNTILR	99.7%	70.2	25	70.2	1	0	0	1883.95	56	71
Glutathione S-transferase P	GSTP1	GSTP1_HUMAN	23.4	100.0%	2	2	2	0.00%	12.9%	PPYTVVYFPVR	99.7%	65.3	25	65.3	1	0	0	1337.73	2	12
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	11	16	40	0.04%	41.5%	GALQNIIPASTGAAK	99.7%	89.3	25	86.9	7	0	0	1411.79	201	215
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	11	16	40	0.04%	41.5%	IISNASCTTNCLAPLAK	99.7%	130	25	127	3	0	0	1833.92	146	162
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	11	16	40	0.04%	41.5%	LISWYDNEFGYSNR	99.7%	82.5	25	82.5	2	0	0	1763.80	310	323
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	11	16	40	0.04%	41.5%	LTGMAFR	97.4%	31.3	25	24.4	2	0	0	811.41	228	234
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	11	16	40	0.04%	41.5%	LVINGNPITIFQER	99.7%	79.5	25	71.6	2	0	0	1613.90	67	80
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	11	16	40	0.04%	41.5%	LVINGNPITIFQERDPSK	99.7%	44	25	41.9	1	2	0	2041.11	67	84
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	11	16	40	0.04%	41.5%	VIISAPSADAPMFVMGVNHEK	95.5%	23	25	22.7	0	1	0	2213.11	119	139
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	11	16	40	0.04%	41.5%	VPTANVSVVDLTCR	99.7%	112	25	107	4	2	0	1530.79	235	248
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	11	16	40	0.04%	41.5%	VVDLMAHMASK	99.7%	74.2	25	61.7	3	0	0	1201.61	324	334
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	11	16	40	0.04%	41.5%	VVDLMAHMASKE	99.7%	75	25	63.9	7	0	0	1330.65	324	335
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	11	16	40	0.04%	41.5%	WGDAGAEYVVESTGVFTTMEK	99.7%	109	25	109	4	0	0	2277.04	87	107
Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	GPD1L_HUMAN	38.4	100.0%	4	4	7	0.01%	12.5%	FCETTIGSK	99.6%	40.2	25	40.2	2	0	0	1042.49	163	171
Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	GPD1L_HUMAN	38.4	100.0%	4	4	7	0.01%	12.5%	ICDEITGR	99.7%	58.5	25	45.8	2	0	0	963.46	103	110
Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	GPD1L_HUMAN	38.4	100.0%	4	4	7	0.01%	12.5%	LQGPQTSAEVYR	99.7%	54.8	25	52.7	2	0	0	1348.69	299	310
Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	GPD1L_HUMAN	38.4	100.0%	4	4	7	0.01%	12.5%	VCIVGSGNWGSAVAK	99.7%	43.8	25	33.9	1	0	0	1504.76	8	22
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	4	4	7	0.01%	7.2%	LPFAAAQIGNSFR	99.7%	66.9	25	61.6	2	0	0	1391.74	319	331
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	4	4	7	0.01%	7.2%	SPITGNDLSPPVSFNLMFK	99.7%	45	25	45	1	0	0	2064.05	265	283
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	4	4	7	0.01%	7.2%	TVNVVQFEPSK	99.7%	46.5	25	40.8	2	0	0	1247.66	491	501
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	4	4	7	0.01%	7.2%	VDDSSGSIGR	99.7%	46.6	25	42.2	2	0	0	992.46	647	656
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	15	0.01%	15.3%	DYFFALAHTVR	99.7%	57.1	25	48.7	2	0	0	1339.68	51	61
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	15	0.01%	15.3%	GLAGLGDVAEVR	99.7%	86.6	25	80	2	0	0	1156.63	18	29
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	15	0.01%	15.3%	IGEEFLTDLSQLK	99.7%	56.8	25	46.5	1	0	0	1492.79	508	520
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	15	0.01%	15.3%	IGEEFLTDLSQLKK	99.5%	31.6	25	30	0	1	0	1620.88	508	521
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	15	0.01%	15.3%	LLPLVSDEVFIR	99.7%	56.1	25	54.6	2	0	0	1400.81	522	533
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	15	0.01%	15.3%	LVTSIGDVVNHDPVVGDR	99.7%	52.3	25	51.5	0	2	0	1891.99	623	640
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	15	0.01%	15.3%	NLAENISR	99.7%	47.9	25	20.1	3	0	0	916.48	271	278
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	15	0.01%	15.3%	VEDVEALDR	99.7%	43.5	25	29.1	2	0	0	1045.52	716	724
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	15	0.01%	15.3%	VIFLENYR	99.7%	62.3	25	52	3	0	0	1053.57	643	650
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	15	0.01%	15.3%	VLYPNDNFFEGK	99.7%	64.5	25	63.8	2	0	0	1442.70	279	290
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	15	0.01%	15.3%	WLLLCNPGLADTIVEK	99.6%	40.2	25	40.2	2	0	0	1841.98	492	507
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	15	0.01%	15.3%	YEFGIFNQK	99.7%	43	25	43	1	0	0	1145.56	162	170
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	APNDFNLR	99.7%	52.8	25	41	2	0	0	946.47	249	256
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	DFNVGDYIQAVLDR	99.7%	109	25	98.8	2	0	0	1624.80	257	270
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	DFSELEPDKFQNK	99.7%	62	25	55.5	2	0	0	1596.75	471	483
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	DYYFALAHTVR	99.7%	56.9	25	44.2	2	0	0	1355.67	51	61
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	EYAQNIWNVEPSDLK	99.7%	55.8	25	50.3	2	0	0	1805.87	820	834
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	EYYEALPELK	99.7%	44.5	25	43.2	2	0	0	1254.63	731	740
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	FSQFLETEYK	99.7%	71.7	25	63.7	4	0	0	1291.62	546	555
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	GIVGVENVAELK	99.7%	51.2	25	40	2	0	0	1227.69	18	29
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	GIVGVENVAELKK	99.7%	71.4	25	70.5	2	0	0	1355.79	18	30
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	HLEIIYEINQK	99.7%	59.1	25	47.1	2	0	0	1399.76	400	410

Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	IDDVAALDK	99.7%	50.8	25	45.3	2	0	0	959.50	716	724
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	IDDVAALDKK	99.7%	54.6	25	35.4	2	0	0	1087.60	716	725
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	IFVDIEK	99.7%	40.9	25	27.7	1	0	0	863.49	353	359
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	IGEDYVKDLSQLTK	97.7%	31.9	25	26.2	1	0	0	1608.85	508	521
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	INPSSMFDVQVK	99.7%	75.6	25	63.4	2	0	0	1364.69	558	569
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	LHSFLGDDVFLR	99.7%	77.2	25	66.4	2	2	0	1418.74	522	533
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	LITSVADVVNNDPMVGSK	99.7%	111	25	107	5	0	0	1874.95	623	640
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	LVIDQIDNGFFSPK	99.7%	92.4	25	87.5	4	0	0	1592.83	741	754
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	MSLIEEEGSKR	99.7%	71.2	25	53.2	4	0	0	1278.64	429	439
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	NLAENISR	99.7%	47.9	25	20.1	3	0	0	916.48	271	278
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	TFAYTNHTVLPEALER	99.7%	42	25	37.2	0	2	0	1861.94	372	387
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	VFADYEAYVK	99.7%	58.2	25	55.3	2	0	0	1204.59	774	783
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	VIFLENYR	99.7%	62.3	25	52	3	0	0	1053.57	643	650
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	VIPATDLSEQISTAGTEASGTGNMK	99.7%	106	25	106	1	3	0	2478.20	657	681
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	VLYPNDNFFEGK	99.7%	64.5	25	63.8	2	0	0	1442.70	279	290
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	VSQLYMNPK	99.7%	58.5	25	45.3	4	0	0	1095.55	788	796
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	WLLLCNPGLAELIAEK	99.7%	47.7	25	47.7	1	0	0	1840.00	492	507
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	WPVDLVEK	99.4%	38.5	25	30.9	2	0	0	985.54	388	395
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	35	72	0.07%	38.3%	YEYGIFNQK	98.2%	32.8	25	32.4	2	0	0	1161.56	162	170
Glyoxylate reductase/hydroxypyruvate reductase	GRHPR	GRHPR_HUMAN	35.7	100.0%	5	6	11	0.01%	21.3%	GEPMPSELKL	98.2%	32.9	25	29.7	1	0	0	1116.56	319	328
Glyoxylate reductase/hydroxypyruvate reductase	GRHPR	GRHPR_HUMAN	35.7	100.0%	5	6	11	0.01%	21.3%	IAAAGLDVTSPEPLPTNHPLLTLK	99.7%	56.2	25	56.2	0	2	0	2468.38	263	286
Glyoxylate reductase/hydroxypyruvate reductase	GRHPR	GRHPR_HUMAN	35.7	100.0%	5	6	11	0.01%	21.3%	ILDAAGANLK	99.7%	57	25	42.7	2	0	0	985.57	67	76
Glyoxylate reductase/hydroxypyruvate reductase	GRHPR	GRHPR_HUMAN	35.7	100.0%	5	6	11	0.01%	21.3%	NTMSLLAANNLLAGLR	99.7%	84.2	25	77.2	4	0	0	1687.92	303	318
Glyoxylate reductase/hydroxypyruvate reductase	GRHPR	GRHPR_HUMAN	35.7	100.0%	5	6	11	0.01%	21.3%	RLPEAIEEVK	99.7%	51	25	36.8	2	0	0	1183.67	125	134
GMP synthase [glutamine-hydrolyzing]	GMPS	GUAA_HUMAN	76.7	100.0%	3	3	3	0.00%	5.9%	ELGLPEELVSR	99.7%	47.9	25	46.4	1	0	0	1241.67	425	435
GMP synthase [glutamine-hydrolyzing]	GMPS	GUAA_HUMAN	76.7	100.0%	3	3	3	0.00%	5.9%	EPPTDVTPTFLTTGVLSTLR	99.7%	43	25	43	1	0	0	2145.14	570	589
GMP synthase [glutamine-hydrolyzing]	GMPS	GUAA_HUMAN	76.7	100.0%	3	3	3	0.00%	5.9%	VVYIFGPPVK	96.0%	29.5	25	25.5	1	0	0	1118.66	560	569
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	11	11	15	0.01%	6.7%	AASSSSPGSPVASSPSR	99.7%	61.3	25	59.1	1	0	0	1531.73	1776	1792
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	11	11	15	0.01%	6.7%	FSCLLPDPR	99.1%	36.4	25	36.4	2	0	0	1104.55	683	691
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	11	11	15	0.01%	6.7%	GATPEGIFLR	98.2%	32.8	25	14.1	2	0	0	1060.58	907	916
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	11	11	15	0.01%	6.7%	LLEAFTER	99.7%	43.3	25	30.6	1	0	0	978.53	801	808
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	11	11	15	0.01%	6.7%	LLITGTEQFNQKPK	99.7%	56.8	25	50.8	1	0	0	1616.90	702	715
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	11	11	15	0.01%	6.7%	LMEIITVENPK	99.7%	49.3	25	41	1	0	0	1286.70	502	512
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	11	11	15	0.01%	6.7%	LNLYAASLR	99.7%	54.4	25	51.2	1	0	0	1020.58	470	478
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	11	11	15	0.01%	6.7%	MQALTYLQR	99.4%	38	25	20.1	1	0	0	1123.59	1562	1570
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	11	11	15	0.01%	6.7%	SEDTTGPITGLALTSVNK	99.7%	68.2	25	63.3	2	0	0	1803.93	74	91
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	11	11	15	0.01%	6.7%	SLEETIIQK	98.7%	34.5	25	27.9	1	0	0	1060.59	945	953
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	11	11	15	0.01%	6.7%	VLNSLTQQEK	99.7%	52	25	39.9	2	0	0	1159.63	596	605
GPI transamidase component PIG-S	PIGS	PIGS_HUMAN	61.7	99.8%	2	2	2	0.00%	5.1%	ASLPYSQISGLNALQLR	99.7%	57.7	25	47.7	1	0	0	1831.01	44	60
GPI transamidase component PIG-S	PIGS	PIGS_HUMAN	61.7	99.8%	2	2	2	0.00%	5.1%	LMVPVTVVFTR	95.4%	28.9	25	28.9	1	0	0	1261.73	61	71
GPI transamidase component PIG-T	PIGT	PIGT_HUMAN	65.7	100.0%	2	2	3	0.00%	3.1%	LYVHTLTITSK	99.4%	38.4	25	38.4	1	0	0	1275.73	395	405
GPI transamidase component PIG-T	PIGT	PIGT_HUMAN	65.7	100.0%	2	2	3	0.00%	3.1%	VSIQFER	99.7%	45.1	25	15.7	2	0	0	878.47	442	448
GPI-anchor transamidase	PIGK	GPI8_HUMAN	45.3	100.0%	3	3	3	0.00%	7.9%	HVANTLSVYR	99.7%	44.7	25	44.7	1	0	0	1159.62	61	70
GPI-anchor transamidase	PIGK	GPI8_HUMAN	45.3	100.0%	3	3	3	0.00%	7.9%	SLCVSTPGHR	99.7%	43.4	25	41.9	1	0	0	1113.55	278	287
GPI-anchor transamidase	PIGK	GPI8_HUMAN	45.3	100.0%	3	3	3	0.00%	7.9%	SYEVTVENFLR	99.7%	47.2	25	41.2	1	0	0	1356.68	123	133
GTP:AMP phosphotransferase AK3, mitochondrial	AK3	KAD3_HUMAN	25.6	100.0%	3	3	4	0.00%	15.9%	AVIMGAPGSGK	99.6%	40	25	26.2	2	0	0	1003.52	10	20
GTP:AMP phosphotransferase AK3, mitochondrial	AK3	KAD3_HUMAN	25.6	100.0%	3	3	4	0.00%	15.9%	TLPQAEALDR	96.0%	29.5	25	4.81	1	0	0	1113.59	95	104
GTP:AMP phosphotransferase AK3, mitochondrial	AK3	KAD3_HUMAN	25.6	100.0%	3	3	4	0.00%	15.9%	TVGIDDLTGEPLIQR	99.4%	37.8	25	29.4	1	0	0	1626.87	147	161
GTPase Era, mitochondrial	ERAL1	ERAL1_HUMAN	48.3	100.0%	4	4	7	0.01%	12.1%	DPNTQSVGNPQR	99.7%	56.3	25	48.1	1	0	0	1312.62	285	296
GTPase Era, mitochondrial	ERAL1	ERAL1_HUMAN	48.3	100.0%	4	4	7	0.01%	12.1%	EIFMLSALSQEDVK	99.5%	39.1	25	32.7	2	0	0	1609.81	304	317
GTPase Era, mitochondrial	ERAL1	ERAL1_HUMAN	48.3	100.0%	4	4	7	0.01%	12.1%	STLSNQLLGR	99.7%	56.2	25	11.1	2	0	0	1088.61	127	136

GTPase Era, mitochondrial	ERAL1	ERAL1_HUMAN	48.3	100.0%	4	4	7	0.01%	12.1%	TAVWEEGPGGELVIQQK	99.7%	59.4	25	47.4	2	0	0	1840.94	372	388
GTPase-activating protein and VPS9 domain-containing protein 1	GAPVD1	GAPD1_HUMAN	165.0	100.0%	2	2	2	0.00%	2.0%	AVETPPLSSVNLLEGLSR	99.7%	58.5	25	56.7	1	0	0	1882.03	387	404
GTPase-activating protein and VPS9 domain-containing protein 1	GAPVD1	GAPD1_HUMAN	165.0	100.0%	2	2	2	0.00%	2.0%	LIASSLVAGEK	99.7%	48.4	25	36	1	0	0	1087.64	109	119
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	9	11	31	0.03%	41.7%	FNVWDTAGQEK	99.7%	68.5	25	55.2	4	0	0	1294.61	61	71
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	9	11	31	0.03%	41.7%	GPIKFNVWDTAGQEK	99.7%	76.9	25	76.6	2	2	0	1689.86	57	71
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	9	11	31	0.03%	41.7%	HLTGEFEK	97.9%	32.2	25	27.4	3	0	0	960.48	30	37
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	9	11	31	0.03%	41.7%	KYVATLGVEVHPLVFHTNR	99.7%	83.7	25	75.7	0	1	0	2180.20	38	56
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	9	11	31	0.03%	41.7%	LVLVGDGGTGK	99.7%	76.6	25	30	2	0	0	1015.58	13	23
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	9	11	31	0.03%	41.7%	NLQYYDISAK	99.7%	56.4	25	56	10	0	0	1214.61	143	152
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	9	11	31	0.03%	41.7%	SNYNFEKPFLWLAR	99.7%	44.6	25	44.6	1	2	0	1784.91	153	166
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	9	11	31	0.03%	41.7%	VCENIPIVLCGNK	99.7%	67.9	25	67.9	2	0	0	1515.77	111	123
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	9	11	31	0.03%	41.7%	YVATLGVEVHPLVFHTNR	99.1%	29.4	25	29.4	0	2	0	2052.10	39	56
GTP-binding protein 10	GTPBP10	GTPBA_HUMAN	42.9	100.0%	4	4	8	0.01%	10.6%	FVAGVGANSK	99.0%	35.4	25	30.9	2	0	0	949.51	67	76
GTP-binding protein 10	GTPBP10	GTPBA_HUMAN	42.9	100.0%	4	4	8	0.01%	10.6%	ILVAQGGLGGK	99.4%	37.9	25	28.9	2	0	0	1012.62	116	126
GTP-binding protein 10	GTPBP10	GTPBA_HUMAN	42.9	100.0%	4	4	8	0.01%	10.6%	LLTNFLPLK	99.7%	43	25	31.1	2	0	0	1058.66	127	135
GTP-binding protein 10	GTPBP10	GTPBA_HUMAN	42.9	100.0%	4	4	8	0.01%	10.6%	TAFETIILLTK	99.7%	58.3	25	53.8	2	0	0	1249.74	249	259
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	7	10	15	0.01%	33.7%	ALAESWNAAFLESSAK	99.7%	112	25	112	2	0	0	1694.84	136	151
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	7	10	15	0.01%	33.7%	ENQTAVDVFR	99.7%	81.7	25	66.2	2	0	0	1178.58	152	161
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	7	10	15	0.01%	33.7%	IAILGYR	94.6%	28.3	25	25.8	1	0	0	805.49	9	15
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	7	10	15	0.01%	33.7%	IILEAEKMDGAASQGK	99.7%	98.7	25	98.7	3	2	0	1660.86	163	178
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	7	10	15	0.01%	33.7%	KIAILGYR	99.6%	40.2	25	25.4	2	0	0	933.59	8	15
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	7	10	15	0.01%	33.7%	VQIPIMLVGNK	96.1%	29.5	25	22.5	1	0	0	1227.71	110	120
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	7	10	15	0.01%	33.7%	VQIPIMLVGNKK	99.3%	37.7	25	34.9	1	1	0	1355.81	110	121
GTP-binding protein SAR1a	SAR1A	SAR1A_HUMAN	22.4	99.8%	2	2	2	0.00%	9.6%	LVFLGLDNAGK	99.7%	56.4	25	56.4	1	0	0	1146.65	28	38
GTP-binding protein SAR1a	SAR1A	SAR1A_HUMAN	22.4	99.8%	2	2	2	0.00%	9.6%	QGYGEGFR	96.1%	29.6	25	22.4	1	0	0	913.42	184	191
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	GBB2_HUMAN	37.3	100.0%	6	6	11	0.01%	22.1%	ACGDSTLTQITAGLDPVGR	99.7%	101	25	98.6	2	0	0	1931.95	24	42
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	GBB2_HUMAN	37.3	100.0%	6	6	11	0.01%	22.1%	AGVLAGHDNR	99.7%	47.5	25	47.5	2	0	0	1009.52	305	314
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	GBB2_HUMAN	37.3	100.0%	6	6	11	0.01%	22.1%	ELPGHTGYLSCCR	99.7%	50.6	25	46.8	1	0	0	1549.69	138	150
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	GBB2_HUMAN	37.3	100.0%	6	6	11	0.01%	22.1%	LIIWDSYTTNK	99.7%	66.2	25	56	2	0	0	1353.71	79	89
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	GBB2_HUMAN	37.3	100.0%	6	6	11	0.01%	22.1%	LLVSASQDGK	99.7%	69	25	58.2	2	0	0	1017.56	69	78
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	GBB2_HUMAN	37.3	100.0%	6	6	11	0.01%	22.1%	TFVSGACDASIK	99.7%	52.8	25	46	2	0	0	1255.60	198	209
Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	GNAS	GNAS1_HUMAN	111.0	100.0%	3	3	4	0.00%	4.5%	LLLLGAGESGK	99.7%	68.9	25	0	6	0	0	1057.63	686	696
Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	GNAS	GNAS1_HUMAN	111.0	100.0%	3	3	4	0.00%	4.5%	TISVILFLNK	99.7%	41.7	25	41.7	1	0	0	1147.71	927	936
Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	GNAS	GNAS1_HUMAN	111.0	100.0%	3	3	4	0.00%	4.5%	VLTSGIFETK	99.7%	57.3	25	53.5	2	0	0	1094.61	845	854
Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	GNAS	GNAS1_HUMAN	111.0	100.0%	3	3	4	0.00%	4.5%	YTTPEDATPEPGEDPR	99.7%	59.7	25	59.7	1	0	0	1774.78	961	976
Guanine nucleotide-binding protein subunit alpha-11	GNA11	GNA11_HUMAN	42.1	100.0%	3	3	5	0.00%	13.1%	IATLGYLPTQQDVLR	99.7%	62.7	25	59.5	2	0	0	1687.94	167	181
Guanine nucleotide-binding protein subunit alpha-11	GNA11	GNA11_HUMAN	42.1	100.0%	3	3	5	0.00%	13.1%	LLLLGTGESGK	99.7%	64.3	25	38.4	2	0	0	1087.64	42	52
Guanine nucleotide-binding protein subunit alpha-11	GNA11	GNA11_HUMAN	42.1	100.0%	3	3	5	0.00%	13.1%	MVDVGGQR	98.4%	33.3	25	32.3	1	0	0	861.42	203	210
Guanine nucleotide-binding protein subunit alpha-11	GNA11	GNA11_HUMAN	42.1	100.0%	3	3	5	0.00%	13.1%	VTTFEHQYVSAIK	99.7%	41.9	25	38.4	1	0	0	1522.79	121	133
Guanine nucleotide-binding protein subunit alpha-13	GNA13	GNA13_HUMAN	44.1	100.0%	2	2	7	0.01%	5.0%	ILLLGAGESGK	99.7%	68.9	25	0	6	0	0	1057.63	51	61
Guanine nucleotide-binding protein subunit alpha-13	GNA13	GNA13_HUMAN	44.1	100.0%	2	2	7	0.01%	5.0%	MVDVGGQR	98.4%	33.3	25	32.3	1	0	0	861.42	220	227
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	16	20	48	0.05%	62.5%	DETNYGIPQR	99.7%	63.8	25	52.4	3	0	0	1192.56	48	57
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	16	20	48	0.05%	62.5%	DGQAMLWDLNEGK	99.7%	97.9	25	93	4	0	0	1492.67	213	225
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	16	20	48	0.05%	62.5%	DKTIIMWK	98.7%	34.5	25	21.9	2	0	0	1034.57	37	44
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	16	20	48	0.05%	62.5%	DVLSVAFSSDNR	99.7%	96	25	95.3	6	0	0	1309.64	107	118
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	16	20	48	0.05%	62.5%	FSPNSSNPIIVSCGWDK	99.7%	104	25	89.6	2	0	0	1907.90	156	172
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	16	20	48	0.05%	62.5%	HLYTLDGGDIINALCFSPNR	99.7%	106	25	106	2	2	0	2276.11	226	245
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	16	20	48	0.05%	62.5%	IIVDELKQEVISTSSK	99.7%	93.3	25	93.3	2	2	0	1789.00	265	280
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	16	20	48	0.05%	62.5%	IWDLEGK	99.0%	35.7	25	20.1	2	0	0	860.45	258	264
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	16	20	48	0.05%	62.5%	LTRDETNYGIPQR	99.7%	49.7	25	42.2	2	0	0	1562.79	45	57
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	16	20	48	0.05%	62.5%	LWDLTTGTTTR	99.7%	82.8	25	78.9	2	0	0	1264.65	89	99

Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	16	20	48	0.05%	62.5%	LWNTLGVCK	99.7%	60.1	25	56.7	4	0	0	1090.57	131	139
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	16	20	48	0.05%	62.5%	TNHIGHTGYLNTVTVSPDGSLCASGGK	99.7%	97.6	25	97.6	0	2	0	2743.31	186	212
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	16	20	48	0.05%	62.5%	VWNLANCK	99.4%	38.4	25	38.4	2	0	0	1004.50	176	183
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	16	20	48	0.05%	62.5%	VWQVTIGTR	99.7%	73.6	25	66	3	0	0	1059.59	309	317
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	16	20	48	0.05%	62.5%	YTVQDESHSEWVSCVR	99.7%	81.1	25	81.1	2	2	0	1981.87	140	155
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	16	20	48	0.05%	62.5%	YWLCAATGPSIK	99.7%	69.7	25	62.8	2	0	0	1366.68	246	257
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	7	7	16	0.02%	13.5%	ELPTVVFR	98.7%	34.4	25	30.1	2	0	0	960.55	198	205
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	7	7	16	0.02%	13.5%	KDPGVPNSAPFK	99.7%	44.1	25	39.9	2	0	0	1256.66	46	57
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	7	7	16	0.02%	13.5%	LLGGFQETCSK	99.7%	45.9	25	45.9	2	0	0	1239.60	243	253
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	7	7	16	0.02%	13.5%	LVLILNK	96.1%	29.5	25	19.7	1	0	0	812.56	173	179
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	7	7	16	0.02%	13.5%	SGFNLEELEK	99.7%	56.5	25	43.7	2	0	0	1165.57	425	434
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	7	7	16	0.02%	13.5%	VGVIGFPNVGK	99.7%	53.7	25	40.7	5	0	0	1086.63	257	267
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	7	7	16	0.02%	13.5%	VIEASDVVLEVLDAR	99.7%	90.3	25	74.3	2	0	0	1627.89	137	151
H/ACA ribonucleoprotein complex subunit 1	GAR1	GAR1_HUMAN	22.3	100.0%	3	3	5	0.00%	10.6%	DFYFSVK	95.0%	28.6	25	19.8	1	0	0	905.44	122	128
H/ACA ribonucleoprotein complex subunit 1	GAR1	GAR1_HUMAN	22.3	100.0%	3	3	5	0.00%	10.6%	FYIDPYK	99.7%	42	25	35.6	2	0	0	945.47	144	150
H/ACA ribonucleoprotein complex subunit 1	GAR1	GAR1_HUMAN	22.3	100.0%	3	3	5	0.00%	10.6%	VDEIFGQLR	99.7%	54.2	25	43.3	2	0	0	1076.57	113	121
H/ACA ribonucleoprotein complex subunit 2	NHP2	NHP2_HUMAN	17.2	99.8%	2	3	10	0.01%	19.0%	NLPYVYIPSK	99.4%	37.9	25	30.2	2	0	0	1193.66	102	111
H/ACA ribonucleoprotein complex subunit 2	NHP2	NHP2_HUMAN	17.2	99.8%	2	3	10	0.01%	19.0%	TYQELLVNQNPIAQPLASR	99.7%	89.6	25	84.8	4	4	0	2155.15	23	41
H/ACA ribonucleoprotein complex subunit 3	NOP10	NOP10_HUMAN	7.7	100.0%	3	4	7	0.01%	56.2%	FSPDDKYSR	99.7%	46.9	25	19	3	0	0	1114.52	35	43
H/ACA ribonucleoprotein complex subunit 3	NOP10	NOP10_HUMAN	7.7	100.0%	3	4	7	0.01%	56.2%	KFDPMGQQTCSAHPAR	99.1%	29.5	25	29.5	0	1	0	1846.83	19	34
H/ACA ribonucleoprotein complex subunit 3	NOP10	NOP10_HUMAN	7.7	100.0%	3	4	7	0.01%	56.2%	VLMTQQPRPVL	99.7%	44.5	25	44.5	3	0	0	1297.73	54	64
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	10	11	19	0.02%	22.8%	ALETLTGALFQRPPLIAAVK	99.7%	44	25	44	0	1	0	2109.24	172	191
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	10	11	19	0.02%	22.8%	APQVVAEAAK	99.7%	42.4	25	37.2	2	0	0	983.55	434	443
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	10	11	19	0.02%	22.8%	DSAVNAICYGAK	99.7%	62.4	25	56.7	2	0	0	1268.59	303	314
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	10	11	19	0.02%	22.8%	EIGDYIR	98.5%	33.7	25	20.2	1	0	0	865.44	82	88
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	10	11	19	0.02%	22.8%	EVVAEVVK	99.1%	36.3	25	27.5	2	0	0	872.51	426	433
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	10	11	19	0.02%	22.8%	HGKPTDSTPATWK	99.6%	33.2	25	33.2	0	2	0	1425.71	401	413
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	10	11	19	0.02%	22.8%	IMLPGVLR	97.1%	30.8	25	18.5	1	0	0	914.55	315	322
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	10	11	19	0.02%	22.8%	LDTSQWPLLLK	99.7%	76.6	25	64.3	2	0	0	1313.75	47	57
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	10	11	19	0.02%	22.8%	LGIFWVSCEAGTYIR	99.7%	56.8	25	56.8	2	0	0	1771.88	213	227
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	10	11	19	0.02%	22.8%	LHNAIEGGTQLSR	99.7%	85.5	25	80.2	2	2	0	1395.73	159	171
HCLS1-associated protein X-1	HAX1	HAX1_HUMAN	31.6	100.0%	5	6	11	0.01%	23.3%	FHDNFGFDDLVR	99.7%	55.2	25	55.2	2	1	0	1481.68	75	86
HCLS1-associated protein X-1	HAX1	HAX1_HUMAN	31.6	100.0%	5	6	11	0.01%	23.3%	GFFGFPGPR	99.7%	41	25	41	2	0	0	981.49	9	17
HCLS1-associated protein X-1	HAX1	HAX1_HUMAN	31.6	100.0%	5	6	11	0.01%	23.3%	IFGGVLESDAR	99.7%	91.9	25	76.6	2	0	0	1163.61	140	150
HCLS1-associated protein X-1	HAX1	HAX1_HUMAN	31.6	100.0%	5	6	11	0.01%	23.3%	TREDNDLDSQVSQEGLGPVLQPQPK	99.7%	51.2	25	51.2	0	2	0	2750.36	181	205
HCLS1-associated protein X-1	HAX1	HAX1_HUMAN	31.6	100.0%	5	6	11	0.01%	23.3%	YPDSHQPR	99.5%	38.8	25	22.5	2	0	0	999.46	132	139
HEAT repeat-containing protein 1	HEATR1	HEAT1_HUMAN	242.4	100.0%	6	6	8	0.01%	3.3%	GWEEALENVIK	98.4%	33.5	25	26.1	1	0	0	1287.66	639	649
HEAT repeat-containing protein 1	HEATR1	HEAT1_HUMAN	242.4	100.0%	6	6	8	0.01%	3.3%	ITSEMGSASQANIR	99.7%	45	25	34.9	1	0	0	1480.71	1792	1805
HEAT repeat-containing protein 1	HEATR1	HEAT1_HUMAN	242.4	100.0%	6	6	8	0.01%	3.3%	LDDTYSFQVINK	99.7%	78.5	25	64.3	1	0	0	1442.72	1337	1348
HEAT repeat-containing protein 1	HEATR1	HEAT1_HUMAN	242.4	100.0%	6	6	8	0.01%	3.3%	LVPDLLAIVQR	99.7%	75.6	25	69.1	2	0	0	1236.77	1644	1654
HEAT repeat-containing protein 1	HEATR1	HEAT1_HUMAN	242.4	100.0%	6	6	8	0.01%	3.3%	TLATTLAPR	99.7%	43.2	25	38	2	0	0	943.56	1812	1820
HEAT repeat-containing protein 1	HEATR1	HEAT1_HUMAN	242.4	100.0%	6	6	8	0.01%	3.3%	VFAEYPGSSAQLR	98.5%	33.7	25	33.7	1	0	0	1424.72	202	214
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	19	0.02%	18.1%	AIQDAILEVLK	99.7%	71.3	25	64.1	3	0	0	1212.72	804	814
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	19	0.02%	18.1%	ATDTINSQGQFPSYLETVTK	99.7%	76.6	25	76.6	1	0	0	2200.08	636	655
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	19	0.02%	18.1%	CSLLDPFAAVR	99.7%	44.5	25	37	2	0	0	1248.64	173	183
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	19	0.02%	18.1%	DVQETLMPQVLTTLEEDSK	99.7%	60.9	25	59.6	1	0	0	2176.07	697	715
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	19	0.02%	18.1%	EGSGLFPDLLVR	99.7%	47.9	25	46.5	2	0	0	1302.71	815	826
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	19	0.02%	18.1%	LFDDVPQVR	99.7%	55.3	25	47.6	2	0	0	1088.57	254	262
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	19	0.02%	18.1%	LIPLLLSSLNDEVPEVR	99.7%	73.4	25	68.7	2	0	0	1907.09	286	302
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	19	0.02%	18.1%	LLPGLEADSKPGR	99.7%	57.9	25	54.9	1	0	0	1352.75	34	46
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	19	0.02%	18.1%	SAELVGTFVSPEVFLK	99.7%	87.8	25	84.4	2	0	0	1722.93	423	438

HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	19	0.02%	18.1%	SVDDVLSHFAQR	99.7%	54.6	25	45.5	1	0	0	1373.68	242	253
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	11	11	19	0.02%	18.1%	TPSASGLLVLASAMR	99.7%	84.1	25	81	2	0	0	1473.81	447	461
HEAT repeat-containing protein 3	HEATR3	HEAT3_HUMAN	74.6	100.0%	2	2	3	0.00%	4.0%	SQAEIINALLK	99.7%	57.7	25	40.7	2	0	0	1199.70	268	278
HEAT repeat-containing protein 3	HEATR3	HEAT3_HUMAN	74.6	100.0%	2	2	3	0.00%	4.0%	VNVVSILGITGSVLAK	99.7%	51.1	25	51.1	1	0	0	1569.96	557	572
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	35.3%	AFYPEEISSMVLTK	99.7%	86.9	25	81.1	6	0	0	1630.80	113	126
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	35.3%	AQIHDLVLVGGSTR	99.7%	91.9	25	87.4	2	1	0	1465.81	329	342
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	35.3%	ARFEELCSDLFR	99.7%	60.3	25	57.4	2	0	0	1542.74	300	311
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	35.3%	ATAGDTHLGGEDFDNR	99.7%	78.9	25	78.9	2	2	0	1675.73	221	236
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	35.3%	DAGVIAGLNVLR	99.7%	102	25	90.5	4	0	0	1197.70	160	171
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	35.3%	DNNLLGR	98.7%	34.5	25	19	2	0	0	801.42	452	458
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	35.3%	FEELCSDLFR	99.7%	50.8	25	50.8	3	0	0	1315.60	302	311
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	35.3%	FGDPVVQSDMK	99.7%	65.3	25	65.3	4	0	0	1238.57	78	88
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	35.3%	IINEPTAAAIAYGLDR	99.7%	114	25	114	4	3	0	1687.90	172	187
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	35.3%	ITITNDKGR	99.7%	51.6	25	37.5	2	0	0	1017.57	501	509
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	35.3%	KFGDPVVQSDMK	99.6%	40.6	25	36.1	2	0	0	1350.67	77	88
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	35.3%	LLQDFFNGR	99.7%	63.5	25	48.5	2	0	0	1109.57	349	357
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	35.3%	LSKEEIER	99.7%	49.8	25	24.2	2	0	0	1003.54	510	517
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	35.3%	LVNHFVEEFK	95.8%	29.2	25	21.2	2	0	0	1261.66	237	246
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	35.3%	LVNHFVEEFKR	99.7%	39	25	37.9	0	2	0	1417.76	237	247
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	35.3%	MVQEAEKYK	98.6%	34	25	27.3	2	0	0	1125.56	518	526
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	35.3%	NALESYAFNMK	99.7%	78.5	25	78.5	5	0	0	1287.60	540	550
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	35.3%	NQVALNPQNTVFDAK	99.7%	100	25	93.3	2	0	0	1658.85	57	71
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	35.3%	NQVALNPQNTVFDAKR	96.7%	24.2	25	24.2	0	1	0	1814.95	57	72
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	35.3%	SAVEDEGLK	99.7%	48.7	25	36.2	2	0	0	947.47	551	559
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	35.3%	TTPSYVAFTDTER	99.7%	94.8	25	89.7	7	0	0	1487.70	37	49
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	35.3%	VEIIANDQGNR	99.7%	76.2	25	0	2	0	0	1228.63	26	36
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	35.3%	VQVSYKGETK	99.7%	42.4	25	36.5	1	0	0	1138.61	103	112
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	35.3%	YKAEDEVQR	99.7%	46.3	25	36.2	3	0	0	1137.55	525	533
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	11	0.01%	14.4%	AFSDPFVEAEK	99.7%	48	25	39.1	2	0	0	1239.59	74	84
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	11	0.01%	14.4%	AGGIETIANEYSDR	99.7%	72.2	25	72.2	1	0	0	1495.70	20	33
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	11	0.01%	14.4%	EFSITDVVPYPISLR	99.7%	50.5	25	50.5	1	0	0	1735.93	391	405
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	11	0.01%	14.4%	FQESEERPK	99.7%	48.5	25	36.7	2	0	0	1149.55	689	697
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	11	0.01%	14.4%	GCALQCAILSPAFK	99.7%	85	25	71.2	2	0	0	1535.77	375	388
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	11	0.01%	14.4%	MIMQDKLEK	99.0%	35.4	25	25	2	0	0	1135.59	604	612
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	11	0.01%	14.4%	SNLAYDIVQLPTGLTGIK	99.7%	81.4	25	81.4	2	0	0	1903.05	85	102
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	11	0.01%	14.4%	TSTVDLPIENQLLWQIDR	99.7%	47.5	25	42.8	1	0	0	2141.12	574	591
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	11	0.01%	14.4%	VLATAFDTTLGGR	99.7%	96.6	25	89.7	2	0	0	1321.71	222	234
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	35	68	0.06%	39.2%	ARFEELNADLFR	99.7%	34.5	25	27.3	0	1	0	1480.75	300	311
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	35	68	0.06%	39.2%	DAGTIAGLNVLR	99.7%	103	25	90.2	2	0	0	1199.67	160	171
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	35	68	0.06%	39.2%	EIAEAYLGK	99.7%	43.5	25	35	2	0	0	993.53	129	137
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	35	68	0.06%	39.2%	FDDAVVQSDMK	99.7%	64.6	25	59.2	1	0	0	1254.57	78	88
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	35	68	0.06%	39.2%	FEELNADLFR	99.7%	61.5	25	55.2	2	0	0	1253.62	302	311
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	35	68	0.06%	39.2%	IINEPTAAAIAYGLDK	99.7%	103	25	101	2	0	0	1659.90	172	187
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	35	68	0.06%	39.2%	IINEPTAAAIAYGLDKK	99.7%	85.6	25	85.6	2	0	0	1787.99	172	188
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	35	68	0.06%	39.2%	ITITNDKGR	99.7%	51.6	25	37.5	2	0	0	1017.57	501	509
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	35	68	0.06%	39.2%	LLQDFFNGK	99.7%	50.4	25	25.2	2	0	0	1081.57	349	357
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	35	68	0.06%	39.2%	LSKEDIER	99.7%	64.3	25	12.8	2	0	0	989.53	510	517
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	35	68	0.06%	39.2%	MKEIAEAYLGK	99.7%	64.6	25	48.3	4	0	0	1252.66	127	137
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	35	68	0.06%	39.2%	MVNHFIAEFK	99.7%	53.9	25	42.6	4	1	0	1235.62	237	246
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	35	68	0.06%	39.2%	MVQEAEKYK	98.6%	34	25	27.3	2	0	0	1125.56	518	526
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	35	68	0.06%	39.2%	NQTAEKEEFEHQQK	98.7%	27.8	25	27.8	0	1	0	1745.81	584	597

Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	35	68	0.06%	39.2%	NQVAMNPTNTVFDAK	99.7%	113	25	108	4	0	0	1665.79	57	71
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	35	68	0.06%	39.2%	NSLESYAFNMK	99.7%	53.9	25	53.9	2	0	0	1319.59	540	550
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	35	68	0.06%	39.2%	RFDDAVVQSDMK	99.7%	69.2	25	65.2	3	0	0	1410.67	77	88
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	35	68	0.06%	39.2%	SFYPEEVSSMVLTK	99.7%	88.9	25	88.9	4	0	0	1616.79	113	126
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	35	68	0.06%	39.2%	SQIHDIVLVGGSTR	99.7%	89.9	25	88.9	2	2	0	1481.81	329	342
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	35	68	0.06%	39.2%	STAGDTHLGGEDFDNR	99.7%	80.8	25	80.8	2	2	0	1691.73	221	236
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	35	68	0.06%	39.2%	TTPSYVAFTDTER	99.7%	94.8	25	89.7	7	0	0	1487.70	37	49
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	35	68	0.06%	39.2%	TVTNAVVTVPAYFNDSQR	99.7%	73.4	25	73.4	2	2	0	1982.00	138	155
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	35	68	0.06%	39.2%	VCNPIITK	99.3%	37.1	25	18.2	2	0	0	944.52	602	609
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	35	68	0.06%	39.2%	VEIIANDQGNR	99.7%	76.2	25	0	2	0	0	1228.63	26	36
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	25	35	68	0.06%	39.2%	VQVEYKGETK	99.7%	57.2	25	51.2	2	0	0	1180.62	103	112
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	11	11	23	0.02%	14.3%	DISTTLNADEAVAR	99.7%	108	25	101	2	0	0	1475.73	361	374
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	11	11	23	0.02%	14.3%	DKLCGPYEK	97.5%	31.5	25	27.2	1	0	0	1109.53	647	655
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	11	11	23	0.02%	14.3%	FQEAEERPK	99.7%	42.5	25	26.6	2	0	0	1133.56	706	714
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	11	11	23	0.02%	14.3%	GCALQCAILSPAFK	99.7%	85	25	71.2	2	0	0	1535.77	375	388
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	11	11	23	0.02%	14.3%	LKETAENSLK	99.7%	41.8	25	16.1	2	0	0	1132.62	125	134
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	11	11	23	0.02%	14.3%	MFEELGQR	95.4%	29	25	29	1	0	0	1009.48	715	722
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	11	11	23	0.02%	14.3%	MIMQDKLEK	99.0%	35.4	25	25	2	0	0	1135.59	621	629
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	11	11	23	0.02%	14.3%	SLDQDPVVR	99.5%	38.6	25	32.5	2	0	0	1028.54	773	781
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	11	11	23	0.02%	14.3%	SQFEELCAELLQK	99.7%	74	25	66.6	2	0	0	1594.78	304	316
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	11	11	23	0.02%	14.3%	SVLDAAQIVGLNCLR	99.7%	89.7	25	89.4	2	0	0	1628.88	155	169
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	11	11	23	0.02%	14.3%	VLGTAFDPFLGGK	99.7%	68.6	25	54.9	5	0	0	1321.72	222	234
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	11	11	20	0.02%	22.0%	AFLDALQNQAEASSK	99.7%	120	25	115	2	0	0	1592.79	182	196
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	11	11	20	0.02%	22.0%	AQLLQPTLEINPR	99.7%	76.3	25	74.4	2	0	0	1492.85	635	647
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	11	11	20	0.02%	22.0%	ELGSSVALYSR	99.7%	52	25	52	2	0	0	1181.62	358	368
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	11	11	20	0.02%	22.0%	ELISNASDALEK	99.7%	84.7	25	77.5	2	0	0	1289.66	115	126
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	11	11	20	0.02%	22.0%	ELLQESALIR	99.7%	75.8	25	62.1	2	0	0	1171.67	403	412
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	11	11	20	0.02%	22.0%	FFEDYGLFMR	99.7%	66	25	63.8	2	0	0	1324.60	440	449
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	11	11	20	0.02%	22.0%	GVVDSEDIPLNLSR	99.7%	123	25	0	15	0	0	1513.79	389	402
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	11	11	20	0.02%	22.0%	LVSDGQALPEMEIHLQTNAEK	98.6%	27.4	25	27.4	0	2	0	2339.16	131	151
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	11	11	20	0.02%	22.0%	NIYYLCAPNR	99.4%	38	25	36.6	2	0	0	1283.62	496	505
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	11	11	20	0.02%	22.0%	SDCKEFSSEAR	99.7%	57.8	25	50.5	1	0	0	1315.56	259	269
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	11	11	20	0.02%	22.0%	TDAPLNIR	99.3%	37.6	25	27.5	2	0	0	899.49	333	340
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	11	11	20	0.02%	22.0%	YESSALPSGQLTSLSEYASR	99.7%	107	25	90.9	1	0	0	2146.03	470	489
Heat shock protein beta-1	HSPB1	HSPB1_HUMAN	22.8	100.0%	3	3	4	0.00%	21.0%	LATQSNEITIPVTFESR	99.7%	72.7	25	72.7	1	0	0	1905.99	172	188
Heat shock protein beta-1	HSPB1	HSPB1_HUMAN	22.8	100.0%	3	3	4	0.00%	21.0%	LFDQAFGLPR	99.7%	60.5	25	52.3	2	0	0	1163.62	28	37
Heat shock protein beta-1	HSPB1	HSPB1_HUMAN	22.8	100.0%	3	3	4	0.00%	21.0%	VSLDVNHFAPDELTVK	99.5%	31.6	25	29.1	0	1	0	1783.92	97	112
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	ADLINNLGTIAK	99.7%	81.9	25	68.9	24	0	0	1242.71	101	112
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	ALLFVPR	99.6%	40.4	25	0	5	0	0	815.51	339	345
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	DNSTMGYMAAK	99.7%	58.5	25	51.5	6	0	0	1188.50	621	631
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	DQVANSAFVER	99.7%	73.4	25	64.1	6	0	0	1235.60	500	510
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	EDQTEYLEER	99.7%	69.9	25	62.3	4	0	0	1311.57	192	201
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	EGLELPEDEEEK	97.9%	32.3	25	32.3	1	0	0	1416.64	547	558
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	EGLELPEDEEEKK	99.6%	40.7	25	38.7	2	0	0	1544.73	547	559
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	EKYIDQEELNK	99.7%	60.3	25	50.5	2	0	0	1408.70	282	292
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	ELHINLIPNK	99.2%	36.8	25	28.1	1	0	0	1190.69	75	84
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	ELHINLIPNKQDR	99.7%	53.2	25	53.2	2	2	0	1589.88	75	87
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	ELISNSSDALDK	99.7%	73.9	25	62.9	2	0	0	1291.64	47	58
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	ELISNSSDALDKIR	99.7%	95.4	25	85.5	2	2	0	1560.82	47	60
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	FENLCK	95.6%	29.1	25	13.8	2	0	0	810.38	568	573
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	FYEQFSK	99.7%	50.4	25	26.6	2	0	0	948.45	437	443

Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	GVVDSEDLPLNISR	99.7%	123	25	0	15	0	0	1513.79	387	400
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	HFSVEGQLEFR	99.7%	71.9	25	70.5	11	2	0	1348.66	328	338
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	HIYYITGETK	99.7%	52.5	25	49.8	2	0	0	1224.63	490	499
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	HLEINPDHSIIETLR	99.7%	44	25	43.3	1	2	0	1786.94	633	647
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	HNDDEQYAWESSAGGSFTVR	99.7%	67.3	25	67.3	2	4	0	2255.96	154	173
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	HSQFIGYPITLFVEK	99.7%	68.5	25	64.2	2	1	0	1778.95	210	224
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	IRYESLTDPSK	99.7%	56	25	49	2	2	0	1308.68	59	69
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	LGIHEDSQNR	99.7%	44.2	25	38.2	4	0	0	1168.57	447	456
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	LGIHEDSQNRK	99.0%	28.9	25	22.9	1	2	0	1296.67	447	457
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	LVTSPCCIVTSTYGWTANMER	99.7%	81.3	25	81.3	4	0	0	2446.12	592	612
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	NPDDITNEEYGEFYK	99.7%	95.3	25	85.3	2	0	0	1833.78	300	314
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	RAPFDLFENR	99.7%	48.1	25	36.9	2	0	0	1264.64	346	355
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	SLTNDWEDHLAVK	99.7%	84.1	25	75.8	8	2	0	1527.74	315	327
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	TDTGEPMGR	99.7%	47.5	25	35.9	2	0	0	963.42	174	182
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	TKFENLCK	94.9%	28.5	25	26.1	2	0	0	1039.52	566	573
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	TKPIWTR	95.1%	28.6	25	22.3	1	0	0	901.53	293	299
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	TLTIVDTGIGMTK	99.7%	114	25	0	23	0	0	1349.73	88	100
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	VILHLKEDQTEYLEER	99.7%	53.6	25	53.5	4	7	0	2015.04	186	201
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	YESLTDPSK	99.7%	54.7	25	48.7	4	0	0	1039.49	61	69
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	YESLTDPSKLDSGK	99.7%	66.9	25	50.5	4	1	0	1539.75	61	74
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	YIDQEELNK	99.7%	63.4	25	43.4	15	0	0	1151.56	284	292
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	19	26	61	0.06%	45.8%	YYTSASGDEMVSLK	99.7%	81.4	25	77.4	4	0	0	1550.70	465	478
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	ADHGEPIGR	97.1%	30.8	25	21.2	2	0	0	951.46	169	177
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	ADLINNLGTIAK	99.7%	81.9	25	68.9	24	0	0	1242.71	96	107
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	AKFENLCK	99.5%	38.8	25	27.4	1	0	0	1009.51	558	565
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	ALLFIPR	99.7%	46.6	25	16.4	7	0	0	829.53	331	337
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	APFDLFENK	99.7%	45	25	40.7	4	0	0	1080.54	339	347
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	APFDLFENKK	99.7%	50.5	25	43.7	2	0	0	1208.63	339	348
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	CLELFSELAEDKENYK	99.7%	45.2	25	43.1	0	1	0	1987.93	412	427
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	DNSTMGYMMAK	99.7%	85.3	25	20.5	11	0	0	1280.50	613	623
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	EDQTEYLEER	99.7%	69.9	25	62.3	4	0	0	1311.57	187	196
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	EGLELPEDEEEK	97.9%	32.3	25	32.3	1	0	0	1416.64	539	550
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	EGLELPEDEEEKK	99.6%	40.7	25	38.7	2	0	0	1544.73	539	551
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	EKYIDQEELNK	99.7%	60.3	25	50.5	2	0	0	1408.70	274	284
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	ELISNASDALDK	99.7%	84	25	75.5	8	0	0	1275.64	42	53
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	ELISNASDALDKIR	99.7%	111	25	88.2	10	2	0	1544.83	42	55
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	ELKIDIIPNPQER	99.7%	44.5	25	44.4	2	0	0	1564.87	70	82
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	EQVANSAFVER	99.7%	81.2	25	68.3	17	0	0	1249.62	492	502
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	FENLCK	95.6%	29.1	25	13.8	2	0	0	810.38	560	565
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	FYEAFSK	99.0%	35.8	25	30.1	4	0	0	891.42	429	435
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	GFEVVYMTEPIDEYCVQQLK	99.7%	103	25	50.8	6	4	0	2464.14	507	526
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	GVVDSEDLPLNISR	99.7%	123	25	0	15	0	0	1513.79	379	392
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	HFSVEGQLEFR	99.7%	71.9	25	70.5	11	2	0	1348.66	320	330
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	HLEINPDHPIVETLR	99.7%	74.3	25	67.7	2	4	0	1782.95	625	639
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	HNDDEQYAWESSAGGSFTVR	99.7%	67.3	25	67.3	2	4	0	2255.96	149	168
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	HSQFIGYPITLYLEK	99.7%	76.7	25	0	3	4	0	1808.96	205	219
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	IDIIPNPQER	99.7%	49.3	25	41.3	4	0	0	1194.65	73	82
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	IRYESLTDPSK	99.7%	56	25	49	2	2	0	1308.68	54	64
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	KFYEAFSK	96.1%	29.6	25	20.5	1	0	0	1019.52	428	435
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	KHLEINPDHPIVETLR	99.7%	46.4	25	46.4	0	2	0	1911.04	624	639
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	LGIHEDSTNR	99.7%	52.7	25	51	8	0	0	1141.56	439	448

Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	LGIHEDSTNRR	99.7%	43.1	25	42.1	0	3	0	1297.66	439	449
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	LVSSPCCIVTSTYGWTANMER	99.7%	97.6	25	97.6	4	4	0	2448.10	584	604
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	NPDDITQEEYGEFYK	99.7%	98.7	25	98.7	10	0	0	1847.80	292	306
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	RAPFDLFENK	99.7%	53.5	25	39.7	6	0	0	1236.64	338	347
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	RLSELLR	99.6%	40.7	25	14.8	3	0	0	886.55	450	456
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	SIYYITGESK	99.7%	69.1	25	60.9	8	0	0	1160.58	482	491
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	SLTNDWEDHLAVK	99.7%	84.1	25	75.8	8	2	0	1527.74	307	319
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	TKPIWTR	95.1%	28.6	25	22.3	1	0	0	901.53	285	291
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	TLTLVDTGIGMTK	99.7%	114	25	0	23	0	0	1349.73	83	95
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	VFIMDSCDELIPEYLNFIR	99.7%	60.6	25	60.6	2	0	0	2390.14	360	378
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	VILHLKEDQTEYLEER	99.7%	53.6	25	53.5	4	7	0	2015.04	181	196
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	YESLTDPSK	99.7%	54.7	25	48.7	4	0	0	1039.49	56	64
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	YESLTDPSKLDSGK	99.7%	66.9	25	50.5	4	1	0	1539.75	56	69
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	YHTSQSGDEMTSLSEYVSR	99.7%	112	25	112	4	9	0	2176.95	457	475
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	44	64	304	0.29%	55.9%	YIDQEELNK	99.7%	63.4	25	43.4	15	0	0	1151.56	276	284
Helicase SKI2W	SKIV2L	SKIV2_HUMAN	137.8	99.9%	2	2	3	0.00%	2.4%	GPATAEVPYPDDLVGFK	97.1%	30.8	25	30.8	1	0	0	1775.89	889	905
Helicase SKI2W	SKIV2L	SKIV2_HUMAN	137.8	99.9%	2	2	3	0.00%	2.4%	TVVAEYAIALAQK	99.7%	61.4	25	61.4	2	0	0	1376.78	339	351
Helicase-like transcription factor	HLTF	HLTF_HUMAN	113.9	100.0%	3	3	3	0.00%	3.0%	ELAAGAFGTK	98.2%	33	25	23.5	1	0	0	964.51	979	988
Helicase-like transcription factor	HLTF	HLTF_HUMAN	113.9	100.0%	3	3	3	0.00%	3.0%	MSELSSSRPK	99.7%	41	25	35.9	1	0	0	1121.56	377	386
Helicase-like transcription factor	HLTF	HLTF_HUMAN	113.9	100.0%	3	3	3	0.00%	3.0%	VILDEGHAIR	99.7%	43.7	25	33	1	0	0	1122.63	554	563
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	8	9	18	0.02%	16.5%	ALPLIVGAQLIHADK	99.7%	65	25	65	1	0	0	1558.93	15	29
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	8	9	18	0.02%	16.5%	GASGSFVVVQK	99.7%	52.1	25	43.9	2	0	0	1078.59	223	233
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	8	9	18	0.02%	16.5%	GQLEQITGK	98.9%	35.2	25	24.5	3	0	0	973.53	312	320
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	8	9	18	0.02%	16.5%	KYVSQYYPK	99.7%	55.7	25	39.6	1	0	0	1175.61	283	291
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	8	9	18	0.02%	16.5%	LEDVLPLAFTR	99.7%	70.6	25	43.8	4	0	0	1273.72	259	269
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	8	9	18	0.02%	16.5%	MDAILTEAIK	98.9%	35.1	25	21	3	0	0	1120.59	161	170
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	8	9	18	0.02%	16.5%	SSAVDPEPQVK	99.7%	55.6	25	38.4	2	0	0	1156.58	248	258
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	8	9	18	0.02%	16.5%	TIPSWATLSASQLAR	99.7%	88.5	25	88.5	2	0	0	1601.86	132	146
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	8	11	36	0.03%	25.9%	DLKDYFTK	99.7%	45.9	25	32	2	0	0	1029.53	84	91
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	8	11	36	0.03%	25.9%	EVYQQQQYGSGGR	99.7%	93.4	25	85.4	13	0	0	1499.69	233	245
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	8	11	36	0.03%	25.9%	EYFGEFGEIEAIELPMDPK	99.7%	56	25	55.8	4	0	0	2214.03	172	190
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	8	11	36	0.03%	25.9%	FGEVVDCTIK	99.7%	66.1	25	0	15	0	0	1167.57	92	101
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	8	11	36	0.03%	25.9%	FGEVVDCTIKMDPNTGR	99.5%	32.3	25	32.3	0	1	0	1954.90	92	108
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	8	11	36	0.03%	25.9%	GFGFILFK	99.7%	43.5	25	36.1	6	0	0	928.53	111	118
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	8	11	36	0.03%	25.9%	GFVFITFK	99.4%	37.8	25	37.8	2	0	0	958.54	196	203
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	8	11	36	0.03%	25.9%	MFVGGLSWDTSK	99.7%	73.6	25	68.7	2	0	0	1343.63	71	82
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	8	11	36	0.03%	25.9%	MFVGGLSWDTSKK	99.7%	73.1	25	63.8	4	2	0	1455.73	71	83
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	7	10	33	0.03%	33.4%	AEIIADKQSGK	99.7%	68.2	25	36.4	4	0	0	1159.63	127	137
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	7	10	33	0.03%	33.4%	AVPKEDIYSGGGGGGSR	99.7%	105	25	101	4	2	0	1606.78	173	189
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	7	10	33	0.03%	33.4%	EDIYSGGGGGGSR	99.7%	105	25	103	4	0	0	1211.53	177	189
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	7	10	33	0.03%	33.4%	GDVAEGDLIEHFSQFGTVEK	99.7%	102	25	102	4	4	0	2178.04	107	126
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	7	10	33	0.03%	33.4%	GFGFVYFQNHDAADK	99.7%	79.7	25	79.7	2	3	0	1715.78	140	154
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	7	10	33	0.03%	33.4%	KLFVGGLK	99.1%	36	25	0	4	0	0	861.56	99	106
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	7	10	33	0.03%	33.4%	LFIGGLNVQTSESGLR	99.7%	124	25	116	4	0	0	1690.91	9	24
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	7	10	33	0.03%	33.4%	SGGGGGGGGSSWGGR	99.7%	91.9	25	89.6	2	0	0	1192.51	270	284
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	15	25	149	0.14%	42.7%	DYFEQYGK	99.7%	47.9	25	47.9	4	0	0	1049.46	123	130
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	15	25	149	0.14%	42.7%	EDSQRPGAHLTVK	99.7%	55.8	25	39.1	9	0	0	1437.74	93	105
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	15	25	149	0.14%	42.7%	EDSQRPGAHLTVKK	99.7%	48.2	25	36.3	1	0	0	1565.84	93	106
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	15	25	149	0.14%	42.7%	EDTEEHHLRDYFEQYGK	99.4%	31.1	25	31.1	0	1	0	2195.96	114	130
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	15	25	149	0.14%	42.7%	GFAFVTFDDHDSVDK	99.7%	80.4	25	73.2	8	3	0	1699.76	147	161
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	15	25	149	0.14%	42.7%	GFAFVTFDDHDSVDKIVIQK	99.7%	45.7	25	23.2	0	2	0	2281.15	147	166

Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	15	25	149	0.14%	42.7%	IEVIEIMTDR	99.7%	80.3	25	73	15	0	0	1218.64	131	140
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	15	25	149	0.14%	42.7%	IFVGGIKEDTEEHHLR	99.7%	92.5	25	0	2	8	0	1879.97	107	122
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	15	25	149	0.14%	42.7%	KIFVGGIK	99.1%	36	25	0	4	0	0	861.56	106	113
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	15	25	149	0.14%	42.7%	KLFIGGLSFETTDESLR	99.7%	66.3	25	58.7	2	2	0	1913.00	15	31
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	15	25	149	0.14%	42.7%	LFIGGLSFETTDESLR	99.7%	129	25	116	25	0	0	1784.91	16	31
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	15	25	149	0.14%	42.7%	NQGGYGGSSSSSSYGSGR	99.7%	140	25	140	14	0	0	1694.70	353	370
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	15	25	149	0.14%	42.7%	RGFAFVTFDDHDSVDK	99.7%	50.8	25	50.5	2	2	0	1855.86	146	161
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	15	25	149	0.14%	42.7%	SESPKEPEQLR	99.7%	36.6	25	31.2	7	5	0	1299.65	4	14
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	15	25	149	0.14%	42.7%	SHFEQWGTLTDCVVMR	99.7%	85	25	85	4	6	0	1965.89	32	47
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	15	25	149	0.14%	42.7%	SSGPYGGGGQYFAKPR	99.7%	83.7	25	72.7	19	9	0	1628.78	337	352
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	15	25	149	0.14%	42.7%	YHTVNGHNCEVR	99.7%	66.4	25	60	3	6	0	1485.67	167	178
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	15	29	100	0.09%	39.2%	EDSVKPGAHLTVK	99.7%	61.2	25	54.1	6	0	0	1380.75	114	126
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	15	29	100	0.09%	39.2%	EDSVKPGAHLTVKK	99.7%	54.2	25	34.8	1	1	0	1508.84	114	127
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	15	29	100	0.09%	39.2%	EDTEEYNLR	99.7%	69.1	25	69.1	4	0	0	1168.51	135	143
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	15	29	100	0.09%	39.2%	EDTEEYNLRDYFEK	99.7%	77.8	25	71	2	0	0	1850.81	135	148
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	15	29	100	0.09%	39.2%	GEEGHDPKEPEQLR	99.7%	45.5	25	41.1	2	2	0	1620.76	22	35
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	15	29	100	0.09%	39.2%	GFAFVTFDDHDTVDK	99.7%	79.5	25	79.5	6	4	0	1713.78	168	182
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	15	29	100	0.09%	39.2%	GFAFVTFDDHDTVDKIVVQK	99.7%	33.5	25	10.1	0	1	0	2281.15	168	187
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	15	29	100	0.09%	39.2%	IETIEVMEDR	99.7%	82.4	25	73.5	14	0	0	1234.60	152	161
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	15	29	100	0.09%	39.2%	IFVGGIKEDTEEYNLR	99.7%	90.2	25	83.5	5	7	0	1882.95	128	143
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	15	29	100	0.09%	39.2%	KIFVGGIK	99.1%	36	25	0	4	0	0	861.56	127	134
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	15	29	100	0.09%	39.2%	LFIGGLSFETTDDSLR	99.7%	125	25	119	6	0	0	1770.89	37	52
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	15	29	100	0.09%	39.2%	SSGSPYGGGYGSGGGSGGYGSR	99.7%	142	25	142	9	1	0	1910.79	355	376
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	15	29	100	0.09%	39.2%	WGTLTDCVVMR	99.7%	60.3	25	49	6	0	0	1337.63	58	68
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	15	29	100	0.09%	39.2%	WGTLTDCVVMRDPQTK	99.7%	51.4	25	51.4	4	6	0	1906.92	58	73
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	15	29	100	0.09%	39.2%	YGKIETIEVMEDR	99.7%	68.1	25	64.2	4	4	0	1582.78	149	161
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	15	29	100	0.09%	39.2%	YHTINGHNCEVK	99.7%	57	25	55.3	2	3	0	1471.67	188	199
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	27	101	0.10%	42.3%	DLKDYFSK	99.2%	36.5	25	29.7	3	0	0	1015.51	112	119
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	27	101	0.10%	42.3%	ESESVDKVMDQK	99.7%	62.7	25	50.8	7	1	0	1394.65	147	158
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	27	101	0.10%	42.3%	EYFGGFGEVESIELPMDNK	99.7%	99.3	25	99.3	8	0	0	2160.98	200	218
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	27	101	0.10%	42.3%	EYFGGFGEVESIELPMDNKTNK	99.7%	49.4	25	47.3	0	2	0	2520.16	200	221
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	27	101	0.10%	42.3%	FGEVVDCTLK	99.7%	66.1	25	0	15	0	0	1167.57	120	129
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	27	101	0.10%	42.3%	FGEVVDCTLKLDPITGR	99.7%	83.5	25	82.4	2	2	0	1919.99	120	136
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	27	101	0.10%	42.3%	GFCFITFK	99.1%	36.3	25	33.3	2	0	0	1019.50	224	231
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	27	101	0.10%	42.3%	GFCFITFKEEEPVK	99.7%	81.8	25	81.8	2	0	0	1730.85	224	237
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	27	101	0.10%	42.3%	GFGFVLFK	99.7%	48.4	25	42.3	14	0	0	914.51	139	146
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	27	101	0.10%	42.3%	HSEAATAQREEWK	99.7%	71.3	25	68.5	2	1	0	1542.73	86	98
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	27	101	0.10%	42.3%	IDASKNEEDEGHSNSSPR	99.7%	85.1	25	85.1	2	4	0	1971.86	68	85
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	27	101	0.10%	42.3%	IFVGGLSPDTPEEK	99.7%	94.2	25	85.8	12	0	0	1488.76	184	197
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	27	101	0.10%	42.3%	IFVGGLSPDTPEEKIR	99.7%	87.9	25	79.2	2	3	0	1757.94	184	199
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	27	101	0.10%	42.3%	KYHNVGLSK	99.5%	38.9	25	29.1	2	0	0	1045.58	243	251
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	27	101	0.10%	42.3%	MFIGGLSWDTTK	99.7%	92	25	89.4	4	0	0	1355.67	99	110
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	27	101	0.10%	42.3%	MFIGGLSWDTTKK	99.7%	74.8	25	74.5	5	1	0	1483.76	99	111
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	27	101	0.10%	42.3%	YHNVGLSK	99.7%	42.5	25	21.3	5	0	0	917.48	244	251
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	12	31	0.03%	23.8%	DAASVDKVLELK	99.7%	61.5	25	46.5	3	0	0	1287.72	198	209
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	12	31	0.03%	23.8%	DLTEYLSR	99.7%	52.2	25	34.2	7	0	0	996.50	163	170
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	12	31	0.03%	23.8%	EYFGAFGEIENIELPMDTK	99.7%	71.9	25	71.9	2	0	0	2219.02	251	269
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	12	31	0.03%	23.8%	FGEVVDCTIK	99.7%	66.1	25	0	15	0	0	1167.57	171	180
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	12	31	0.03%	23.8%	GFCFITYTDEEPVK	99.7%	57.6	25	57.6	2	0	0	1705.78	275	288
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	12	31	0.03%	23.8%	GFCFITYTDEEPVKK	99.7%	76.8	25	73.9	4	2	0	1833.87	275	289
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	12	31	0.03%	23.8%	GFGFVLFK	99.7%	48.4	25	42.3	14	0	0	914.51	190	197

Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	12	31	0.03%	23.8%	MFIGGLSWDTSK	99.7%	76.3	25	72.1	4	0	0	1357.65	150	161
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	12	31	0.03%	23.8%	MFIGGLSWDTSKK	99.7%	78.2	25	68.9	4	1	0	1469.75	150	162
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	12	31	0.03%	23.8%	QLAPLLPSLAPSSAR	99.1%	36.3	25	35	2	0	0	1520.88	37	51
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	8	11	28	0.03%	37.1%	ATENDIYNFFSPLNPVR	99.7%	84.4	25	84.4	21	4	0	1996.98	300	316
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	8	11	28	0.03%	37.1%	DLSYCLSGMYDHR	99.7%	64.9	25	64.9	3	0	0	1616.68	263	275
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	8	11	28	0.03%	37.1%	FMSVQRPGPYDRPGTAR	95.6%	23.1	25	23.1	0	1	0	1934.97	201	217
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	8	11	28	0.03%	37.1%	HSGPNSADSANDGFVR	99.7%	96.8	25	95.5	3	3	0	1630.72	99	114
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	8	11	28	0.03%	37.1%	ITGEAFVQFASQELAEK	99.7%	107	25	97.3	6	0	0	1867.94	151	167
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	8	11	28	0.03%	37.1%	QSGEAFVELGSEDDVK	99.7%	128	25	123	3	0	0	1709.79	53	68
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	8	11	28	0.03%	37.1%	TEMDWVLK	99.2%	36.4	25	19.8	2	0	0	1021.50	91	98
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	8	11	28	0.03%	37.1%	VHIEIGPDGR	99.7%	61.4	25	58.5	8	0	0	1092.58	317	326
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	8	11	28	0.03%	37.1%	VTGEADVEFATHEEAVAAMSK	99.7%	49.6	25	49.6	0	3	0	2208.01	327	347
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	8	11	28	0.03%	37.1%	YGDSEFTVQSTTGHCVHMR	99.7%	67.2	25	67.2	0	4	0	2211.95	276	294
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	19	110	0.10%	41.2%	ATENDIYNFFSPLNPVR	99.7%	84.4	25	84.4	21	4	0	1996.98	300	316
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	19	110	0.10%	41.2%	DLNYCFSGMSDHR	99.7%	67.8	25	67.8	9	0	0	1601.65	263	275
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	19	110	0.10%	41.2%	EGRPSGEAFVELESEDEVK	99.7%	119	25	118	4	7	0	2106.98	50	68
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	19	110	0.10%	41.2%	GLPWSCSADEVQR	99.7%	81.6	25	78.4	4	0	0	1504.69	17	29
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	19	110	0.10%	41.2%	HTGPNSPDTANDGFVR	99.7%	88	25	88	5	10	0	1684.77	99	114
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	19	110	0.10%	41.2%	IQNGAQGIR	99.7%	67.2	25	51.1	5	0	0	956.53	36	44
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	19	110	0.10%	41.2%	SNNVEMDWVLK	99.7%	67.7	25	62.2	6	0	0	1334.64	88	98
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	19	110	0.10%	41.2%	STGEAFVQFASQEIAEK	99.7%	115	25	115	12	0	0	1841.89	151	167
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	19	110	0.10%	41.2%	VHIEIGPDGR	99.7%	61.4	25	58.5	8	0	0	1092.58	317	326
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	19	110	0.10%	41.2%	VTGEADVEFATHEDAVAAMSK	99.7%	50	25	43.9	0	5	0	2194.00	327	347
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	19	110	0.10%	41.2%	YGDGGSTFQSTTGHCVHMR	99.7%	65.9	25	65.9	0	9	0	2113.88	276	294
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	19	110	0.10%	41.2%	YVELFLNSTAGASGGAYEHR	98.8%	28.1	25	24.9	0	1	0	2142.03	356	375
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	7	9	24	0.02%	36.7%	ATENDIYNFFSPLNPMR	99.7%	70.5	25	70.5	6	0	0	2028.95	300	316
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	7	9	24	0.02%	36.7%	DLNYCFSGMSDHR	99.7%	67.8	25	67.8	9	0	0	1601.65	263	275
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	7	9	24	0.02%	36.7%	EGRPSGEAFVELESEEEVK	99.7%	38.9	25	38	0	1	0	2121.00	50	68
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	7	9	24	0.02%	36.7%	GLPWSCSADEVMR	99.7%	60.7	25	54.5	2	0	0	1523.66	17	29
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	7	9	24	0.02%	36.7%	HTGPNSPDTANDGFVR	99.7%	88	25	88	5	10	0	1684.77	99	114
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	7	9	24	0.02%	36.7%	IQNGTSGIR	99.5%	38.8	25	22.5	3	0	0	945.51	36	44
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	7	9	24	0.02%	36.7%	SNSVEMDWVLK	99.4%	38.2	25	27.9	4	0	0	1307.63	88	98
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	7	9	24	0.02%	36.7%	STGEAFVQFASQEIAEK	99.7%	115	25	115	12	0	0	1841.89	151	167
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	7	9	24	0.02%	36.7%	VHIEIGPDGR	99.7%	61.4	25	58.5	8	0	0	1092.58	317	326
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	7	9	24	0.02%	36.7%	VTGEADVEFATHEDAVAAMAK	99.3%	30.2	25	4.84	0	1	0	2178.00	327	347
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	7	9	24	0.02%	36.7%	YGDGGSSFQSTTGHCVHMR	99.7%	67.3	25	67.3	0	7	0	2083.87	276	294
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	13	41	0.04%	37.0%	ATENDIANFFSPLNPIR	99.7%	77.9	25	76.4	7	1	0	1918.97	206	222
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	13	41	0.04%	37.0%	ATGEADVEFVTHEDAVAAMSK	99.7%	64.5	25	63.4	0	4	0	2178.00	233	253
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	13	41	0.04%	37.0%	DGMDNQGGYGSVGR	99.7%	79.8	25	79.8	5	0	0	1428.58	288	301
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	13	41	0.04%	37.0%	EIAENALGK	99.7%	51.8	25	51.8	4	0	0	944.50	68	76
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	13	41	0.04%	37.0%	HNGPNDASDGTVR	99.7%	60.1	25	44.1	2	0	0	1339.60	7	19
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	13	41	0.04%	37.0%	STGEAFVQFASK	99.7%	74.8	25	64.3	9	0	0	1271.63	56	67
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	13	41	0.04%	37.0%	VHIDIGADGR	99.7%	63.5	25	52.9	3	0	0	1052.55	223	232
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	13	41	0.04%	37.0%	YIEIFR	98.9%	35	25	0	1	0	0	840.46	85	90
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	13	41	0.04%	37.0%	YIELFLNSTPGGGSGMGGSGMGGYGR	99.7%	104	25	103	3	2	0	2554.13	262	287
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	22	83	0.08%	38.7%	DLAGSIIGK	99.7%	54.8	25	36.5	4	0	0	873.50	397	405
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	22	83	0.08%	38.7%	DYDDMSPR	99.5%	39.1	25	39.1	4	0	0	998.39	279	286
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	22	83	0.08%	38.7%	GGDLMAYDR	99.7%	65.2	25	59.1	5	0	0	1013.44	317	325
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	22	83	0.08%	38.7%	GGDLMAYDRR	98.3%	33.1	25	19.8	3	0	0	1153.54	317	326
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	22	83	0.08%	38.7%	GSDFDCELR	99.7%	54.5	25	53.9	4	0	0	1098.45	140	148
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	22	83	0.08%	38.7%	GSYGDLGGPIITTQVTIPK	99.7%	88.3	25	86.4	4	0	0	1917.03	378	396

Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	22	83	0.08%	38.7%	IDEPLEGSEDR	99.7%	81.9	25	73.1	4	0	0	1259.58	423	433
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	22	83	0.08%	38.7%	IILDLISESPIK	99.7%	99.3	25	93.4	14	0	0	1340.80	208	219
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	22	83	0.08%	38.7%	IITITGTQDQIQNAQYLLQNSVK	99.7%	66.5	25	66.5	0	5	0	2589.39	434	456
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	22	83	0.08%	38.7%	ILSISADIETIGEILKK	99.2%	36.4	25	36.4	1	0	0	1843.08	87	103
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	22	83	0.08%	38.7%	LFQECCPHSTDR	99.7%	82.8	25	82.8	4	3	0	1549.65	180	191
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	22	83	0.08%	38.7%	LLIHQSLAGGIIGVK	99.7%	56	25	56	0	4	0	1518.94	149	163
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	22	83	0.08%	38.7%	NTDEMVELR	99.7%	76.2	25	55.7	8	0	0	1106.51	38	46
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	22	83	0.08%	38.7%	RDYDDMSPR	98.1%	32.8	25	32.8	1	0	0	1154.49	278	286
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	22	83	0.08%	38.7%	RPAEDMEEEQAFKR	99.7%	94.9	25	94.9	1	6	0	1735.81	22	35
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	22	83	0.08%	38.7%	VVLIGGKPDR	99.7%	50.1	25	32.5	8	0	0	1053.64	192	201
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	19	30	133	0.13%	45.5%	AITHLNNNFMFGQK	99.7%	79.2	25	78.8	8	6	0	1650.81	435	448
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	19	30	133	0.13%	45.5%	ASLNGADIYSGCCTLK	99.7%	101	25	91.3	4	0	0	1729.79	249	264
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	19	30	133	0.13%	45.5%	IEYAKPTR	99.7%	61.5	25	50.8	10	0	0	977.54	265	272
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	19	30	133	0.13%	45.5%	ISRPGDSDDSR	99.7%	39.9	25	30.3	4	6	0	1204.56	179	189
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	19	30	133	0.13%	45.5%	LCFSTAQHAS	99.7%	54.6	25	52.9	5	0	0	1121.50	580	589
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	19	30	133	0.13%	45.5%	LNVCVSK	99.7%	43.9	25	30.9	5	0	0	819.44	449	455
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	19	30	133	0.13%	45.5%	MGPPVGGHR	99.7%	43.3	25	27	4	0	0	907.46	345	353
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	19	30	133	0.13%	45.5%	NDQDTWDYTNPNLSGQGDPGSNPNKR	99.7%	99.7	25	99.7	0	4	0	2890.26	278	303
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	19	30	133	0.13%	45.5%	NGVQAMVEFDSVQSAQR	99.7%	129	25	129	4	0	0	1881.88	230	246
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	19	30	133	0.13%	45.5%	NPNGPYPYTLK	99.5%	38.6	25	25.5	3	0	0	1263.64	569	579
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	19	30	133	0.13%	45.5%	QPAIMPGQSYGLEDGSCSYK	99.7%	76.6	25	76.6	4	0	0	2187.97	456	475
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	19	30	133	0.13%	45.5%	QPAIMPGQSYGLEDGSCSYKDFSESR	99.7%	76.9	25	76.9	0	2	0	2925.27	456	481
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	19	30	133	0.13%	45.5%	SDALETLGFLNHYQMK	99.7%	67.5	25	67.5	8	4	0	1866.91	553	568
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	19	30	133	0.13%	45.5%	SKPGAAMVEMADGYAVDR	99.7%	85.6	25	36.2	8	13	0	1883.86	417	434
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	19	30	133	0.13%	45.5%	SSSGLLEWESK	99.7%	60.8	25	47.6	4	0	0	1222.60	542	552
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	19	30	133	0.13%	45.5%	TDNAGDQHGGGGGGGGGAGAAGGGGGGENYDDPHK	99.7%	36.8	25	36.8	0	1	0	2981.20	63	97
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	19	30	133	0.13%	45.5%	TPASPVVHIR	99.7%	55	25	53	5	0	0	1076.62	98	107
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	19	30	133	0.13%	45.5%	VFNVFCLYGNVEK	99.7%	105	25	95.2	17	0	0	1588.78	399	411
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	19	30	133	0.13%	45.5%	YYGGGSEGGR	99.7%	47.2	25	45	4	0	0	1002.43	47	56
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	ACQIFVR	99.7%	48.9	25	39.6	2	0	0	893.47	652	658
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	ADILEDKDGK	99.7%	52.5	25	48.2	7	0	0	1103.56	233	242
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	AFITNIPFDVK	99.7%	89.1	25	72.3	13	0	0	1264.69	73	83
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	DKFNECGHVLYADIK	99.7%	67.1	25	57.8	2	0	0	1808.86	671	685
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	EVFSMAGVVVR	99.7%	66.7	25	52.3	2	0	0	1193.63	222	232
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	FESPEVAER	99.7%	46.8	25	37.3	5	0	0	1063.51	699	707
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	FGSGMNMGR	99.7%	57.5	25	13.9	10	0	0	972.40	363	371
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	FNECGHVLYADIK	99.7%	63.7	25	55	1	0	0	1565.74	673	685
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	GCAVVEFK	99.7%	51.7	25	32.7	3	0	0	909.45	113	120
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	GGNRFEPYANPTK	99.7%	38.7	25	32.2	2	2	0	1450.71	57	69
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	GIGMGNIGPAGMGMEGIGFGINK	99.7%	113	25	113	9	3	0	2226.04	323	345
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	GNFGGSFAGSFGGAGGHAPGVAR	99.7%	133	25	133	2	4	0	2034.95	628	650
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	HSLSGRPLK	98.9%	35.3	25	18.6	1	0	0	994.58	135	143
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	INEILSNALK	99.7%	71.2	25	55.7	8	0	0	1114.65	372	381
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	INEILSNALKR	99.7%	49.6	25	42.6	2	0	0	1270.75	372	382
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	KACQIFVR	99.7%	62.6	25	52.7	2	0	0	1021.56	651	658
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	LGSTVFVANLDYK	99.7%	93.3	25	86.3	3	0	0	1426.76	202	214
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	LKEVFSMAGVVVR	99.7%	80.1	25	70	3	6	0	1450.81	220	232
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	MEEESGAPGVPSGNGAPGPK	99.7%	51.8	25	51.8	1	0	0	1867.85	18	37
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	MGAGLGHGMDR	99.7%	81.2	25	75	10	0	0	1117.49	419	429
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	MGAGMGFGLER	99.7%	89.5	25	61.8	14	0	0	1141.51	486	496
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	MGANNLER	99.7%	70.9	25	61.4	4	0	0	904.43	558	565

Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	MGANSLER	99.7%	70.9	25	57	7	0	0	877.42	571	578
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	MGGMEGPFGGGMENMGR	99.7%	79.1	25	79.1	11	0	0	1714.68	346	362
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	MGLAMGGGGGASFDR	99.7%	104	25	47.8	10	0	0	1399.61	607	621
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	MGLSMER	99.7%	51	25	46.9	6	0	0	839.38	525	531
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	MGLVMDR	99.7%	50.2	25	41.5	7	0	0	821.40	437	443
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	MGPAMGPALGAGIER	99.7%	76.7	25	67.2	13	0	0	1459.70	592	606
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	MGPLGLDHMASSIER	99.7%	90.1	25	90.1	8	4	0	1613.78	457	471
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	MGPVMDR	95.0%	28.6	25	0.53	2	0	0	821.36	544	550
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	MVPAGMGAGLER	99.7%	59.8	25	56.8	8	0	0	1188.59	532	543
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	NLPFDFTWK	98.4%	33.5	25	27.8	1	0	0	1167.58	659	667
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	QGGGGGGGSVPGIER	99.7%	91.4	25	90.5	6	0	0	1284.63	389	403
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	VGEVTYVELLMDAEGK	99.7%	113	25	110	8	0	0	1768.87	95	110
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	VGQTIER	99.7%	49.8	25.4	29.1	6	0	0	802.44	504	510
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	VKEDPDGEHAR	99.5%	39.4	25	29.9	2	0	0	1252.59	144	154
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	37	57	222	0.21%	54.1%	WQSLKDLVK	99.3%	37.1	25	30.3	2	0	0	1116.64	84	92
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	21	28	164	0.16%	38.4%	AGPIWDLR	99.7%	68.9	25	54.1	6	0	0	927.50	185	192
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	21	28	164	0.16%	38.4%	DLFEDELVPLFEK	99.7%	101	25	95.1	15	0	0	1593.80	172	184
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	21	28	164	0.16%	38.4%	DSDLSHVQNK	99.7%	53.4	25	46.3	9	0	0	1142.54	82	91
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	21	28	164	0.16%	38.4%	DYAFIHFDER	99.7%	60.8	25	51.5	2	0	0	1312.60	372	381
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	21	28	164	0.16%	38.4%	EFNEDGALAVLQQFK	99.7%	75.4	25	67.4	8	0	0	1708.85	67	81
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	21	28	164	0.16%	38.4%	EQILEEFSK	99.5%	38.9	25	18.2	6	0	0	1122.57	257	265
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	21	28	164	0.16%	38.4%	GFCFLEYEDHK	99.7%	53.6	25	53.6	8	1	0	1444.62	287	297
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	21	28	164	0.16%	38.4%	GYAFVTFCTK	99.7%	62	25	62	6	0	0	1193.57	204	213
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	21	28	164	0.16%	38.4%	HIGVCISVANNR	99.7%	44.5	25	0	6	2	0	1339.69	233	244
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	21	28	164	0.16%	38.4%	LDEIYVAGLVAHSDLDER	99.7%	102	25	100	1	0	0	2015.01	43	60
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	21	28	164	0.16%	38.4%	LFVGSIPK	99.7%	42	25	26.6	4	0	0	860.52	245	252
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	21	28	164	0.16%	38.4%	LKDYAFIHFDER	99.7%	50.1	25	46	0	2	0	1553.77	370	381
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	21	28	164	0.16%	38.4%	LMMDPLTGLNR	99.7%	74.5	25	69.2	19	0	0	1260.64	193	203
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	21	28	164	0.16%	38.4%	LYNNHEIR	99.7%	45.9	25	17.6	8	0	0	1058.54	222	229
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	21	28	164	0.16%	38.4%	NLANTVTEEILEK	99.7%	107	25	97.1	8	0	0	1473.78	344	356
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	21	28	164	0.16%	38.4%	SAFLCGVMK	99.7%	55.2	25	49.2	10	0	0	1012.50	92	100
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	21	28	164	0.16%	38.4%	SENQEFYQDTFGQQWK	99.7%	84.7	25	84.7	2	0	0	2034.88	608	623
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	21	28	164	0.16%	38.4%	TGYTLDVTTGQR	99.7%	83.7	25	79.6	12	0	0	1311.65	131	142
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	21	28	164	0.16%	38.4%	TKEQILEEFSK	99.7%	72.6	25	72.6	10	2	0	1351.71	255	265
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	21	28	164	0.16%	38.4%	VTEGLTDVILYHQPDDK	99.7%	80.9	25	80.9	5	6	0	1942.98	266	282
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	21	28	164	0.16%	38.4%	YGGPPPDSVYSGQQPSVGTEIFVGK	99.7%	69.7	25	68.9	2	4	0	2566.25	144	168
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	152	0.14%	39.7%	AGPIWDLR	99.7%	68.9	25	54.1	6	0	0	927.50	188	195
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	152	0.14%	39.7%	DLYEDELVPLFEK	99.7%	88.4	25	82.4	19	0	0	1609.80	175	187
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	152	0.14%	39.7%	DYAFVHFEDR	99.7%	51.7	25	51.6	3	0	0	1298.58	375	384
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	152	0.14%	39.7%	EFNEEGALSVLQQFK	99.7%	103	25	91.6	10	0	0	1738.86	70	84
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	152	0.14%	39.7%	ENILEEFSK	99.7%	46.1	25	39.5	2	0	0	1108.55	260	268
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	152	0.14%	39.7%	ESDLSHVQNK	99.7%	55.4	25	41.3	4	0	0	1156.56	85	94
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	152	0.14%	39.7%	GFCFLEYEDHK	99.7%	53.6	25	53.6	8	1	0	1444.62	290	300
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	152	0.14%	39.7%	GYAFITFCGK	99.7%	74.6	25	68.8	7	0	0	1163.56	207	216
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	152	0.14%	39.7%	HLGVCISVANNR	99.7%	44.5	25	0	6	2	0	1339.69	236	247
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	152	0.14%	39.7%	LCDSYEIRPGK	99.7%	65.6	25	50.6	6	2	0	1337.65	225	235
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	152	0.14%	39.7%	LFVGSIPK	99.7%	42	25	26.6	4	0	0	860.52	248	255
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	152	0.14%	39.7%	LKDYAFVHFEDR	99.7%	74.4	25	74.4	2	4	0	1539.76	373	384
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	152	0.14%	39.7%	LMMDPLSGQNR	99.7%	68.1	25	47	20	0	0	1261.60	196	206
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	152	0.14%	39.7%	NLATTVTEEILEK	99.7%	126	25	115	22	0	0	1460.78	347	359
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	152	0.14%	39.7%	SAFLCGVMK	99.7%	55.2	25	49.2	10	0	0	1012.50	95	103

Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	152	0.14%	39.7%	SFSEFGK	97.1%	30.9	25	27.2	2	0	0	801.38	360	366
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	152	0.14%	39.7%	STAYEDYYYHPPPR	99.7%	61.2	25	61.2	3	5	0	1758.78	428	441
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	152	0.14%	39.7%	TGYTLDVTTGQR	99.7%	83.7	25	79.6	12	0	0	1311.65	134	145
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	152	0.14%	39.7%	TKENILEEFSK	99.7%	63.5	25	56.2	9	0	0	1337.69	258	268
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	152	0.14%	39.7%	TLIEAGLPQK	99.7%	71.3	25	71.3	4	0	0	1069.63	32	41
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	152	0.14%	39.7%	VQESTKGPDEAK	99.7%	63.2	25	56	11	1	0	1288.64	115	126
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	152	0.14%	39.7%	VTEGLVDVILYHQPDDK	99.7%	90.7	25	87.4	4	6	0	1941.00	269	285
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	152	0.14%	39.7%	YGGPPPDSVYSGVQPGIGTEVFVGK	99.7%	75.9	25	75.9	2	4	0	2507.25	147	171
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	AEGGGGGGRPGAPAAGDGK	99.7%	62.2	25	59	3	2	0	1538.73	216	234
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	AEGGGGGGRPGAPAAGDGKTEQK	99.7%	49.4	25	49.4	0	4	0	2024.97	216	238
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	DCEVVMMIGLPGAGK	99.7%	94.6	25	18.9	8	0	0	1592.75	496	510
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	DIDIHEVR	99.7%	47.2	25	38.9	10	0	0	996.51	353	360
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	DLPEHAVLK	99.5%	39.1	25	31.5	6	0	0	1021.57	627	635
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	EKPYFPIPEEYTFIQNVPLEDR	99.7%	33.5	25	33.5	0	1	0	2724.36	463	484
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	FIEIAAR	99.7%	46.9	25	30.1	13	0	0	819.47	566	572
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	GKVCFEMK	99.3%	37.7	25	27.6	2	0	0	998.48	332	339
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	GYFEYIEENK	99.7%	59.4	25	53.9	5	0	0	1291.58	256	265
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	GYFEYIEENKYSR	99.7%	70.2	25	68.7	6	3	0	1697.78	256	268
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	KAEGGGGGGRPGAPAAGDGK	99.7%	37.1	25	37.1	0	4	0	1666.83	215	234
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	KAVVVCPK	99.5%	38.8	25	23.3	5	0	0	900.53	602	609
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	KDCEVVMMIGLPGAGK	99.7%	80.9	25	80.9	6	5	0	1704.85	495	510
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	KMCLFAGFQR	99.7%	41.7	25	36.1	2	2	0	1273.62	592	601
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	LLEQYKEESK	99.7%	59.2	25	49.1	14	0	0	1266.66	665	674
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	LNTLLQR	99.7%	60.8	25	24.7	6	0	0	857.52	552	558
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	LQAALDDEEAGGRPAMEPGNGSLDLGGDSAGR	99.7%	107	25	107	0	4	0	3142.43	38	69
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	LSASSLTMESFAFLWAGGR	99.7%	91.6	25	81.8	2	0	0	2047.00	306	324
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	MCLFAGFQR	99.7%	67	25	65	18	0	0	1145.52	593	601
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	MMVAGFK	98.8%	34.7	25	20.5	3	0	0	815.38	537	543
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	MMVAGFKK	98.8%	34.9	25	27.1	1	0	0	911.48	537	544
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	NFILDQTNVSAAAQR	99.7%	146	25	127	22	2	0	1647.84	576	590
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	NGQDLGVAFK	99.7%	65.1	25	62.7	7	0	0	1048.54	424	433
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	RNFILDQTNVSAAAQR	99.7%	44.5	25	37.4	0	2	0	1803.95	575	590
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	SSGPTSLFAVTVAPPGAR	99.7%	65.6	25	60.3	13	3	0	1714.91	187	204
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	TCNCETEDYGEK	99.7%	65	25	65	2	0	0	1505.55	388	399
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	VCFEMK	95.4%	28.9	25	22.1	1	0	0	829.36	334	339
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	VSELKEELK	99.7%	43.6	25	21.3	2	0	0	1074.60	13	21
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	VTEKIPVR	98.9%	35.3	25	29.6	1	0	0	941.58	340	347
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	209	0.20%	34.7%	YNILGTNTIMDK	99.7%	86.6	25	69.5	19	0	0	1382.70	525	536
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	13	14	46	0.04%	21.1%	AIVICPTDEDLKDR	95.6%	23.1	25	23.1	0	1	0	1644.83	528	541
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	13	14	46	0.04%	21.1%	EALGGQALYPHVLVK	99.7%	71.1	25	58.2	6	0	0	1594.90	361	375
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	13	14	46	0.04%	21.1%	HLPSTEPDPHVVR	99.7%	42	25	39.7	0	6	0	1483.77	271	283
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	13	14	46	0.04%	21.1%	INEEISVK	99.7%	42.7	25	27.3	3	0	0	931.51	263	270
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	13	14	46	0.04%	21.1%	NCAVEFNFGQR	99.7%	64.7	25	64.7	4	0	0	1341.60	376	386
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	13	14	46	0.04%	21.1%	NPPGASTYNK	99.5%	39.5	25	36.9	4	0	0	1048.51	722	731
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	13	14	46	0.04%	21.1%	NYILDQTNVYGSAQR	99.7%	138	25	129	6	0	0	1741.85	501	515
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	13	14	46	0.04%	21.1%	QGAPTSFLPPEASQLKPDR	99.7%	50.3	25	50.3	0	2	0	2039.06	147	165
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	13	14	46	0.04%	21.1%	QNQFYDTQVIK	99.7%	41.1	25	1.84	2	0	0	1383.69	107	117
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	13	14	46	0.04%	21.1%	RPLEMEQQQAYRPEMK	99.2%	30	25	25.4	0	1	0	2065.98	127	142
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	13	14	46	0.04%	21.1%	TDEEGKDVPDHAVLEMK	99.7%	38.9	25	38.9	0	1	0	1928.89	546	562
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	13	14	46	0.04%	21.1%	VCFEMK	95.4%	28.9	25	22.1	1	0	0	829.36	257	262
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	13	14	46	0.04%	21.1%	WDVLIQQATQCLNR	99.7%	103	25	89.7	5	0	0	1744.88	477	490

Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	13	14	46	0.04%	21.1%	YNILGTNAIMDK	99.7%	50.1	25	48.6	5	0	0	1368.68	450	461
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	15	18	38	0.04%	21.2%	ANFSLPEK	99.7%	59.8	25	40	2	0	0	905.47	594	601
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	15	18	38	0.04%	21.2%	DLLVQQASQCLSK	99.7%	115	25	110	3	0	0	1489.77	509	521
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	15	18	38	0.04%	21.2%	DRYGGQPLFSEK	99.1%	36	25	30	2	0	0	1396.69	262	273
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	15	18	38	0.04%	21.2%	EGCTEVSLLR	99.7%	53.5	25	37	4	0	0	1163.57	306	315
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	15	18	38	0.04%	21.2%	EVEGDDVPESIMLEMK	99.7%	88.4	25	87.3	2	0	0	1820.83	578	593
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	15	18	38	0.04%	21.2%	FPTLWSGAR	99.7%	49.8	25	40.6	1	0	0	1034.54	274	282
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	15	18	38	0.04%	21.2%	GLEEPEMDPK	99.7%	45	25	43.3	4	0	0	1144.52	497	506
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	15	18	38	0.04%	21.2%	MKGLEEPEMDPK	99.7%	46.2	25	46.2	1	0	0	1435.64	495	506
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	15	18	38	0.04%	21.2%	NFILDQCNVYNSGQR	99.7%	107	25	104	2	0	0	1827.84	532	546
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	15	18	38	0.04%	21.2%	NYYGYQGYR	99.7%	47.2	25	42.3	2	0	0	1183.52	739	747
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	15	18	38	0.04%	21.2%	SGDETPGSEVPGDK	99.7%	64.5	25	61.5	2	0	0	1374.60	161	174
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	15	18	38	0.04%	21.2%	TIEECEVILMVGLPGSGK	99.7%	58.8	25	56	2	0	0	1931.98	448	465
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	15	18	38	0.04%	21.2%	VTQNLPMK	99.7%	59.6	25	35.6	4	0	0	930.51	298	305
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	15	18	38	0.04%	21.2%	YGGQPLFSEK	99.7%	54.3	25	46.3	2	0	0	1125.56	264	273
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	15	18	38	0.04%	21.2%	YNVLGAETVLNQMR	99.7%	106	25	100	5	0	0	1607.82	481	494
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	38	229	0.22%	61.5%	DYFEEYGK	99.7%	45.1	25	43.7	3	0	0	1050.44	130	137
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	38	229	0.22%	61.5%	DYFEEYGKIDTIEIITDR	99.7%	52.4	25	49.3	1	2	0	2220.07	130	147
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	38	229	0.22%	61.5%	EESGKPGAHVTVK	99.7%	74.9	25	61.4	12	1	0	1338.70	100	112
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	38	229	0.22%	61.5%	EESGKPGAHVTVKK	99.4%	38.1	25	30.2	2	0	0	1466.80	100	113
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	38	229	0.22%	61.5%	GFGDGYNGYGGGPGGGNFGGSPGYGGGR	99.7%	124	25	124	4	3	0	2495.04	239	266
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	38	229	0.22%	61.5%	GFGFVTFDDHDPVDK	99.7%	96.7	25	91.5	10	10	0	1695.77	154	168
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	38	229	0.22%	61.5%	GFGFVTFDDHDPVDKIVLQK	99.7%	55.4	25	55.4	2	4	0	2277.16	154	173
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	38	229	0.22%	61.5%	GGGGNFGPGPGSNFR	99.7%	63.8	25	63.8	15	0	0	1377.63	214	228
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	38	229	0.22%	61.5%	GGNFGFGDSR	99.7%	65.3	25	47.8	22	0	0	1013.44	204	213
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	38	229	0.22%	61.5%	IDTIEIITDR	99.7%	101	25	92	9	0	0	1188.65	138	147
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	38	229	0.22%	61.5%	KLFIGGLSFETTEESLR	99.7%	53	25	53	0	2	0	1927.02	22	38
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	38	229	0.22%	61.5%	KLFVGGIK	99.1%	36	25	0	4	0	0	861.56	113	120
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	38	229	0.22%	61.5%	LFIGGLSFETTEESLR	99.7%	108	25	108	29	0	0	1798.92	23	38
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	38	229	0.22%	61.5%	LFVGGIKEDTEEHHLR	99.7%	92.5	25	0	2	8	0	1879.97	114	129
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	38	229	0.22%	61.5%	LTDCVVMR	99.7%	59.7	25	53.3	13	0	0	993.49	47	54
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	38	229	0.22%	61.5%	LTDCVVMRDPASK	99.7%	68.4	25	58.5	6	1	0	1491.73	47	59
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	38	229	0.22%	61.5%	NMGGPYGGGNYGPGGSGGSGGYGGR	99.7%	179	25	179	13	7	0	2205.90	326	350
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	38	229	0.22%	61.5%	NYYEQWGK	99.6%	40.6	25	40.6	7	0	0	1087.48	39	46
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	38	229	0.22%	61.5%	QEMQEVQSSR	99.7%	78.4	25	72.7	10	0	0	1221.55	191	200
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	38	229	0.22%	61.5%	RGFGFVTFDDHDPVDK	99.7%	42	25	42	0	2	0	1851.87	153	168
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	38	229	0.22%	61.5%	TLETVPLER	99.7%	46.2	25	46.2	12	0	0	1057.59	4	12
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	38	229	0.22%	61.5%	YHTINGHNAEVR	99.7%	73.8	25	57.9	5	4	0	1410.69	174	185
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	38	229	0.22%	61.5%	YHTINGHNAEVRK	99.7%	41.2	25	41.2	1	3	0	1538.78	174	186
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	19	26	256	0.24%	45.1%	AAVAGEDGR	99.4%	37.9	25	34.3	2	0	0	845.41	65	73
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	19	26	256	0.24%	45.1%	GDDLQAIKK	99.7%	57.4	25	47.6	4	0	0	987.55	190	198
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	19	26	256	0.24%	45.1%	GDDQLELIK	99.7%	52.9	25	24.7	2	0	0	1030.54	276	284
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	19	26	256	0.24%	45.1%	GDDQLELIKDDEK	99.7%	43.3	25	39.5	2	0	0	1517.73	276	288
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	19	26	256	0.24%	45.1%	GFAFVQYVNER	99.7%	93.2	25	92.9	35	0	0	1329.66	51	61
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	19	26	256	0.24%	45.1%	IVGCSVHK	99.7%	51.6	25	43.3	4	0	0	899.48	43	50
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	19	26	256	0.24%	45.1%	KSDVEAIFSK	99.7%	65.8	25	53.1	20	0	0	1123.60	30	39
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	19	26	256	0.24%	45.1%	LKGDDLQAIK	96.7%	30.3	25	20.2	2	0	0	1100.63	188	197
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	19	26	256	0.24%	45.1%	MIAGQVLDINLAAEPK	99.7%	137	25	137	63	6	0	1682.91	74	89
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	19	26	256	0.24%	45.1%	MYSYPAR	99.7%	43.9	25	36	12	0	0	903.40	136	142
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	19	26	256	0.24%	45.1%	NDKSEEEQSSSSVK	99.7%	82.4	25	78.6	2	2	0	1553.69	230	243
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	19	26	256	0.24%	45.1%	QKVDSLLENLEK	99.7%	68.5	25	56	10	4	0	1415.77	205	216

Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	19	26	256	0.24%	45.1%	SDVEAIFSK	99.7%	61.3	25	55.8	17	0	0	995.50	31	39
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	19	26	256	0.24%	45.1%	SDVEAIFSKYGK	99.7%	48.2	25	45.2	1	0	0	1343.68	31	42
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	19	26	256	0.24%	45.1%	VDSLLENLEK	99.7%	68.1	25	48.5	7	0	0	1159.62	207	216
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	19	26	256	0.24%	45.1%	VDSLLENLEKIEK	99.7%	52.2	25	52.2	2	0	0	1529.84	207	219
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	19	26	256	0.24%	45.1%	VFIGNLNTLVVK	99.7%	104	25	98.8	44	0	0	1316.79	18	29
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	19	26	256	0.24%	45.1%	VFIGNLNTLVVKK	99.7%	64.4	25	64.4	2	2	0	1444.89	18	30
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	19	26	256	0.24%	45.1%	VPPPPPIAR	99.1%	36.2	25	32.8	11	0	0	943.57	143	151
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	11	12	22	0.02%	13.6%	ASGVEGADVVK	99.7%	48	25	31	1	0	0	1031.54	177	187
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	11	12	22	0.02%	13.6%	CNVSFLLSEDGSGK	99.7%	69.4	25	61.3	1	0	0	1512.70	886	899
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	11	12	22	0.02%	13.6%	FLLSESGSGK	99.6%	40.3	25	29	2	0	0	1024.53	442	451
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	11	12	22	0.02%	13.6%	FLSQIESDR	99.7%	66.1	25	49.1	2	0	0	1094.55	786	794
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	11	12	22	0.02%	13.6%	GAALITAVGVR	99.7%	77.8	25	64.9	2	0	0	1027.63	900	910
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	11	12	22	0.02%	13.6%	GAAMVTAVAYR	99.7%	100	25	84	4	0	0	1125.57	452	462
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	11	12	22	0.02%	13.6%	GDFIALDLGGSSFR	99.7%	81.1	25	81.1	2	0	0	1454.73	78	91
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	11	12	22	0.02%	13.6%	HIDLVEGDEGR	99.7%	44.9	25	44.9	2	0	0	1239.60	244	254
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	11	12	22	0.02%	13.6%	LALLQVR	99.7%	43.2	25	23.6	2	0	0	812.54	795	801
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	11	12	22	0.02%	13.6%	LSDETLIDIMTR	99.7%	72.8	25	68.2	2	0	0	1406.72	31	42
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	11	12	22	0.02%	13.6%	SANLVAATLGAILNR	99.7%	92.9	25	78.4	2	0	0	1483.86	382	396
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	6	9	16	0.02%	14.3%	ISICSSDKR	99.2%	36.8	25	29.9	2	0	0	1065.54	405	413
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	6	9	16	0.02%	14.3%	LGCFNLTIK	99.7%	60	25	42.4	2	0	0	1065.58	271	279
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	6	9	16	0.02%	14.3%	LHISPSNMTNQNTNEYLEK	99.7%	34.8	25	34.8	0	1	0	2249.05	343	361
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	6	9	16	0.02%	14.3%	SIRPDNMSEYSK	99.5%	39.4	25	26.7	3	1	0	1426.66	78	89
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	6	9	16	0.02%	14.3%	VMTVSFHK	99.7%	45.9	25	40.7	3	0	0	948.50	193	200
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	6	9	16	0.02%	14.3%	YGEYFPGTGDLR	99.7%	53.5	25	53.5	4	0	0	1374.63	201	212
Histone deacetylase 2	HDAC2	HDAC2_HUMAN	55.4	100.0%	2	2	3	0.00%	10.2%	LGCFNLTVK	99.7%	56.7	25	52.9	2	0	0	1051.56	272	280
Histone deacetylase 2	HDAC2	HDAC2_HUMAN	55.4	100.0%	2	2	3	0.00%	10.2%	SIRPDNMSEYSK	99.5%	39.4	25	26.7	3	1	0	1426.66	79	90
Histone deacetylase 2	HDAC2	HDAC2_HUMAN	55.4	100.0%	2	2	3	0.00%	10.2%	VMTVSFHK	99.7%	45.9	25	40.7	3	0	0	948.50	194	201
Histone deacetylase 2	HDAC2	HDAC2_HUMAN	55.4	100.0%	2	2	3	0.00%	10.2%	YGEYFPGTGDLR	99.7%	53.5	25	53.5	4	0	0	1374.63	202	213
Histone deacetylase 2	HDAC2	HDAC2_HUMAN	55.4	100.0%	2	2	3	0.00%	10.2%	YYAVNFPMR	99.1%	36	25	34.7	1	0	0	1176.55	222	230
Histone deacetylase 8	HDAC8	HDAC8_HUMAN	41.8	99.8%	2	2	3	0.00%	7.4%	FSPGFFPGTGDVSDVGLGK	99.5%	38.9	25	38.7	2	0	0	1883.92	203	221
Histone deacetylase 8	HDAC8	HDAC8_HUMAN	41.8	99.8%	2	2	3	0.00%	7.4%	IQQILNYIK	96.7%	30.3	25	24.8	1	0	0	1132.67	362	370
Histone deacetylase complex subunit SAP18	SAP18	SAP18_HUMAN	17.6	100.0%	4	8	19	0.02%	15.7%	EIGSTMSGR	97.6%	31.7	25	28.9	1	0	0	937.44	105	113
Histone deacetylase complex subunit SAP18	SAP18	SAP18_HUMAN	17.6	100.0%	4	8	19	0.02%	15.7%	GTDDSMTLQSQK	99.7%	72.8	25	49.7	5	0	0	1310.59	115	126
Histone deacetylase complex subunit SAP18	SAP18	SAP18_HUMAN	17.6	100.0%	4	8	19	0.02%	15.7%	KGTDDSMTLQSQK	99.7%	87.6	25	77.7	6	1	0	1438.68	114	126
Histone deacetylase complex subunit SAP18	SAP18	SAP18_HUMAN	17.6	100.0%	4	8	19	0.02%	15.7%	VKEIGSTMSGR	99.7%	62.2	25	52.2	6	0	0	1164.60	103	113
Histone H1.0	H1F0	H10_HUMAN	20.9	100.0%	3	4	9	0.01%	18.6%	TENSTSAPAAKPK	99.7%	51.6	25	49.2	3	0	0	1301.67	2	14
Histone H1.0	H1F0	H10_HUMAN	20.9	100.0%	3	4	9	0.01%	18.6%	VGENADSQIK	99.7%	57	25	49.3	3	0	0	1060.53	60	69
Histone H1.0	H1F0	H10_HUMAN	20.9	100.0%	3	4	9	0.01%	18.6%	YSDMIVAAIQAEK	99.7%	56.5	25	56.5	3	0	0	1438.72	28	40
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	9	12	124	0.12%	30.1%	ALAAAGYDVEK	99.7%	76.9	25	68.9	31	0	0	1107.57	65	75
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	9	12	124	0.12%	30.1%	ALAAAGYDVEKNNSR	99.7%	102	25	102	8	2	0	1578.79	65	79
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	9	12	124	0.12%	30.1%	ASGPPVSELITK	99.7%	81.8	25	74.6	20	0	0	1198.67	35	46
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	9	12	124	0.12%	30.1%	KALAAAGYDVEK	99.7%	70.1	25	63.5	3	2	0	1235.66	64	75
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	9	12	124	0.12%	30.1%	KASGPPVSELITK	99.7%	81.4	25	76.8	18	3	0	1326.76	34	46
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	9	12	124	0.12%	30.1%	SETAPAAPAAPAPAEK	99.7%	65.2	25	0	2	0	0	1478.75	2	17
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	9	12	124	0.12%	30.1%	SGVSLAALK	99.7%	59.8	25	39.9	4	0	0	845.51	55	63
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	9	12	124	0.12%	30.1%	SGVSLAALKK	99.7%	74.3	25	71.5	30	0	0	973.60	55	64
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	9	12	124	0.12%	30.1%	SLVSKGTLVQTK	99.5%	39.1	25	32.9	1	0	0	1260.75	86	97
Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	6	6	24	0.02%	23.5%	AGGSAALSPSK	99.7%	71.3	25	59.6	2	0	0	945.50	24	34
Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	6	6	24	0.02%	23.5%	ALVQNDTLLQVK	99.7%	82.4	25	72.6	6	0	0	1341.77	95	106
Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	6	6	24	0.02%	23.5%	GAPAAATAPAPTAHK	99.7%	80.7	25	80.7	7	0	0	1331.71	129	143
Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	6	6	24	0.02%	23.5%	RGAPAAATAPAPTAHK	99.7%	47.2	25	45.4	0	2	0	1487.81	128	143

Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	6	6	24	0.02%	23.5%	YSQLVVETIR	99.7%	95.6	25	81.3	6	0	0	1207.67	48	57
Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	6	6	24	0.02%	23.5%	YSQLVVETIRR	99.7%	41.6	25	28.9	0	1	0	1363.77	48	58
Histone H2A type 1-B/E	HIST1H2AB	H2A1B_HUMAN	14.1	100.0%	5	6	31	0.03%	35.4%	AGLQFPVGR	99.7%	70.2	25	57.7	18	0	0	944.53	22	30
Histone H2A type 1-B/E	HIST1H2AB	H2A1B_HUMAN	14.1	100.0%	5	6	31	0.03%	35.4%	HLQLAIR	99.3%	37.3	25	26.7	3	0	0	850.53	83	89
Histone H2A type 1-B/E	HIST1H2AB	H2A1B_HUMAN	14.1	100.0%	5	6	31	0.03%	35.4%	HLQLAIRNDEELNK	97.1%	24.7	25	24.7	0	2	0	1692.90	83	96
Histone H2A type 1-B/E	HIST1H2AB	H2A1B_HUMAN	14.1	100.0%	5	6	31	0.03%	35.4%	NDEELNKLLGR	99.7%	69.3	25	53.9	2	0	0	1300.69	90	100
Histone H2A type 1-B/E	HIST1H2AB	H2A1B_HUMAN	14.1	100.0%	5	6	31	0.03%	35.4%	VTIAQGGVLPNIQAVLLPK	99.7%	45.4	25	45.4	5	1	0	1931.17	101	119
Histone H2B type 1-B	HIST1H2BB	H2B1B_HUMAN	14.0	99.8%	2	2	3	0.00%	27.0%	AMGIMNSFVNDIFER	99.7%	114	25	114	19	0	0	1743.82	59	73
Histone H2B type 1-B	HIST1H2BB	H2B1B_HUMAN	14.0	99.8%	2	2	3	0.00%	27.0%	ESYSIYVYK	95.8%	29.2	25	27.1	1	0	0	1151.56	36	44
Histone H2B type 1-B	HIST1H2BB	H2B1B_HUMAN	14.0	99.8%	2	2	3	0.00%	27.0%	KESYSIYVYK	99.7%	60.8	25	53.5	2	0	0	1279.66	35	44
Histone H2B type 1-B	HIST1H2BB	H2B1B_HUMAN	14.0	99.8%	2	2	3	0.00%	27.0%	LLLPGELAK	99.7%	46.3	25	15.3	11	0	0	953.60	101	109
Histone H2B type 1-C/E/F/G/I	HIST1H2BC	H2B1C_HUMAN	13.9	100.0%	4	5	35	0.03%	27.0%	AMGIMNSFVNDIFER	99.7%	114	25	114	19	0	0	1743.82	59	73
Histone H2B type 1-C/E/F/G/I	HIST1H2BC	H2B1C_HUMAN	13.9	100.0%	4	5	35	0.03%	27.0%	ESYSVYVYK	99.6%	40.8	25	40.8	2	0	0	1137.55	36	44
Histone H2B type 1-C/E/F/G/I	HIST1H2BC	H2B1C_HUMAN	13.9	100.0%	4	5	35	0.03%	27.0%	KESYSVYVYK	99.7%	60.5	25	51.9	3	0	0	1265.64	35	44
Histone H2B type 1-C/E/F/G/I	HIST1H2BC	H2B1C_HUMAN	13.9	100.0%	4	5	35	0.03%	27.0%	LLLPGELAK	99.7%	46.3	25	15.3	11	0	0	953.60	101	109
Histone H3.1t	HIST3H3	H31T_HUMAN	15.5	100.0%	4	4	15	0.01%	19.9%	EIAQDFK	97.9%	32.3	25	20.4	3	0	0	850.43	74	80
Histone H3.1t	HIST3H3	H31T_HUMAN	15.5	100.0%	4	4	15	0.01%	19.9%	EIAQDFKTDLR	99.7%	50	25	36.6	5	0	0	1335.69	74	84
Histone H3.1t	HIST3H3	H31T_HUMAN	15.5	100.0%	4	4	15	0.01%	19.9%	STELLIR	99.7%	55.2	25	36.1	5	0	0	831.49	58	64
Histone H3.1t	HIST3H3	H31T_HUMAN	15.5	100.0%	4	4	15	0.01%	19.9%	YRPGTVALR	97.1%	30.8	25	23.7	2	0	0	1032.59	42	50
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	9	57	0.05%	51.5%	DAVTYTEHAK	99.7%	54.1	25	51	11	0	0	1134.54	69	78
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	9	57	0.05%	51.5%	DNIQGITKPAIR	99.7%	70.3	25	61.8	9	4	0	1325.75	25	36
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	9	57	0.05%	51.5%	ISGLIYEETR	99.7%	73.2	25	63.4	11	0	0	1180.62	47	56
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	9	57	0.05%	51.5%	TVTAMDVVYALK	99.7%	75.4	25	65.2	9	0	0	1326.70	81	92
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	9	57	0.05%	51.5%	TVTAMDVVYALKR	99.7%	43.6	25	43.6	3	0	0	1466.80	81	93
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	9	57	0.05%	51.5%	VFLENVIR	99.7%	55.6	25	47.1	10	0	0	989.58	61	68
Histone-binding protein RBBP4	RBBP4	RBBP4_HUMAN	47.7	100.0%	3	3	5	0.00%	6.4%	LMIWDTR	97.0%	30.7	25	27.5	1	0	0	934.48	252	258
Histone-binding protein RBBP4	RBBP4	RBBP4_HUMAN	47.7	100.0%	3	3	5	0.00%	6.4%	TVALWDLR	99.7%	64.4	25	42.2	2	0	0	973.55	297	304
Histone-binding protein RBBP4	RBBP4	RBBP4_HUMAN	47.7	100.0%	3	3	5	0.00%	6.4%	YMPQNPCIIATK	99.2%	37	25	26.5	2	0	0	1435.71	132	143
Hornerin	HRNR	HORN_HUMAN	282.4	100.0%	4	5	25	0.02%	2.7%	GEQHGSSSGSSSSYGQHGSGSR	98.7%	27.9	25	27.9	0	2	0	2122.88	1910	1931
Hornerin	HRNR	HORN_HUMAN	282.4	100.0%	4	5	25	0.02%	2.7%	GPYESGSGHSSGLGHQESR	99.0%	28.9	25	28.9	0	2	0	1928.85	572	590
Hornerin	HRNR	HORN_HUMAN	282.4	100.0%	4	5	25	0.02%	2.7%	GPYESGSGHSSGLGHR	99.7%	60	25	54.4	2	16	0	1584.72	1038	1053
Hornerin	HRNR	HORN_HUMAN	282.4	100.0%	4	5	25	0.02%	2.7%	QSLGHGQHGSGSGQSPSPSR	99.7%	54.1	25	53.4	0	3	0	1947.90	992	1011
Huntingtin	HTT	HD_HUMAN	347.6	100.0%	3	3	4	0.00%	1.2%	AALPSLTNPPSLSPIR	99.7%	48.6	25	48.6	1	0	0	1633.93	1167	1182
Huntingtin	HTT	HD_HUMAN	347.6	100.0%	3	3	4	0.00%	1.2%	LFEPLVIK	98.5%	33.8	25	26.1	2	0	0	958.60	1424	1431
Huntingtin	HTT	HD_HUMAN	347.6	100.0%	3	3	4	0.00%	1.2%	NSAASGLFIQAIQSR	99.7%	52.8	25	44.5	1	0	0	1562.83	1946	1960
Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	HMGCL_HUMAN	34.4	99.8%	2	2	2	0.00%	7.4%	AAQSANISVR	99.7%	51.3	25	37.4	1	0	0	1016.55	156	165
Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	HMGCL_HUMAN	34.4	99.8%	2	2	2	0.00%	7.4%	FPGINYPVLTPNLK	99.6%	39.8	25	26.2	1	0	0	1572.88	98	111
Hydroxysteroid dehydrogenase-like protein 2	HSDL2	HSDL2_HUMAN	45.4	100.0%	3	3	8	0.01%	9.6%	LAGCTVFITGASR	99.7%	96.2	25	78.2	4	0	0	1352.70	8	20
Hydroxysteroid dehydrogenase-like protein 2	HSDL2	HSDL2_HUMAN	45.4	100.0%	3	3	8	0.01%	9.6%	LLGTIYTAAEEIEAVGGK	99.7%	58.6	25	58.6	2	0	0	1834.98	50	67
Hydroxysteroid dehydrogenase-like protein 2	HSDL2	HSDL2_HUMAN	45.4	100.0%	3	3	8	0.01%	9.6%	SGAVEETFR	99.7%	46.5	25	40.6	2	0	0	995.48	307	315
Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	HPRT_HUMAN	24.6	100.0%	6	7	12	0.01%	30.3%	FFADLLDYIK	99.2%	36.6	25	36.6	2	0	0	1244.66	74	83
Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	HPRT_HUMAN	24.6	100.0%	6	7	12	0.01%	30.3%	SIPMTVDFIR	98.0%	32.4	25	17.7	1	0	0	1178.62	92	101
Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	HPRT_HUMAN	24.6	100.0%	6	7	12	0.01%	30.3%	SYCNDQSTGDIK	99.7%	65.3	25	65.3	1	0	0	1387.58	104	115
Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	HPRT_HUMAN	24.6	100.0%	6	7	12	0.01%	30.3%	TMQTLLSLVR	99.7%	71.2	25	40.2	2	0	0	1161.67	142	151
Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	HPRT_HUMAN	24.6	100.0%	6	7	12	0.01%	30.3%	VFIPHGLIMDR	99.7%	40.5	25	37.2	0	4	0	1297.71	35	45
Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	HPRT_HUMAN	24.6	100.0%	6	7	12	0.01%	30.3%	VIGGDDLSTLTGK	99.7%	101	25	92.6	2	0	0	1275.68	116	128
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	21	25	38	0.04%	27.5%	AANSLEAFIFETQDK	99.7%	89.6	25	79.2	2	1	0	1683.82	739	753
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	21	25	38	0.04%	27.5%	AEAGPEGVAPAPEGEK	99.7%	83.5	25	74.4	2	0	0	1508.72	670	685
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	21	25	38	0.04%	27.5%	AEAGPEGVAPAPEGEKK	99.7%	53.6	25	53.6	1	2	0	1636.82	670	686
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	21	25	38	0.04%	27.5%	AVGKEELGK	99.6%	40.1	25	30.4	2	0	0	930.53	399	407
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	21	25	38	0.04%	27.5%	DAVITVPVFFNQAER	99.7%	52.4	25	37.5	2	0	0	1705.89	171	185

Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	21	25	38	0.04%	27.5%	DAVVYPILVEFTR	99.7%	75.2	25	75.2	2	0	0	1521.83	439	451
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	21	25	38	0.04%	27.5%	EAGMQPQLQIR	97.6%	31.7	25	22.7	1	0	0	1270.66	252	262
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	21	25	38	0.04%	27.5%	EVEEEPGIHSLK	99.7%	49.6	25	38.6	1	0	0	1366.69	452	463
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	21	25	38	0.04%	27.5%	FFGDSAASMAIK	99.7%	59.4	25	53.5	2	0	0	1244.60	80	91
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	21	25	38	0.04%	27.5%	KYPDYESK	95.4%	29	25	24.3	1	0	0	1029.49	530	537
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	21	25	38	0.04%	27.5%	LAGLFNEQR	99.7%	63.6	25	55.4	2	0	0	1047.56	283	291
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	21	25	38	0.04%	27.5%	LGNTISSLFGGGTTPDAK	99.7%	110	25	110	2	0	0	1735.89	577	594
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	21	25	38	0.04%	27.5%	LYQPEYQEVSTEEQREEISGK	99.7%	34.9	25	32.2	0	2	0	2542.19	754	774
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	21	25	38	0.04%	27.5%	MGPYPQR	98.6%	34	25	23.4	2	0	0	864.40	473	479
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	21	25	38	0.04%	27.5%	NINADEAAAMGAVYQAAALSK	99.7%	73.7	25	73.7	1	0	0	2079.02	408	428
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	21	25	38	0.04%	27.5%	TLGGLEMELR	99.7%	54.9	25	49.1	3	0	0	1118.59	269	278
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	21	25	38	0.04%	27.5%	VAIVKPGVPMEIVLNK	95.5%	23.1	25	21.5	0	1	0	1723.02	47	62
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	21	25	38	0.04%	27.5%	VEFEELCADLFER	99.7%	76.8	25	76.7	2	0	0	1656.76	346	358
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	21	25	38	0.04%	27.5%	VESVFETLVEDSAEEESTLTK	99.7%	61	25	61	1	0	0	2342.11	556	576
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	21	25	38	0.04%	27.5%	VLQLINDNTATALSYGVFR	99.7%	118	25	113	2	0	0	2095.12	199	217
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	21	25	38	0.04%	27.5%	YFQHLLGK	96.5%	30.1	25	30.1	1	0	0	1005.55	99	106
Ig kappa chain V-II region RPMI 6410	IGKV2-30	KV206_HUMAN	14.7	100.0%	3	4	317	0.30%	18.0%	FSGSGSGTDFTLK	99.7%	103	25	0	299	0	0	1303.62	87	99
Ig kappa chain V-II region RPMI 6410	IGKV2-30	KV206_HUMAN	14.7	100.0%	3	4	317	0.30%	18.0%	FSGSGSGTDFTLKISR	99.7%	87.2	25	0	4	13	0	1659.83	87	102
Ig kappa chain V-II region RPMI 6410	IGKV2-30	KV206_HUMAN	14.7	100.0%	3	4	317	0.30%	18.0%	LIYKVSNR	97.1%	30.9	25	19.1	1	0	0	992.59	72	79
Immunoglobulin-binding protein 1	IGBP1	IGBP1_HUMAN	39.2	100.0%	2	2	4	0.00%	6.8%	LPELFETGR	99.7%	44.9	25	39.5	2	0	0	1061.56	12	20
Immunoglobulin-binding protein 1	IGBP1	IGBP1_HUMAN	39.2	100.0%	2	2	4	0.00%	6.8%	YLLVPAFQGALTMK	99.5%	39.2	25	36.2	2	0	0	1567.86	78	91
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	7	8	15	0.01%	17.4%	ASLSLIEK	99.6%	40.1	25	32.8	1	0	0	860.51	487	494
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	7	8	15	0.01%	17.4%	EATWTMSNITAGR	99.7%	64.6	25	59.5	4	0	0	1437.68	354	366
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	7	8	15	0.01%	17.4%	FVSFLGR	98.0%	32.5	25	23	2	0	0	825.46	124	130
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	7	8	15	0.01%	17.4%	GINSSNVENQLQATQAAR	99.7%	107	25	98.4	2	0	0	1900.95	84	101
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	7	8	15	0.01%	17.4%	NLTWTLSNLCR	99.7%	69.9	25	0	2	0	0	1377.69	228	238
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	7	8	15	0.01%	17.4%	NPAPPIDAVEQILPTLVR	99.7%	78.5	25	78.5	2	0	0	1943.10	241	258
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	7	8	15	0.01%	17.4%	NVSSFPDDATSPLQENR	99.7%	107	25	99.1	2	0	0	1876.87	52	68
Importin subunit alpha-4	KPNA3	IMA4_HUMAN	57.8	99.8%	2	2	4	0.00%	5.2%	DSQVVQVVLDGLK	99.7%	42.7	25	29.4	2	0	0	1399.78	424	436
Importin subunit alpha-4	KPNA3	IMA4_HUMAN	57.8	99.8%	2	2	4	0.00%	5.2%	EAAWAISNLTISGR	99.7%	62.9	25	62.5	2	0	0	1488.78	387	400
Importin subunit alpha-5	KPNA1	IMA5_HUMAN	60.2	100.0%	5	5	9	0.01%	14.1%	EAAWAITNATSGGSAEQIK	99.7%	141	25	129	1	0	0	1904.93	399	417
Importin subunit alpha-5	KPNA1	IMA5_HUMAN	60.2	100.0%	5	5	9	0.01%	14.1%	EACWTISNITAGNR	99.7%	61.1	25	57.2	2	0	0	1592.75	357	370
Importin subunit alpha-5	KPNA1	IMA5_HUMAN	60.2	100.0%	5	5	9	0.01%	14.1%	EPNPPIDEVISTPGVVAR	99.7%	78.4	25	78.4	2	0	0	1890.00	113	130
Importin subunit alpha-5	KPNA1	IMA5_HUMAN	60.2	100.0%	5	5	9	0.01%	14.1%	IVQVALNGLENILR	99.6%	40.5	25	40.5	2	0	0	1551.92	439	452
Importin subunit alpha-5	KPNA1	IMA5_HUMAN	60.2	100.0%	5	5	9	0.01%	14.1%	NAVWALSNLCR	99.7%	46.5	25	46.5	2	0	0	1303.66	231	241
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	20	23	48	0.05%	28.9%	AAVENLPTFLVELSR	99.7%	105	25	102	7	0	0	1658.91	28	42
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	20	23	48	0.05%	28.9%	ANFDKESER	99.7%	63.3	25	54.6	2	0	0	1095.51	207	215
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	20	23	48	0.05%	28.9%	DTAAWTVGR	99.7%	57	25	45.4	1	0	0	976.48	426	434
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	20	23	48	0.05%	28.9%	ESCLEAYTGIVQGLK	99.7%	99.8	25	94	2	0	0	1667.83	763	777
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	20	23	48	0.05%	28.9%	GALQYLVPILTQTLTK	99.7%	60.1	25	60.1	2	0	0	1759.04	317	332
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	20	23	48	0.05%	28.9%	GDQENVHPDVMLVQPR	99.7%	43.3	25	43.3	0	1	0	1849.89	778	793
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	20	23	48	0.05%	28.9%	LAATNALLNSLEFTK	99.7%	114	25	109	2	0	0	1605.88	192	206
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	20	23	48	0.05%	28.9%	LLETTDRPDGHQNNLR	99.7%	44.8	25	41.5	0	2	0	1878.94	510	525
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	20	23	48	0.05%	28.9%	NSLTSKDPDIK	98.9%	35.4	25	7.86	2	0	0	1217.64	63	73
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	20	23	48	0.05%	28.9%	SDYDMVDYLNELR	99.7%	86.8	25	86.8	2	0	0	1632.72	750	762
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	20	23	48	0.05%	28.9%	SNEILTAIIQGMR	99.7%	98.4	25	89.5	4	0	0	1445.78	170	182
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	20	23	48	0.05%	28.9%	SSAYESLMEIVK	99.7%	90.6	25	86.2	4	0	0	1356.67	526	537
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	20	23	48	0.05%	28.9%	TTLVIMER	99.7%	46.1	25	24.3	3	0	0	962.53	550	557
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	20	23	48	0.05%	28.9%	TVSPDRLELEAAQK	99.7%	50.2	25	42.4	2	0	0	1556.83	10	23
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	20	23	48	0.05%	28.9%	VAAGLQIK	99.7%	45.2	25	33.1	2	0	0	799.50	55	62
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	20	23	48	0.05%	28.9%	VAALQNLVK	99.5%	39	25	33	2	0	0	955.59	235	243

Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	20	23	48	0.05%	28.9%	VLANPGNSQVAR	99.7%	77.8	25	70.7	2	0	0	1225.66	43	54
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	20	23	48	0.05%	28.9%	WLAIDANAR	97.9%	32.1	25	26.8	2	0	0	1029.55	80	88
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	20	23	48	0.05%	28.9%	YLEVVLNTLQQASQAQVDK	99.7%	104	25	104	2	0	0	2147.13	731	749
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	20	23	48	0.05%	28.9%	YMEAFKPFLGIGLK	99.7%	66.1	25	66.1	2	0	0	1613.88	646	659
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	11	13	20	0.02%	12.8%	ALLTFYHVTK	98.1%	32.7	25	29.7	2	0	0	1192.67	147	156
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	11	13	20	0.02%	12.8%	FIVQCMNLIK	99.7%	44.1	25	34.7	1	0	0	1265.67	316	325
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	11	13	20	0.02%	12.8%	IFQNMSPLLELSSENLR	99.7%	87.4	25	87.4	4	0	0	2007.02	688	704
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	11	13	20	0.02%	12.8%	LTVDDFEFR	99.7%	53.9	25	50.3	2	0	0	1141.55	541	549
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	11	13	20	0.02%	12.8%	MAFFTYPTLTEICR	99.7%	50.8	25	42.9	2	0	0	1749.83	354	367
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	11	13	20	0.02%	12.8%	MDNITQPER	99.7%	48.7	25	40.7	1	0	0	1103.52	836	844
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	11	13	20	0.02%	12.8%	NFEDSSPETLEAHK	99.7%	72	25	61.2	2	0	0	1603.72	338	351
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	11	13	20	0.02%	12.8%	NYAYKPSK	95.6%	29.1	25	17.8	1	0	0	970.50	330	337
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	11	13	20	0.02%	12.8%	SIGTDNVCR	99.7%	53.7	25	47.7	2	0	0	1021.47	255	263
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	11	13	20	0.02%	12.8%	VAPHALSEEEK	97.9%	32.3	25	25.3	1	0	0	1209.61	77	87
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	11	13	20	0.02%	12.8%	VTEDEEPPTEQDKR	99.7%	55.6	25	54.8	1	1	0	1672.77	905	918
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	47	0.04%	21.4%	ACYALENFVENLGPK	99.7%	99.1	25	99.1	2	0	0	1724.83	458	472
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	47	0.04%	21.4%	AQELQAVLGLS	99.7%	61.6	25	43	2	0	0	1128.63	1071	1081
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	47	0.04%	21.4%	ATEQLQIVLR	99.7%	67.2	25	32.7	2	0	0	1170.68	24	33
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	47	0.04%	21.4%	DNICGALAR	99.7%	45.2	25	38.2	2	0	0	989.48	959	967
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	47	0.04%	21.4%	ELLLPDTER	98.8%	34.6	25	28.1	1	0	0	1085.58	12	20
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	47	0.04%	21.4%	EVMPLLLAYLK	99.7%	63.3	25	54.9	6	0	0	1289.75	435	445
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	47	0.04%	21.4%	GLEDPSQVVR	99.7%	59.4	25	31.2	2	0	0	1099.57	402	411
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	47	0.04%	21.4%	ILCCLTFLVK	99.7%	41.9	25	38.7	2	0	0	1266.70	267	276
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	47	0.04%	21.4%	LAELCGVLK	99.7%	55.8	25	40.6	3	0	0	1002.57	793	801
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	47	0.04%	21.4%	LIMAMQTLIPIDEAK	99.7%	53.2	25	46.7	4	0	0	1686.92	206	220
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	47	0.04%	21.4%	LLECPHLNVR	99.7%	42.8	25	34.4	1	0	0	1250.67	705	714
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	47	0.04%	21.4%	LLMASPTR	96.7%	30.3	25	18.4	2	0	0	904.49	968	975
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	47	0.04%	21.4%	LLNETLGEVGSPGLLFYSLR	99.7%	82.3	25	82.3	1	0	0	2178.18	163	182
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	47	0.04%	21.4%	LLPVLLSTAQEADPEVR	99.7%	84.9	25	80.2	2	0	0	1851.02	900	916
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	47	0.04%	21.4%	NVALGNAIR	98.6%	34.1	25	25.8	1	0	0	927.54	256	264
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	47	0.04%	21.4%	QFAAVLTR	99.4%	38.4	25	17.2	2	0	0	905.52	55	62
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	47	0.04%	21.4%	SCGTLTLKPPGR	97.6%	31.6	25	30.3	1	0	0	1286.69	781	792
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	47	0.04%	21.4%	SLILTALQR	99.7%	59.8	25	47.3	3	0	0	1014.63	82	90
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	47	0.04%	21.4%	TLTTMAPYLSTEDVPLAR	99.7%	76.7	25	76.7	4	0	0	1995.01	183	200
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	47	0.04%	21.4%	VVPSYMQAVNR	99.7%	46.2	25	42.8	4	0	0	1279.65	751	761
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	21	24	71	0.07%	24.2%	ATAAFILANEHNVALFK	99.7%	62.2	25	53.4	2	0	0	1829.99	196	212
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	21	24	71	0.07%	24.2%	EFQQYLPVVMGPLMK	99.7%	48.7	25	43.8	2	0	0	1779.92	618	632
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	21	24	71	0.07%	24.2%	EGFVEYTEQVVK	99.7%	67.8	25	57.6	2	0	0	1427.71	694	705
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	21	24	71	0.07%	24.2%	FLFDSVSSQNVGLR	99.7%	95.8	25	93.1	7	0	0	1568.81	135	148
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	21	24	71	0.07%	24.2%	FMQDASDVMQLLLK	99.7%	136	25	122	5	0	0	1638.82	573	586
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	21	24	71	0.07%	24.2%	FVPYYDLFMPSLK	99.7%	64.5	25	0	8	0	0	1635.81	527	539
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	21	24	71	0.07%	24.2%	HIVENAVQK	97.9%	32.2	25	29.9	2	0	0	1037.57	540	548
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	21	24	71	0.07%	24.2%	KQAEETYENIPGQSK	99.3%	30.2	25	26.8	0	1	0	1721.83	27	41
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	21	24	71	0.07%	24.2%	LQELIQK	99.4%	38.2	25	8.14	2	0	0	871.52	497	503
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	21	24	71	0.07%	24.2%	LVLEQVVTSIASVADTAEEK	99.7%	91.1	25	86.9	2	2	0	2102.12	507	526
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	21	24	71	0.07%	24.2%	QAEETYENIPGQSK	99.7%	65.4	25	55	1	0	0	1593.74	28	41
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	21	24	71	0.07%	24.2%	QMAAVLLR	99.7%	54.6	25	35.2	2	0	0	901.53	60	67
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	21	24	71	0.07%	24.2%	SLLIPYLDNLVK	99.7%	43.9	25	24.1	2	0	0	1387.82	476	487
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	21	24	71	0.07%	24.2%	SLVEIADTVPK	99.7%	84.4	25	72.4	7	0	0	1171.66	239	249
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	21	24	71	0.07%	24.2%	STACQMLVCYAK	99.7%	65.2	25	65.2	2	0	0	1431.64	679	690
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	21	24	71	0.07%	24.2%	TIECISLIGLAVGK	99.7%	99.9	25	96.1	7	0	0	1473.83	557	570

Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	21	24	71	0.07%	24.2%	VAAAESMPLLLECAR	99.7%	64.3	25	62.6	3	0	0	1630.83	721	735
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	21	24	71	0.07%	24.2%	VCDIAAELAR	99.7%	68.9	25	43.1	5	0	0	1117.57	109	118
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	21	24	71	0.07%	24.2%	VIAALLQTMEDQGNQR	99.7%	114	25	113	3	0	0	1786.91	442	457
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	21	24	71	0.07%	24.2%	VQAHAAAALINFTEDCPK	99.7%	37.1	25	37.1	0	2	0	1955.96	458	475
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	21	24	71	0.07%	24.2%	VSDILHSIFSSYK	99.7%	67.3	25	60.2	2	0	0	1495.78	842	854
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	23	62	0.06%	23.0%	AFAVGVQQVLLK	99.7%	88.4	25	74.5	7	0	0	1272.77	295	306
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	23	62	0.06%	23.0%	AIFQTIQNR	99.7%	50.7	25	41.4	5	0	0	1090.60	964	972
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	23	62	0.06%	23.0%	DGALHMIGSLAEILLK	99.7%	38.6	25	34.4	0	2	0	1696.93	430	445
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	23	62	0.06%	23.0%	ENIVEAIIHSPELIR	99.7%	62.8	25	55.7	2	2	0	1732.96	93	107
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	23	62	0.06%	23.0%	ETENDDLTNVIQK	99.7%	67.5	25	61.2	4	0	0	1518.73	552	564
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	23	62	0.06%	23.0%	EYNEFAEVFLK	99.7%	70.8	25	68.5	4	0	0	1388.67	284	294
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	23	62	0.06%	23.0%	FIQLLSDQSDQSVLIQK	99.7%	120	25	116	2	0	0	1962.05	185	201
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	23	62	0.06%	23.0%	GIDQCIPLFVEAALER	99.7%	65.6	25	63.3	3	0	0	1830.94	753	768
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	23	62	0.06%	23.0%	GTMDPALR	99.0%	35.5	25	26.5	4	0	0	876.42	12	19
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	23	62	0.06%	23.0%	LLEVIILQCK	99.7%	66.6	25	66.6	4	0	0	1228.73	741	750
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	23	62	0.06%	23.0%	QLQDIATLADQR	99.7%	46.2	25	31.8	3	0	0	1371.72	991	1002
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	23	62	0.06%	23.0%	SDQNLQTALELTR	99.7%	77.6	25	61.2	4	0	0	1488.77	490	502
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	23	62	0.06%	23.0%	SPLVAAMQHFLPVLK	99.7%	52.5	25	52.5	1	0	0	1650.94	168	182
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	23	62	0.06%	23.0%	TMGFCYQILTEPNADPR	99.7%	56.2	25	56.2	2	0	0	2012.92	411	427
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	23	62	0.06%	23.0%	VLTGVAGEDAECHAAK	99.7%	106	25	106	4	1	0	1627.77	725	740
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	23	62	0.06%	23.0%	VQLTTCIHHIIK	97.1%	24.6	25	19.9	0	1	0	1462.82	108	119
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	23	62	0.06%	23.0%	WALHILAR	99.7%	54.6	25	48.5	2	0	0	979.58	263	270
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	23	62	0.06%	23.0%	YGSPGNVSK	98.1%	32.7	25	25.2	2	0	0	908.45	275	283
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	23	62	0.06%	23.0%	YLEMIYSMCK	99.7%	58.8	25	51.2	3	0	0	1337.59	714	723
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	5	5	7	0.01%	6.6%	ETENDDVTNVIQK	99.7%	59.5	25	56.3	1	0	0	1504.71	553	565
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	5	5	7	0.01%	6.6%	EYFEFSEFFLK	99.6%	39.8	25	39.8	1	0	0	1485.69	285	295
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	5	5	7	0.01%	6.6%	IAAENELNQSYK	99.7%	70	25	70	1	0	0	1379.68	20	31
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	5	5	7	0.01%	6.6%	IINFAPSLLR	99.7%	42.5	25	36.2	2	0	0	1143.69	32	41
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	5	5	7	0.01%	6.6%	LLEVIILQCK	99.7%	66.6	25	66.6	4	0	0	1228.73	741	750
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	5	5	7	0.01%	6.6%	TYAVGIQQVLLK	99.7%	88.9	25	81.8	2	0	0	1332.79	296	307
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	12	15	26	0.02%	14.9%	EALVDTLTGILSPVQEVR	99.7%	94.4	25	91.4	2	0	0	1940.07	23	40
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	12	15	26	0.02%	14.9%	ELGENLDQILR	99.7%	44.2	25	38.5	1	0	0	1299.69	777	787
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	12	15	26	0.02%	14.9%	EVTDTQMPLVAPVILPEMYK	99.7%	52.2	25	51.8	3	0	0	2274.18	176	195
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	12	15	26	0.02%	14.9%	FRPPETTER	99.1%	36.4	25	22.3	2	0	0	1132.57	96	104
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	12	15	26	0.02%	14.9%	IFTMAEVYGIR	99.7%	72.2	25	64.8	2	0	0	1299.68	196	206
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	12	15	26	0.02%	14.9%	LIINELSNVMEANAAR	99.7%	122	25	113	3	0	0	1757.92	920	935
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	12	15	26	0.02%	14.9%	LIPTLVSIMQAPADK	99.7%	74.6	25	74.6	4	0	0	1612.90	647	661
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	12	15	26	0.02%	14.9%	QLASVILK	99.7%	53.1	25	27.5	1	0	0	871.56	75	82
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	12	15	26	0.02%	14.9%	VKGEEIYSMDEGIR	99.3%	30.3	25	30.3	0	1	0	1641.78	883	896
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	12	15	26	0.02%	14.9%	VSSVALCK	99.4%	37.8	25	20.2	2	0	0	863.47	858	865
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	12	15	26	0.02%	14.9%	WTNIPLLVK	99.2%	36.5	25	23.2	1	0	0	1083.66	908	916
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	12	15	26	0.02%	14.9%	YSNDPVVASLAQDIFK	99.7%	93	25	83.1	4	0	0	1766.90	616	631
Inactive hydroxysteroid dehydrogenase-like protein 1	HSDL1	HSDL1_HUMAN	37.0	100.0%	4	4	7	0.01%	10.9%	AYAEELASR	99.7%	62.4	25	55.9	2	0	0	1009.49	82	90
Inactive hydroxysteroid dehydrogenase-like protein 1	HSDL1	HSDL1_HUMAN	37.0	100.0%	4	4	7	0.01%	10.9%	AYLDHFSR	99.2%	36.8	25	27.8	2	0	0	1008.49	223	230
Inactive hydroxysteroid dehydrogenase-like protein 1	HSDL1	HSDL1_HUMAN	37.0	100.0%	4	4	7	0.01%	10.9%	GLNIILISR	99.7%	71.8	25	66.8	2	0	0	998.64	91	99
Inactive hydroxysteroid dehydrogenase-like protein 1	HSDL1	HSDL1_HUMAN	37.0	100.0%	4	4	7	0.01%	10.9%	NEEKLQVVAK	99.7%	41.4	25	30.5	1	0	0	1157.65	100	109
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	4	4	7	0.01%	24.2%	IDLPEYQGEPDEISIQK	99.7%	55.7	25	54.7	1	0	0	1973.97	40	56
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	4	4	7	0.01%	24.2%	IVFVTGNAK	99.7%	42.9	25	36.7	2	0	0	948.55	10	18
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	4	4	7	0.01%	24.2%	KIVFVTGNAK	98.7%	34.4	25	34.4	2	0	0	1076.65	9	18
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	4	4	7	0.01%	24.2%	SAYALCTFALSTGDPSQPVR	99.7%	68.6	25	68.6	2	0	0	2141.03	111	130
Inosine-5'-monophosphate dehydrogenase 2	IMPDH2	IMDH2_HUMAN	55.8	100.0%	3	3	5	0.00%	7.4%	EANEILQR	99.7%	41.8	25	21.7	2	0	0	972.51	196	203

Inosine-5'-monophosphate dehydrogenase 2	IMPDH2	IMDH2_HUMAN	55.8	100.0%	3	3	5	0.00%	7.4%	TSSAQVEGGVHSLHSYEK	99.6%	33.4	25	31	0	1	0	1915.91	494	511
Inosine-5'-monophosphate dehydrogenase 2	IMPDH2	IMDH2_HUMAN	55.8	100.0%	3	3	5	0.00%	7.4%	VAQGVSGAVQDK	99.7%	68.4	25	57.2	2	0	0	1158.61	439	450
Insulin receptor substrate 4	IRS4	IRS4_HUMAN	133.8	100.0%	8	8	13	0.01%	7.6%	AAVSAFPTDSLER	99.7%	59.4	25	51.1	2	0	0	1363.69	1098	1110
Insulin receptor substrate 4	IRS4	IRS4_HUMAN	133.8	100.0%	8	8	13	0.01%	7.6%	ANPLSLDSAR	99.7%	58.2	25	50.4	2	0	0	1043.55	985	994
Insulin receptor substrate 4	IRS4	IRS4_HUMAN	133.8	100.0%	8	8	13	0.01%	7.6%	GAQDVAGGSNPGAHNPSANLAR	98.5%	27.1	25	27.1	0	1	0	2060.99	1177	1198
Insulin receptor substrate 4	IRS4	IRS4_HUMAN	133.8	100.0%	8	8	13	0.01%	7.6%	LAPSPARPR	99.0%	35.8	25	35.8	2	0	0	964.57	436	444
Insulin receptor substrate 4	IRS4	IRS4_HUMAN	133.8	100.0%	8	8	13	0.01%	7.6%	LETADAPAR	97.8%	32	25	17.7	1	0	0	943.48	100	108
Insulin receptor substrate 4	IRS4	IRS4_HUMAN	133.8	100.0%	8	8	13	0.01%	7.6%	LLQEEEQER	99.7%	48.9	25	30.6	3	0	0	1173.57	1074	1082
Insulin receptor substrate 4	IRS4	IRS4_HUMAN	133.8	100.0%	8	8	13	0.01%	7.6%	SQSFFAAAR	99.5%	38.6	25	29.5	1	0	0	984.49	1089	1097
Insulin receptor substrate 4	IRS4	IRS4_HUMAN	133.8	100.0%	8	8	13	0.01%	7.6%	WFQPVANAADAEAVR	99.7%	83.5	25	78.5	1	0	0	1644.81	1162	1176
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	24	39	142	0.14%	46.6%	AIETFSGK	99.7%	47.9	25	43.2	2	0	0	852.45	53	60
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	24	39	142	0.14%	46.6%	AISVHSTPEGCSSACK	99.7%	79.8	25	79.8	4	5	0	1690.75	243	258
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	24	39	142	0.14%	46.6%	DQTPDENDQVIVK	99.7%	89.2	25	80.8	4	0	0	1500.72	526	538
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	24	39	142	0.14%	46.6%	EEVKLETHIR	99.7%	67.1	25	57.9	3	2	0	1253.68	484	493
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	24	39	142	0.14%	46.6%	IIGHFYASQMAQR	99.7%	70.8	25	64.8	8	8	0	1521.76	539	551
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	24	39	142	0.14%	46.6%	ILAHNNFVGR	99.7%	57.2	25	52.4	4	0	0	1140.63	281	290
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	24	39	142	0.14%	46.6%	IRDILAQVK	99.7%	52	25	29.5	4	0	0	1055.66	553	561
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	24	39	142	0.14%	46.6%	ISYSGQFLVK	99.7%	69.5	25	64.7	2	0	0	1141.63	27	36
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	24	39	142	0.14%	46.6%	ITISSLQDLTLYNPER	99.7%	68.4	25	68.4	6	0	0	1862.99	310	325
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	24	39	142	0.14%	46.6%	LEIEHSVPK	99.6%	39.9	25	36.4	2	0	0	1051.58	68	76
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	24	39	142	0.14%	46.6%	LKEENFFGPK	99.7%	50.1	25	47.9	2	4	0	1208.63	474	483
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	24	39	142	0.14%	46.6%	LLVPTQYVGAIIGK	99.7%	101	25	100	13	2	0	1471.89	200	213
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	24	39	142	0.14%	46.6%	LNGHQLENHALK	99.7%	35	25	35	2	2	0	1373.73	139	150
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	24	39	142	0.14%	46.6%	LYIGNLNESVTPADLEK	99.7%	104	25	90.4	5	0	0	1875.97	4	20
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	24	39	142	0.14%	46.6%	MILEIMHK	99.7%	49.4	25	39.6	5	0	0	1014.55	259	266
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	24	39	142	0.14%	46.6%	MVIITGPPEAQFK	99.7%	72.7	25	61.3	9	0	0	1430.77	453	465
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	24	39	142	0.14%	46.6%	QGSPVAAGAPAK	99.7%	54	25	51.5	4	0	0	1053.57	179	190
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	24	39	142	0.14%	46.6%	QQQVDIPLR	99.7%	66.8	25	53.3	8	0	0	1096.61	191	199
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	24	39	142	0.14%	46.6%	RLEIEHSVPK	99.7%	35.1	25	31.7	3	4	0	1207.68	67	76
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	24	39	142	0.14%	46.6%	SGYAFVDCPDEHWAMK	99.7%	79.8	25	77.1	3	3	0	1912.80	37	52
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	24	39	142	0.14%	46.6%	TADEVPLK	99.7%	45.4	25	33	4	0	0	872.47	273	280
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	24	39	142	0.14%	46.6%	TVNELQNLTAAEVVVPR	99.7%	111	25	94.5	6	4	0	1853.01	509	525
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	24	39	142	0.14%	46.6%	VSYIPDEQIAQGPENGR	99.7%	81.1	25	81.1	4	0	0	1872.91	151	167
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	24	39	142	0.14%	46.6%	VSYIPDEQIAQGPENGRR	99.7%	57.1	25	54.9	1	0	0	2029.01	151	168
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	11	13	39	0.04%	29.4%	DQTPDENEEVIVR	99.7%	66.9	25	53	2	0	0	1543.72	548	560
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	11	13	39	0.04%	29.4%	IAPAEGPDVSER	99.7%	49.8	25	48	4	0	0	1240.62	463	474
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	11	13	39	0.04%	29.4%	IIGHFFASQTAQR	99.7%	52.1	25	44.7	3	2	0	1475.78	561	573
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	11	13	39	0.04%	29.4%	ILVPTQFVGAIIGK	99.7%	106	25	0	5	0	0	1455.89	198	211
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	11	13	39	0.04%	29.4%	ISYIPDEEVSSPSPPQR	99.7%	77.2	25	77.2	4	0	0	1900.93	152	168
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	11	13	39	0.04%	29.4%	ITISSLQDLSIYNPER	99.7%	75.3	25	73.3	2	0	0	1848.97	308	323
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	11	13	39	0.04%	29.4%	LAEEIPLK	99.1%	36.3	25	36.3	3	0	0	912.54	271	278
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	11	13	39	0.04%	29.4%	LSGHQFENYSFK	99.5%	39.5	25	37.9	3	4	0	1456.69	140	151
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	11	13	39	0.04%	29.4%	LYIGNLSPAVTADDLR	99.7%	60.2	25	60.2	2	0	0	1717.91	5	20
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	11	13	39	0.04%	29.4%	MVIITGPPEAQFK	99.7%	72.7	25	61.3	9	0	0	1430.77	475	487
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	11	13	39	0.04%	29.4%	SGYAFVDYPDQNWAIR	99.7%	85.8	25	85.8	4	0	0	1901.88	38	53
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	11	13	39	0.04%	29.4%	TVNELQNLTSAEVIVPR	99.7%	42.9	25	39.1	2	0	0	1883.02	531	547
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	11	13	39	0.04%	29.4%	YPQGVASQR	99.7%	58.2	25	45.6	4	0	0	1005.51	589	597
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	18	22	50	0.05%	44.7%	ALQSGPPQSR	99.5%	39.2	25	30.5	2	0	0	1040.55	568	577
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	18	22	50	0.05%	44.7%	DQTPDENDQVVVK	99.7%	84	25	73.9	2	0	0	1486.70	526	538
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	18	22	50	0.05%	44.7%	FTEEIPLK	99.0%	35.7	25	24.3	2	0	0	976.54	273	280
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	18	22	50	0.05%	44.7%	IAPAEAPDAK	99.7%	60.7	25	60.7	4	0	0	982.52	441	450

Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	18	22	50	0.05%	44.7%	IELHGKPIEVEHSVPK	99.7%	39.3	25	39.3	0	1	0	1812.00	61	76
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	18	22	50	0.05%	44.7%	IKEENFVSPK	99.7%	49.7	25	23.6	2	0	0	1190.64	474	483
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	18	22	50	0.05%	44.7%	ILAHNNFVGR	99.7%	57.2	25	52.4	4	0	0	1140.63	281	290
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	18	22	50	0.05%	44.7%	IPVSGPFLVK	99.6%	40.1	25	40.1	3	0	0	1056.65	27	36
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	18	22	50	0.05%	44.7%	ITGHFYACQVAQR	99.7%	63.8	25	60	2	2	0	1550.75	539	551
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	18	22	50	0.05%	44.7%	ITISPLQELTLYNPER	99.7%	79.6	25	79.6	4	0	0	1887.02	310	325
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	18	22	50	0.05%	44.7%	LLVPTQFVGAIIGK	99.7%	106	25	0	5	0	0	1455.89	200	213
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	18	22	50	0.05%	44.7%	LNGFQLENFTLK	99.7%	63.5	25	53.5	2	0	0	1423.76	139	150
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	18	22	50	0.05%	44.7%	LYIGNLSENAAPSDLESIFK	99.7%	72.7	25	72.7	2	0	0	2181.11	4	23
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	18	22	50	0.05%	44.7%	MVIITGPPEAQFK	99.7%	72.7	25	61.3	9	0	0	1430.77	453	465
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	18	22	50	0.05%	44.7%	SILEIMHK	96.3%	29.8	25	22	1	0	0	970.54	259	266
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	18	22	50	0.05%	44.7%	SITILSTPEGTSAACK	99.7%	88.3	25	83.3	2	0	0	1635.83	243	258
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	18	22	50	0.05%	44.7%	TGYAFVDCPDESWALK	99.7%	77.1	25	77.1	2	0	0	1858.83	37	52
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	18	22	50	0.05%	44.7%	TVNELQNLSSAEVVVPR	99.7%	86	25	76.3	2	2	0	1854.99	509	525
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	18	22	50	0.05%	44.7%	VAYIPDEMAAQQNPLQQPR	99.7%	99.2	25	99.2	4	2	0	2169.08	151	169
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	18	22	50	0.05%	44.7%	VPSFAAGR	99.7%	47	25	41.1	2	0	0	804.44	494	501
Integrator complex subunit 1	INTS1	INT1_HUMAN	244.3	99.8%	2	2	2	0.00%	1.2%	DAAAALSSASALTGLTK	96.5%	30.1	25	30.1	1	0	0	1547.83	60	76
Integrator complex subunit 1	INTS1	INT1_HUMAN	244.3	99.8%	2	2	2	0.00%	1.2%	LQDLLLGPK	98.8%	35	25	30.3	1	0	0	996.61	954	962
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	100.0%	8	8	17	0.02%	17.2%	DLKPSNIFLVDTK	99.7%	50.4	25	40.2	2	0	0	1489.83	414	426
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	100.0%	8	8	17	0.02%	17.2%	EIELIGSGGFGQVFK	99.7%	97.6	25	93.3	2	0	0	1580.83	269	283
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	100.0%	8	8	17	0.02%	17.2%	GVDYIHSK	98.2%	32.9	25	20	1	0	0	918.47	401	408
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	100.0%	8	8	17	0.02%	17.2%	IGDFGLVTSLK	99.7%	91.2	25	81.1	2	0	0	1149.65	430	440
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	100.0%	8	8	17	0.02%	17.2%	LAVEILNK	99.7%	53.4	25	36.7	2	0	0	899.56	70	77
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	100.0%	8	8	17	0.02%	17.2%	LAYLQILSEETSVK	99.7%	114	25	113	2	0	0	1593.87	160	173
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	100.0%	8	8	17	0.02%	17.2%	VLALELFEQITK	99.7%	94.7	25	94.7	5	0	0	1403.81	389	400
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	100.0%	8	8	17	0.02%	17.2%	YMSPEQISSQDYGK	99.7%	60.7	25	60.7	1	0	0	1632.72	454	467
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	15	24	71	0.07%	47.6%	AAEAAINILK	99.7%	69.3	25	58.7	10	0	0	1013.60	91	100
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	15	24	71	0.07%	47.6%	ANASICFAVPDPLMPDPSK	99.7%	80.7	25	79	8	0	0	2029.97	101	119
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	15	24	71	0.07%	47.6%	EDSGTFSLGK	99.7%	64.1	25	61.8	4	0	0	1040.49	16	25
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	15	24	71	0.07%	47.6%	EYTTICR	96.6%	30.2	25	23.2	1	0	0	942.44	158	164
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	15	24	71	0.07%	47.6%	HRAEAPPLER	99.0%	35.5	25	27.6	2	0	0	1175.63	6	15
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	15	24	71	0.07%	47.6%	LESFMETGK	99.7%	59.5	25	50.5	7	0	0	1041.49	165	173
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	15	24	71	0.07%	47.6%	LPEYTLSQEGGPAHK	99.7%	82.8	25	76.8	3	3	0	1626.81	142	156
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	15	24	71	0.07%	47.6%	LPEYTLSQEGGPAHKR	99.7%	70.9	25	70.9	1	2	0	1782.91	142	157
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	15	24	71	0.07%	47.6%	MITAKPGK	95.0%	28.5	25	22.3	1	0	0	845.49	26	33
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	15	24	71	0.07%	47.6%	REYTTICR	98.9%	35.2	25	23.9	2	0	0	1098.54	157	164
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	15	24	71	0.07%	47.6%	SDVQIHVPTFTFR	99.7%	61	25	60.7	4	4	0	1546.80	57	69
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	15	24	71	0.07%	47.6%	SLLSIPNTDYIQLLSEIAK	99.7%	47.9	25	47.9	1	0	0	2118.17	232	250
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	15	24	71	0.07%	47.6%	TPIQVLHEYGMK	99.7%	70.4	25	65.6	7	4	0	1431.73	34	45
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	15	24	71	0.07%	47.6%	VTVGDITCTGEGTSK	99.7%	110	25	108	4	0	0	1524.72	70	84
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	15	24	71	0.07%	47.6%	VTVGDITCTGEGTSKK	99.7%	86.1	25	85.4	2	1	0	1652.82	70	85
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	16	24	110	0.10%	40.5%	AQDPSEVLTMLTNETGFEISSSDATVK	99.5%	32.2	25	32.2	0	1	0	2870.36	148	174
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	16	24	110	0.10%	40.5%	GTMTTGHNVADLVVILK	99.7%	82	25	69.2	4	4	0	1768.96	111	127
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	16	24	110	0.10%	40.5%	ILITTVPPNLR	99.7%	45.7	25	45.7	12	0	0	1236.77	175	185
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	16	24	110	0.10%	40.5%	ILITTVPPNLRK	99.5%	38.7	25	38.7	2	2	0	1364.86	175	186
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	16	24	110	0.10%	40.5%	ILPTLEAVAALGNK	99.7%	99.5	25	92.8	13	2	0	1409.84	128	141
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	16	24	110	0.10%	40.5%	ILSHGGFR	99.7%	56.8	25	44.4	2	0	0	886.49	320	327
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	16	24	110	0.10%	40.5%	ILSHGGFRK	94.9%	28.5	25	19	1	0	0	1014.58	320	328
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	16	24	110	0.10%	40.5%	KLDPELHLDIK	99.7%	66.2	25	40.2	2	3	0	1320.75	186	196
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	16	24	110	0.10%	40.5%	LDPELHLDIK	99.7%	41.8	25	35.6	2	0	0	1192.66	187	196
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	16	24	110	0.10%	40.5%	NQDLAPNSAEQASILSLVTK	99.7%	116	25	116	12	8	0	2099.10	61	80

Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	16	24	110	0.10%	40.5%	QPLALNVAYR	99.7%	69	25	53	12	0	0	1144.65	260	269
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	16	24	110	0.10%	40.5%	RNQDLAPNSAEQASILSLVTK	99.7%	78	25	77.9	0	2	0	2255.20	60	80
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	16	24	110	0.10%	40.5%	VKPAPDETSFSEALLK	99.7%	68.4	25	62	4	4	0	1731.92	44	59
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	16	24	110	0.10%	40.5%	VKPAPDETSFSEALLKR	99.7%	69.5	25	66.8	2	0	0	1888.02	44	60
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	16	24	110	0.10%	40.5%	VLQSALAAIR	99.7%	90.6	25	79.4	10	0	0	1041.64	197	206
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	16	24	110	0.10%	40.5%	WFEENASQSTVK	99.7%	79.9	25	79.9	6	0	0	1425.66	210	221
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	AEPPQAMNALMR	99.7%	53.8	25	48.9	10	0	0	1328.65	397	408
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	AVSDWIDEQEK	99.7%	71.2	25	58.4	4	0	0	1319.61	44	54
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	AYAALAALEK	99.7%	87.6	25	61.2	19	0	0	1020.57	578	587
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	CLAALASLR	99.7%	78.3	25	61	8	0	0	974.55	203	211
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	EATDAIGHLDR	99.7%	77.7	25	55.2	12	0	0	1197.59	298	308
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	EDITQSAQHALR	99.7%	63.6	25	50.9	10	3	0	1368.69	312	323
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	EPPLSLTIHLTSPVVR	99.7%	73.9	25	73.9	2	4	0	1759.01	162	177
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	FNYSGSGGR	99.7%	70.9	25	59	5	0	0	944.42	807	815
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	FVMEVEVDGQK	99.7%	71.1	25	64.3	11	0	0	1296.61	555	565
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	GDLDLELVLLCK	99.7%	77.4	25	72.9	2	0	0	1387.75	106	117
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	GWPLELLCEK	99.7%	60.2	25	0	13	0	0	1244.63	248	257
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	GYNHGQGSYSYSNSYNSPGGGGGSDYNYESK	99.7%	75.4	25	75.4	0	2	0	3253.30	776	806
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	HGKNPVMELNEK	99.1%	29.2	25	25.9	0	2	0	1395.71	524	535
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	HSSVYPTQEELEAVQNMVSHTER	99.7%	45.8	25	45.8	0	1	0	2671.24	18	40
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	IFVNDDR	99.7%	42.8	25	26.8	2	0	0	878.44	6	12
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	IFVNDDRHVMAK	99.7%	62	25	57.5	4	2	0	1460.73	6	17
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	LAAFGQLHK	99.7%	57.5	25	44.5	15	0	0	984.56	324	332
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	LFPDTPLALDANK	99.7%	67.1	25	58.8	11	0	0	1414.76	588	600
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	LFPDTPLALDANKK	99.7%	85.4	25	74.3	6	1	0	1542.85	588	601
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	LNQLKPGLQYK	99.7%	56.9	25	44.8	10	4	0	1301.76	409	419
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	LVSQTGPVHAPIFTMSVEVDGNSFEASGPSK	99.7%	67.8	25	67.8	0	1	0	3204.55	420	450
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	NADHSMNYQYR	99.7%	57.7	25	57.7	6	4	0	1414.58	884	894
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	NENPVDYTVQIPPSTTYAITPMK	99.7%	68.1	25	68.1	4	2	0	2579.27	349	371
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	NPVMELNEK	99.7%	59.3	25	50.1	10	0	0	1089.52	527	535
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	NPVMELNEKR	99.7%	57.2	25	48.1	4	0	0	1229.63	527	536
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	NTKEPPLSLTIHLTSPVVR	99.6%	32.5	25	32.5	0	1	0	2102.20	159	177
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	RPMEEDGEEKSPSK	99.7%	52.1	25	52.1	3	9	0	1618.74	372	385
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	SCVIVIR	99.7%	46.8	25	0	2	0	0	846.49	225	231
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	SGGNSYGSGGASYNPGSHGGYGGGSGGGSSYQGK	99.7%	87.9	25	87.9	0	2	0	3012.24	816	849
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	SIGTANRPMGAGEALR	99.7%	58.2	25	53.9	3	3	0	1600.82	258	273
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	SIGTANRPMGAGEALRR	99.7%	51.4	25	50.4	0	3	0	1756.92	258	274
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	VLAGETLSVNDPPDVLDR	99.7%	102	25	102	10	2	0	1909.99	183	200
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	VLECLASGIVMPDGSGIYDPCEK	99.7%	98.3	25	98.3	4	2	0	2526.16	275	297
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	VLGMDPLPSK	99.7%	56.6	25	53.8	10	0	0	1056.58	333	342
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	VLQDMGLPTGAEGR	99.7%	85.2	25	78.5	15	0	0	1443.73	461	474
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	VPTWGPLR	99.7%	52.8	25	16.3	2	0	0	925.53	240	247
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	YELISETGGSHDK	99.7%	76.9	25	65.3	2	0	0	1435.67	541	553
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	65	276	0.26%	51.8%	YELISETGGSHDKR	99.7%	77.6	25	74	6	3	0	1591.77	541	554
Intraflagellar transport protein 27 homolog	IFT27	IFT27_HUMAN	20.5	99.8%	2	2	3	0.00%	15.6%	SQAPGISLPGVLVGNK	99.7%	86.9	25	84.5	2	0	0	1536.87	109	124
Intraflagellar transport protein 27 homolog	IFT27	IFT27_HUMAN	20.5	99.8%	2	2	3	0.00%	15.6%	SYTLTTGMDLVVK	96.5%	30.1	25	25.8	1	0	0	1443.74	35	47
Iron-sulfur protein NUBPL	NUBPL	NUBPL_HUMAN	34.1	100.0%	3	3	5	0.00%	16.9%	AIGLLDVDVYGPSVPK	99.7%	86.8	25	86.8	2	0	0	1642.91	100	115
Iron-sulfur protein NUBPL	NUBPL	NUBPL_HUMAN	34.1	100.0%	3	3	5	0.00%	16.9%	EASDTGQPIVFSQPESDEAK	99.7%	64.4	25	64.4	1	0	0	2134.98	282	301
Iron-sulfur protein NUBPL	NUBPL	NUBPL_HUMAN	34.1	100.0%	3	3	5	0.00%	16.9%	STTAVNLALALAANDSSK	99.7%	64.1	25	64.1	2	0	0	1746.92	82	99
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	11	15	30	0.03%	33.1%	APIQWEER	99.7%	66.9	25	57.4	2	0	0	1028.52	59	66
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	11	15	30	0.03%	33.1%	CSDFTEEICR	99.7%	68.1	25	65.1	2	0	0	1316.52	351	360

Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	11	15	30	0.03%	33.1%	DMANPTALLLSAVMMLR	99.7%	64	25	60.3	3	2	0	1894.94	300	316
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	11	15	30	0.03%	33.1%	HMGLFDHAAR	99.7%	41.1	25	39.3	2	0	0	1170.55	317	326
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	11	15	30	0.03%	33.1%	IAEFAFEYAR	99.7%	80.2	25	69.9	2	0	0	1216.60	179	188
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	11	15	30	0.03%	33.1%	IEAACFATIK	99.7%	61.8	25	54.7	2	0	0	1123.58	327	336
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	11	15	30	0.03%	33.1%	LITEGASKR	99.6%	40.8	25	13.7	1	0	0	974.56	170	178
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	11	15	30	0.03%	33.1%	MSDGLFLQK	99.7%	58.9	25	53.7	4	0	0	1038.53	206	214
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	11	15	30	0.03%	33.1%	NVTAIQGPGGK	99.7%	60.5	25	59.9	2	0	0	1041.57	67	77
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	11	15	30	0.03%	33.1%	TPIAAGHPSMNLLLR	99.7%	69	25	69	4	2	0	1590.88	101	115
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	11	15	30	0.03%	33.1%	TPYTDVNIVTIR	99.7%	74.9	25	64.3	2	0	0	1391.75	135	146
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	10	14	30	0.03%	31.2%	DMGGYSTTTDFIK	99.7%	76.7	25	70.3	4	0	0	1435.64	362	374
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	10	14	30	0.03%	31.2%	EQTEGEYSSLEHESAR	99.7%	85.2	25	80.9	2	2	0	1851.80	165	180
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	10	14	30	0.03%	31.2%	FAFDYATKK	99.7%	43.4	25	37.7	2	0	0	1090.56	200	208
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	10	14	30	0.03%	31.2%	GELASYDMR	99.7%	53.5	25	51.2	4	0	0	1041.47	123	131
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	10	14	30	0.03%	31.2%	HLNLEYHSSMIADAVK	95.5%	23	25	23	0	1	0	1843.90	335	350
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	10	14	30	0.03%	31.2%	HNNLDLVIIR	99.7%	57.6	25	48.8	2	0	0	1206.70	155	164
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	10	14	30	0.03%	31.2%	LGDGLFLQCCEEVAELYPK	99.7%	50.1	25	50.1	2	0	0	2241.06	224	242
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	10	14	30	0.03%	31.2%	NIANPTAMLLSASNMLR	99.7%	127	25	125	8	0	0	1816.94	318	334
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	10	14	30	0.03%	31.2%	SVIGHLQTK	99.0%	35.7	25	35.7	2	0	0	982.57	375	383
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	10	14	30	0.03%	31.2%	TRDMGGYSTTTDFIK	99.7%	41.9	25	41.6	1	0	0	1708.79	360	374
Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G	IDH3G_HUMAN	42.8	100.0%	4	4	8	0.01%	10.4%	LGDGLFLQCCR	99.7%	52.4	25	51.4	2	0	0	1338.63	227	237
Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G	IDH3G_HUMAN	42.8	100.0%	4	4	8	0.01%	10.4%	LHSYATSIR	98.1%	32.6	25	22.8	2	0	0	1047.56	341	349
Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G	IDH3G_HUMAN	42.8	100.0%	4	4	8	0.01%	10.4%	SLPGVVTR	99.7%	51.9	25	41.3	2	0	0	828.49	150	157
Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G	IDH3G_HUMAN	42.8	100.0%	4	4	8	0.01%	10.4%	TSLDLYANVIHCK	99.7%	62.2	25	56.2	2	0	0	1533.77	137	149
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	24	45	0.04%	45.8%	ATDFVADR	99.4%	38.5	25	32.5	1	0	0	894.43	181	188
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	24	45	0.04%	45.8%	CATITPDEAR	99.7%	43.8	25	35.5	2	0	0	1133.53	113	122
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	24	45	0.04%	45.8%	DQTDDQVTIDSALATQK	99.7%	149	25	149	2	0	0	1848.88	90	106
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	24	45	0.04%	45.8%	FKDIFQEIFDK	99.7%	43.9	25	39.7	2	0	0	1429.74	262	272
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	24	45	0.04%	45.8%	GKLDGNQDLIR	99.7%	64.8	25	51.3	2	1	0	1228.66	383	393
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	24	45	0.04%	45.8%	GRPTSTNPIASIFAWTR	99.6%	32.9	25	30.5	0	2	0	1874.99	361	377
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	24	45	0.04%	45.8%	IIWQFIK	98.7%	34.2	25	23.6	2	0	0	947.57	61	67
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	24	45	0.04%	45.8%	LIDDMVAQVLK	99.7%	89.3	25	73.1	4	0	0	1244.69	289	299
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	24	45	0.04%	45.8%	LILPHVDIQLK	99.7%	50.8	25	37.2	2	1	0	1288.80	70	80
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	24	45	0.04%	45.8%	LNEHFLNTTDFLDTIK	99.7%	68.8	25	68.8	2	2	0	1920.97	427	442
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	24	45	0.04%	45.8%	LVPGWTKPITIGR	96.1%	23.6	25	7.26	0	1	0	1437.86	160	172
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	24	45	0.04%	45.8%	NILGGTVFR	99.3%	37.6	25	27.4	2	0	0	976.56	141	149
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	24	45	0.04%	45.8%	NILGGTVFREPIICK	99.7%	55.3	25	55.3	1	0	0	1716.95	141	155
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	24	45	0.04%	45.8%	SSGGFVWACK	99.7%	84	25	75.6	2	0	0	1098.50	300	309
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	24	45	0.04%	45.8%	TIEAEAAHGTVTR	99.7%	87.4	25	82.3	3	0	0	1355.69	341	353
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	24	45	0.04%	45.8%	VAKPVVEMDGDEMTR	99.7%	63.5	25	63.5	0	5	0	1708.79	46	60
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	24	45	0.04%	45.8%	VCVETVESGAMTK	99.7%	115	25	104	4	0	0	1410.66	401	413
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	18	24	45	0.04%	45.8%	YFDLGLPNR	99.7%	51.2	25	40.8	2	0	0	1094.56	81	89
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	AEPDHMVLGK	97.1%	30.9	25	28	1	0	0	1112.54	894	903
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	APLKPYPVSPSDK	99.7%	63.4	25	60.3	2	2	0	1398.76	1039	1051
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	AVPSWFVR	98.4%	33.4	25	29.5	2	0	0	961.53	411	418
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	CNLVPTDEITVYYK	97.1%	30.8	25	23.7	2	0	0	1714.84	1001	1014
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	DVLLPWYNAYR	99.7%	52	25	48.6	2	0	0	1409.72	651	661
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	EEEGTGVVHQAPYFGAEDYR	99.7%	58.1	25	58.1	0	1	0	2254.00	315	334
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	EFEDAFPADFIAEGIDQTR	99.7%	77.2	25	77.2	2	0	0	2170.99	547	565
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	EIVVIHQDPEALK	99.7%	71.8	25	57.4	2	0	0	1490.82	849	861
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	ESVDHLTIPSR	99.7%	44.7	25	31.2	2	0	0	1253.65	501	511
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	FLIQNVLR	99.7%	41.4	25	25.7	4	0	0	1002.61	662	669

Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	FVDILTNWYVR	99.7%	63.2	25	57.2	4	0	0	1425.75	726	736
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	GSELEITLTR	99.7%	66.9	25	43.4	2	0	0	1118.61	1062	1071
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	LESDYEILER	99.7%	79.4	25	60.9	2	0	0	1266.62	269	278
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	LFLNETQTQEITEDIPVK	99.7%	123	25	111	2	0	0	2118.10	1227	1244
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	LLILMEAR	99.7%	66.2	25	50.3	4	0	0	974.57	255	262
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	LYLINSPVVR	99.7%	64.2	25	55	3	0	0	1173.70	625	634
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	MGITEYNNQCR	99.7%	61.7	25	61.7	3	0	0	1401.59	111	121
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	NNDLCYWVPELVR	99.7%	62	25	56.8	2	0	0	1677.81	429	441
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	NVIVNGLVLASDGQK	99.7%	101	25	101	2	0	0	1526.85	586	600
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	QLSSEELEQFQK	99.7%	83.7	25	82	2	0	0	1465.72	918	929
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	TESAVSQMQSVIELGR	99.7%	108	25	105	4	0	0	1734.87	818	833
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	TVYVSVLPTTADF	98.5%	33.8	25	18	2	0	0	1412.73	1250	1262
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	VCMDFNIIR	99.3%	37.5	25	30.9	1	0	0	1183.56	335	343
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	VENMVDQLLR	99.7%	99.8	25	83.6	4	0	0	1216.64	419	428
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	VLIDPVSVQDK	96.3%	29.8	25	24.1	1	0	0	1212.68	786	796
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	VREELIDK	96.0%	29.5	25	15.6	1	0	0	1001.56	809	816
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	YAHQSGFHVDR	97.1%	24.6	25	24.6	0	1	0	1316.61	71	81
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	28	33	64	0.06%	26.3%	YIIEELNVR	99.7%	57.8	25	11.6	2	0	0	1148.63	869	877
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	25	43	0.04%	23.8%	ASPLLPANHVTMAK	99.7%	41.1	25	39.8	3	0	0	1449.79	373	386
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	25	43	0.04%	23.8%	AVLEEGTDVVIK	99.7%	89.8	25	81.8	3	0	0	1272.70	434	445
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	25	43	0.04%	23.8%	DQLGGWFQSSLLTSVAAR	99.7%	83.9	25	83.9	2	0	0	1935.99	626	643
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	25	43	0.04%	23.8%	DSFLGSIPGK	99.7%	66.1	25	42.5	2	0	0	1020.54	887	896
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	25	43	0.04%	23.8%	EAQNLSAMEIR	99.7%	63.1	25	53.8	4	0	0	1261.62	171	181
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	25	43	0.04%	23.8%	ELSNFYFSIIK	99.7%	64.6	25	52.3	2	0	0	1360.71	793	803
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	25	43	0.04%	23.8%	EMTADVIELK	99.7%	52.6	25	30.6	4	0	0	1148.59	948	957
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	25	43	0.04%	23.8%	EPPYGADVLR	97.9%	32.2	25	21.9	1	0	0	1116.57	688	697
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	25	43	0.04%	23.8%	FLINLEGGDIR	99.7%	79	25	58.5	2	0	0	1246.68	960	970
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	25	43	0.04%	23.8%	FLINLEGGDIREESSYK	99.3%	30.5	25	27.7	0	1	0	1969.99	960	976
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	25	43	0.04%	23.8%	FPLLKPSPK	99.7%	43.6	25	35.8	2	0	0	1026.63	273	281
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	25	43	0.04%	23.8%	QQPDTELEIQQK	99.7%	43.4	25	32.1	1	0	0	1456.73	79	90
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	25	43	0.04%	23.8%	SCQTALVEILDVIVR	99.7%	122	25	114	2	0	0	1715.94	818	832
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	25	43	0.04%	23.8%	SGDLYVLAADK	99.7%	84	25	74.4	2	0	0	1151.59	326	336
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	25	43	0.04%	23.8%	SYKPVFWSPSSR	97.4%	31.3	25	19.4	2	0	0	1440.73	239	250
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	25	43	0.04%	23.8%	TALAEAELEYNPEHVSR	99.7%	79.3	25	79.3	1	2	0	1928.93	251	267
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	25	43	0.04%	23.8%	TGWISTSSIWK	99.6%	39.8	25	34.5	1	0	0	1265.65	861	871
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	25	43	0.04%	23.8%	TKDEYLINSQTTEHIVK	99.7%	52.8	25	43.9	0	2	0	2019.04	539	555
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	25	43	0.04%	23.8%	TVIVHGFTLGEK	99.7%	56.8	25	50.8	1	1	0	1300.73	650	661
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	20	25	43	0.04%	23.8%	YTAESSDTLCPR	99.7%	100	25	89.1	2	0	0	1399.62	993	1004
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	2	2	4	0.00%	3.0%	HPEAEMAQNSVR	97.7%	31.9	25	28.6	2	0	0	1384.63	466	477
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	2	2	4	0.00%	3.0%	LNYGIPAIVK	99.7%	42	25	34.3	2	0	0	1087.65	478	487
Katanin p60 ATPase-containing subunit A1	KATNA1	KTNA1_HUMAN	56.0	100.0%	2	2	4	0.00%	3.9%	DIISQNPNVR	99.7%	49.1	25	35.5	2	0	0	1155.61	198	207
Katanin p60 ATPase-containing subunit A1	KATNA1	KTNA1_HUMAN	56.0	100.0%	2	2	4	0.00%	3.9%	SVSAADIER	99.7%	55.5	25	30.3	2	0	0	947.48	472	480
Keratin-associated protein 11-1	KRTAP11-1	KR111_HUMAN	17.1	99.8%	2	2	4	0.00%	15.3%	TSCVSNPCQVTCSR	99.7%	77.9	25	73.7	2	0	0	1655.69	74	87
Keratin-associated protein 11-1	KRTAP11-1	KR111_HUMAN	17.1	99.8%	2	2	4	0.00%	15.3%	TYQQSCVSSCR	99.7%	64.1	25	64.1	2	0	0	1375.57	150	160
Keratin-associated protein 19-5	KRTAP19-5	KR195_HUMAN	7.6	99.8%	2	2	3	0.00%	52.8%	LGYGGGYGGYGYGSGFGGYGYR	99.7%	69.7	25	69.7	1	0	0	2184.94	35	56
Keratin-associated protein 19-5	KRTAP19-5	KR195_HUMAN	7.6	99.8%	2	2	3	0.00%	52.8%	SCRPSCYGGYGFSGFY	99.7%	58.6	25	58.6	2	0	0	1864.74	57	72
Keratin-associated protein 24-1	KRTAP24-1	KR241_HUMAN	27.7	99.8%	2	2	4	0.00%	9.1%	SLSYIPSTFPPLR	99.7%	44.1	25	44.1	3	0	0	1477.81	230	242
Keratin-associated protein 24-1	KRTAP24-1	KR241_HUMAN	27.7	99.8%	2	2	4	0.00%	9.1%	YLCSGSRPLK	97.3%	31.2	25	23.4	1	0	0	1180.61	243	252
KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	KHDR1_HUMAN	48.2	100.0%	3	5	7	0.01%	8.6%	ILGPQGNTIK	97.5%	31.5	25	25.1	1	0	0	1040.61	176	185
KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	KHDR1_HUMAN	48.2	100.0%	3	5	7	0.01%	8.6%	KDDEENYLDLFSHK	99.7%	35.6	25	35.6	0	1	0	1752.81	139	152
KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	KHDR1_HUMAN	48.2	100.0%	3	5	7	0.01%	8.6%	SGSMDPSGAHPSVR	99.7%	53.3	25	53.3	3	2	0	1384.63	18	31

Kidney mitochondrial carrier protein 1	SLC25A30	KMCP1_HUMAN	32.5	99.8%	2	2	4	0.00%	9.6%	AAIVVGVELPVYDITK	99.7%	56.9	25	56.9	2	0	0	1686.97	172	187
Kidney mitochondrial carrier protein 1	SLC25A30	KMCP1_HUMAN	32.5	99.8%	2	2	4	0.00%	9.6%	ALYSGIAPAMLR	99.7%	44.5	25	44.5	2	0	0	1278.69	67	78
Kinesin-like protein KIF11	KIF11	KIF11_HUMAN	119.2	99.8%	2	2	3	0.00%	2.4%	LNLVDLAGSENIGR	99.7%	66.1	25	62.2	1	0	0	1470.79	261	274
Kinesin-like protein KIF11	KIF11	KIF11_HUMAN	119.2	99.8%	2	2	3	0.00%	2.4%	TVLQELINVLK	99.7%	43.5	25	34.5	2	0	0	1269.78	619	629
Kinesin-like protein KIF22	KIF22	KIF22_HUMAN	73.3	99.8%	2	2	4	0.00%	3.8%	ALMDLLQLTR	99.7%	48.8	25	32.1	3	0	0	1173.67	150	159
Kinesin-like protein KIF22	KIF22	KIF22_HUMAN	73.3	99.8%	2	2	4	0.00%	3.8%	VLDLLDPASGDLVIR	99.5%	38.8	25	38.8	1	0	0	1595.90	184	198
Kinesin-like protein KIF23	KIF23	KIF23_HUMAN	110.1	100.0%	2	2	2	0.00%	2.4%	NLQQELETQNQK	99.7%	53.6	25	38.8	1	0	0	1472.73	588	599
Kinesin-like protein KIF23	KIF23	KIF23_HUMAN	110.1	100.0%	2	2	2	0.00%	2.4%	STEEAFEVFWR	99.7%	47.7	25	47.7	1	0	0	1400.65	272	282
Kinetochore-associated protein 1	KNTC1	KNTC1_HUMAN	250.8	99.9%	2	2	3	0.00%	1.0%	LGISFQPVFR	99.7%	66.6	25	65.9	2	0	0	1163.66	1414	1423
Kinetochore-associated protein 1	KNTC1	KNTC1_HUMAN	250.8	99.9%	2	2	3	0.00%	1.0%	VLAPELIPSILEK	99.7%	49.6	25	49.6	1	0	0	1421.86	727	739
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	5	5	9	0.01%	14.7%	GLLEESSFATLFPK	99.7%	67.9	25	67.2	2	0	0	1538.81	53	66
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	5	5	9	0.01%	14.7%	ILQDDVACDIIK	99.7%	85.9	25	70.7	2	0	0	1402.73	135	146
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	5	5	9	0.01%	14.7%	LGALTAEEIALK	99.7%	70.6	25	40.3	2	0	0	1228.71	358	369
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	5	5	9	0.01%	14.7%	SVSFEQAVR	98.0%	32.4	25	24.6	1	0	0	1022.53	126	134
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	5	5	9	0.01%	14.7%	TFDPYIIIR	99.7%	41.5	25	32.2	2	0	0	1137.63	107	115
Kynurenine--oxoglutarate transaminase 3	CCBL2	KAT3_HUMAN	51.4	100.0%	3	4	5	0.00%	7.3%	GFGHPSLVK	97.1%	30.9	25	18.8	1	0	0	941.52	100	108
Kynurenine--oxoglutarate transaminase 3	CCBL2	KAT3_HUMAN	51.4	100.0%	3	4	5	0.00%	7.3%	IAAIDSLNQYTR	99.7%	55.8	25	51	2	0	0	1364.72	88	99
Kynurenine--oxoglutarate transaminase 3	CCBL2	KAT3_HUMAN	51.4	100.0%	3	4	5	0.00%	7.3%	MAGATPVFIPLR	99.7%	47.1	25	29.4	2	0	0	1272.71	168	179
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	8	8	12	0.01%	17.7%	FIPEITISDILR	99.7%	75.9	25	72.6	2	0	0	1416.81	388	399
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	8	8	12	0.01%	17.7%	GDYLLLKPEK	95.2%	28.7	25	24.9	1	0	0	1175.67	283	292
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	8	8	12	0.01%	17.7%	HPSLSIGVLEK	97.9%	32.3	25	29	1	0	0	1179.67	71	81
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	8	8	12	0.01%	17.7%	ISELSGCTPDPR	99.7%	49.3	25	40.3	2	0	0	1331.63	266	277
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	8	8	12	0.01%	17.7%	LIQQEDIK	99.4%	38.1	25	22.4	1	0	0	986.55	166	173
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	8	8	12	0.01%	17.7%	LIQQEDIKK	99.6%	40	25	21.1	1	0	0	1114.65	166	174
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	8	8	12	0.01%	17.7%	LIVAVEQEEIPR	99.7%	62.1	25	41.1	2	0	0	1395.78	137	148
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	8	8	12	0.01%	17.7%	MDGSIWLGPNAVLAFK	99.7%	42.6	25	42.6	2	0	0	1734.89	319	334
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	4	4	7	0.01%	17.4%	IAWALSR	99.6%	39.9	25	28	2	0	0	816.47	89	95
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	4	4	7	0.01%	17.4%	KSLDFYTR	99.5%	39.3	25	23.8	1	0	0	1029.54	44	51
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	4	4	7	0.01%	17.4%	RFEELGVK	99.2%	36.8	25	11.7	2	0	0	977.54	141	148
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	4	4	7	0.01%	17.4%	VLGMTLIQK	99.7%	51.6	25	45.6	2	0	0	1002.60	52	60
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	7	20	0.02%	13.7%	KFADGEVVR	99.7%	42.3	25	37.4	2	0	0	1020.55	5	13
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	7	20	0.02%	13.7%	LTPLILKPFGNSISR	99.7%	51.4	25	51.4	2	0	0	1655.98	117	131
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	7	20	0.02%	13.7%	NDLSPASSGNAVYDFFIGR	99.7%	101	25	101	6	0	0	2029.96	354	372
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	7	20	0.02%	13.7%	NLLVSGWWGFVR	99.7%	45.2	25	45.2	1	0	0	1433.77	533	544
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	7	20	0.02%	13.7%	TFEVTPIR	99.3%	37.6	25	31.9	3	0	0	962.53	196	203
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	7	20	0.02%	13.7%	VVEGTPLIDGR	99.7%	61.7	25	47.6	4	0	0	1155.64	280	290
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	7	20	0.02%	13.7%	YNGEPEHIER	99.7%	50.1	25	40	2	0	0	1243.57	132	141
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	25	29	53	0.05%	36.2%	AGGPTTPLSPTR	99.7%	72.3	25	64.2	4	0	0	1154.62	15	26
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	25	29	53	0.05%	36.2%	ALYETELADAR	99.7%	86	25	64.4	2	0	0	1251.62	80	90
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	25	29	53	0.05%	36.2%	DAALATALGDK	99.5%	39.2	25	32.8	1	0	0	1045.55	146	156
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	25	29	53	0.05%	36.2%	DAALATALGDKK	99.7%	69.6	25	50.4	2	0	0	1173.65	146	157
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	25	29	53	0.05%	36.2%	DQMQQQLNDYEQLLDVK	99.7%	91.8	25	91.8	2	0	0	2108.00	351	367
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	25	29	53	0.05%	36.2%	ESDLNGAQIK	98.7%	34.4	25	28	1	0	0	1074.54	125	134
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	25	29	53	0.05%	36.2%	IESLSSQLSNLQK	99.7%	51.2	25	32.1	1	0	0	1446.78	300	312
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	25	29	53	0.05%	36.2%	IGDTSVSYK	99.7%	65.4	25	65	2	0	0	969.49	475	483
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	25	29	53	0.05%	36.2%	IQELEDLLAK	99.7%	71.1	25	34.2	4	0	0	1171.66	321	330
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	25	29	53	0.05%	36.2%	KESDLNGAQIK	99.6%	40	25	18.1	2	0	0	1202.64	124	134
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	25	29	53	0.05%	36.2%	KIGDTSVSYK	99.7%	51.8	25	46.7	1	0	0	1097.58	474	483
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	25	29	53	0.05%	36.2%	KLLEGEEER	99.7%	66.5	25	38.7	2	0	0	1102.57	379	387
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	25	29	53	0.05%	36.2%	KQLADETLLK	98.5%	33.7	25	21.7	2	0	0	1158.67	182	191
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	25	29	53	0.05%	36.2%	LAQALHEMR	99.7%	71.5	25	65	4	0	0	1084.56	242	250

Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	25	29	53	0.05%	36.2%	LLEGEEERLK	99.7%	41.7	25	34.7	2	0	0	1215.66	380	389
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	25	29	53	0.05%	36.2%	LQEKEELR	99.7%	48.8	25	22.8	2	0	0	1044.57	30	37
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	25	29	53	0.05%	36.2%	LREYEAALNSK	99.7%	50	25	32.8	2	0	0	1293.68	135	145
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	25	29	53	0.05%	36.2%	LSSEMNTSTVNSAR	99.7%	116	25	107	4	0	0	1496.70	277	290
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	25	29	53	0.05%	36.2%	LVEVDSGR	99.6%	40	25	31.4	1	0	0	874.46	227	234
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	25	29	53	0.05%	36.2%	LYKEELEQTYHAK	99.7%	64	25	58.9	1	4	0	1651.83	259	271
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	25	29	53	0.05%	36.2%	MRIESLSSQLSNLQK	99.7%	47.7	25	39.2	1	0	0	1749.92	298	312
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	25	29	53	0.05%	36.2%	NQNSWGTGEDVK	99.7%	48.9	25	48.3	2	0	0	1334.60	517	528
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	25	29	53	0.05%	36.2%	QIEYEYK	97.3%	31.1	25	22.7	1	0	0	972.47	235	241
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	25	29	53	0.05%	36.2%	QLADETLLK	99.6%	40.5	25	29.6	2	0	0	1030.58	183	191
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	25	29	53	0.05%	36.2%	SMYEEEINETR	99.7%	79.9	25	75.5	1	0	0	1416.59	210	220
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	10	10	18	0.02%	21.7%	AGGPATPLSPTR	99.7%	52.5	25	42.4	2	0	0	1124.61	9	20
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	10	10	18	0.02%	21.7%	ALYESELADAR	99.7%	52.5	25	39.9	2	0	0	1237.61	74	84
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	10	10	18	0.02%	21.7%	ATSSSSGSLSATGR	99.7%	107	25	106	2	0	0	1268.61	397	410
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	10	10	18	0.02%	21.7%	EGELTVAQGR	99.7%	65.6	25	39.8	3	0	0	1059.54	119	128
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	10	10	18	0.02%	21.7%	GLESDVAELR	99.7%	83.9	25	61.3	2	0	0	1088.56	152	161
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	10	10	18	0.02%	21.7%	ISEKEEVTTR	99.7%	74	25	50.8	2	0	0	1191.62	58	67
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	10	10	18	0.02%	21.7%	KLLEGEEER	99.7%	66.5	25	38.7	2	0	0	1102.57	373	381
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	10	10	18	0.02%	21.7%	LELEQTYQAK	99.2%	36.5	25	33	1	0	0	1222.63	256	265
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	10	10	18	0.02%	21.7%	LLEGEEERLK	99.7%	41.7	25	34.7	2	0	0	1215.66	374	383
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	10	10	18	0.02%	21.7%	LQEKEELR	99.7%	48.8	25	22.8	2	0	0	1044.57	24	31
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	10	10	18	0.02%	21.7%	LSSDQNDKAASAAR	99.7%	42.6	25	38.8	1	0	0	1433.70	271	284
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	10	10	18	0.02%	21.7%	QVLEGEEIAYK	99.7%	64.5	25	56.7	2	0	0	1278.66	486	496
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	10	10	18	0.02%	21.7%	RLVEVDSSR	97.9%	32.3	25	21.4	1	0	0	1060.57	220	228
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	18	21	44	0.04%	19.6%	DYEAGQLYGLEK	99.7%	57	25	34.2	1	0	0	1385.66	981	992
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	18	21	44	0.04%	19.6%	ETESAPGSPR	99.7%	47.9	25	43.5	6	0	0	1030.48	514	523
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	18	21	44	0.04%	19.6%	FQHPSHELLK	97.2%	31	25	17.5	1	0	0	1235.65	872	881
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	18	21	44	0.04%	19.6%	FQQVPTDALANK	99.7%	64.3	25	54.2	4	0	0	1331.70	742	753
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	18	21	44	0.04%	19.6%	FSHLTSLPQQLPSQQLMSK	98.5%	27.1	25	26.2	0	1	0	2186.13	579	597
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	18	21	44	0.04%	19.6%	FWSFFLR	99.7%	49.7	25	43.9	3	0	0	1002.52	918	924
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	18	21	44	0.04%	19.6%	GLSASLPDLDSENWIEVK	99.7%	77.8	25	75.8	2	0	0	1972.99	544	561
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	18	21	44	0.04%	19.6%	ILIVTQTPHYMR	99.7%	60.3	25	53.6	4	2	0	1471.81	643	654
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	18	21	44	0.04%	19.6%	KFDGVEGPR	99.7%	46.5	25	36.6	2	0	0	1004.52	367	375
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	18	21	44	0.04%	19.6%	LFGAPEPSTIAR	99.7%	41.7	25	15.2	2	0	0	1258.68	754	765
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	18	21	44	0.04%	19.6%	LGIGQSQEMNTLFR	99.7%	74.7	25	63.6	4	0	0	1609.80	904	917
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	18	21	44	0.04%	19.6%	LQEYLGK	98.8%	34.7	25	16.9	2	0	0	850.47	1011	1017
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	18	21	44	0.04%	19.6%	QIEYYFSVDNLER	99.7%	69.5	25	68.9	2	0	0	1675.80	410	422
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	18	21	44	0.04%	19.6%	SLPTTVPESPNYR	99.7%	44.8	25	41.2	2	0	0	1460.74	766	778
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	18	21	44	0.04%	19.6%	SVQPQSHKPQPTR	99.7%	47	25	42.9	1	0	0	1489.79	186	198
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	18	21	44	0.04%	19.6%	THFDYQFGYR	99.0%	35.7	25	35.7	2	0	0	1333.60	357	366
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	18	21	44	0.04%	19.6%	VQALTTDISLIFAALK	97.8%	32	25	32	1	0	0	1703.99	447	462
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	18	21	44	0.04%	19.6%	YGLECLFR	99.7%	58.6	25	56	2	0	0	1057.51	949	956
La-related protein 7	LARP7	LARP7_HUMAN	66.9	100.0%	7	7	10	0.01%	13.9%	AIEFLNNPPEEAPR	99.7%	88.5	25	86.5	2	0	0	1596.80	182	195
La-related protein 7	LARP7	LARP7_HUMAN	66.9	100.0%	7	7	10	0.01%	13.9%	EENMDTSNTSISK	99.1%	35.9	25	35.9	1	0	0	1471.62	238	250
La-related protein 7	LARP7	LARP7_HUMAN	66.9	100.0%	7	7	10	0.01%	13.9%	GFAFVEFETK	99.7%	65.9	25	56.8	2	0	0	1174.58	167	176
La-related protein 7	LARP7	LARP7_HUMAN	66.9	100.0%	7	7	10	0.01%	13.9%	LEILSGDHEQR	99.7%	70.7	25	61.3	1	0	0	1296.65	521	531
La-related protein 7	LARP7	LARP7_HUMAN	66.9	100.0%	7	7	10	0.01%	13.9%	MGEEVIPLR	99.7%	51.3	25	48.4	1	0	0	1043.56	369	377
La-related protein 7	LARP7	LARP7_HUMAN	66.9	100.0%	7	7	10	0.01%	13.9%	TVYVELLPK	97.0%	30.6	25	30.1	1	0	0	1061.62	126	134
La-related protein 7	LARP7	LARP7_HUMAN	66.9	100.0%	7	7	10	0.01%	13.9%	VNATGPQFVSGVIVK	99.7%	59.9	25	53.4	2	0	0	1515.85	444	458
Large neutral amino acids transporter small subunit 1	SLC7A5	LAT1_HUMAN	55.0	100.0%	3	4	9	0.01%	9.5%	ALAAPAAEEKEEAR	99.7%	84.5	25	84.5	2	2	0	1455.74	10	23
Large neutral amino acids transporter small subunit 1	SLC7A5	LAT1_HUMAN	55.0	100.0%	3	4	9	0.01%	9.5%	GDVSNLDPNFSFEGTK	99.7%	53.3	25	47.2	1	0	0	1726.79	222	237

Large neutral amino acids transporter small subunit 1	SLC7A5	LAT1_HUMAN	55.0	100.0%	3	4	9	0.01%	9.5%	SADGSAPAGEGEGVTLQR	99.7%	83.1	25	83.1	4	0	0	1701.80	31	48
Lethal(2) giant larvae protein homolog 1	LLGL1	L2GL1_HUMAN	115.4	99.9%	2	2	5	0.00%	2.4%	APVVAIAVLDGR	99.7%	107	25	102	4	0	0	1180.70	788	799
Lethal(2) giant larvae protein homolog 1	LLGL1	L2GL1_HUMAN	115.4	99.9%	2	2	5	0.00%	2.4%	TGPLPWPAGFQPR	99.6%	40.3	25	31.3	1	0	0	1423.75	578	590
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	AENQPIRDVLK	95.1%	28.7	25	14.6	1	0	0	1282.71	673	683
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	AFAETHIK	99.7%	46.1	25	39.1	2	0	0	916.49	1091	1098
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	AGDMENAENILTVMR	99.7%	72.3	25	72.3	4	0	0	1663.78	245	259
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	AGYPQYVSEILEK	99.7%	76.4	25	67.3	2	0	0	1496.76	315	327
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	CVANNQVETLEK	99.7%	66	25	56.5	2	0	0	1404.68	930	941
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	DAGIEPGPDTYLALLNAYAEK	99.7%	54.9	25	54.9	1	0	0	2221.10	260	280
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	DAHLLVESK	99.7%	56	25	44.3	2	0	0	1011.55	641	649
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	DLPVTEAVFSALVTGHAR	99.7%	94	25	94	2	0	0	1883.00	227	244
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	EKDIQEESTFSSR	99.7%	75.4	25	71.4	2	0	0	1555.72	65	77
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	EQNIVFNAETYSNLIK	99.7%	87	25	86.7	2	0	0	1882.95	1060	1075
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	GAYDIFLNAK	99.7%	60	25	52.7	2	0	0	1111.58	1050	1059
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	GDLSTALEVAIDCYEK	99.7%	56.5	25	51.8	2	0	0	1783.84	836	851
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	GDVENIEVVQK	99.7%	68.6	25	55.2	2	0	0	1229.64	1153	1163
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	GFTLNDAANSR	99.7%	86.7	25	72.8	2	0	0	1165.56	1099	1109
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	IPENIYR	97.2%	31	25	18.6	2	0	0	904.49	618	624
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	IQEENVIPR	99.7%	55.7	25	48	2	0	0	1097.60	981	989
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	ISIMAER	99.7%	50.6	25	38.4	2	0	0	835.43	1237	1243
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	KIIETPGIR	99.7%	55.2	25	48.3	2	0	0	1026.63	909	917
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	LDDLFLKR	99.7%	50.3	25	38.8	2	0	0	1019.59	1351	1358
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	LDSSAVLDTGK	99.7%	74.3	25	66.7	2	0	0	1105.57	740	750
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	LGAVYDVSHYNALLK	99.7%	78.8	25	73.8	2	1	0	1662.89	156	170
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	LIASYCNVGDIEGASK	99.7%	120	25	120	2	0	0	1696.82	203	218
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	LIITQVR	98.1%	32.7	25	13.4	2	0	0	842.55	1110	1116
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	LLMSEDYFTQAMEVK	99.7%	98.5	25	98.5	5	0	0	1804.85	1076	1090
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	LQDAINILK	99.7%	57	25	48.2	2	0	0	1027.61	764	772
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	LVEKGETDLIQK	99.7%	50.2	25	39.4	2	0	0	1372.77	865	876
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	MEEANIQPNR	99.7%	62	25	51.9	4	0	0	1217.56	188	197
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	MLNGLEDSIGLSK	99.7%	71.4	25	69.2	3	0	0	1376.71	1164	1176
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	MVFINNIALAQIK	99.7%	97.7	25	94.5	4	0	0	1474.85	1177	1189
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	NLLESYHVPELIK	99.7%	48.9	25	39.8	1	0	0	1554.85	628	640
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	NVQGIIEILK	99.7%	66	25	57.2	2	0	0	1126.68	454	463
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	SCGSLLPELK	99.7%	47.8	25	37.9	2	0	0	1103.58	129	138
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	SEAANGNLDFVLSFLK	99.7%	63.5	25	63.5	2	0	0	1724.89	514	529
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	SGGLGGSHALLLLR	99.7%	63.7	25	56.4	2	2	0	1350.79	115	128
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	SNTLPISLQSIR	99.7%	80.1	25	54.8	2	0	0	1328.75	530	541
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	SVLELIPELNEK	99.6%	39.8	25	38.6	2	0	0	1383.77	1306	1317
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	SYVSEKDVTSAK	99.7%	73.7	25	69.9	2	0	0	1313.66	1327	1338
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	TVLDQQQTPSR	99.7%	72.3	25	52.6	2	0	0	1272.65	1129	1139
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	TVQLTSSELESTLETLK	99.7%	97.4	25	89.9	2	0	0	1878.99	656	672
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	VIEEQLEPAVEK	99.7%	69	25	66.2	1	0	0	1383.74	1225	1236
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	VIEPQYFGLAYLFR	98.4%	33.6	25	25.9	1	0	0	1715.92	1210	1223
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	42	49	92	0.09%	36.3%	VYLQNEYK	99.7%	44.6	25	34.8	2	0	0	1056.54	171	178
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	5	5	10	0.01%	8.5%	GTAAILEYLR	99.7%	70.7	25	54.1	2	0	0	1106.62	588	597
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	5	5	10	0.01%	8.5%	LQTINLSFNR	99.7%	62.4	25	53.1	2	0	0	1205.66	497	506
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	5	5	10	0.01%	8.5%	SNIVTSINFSK	99.7%	47.6	25	44.9	2	0	0	1209.65	424	434
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	5	5	10	0.01%	8.5%	SVPDEIILLR	99.7%	50.8	25	31.9	2	0	0	1154.68	303	312
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	5	5	10	0.01%	8.5%	TLLLDGNPFR	99.7%	48	25	44.2	2	0	0	1145.63	569	578
Leucine-rich repeat-containing protein 47	LRRC47	LRC47_HUMAN	63.5	100.0%	4	4	6	0.01%	9.1%	DGPSLLVVEQVR	99.7%	53.6	25	41.4	1	0	0	1311.73	543	554

Leucine-rich repeat-containing protein 47	LRRC47	LRC47_HUMAN	63.5	100.0%	4	4	6	0.01%	9.1%	ELLLTGPGLEER	99.7%	67	25	56.6	1	0	0	1326.73	23	34
Leucine-rich repeat-containing protein 47	LRRC47	LRC47_HUMAN	63.5	100.0%	4	4	6	0.01%	9.1%	NALGPGLSPELGPLPALR	99.7%	60.8	25	60.8	2	0	0	1772.01	85	102
Leucine-rich repeat-containing protein 47	LRRC47	LRC47_HUMAN	63.5	100.0%	4	4	6	0.01%	9.1%	TAATLATHELR	99.7%	80.8	25	72.6	2	0	0	1183.64	371	381
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	34	0.03%	19.4%	CEFAVGYQR	99.2%	36.6	25	32.1	1	0	0	1129.51	70	78
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	34	0.03%	19.4%	ELAVEGMHR	99.5%	38.6	25	33	2	0	0	1057.51	837	845
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	34	0.03%	19.4%	ELMGEEILGASLSAPLTSYK	99.7%	64.8	25	64.8	3	0	0	2109.08	351	370
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	34	0.03%	19.4%	EVWDYVFFK	99.7%	43	25	40.1	1	0	0	1232.60	633	641
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	34	0.03%	19.4%	FDDPLLGPR	99.7%	62.1	25	42.8	2	0	0	1029.54	1118	1126
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	34	0.03%	19.4%	GFYEGIMLVDGFK	99.7%	68	25	62.1	4	0	0	1475.72	471	483
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	34	0.03%	19.4%	GTGVVTSVPSDSPDDIAALR	99.7%	77.4	25	77.4	2	0	0	1956.99	385	404
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	34	0.03%	19.4%	ILDLQLEFDEK	99.7%	65.4	25	64.6	2	0	0	1362.72	1007	1017
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	34	0.03%	19.4%	MIDAGDALIYMEPEK	99.7%	62.8	25	62.8	1	0	0	1695.80	498	512
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	34	0.03%	19.4%	QTGEGVGPQEYTLLK	99.7%	60.8	25	49.8	2	0	0	1619.83	254	268
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	34	0.03%	19.4%	SFITTDVNPYYDSFVR	99.7%	94.9	25	91.9	2	0	0	1923.91	204	219
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	34	0.03%	19.4%	SGPASTFNDR	96.6%	30.1	25	8.53	1	0	0	1051.48	786	795
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	34	0.03%	19.4%	STGNFLTLTQAIDK	99.7%	90.4	25	81.2	2	0	0	1508.80	720	733
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	34	0.03%	19.4%	TGFFEFQAAK	99.7%	57.7	25	51	2	0	0	1145.56	823	832
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	34	0.03%	19.4%	VDIGDTIIYLVH	99.7%	82	25	79.9	2	0	0	1357.74	1165	1176
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	34	0.03%	19.4%	VFASELNAGIIK	99.7%	92.6	25	81.4	2	0	0	1261.72	796	807
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	34	0.03%	19.4%	VFEVNASNLEK	99.7%	71.1	25	64.2	2	0	0	1249.64	29	39
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	34	0.03%	19.4%	VIASELGSMPELK	99.7%	51.2	25	46.1	1	0	0	1373.73	971	983
Leukotriene A-4 hydrolase	LTA4H	LKHA4_HUMAN	69.3	99.9%	2	2	3	0.00%	3.9%	GSPMEISLPIALSK	99.7%	42.5	25	31.4	2	0	0	1458.79	84	97
Leukotriene A-4 hydrolase	LTA4H	LKHA4_HUMAN	69.3	99.9%	2	2	3	0.00%	3.9%	TFGETHPFTK	99.7%	51.9	25	51.2	1	0	0	1164.57	356	365
LINE-1 retrotransposable element ORF1 protein	L1RE1	LORF1_HUMAN	40.1	99.8%	2	2	4	0.00%	6.8%	DFVTTRPALK	99.0%	35.7	25	32.4	2	0	0	1147.65	305	314
LINE-1 retrotransposable element ORF1 protein	L1RE1	LORF1_HUMAN	40.1	99.8%	2	2	4	0.00%	6.8%	LTADLSAETLQAR	99.7%	86.3	25	74.3	2	0	0	1388.74	249	261
Lipase maturation factor 2	LMF2	LMF2_HUMAN	79.7	99.8%	2	2	3	0.00%	2.8%	FVQALLAPCSLR	95.3%	28.8	25	28.8	1	0	0	1374.76	651	662
Lipase maturation factor 2	LMF2	LMF2_HUMAN	79.7	99.8%	2	2	3	0.00%	2.8%	LVQSQVAR	98.7%	34.2	25	16.4	2	0	0	900.53	539	546
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	8	8	10	0.01%	3.5%	DLSKPIGALNPK	98.3%	33.3	25	32.5	1	0	0	1252.73	2268	2279
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	8	8	10	0.01%	3.5%	EIFVDFAPFLSR	98.0%	32.5	25	32.5	1	0	0	1440.75	1813	1824
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	8	8	10	0.01%	3.5%	IQNPQILK	95.4%	28.9	25	20.1	1	0	0	953.58	813	820
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	8	8	10	0.01%	3.5%	LINDCHGSVSEASSEQK	99.0%	28.8	25	28.8	0	1	0	1860.84	1224	1240
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	8	8	10	0.01%	3.5%	NPLGSTHPEATLK	99.7%	49.2	25	37	1	0	0	1364.72	1998	2010
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	8	8	10	0.01%	3.5%	SAAAIALPPIAK	99.7%	64.5	25	60.7	2	0	0	1122.69	213	224
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	8	8	10	0.01%	3.5%	VGVGTSFGLPQTR	99.7%	48	25	48	1	0	0	1318.71	2183	2195
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	8	8	10	0.01%	3.5%	YGPDAFFNFPGK	99.7%	61.2	25	55.8	2	0	0	1359.64	201	212
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	159	0.15%	60.8%	DLADELALVDVIEDK	99.7%	119	25	119	3	0	0	1657.85	43	57
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	159	0.15%	60.8%	DQLIYNLLK	99.7%	64.9	25	46	8	0	0	1119.64	6	14
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	159	0.15%	60.8%	DQLIYNLLKEEQTPQNK	99.7%	106	25	99.2	2	2	0	2074.08	6	22
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	159	0.15%	60.8%	DYNVTANSK	99.7%	58.8	25	54	12	0	0	1011.47	82	90
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	159	0.15%	60.8%	FIIPNVVK	98.7%	34.2	25	21.1	2	0	0	929.58	119	126
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	159	0.15%	60.8%	GEMMDLQHGSLFLR	99.7%	73.6	25	73.6	5	6	0	1633.78	60	73
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	159	0.15%	60.8%	GYTSWAIGLSVADLAESIMK	99.7%	73.8	25	73.8	2	0	0	2128.06	246	265
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	159	0.15%	60.8%	ITVVGVGAVGMACAISILMK	99.7%	47.5	25	45	4	1	0	2006.08	23	42
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	159	0.15%	60.8%	IVSGKDYNVTANSK	99.7%	87.7	25	82.5	4	3	0	1495.78	77	90
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	159	0.15%	60.8%	KSADTLWGIQK	99.1%	29.4	25	21.8	0	1	0	1246.68	318	328
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	159	0.15%	60.8%	LKGEMMDLQHGSLFLR	97.8%	25.7	25	2.59	0	2	0	1890.96	58	73
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	159	0.15%	60.8%	LLIVSNPVDILTYVAWK	99.7%	133	25	0	4	0	0	1944.12	133	149
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	159	0.15%	60.8%	LVIITAGAR	99.7%	74	25	57.2	24	0	0	913.58	91	99
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	159	0.15%	60.8%	QVVESAYEVIK	99.7%	69.6	25	63.1	14	0	0	1264.68	233	243
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	159	0.15%	60.8%	RVHPVSTMIK	99.5%	38.6	25	28.2	2	0	0	1167.67	269	278
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	159	0.15%	60.8%	SADTLWGIQK	99.7%	60	25	39	7	0	0	1118.58	319	328

L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	159	0.15%	60.8%	TLHPDLGTDK	99.7%	45.1	25	42.2	2	0	0	1096.56	213	222
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	159	0.15%	60.8%	TLHPDLGTDKDK	99.6%	32.5	25	29.3	1	2	0	1339.69	213	224
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	159	0.15%	60.8%	VIGSGCNLDSAR	99.7%	84.2	25	74.2	20	0	0	1248.60	158	169
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	159	0.15%	60.8%	VTLTSEEEAR	99.7%	79	25	72.3	26	0	0	1134.56	306	315
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	25	126	0.12%	46.7%	DYSVTANSK	96.0%	29.5	25	22.8	1	0	0	984.46	83	91
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	25	126	0.12%	46.7%	EKLIAPVAEEEATVPNNK	99.7%	101	25	96.7	2	2	0	1952.03	6	23
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	25	126	0.12%	46.7%	FIIPQIVK	99.7%	47.9	25	43.8	3	0	0	957.61	120	127
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	25	126	0.12%	46.7%	GEMMDLQHGSLFLQTPK	99.7%	90	25	88.1	6	6	0	1931.94	61	77
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	25	126	0.12%	46.7%	GLTSVINQK	99.7%	61.6	25	43.8	9	0	0	959.55	300	308
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	25	126	0.12%	46.7%	ITVVGVGQVGMACAISILGK	99.7%	140	25	140	17	5	0	1973.09	24	43
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	25	126	0.12%	46.7%	IVADKDYSVTANSK	99.7%	84	25	80.2	12	3	0	1510.77	78	91
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	25	126	0.12%	46.7%	IVVVTAGVR	99.7%	76.1	25	56.4	7	0	0	913.58	92	100
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	25	126	0.12%	46.7%	KSADTLWDIQK	99.7%	56.7	25	47.3	2	0	0	1304.68	319	329
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	25	126	0.12%	46.7%	LIAPVAEEEATVPNNK	99.7%	83.6	25	73.6	14	2	0	1694.90	8	23
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	25	126	0.12%	46.7%	LKDDEVAQLK	99.7%	65.2	25	53.1	3	0	0	1158.64	309	318
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	25	126	0.12%	46.7%	LKGEMMDLQHGSLFLQTPK	97.0%	24.6	25	24	0	1	0	2205.10	59	77
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	25	126	0.12%	46.7%	MVVESAYEVIK	99.7%	81.6	25	77.9	19	0	0	1267.66	234	244
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	25	126	0.12%	46.7%	SADTLWDIQK	99.7%	70.8	25	62.2	9	0	0	1176.59	320	329
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	25	126	0.12%	46.7%	SLADELALVDVLEDK	99.7%	120	25	104	3	0	0	1629.86	44	58
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	15	25	126	0.12%	46.7%	VIGSGCNLDSAR	99.7%	84.2	25	74.2	20	0	0	1248.60	159	170
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	7	7	12	0.01%	9.2%	DIIALNPLYR	99.7%	62.7	25	52.2	2	0	0	1187.68	302	311
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	7	7	12	0.01%	9.2%	EIFDIAFPDEQAEALAVER	99.7%	52.7	25	47.3	1	0	0	2163.06	941	959
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	7	7	12	0.01%	9.2%	FSVGGMTDVAEIK	99.7%	69.4	25	63.5	1	0	0	1353.67	547	559
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	7	7	12	0.01%	9.2%	ILEFIAVSQLR	99.7%	52.3	25	52.3	2	0	0	1288.76	501	511
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	7	7	12	0.01%	9.2%	LAQPYVGVFLK	99.7%	52.8	25	52.5	2	0	0	1234.72	159	169
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	7	7	12	0.01%	9.2%	LSSDVLTLLIK	99.7%	79.8	25	59.3	2	0	0	1201.74	691	701
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	7	7	12	0.01%	9.2%	TENPLILIDEVDK	98.8%	34.9	25	34.9	2	0	0	1498.80	582	594
Long-chain fatty acid transport protein 4	SLC27A4	S27A4_HUMAN	72.1	99.8%	2	2	6	0.01%	3.1%	ILSFVYPIR	99.7%	51.8	25	36.2	2	0	0	1107.66	409	417
Long-chain fatty acid transport protein 4	SLC27A4	S27A4_HUMAN	72.1	99.8%	2	2	6	0.01%	3.1%	TVPILFASTVR	99.7%	58.2	25	56.7	4	0	0	1203.71	75	85
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	9	9	15	0.01%	15.3%	AKPVNSKPDSAYR	98.4%	33.3	25	31.6	1	0	0	1432.75	57	69
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	9	9	15	0.01%	15.3%	IGYSSPQTLADQSSK	99.7%	79.5	25	79.4	2	0	0	1581.78	349	363
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	9	9	15	0.01%	15.3%	LKDIVSLVPR	99.7%	51	25	45.6	2	0	0	1139.71	221	230
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	9	9	15	0.01%	15.3%	LLLCGGAPLSATTQR	99.7%	85.4	25	72.7	2	0	0	1557.84	447	461
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	9	9	15	0.01%	15.3%	LSPEPWTPETGLVTDAFK	99.7%	68.5	25	65.2	2	0	0	1988.00	682	699
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	9	9	15	0.01%	15.3%	NLFILAYNYK	99.7%	56.2	25	38.7	2	0	0	1258.68	407	416
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	9	9	15	0.01%	15.3%	NTPLCDSFVFR	99.4%	38.4	25	34.7	2	0	0	1355.64	425	435
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	9	9	15	0.01%	15.3%	THYQADIER	96.7%	30.2	25	28.3	1	0	0	1132.54	707	715
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	9	9	15	0.01%	15.3%	VSEMSSFQR	99.7%	50.1	25	44.1	1	0	0	1086.49	398	406
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	9	10	22	0.02%	26.5%	EVTWEVLEGEVEK	99.7%	68.6	25	60.9	1	0	0	1546.76	300	312
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	9	10	22	0.02%	26.5%	GSIFVVFDSIESAK	99.7%	102	25	98	2	0	0	1498.78	152	165
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	9	10	22	0.02%	26.5%	IIEDQQESLNK	99.7%	85.1	25	72.2	4	0	0	1316.67	318	328
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	9	10	22	0.02%	26.5%	KFVETPGQK	98.5%	33.7	25	30	2	0	0	1033.57	166	174
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	9	10	22	0.02%	26.5%	LDEGWVPLEIMIK	99.7%	67.8	25	57.6	3	0	0	1542.82	42	54
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	9	10	22	0.02%	26.5%	LTTDFNVIVEALSK	99.7%	94.9	25	89.9	4	0	0	1549.85	61	74
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	9	10	22	0.02%	26.5%	QKLEEDAEMK	99.5%	39.5	25	35.7	3	0	0	1220.58	215	224
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	9	10	22	0.02%	26.5%	SPSKPLPEVTDEYKNDVK	99.5%	31.9	25	31.9	0	2	0	2046.04	92	109
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	9	10	22	0.02%	26.5%	WIDFVR	99.2%	36.9	25	14.7	1	0	0	835.45	261	266
Lymphoid-specific helicase	HELLS	HELLS_HUMAN	97.1	100.0%	2	2	2	0.00%	2.4%	EVVVYAPLSK	99.7%	48	25	46.5	1	0	0	1104.63	465	474
Lymphoid-specific helicase	HELLS	HELLS_HUMAN	97.1	100.0%	2	2	2	0.00%	2.4%	MEQQQLEEQK	99.7%	48.2	25	38.4	1	0	0	1306.59	86	95
Lys-63-specific deubiquitinase BRCC36	BRCC3	BRCC3_HUMAN	36.1	99.9%	2	2	3	0.00%	6.3%	FAYTGTEMR	96.8%	30.4	25	30.4	1	0	0	1091.48	52	60
Lys-63-specific deubiquitinase BRCC36	BRCC3	BRCC3_HUMAN	36.1	99.9%	2	2	3	0.00%	6.3%	VCLESAVELPK	99.7%	49.3	25	36.5	2	0	0	1244.66	227	237

Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	7	7	11	0.01%	11.4%	IAPELYHK	99.6%	39.6	25	16.6	1	0	0	970.54	298	305
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	7	7	11	0.01%	11.4%	LIFYDLR	99.4%	38.2	25	36.4	2	0	0	939.53	142	148
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	7	7	11	0.01%	11.4%	LQVMANSR	97.5%	31.5	25	22.7	1	0	0	934.48	154	161
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	7	7	11	0.01%	11.4%	MLVVGGIDR	99.7%	44.8	25	34.8	2	0	0	959.53	306	314
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	7	7	11	0.01%	11.4%	RGDIIGVQGNPGK	99.7%	51.1	25	47	2	0	0	1310.72	178	190
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	7	7	11	0.01%	11.4%	SEEEFIHINNK	99.7%	56.8	25	56.8	1	0	0	1359.65	165	175
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	7	7	11	0.01%	11.4%	VAMFLTDSNNIK	99.7%	41.6	25	40.7	2	0	0	1352.69	554	565
Lysophosphatidylcholine acyltransferase 1	LPCAT1	PCAT1_HUMAN	59.2	100.0%	4	4	6	0.01%	9.0%	AAPASSAGASDAR	99.7%	75.2	25	75.2	2	0	0	1131.54	10	22
Lysophosphatidylcholine acyltransferase 1	LPCAT1	PCAT1_HUMAN	59.2	100.0%	4	4	6	0.01%	9.0%	NPALYASNVR	99.7%	87.1	25	82.4	2	0	0	1104.58	286	295
Lysophosphatidylcholine acyltransferase 1	LPCAT1	PCAT1_HUMAN	59.2	100.0%	4	4	6	0.01%	9.0%	TALGVAELTVTDLFR	99.7%	99.7	25	95.5	1	0	0	1605.88	447	461
Lysophosphatidylcholine acyltransferase 1	LPCAT1	PCAT1_HUMAN	59.2	100.0%	4	4	6	0.01%	9.0%	TLDTIQLAFK	99.7%	46.1	25	31.4	1	0	0	1149.65	417	426
Lysophospholipid acyltransferase 7	MBOAT7	MBOA7_HUMAN	52.8	99.8%	2	2	3	0.00%	5.1%	AASLEYDYETIR	99.6%	39.8	25	34.6	1	0	0	1430.68	289	300
Lysophospholipid acyltransferase 7	MBOAT7	MBOA7_HUMAN	52.8	99.8%	2	2	3	0.00%	5.1%	AASQPTSLAPEK	99.1%	35.9	25	21.9	2	0	0	1199.63	457	468
Lysosomal protective protein	CTSA	PPGB_HUMAN	54.5	100.0%	2	2	3	0.00%	4.2%	FLNKQPY	98.6%	34.1	25	26.1	1	0	0	909.48	474	480
Lysosomal protective protein	CTSA	PPGB_HUMAN	54.5	100.0%	2	2	3	0.00%	4.2%	YGDSGEQIAGFVK	99.7%	81.3	25	75.1	2	0	0	1370.66	430	442
Lysozyme C	LYZ	LYSC_HUMAN	16.5	99.8%	2	2	3	0.00%	12.8%	LGMDGYR	95.6%	29.1	25	25.9	1	0	0	827.37	33	39
Lysozyme C	LYZ	LYSC_HUMAN	16.5	99.8%	2	2	3	0.00%	12.8%	STDYGIFQINSR	99.7%	42.7	25	36.6	2	0	0	1400.68	69	80
Macrophage migration inhibitory factor	MIF	MIF_HUMAN	12.5	99.8%	2	3	6	0.01%	17.4%	LLCGLLAER	99.7%	72.7	25	55.1	2	0	0	1044.59	79	87
Macrophage migration inhibitory factor	MIF	MIF_HUMAN	12.5	99.8%	2	3	6	0.01%	17.4%	PMFIVNTNVPR	99.7%	72.3	25	66.5	4	0	0	1303.68	2	12
Magnesium transporter protein 1	MAGT1	MAGT1_HUMAN	38.0	100.0%	4	4	8	0.01%	11.0%	GFSAEQIAR	99.7%	48.2	25	30.1	3	0	0	978.50	160	168
Magnesium transporter protein 1	MAGT1	MAGT1_HUMAN	38.0	100.0%	4	4	8	0.01%	11.0%	RGDTYELQVR	99.7%	45.2	25	37.4	2	0	0	1236.63	150	159
Magnesium transporter protein 1	MAGT1	MAGT1_HUMAN	38.0	100.0%	4	4	8	0.01%	11.0%	VSQLMEWTNK	99.7%	52.7	25	41.7	1	0	0	1235.61	41	50
Magnesium transporter protein 1	MAGT1	MAGT1_HUMAN	38.0	100.0%	4	4	8	0.01%	11.0%	YSSAFTNR	99.7%	59.7	25	52.2	2	0	0	945.44	106	113
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	5	5	8	0.01%	21.9%	GCDVVVIPAGVPR	96.8%	30.4	25	30.4	1	0	0	1338.72	92	104
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	5	5	8	0.01%	21.9%	IFGVTTLDIVR	99.7%	55	25	45.8	2	0	0	1233.72	166	176
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	5	5	8	0.01%	21.9%	SQETECTYFSTPLLLGK	99.7%	74.9	25	74.9	2	0	0	1973.95	280	296
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	5	5	8	0.01%	21.9%	VAVLGASGGIGQPLSLLLK	99.7%	109	25	109	2	0	0	1793.09	27	45
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	5	5	8	0.01%	21.9%	VDFPQDQLTALTGR	99.7%	64	25	52.6	1	0	0	1560.80	216	229
Malectin	MLEC	MLEC_HUMAN	32.2	100.0%	3	3	5	0.00%	14.0%	FAEVYFAQSQQK	99.7%	92.1	25	92.1	2	0	0	1445.71	127	138
Malectin	MLEC	MLEC_HUMAN	32.2	100.0%	3	3	5	0.00%	14.0%	LSVQGEVSTFTGK	99.7%	90.7	25	86.1	1	0	0	1352.71	178	190
Malectin	MLEC	MLEC_HUMAN	32.2	100.0%	3	3	5	0.00%	14.0%	VCALYIMAGTVDDVPK	99.7%	80.7	25	67.6	2	0	0	1751.87	205	220
Malonyl-CoA-acyl carrier protein transacylase, mitochondrial	MCAT	FABD_HUMAN	43.0	99.8%	2	2	3	0.00%	5.4%	LLAQQLVSPVK	99.7%	52.8	25	52.8	2	0	0	1195.74	315	325
Malonyl-CoA-acyl carrier protein transacylase, mitochondrial	MCAT	FABD_HUMAN	43.0	99.8%	2	2	3	0.00%	5.4%	VISGHQEALR	99.7%	49	25	42.1	1	0	0	1109.61	237	246
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	5	5	8	0.01%	11.9%	AVILIGGPQK	98.9%	35.2	25	30.9	2	0	0	995.63	4	13
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	5	5	8	0.01%	11.9%	GNVYIHPTAK	98.9%	35.2	25	35.2	1	0	0	1099.59	285	294
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	5	5	8	0.01%	11.9%	GVTVGEGVR	99.7%	43.5	25	27.5	1	0	0	873.48	310	318
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	5	5	8	0.01%	11.9%	LLPAITILGCR	99.7%	46.4	25	46.4	2	0	0	1226.73	380	390
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	5	5	8	0.01%	11.9%	SAGSALYASR	99.7%	57.9	25	52.7	2	0	0	982.50	250	259
Mannose-1-phosphate guanyltransferase beta	GMPPB	GMPPB_HUMAN	39.8	100.0%	4	4	8	0.01%	16.9%	ALILVGGYGTR	99.7%	77	25	77	2	0	0	1119.65	3	13
Mannose-1-phosphate guanyltransferase beta	GMPPB	GMPPB_HUMAN	39.8	100.0%	4	4	8	0.01%	16.9%	ISMSHEEEPLGTAGPLALAR	99.7%	40	25	38.9	0	2	0	2095.05	75	94
Mannose-1-phosphate guanyltransferase beta	GMPPB	GMPPB_HUMAN	39.8	100.0%	4	4	8	0.01%	16.9%	LCSGPGIVGNVLVDPSAR	99.7%	68.1	25	67	2	0	0	1810.95	244	261
Mannose-1-phosphate guanyltransferase beta	GMPPB	GMPPB_HUMAN	39.8	100.0%	4	4	8	0.01%	16.9%	YGVVVCEADTGR	99.7%	65	25	63.8	2	0	0	1325.62	144	155
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	ALWFQGR	97.1%	30.8	25	16.5	1	0	0	877.47	556	562
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	DDWEEKR	99.7%	42	25	17.6	4	0	0	977.43	176	182
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	DLDELSR	98.6%	34.2	25	27.6	1	0	0	847.42	121	127
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	DLDELSRYPEDK	99.7%	57.2	25	53.9	4	0	0	1479.70	121	132
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	DLSAAGIGLLAAATQSLSMPASLGR	99.7%	115	25	115	2	1	0	2387.26	20	44
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	DSFDDRGPSLNPVLDYDHGSR	99.7%	47.6	25	47.6	0	4	0	2362.07	187	207
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	EDAMAMVDHCLK	99.7%	63.7	25	63.5	5	0	0	1419.61	543	554
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	EWSQHINGASHSR	99.5%	32.3	25	32.3	0	2	0	1508.70	305	317
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	FDQKQELGR	99.7%	51.4	25	39.3	4	0	0	1120.57	488	496

Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	FDSEYER	99.7%	47.4	25	47.4	4	0	0	945.39	246	252
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	GAPPSSNIEDFHGLLPK	99.7%	71.7	25	68.8	4	0	0	1778.91	271	287
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	GDADQASNILASFGLSAR	99.7%	105	25	105	6	4	0	1792.88	103	120
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	GNLGAGNGNLQGPR	99.7%	80.6	25	80.6	5	0	0	1324.67	374	387
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	GPGPLQER	99.7%	49.5	25	40.4	6	0	0	853.45	256	263
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	GPLPLSSQHR	99.7%	48	25	42	4	0	0	1091.60	93	102
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	GPSLNPVLDYDHGSR	99.7%	92.4	25	92.4	2	4	0	1626.79	193	207
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	GYPHLCSICDLPVHSNK	99.7%	43.9	25	43.9	0	4	0	1996.94	288	304
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	IEELDQENEAALENGIK	99.7%	102	25	102	1	0	0	1914.93	720	736
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	IGPYQPNVPVGIDYVIPK	99.7%	64.2	25	64.2	7	0	0	1969.08	781	798
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	IKKPEGKPDQK	99.2%	29.7	25	25.6	1	4	0	1267.74	477	487
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	IKNYILMR	97.9%	32.2	25	14.7	1	0	0	1050.61	523	530
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	ITPENLPQILLQLK	99.7%	83.6	25	76.5	6	0	0	1619.97	133	146
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	LCSLFYTNEEVAK	99.7%	71.2	25	65.3	5	0	0	1573.76	805	817
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	MDYEDDRLR	99.7%	46.3	25	38.4	6	0	0	1212.53	217	225
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	NTHCSSLPHYQK	99.7%	57.4	25	57.4	4	0	0	1471.67	818	829
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	NYILMR	98.6%	34.1	25	22.6	5	0	0	809.43	525	530
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	RTEEGPTLSYGR	99.7%	63.2	25	49.8	4	1	0	1365.68	149	160
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	SFQQSSLSR	99.7%	66.1	25	43.1	2	0	0	1039.52	4	12
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	SQAFIEMETR	99.7%	64.6	25	57.7	10	0	0	1211.57	533	542
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	SQESGYYDR	99.7%	50.5	25	50.5	6	0	0	1104.46	208	216
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	TEEGPTLSYGR	99.7%	56.4	25	45.7	5	0	0	1209.57	150	160
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	VIHLSNLPHSGYSDSAVLK	99.7%	67.7	25	67.7	2	6	0	2037.08	497	515
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	33	44	157	0.15%	43.3%	VVHIMDFQR	99.7%	47.3	25	39.6	10	0	0	1144.59	399	407
MAX gene-associated protein	MGA	MGAP_HUMAN	331.8	99.8%	2	2	3	0.00%	1.0%	ISNPSAFSIVPR	99.7%	49.1	25	40.9	2	0	0	1287.71	2208	2219
MAX gene-associated protein	MGA	MGAP_HUMAN	331.8	99.8%	2	2	3	0.00%	1.0%	VLQSEGEAVDPEANVIK	99.7%	51.3	25	51.3	1	0	0	1797.92	1954	1970
Mediator of DNA damage checkpoint protein 1	MDC1	MDC1_HUMAN	226.7	100.0%	5	5	9	0.01%	3.5%	EGAQVPTGR	98.5%	33.7	25	23.9	2	0	0	914.47	664	672
Mediator of DNA damage checkpoint protein 1	MDC1	MDC1_HUMAN	226.7	100.0%	5	5	9	0.01%	3.5%	NQLVTPEPTSR	98.2%	32.9	25	23	2	0	0	1241.65	1585	1595
Mediator of DNA damage checkpoint protein 1	MDC1	MDC1_HUMAN	226.7	100.0%	5	5	9	0.01%	3.5%	TPEPVVPTAPEPHPTTSTDQPVTPK	98.0%	26.1	25	26.1	0	2	0	2623.33	1608	1632
Mediator of DNA damage checkpoint protein 1	MDC1	MDC1_HUMAN	226.7	100.0%	5	5	9	0.01%	3.5%	TPESIVPIAPELQPSTSR	99.7%	66	25	66	2	0	0	1922.02	1567	1584
Mediator of DNA damage checkpoint protein 1	MDC1	MDC1_HUMAN	226.7	100.0%	5	5	9	0.01%	3.5%	TPETLVPTAPK	99.7%	52.4	25	47.7	1	0	0	1153.65	1403	1413
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	5	5	8	0.01%	3.6%	EVGNALLNVVLK	99.7%	45.8	25	26.7	2	0	0	1268.76	1121	1132
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	5	5	8	0.01%	3.6%	FLELLPVSK	97.9%	32.2	25	32.2	1	0	0	1045.63	974	982
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	5	5	8	0.01%	3.6%	FLTEVLLPIVK	99.7%	57.3	25	52	2	0	0	1271.80	1230	1240
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	5	5	8	0.01%	3.6%	LFDLLYPEK	99.7%	46	25	37.2	2	0	0	1137.62	398	406
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	5	5	8	0.01%	3.6%	YNIVTLDR	99.7%	44.3	25	38.6	1	0	0	993.54	857	864
Melanoma-associated antigen D2	MAGED2	MAGD2_HUMAN	65.0	100.0%	5	5	8	0.01%	8.8%	ALEVSEDVK	99.1%	36.1	25	19.5	1	0	0	989.52	48	56
Melanoma-associated antigen D2	MAGED2	MAGD2_HUMAN	65.0	100.0%	5	5	8	0.01%	8.8%	EYTDVYPEIIER	99.7%	60.8	25	60.8	2	0	0	1526.74	312	323
Melanoma-associated antigen D2	MAGED2	MAGD2_HUMAN	65.0	100.0%	5	5	8	0.01%	8.8%	GPIAFWAR	99.6%	40.5	25	34.5	1	0	0	917.50	220	227
Melanoma-associated antigen D2	MAGED2	MAGD2_HUMAN	65.0	100.0%	5	5	8	0.01%	8.8%	LQSSQEPEAPPPR	99.7%	73.8	25	67.5	2	0	0	1435.72	262	274
Melanoma-associated antigen D2	MAGED2	MAGD2_HUMAN	65.0	100.0%	5	5	8	0.01%	8.8%	SSEAVIWEVLR	99.7%	60.8	25	22.2	2	0	0	1288.69	386	396
Melanoma-associated antigen G1	NDNL2	MAGG1_HUMAN	34.3	99.8%	2	2	3	0.00%	9.2%	GPGGSQGSQGPSPQGAR	99.3%	37	25	37	2	0	0	1524.72	53	69
Melanoma-associated antigen G1	NDNL2	MAGG1_HUMAN	34.3	99.8%	2	2	3	0.00%	9.2%	VSELVQFLLIK	99.7%	49.3	25	36.2	1	0	0	1288.79	89	99
Metaxin-1	MTX1	MTX1_HUMAN	51.5	99.8%	2	2	2	0.00%	6.2%	QGADTLAFMSLLEEK	99.7%	42.6	25	37	1	0	0	1652.82	238	252
Metaxin-1	MTX1	MTX1_HUMAN	51.5	99.8%	2	2	2	0.00%	6.2%	QTPAGPETEEEPYR	99.7%	56.3	25	54.5	1	0	0	1603.72	403	416
Metaxin-2	MTX2	MTX2_HUMAN	29.8	100.0%	4	4	8	0.01%	20.2%	ANAEYMSPSGK	99.7%	45	25	45	3	0	0	1170.51	61	71
Metaxin-2	MTX2	MTX2_HUMAN	29.8	100.0%	4	4	8	0.01%	20.2%	LGTQPYFFNK	99.7%	50.9	25	40.1	2	0	0	1214.62	197	206
Metaxin-2	MTX2	MTX2_HUMAN	29.8	100.0%	4	4	8	0.01%	20.2%	NYSNLLAFCR	99.7%	56	25	46.7	2	0	0	1257.60	238	247
Metaxin-2	MTX2	MTX2_HUMAN	29.8	100.0%	4	4	8	0.01%	20.2%	VPFIHVGNQVVSELGPIVQFVK	99.7%	51.8	25	51.6	0	1	0	2406.35	72	93
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	36.6%	ADKNEVAAEVAK	99.7%	58.3	25	37.7	2	0	0	1244.65	864	875
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	36.6%	AEVLISTVGPEDCVVPFLTRPK	99.7%	55.8	25	55.8	0	2	0	2427.30	26	47

Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	36.6%	ALEEGLTPQEICDK	99.7%	41.6	25	40.5	1	0	0	1602.77	322	335
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	36.6%	ALTHIDHSLSR	99.7%	37.2	25	34.3	2	2	0	1249.66	120	130
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	36.6%	FFGGYVPEMVLTPDDQR	99.7%	78.6	25	77.9	4	0	0	1970.93	664	680
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	36.6%	FVEGVCPFCGYEEAR	99.7%	72.3	25	72.3	2	0	0	1819.78	400	414
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	36.6%	GEDVLGSVR	99.7%	51.5	25	42.8	1	0	0	931.48	110	118
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	36.6%	GFVLQDTVEQLR	99.7%	80.8	25	67.2	4	0	0	1404.75	377	388
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	36.6%	GLESLPPLRPQQNPVLPVAGER	99.7%	34.8	25	34.8	0	2	0	2367.31	243	264
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	36.6%	GVGVFGDMAQDTGIPADIWR	99.7%	101	25	100	4	0	0	2121.01	599	618
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	36.6%	ITQDIFQQLLK	99.7%	74.8	25	58.5	6	0	0	1346.77	365	375
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	36.6%	KGEDVLGSVR	99.7%	62.7	25	54.1	2	0	0	1059.58	109	118
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	36.6%	LENDQIESLR	99.7%	84.4	25	70.8	2	0	0	1216.62	805	814
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	36.6%	LFVSDGVPGCLPVLAAAGR	99.7%	101	25	96.8	2	0	0	1899.02	3	21
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	36.6%	LINAVELK	99.7%	59.2	25	45.2	2	0	0	899.56	424	431
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	36.6%	NNSELLNNLGNFINR	99.7%	110	25	106	2	0	0	1731.88	642	656
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	36.6%	NPEQVDLYQFMAK	99.7%	72.4	25	67.3	4	0	0	1598.75	542	554
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	36.6%	QLAVAEGKPPEAPK	99.7%	88.6	25	83.6	2	0	0	1434.80	882	895
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	36.6%	QPQPSPAEGR	99.5%	38.6	25	32.4	2	0	0	1066.53	205	214
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	36.6%	QQGVLALRPYLQK	99.7%	62.4	25	59	2	0	0	1513.89	192	204
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	36.6%	RLEEWLGR	99.7%	43.2	25	20.3	2	0	0	1058.57	460	467
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	36.6%	SCPVVQSSQHLFLDLPK	99.7%	81.5	25	74	2	2	0	1955.01	440	456
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	36.6%	TLPGSDWTPNAQFITR	99.7%	74.9	25	71.9	2	0	0	1803.90	468	483
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	36.6%	VPVLQLDSGNYLFSTSAICR	99.7%	143	25	143	2	0	0	2240.14	48	67
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	19	180	0.17%	37.7%	AHAAQVTCVAASPHK	99.7%	93.2	25	90.8	6	10	0	1547.77	165	179
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	19	180	0.17%	37.7%	AHAAQVTCVAASPHKDSVFLSCSEDNR	99.7%	73.8	25	73.8	0	4	0	2957.36	165	191
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	19	180	0.17%	37.7%	CWAGSLWLFK	99.7%	46.8	25	44.9	6	0	0	1267.63	53	62
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	19	180	0.17%	37.7%	DSVFLSCSEDNR	99.7%	71.1	25	66.1	12	0	0	1428.61	180	191
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	19	180	0.17%	37.7%	ETPPPLVPPAAR	99.7%	44.8	25	38.3	5	0	0	1244.70	4	15
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	19	180	0.17%	37.7%	EWNLPPNAPACMER	99.7%	72.9	25	72.9	24	0	0	1684.76	16	29
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	19	180	0.17%	37.7%	FCKYEHDDIVSTVSVLSSGTQAVSGSK	99.7%	104	25	102	0	3	0	2901.39	119	145
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	19	180	0.17%	37.7%	ILLWDTR	99.7%	53.3	25	45.3	18	0	0	916.53	192	198
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	19	180	0.17%	37.7%	KETPPPLVPPAAR	99.7%	50.7	25	44.9	4	1	0	1372.79	3	15
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	19	180	0.17%	37.7%	SDGALLLGASSLSGR	99.7%	126	25	118	31	0	0	1403.75	38	52
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	19	180	0.17%	37.7%	VWDLAQQVVLSSYR	99.7%	118	25	113	18	6	0	1663.88	151	164
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	19	180	0.17%	37.7%	YEHDDIVSTVSVLSSGTQAVSGSK	99.7%	128	25	128	9	11	0	2466.20	122	145
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	19	180	0.17%	37.7%	YRSDGALLLGASSLSGR	99.7%	100	25	94.5	4	8	0	1722.91	36	52
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	7	10	34	0.03%	56.1%	DRSDCLGEHLYVMVNAK	99.7%	47.7	25	47.7	0	2	0	2006.94	69	85
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	7	10	34	0.03%	56.1%	FEEESKEPVADEEEEDSDDDVEPITEFR	99.7%	62.1	25	62.1	0	1	0	3314.39	86	113
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	7	10	34	0.03%	56.1%	GLGTGTLYIAESR	99.7%	105	25	97.5	10	0	0	1337.71	31	43
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	7	10	34	0.03%	56.1%	LEGMLSQSVSSQYNMAGVR	99.7%	108	25	105	6	3	0	2056.98	188	206
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	7	10	34	0.03%	56.1%	QQPDTEAVLNGK	99.7%	81.4	25	79.7	4	0	0	1299.65	19	30
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	7	10	34	0.03%	56.1%	SFPPPGPAEGLLR	99.7%	44.7	25	39.7	5	0	0	1337.72	6	18
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	7	10	34	0.03%	56.1%	TEDSIRDYEDGMEVDTTPTVAGQFEDADVDH	99.7%	80	25	80	0	3	0	3473.45	207	237
Methylsterol monooxygenase 1	MSMO1	MSMO1_HUMAN	35.2	99.8%	2	2	3	0.00%	7.2%	IFGTDSQYNAYNEK	99.7%	96.2	25	96.2	1	0	0	1649.74	271	284
Methylsterol monooxygenase 1	MSMO1	MSMO1_HUMAN	35.2	99.8%	2	2	3	0.00%	7.2%	WYFLLAR	97.6%	31.7	25	31.4	2	0	0	968.54	135	141
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	10	11	19	0.02%	36.9%	DLADVAAR	97.3%	31.1	25	13.9	2	0	0	830.44	102	109
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	10	11	19	0.02%	36.9%	EAEREGATEEAVR	99.7%	44.3	25	30.7	2	1	0	1446.68	110	122
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	10	11	19	0.02%	36.9%	EIIIEERPGQELTDVNGVR	99.7%	55.8	25	49.7	0	2	0	2167.14	294	312
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	10	11	19	0.02%	36.9%	GSLQILDQLLLPK	99.7%	71.7	25	50.5	2	0	0	1437.87	11	23
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	10	11	19	0.02%	36.9%	GVSAVVVGADR	99.7%	80.9	25	68.2	2	0	0	1029.57	239	249
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	10	11	19	0.02%	36.9%	TALTTTISSR	99.7%	68.2	25	60.7	2	0	0	1050.58	351	360
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	10	11	19	0.02%	36.9%	VGTYQLAIVAK	99.7%	74.1	25	68.2	2	0	0	1162.68	260	270

Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	10	11	19	0.02%	36.9%	VICCTEDMLEK	99.7%	48.2	25	44.6	1	0	0	1413.61	125	135
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	10	11	19	0.02%	36.9%	VTVLTHCNTGALATAGYGTALGVIR	99.7%	37	25	37	0	1	0	2516.33	162	186
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	10	11	19	0.02%	36.9%	YEAVGSVHQAWEAIR	99.7%	46.2	25	40.6	0	2	0	1715.85	27	41
Methyltransferase-like protein 13	METTL13	MET13_HUMAN	78.8	99.8%	2	2	3	0.00%	3.3%	LAEAVQER	99.3%	37.3	25	13.3	1	0	0	915.49	242	249
Methyltransferase-like protein 13	METTL13	MET13_HUMAN	78.8	99.8%	2	2	3	0.00%	3.3%	LATPELLETAQALER	99.7%	85.2	25	75.1	2	0	0	1654.90	660	674
Microsomal glutathione S-transferase 1	MGST1	MGST1_HUMAN	17.6	100.0%	3	6	16	0.02%	27.1%	IYHTIAYLTPLPQPNR	99.7%	68.4	25	68.4	2	1	0	1897.03	115	130
Microsomal glutathione S-transferase 1	MGST1	MGST1_HUMAN	17.6	100.0%	3	6	16	0.02%	27.1%	KVFANPEDCVAFGK	99.7%	67	25	54	2	2	0	1581.77	42	55
Microsomal glutathione S-transferase 1	MGST1	MGST1_HUMAN	17.6	100.0%	3	6	16	0.02%	27.1%	MMLMSTATAFYR	99.7%	104	25	104	9	0	0	1422.66	27	38
Microtubule-associated protein 1B	MAP1B	MAP1B_HUMAN	270.6	100.0%	2	2	4	0.00%	1.0%	AVLDALLEGK	99.7%	44.8	25	33.2	2	0	0	1028.60	2400	2409
Microtubule-associated protein 1B	MAP1B	MAP1B_HUMAN	270.6	100.0%	2	2	4	0.00%	1.0%	SVGNTIDPVILFQK	99.7%	56.8	25	51.7	2	0	0	1530.85	401	414
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	4	4	6	0.01%	0.8%	APAVQDLLTR	99.7%	57.6	25	51.8	2	0	0	1083.62	3340	3349
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	4	4	6	0.01%	0.8%	FLQQEQSVFR	98.4%	33.3	25	23.4	1	0	0	1281.66	155	164
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	4	4	6	0.01%	0.8%	GEPVLLVGETGTGK	99.7%	90.7	25	90.7	2	0	0	1356.74	670	683
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	4	4	6	0.01%	0.8%	LLEEAQLQDLEK	99.7%	54.7	25	53.6	1	0	0	1428.76	222	233
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	13	13	22	0.02%	17.0%	ADPLALAAEK	99.2%	36.6	25	29.5	1	0	0	998.55	61	70
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	13	13	22	0.02%	17.0%	AMVEAVQLIADGK	99.7%	84.4	25	74.3	2	0	0	1344.72	197	209
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	13	13	22	0.02%	17.0%	DLGEEALNEYLK	99.7%	60.7	25	50.5	2	0	0	1393.68	904	915
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	13	13	22	0.02%	17.0%	EESFGPIMVISK	97.8%	32.1	25	32.1	1	0	0	1336.68	824	835
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	13	13	22	0.02%	17.0%	FLFPEGIK	98.5%	33.7	25	20	1	0	0	950.53	189	196
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	13	13	22	0.02%	17.0%	GVINIIPGSGGIAGQR	99.5%	38.9	25	38.9	2	0	0	1508.85	642	657
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	13	13	22	0.02%	17.0%	HGSIIYHPSILPR	99.7%	36.3	25	0	0	2	0	1489.83	122	134
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	13	13	22	0.02%	17.0%	IPQPEEGATYEGIQK	99.7%	75.2	25	0	2	0	0	1659.82	213	227
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	13	13	22	0.02%	17.0%	LGFTGSTPIGK	99.7%	60.6	25	54.9	2	0	0	1077.59	667	677
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	13	13	22	0.02%	17.0%	LLQYCETGVK	99.7%	43.4	25	37.4	2	0	0	1210.61	779	788
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	13	13	22	0.02%	17.0%	SPLIIFNDCELDK	99.7%	52	25	48.4	2	0	0	1563.77	699	711
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	13	13	22	0.02%	17.0%	VSYASLADVDK	99.7%	61.6	25	58.8	2	0	0	1167.59	474	484
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	13	13	22	0.02%	17.0%	VVGVFTVPDKDGK	99.7%	43.8	25	35.8	1	0	0	1360.75	48	60
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	17	34	0.03%	50.6%	AVIGMTAGATGAFVGTPAEVALIR	99.7%	115	25	115	4	4	0	2273.23	123	146
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	17	34	0.03%	50.6%	AVVVNAAQLASYSQSK	99.7%	131	25	125	1	0	0	1635.87	191	206
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	17	34	0.03%	50.6%	EEGVLTLWR	99.7%	53.8	25	43.9	1	0	0	1102.59	174	182
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	17	34	0.03%	50.6%	FLFGGLAGMGATVFVQPLDLVK	99.7%	47.8	25	47.8	1	0	0	2296.24	25	46
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	17	34	0.03%	50.6%	GIYTGLSAGLLR	99.7%	73	25	64.4	2	0	0	1220.70	79	90
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	17	34	0.03%	50.6%	ITREEGVLTLWR	99.2%	30	25	25.1	0	1	0	1472.82	171	182
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	17	34	0.03%	50.6%	LGIYTVLFER	99.7%	81.9	25	78.1	6	0	0	1210.68	99	108
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	17	34	0.03%	50.6%	LTGADGTPPGFLLK	99.7%	49.4	25	39.9	2	0	0	1386.76	109	122
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	17	34	0.03%	50.6%	MIDGKPEYK	99.0%	35.8	25	29.4	2	0	0	1080.54	252	260
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	17	34	0.03%	50.6%	MTADGRLPADQR	99.3%	37.3	25	25.1	1	0	0	1330.65	147	158
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	17	34	0.03%	50.6%	NVFNALIR	99.7%	44	25	29.6	3	0	0	946.55	163	170
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	17	34	0.03%	50.6%	TSFHALTSILK	99.7%	68.3	25	53.8	2	2	0	1217.69	63	73
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	17	34	0.03%	50.6%	YEGFFSLWK	95.8%	29.2	25	26.9	2	0	0	1176.57	272	280
Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20	MCAT_HUMAN	32.9	100.0%	4	4	6	0.01%	14.3%	CLLQIQASSGESK	99.7%	104	25	94.2	2	0	0	1420.71	136	148
Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20	MCAT_HUMAN	32.9	100.0%	4	4	6	0.01%	14.3%	ELIRDEGVTSLYK	99.7%	47.1	25	46.7	1	0	0	1522.81	255	267
Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20	MCAT_HUMAN	32.9	100.0%	4	4	6	0.01%	14.3%	VSELSAPR	97.2%	31	25	14.8	1	0	0	858.47	204	211
Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20	MCAT_HUMAN	32.9	100.0%	4	4	6	0.01%	14.3%	YTGTLDCAK	99.7%	45.3	25	33.8	2	0	0	1028.47	149	157
Mitochondrial carrier homolog 2	MTCH2	MTCH2_HUMAN	33.3	100.0%	3	3	4	0.00%	12.5%	GLFTGLTPR	99.7%	51.5	25	25	1	0	0	961.55	69	77
Mitochondrial carrier homolog 2	MTCH2	MTCH2_HUMAN	33.3	100.0%	3	3	4	0.00%	12.5%	SMVQFIGR	97.7%	31.9	25	22.1	1	0	0	937.49	148	155
Mitochondrial carrier homolog 2	MTCH2	MTCH2_HUMAN	33.3	100.0%	3	3	4	0.00%	12.5%	VLQHYQESDKGEELGPGNVQK	99.7%	34.5	25	34.5	0	2	0	2355.16	91	111
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	26	0.02%	48.4%	FAIYETVR	99.4%	38.5	25	29.2	2	0	0	998.53	79	86
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	26	0.02%	48.4%	GALVTVGQLSCYDQAK	99.7%	91.1	25	91.1	2	0	0	1709.85	171	186
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	26	0.02%	48.4%	GEYQGVFHCAVETAK	99.7%	60.2	25	60.2	2	0	0	1695.78	232	246
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	26	0.02%	48.4%	GSQGPLPFHEK	97.3%	31.1	25	20.8	2	0	0	1196.61	92	102

Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	26	0.02%	48.4%	LFSGATMASSR	99.7%	68.5	25	59.3	2	0	0	1143.55	160	170
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	26	0.02%	48.4%	LGPLAFYK	99.7%	55.1	25	42	2	0	0	908.52	247	254
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	26	0.02%	48.4%	NYAHALDGLYR	99.7%	50.8	25	45.8	2	0	0	1292.64	140	150
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	26	0.02%	48.4%	QMTYSLTR	99.7%	60.8	25	50.9	2	0	0	999.49	71	78
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	26	0.02%	48.4%	TDGILALYSGLSASLCR	99.7%	93.4	25	90.4	2	0	0	1796.92	54	70
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	26	0.02%	48.4%	VHLQTQQEVK	99.7%	51.8	25	49.5	2	2	0	1209.66	32	41
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	26	0.02%	48.4%	VLLGSVSGLAGGFVGTPADLVNVR	99.7%	73.9	25	73.9	2	2	0	2298.28	103	126
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	6	6	13	0.01%	30.1%	KLYPTVGKPSSS	99.7%	42.7	25	34	2	0	0	1263.69	155	166
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	6	6	13	0.01%	30.1%	LYPTVGKPSSS	99.7%	43.8	25	30.4	2	0	0	1135.60	156	166
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	6	6	13	0.01%	30.1%	SVDFLLDSSLR	99.7%	76.9	25	51	2	0	0	1251.66	144	154
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	6	6	13	0.01%	30.1%	SVDFLLDSSLRK	99.7%	70.8	25	61.9	2	0	0	1379.75	144	155
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	6	6	13	0.01%	30.1%	VCAASLYVLGTATR	99.7%	104	25	90.9	1	0	0	1481.78	103	116
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	6	6	13	0.01%	30.1%	YLGYANEVGEAFR	99.7%	83.7	25	81.4	4	0	0	1488.71	21	33
Mitochondrial folate transporter/carrier	SLC25A32	MFTC_HUMAN	35.4	99.8%	2	2	3	0.00%	8.3%	FAVSDGLELRPK	99.7%	71.9	25	67.5	2	0	0	1331.73	50	61
Mitochondrial folate transporter/carrier	SLC25A32	MFTC_HUMAN	35.4	99.8%	2	2	3	0.00%	8.3%	IFAVAATYPYQVVR	99.7%	59.5	25	50.6	1	0	0	1597.87	236	249
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	8	8	13	0.01%	32.5%	GAAVNLTLVTPEK	99.7%	62.4	25	55.6	2	0	0	1312.75	68	80
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	8	8	13	0.01%	32.5%	GLGATLLR	94.9%	28.5	25	10.4	1	0	0	800.50	189	196
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	8	8	13	0.01%	32.5%	GVNEDTYSGILDCAR	99.7%	103	25	103	2	0	0	1669.75	259	273
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	8	8	13	0.01%	32.5%	HEGPSAFLK	95.0%	28.6	25	24.9	1	0	0	985.51	278	286
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	8	8	13	0.01%	32.5%	ILAAQGQLSAQGGAQPSVEAPAAPRPTATQLTR	99.7%	131	25	131	0	1	0	3256.74	143	175
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	8	8	13	0.01%	32.5%	IQLQDAGR	99.7%	48.5	25	30.9	2	0	0	900.49	129	136
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	8	8	13	0.01%	32.5%	LAANDFFR	99.7%	55.5	25	42	2	0	0	953.48	84	91
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	8	8	13	0.01%	32.5%	VYTSMSDCLIK	99.7%	50.6	25	45.3	2	0	0	1316.62	45	55
Mitochondrial import inner membrane translocase subunit Tim13	TIMM13	TIM13_HUMAN	10.5	100.0%	3	3	4	0.00%	36.8%	LDPGLIMEQVK	97.3%	31.1	25	27.4	1	0	0	1258.67	17	27
Mitochondrial import inner membrane translocase subunit Tim13	TIMM13	TIM13_HUMAN	10.5	100.0%	3	3	4	0.00%	36.8%	VQIAVANAQELLQR	99.7%	97.5	25	83.6	2	0	0	1552.88	28	41
Mitochondrial import inner membrane translocase subunit Tim13	TIMM13	TIM13_HUMAN	10.5	100.0%	3	3	4	0.00%	36.8%	YMDAWNTVSR	99.7%	42	25	42	1	0	0	1242.56	73	82
Mitochondrial import inner membrane translocase subunit Tim21	TIMM21	TIM21_HUMAN	28.2	99.8%	2	2	3	0.00%	8.5%	ENPGSGEYDFR	99.7%	52	25	45	1	0	0	1270.53	214	224
Mitochondrial import inner membrane translocase subunit Tim21	TIMM21	TIM21_HUMAN	28.2	99.8%	2	2	3	0.00%	8.5%	FYIEGSEPGK	99.7%	50.5	25	48.5	2	0	0	1126.54	195	204
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	8	9	21	0.02%	28.9%	AQGPQQQPGSEGPSYAK	99.7%	81.2	25	77.6	6	0	0	1729.81	48	64
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	8	9	21	0.02%	28.9%	IPDEFDNDPILVQQLR	99.7%	76.9	25	61.1	2	0	0	1911.98	98	113
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	8	9	21	0.02%	28.9%	QNLFLGSLTSR	99.7%	59.4	25	46.2	3	0	0	1235.67	335	345
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	8	9	21	0.02%	28.9%	RAPDQAAEIGSR	99.7%	54.1	25	48	2	2	0	1270.65	32	43
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	8	9	21	0.02%	28.9%	TIALNGVEDVR	99.7%	89.8	25	77	2	0	0	1186.64	285	295
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	8	9	21	0.02%	28.9%	TVLEHYALEDDPLAAFK	99.7%	36.9	25	35.5	0	1	0	1931.98	296	312
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	8	9	21	0.02%	28.9%	VLLDLSAFLK	99.7%	47.8	25	47.8	2	0	0	1118.68	275	284
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	8	9	21	0.02%	28.9%	VVVVDCKK	97.5%	31.5	25	31.5	1	0	0	946.54	244	251
Mitochondrial import receptor subunit TOM22 homolog	TOMM22	TOM22_HUMAN	15.5	100.0%	3	5	14	0.01%	33.8%	LQMEQQQQLQQR	99.7%	73.8	25	60	9	0	0	1557.78	106	117
Mitochondrial import receptor subunit TOM22 homolog	TOMM22	TOM22_HUMAN	15.5	100.0%	3	5	14	0.01%	33.8%	LWGLTEMFPER	99.7%	48.5	25	40.4	4	0	0	1394.68	48	58
Mitochondrial import receptor subunit TOM22 homolog	TOMM22	TOM22_HUMAN	15.5	100.0%	3	5	14	0.01%	33.8%	QILLGPNTGLSGGMPGALPSLPGKI	99.3%	37.7	25	37.7	1	0	0	2404.33	118	142
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	6	10	20	0.02%	21.1%	ELFPIQMEGVK	99.7%	52.8	25	40.6	4	0	0	1290.68	92	102
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	6	10	20	0.02%	21.1%	FVNWQVDGEYR	99.7%	66.6	25	66.2	2	0	0	1412.66	185	195
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	6	10	20	0.02%	21.1%	GSVDSNWIVGATLEK	99.7%	102	25	91.8	2	0	0	1575.80	316	330
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	6	10	20	0.02%	21.1%	MAIQTQQSK	99.4%	38.1	25	33.5	2	0	0	1034.53	176	184
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	6	10	20	0.02%	21.1%	MQDTSVSFGYQLDLPK	99.7%	93.3	25	93.3	4	0	0	1844.87	294	309
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	6	10	20	0.02%	21.1%	RPGEEGTVMSLAGK	99.7%	63	25	56.8	4	2	0	1447.72	240	253
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	20	52	0.05%	26.4%	AAMDNSEIAGEKK	99.7%	68.6	25	59.2	5	0	0	1363.65	258	270
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	20	52	0.05%	26.4%	AVDEAADALLK	99.7%	72.7	25	57.2	4	0	0	1115.59	287	297
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	20	52	0.05%	26.4%	ELDSITPEVLPGWK	99.7%	48.6	25	47.4	4	0	0	1583.83	372	385
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	20	52	0.05%	26.4%	ERPPEEVAAR	99.7%	43.7	25	33.5	4	0	0	1153.60	196	205
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	20	52	0.05%	26.4%	EVAGAKPHITAAEGK	99.7%	44.6	25	36.8	1	1	0	1478.80	316	330
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	20	52	0.05%	26.4%	GIEQAVQSHAVAEEEAR	99.7%	49.9	25	47.5	0	3	0	1823.89	548	564

Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	20	52	0.05%	26.4%	GVYSEETLR	99.7%	66.5	25	55	4	0	0	1053.52	624	632
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	20	52	0.05%	26.4%	ISSVSEVMK	95.0%	28.6	25	16.9	1	0	0	995.51	111	119
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	20	52	0.05%	26.4%	LFEMVLGPAAYNVPLPK	99.6%	40	25	36.4	1	0	0	1859.01	85	101
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	20	52	0.05%	26.4%	LHNMIVDLDNVVK	99.6%	40.4	25	34.3	1	0	0	1509.81	331	343
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	20	52	0.05%	26.4%	LSEQELQFR	99.7%	70.9	25	38.6	4	0	0	1149.59	517	525
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	20	52	0.05%	26.4%	SEFEQNLSEK	99.7%	51.6	25	42.5	4	0	0	1210.56	507	516
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	20	52	0.05%	26.4%	TSSAETPTIPLGSAVEAIK	99.7%	83.2	25	79.3	2	0	0	1872.00	582	600
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	20	52	0.05%	26.4%	VAMIDETR	99.3%	37.4	25	26.9	4	0	0	934.47	645	652
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	20	52	0.05%	26.4%	VVSQYHELVVQAR	99.7%	72.7	25	67.2	3	2	0	1527.83	354	366
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	20	52	0.05%	26.4%	YSTSGSSGLTTGK	99.7%	71.6	25	69.8	4	0	0	1245.60	33	45
Mitochondrial inner membrane protein OXA1L	OXA1L	OXA1L_HUMAN	48.5	100.0%	5	6	10	0.01%	11.3%	ASSEMALYQK	99.7%	64.2	25	48.4	3	0	0	1143.54	198	207
Mitochondrial inner membrane protein OXA1L	OXA1L	OXA1L_HUMAN	48.5	100.0%	5	6	10	0.01%	11.3%	CLIFPLIVTGQR	99.7%	65	25	52.6	2	0	0	1416.80	153	164
Mitochondrial inner membrane protein OXA1L	OXA1L	OXA1L_HUMAN	48.5	100.0%	5	6	10	0.01%	11.3%	EGFLESFKK	94.9%	28.5	25	19.8	1	0	0	1084.57	359	367
Mitochondrial inner membrane protein OXA1L	OXA1L	OXA1L_HUMAN	48.5	100.0%	5	6	10	0.01%	11.3%	LAGDHIEYYK	99.7%	51.4	25	44	2	0	0	1208.59	188	197
Mitochondrial inner membrane protein OXA1L	OXA1L	OXA1L_HUMAN	48.5	100.0%	5	6	10	0.01%	11.3%	NQLELAAR	99.7%	57.7	25	33.7	2	0	0	914.51	387	394
Mitochondrial pyruvate carrier 2	MPC2	MPC2_HUMAN	14.3	99.8%	2	2	3	0.00%	14.2%	TVFFWAPIMK	98.6%	34.2	25	21	1	0	0	1255.65	40	49
Mitochondrial pyruvate carrier 2	MPC2	MPC2_HUMAN	14.3	99.8%	2	2	3	0.00%	14.2%	YSLVIIPK	99.7%	47.5	25	46.6	2	0	0	932.58	85	92
Mitochondrial Rho GTPase 2	RHOT2	MIRO2_HUMAN	68.1	100.0%	4	4	7	0.01%	6.6%	ILLLGEAQVGK	99.7%	66.9	25	39.4	2	0	0	1140.70	7	17
Mitochondrial Rho GTPase 2	RHOT2	MIRO2_HUMAN	68.1	100.0%	4	4	7	0.01%	6.6%	NISELFYYAQK	96.1%	29.5	25	11	1	0	0	1375.69	154	164
Mitochondrial Rho GTPase 2	RHOT2	MIRO2_HUMAN	68.1	100.0%	4	4	7	0.01%	6.6%	SAFLQAFLGR	99.7%	60.4	25	57.2	2	0	0	1109.61	430	439
Mitochondrial Rho GTPase 2	RHOT2	MIRO2_HUMAN	68.1	100.0%	4	4	7	0.01%	6.6%	VPIILVGNK	99.7%	47.4	25	0	2	0	0	952.62	111	119
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	18	37	0.04%	51.6%	DSIIYLTADSPNVMTTFR	99.7%	91	25	91	4	0	0	2044.01	285	302
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	18	37	0.04%	51.6%	ELQNTVSQLLESEGWNRR	98.7%	27.8	25	27.8	0	1	0	2159.08	219	236
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	18	37	0.04%	51.6%	EVPEHITEEELK	99.7%	59.5	25	44.4	2	0	0	1452.72	107	118
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	18	37	0.04%	51.6%	LLETTEEDKQK	99.7%	72.4	25	63.3	2	0	0	1333.68	165	175
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	18	37	0.04%	51.6%	LLLTSTEK	99.7%	43.7	25	33	3	0	0	904.54	269	276
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	18	37	0.04%	51.6%	LNLATECLPLDK	99.7%	71.2	25	50.7	2	0	0	1386.73	329	340
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	18	37	0.04%	51.6%	NESTPPSEELELDKWK	99.7%	71.5	25	65.7	2	0	0	1901.91	52	67
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	18	37	0.04%	51.6%	NFLFLR	98.9%	35.2	25	11.3	2	0	0	809.47	176	181
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	18	37	0.04%	51.6%	NLTLDQMIR	97.7%	31.7	25	13.2	1	0	0	1119.58	350	358
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	18	37	0.04%	51.6%	NNGNWQEALQFVPK	99.7%	50.8	25	41.7	2	0	0	1644.81	365	378
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	18	37	0.04%	51.6%	NVDPFHIYFCNLK	99.7%	52.2	25	45.2	2	0	0	1666.80	237	249
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	18	37	0.04%	51.6%	SMQPGTSLAK	99.7%	41.1	25	34	2	0	0	1019.52	316	325
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	18	37	0.04%	51.6%	SSVQEECVSTISSSKDEDPLAATR	99.7%	55.3	25	55.3	0	2	0	2596.20	72	95
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	18	37	0.04%	51.6%	TLMECVSNTAK	99.7%	56.9	25	56.9	4	0	0	1253.59	119	129
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	18	37	0.04%	51.6%	VYVIGSFVDK	99.7%	50.8	25	50.3	3	0	0	1126.61	306	315
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	18	37	0.04%	51.6%	YLQWEIGNK	99.7%	43.1	25	41.4	2	0	0	1150.59	341	349
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	17	18	37	0.04%	51.6%	YQEKWDK	97.7%	31.9	25	20	1	0	0	996.48	262	268
Mitochondrial ribonuclease P protein 3	KIAA0391	MRRP3_HUMAN	67.3	100.0%	4	4	7	0.01%	8.6%	EALLLLEDIKK	99.7%	45.3	25	42.8	2	0	0	1284.78	228	238
Mitochondrial ribonuclease P protein 3	KIAA0391	MRRP3_HUMAN	67.3	100.0%	4	4	7	0.01%	8.6%	ESQLLLNVVSQLAK	99.7%	74.6	25	70.1	2	0	0	1541.89	422	435
Mitochondrial ribonuclease P protein 3	KIAA0391	MRRP3_HUMAN	67.3	100.0%	4	4	7	0.01%	8.6%	LLDILSYLR	99.7%	62.3	25	62.3	2	0	0	1105.66	301	309
Mitochondrial ribonuclease P protein 3	KIAA0391	MRRP3_HUMAN	67.3	100.0%	4	4	7	0.01%	8.6%	SRPPFDVVIDGLNVAK	96.4%	23.8	25	23.8	0	1	0	1726.95	400	415
Mitochondrial thiamine pyrophosphate carrier	SLC25A19	TPC_HUMAN	35.5	100.0%	3	3	4	0.00%	8.8%	ALISPFDVIK	99.0%	35.5	25	34.6	1	0	0	1102.65	31	40
Mitochondrial thiamine pyrophosphate carrier	SLC25A19	TPC_HUMAN	35.5	100.0%	3	3	4	0.00%	8.8%	EGALGFFK	99.5%	39	25	30.8	2	0	0	868.46	276	283
Mitochondrial thiamine pyrophosphate carrier	SLC25A19	TPC_HUMAN	35.5	100.0%	3	3	4	0.00%	8.8%	VGYDPKPDGR	97.7%	31.8	25	27.3	1	0	0	1103.55	2	11
Mitochondrial translocator assembly and maintenance protein 41 homolog	TAMM41	TAM41_HUMAN	51.1	99.8%	2	2	4	0.00%	6.0%	ELYGSILQENPQVVYK	99.7%	85.1	25	85.1	2	0	0	1879.98	214	229
Mitochondrial translocator assembly and maintenance protein 41 homolog	TAMM41	TAM41_HUMAN	51.1	99.8%	2	2	4	0.00%	6.0%	IISVNEDVTLR	98.8%	34.9	25	33.1	2	0	0	1258.70	140	150
Mitotic checkpoint protein BUB3	BUB3	BUB3_HUMAN	37.2	100.0%	4	4	7	0.01%	15.2%	LNQPPEDGISSVK	98.9%	35.4	25	35.4	2	0	0	1383.71	9	21
Mitotic checkpoint protein BUB3	BUB3	BUB3_HUMAN	37.2	100.0%	4	4	7	0.01%	15.2%	TPCNAGTFSQPEK	99.7%	43.7	25	36.9	1	0	0	1436.65	127	139
Mitotic checkpoint protein BUB3	BUB3	BUB3_HUMAN	37.2	100.0%	4	4	7	0.01%	15.2%	VAVEYLDPSPEVQK	99.7%	52.6	25	50.7	2	0	0	1573.81	203	216
Mitotic checkpoint protein BUB3	BUB3	BUB3_HUMAN	37.2	100.0%	4	4	7	0.01%	15.2%	VYTLSVSGDR	99.7%	70.9	25	61.1	2	0	0	1096.56	140	149

Mitotic spindle assembly checkpoint protein MAD2A	MAD2L1	MD2L1_HUMAN	23.5	100.0%	2	2	3	0.00%	9.3%	GIYPSETFTR	99.4%	37.8	25	37.5	2	0	0	1170.58	36	45
Mitotic spindle assembly checkpoint protein MAD2A	MAD2L1	MD2L1_HUMAN	23.5	100.0%	2	2	3	0.00%	9.3%	WQFDIECDK	98.1%	32.7	25	32.3	1	0	0	1240.53	100	108
Mitotic spindle-associated MMXD complex subunit MIP18	FAM96B	MIP18_HUMAN	17.7	100.0%	3	3	5	0.00%	30.7%	EIFDLIR	99.7%	42.2	25	20.6	2	0	0	905.51	45	51
Mitotic spindle-associated MMXD complex subunit MIP18	FAM96B	MIP18_HUMAN	17.7	100.0%	3	3	5	0.00%	30.7%	SGERPVTAGEEDEQVPDSIDAR	99.7%	33.7	25	22.5	0	1	0	2357.09	23	44
Mitotic spindle-associated MMXD complex subunit MIP18	FAM96B	MIP18_HUMAN	17.7	100.0%	3	3	5	0.00%	30.7%	VGGGGVGGGLLENANPLIYQR	99.7%	83.8	25	83.8	2	0	0	2041.08	2	22
MKI67 FHA domain-interacting nucleolar phosphoprotein	NIFK	MK67I_HUMAN	34.2	100.0%	4	4	6	0.01%	17.4%	GIDYDFPSLILQK	99.7%	63.1	25	63.1	3	0	0	1508.80	180	192
MKI67 FHA domain-interacting nucleolar phosphoprotein	NIFK	MK67I_HUMAN	34.2	100.0%	4	4	6	0.01%	17.4%	GYAFVEFESEDVAK	99.7%	61	25	56.5	1	0	0	1590.73	87	100
MKI67 FHA domain-interacting nucleolar phosphoprotein	NIFK	MK67I_HUMAN	34.2	100.0%	4	4	6	0.01%	17.4%	IVAETMNNYLFGER	99.7%	57.3	25	54.1	1	0	0	1656.81	101	114
MKI67 FHA domain-interacting nucleolar phosphoprotein	NIFK	MK67I_HUMAN	34.2	100.0%	4	4	6	0.01%	17.4%	VSGTLDTPEK	99.7%	41.2	25	22.2	1	0	0	1046.54	217	226
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	10	10	15	0.01%	11.7%	AIFQEVHVQSLPQVDR	97.1%	24.7	25	24.3	0	1	0	1865.99	133	148
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	10	10	15	0.01%	11.7%	EDLILSLR	99.7%	45.3	25	15.7	2	0	0	958.56	239	246
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	10	10	15	0.01%	11.7%	EVFQTASER	99.7%	53.5	25	41.2	2	0	0	1066.52	308	316
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	10	10	15	0.01%	11.7%	FAEFLLPLLIEK	99.7%	66.6	25	57.6	3	0	0	1432.85	255	266
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	10	10	15	0.01%	11.7%	FLNLSSSPSMAVR	99.7%	46.6	25	46.6	1	0	0	1424.72	959	971
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	10	10	15	0.01%	11.7%	GEWFLLGSPGS	97.7%	31.8	25	20.6	1	0	0	1149.56	1020	1030
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	10	10	15	0.01%	11.7%	IVHDLISR	99.2%	36.9	25	35.2	1	0	0	952.56	196	203
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	10	10	15	0.01%	11.7%	LLQAAAGASAR	99.7%	90.3	25	84.4	2	0	0	1028.58	374	384
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	10	10	15	0.01%	11.7%	LPTPVLLPYKPQVIR	98.1%	26.4	25	26.4	0	1	0	1734.07	984	998
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	10	10	15	0.01%	11.7%	VEAEGLAALHSLTACLSR	99.7%	38.9	25	37.4	0	1	0	1897.98	317	334
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	6	6	14	0.01%	22.8%	EFNLLDPK	97.0%	30.7	25	14.8	1	0	0	975.51	188	195
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	6	6	14	0.01%	22.8%	EFPSSFESLVR	99.7%	49.6	25	49	2	0	0	1297.64	135	145
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	6	6	14	0.01%	22.8%	ELVVLPR	98.8%	34.7	25	13.2	2	0	0	825.52	42	48
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	6	6	14	0.01%	22.8%	ITDFQFK	99.2%	36.8	25	18	2	0	0	898.47	35	41
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	6	6	14	0.01%	22.8%	KAYLEPEHTK	99.7%	39.4	25	37.9	0	3	0	1215.64	23	32
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	6	6	14	0.01%	22.8%	LVTDEDVFPTK	99.7%	64.7	25	57.5	4	0	0	1263.65	121	131
Monocarboxylate transporter 1	SLC16A1	MOT1_HUMAN	53.9	100.0%	4	5	16	0.02%	8.4%	DLHDANTDLIGR	99.7%	54.1	25	52	8	1	0	1339.66	225	236
Monocarboxylate transporter 1	SLC16A1	MOT1_HUMAN	53.9	100.0%	4	5	16	0.02%	8.4%	ESKEEETSIDVAGKPNEVTK	99.7%	44.5	25	44.5	0	4	0	2190.08	460	479
Monocarboxylate transporter 1	SLC16A1	MOT1_HUMAN	53.9	100.0%	4	5	16	0.02%	8.4%	KDLHDANTDLIGR	99.7%	48.8	25	47.8	0	1	0	1467.76	224	236
Monocarboxylate transporter 1	SLC16A1	MOT1_HUMAN	53.9	100.0%	4	5	16	0.02%	8.4%	LNDMYGDYK	98.7%	34.3	25	28.2	2	0	0	1118.48	412	420
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	45	0.04%	27.1%	AEIDLVCELAK	99.7%	75.7	25	59.7	2	0	0	1260.65	808	818
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	45	0.04%	27.1%	ASGLVPNVVVLVATVR	99.7%	59.9	25	59.9	2	0	0	1593.97	730	745
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	45	0.04%	27.1%	AVIELLEK	99.7%	41.9	25	15.9	2	0	0	914.56	206	213
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	45	0.04%	27.1%	DFILPISDVR	99.7%	46.1	25	37.4	2	0	0	1174.65	926	935
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	45	0.04%	27.1%	DIELSPEAQAK	99.7%	62.4	25	54.4	2	0	0	1200.61	881	891
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	45	0.04%	27.1%	DVDGVTDINLGK	99.7%	76.3	25	68.5	2	0	0	1245.63	178	189
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	45	0.04%	27.1%	EFSEIQLAR	99.7%	63.5	25	34	2	0	0	1092.57	531	539
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	45	0.04%	27.1%	EIGLLADEIEIYGK	99.7%	92.9	25	91.9	2	0	0	1562.83	380	393
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	45	0.04%	27.1%	EVLSLLQEK	99.5%	38.9	25	25.8	2	0	0	1058.61	84	92
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	45	0.04%	27.1%	FQFLYDVQVPIVDK	99.7%	94.1	25	92.3	2	0	0	1710.91	855	868
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	45	0.04%	27.1%	ILHENTQTDK	98.6%	27.4	25	23.5	2	1	0	1198.61	507	516
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	45	0.04%	27.1%	IQNMVSSGR	99.7%	52.3	25	45.2	2	0	0	991.50	327	335
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	45	0.04%	27.1%	KITIGQGNTEK	99.7%	49.1	25	36.1	2	0	0	1188.66	586	596
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	45	0.04%	27.1%	LDIDPSTITWQR	99.4%	38.3	25	32.8	1	0	0	1444.74	564	575
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	45	0.04%	27.1%	LQPLSPVPSDIEISR	99.7%	68.6	25	68.6	2	0	0	1650.91	353	367
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	45	0.04%	27.1%	LVPLVNGVR	99.2%	36.9	25	33.9	1	0	0	966.61	522	530
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	45	0.04%	27.1%	MHGGGPSVTAGVPLKK	99.7%	35	25	34.9	0	4	0	1535.84	749	764
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	45	0.04%	27.1%	SGQPVTADDLGVTGALTVLMK	99.7%	91.7	25	91.7	2	0	0	2073.09	639	659
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	45	0.04%	27.1%	TDPSTLTEEEVSK	99.7%	78.9	25	70.9	2	0	0	1435.68	548	560
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	45	0.04%	27.1%	TIAQAVYGAK	99.7%	50.4	25	28	2	0	0	1021.57	871	880
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	45	0.04%	27.1%	VLNALKPEK	99.7%	44.9	25	36	2	0	0	1011.62	169	177
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	45	0.04%	27.1%	YVLVAGITPTPLGEGK	99.7%	100	25	100	2	0	0	1614.91	414	429

Motile sperm domain-containing protein 2	MOSPD2	MSPD2_HUMAN	59.7	100.0%	4	4	7	0.01%	8.5%	EISVNDLNESSIPR	99.7%	73.9	25	73.9	1	0	0	1572.79	74	87
Motile sperm domain-containing protein 2	MOSPD2	MSPD2_HUMAN	59.7	100.0%	4	4	7	0.01%	8.5%	LIAFWLER	99.7%	52.6	25	40.3	2	0	0	1047.60	128	135
Motile sperm domain-containing protein 2	MOSPD2	MSPD2_HUMAN	59.7	100.0%	4	4	7	0.01%	8.5%	TLIVLTNVTK	99.7%	49.7	25	49.7	2	0	0	1101.69	348	357
Motile sperm domain-containing protein 2	MOSPD2	MSPD2_HUMAN	59.7	100.0%	4	4	7	0.01%	8.5%	TWLGPEAVSLLK	99.5%	39.4	25	24.1	2	0	0	1313.75	200	211
mRNA export factor	RAE1	RAE1L_HUMAN	41.0	100.0%	5	5	6	0.01%	16.0%	CWEVQDSGQTIPK	99.7%	62.3	25	62.3	1	0	0	1547.72	68	80
mRNA export factor	RAE1	RAE1L_HUMAN	41.0	100.0%	5	5	6	0.01%	16.0%	GHEFYNPQK	97.9%	32.2	25	22.5	1	0	0	1119.52	341	349
mRNA export factor	RAE1	RAE1L_HUMAN	41.0	100.0%	5	5	6	0.01%	16.0%	NAAEELKPR	98.8%	34.9	25	25.2	2	0	0	1027.55	357	365
mRNA export factor	RAE1	RAE1L_HUMAN	41.0	100.0%	5	5	6	0.01%	16.0%	QNKPTGFALGSIEGR	99.7%	34.6	25	34.3	0	1	0	1574.83	225	239
mRNA export factor	RAE1	RAE1L_HUMAN	41.0	100.0%	5	5	6	0.01%	16.0%	SSNPMMVLQLPER	99.6%	39.9	25	28.8	1	0	0	1533.74	160	172
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	9	11	19	0.02%	40.6%	EGDVLTPEQAR	99.7%	43.8	25	32	2	0	0	1214.60	178	188
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	9	11	19	0.02%	40.6%	GEVGLLFTNR	99.7%	73.3	25	67.3	2	0	0	1105.60	98	107
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	9	11	19	0.02%	40.6%	GVVTLLSDYEVCK	99.7%	69.4	25	63.7	1	0	0	1482.75	165	177
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	9	11	19	0.02%	40.6%	QNLIEELRK	99.5%	39.5	25	16.7	1	0	0	1142.65	24	32
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	9	11	19	0.02%	40.6%	SPSDEYKDNLHQVSK	99.7%	53.2	25	53.2	2	2	0	1746.83	80	94
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	9	11	19	0.02%	40.6%	TKEEVNEWFTK	99.7%	53.5	25	49.4	2	0	0	1410.69	108	118
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	9	11	19	0.02%	40.6%	YLFIFSVANMR	99.7%	49.7	25	49.7	4	0	0	1360.71	39	49
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	9	11	19	0.02%	40.6%	YMWDSQSGR	99.7%	41.2	25	41.2	1	0	0	1129.47	206	214
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	9	11	19	0.02%	40.6%	YTEMDYAR	99.6%	39.9	25	39.9	2	0	0	1064.44	119	126
Msx2-interacting protein	SPEN	MINT_HUMAN	402.2	100.0%	2	2	2	0.00%	0.5%	GLDDTVSIASR	99.7%	58.8	25	36.5	1	0	0	1133.58	90	100
Msx2-interacting protein	SPEN	MINT_HUMAN	402.2	100.0%	2	2	2	0.00%	0.5%	YGLVFFR	98.8%	34.8	25	33.3	1	0	0	901.49	378	384
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	8	8	13	0.01%	22.1%	ACGNFGIPCELR	99.7%	47.2	25	42.2	2	0	0	1393.64	287	298
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	8	8	13	0.01%	22.1%	ASILNTWISLK	99.7%	54.4	25	52.7	2	0	0	1245.72	404	414
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	8	8	13	0.01%	22.1%	DQITAGNAAR	96.9%	30.5	25	3.33	1	0	0	1016.51	37	46
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	8	8	13	0.01%	22.1%	EIVLADVIDNDSWR	99.7%	118	25	110	2	0	0	1644.82	202	215
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	8	8	13	0.01%	22.1%	EVTPEGLQMVK	99.7%	50.8	25	41.4	1	0	0	1230.64	236	246
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	8	8	13	0.01%	22.1%	ITSCIFQLLQEAGIK	99.7%	111	25	103	1	0	0	1720.93	60	74
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	8	8	13	0.01%	22.1%	NFEWVAER	98.1%	32.7	25	29	2	0	0	1050.50	248	255
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	8	8	13	0.01%	22.1%	TKEVYELLDSPGK	99.7%	78.4	25	76.9	2	0	0	1478.77	18	30
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	61	0.06%	18.8%	AGALHAQVER	98.7%	34.3	25	16.8	1	0	0	1051.56	897	906
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	61	0.06%	18.8%	ALVDILSEVSK	99.7%	106	25	97.3	4	0	0	1173.67	180	190
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	61	0.06%	18.8%	AQDSSLHMPER	99.7%	47.9	25	47.5	2	0	0	1286.58	433	443
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	61	0.06%	18.8%	EIPSATQSPISK	99.7%	58.8	25	51.5	3	0	0	1257.67	1156	1167
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	61	0.06%	18.8%	ELEAHSAEAR	99.7%	53.9	25	44.6	3	0	0	1112.53	582	591
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	61	0.06%	18.8%	EQLMTVLQAGK	99.6%	40.2	25	34	1	0	0	1233.65	758	768
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	61	0.06%	18.8%	EVVEQGLLK	99.7%	50.6	25	39.1	4	0	0	1014.58	287	295
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	61	0.06%	18.8%	GNTAEGCVHETQEK	99.7%	75.4	25	74.9	3	0	0	1559.68	936	949
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	61	0.06%	18.8%	HQACLLLQK	98.4%	33.3	25	26.7	2	0	0	1110.61	1028	1036
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	61	0.06%	18.8%	KPTSQIPETK	99.7%	48.6	25	46.6	4	0	0	1128.63	489	498
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	61	0.06%	18.8%	LITGLGVGR	99.7%	61.4	25	53.2	2	0	0	885.55	77	85
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	61	0.06%	18.8%	LLEYLR	99.0%	35.7	25	20.8	1	0	0	806.48	57	62
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	61	0.06%	18.8%	LLGAALPLLTK	99.7%	54	25	54	4	0	0	1109.73	308	318
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	61	0.06%	18.8%	LPAIALDLLR	99.7%	72.3	25	63.2	2	0	0	1094.69	264	273
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	61	0.06%	18.8%	LVGSVNLFSDENVPR	99.7%	95.4	25	86.8	4	0	0	1645.85	232	246
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	61	0.06%	18.8%	NSPLTVPMFLSLFSR	99.7%	58	25	58	1	0	0	1724.90	990	1004
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	61	0.06%	18.8%	QLMGQVLAK	99.7%	64.8	25	45	2	0	0	987.57	1054	1062
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	61	0.06%	18.8%	SPAESCDLLGDIQTCIR	99.7%	80.2	25	80.2	2	0	0	1934.90	609	625
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	61	0.06%	18.8%	SPAPGAPTR	99.6%	40.1	25	25.8	3	0	0	853.45	1232	1240
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	61	0.06%	18.8%	SPLSALAR	99.7%	63.8	25	32.2	3	0	0	814.48	1290	1297
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	61	0.06%	18.8%	SPSLLQSGAK	99.7%	51.1	25	40.7	4	0	0	987.55	1308	1317
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	61	0.06%	18.8%	VLDLVEVLVTK	99.7%	84.3	25	84.3	2	0	0	1227.76	828	838
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	23	23	61	0.06%	18.8%	VYSTALSSFLTK	99.7%	97.3	25	90.3	4	0	0	1316.71	977	988

Myeloid leukemia factor 2	MLF2	MLF2_HUMAN	28.1	99.8%	2	2	3	0.00%	8.5%	LAIQGPEDSPSR	99.7%	41.6	25	35.2	1	0	0	1269.64	230	241
Myeloid leukemia factor 2	MLF2	MLF2_HUMAN	28.1	99.8%	2	2	3	0.00%	8.5%	VYQETSEMR	99.7%	66.1	25	54.3	2	0	0	1142.51	120	128
Myosin light polypeptide 6	MYL6	MYL6_HUMAN	16.9	100.0%	5	6	12	0.01%	37.1%	ALGQNPTNAEVLK	99.7%	52.7	25	49.2	4	0	0	1354.73	38	50
Myosin light polypeptide 6	MYL6	MYL6_HUMAN	16.9	100.0%	5	6	12	0.01%	37.1%	EAFQLFDR	99.7%	49.3	25	42.5	2	0	0	1025.51	14	21
Myosin light polypeptide 6	MYL6	MYL6_HUMAN	16.9	100.0%	5	6	12	0.01%	37.1%	HVLVTLGEK	95.3%	28.8	25	28.8	1	0	0	995.59	111	119
Myosin light polypeptide 6	MYL6	MYL6_HUMAN	16.9	100.0%	5	6	12	0.01%	37.1%	ILYSQCGDVMR	99.7%	64.5	25	64.5	4	0	0	1357.62	27	37
Myosin light polypeptide 6	MYL6	MYL6_HUMAN	16.9	100.0%	5	6	12	0.01%	37.1%	NKDQGTYEDYVEGLR	99.7%	42.5	25	42.5	0	1	0	1786.82	80	94
Myosin regulatory light chain 12A	MYL12A	ML12A_HUMAN	19.8	100.0%	3	3	10	0.01%	18.7%	FTDEEVDELYR	99.7%	70.8	25	70.8	2	0	0	1415.63	133	143
Myosin regulatory light chain 12A	MYL12A	ML12A_HUMAN	19.8	100.0%	3	3	10	0.01%	18.7%	GNFNYIEFTR	99.7%	60.9	25	50.4	4	0	0	1260.60	151	160
Myosin regulatory light chain 12A	MYL12A	ML12A_HUMAN	19.8	100.0%	3	3	10	0.01%	18.7%	LNGTDPEDVIR	99.7%	42.8	25	31.2	4	0	0	1228.62	93	103
Myosin-10	MYH10	MYH10_HUMAN	229.0	100.0%	2	2	2	0.00%	1.7%	ALELDPNLYR	99.7%	47.3	25	47.3	1	0	0	1203.64	753	762
Myosin-10	MYH10	MYH10_HUMAN	229.0	100.0%	2	2	2	0.00%	1.7%	LDPHLVLDQLR	99.2%	36.8	25	30	2	0	0	1318.75	690	700
Myosin-10	MYH10	MYH10_HUMAN	229.0	100.0%	2	2	2	0.00%	1.7%	SDLLLEGFNNYR	98.1%	32.7	25	32.7	1	0	0	1440.71	297	308
Myosin-9	MYH9	MYH9_HUMAN	226.5	100.0%	2	2	4	0.00%	1.4%	LDPHLVLDQLR	99.2%	36.8	25	30	2	0	0	1318.75	683	693
Myosin-9	MYH9	MYH9_HUMAN	226.5	100.0%	2	2	4	0.00%	1.4%	QLLQANPILEAFGNAK	99.7%	62.7	25	62.7	2	0	0	1726.95	210	225
Myotrophin	MTPN	MTPN_HUMAN	12.9	100.0%	2	2	3	0.00%	25.4%	GPDGLTAFEATDNQAIK	99.7%	85.5	25	85.5	2	0	0	1747.85	98	114
Myotrophin	MTPN	MTPN_HUMAN	12.9	100.0%	2	2	3	0.00%	25.4%	NGDLDEVKDYVAK	99.7%	45.6	25	45.6	1	0	0	1465.72	12	24
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	16	0.02%	8.7%	AGFVPVYLR	99.5%	38.9	25	30.9	2	0	0	1021.58	726	734
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	16	0.02%	8.7%	ASEVFLQR	99.7%	63.8	25	45.1	2	0	0	949.51	521	528
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	16	0.02%	8.7%	EELEALFLPYDLK	99.7%	66.4	25	64.9	2	0	0	1579.83	811	823
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	16	0.02%	8.7%	ILIENGVAER	99.7%	49.2	25	39.8	2	0	0	1113.63	12	21
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	16	0.02%	8.7%	LDYLGVSYGLTPR	99.7%	77.6	25	68.3	2	0	0	1453.77	706	718
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	16	0.02%	8.7%	QQSAQSQVSTTAENK	99.7%	102	25	90.4	2	0	0	1606.77	433	447
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	16	0.02%	8.7%	SLFVVVGDR	99.7%	51.3	25	47.2	2	0	0	991.56	24	32
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	16	0.02%	8.7%	TEAHQDVVGR	99.7%	54.5	25	50.3	1	0	0	1111.55	173	182
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	16	0.02%	8.7%	YRTEAHQDVVGR	96.7%	24.2	25	24.2	0	1	0	1430.71	171	182
N-acetyltransferase 14	NAT14	NAT14_HUMAN	21.7	100.0%	2	3	5	0.00%	15.5%	AWAGGMGEPR	99.7%	42	25	33	3	0	0	1047.47	153	162
N-acetyltransferase 14	NAT14	NAT14_HUMAN	21.7	100.0%	2	3	5	0.00%	15.5%	GSGDVCGVLALAPGTNAGDGAR	99.7%	94.4	25	94.4	2	0	0	2014.96	103	124
N-acylneuraminate cytidylyltransferase	CMAS	NEUA_HUMAN	48.4	99.8%	2	2	3	0.00%	6.0%	GAATSVSNPR	99.7%	70.6	25	55.3	2	0	0	959.49	7	16
N-acylneuraminate cytidylyltransferase	CMAS	NEUA_HUMAN	48.4	99.8%	2	2	3	0.00%	6.0%	VGLSGAPADACSTAQK	99.7%	57.1	25	55	1	0	0	1532.74	384	399
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	4	4	6	0.01%	4.0%	AQYPIADLVK	99.0%	35.6	25	18.5	1	0	0	1117.63	940	949
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	4	4	6	0.01%	4.0%	FFTGQITAAGK	99.7%	53.6	25	48.8	2	0	0	1140.60	214	224
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	4	4	6	0.01%	4.0%	TVAELEAEK	96.5%	30.1	25	17.4	1	0	0	989.52	454	462
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	4	4	6	0.01%	4.0%	VALSPAGVQNLVK	99.7%	68.1	25	59.9	2	0	0	1295.77	72	84
NAD(P)H-hydrate epimerase	APOA1BP	NNRE_HUMAN	31.7	100.0%	3	3	5	0.00%	12.8%	GNAGGIQPDLLISLTAPK	99.7%	45.3	25	45.3	2	0	0	1764.99	228	245
NAD(P)H-hydrate epimerase	APOA1BP	NNRE_HUMAN	31.7	100.0%	3	3	5	0.00%	12.8%	LFGYEPTIYYPK	99.7%	43.7	25	43.7	2	0	0	1490.76	133	144
NAD(P)H-hydrate epimerase	APOA1BP	NNRE_HUMAN	31.7	100.0%	3	3	5	0.00%	12.8%	YHYLGGR	97.5%	31.5	25	22.5	1	0	0	865.43	255	261
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3	NDUFAF3	NDUF3_HUMAN	20.4	100.0%	3	3	4	0.00%	17.4%	IEIVVVGTGDR	99.7%	52.3	25	47.9	1	0	0	1157.65	112	122
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3	NDUFAF3	NDUF3_HUMAN	20.4	100.0%	3	3	4	0.00%	17.4%	LQSQVLQAMR	99.7%	42.7	25	35	1	0	0	1173.64	126	135
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3	NDUFAF3	NDUF3_HUMAN	20.4	100.0%	3	3	4	0.00%	17.4%	LSPADDELYQR	99.7%	48.6	25	45.4	2	0	0	1306.63	34	44
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4	NDUFAF4	NDUF4_HUMAN	20.3	99.9%	2	2	3	0.00%	10.9%	EQISLYPEVK	99.2%	36.6	25	31.8	2	0	0	1205.64	42	51
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4	NDUFAF4	NDUF4_HUMAN	20.3	99.9%	2	2	3	0.00%	10.9%	HPSTNSLLR	95.5%	29	25	17.1	1	0	0	1024.55	33	41
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	8	8	15	0.01%	20.0%	FDKGPWLK	98.5%	33.6	25	17.4	2	0	0	990.54	278	285
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	8	8	15	0.01%	20.0%	FYDDPR	98.3%	33.2	25	33.2	2	0	0	812.36	117	122
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	8	8	15	0.01%	20.0%	ITSAYLQDIENAYK	99.7%	85.6	25	75.4	2	0	0	1628.82	229	242
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	8	8	15	0.01%	20.0%	KVVEDIEYLK	99.7%	58.5	25	49.1	2	0	0	1235.69	268	277
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	8	8	15	0.01%	20.0%	LQSWLYSSR	99.7%	48	25	39.1	2	0	0	1139.58	131	139
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	8	8	15	0.01%	20.0%	VITVDGNICTGK	99.7%	84.6	25	76.5	2	0	0	1276.66	59	70
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	8	8	15	0.01%	20.0%	VVEDIEYLK	99.7%	51.6	25	51.6	2	0	0	1107.59	269	277
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	8	8	15	0.01%	20.0%	YSPGYNTEVGDK	99.7%	47.2	25	44.8	1	0	0	1329.60	339	350
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	100.0%	7	8	17	0.02%	52.4%	FNVTGTPEQYVPYSTTR	99.7%	72.4	25	70.2	3	0	0	1959.94	115	131

NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	100.0%	7	8	17	0.02%	52.4%	GLQQITGHGGLR	99.7%	60.3	25	49.3	3	2	0	1236.68	10	21
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	100.0%	7	8	17	0.02%	52.4%	IQEWIPPSTPYK	99.7%	49.3	25	40.4	2	0	0	1458.76	134	145
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	100.0%	7	8	17	0.02%	52.4%	VGTLVGEDK	99.7%	65.6	25	33.1	2	0	0	917.49	35	43
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	100.0%	7	8	17	0.02%	52.4%	VGTLVGEDKYGNK	99.7%	41.1	25	35.5	2	0	0	1379.72	35	47
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	100.0%	7	8	17	0.02%	52.4%	WVVYTTEMNGK	99.6%	40.1	25	40.1	1	0	0	1343.63	61	71
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	100.0%	7	8	17	0.02%	52.4%	YYEDNKQFFGR	99.7%	50.5	25	50.5	2	0	0	1466.67	48	58
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	NDUAD_HUMAN	16.7	100.0%	5	6	11	0.01%	30.6%	ENLEEEAIIMK	99.7%	79.2	25	63.4	4	0	0	1318.66	89	99
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	NDUAD_HUMAN	16.7	100.0%	5	6	11	0.01%	30.6%	IALLPLLQAETDR	99.7%	56.2	25	56.2	2	0	0	1452.84	69	81
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	NDUAD_HUMAN	16.7	100.0%	5	6	11	0.01%	30.6%	LQIEDFEAR	99.7%	52.3	25	46.1	2	0	0	1120.56	60	68
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	NDUAD_HUMAN	16.7	100.0%	5	6	11	0.01%	30.6%	RLQIEDFEAR	99.6%	40.3	25	31.8	1	0	0	1276.66	59	68
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	NDUAD_HUMAN	16.7	100.0%	5	6	11	0.01%	30.6%	VGESVFHTTR	99.7%	76.1	25	69.1	2	0	0	1132.57	106	115
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	NDUFA4	NDUA4_HUMAN	9.4	100.0%	2	2	3	0.00%	22.2%	FYSVNVDYSK	99.7%	65.2	25	53.6	2	0	0	1221.58	64	73
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	NDUFA4	NDUA4_HUMAN	9.4	100.0%	2	2	3	0.00%	22.2%	LGPNDQYK	99.7%	45	25	34.2	1	0	0	934.46	56	63
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	NDUA5_HUMAN	13.5	100.0%	4	5	10	0.01%	31.0%	ILDVLEEIPK	99.7%	48	25	48	2	0	0	1168.68	31	40
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	NDUA5_HUMAN	13.5	100.0%	4	5	10	0.01%	31.0%	KYTEQITNEK	99.7%	52.2	25	42.8	2	0	0	1253.64	46	55
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	NDUA5_HUMAN	13.5	100.0%	4	5	10	0.01%	31.0%	TTGLVGLAVCNTPHER	99.7%	82.4	25	82.4	2	2	0	1724.88	8	23
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	NDUA5_HUMAN	13.5	100.0%	4	5	10	0.01%	31.0%	YTEQITNEK	99.7%	57.1	25	34.7	2	0	0	1125.54	47	55
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	NDUFA6	NDUA6_HUMAN	17.9	100.0%	4	5	9	0.01%	18.8%	FFHETEAPRPK	99.6%	40	25	39	2	2	0	1358.69	132	142
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	NDUFA6	NDUA6_HUMAN	17.9	100.0%	4	5	9	0.01%	18.8%	GKIELEETIK	99.7%	42.5	25	30	2	0	0	1159.66	112	121
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	NDUFA6	NDUA6_HUMAN	17.9	100.0%	4	5	9	0.01%	18.8%	IELEETIK	98.5%	33.6	25	21.4	1	0	0	974.54	114	121
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	NDUFA6	NDUA6_HUMAN	17.9	100.0%	4	5	9	0.01%	18.8%	VVDLLVIK	99.7%	51.2	25	46.6	2	0	0	898.60	104	111
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	19	32	0.03%	48.5%	DAFPEAIIVKPSDIFGR	99.7%	50.5	25	39.3	2	0	0	1875.00	193	209
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	19	32	0.03%	48.5%	FGPIPLGSLGWK	99.7%	56	25	54.4	2	0	0	1271.71	223	234
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	19	32	0.03%	48.5%	FIHVSHLNANIK	99.7%	59.3	25	50.8	2	0	0	1392.77	164	175
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	19	32	0.03%	48.5%	FLNSFASMHR	99.7%	42.9	25	35.6	3	0	0	1209.58	213	222
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	19	32	0.03%	48.5%	IPQAIAQLSK	99.7%	61.8	25	57	2	0	0	1068.64	148	157
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	19	32	0.03%	48.5%	MGSQVIIPYR	99.7%	66	25	54.2	3	0	0	1163.62	76	85
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	19	32	0.03%	48.5%	NFDFEDVFVK	99.7%	53.8	25	19.6	2	0	0	1259.59	138	147
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	19	32	0.03%	48.5%	QPVYVVDVSK	99.7%	41.3	25	38.4	2	0	0	1133.62	238	247
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	19	32	0.03%	48.5%	SFAFVGPSR	99.7%	49.8	25	37.6	2	0	0	967.50	262	270
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	19	32	0.03%	48.5%	SSVSGIVATVFGATGFLGR	99.7%	47.8	25	47.8	1	0	0	1825.98	49	67
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	19	32	0.03%	48.5%	VFEISPFEPWITR	99.7%	64.6	25	61.2	2	0	0	1620.84	304	316
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	19	32	0.03%	48.5%	VVQHSNVVINLIGR	99.7%	34.5	25	34.5	1	2	0	1547.90	119	132
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	19	32	0.03%	48.5%	WLSAEIEDVKPAK	99.7%	67.3	25	55.5	2	0	0	1485.79	361	373
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	19	32	0.03%	48.5%	YIFAVAHR	97.9%	32.2	25	18.3	1	0	0	976.54	279	286
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	19	32	0.03%	48.5%	YLLFHLVK	97.4%	31.3	25	24.8	1	0	0	1032.62	271	278
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	19	32	0.03%	48.5%	YVVNHLGR	96.4%	30	25	22.6	2	0	0	957.53	68	75
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	NDUFB4	NDUB4_HUMAN	15.2	100.0%	4	4	13	0.01%	41.1%	EYLLQYNDPNRR	95.7%	23.2	25	14.1	0	1	0	1580.78	46	57
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	NDUFB4	NDUB4_HUMAN	15.2	100.0%	4	4	13	0.01%	41.1%	GLIENPALLR	99.7%	66.6	25	54.9	4	0	0	1095.65	58	67
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	NDUFB4	NDUB4_HUMAN	15.2	100.0%	4	4	13	0.01%	41.1%	TINVYPNFRPTPK	99.7%	53	25	50.3	4	0	0	1546.84	73	85
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	NDUFB4	NDUB4_HUMAN	15.2	100.0%	4	4	13	0.01%	41.1%	TLPETLDPAEYNISPETR	99.7%	78.1	25	78.1	4	0	0	2046.00	13	30
NADH dehydrogenase [ubiquinone] 1 subunit C2	NDUFC2	NDUC2_HUMAN	14.2	100.0%	3	3	3	0.00%	23.5%	EDYLYAVR	97.6%	31.6	25	31.4	1	0	0	1028.50	78	85
NADH dehydrogenase [ubiquinone] 1 subunit C2	NDUFC2	NDUC2_HUMAN	14.2	100.0%	3	3	3	0.00%	23.5%	LHPEDFPEEDKK	97.4%	25.1	25	23.5	0	1	0	1483.71	95	106
NADH dehydrogenase [ubiquinone] 1 subunit C2	NDUFC2	NDUC2_HUMAN	14.2	100.0%	3	3	3	0.00%	23.5%	TYGEIFEK	95.0%	28.5	25	27.2	1	0	0	986.48	107	114
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	6	6	11	0.01%	13.8%	EAYEAGLIGK	99.7%	53.7	25	42.9	2	0	0	1050.55	175	184
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	6	6	11	0.01%	13.8%	GGAGFPTGLK	99.0%	35.8	25	26.6	2	0	0	904.49	89	98
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	6	6	11	0.01%	13.8%	GGTWFAGFGR	99.7%	50.8	25	43.2	2	0	0	1055.51	258	267
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	6	6	11	0.01%	13.8%	GPDWILGEIK	99.7%	47.6	25	47.2	2	0	0	1127.61	72	81
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	6	6	11	0.01%	13.8%	HFRPELEER	99.4%	31	25	25.4	0	1	0	1212.61	441	449
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	6	6	11	0.01%	13.8%	NACGSGYDFDVFVVR	99.7%	90.1	25	90.1	2	0	0	1705.76	185	199
NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	NDUFV2	NDUV2_HUMAN	27.4	99.8%	2	2	3	0.00%	9.6%	AAAVLPVLDLAQR	99.7%	74.9	25	74.9	2	0	0	1336.79	76	88

NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	NDUFV2	NDUV2_HUMAN	27.4	99.8%	2	2	3	0.00%	9.6%	NSDSILEAIQK	99.7%	73.2	25	59.7	1	0	0	1217.64	144	154
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	6	6	10	0.01%	15.6%	GEFGVYLVSDGSSRPYR	98.6%	33.9	25	25.3	1	0	0	1888.92	405	421
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	6	6	10	0.01%	15.6%	IIAQCLNK	97.8%	31.9	25	11.9	2	0	0	959.53	343	350
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	6	6	10	0.01%	15.6%	LVMELSGEMVR	99.7%	63.4	25	57.1	2	0	0	1295.63	97	107
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	6	6	10	0.01%	15.6%	MFEFYER	98.7%	34.3	25	25.8	2	0	0	1021.44	210	216
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	6	6	10	0.01%	15.6%	NITLNFGPQHPAAHGVLR	99.7%	34.7	25	34.1	0	2	0	1942.04	79	96
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	6	6	10	0.01%	15.6%	TYLQALPYFDR	99.7%	43.5	25	43.5	1	0	0	1386.71	128	138
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	16	0.02%	39.0%	AANWYER	99.0%	35.6	25	30.7	2	0	0	909.42	162	168
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	16	0.02%	39.0%	DFPLSGYVELR	99.7%	71.3	25	56.2	2	0	0	1295.66	201	211
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	16	0.02%	39.0%	ESAGADTRPTVRPR	99.3%	30.2	25	27.1	0	2	0	1512.79	37	50
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	16	0.02%	39.0%	ILTDYGFEGHPFR	99.7%	48.8	25	48.8	2	0	0	1551.76	187	199
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	16	0.02%	39.0%	QLSAFGEYVAEILPK	99.7%	82.3	25	82.1	2	0	0	1664.89	57	71
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	16	0.02%	39.0%	SLVDLTAVDVPTR	99.7%	88.7	25	86.4	2	0	0	1385.76	110	122
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	16	0.02%	39.0%	TYTDELTPIESAVSVFK	99.5%	39.2	25	35.5	2	0	0	1899.96	145	161
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	16	0.02%	39.0%	VVAEPVELAQEFR	99.7%	81.5	25	76.9	2	0	0	1486.79	219	231
NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	NDUFS6	NDUS6_HUMAN	13.7	99.8%	2	3	6	0.01%	21.8%	TGTCGYCGLQFR	99.7%	41.3	25	41.3	2	0	0	1419.61	109	120
NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	NDUFS6	NDUS6_HUMAN	13.7	99.8%	2	3	6	0.01%	21.8%	VIACDGGGGALGHPK	99.7%	63.2	25	49.9	2	2	0	1408.70	84	98
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	NDUS7_HUMAN	23.6	100.0%	4	6	21	0.02%	15.5%	KVYDQMPEPR	99.2%	36.8	25	30	3	0	0	1278.61	136	145
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	NDUS7_HUMAN	23.6	100.0%	4	6	21	0.02%	15.5%	LDDLVNWAR	99.7%	77.1	25	53.8	4	0	0	1101.57	67	75
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	NDUS7_HUMAN	23.6	100.0%	4	6	21	0.02%	15.5%	QSDVMIVAGTLTNK	99.7%	128	25	119	9	0	0	1476.77	116	129
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	NDUS7_HUMAN	23.6	100.0%	4	6	21	0.02%	15.5%	VYDQMPEPR	99.7%	54.1	25	54.1	5	0	0	1150.52	137	145
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	NDUS8_HUMAN	23.7	100.0%	4	4	8	0.01%	23.8%	GLGMTLSYLFR	99.7%	49.6	25	44.7	2	0	0	1257.67	67	77
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	NDUS8_HUMAN	23.7	100.0%	4	4	8	0.01%	23.8%	LCEAICPAQAITIEAEPR	99.7%	88.7	25	78.6	2	0	0	2042.00	116	133
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	NDUS8_HUMAN	23.7	100.0%	4	4	8	0.01%	23.8%	TLLWTELFR	99.7%	43.4	25	40.2	2	0	0	1178.66	58	66
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	NDUS8_HUMAN	23.7	100.0%	4	4	8	0.01%	23.8%	YVNMQDPEMDMK	99.7%	51.7	25	37.9	2	0	0	1548.60	38	49
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	13	13	20	0.02%	24.1%	ALSEIAGMTLPYDTLDQVR	99.7%	81.8	25	80.9	2	0	0	2093.06	625	643
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	13	13	20	0.02%	24.1%	DVAAIAGGLVDAEALVALK	99.7%	60.9	25	54	1	0	0	1796.02	337	355
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	13	13	20	0.02%	24.1%	FASEIAGVDDLGTTGR	99.7%	122	25	119	2	0	0	1608.79	185	200
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	13	13	20	0.02%	24.1%	FEAPLFNAR	99.7%	50.8	25	46.8	2	0	0	1064.55	409	417
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	13	13	20	0.02%	24.1%	GLLTYTSWEDALSR	99.7%	51.9	25	51.9	1	0	0	1611.80	312	325
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	13	13	20	0.02%	24.1%	LEEVSPNLVR	97.1%	30.8	25	6.76	1	0	0	1155.64	646	655
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	13	13	20	0.02%	24.1%	LSVAGNCR	98.9%	35.2	25	24.1	1	0	0	876.44	69	76
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	13	13	20	0.02%	24.1%	LVNQQLLADPLVPPQLTIK	99.3%	37.5	25	34.3	2	0	0	2100.24	674	692
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	13	13	20	0.02%	24.1%	NDGAAILAAVSSIAQK	99.7%	104	25	102	2	0	0	1528.83	484	499
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	13	13	20	0.02%	24.1%	SATYVNTEGR	99.7%	51.8	25	44	2	0	0	1097.52	593	602
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	13	13	20	0.02%	24.1%	VAGMLQSFQGK	99.7%	54.3	25	49.8	1	0	0	1181.60	326	336
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	13	13	20	0.02%	24.1%	VAVTPPGLAR	96.7%	30.3	25	30.3	1	0	0	980.59	608	617
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	13	13	20	0.02%	24.1%	VLFLLGADGGCITR	99.7%	88.7	25	76.6	2	0	0	1491.80	544	557
NADH-ubiquinone oxidoreductase chain 1	MT-ND1	NU1M_HUMAN	35.7	99.8%	2	3	4	0.00%	8.5%	GPNVVGPYGLLQPFADAMK	99.7%	62.3	25	62.3	2	0	0	1974.02	36	54
NADH-ubiquinone oxidoreductase chain 1	MT-ND1	NU1M_HUMAN	35.7	99.8%	2	3	4	0.00%	8.5%	ILGYMQLR	99.7%	51.3	25	44.1	2	0	0	993.56	27	34
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	8	8	19	0.02%	31.1%	AMIENFNAK	99.7%	45.2	25	33.4	2	0	0	1037.51	97	105
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	8	8	19	0.02%	31.1%	DLTQMADELRR	99.2%	36.7	25	35.3	2	0	0	1347.67	150	160
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	8	8	19	0.02%	31.1%	HVVLGAIENK	97.9%	32.3	25	28.7	1	0	0	1079.62	170	179
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	8	8	19	0.02%	31.1%	HVVLGAIENKVESK	99.7%	35.8	25	35.8	0	2	0	1522.86	170	183
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	8	8	19	0.02%	31.1%	MEEDPDDVPHGHITSLAVK	99.7%	56	25	54.6	0	2	0	2105.98	60	78
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	8	8	19	0.02%	31.1%	YVSLHVR	99.5%	39.5	25	25.7	4	0	0	873.49	106	112
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	8	8	19	0.02%	31.1%	YYADGEDAYAMK	99.7%	57.8	25	57.8	3	0	0	1396.57	137	148
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	8	8	19	0.02%	31.1%	YYADGEDAYAMKR	99.7%	66.7	25	66.7	3	0	0	1568.67	137	149
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	30	59	0.06%	25.8%	AIELATTLDESLTNR	99.7%	91.4	25	72.6	2	0	0	1646.86	783	797
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	30	59	0.06%	25.8%	ALKPANMLER	98.5%	33.8	25	13.2	1	0	0	1142.64	267	276
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	30	59	0.06%	25.8%	DLSLLQIQMR	99.7%	76.6	25	64.2	4	0	0	1216.67	119	128

N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	30	59	0.06%	25.8%	EALEHLCTYEK	99.7%	46.7	25	27.7	2	0	0	1392.65	208	218
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	30	59	0.06%	25.8%	EEAYELVR	99.7%	48.9	25	35.7	2	0	0	1008.50	63	70
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	30	59	0.06%	25.8%	FAEHGETLAMK	99.7%	55.6	25	54.7	4	2	0	1233.59	42	52
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	30	59	0.06%	25.8%	FKECLDK	98.3%	33.3	25	14.9	2	0	0	939.46	306	312
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	30	59	0.06%	25.8%	FLLMLQSVK	99.7%	51.6	25	32.3	4	0	0	1094.63	688	696
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	30	59	0.06%	25.8%	GCPPVFNTLR	96.7%	30.4	25	17.6	1	0	0	1160.59	321	330
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	30	59	0.06%	25.8%	GLTLNCLGK	98.9%	35.2	25	18.6	2	0	0	975.53	53	61
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	30	59	0.06%	25.8%	ILEEFRK	99.7%	42	25	35.1	2	0	0	934.54	170	176
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	30	59	0.06%	25.8%	IYEEAWTK	97.5%	31.5	25	20.9	2	0	0	1039.51	279	286
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	30	59	0.06%	25.8%	KEEAYELVR	99.7%	63.6	25	52.6	2	0	0	1136.59	62	70
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	30	59	0.06%	25.8%	LEDAADVYR	99.7%	70.9	25	65.2	2	0	0	1051.51	240	248
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	30	59	0.06%	25.8%	LFGATNPK	99.2%	36.4	25	17.4	2	0	0	847.47	741	748
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	30	59	0.06%	25.8%	LFNTAVCESK	99.7%	66.2	25	56.5	2	0	0	1168.57	715	724
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	30	59	0.06%	25.8%	LPLNFLSGEK	99.7%	55.9	25	43.3	2	0	0	1117.63	296	305
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	30	59	0.06%	25.8%	MVYYLDPSSQK	99.7%	57.9	25	47.6	4	0	0	1346.63	771	781
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	30	59	0.06%	25.8%	NPENWAYYK	99.7%	59.6	25	59.2	2	0	0	1184.54	254	262
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	30	59	0.06%	25.8%	RLPLNFLSGEK	99.7%	56.4	25	50	2	0	0	1273.73	295	305
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	30	59	0.06%	25.8%	VAIIEELVVGYETSLK	99.7%	80.2	25	80.2	3	0	0	1762.98	339	354
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	30	59	0.06%	25.8%	VETPLEEAIK	98.8%	34.8	25	23.3	2	0	0	1128.61	650	659
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	30	59	0.06%	25.8%	WDKDNLQILR	99.7%	34.2	25	20	0	2	0	1300.70	109	118
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	30	59	0.06%	25.8%	WMDEAQALDTADR	99.7%	98.9	25	60.3	4	0	0	1537.66	430	442
N-alpha-acetyltransferase 20	NAA20	NAA20_HUMAN	20.4	100.0%	4	5	9	0.01%	21.9%	AFTCDDLFR	98.7%	34.2	25	21.9	1	0	0	1144.51	6	14
N-alpha-acetyltransferase 20	NAA20	NAA20_HUMAN	20.4	100.0%	4	5	9	0.01%	21.9%	LMELLEEISER	99.7%	70	25	61.2	4	0	0	1361.70	92	102
N-alpha-acetyltransferase 20	NAA20	NAA20_HUMAN	20.4	100.0%	4	5	9	0.01%	21.9%	QLGYSVYR	99.6%	40	25	30	2	0	0	985.51	125	132
N-alpha-acetyltransferase 20	NAA20	NAA20_HUMAN	20.4	100.0%	4	5	9	0.01%	21.9%	VSNQVAVNMYK	99.7%	57	25	57	2	0	0	1252.64	114	124
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	16.3%	DIQYPFLGPVPTR	99.7%	51.7	25	45	2	0	0	1502.80	748	760
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	16.3%	DTSEYIIQAYK	99.7%	69.9	25	69.8	2	0	0	1330.65	576	586
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	16.3%	FINQLLGVVPLSTPTEDK	99.7%	91.6	25	89	2	0	0	1971.08	384	401
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	16.3%	IPEFIAFR	99.7%	50.6	25	34.4	2	0	0	992.56	593	600
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	16.3%	LALPADIR	99.6%	39.7	25	27	2	0	0	868.53	402	409
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	16.3%	LGDPEELMFQYFK	99.7%	47.3	25	43.2	1	0	0	1616.77	345	357
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	16.3%	LLLQQLEATLETGK	99.7%	65.1	25	65.1	1	0	0	1556.89	729	742
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	16.3%	LNNSLHFAQVR	98.3%	26.7	25	20.9	0	1	0	1298.70	603	613
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	16.3%	LSLEEETLWLR	99.6%	40.6	25	35.5	2	0	0	1388.74	678	688
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	16.3%	LTSEIQSR	99.0%	35.6	25	24.5	2	0	0	933.50	224	231
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	16.3%	SLLDQLKDVFSK	99.7%	63.3	25	57.7	2	0	0	1392.77	807	818
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	16.3%	TMFLPLAER	98.5%	33.7	25	27.4	1	0	0	1093.57	171	179
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	16.3%	VFVDLLPATQCTK	99.7%	53.8	25	48.7	2	0	0	1491.79	371	383
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	16.3%	YQEALDVIR	99.7%	46.5	25	34.4	2	0	0	1106.58	209	217
Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACA	NACAM_HUMAN	205.4	100.0%	3	3	8	0.01%	2.0%	IEDLSQQAQLAAAEK	99.7%	113	25	107	3	0	0	1614.83	1991	2005
Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACA	NACAM_HUMAN	205.4	100.0%	3	3	8	0.01%	2.0%	NILFVITKPDVYK	99.7%	65.9	25	65.9	2	0	0	1549.90	1964	1976
Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACA	NACAM_HUMAN	205.4	100.0%	3	3	8	0.01%	2.0%	SPASDTYIVFGEAK	99.7%	95.5	25	95.5	3	0	0	1484.73	1977	1990
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	6	6	11	0.01%	6.1%	AAEDLFVNIR	99.7%	80.7	25	66	2	0	0	1147.61	306	315
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	6	6	11	0.01%	6.1%	ASLGLADHR	99.7%	73	25	62.8	2	0	0	939.50	502	510
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	6	6	11	0.01%	6.1%	ELATVLSDQPGLLGPK	99.7%	78.2	25	78.2	2	0	0	1637.91	352	367
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	6	6	11	0.01%	6.1%	NNNQQLAQLQK	99.7%	60.6	25	53.2	1	0	0	1298.68	71	81
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	6	6	11	0.01%	6.1%	QVEDGEVFDFR	99.7%	60.9	25	60.4	2	0	0	1340.61	474	484
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	6	6	11	0.01%	6.1%	SLSELLGPYGMK	99.4%	37.9	25	32.7	2	0	0	1294.67	838	849
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	7	7	12	0.01%	16.1%	DAAAVGNHVAK	99.7%	62.3	25	40.9	2	0	0	1052.55	353	363
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	7	7	12	0.01%	16.1%	EGQGNLPVR	99.3%	37.4	25	33.8	2	0	0	969.51	318	326
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	7	7	12	0.01%	16.1%	FTVVVATQLPESTSLR	99.7%	51.3	25	51.3	1	0	0	1747.96	123	138

NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	7	7	12	0.01%	16.1%	LADVLWNSQIPLLICR	99.7%	66.8	25	65.7	1	0	0	1911.05	139	154
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	7	7	12	0.01%	16.1%	LLCSNSAFLR	99.5%	39.5	25	24.6	2	0	0	1180.61	382	391
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	7	7	12	0.01%	16.1%	TYGLVGYMR	99.2%	36.5	25	30.7	2	0	0	1059.53	155	163
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	7	7	12	0.01%	16.1%	YPGVSNYQVEEDIGK	99.7%	61.3	25	61.3	2	0	0	1697.80	442	456
Neurochondrin	NCDN	NCDN_HUMAN	78.9	100.0%	3	3	4	0.00%	5.2%	IFDAVGFTFPNR	99.7%	58.4	25	50.6	1	0	0	1383.71	76	87
Neurochondrin	NCDN	NCDN_HUMAN	78.9	100.0%	3	3	4	0.00%	5.2%	IPILSTFLTAR	99.7%	46.5	25	44.4	2	0	0	1231.74	130	140
Neurochondrin	NCDN	NCDN_HUMAN	78.9	100.0%	3	3	4	0.00%	5.2%	LLSTSPALQGTPASR	99.6%	39.8	25	27.7	1	0	0	1498.82	579	593
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	3	3	5	0.00%	4.5%	EIEAEIQALR	99.7%	56.8	25	45	1	0	0	1171.63	128	137
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	3	3	5	0.00%	4.5%	EYQDLLNVK	99.7%	58.5	25	57	6	0	0	1121.58	383	391
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	3	3	5	0.00%	4.5%	LRDDTEAAIR	99.7%	49.4	25	28.5	2	0	0	1159.61	195	204
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	3	3	5	0.00%	4.5%	VQSLQDEVAFLR	99.7%	78.8	25	68.4	2	0	0	1404.75	224	235
Neutral alpha-glucosidase AB	GANAB	GANAB_HUMAN	106.9	99.8%	2	2	2	0.00%	3.2%	SLLLSVNAR	97.2%	31	25	21	1	0	0	972.58	165	173
Neutral alpha-glucosidase AB	GANAB	GANAB_HUMAN	106.9	99.8%	2	2	2	0.00%	3.2%	VSQGSKDPAEGDGAQPEETPR	98.6%	27.4	25	27.4	0	1	0	2154.99	186	206
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	8	8	34	0.03%	18.9%	EVLDSFLDLAR	99.7%	83.4	25	73.3	8	0	0	1277.67	179	189
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	8	8	34	0.03%	18.9%	GPAGDATVASEK	99.7%	84	25	74	4	0	0	1102.54	526	537
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	8	8	34	0.03%	18.9%	IVEMEDVGLLFAR	99.7%	56.9	25	56.9	2	0	0	1491.79	289	301
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	8	8	34	0.03%	18.9%	LGPEGELLIR	99.7%	76.7	25	68.3	3	0	0	1096.64	248	257
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	8	8	34	0.03%	18.9%	LSAFVFPGELLLR	99.7%	67.2	25	64.8	2	0	0	1461.85	86	98
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	8	8	34	0.03%	18.9%	NIFPSNLVSAAFR	99.7%	53.8	25	51.3	5	0	0	1435.77	190	202
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	8	8	34	0.03%	18.9%	SELPLDPLPVPTEEGNPLLK	99.7%	66.4	25	66.4	6	0	0	2158.16	503	522
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	8	8	34	0.03%	18.9%	STEPELIQVK	99.7%	50.5	25	43	4	0	0	1143.63	493	502
NF-kappa-B inhibitor-interacting Ras-like protein 2	NKIRAS2	KBRS2_HUMAN	21.5	99.8%	2	2	2	0.00%	12.0%	RVDPDVAQHWAK	98.6%	27.4	25	27.2	0	1	0	1421.73	129	140
NF-kappa-B inhibitor-interacting Ras-like protein 2	NKIRAS2	KBRS2_HUMAN	21.5	99.8%	2	2	2	0.00%	12.0%	VVVCGQASVGK	99.7%	47.3	25	46.9	1	0	0	1103.59	7	17
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	10	11	20	0.02%	15.7%	DASGQPIFNASAK	98.4%	33.4	25	33	1	0	0	1305.64	323	335
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	10	11	20	0.02%	15.7%	EDLLDQLK	94.7%	28.4	25	2.45	1	0	0	973.52	667	674
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	10	11	20	0.02%	15.7%	EGLGLDVER	99.7%	49.3	25	39.8	2	0	0	987.51	589	597
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	10	11	20	0.02%	15.7%	GAVEDVISR	99.7%	55.1	25	38.6	4	0	0	945.50	525	533
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	10	11	20	0.02%	15.7%	LLTDGYACEVR	99.7%	53.4	25	47.4	2	0	0	1296.63	235	245
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	10	11	20	0.02%	15.7%	MTVEYVYER	99.7%	46.7	25	42.5	1	0	0	1189.56	464	472
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	10	11	20	0.02%	15.7%	SESHTDLTFSR	99.7%	41.6	25	39.9	1	2	0	1279.59	616	626
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	10	11	20	0.02%	15.7%	SGEGIREPISVK	96.8%	30.4	25	16.8	2	0	0	1271.70	572	583
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	10	11	20	0.02%	15.7%	TNPEYIYAPLK	99.7%	64.2	25	62.8	2	0	0	1308.68	212	222
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	10	11	20	0.02%	15.7%	VILESEVIAEAVGVK	99.7%	67.2	25	61.9	2	0	0	1555.89	482	496
NHP2-like protein 1	NHP2L1	NH2L1_HUMAN	14.2	100.0%	3	3	5	0.00%	27.3%	AYPLADAHLTK	96.3%	29.8	25	26.8	1	0	0	1199.64	10	20
NHP2-like protein 1	NHP2L1	NH2L1_HUMAN	14.2	100.0%	3	3	5	0.00%	27.3%	LLDLVQQSCNYK	99.7%	73.8	25	73.4	2	0	0	1480.75	22	33
NHP2-like protein 1	NHP2L1	NH2L1_HUMAN	14.2	100.0%	3	3	5	0.00%	27.3%	QQIQSIQQSIER	99.7%	68.7	25	61.8	2	0	0	1457.77	114	125
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	9	11	19	0.02%	17.8%	AMAAVPQDVVR	98.0%	32.5	25	15.8	2	0	0	1172.61	115	125
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	9	11	19	0.02%	17.8%	AVSDWLIASVEGR	99.7%	93.5	25	74.1	2	0	0	1402.73	195	207
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	9	11	19	0.02%	17.8%	DPEFVFYDQLK	99.7%	66.8	25	55.6	2	0	0	1400.67	501	511
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	9	11	19	0.02%	17.8%	ELETVAAHQFPEVR	99.7%	69.1	25	60.6	3	1	0	1625.83	340	353
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	9	11	19	0.02%	17.8%	IIAEALTR	99.7%	42.4	25	13.3	1	0	0	886.54	417	424
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	9	11	19	0.02%	17.8%	LLDFSYEQYQK	99.7%	77.3	25	74	2	0	0	1433.69	89	99
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	9	11	19	0.02%	17.8%	MQQYDLQGQPYGTR	99.7%	65.3	25	58.9	2	0	0	1700.77	51	64
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	9	11	19	0.02%	17.8%	SSIMDVRSR	98.6%	33.9	25	1.02	1	0	0	1050.54	397	405
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	9	11	19	0.02%	17.8%	TMAAEVLSR	99.6%	39.9	25	31.5	3	0	0	993.50	74	82
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	16	27	0.03%	39.7%	AVPEGFVIPR	99.7%	50.6	25	44.7	3	0	0	1084.62	118	127
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	16	27	0.03%	39.7%	DVYKEHFQDDVFNEK	99.7%	36	25	36	0	2	0	1912.87	85	99
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	16	27	0.03%	39.7%	GTDTVAGLALIK	99.7%	78.9	25	46.1	2	0	0	1158.67	217	228
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	16	27	0.03%	39.7%	GVSSQETAGIGASAHLVNFK	99.7%	89.1	25	89.1	1	1	0	1973.01	197	216
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	16	27	0.03%	39.7%	GWNYILEK	99.7%	41.2	25	26.5	2	0	0	1022.53	100	107
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	16	27	0.03%	39.7%	KFPVTENSK	98.7%	34.3	25	18.4	1	0	0	1049.56	331	339

Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	16	27	0.03%	39.7%	MWSIENIAFGSGGGLLQK	99.7%	56.5	25	54.8	1	0	0	1907.97	372	389
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	16	27	0.03%	39.7%	NAQLNIELEAAHH	99.7%	67.2	25	67.2	2	0	0	1459.73	479	491
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	16	27	0.03%	39.7%	STQAPLIIRPDSGNPLDTVLK	98.2%	26.4	25	21.7	0	1	0	2235.23	303	323
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	16	27	0.03%	39.7%	SYSFDEIRK	99.4%	38.2	25	25	2	0	0	1144.56	470	478
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	16	27	0.03%	39.7%	VIQGDGVDINTLQEIVEGMK	99.7%	123	25	123	4	0	0	2158.11	350	369
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	16	27	0.03%	39.7%	YDGHLPIEIK	99.4%	38.2	25	30.1	2	0	0	1184.63	108	117
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	16	27	0.03%	39.7%	YEETVFYGLQYILNK	99.7%	72.2	25	72.2	1	0	0	1879.95	54	68
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	16	27	0.03%	39.7%	YLLETSGNLDGLEYK	99.7%	80.9	25	75.9	2	0	0	1714.85	175	189
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	12	19	53	0.05%	31.6%	AAPGAEFAPNKR	99.7%	64.4	25	59.6	4	0	0	1228.64	457	468
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	12	19	53	0.05%	31.6%	AGEVFIHK	99.7%	54.3	25	35.8	5	0	0	900.49	100	107
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	12	19	53	0.05%	31.6%	AVVIVDDR	99.7%	42	25	32.3	4	0	0	886.50	177	184
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	12	19	53	0.05%	31.6%	EKLEMEMEAAR	99.7%	56.5	25	22.4	2	0	0	1352.62	294	304
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	12	19	53	0.05%	31.6%	FACHSASLTVR	99.7%	64.1	25	60.6	4	2	0	1248.62	143	153
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	12	19	53	0.05%	31.6%	FAQPGSFEYEYAMR	99.7%	84.4	25	82.4	5	0	0	1711.74	257	270
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	12	19	53	0.05%	31.6%	FGQAATMEGIGAIGGTPPAFNR	99.7%	89.6	25	88.4	2	2	0	2179.06	435	456
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	12	19	53	0.05%	31.6%	GIVEFSGKPAAR	99.7%	50.8	25	48	4	1	0	1231.68	191	202
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	12	19	53	0.05%	31.6%	LFVGNLPPDITEEEMR	99.7%	69.7	25	66.3	4	0	0	1875.92	76	91
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	12	19	53	0.05%	31.6%	MEELHNQEVQK	99.7%	66.8	25	17.5	4	0	0	1384.65	326	336
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	12	19	53	0.05%	31.6%	MGQMAMGGAMGINNR	99.7%	64.4	25	59.5	4	0	0	1602.65	384	398
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	12	19	53	0.05%	31.6%	VELDNMPLR	99.7%	68.7	25	47.7	6	0	0	1086.56	127	135
NTF2-related export protein 1	NXT1	NXT1_HUMAN	15.8	100.0%	3	4	9	0.01%	21.4%	AAEEFVNVYYTTMDK	99.7%	55.4	25	53.2	4	0	0	1780.81	16	30
NTF2-related export protein 1	NXT1	NXT1_HUMAN	15.8	100.0%	3	4	9	0.01%	21.4%	IASDCFR	99.7%	46.2	25	38.6	4	0	0	868.40	128	134
NTF2-related export protein 1	NXT1	NXT1_HUMAN	15.8	100.0%	3	4	9	0.01%	21.4%	TYVDQACR	96.9%	30.6	25	25.1	1	0	0	1012.45	8	15
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	7	7	15	0.01%	9.9%	ANNYNEAVYLVR	99.7%	54.2	25	47	2	0	0	1425.71	118	129
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	7	7	15	0.01%	9.9%	ATNDEIFSILK	99.7%	69	25	62.3	4	0	0	1250.66	512	522
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	7	7	15	0.01%	9.9%	DGVLEEQIER	99.7%	61.1	25	46.1	2	0	0	1187.59	685	694
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	7	7	15	0.01%	9.9%	IFANTESYLK	99.7%	66.6	25	54.4	2	0	0	1185.62	195	204
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	7	7	15	0.01%	9.9%	NLFLVIFQR	99.7%	61.2	25	59.5	3	0	0	1149.68	708	716
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	7	7	15	0.01%	9.9%	NYNFGGEFVEAMIR	99.7%	81.8	25	81.8	1	0	0	1646.76	97	110
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	7	7	15	0.01%	9.9%	TCAAQLVSYPGK	99.7%	67.4	25	64.8	1	0	0	1294.65	331	342
Nuclear cap-binding protein subunit 2	NCBP2	NCBP2_HUMAN	18.0	99.9%	2	2	4	0.00%	15.4%	SDSYVELSQYR	99.7%	51.6	25	42.6	2	0	0	1346.62	11	21
Nuclear cap-binding protein subunit 2	NCBP2	NCBP2_HUMAN	18.0	99.9%	2	2	4	0.00%	15.4%	TACGFCFVEYYSR	99.7%	51.5	25	51.5	2	0	0	1659.69	79	91
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	12	12	20	0.02%	6.2%	AADALEEQQR	99.7%	59.7	25	50.1	1	0	0	1130.54	725	734
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	12	12	20	0.02%	6.2%	AVQAQGGESQQEAQR	99.7%	87.7	25	87.2	2	0	0	1586.75	1574	1588
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	12	12	20	0.02%	6.2%	DSAQTSVTQAQR	99.7%	66	25	60	2	0	0	1291.62	632	643
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	12	12	20	0.02%	6.2%	ELVKEPAR	97.7%	31.8	25	20.7	2	0	0	941.54	936	943
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	12	12	20	0.02%	6.2%	HQVEQLSSSLK	99.7%	45.2	25	45.2	2	0	0	1255.66	551	561
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	12	12	20	0.02%	6.2%	LADDLSTLQEK	99.7%	62.5	25	48.6	2	0	0	1232.64	898	908
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	12	12	20	0.02%	6.2%	LGHELQQAGLK	99.7%	45.9	25	44.9	1	0	0	1193.66	1655	1665
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	12	12	20	0.02%	6.2%	LLQAETASNSAR	99.7%	84.9	25	79.3	2	0	0	1260.65	1271	1282
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	12	12	20	0.02%	6.2%	QELTSQAER	99.5%	38.6	25	16.6	2	0	0	1061.52	1313	1321
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	12	12	20	0.02%	6.2%	SAPASQASLR	99.7%	49.5	25	38.7	2	0	0	987.52	1840	1849
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	12	12	20	0.02%	6.2%	SQAGVSSGAPPGR	99.5%	39.2	25	39.2	1	0	0	1170.59	1887	1899
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	12	12	20	0.02%	6.2%	YVQELAAVR	99.1%	36.2	25	29.9	1	0	0	1048.58	1476	1484
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	16	0.02%	11.5%	AIYAALSGNLK	99.7%	56.5	25	36.8	2	0	0	1120.64	426	436
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	16	0.02%	11.5%	EADLDVATITK	99.7%	58.9	25	51.1	2	0	0	1175.62	627	637
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	16	0.02%	11.5%	EYLGANWTLEK	99.5%	38.9	25	34.4	1	0	0	1323.66	481	491
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	16	0.02%	11.5%	GHLDALTADVK	99.7%	54.4	25	49.6	2	0	0	1139.61	804	814
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	16	0.02%	11.5%	IDVIDWLVFDPAQR	99.7%	50.2	25	50.2	1	0	0	1686.89	672	685
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	16	0.02%	11.5%	SGFGEISSPVIR	99.7%	48.4	25	32.3	2	0	0	1248.66	4	15
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	16	0.02%	11.5%	TVVEALFQR	99.7%	61	25	57.9	2	0	0	1062.59	251	259

Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	16	0.02%	11.5%	VFEELQATDK	99.7%	72.2	25	61.3	2	0	0	1179.59	492	501
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	16	0.02%	11.5%	VLLQASQDENFGNTTPR	99.7%	110	25	110	2	0	0	1889.94	32	48
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	18	30	0.03%	18.5%	AAFLQYCR	96.0%	29.5	25	16.8	1	0	0	1028.50	524	531
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	18	30	0.03%	18.5%	DGIQLSEYLPEVK	99.7%	53.7	25	46.6	2	0	0	1490.77	1111	1123
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	18	30	0.03%	18.5%	DLLQADQLGSLK	99.7%	70.9	25	61.3	2	0	0	1300.71	1124	1135
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	18	30	0.03%	18.5%	EYEIPSNLTPADVFFR	99.7%	67.2	25	65.6	2	0	0	1897.93	676	691
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	18	30	0.03%	18.5%	FLLHQETLPEQLLAEK	98.5%	27.3	25	20.5	0	1	0	1909.04	1001	1016
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	18	30	0.03%	18.5%	GLPLGSAVSSPVLFSPVGR	99.7%	94.1	25	94.1	2	0	0	1840.03	36	54
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	18	30	0.03%	18.5%	HAYSWDINR	95.2%	28.8	25	23.8	1	0	0	1161.54	306	314
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	18	30	0.03%	18.5%	IEEMAEQER	99.7%	52.8	25	27	1	0	0	1134.51	992	1000
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	18	30	0.03%	18.5%	LAALASDFSEDMLQEK	99.7%	64.9	25	57.2	1	0	0	1767.85	976	991
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	18	30	0.03%	18.5%	LLLCEHAEK	99.7%	52.5	25	50.9	2	0	0	1112.58	638	646
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	18	30	0.03%	18.5%	LSAAIVLK	99.4%	38.3	25	9.44	2	0	0	814.54	647	654
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	18	30	0.03%	18.5%	LSDLVNTAILIALNK	99.7%	82	25	82	1	0	0	1597.95	660	674
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	18	30	0.03%	18.5%	NETIAQEDKIK	99.7%	54.7	25	37.8	2	0	0	1288.67	510	520
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	18	30	0.03%	18.5%	NSGLVSITSR	99.7%	69.7	25	63.2	2	0	0	1033.56	467	476
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	18	30	0.03%	18.5%	SNPYFEFVLK	99.0%	35.6	25	29.3	2	0	0	1243.64	1136	1145
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	18	30	0.03%	18.5%	SSFYSLTSSNISK	99.7%	100	25	87.6	2	0	0	1420.70	284	296
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	18	30	0.03%	18.5%	TFGSSLPVK	99.1%	36.2	25	30.3	2	0	0	935.52	83	91
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	18	18	30	0.03%	18.5%	VAYPQADSNLR	99.7%	59.7	25	47	2	0	0	1233.62	788	798
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	7	7	15	0.01%	5.2%	CYLVTGEGQK	97.9%	32.1	25	27.8	1	0	0	1154.55	916	925
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	7	7	15	0.01%	5.2%	DLLILQQLLMR	99.7%	59.6	25	58.4	2	0	0	1355.81	733	743
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	7	7	15	0.01%	5.2%	LLSTYLER	99.7%	58.1	25	43.2	2	0	0	994.56	1291	1298
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	7	7	15	0.01%	5.2%	LPLTPVFEGLAFK	99.7%	58.6	25	47.5	1	0	0	1431.82	1237	1249
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	7	7	15	0.01%	5.2%	SEDGEIVSTPR	99.7%	77.2	25	67.3	4	0	0	1189.57	949	959
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	7	7	15	0.01%	5.2%	SFVELSGAER	99.7%	59.2	25	54.4	2	0	0	1094.55	44	53
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	7	7	15	0.01%	5.2%	TAPLLLSYYLIK	99.7%	54.2	25	54.2	3	0	0	1394.83	766	777
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	25	37	0.04%	12.1%	AQIEQVIANCEHK	99.7%	86.8	25	86.8	2	0	0	1539.76	1207	1219
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	25	37	0.04%	12.1%	ASTEGVAIQGQQGTR	99.7%	88.3	25	78.7	2	0	0	1502.76	70	84
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	25	37	0.04%	12.1%	DACDGHEIGR	99.7%	52.6	25	50.1	2	0	0	1129.47	1484	1493
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	25	37	0.04%	12.1%	DLPSADSVQYR	99.7%	44.9	25	37	2	0	0	1250.60	572	582
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	25	37	0.04%	12.1%	ENLFMDLLR	99.7%	62.2	25	44.8	2	0	0	1150.59	860	868
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	25	37	0.04%	12.1%	FQDDNVEGDKVSK	99.7%	58.5	25	24.8	1	1	0	1480.69	1733	1745
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	25	37	0.04%	12.1%	FTDELMEQGLTYK	99.7%	82.4	25	75.1	2	0	0	1574.74	173	185
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	25	37	0.04%	12.1%	IQQGALELLR	99.7%	84.2	25	73.6	2	0	0	1140.67	1566	1575
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	25	37	0.04%	12.1%	KADNVVNIAR	99.7%	55	25	39.8	2	0	0	1099.62	892	901
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	25	37	0.04%	12.1%	KPVSTTNLQDPGVLGCPR	98.7%	27.6	25	26.9	0	1	0	1939.01	1013	1030
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	25	37	0.04%	12.1%	LAWALALR	99.7%	54.1	25	40.5	2	0	0	913.56	331	338
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	25	37	0.04%	12.1%	LTAPEDVFSK	99.7%	42	25	35.8	2	0	0	1106.57	1452	1461
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	25	37	0.04%	12.1%	LVGDFTHDQSISQK	99.7%	46.9	25	46.9	1	0	0	1574.78	933	946
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	25	37	0.04%	12.1%	MLALALLDR	99.7%	55.9	25	50.4	4	0	0	1015.60	1494	1502
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	25	37	0.04%	12.1%	QCLGLLSR	98.2%	32.8	25	13.7	1	0	0	946.51	1714	1721
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	25	37	0.04%	12.1%	QLDTYAPFPGK	99.7%	44.2	25	37.7	1	0	0	1236.63	829	839
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	25	37	0.04%	12.1%	QYIATIHSR	99.5%	38.7	25	29	1	0	0	1088.58	305	313
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	25	37	0.04%	12.1%	SVSGFLHFDTATK	99.5%	39.3	25	39.3	2	0	0	1409.71	1165	1177
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	25	37	0.04%	12.1%	TLQSLLTPQPPLLK	99.7%	43.2	25	41.9	1	0	0	1548.94	1535	1548
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	25	37	0.04%	12.1%	YLYHGNTNPELAFESAK	99.4%	31.4	25	31.4	0	1	0	1953.93	902	918
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	25	37	0.04%	12.1%	YSFIQALVR	99.7%	56.8	25	47.7	2	0	0	1096.61	1993	2001
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	6	7	13	0.01%	12.3%	DAAFATLVSDR	99.7%	77.6	25	68.3	2	0	0	1165.58	495	505
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	6	7	13	0.01%	12.3%	DVDVYSQILR	99.7%	54	25	46.7	2	0	0	1207.63	60	69
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	6	7	13	0.01%	12.3%	EADASPASAGICR	99.7%	62.3	25	62.3	2	0	0	1304.59	219	231

Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	6	7	13	0.01%	12.3%	FADAASLLLSLMTSR	99.7%	44	25	44	2	0	0	1595.85	553	567
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	6	7	13	0.01%	12.3%	IMLGDEAALLEQK	99.7%	58.8	25	55.6	2	0	0	1430.76	286	298
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	6	7	13	0.01%	12.3%	TMPILSPGNTQTLTELELK	99.7%	87	25	85.9	3	0	0	2086.11	239	257
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	18	19	38	0.04%	26.7%	AQHQLGEFK	99.6%	40.5	25	32.9	2	0	0	1057.54	341	349
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	18	19	38	0.04%	26.7%	AVYCIIGR	99.7%	49.7	25	37.2	2	0	0	951.51	389	396
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	18	19	38	0.04%	26.7%	CGDLLAASQVVNR	99.7%	69.7	25	58.2	2	0	0	1402.71	328	340
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	18	19	38	0.04%	26.7%	DNALLSAIEESR	99.7%	103	25	97.1	2	0	0	1317.66	107	118
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	18	19	38	0.04%	26.7%	EALQYFYFLR	99.7%	42.9	25	28	3	0	0	1349.69	546	555
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	18	19	38	0.04%	26.7%	FTSDTKPIINK	99.7%	58	25	47.7	2	0	0	1263.69	601	611
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	18	19	38	0.04%	26.7%	GLDISHISQR	99.7%	54.7	25	48.3	2	0	0	1125.60	68	77
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	18	19	38	0.04%	26.7%	LESLSAATTFEPLEPVKDTDIQGFLK	99.7%	44.6	25	44.6	0	2	0	2849.48	78	103
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	18	19	38	0.04%	26.7%	LLMLYTR	99.7%	45.2	25	42.2	2	0	0	909.52	531	537
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	18	19	38	0.04%	26.7%	LLSPVVPQISAPQSNK	99.7%	60.7	25	60.7	2	0	0	1677.95	645	660
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	18	19	38	0.04%	26.7%	LTLSQFQK	99.7%	55.8	25	47.3	2	0	0	964.55	435	442
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	18	19	38	0.04%	26.7%	LVPLNQESVEER	99.7%	63.8	25	59.1	2	0	0	1412.74	719	730
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	18	19	38	0.04%	26.7%	NLQEIQQAGER	99.7%	71.4	25	34.5	2	0	0	1285.65	32	42
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	18	19	38	0.04%	26.7%	NMALSIAER	97.9%	32.3	25	30.4	1	0	0	1004.52	665	673
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	18	19	38	0.04%	26.7%	QMTDVLLTPATDALK	99.7%	61.6	25	48.2	2	0	0	1616.86	229	243
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	18	19	38	0.04%	26.7%	SSGQSAQLLSHEPGDPPCLR	99.7%	46	25	35.9	0	2	0	2136.01	505	524
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	18	19	38	0.04%	26.7%	TLITFAGMIPYR	99.7%	58.7	25	50	5	0	0	1382.75	791	802
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	18	19	38	0.04%	26.7%	VIEDRDSQLR	95.5%	29	25	19.3	1	0	0	1230.64	777	786
Nuclear pore complex protein Nup98-Nup96	NUP98	NUP98_HUMAN	197.6	100.0%	4	4	6	0.01%	2.7%	LALLLSQFVGSQSVR	99.7%	55.2	25	55.2	2	0	0	1617.93	1358	1372
Nuclear pore complex protein Nup98-Nup96	NUP98	NUP98_HUMAN	197.6	100.0%	4	4	6	0.01%	2.7%	LPISASHSSK	97.2%	31	25	21.6	1	0	0	1026.56	1031	1040
Nuclear pore complex protein Nup98-Nup96	NUP98	NUP98_HUMAN	197.6	100.0%	4	4	6	0.01%	2.7%	NSPVEAVFSYLTGK	99.7%	52.7	25	52.7	1	0	0	1511.77	1328	1341
Nuclear pore complex protein Nup98-Nup96	NUP98	NUP98_HUMAN	197.6	100.0%	4	4	6	0.01%	2.7%	SITADPLDYR	99.7%	45.7	25	37	2	0	0	1150.57	1514	1523
Nuclear pore membrane glycoprotein 210	NUP210	PO210_HUMAN	205.1	100.0%	4	4	6	0.01%	2.5%	AVDPTSGQLYGLAR	99.7%	60.1	25	49	1	0	0	1447.75	1259	1272
Nuclear pore membrane glycoprotein 210	NUP210	PO210_HUMAN	205.1	100.0%	4	4	6	0.01%	2.5%	TVSVGLTLLR	99.7%	48.6	25	36.5	1	0	0	1058.66	1448	1457
Nuclear pore membrane glycoprotein 210	NUP210	PO210_HUMAN	205.1	100.0%	4	4	6	0.01%	2.5%	VFGAPEVLENLEVK	99.7%	59.1	25	53.2	2	0	0	1543.84	1711	1724
Nuclear pore membrane glycoprotein 210	NUP210	PO210_HUMAN	205.1	100.0%	4	4	6	0.01%	2.5%	VGQALELPLR	99.7%	61	25	61	2	0	0	1095.65	549	558
Nuclear receptor coactivator 5	NCOA5	NCOA5_HUMAN	65.5	100.0%	4	4	6	0.01%	6.9%	DPYGFGDSR	95.4%	28.9	25	25.1	1	0	0	1013.43	14	22
Nuclear receptor coactivator 5	NCOA5	NCOA5_HUMAN	65.5	100.0%	4	4	6	0.01%	6.9%	MADEAILQER	99.7%	53.3	25	48.7	2	0	0	1191.57	316	325
Nuclear receptor coactivator 5	NCOA5	NCOA5_HUMAN	65.5	100.0%	4	4	6	0.01%	6.9%	NMPQADAMVLVAR	99.7%	52.7	25	38.5	1	0	0	1431.71	280	292
Nuclear receptor coactivator 5	NCOA5	NCOA5_HUMAN	65.5	100.0%	4	4	6	0.01%	6.9%	QYFEEIQR	99.4%	38.2	25	33.3	2	0	0	1112.54	183	190
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	6	6	10	0.01%	12.3%	DQSTYISAIR	99.7%	58.5	25	27.3	1	0	0	1153.58	333	342
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	6	6	10	0.01%	12.3%	IIEENIPELLSLNLSNNR	99.7%	65	25	65	1	0	0	2081.12	259	276
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	6	6	10	0.01%	12.3%	ILNLSGNELK	99.7%	59.5	25	47	2	0	0	1100.63	295	304
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	6	6	10	0.01%	12.3%	LDDMSSIVQK	99.7%	41.8	25	35.1	2	0	0	1151.56	280	289
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	6	6	10	0.01%	12.3%	LNVVAFLNELPK	99.7%	65.1	25	63.2	2	0	0	1356.79	460	471
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	6	6	10	0.01%	12.3%	SDPDLVAQNIDVVLNR	99.7%	77.3	25	76.4	2	0	0	1767.92	234	249
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	13	15	46	0.04%	54.3%	AADPPAENSSAPEAEQGGAE	99.6%	40.8	25	40.8	2	0	0	1897.80	305	324
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	13	15	46	0.04%	54.3%	EDGNEEDKENQGDETQGQQPPQR	99.7%	60.3	25	60.3	0	2	0	2628.10	257	279
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	13	15	46	0.04%	54.3%	EDVFVHQTAIK	99.7%	54.7	25	43.1	3	0	0	1286.67	82	92
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	13	15	46	0.04%	54.3%	GAEAANVTGPGGVPVQGSK	99.7%	116	25	116	4	0	0	1695.87	119	137
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	13	15	46	0.04%	54.3%	NDTKEDVFVHQTAIK	99.7%	92.1	25	88	4	5	0	1744.89	78	92
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	13	15	46	0.04%	54.3%	NEGSESAPEGQAQQR	99.7%	93.4	25	90.2	2	0	0	1587.70	171	185
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	13	15	46	0.04%	54.3%	NGYGFINR	99.7%	57.6	25	52.4	5	0	0	940.46	70	77
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	13	15	46	0.04%	54.3%	NYQQNYQNSESGEK	99.7%	87.2	25	87.2	2	0	0	1688.71	157	170
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	13	15	46	0.04%	54.3%	NYQQNYQNSESGEKNEGSESAPEGQAQQR	99.7%	91.9	25	91.9	0	2	0	3257.40	157	185
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	13	15	46	0.04%	54.3%	RPENPKPQDGKETK	99.3%	30.2	25	30.2	0	2	0	1623.85	291	304
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	13	15	46	0.04%	54.3%	RPQYSNPPVQGEVMEGADNQGAGEQGRPVR	99.7%	69.8	25	69.8	0	4	0	3223.53	205	234
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	13	15	46	0.04%	54.3%	RRPENPKPQDGK	98.4%	27	25	27	0	2	0	1421.76	290	301

Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	13	15	46	0.04%	54.3%	SVGDGETVEFDVVEGEK	99.7%	114	25	108	7	0	0	1795.82	102	118
Nucleolar and coiled-body phosphoprotein 1	NOLC1	NOLC1_HUMAN	73.6	99.8%	2	2	6	0.01%	3.4%	DNQLSEVANK	99.3%	37.1	25	30.8	1	0	0	1117.55	24	33
Nucleolar and coiled-body phosphoprotein 1	NOLC1	NOLC1_HUMAN	73.6	99.8%	2	2	6	0.01%	3.4%	VAGGAAPSKPASAK	98.2%	32.8	25	28.7	5	0	0	1211.67	497	510
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	13	25	0.02%	15.6%	DLIGCLQK	98.5%	33.7	25	15.3	1	0	0	946.50	214	221
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	13	25	0.02%	15.6%	DREIQLEISGK	99.7%	60.7	25	59.7	2	0	0	1287.69	627	637
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	13	25	0.02%	15.6%	EEGTPLTLYYSHWR	99.7%	45	25	42.6	1	0	0	1751.84	610	623
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	13	25	0.02%	15.6%	LFHEVVQAFR	99.7%	49.8	25	48.1	2	2	0	1245.67	169	178
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	13	25	0.02%	15.6%	LSNVNLQEK	99.7%	46.2	25	35.5	2	0	0	1044.57	508	516
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	13	25	0.02%	15.6%	MLQPSSSPLWGK	99.7%	51.2	25	40.7	2	0	0	1330.68	234	245
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	13	25	0.02%	15.6%	NSVPVTVAMVER	99.7%	75	25	67.8	2	0	0	1301.69	145	156
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	13	25	0.02%	15.6%	QVQQLLGK	99.7%	44.1	25	30.9	1	0	0	913.55	569	576
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	13	25	0.02%	15.6%	SPDKPGGSPSASR	99.7%	33.7	25	30.9	1	2	0	1242.61	49	61
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	13	25	0.02%	15.6%	VLAFLVLSR	99.7%	68.5	25	68.5	5	0	0	1017.65	311	319
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	13	25	0.02%	15.6%	VQENSAYICSR	99.7%	76.8	25	76.8	2	0	0	1326.61	577	587
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	9	9	18	0.02%	14.6%	FAAHLIAGAPSEGSGALKPELSR	99.7%	41	25	38.5	0	2	0	2279.21	707	729
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	9	9	18	0.02%	14.6%	FLQGDSFLNEDLNQLIK	99.7%	72.4	25	72.4	2	0	0	1994.02	761	777
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	9	9	18	0.02%	14.6%	FYLENLEQMVK	99.7%	67.5	25	56.6	2	0	0	1413.71	307	317
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	9	9	18	0.02%	14.6%	IRPLTEAEK	95.2%	28.8	25	12.5	1	0	0	1056.60	275	283
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	9	9	18	0.02%	14.6%	KPIPLENPK	99.0%	35.5	25	35.5	2	0	0	1035.62	60	68
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	9	9	18	0.02%	14.6%	LGQASLGVIK	99.7%	72.3	25	37.5	2	0	0	985.60	394	403
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	9	9	18	0.02%	14.6%	NYEVRPEMLK	98.2%	32.9	25	21.8	2	0	0	1278.65	413	422
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	9	9	18	0.02%	14.6%	SPLLPAVLEGLAK	99.7%	46.4	25	46.4	3	0	0	1307.79	512	524
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	9	9	18	0.02%	14.6%	YSSEVATESPLDFTK	99.7%	68.9	25	65.2	2	0	0	1673.79	779	793
Nucleolar complex protein 4 homolog	NOC4L	NOC4L_HUMAN	58.5	100.0%	3	4	5	0.00%	5.8%	LFGALLER	99.7%	53	25	33.7	1	0	0	918.54	56	63
Nucleolar complex protein 4 homolog	NOC4L	NOC4L_HUMAN	58.5	100.0%	3	4	5	0.00%	5.8%	LGELLGHPSFQVK	99.7%	43.9	25	41.7	1	1	0	1424.79	103	115
Nucleolar complex protein 4 homolog	NOC4L	NOC4L_HUMAN	58.5	100.0%	3	4	5	0.00%	5.8%	RLEAVLASR	99.7%	50.7	25	34	2	0	0	1014.61	17	25
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	6	6	12	0.01%	9.6%	ADVDVQPYAFTTK	99.7%	81.6	25	81.6	2	0	0	1454.72	191	203
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	6	6	12	0.01%	9.6%	FTQQNYHDR	99.7%	40.9	25	34.6	2	0	0	1208.54	53	61
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	6	6	12	0.01%	9.6%	IAELSEDDQK	99.7%	43.3	25	39.2	2	0	0	1147.55	296	305
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	6	6	12	0.01%	9.6%	LALGQINIAK	99.7%	46.4	25	46	2	0	0	1040.65	94	103
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	6	6	12	0.01%	9.6%	LPTIDPNTR	99.7%	48.6	25	44.3	2	0	0	1026.56	161	169
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	6	6	12	0.01%	9.6%	LSQILTDFPK	99.7%	67.9	25	54.3	2	0	0	1161.65	62	71
Nucleolar MIF4G domain-containing protein 1	NOM1	NOM1_HUMAN	96.3	100.0%	4	4	6	0.01%	5.6%	ASGAGSEFQDQTR	99.7%	66.1	25	61.2	1	0	0	1353.60	532	544
Nucleolar MIF4G domain-containing protein 1	NOM1	NOM1_HUMAN	96.3	100.0%	4	4	6	0.01%	5.6%	NAGSGSETQLR	99.7%	61.2	25	50.6	1	0	0	1119.54	584	594
Nucleolar MIF4G domain-containing protein 1	NOM1	NOM1_HUMAN	96.3	100.0%	4	4	6	0.01%	5.6%	TRPSAAATAAAR	99.2%	36.5	25	29.2	2	0	0	1143.62	160	171
Nucleolar MIF4G domain-containing protein 1	NOM1	NOM1_HUMAN	96.3	100.0%	4	4	6	0.01%	5.6%	TYNPFYAFLASK	99.7%	46.8	25	44.5	2	0	0	1421.71	702	713
Nucleolar pre-ribosomal-associated protein 1	URB1	NPA1P_HUMAN	254.4	100.0%	2	2	3	0.00%	1.2%	ILLTLVANPYSYTDK	99.7%	86.6	25	86.6	2	0	0	1710.93	703	717
Nucleolar pre-ribosomal-associated protein 1	URB1	NPA1P_HUMAN	254.4	100.0%	2	2	3	0.00%	1.2%	ISTINILLSTLK	99.7%	60.6	25	51.7	1	0	0	1315.82	237	248
Nucleolar protein 16	NOP16	NOP16_HUMAN	21.2	100.0%	4	6	11	0.01%	24.2%	AMEVDIEERPK	99.7%	55	25	53.4	3	0	0	1332.65	75	85
Nucleolar protein 16	NOP16	NOP16_HUMAN	21.2	100.0%	4	6	11	0.01%	24.2%	DEKNYYQDTPK	99.7%	45.2	25	45.2	2	0	0	1400.63	136	146
Nucleolar protein 16	NOP16	NOP16_HUMAN	21.2	100.0%	4	6	11	0.01%	24.2%	FGYSVNR	97.1%	30.8	25	24.1	2	0	0	842.42	13	19
Nucleolar protein 16	NOP16	NOP16_HUMAN	21.2	100.0%	4	6	11	0.01%	24.2%	QNLAEMGLAVDPNR	99.7%	63.5	25	56.6	4	0	0	1527.76	51	64
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	10	11	19	0.02%	19.7%	EEPVSSGPEEAVGK	99.7%	45.3	25	45.3	1	0	0	1414.67	565	578
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	10	11	19	0.02%	19.7%	ELNEDKLEK	99.6%	39.9	25	24.6	1	0	0	1117.57	222	230
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	10	11	19	0.02%	19.7%	IDCFSEVPTSVFGEK	99.7%	52.3	25	52.3	2	0	0	1714.80	382	396
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	10	11	19	0.02%	19.7%	IINDNATYCR	99.7%	51.6	25	51.6	2	0	0	1239.58	203	212
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	10	11	19	0.02%	19.7%	LAQFIGNR	99.6%	40	25	21	2	0	0	918.52	213	220
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	10	11	19	0.02%	19.7%	LREQVEER	98.5%	33.8	25	11.5	2	0	0	1058.56	397	404
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	10	11	19	0.02%	19.7%	MSQVAPSLSALIGEAVGAR	99.7%	77	25	72.3	3	0	0	1856.99	289	307
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	10	11	19	0.02%	19.7%	STPKEETVNDPEEAGHR	98.2%	26.6	25	26.6	0	2	0	1895.87	537	553
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	10	11	19	0.02%	19.7%	VLLGVGDPK	99.7%	47.1	25	41.7	2	0	0	897.54	91	99

Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	10	11	19	0.02%	19.7%	VVSLSEYR	99.7%	60.6	25	45.8	2	0	0	952.51	271	278
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	7	9	14	0.01%	16.1%	EAHEPLAVADAK	99.7%	53.5	25	51.7	2	1	0	1250.64	82	93
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	7	9	14	0.01%	16.1%	HAASTVQILGAEK	99.7%	80.2	25	75.6	1	0	0	1324.72	311	323
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	7	9	14	0.01%	16.1%	IISDNLTYCK	99.7%	55.1	25	55.1	2	0	0	1226.61	197	206
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	7	9	14	0.01%	16.1%	LIAHAGSLLNLAK	99.7%	46.6	25	46.6	0	2	0	1320.80	298	310
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	7	9	14	0.01%	16.1%	LSELLPEEVEAEVK	99.7%	56.3	25	53.5	2	0	0	1584.84	222	235
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	7	9	14	0.01%	16.1%	SQMDGLIPGVEPR	99.7%	49.4	25	33.5	2	0	0	1398.70	121	133
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	7	9	14	0.01%	16.1%	TQLYEYLQNR	99.7%	73.2	25	70.9	2	0	0	1327.66	269	278
Nucleolar protein 9	NOP9	NOP9_HUMAN	69.4	99.8%	2	2	4	0.00%	4.6%	GSSVDGSPLLLFLR	99.7%	45.1	25	32.3	2	0	0	1460.81	311	324
Nucleolar protein 9	NOP9	NOP9_HUMAN	69.4	99.8%	2	2	4	0.00%	4.6%	TLLQVLGGTILESER	99.7%	66.1	25	66.1	2	0	0	1628.92	209	223
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	AAVIGDVIR	99.7%	63.3	25	46.6	2	0	0	913.55	424	432
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	AEPSEVDMNSPK	99.7%	58.9	25	47.2	1	0	0	1319.58	62	73
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	APQVLVLAPTR	99.7%	65.8	25	65.8	4	0	0	1164.71	260	270
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	DFSDITKK	99.3%	37	25	23.4	2	0	0	953.49	279	286
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	DSEDNPQTLLFSATCPHWVFNVAK	99.7%	76	25	76	0	2	0	2776.30	364	387
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	DVESYIHR	99.7%	43.3	25	33.6	2	0	0	1018.50	517	524
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	EAQELSQNSAIK	99.7%	61.1	25	51.3	4	0	0	1317.66	450	461
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	EEYQLVQVEQK	99.7%	77.6	25	69.4	2	0	0	1392.70	545	555
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	EGAFSNFPISEETIK	99.7%	67.1	25	67.1	6	0	0	1668.81	185	199
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	ELKEQLGEEIDSK	99.7%	77	25	68.2	2	0	0	1517.77	656	668
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	GAVEALAAALAHISGATSVDQR	99.7%	83.5	25	83.5	0	2	0	2108.11	606	627
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	GRAPQVLVLAPTR	99.7%	59.9	25	59.9	2	0	0	1377.83	258	270
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	GVTFLFPIQAK	99.7%	64.9	25	43	2	0	0	1220.70	205	215
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	IGVPSATEIIK	99.7%	44.9	25	44.9	3	0	0	1127.67	563	573
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	KAEPSEVDMNSPK	99.7%	67.4	25	60.9	4	2	0	1431.68	61	73
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	KEAQELSQNSAIK	98.3%	26.7	25	19.5	0	1	0	1445.76	449	461
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	LGVCFDVPTASVTEIQEK	99.7%	76	25	72.2	2	0	0	1992.99	679	696
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	LHGELQDR	99.7%	43.9	25	38.2	2	0	0	967.50	248	255
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	LLDSVPPTAISHFK	99.7%	47.8	25	42.1	2	2	0	1524.84	582	595
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	LSVACFYGGTPYGGQFER	99.7%	84.7	25	82.5	2	0	0	2008.92	287	304
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	NEEPSEEEIDAPKPK	99.7%	72.7	25	65.9	2	2	0	1711.80	117	131
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	NGIDILVGTPGR	99.7%	77.3	25	64	3	0	0	1211.67	307	318
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	NGSFGVLVATNVAAR	99.7%	86.4	25	86.4	2	0	0	1475.80	485	499
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	QDAQSLHGDIPQK	99.7%	72.7	25	70.1	2	1	0	1436.71	462	474
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	SDAGLESDTAMK	99.7%	73.9	25	73.9	4	0	0	1240.54	7	18
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	SDKTEEIAEEEETVFPK	99.7%	108	25	94.9	2	1	0	1980.93	38	54
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	STYEQVDLIGK	99.7%	78.6	25	70.7	3	0	0	1252.64	392	402
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	STYEQVDLIGKK	99.7%	62.4	25	39.2	2	0	0	1380.74	392	403
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	TAITVEHLAIK	99.7%	76.7	25	75.7	4	0	0	1195.70	407	417
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	TFSFAIPLIEK	99.7%	61	25	59	3	0	0	1265.71	237	247
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	TIIFCETKK	94.7%	28.3	25	13.2	1	0	0	1139.61	441	449
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	39	87	0.08%	47.4%	WQLSVATEQPELEGPR	99.7%	86.1	25	86.1	2	0	0	1839.92	703	718
Nucleolar transcription factor 1	UBTF	UBF1_HUMAN	89.4	100.0%	3	3	4	0.00%	4.6%	FLESLPEEEQQR	99.7%	56.1	25	41.2	1	0	0	1504.73	361	372
Nucleolar transcription factor 1	UBTF	UBF1_HUMAN	89.4	100.0%	3	3	4	0.00%	4.6%	TLTELILDAQEHVK	99.7%	60.6	25	60.6	2	0	0	1609.88	84	97
Nucleolar transcription factor 1	UBTF	UBF1_HUMAN	89.4	100.0%	3	3	4	0.00%	4.6%	WVEISNEVR	99.5%	39.2	25	30.4	1	0	0	1131.58	72	80
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	182	0.17%	33.1%	ALELTGLK	99.7%	64.4	25	50.9	5	0	0	844.51	363	370
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	182	0.17%	33.1%	ALVATPGKK	94.6%	28.3	25	22.5	1	0	0	884.56	117	125
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	182	0.17%	33.1%	EAMEDGEIDGNK	99.7%	66	25	66	6	0	0	1307.54	628	639
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	182	0.17%	33.1%	EAMEDGEIDGNKVTLDWAKPK	99.7%	67.4	25	67.4	0	6	0	2346.13	628	648
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	182	0.17%	33.1%	ESFDGSVR	99.6%	40.8	25	33.3	4	0	0	896.41	590	597
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	182	0.17%	33.1%	EVFEDAAEIR	99.7%	71	25	53.3	6	0	0	1178.57	411	420

Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	182	0.17%	33.1%	FGYVDFESAEDLEK	99.7%	106	25	104	8	0	0	1648.74	349	362
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	182	0.17%	33.1%	GFGFVDFNSEEDAK	99.7%	83.3	25	83.3	20	0	0	1561.68	611	624
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	182	0.17%	33.1%	GIAYIEFK	99.7%	46	25	34	6	0	0	940.51	430	437
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	182	0.17%	33.1%	GLSEDTTEETLK	99.7%	80.7	25	66.7	7	0	0	1322.63	578	589
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	182	0.17%	33.1%	GLSEDTTEETLKESFDGSVR	99.7%	102	25	97.8	4	8	0	2200.03	578	597
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	182	0.17%	33.1%	GYAFIEFASFEDAK	99.7%	109	25	104	8	0	0	1594.74	524	537
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	182	0.17%	33.1%	KFGYVDFESAEDLEK	99.7%	70.9	25	63.2	5	0	0	1776.83	348	362
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	182	0.17%	33.1%	KVAVATPAK	95.5%	29	25	24.1	1	0	0	884.56	71	79
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	182	0.17%	33.1%	LELQGPR	99.7%	53.2	25	42.3	8	0	0	812.46	555	561
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	182	0.17%	33.1%	NDLAVVDVR	99.7%	88.7	25	77.6	11	0	0	1000.54	334	342
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	182	0.17%	33.1%	QKVEGTEPTTAFNLFVGNLNFNK	97.9%	26	25	26	0	1	0	2568.31	296	318
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	182	0.17%	33.1%	SISLYYTGEK	99.7%	62.2	25	54.7	12	0	0	1160.58	458	467
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	182	0.17%	33.1%	TEADAEKTFEEK	99.7%	75.5	25	61.4	4	0	0	1397.64	438	449
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	182	0.17%	33.1%	TGISDVFAK	99.7%	72.3	25	55.4	10	0	0	937.50	325	333
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	182	0.17%	33.1%	TLVLSNLSYSATEETLQEVFEK	99.7%	122	25	122	4	3	0	2501.27	487	508
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	182	0.17%	33.1%	VAVATPAKK	99.5%	39.2	25	25.3	5	0	0	884.56	72	80
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	182	0.17%	33.1%	VEGTEPTTAFNLFVGNLNFNK	99.7%	93.4	25	92	8	7	0	2312.16	298	318
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	182	0.17%	33.1%	VFGNEIK	98.5%	33.8	25	11.4	2	0	0	806.44	371	377
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	182	0.17%	33.1%	VTLDWAKPK	99.7%	53.8	25	50.2	3	0	0	1057.60	640	648
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	26	32	182	0.17%	33.1%	VTQDELKEVFEDAAEIR	99.7%	104	25	95.8	3	6	0	1991.99	404	420
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	10	16	72	0.07%	38.4%	ADKDYHFK	99.7%	52.7	25	43.2	1	0	0	1023.49	25	32
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	10	16	72	0.07%	38.4%	DELHIVEAEAMNYEGSPIK	99.7%	78.6	25	78.6	2	4	0	2161.01	55	73
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	10	16	72	0.07%	38.4%	GPSSVEDIK	99.7%	69.3	25	58.3	13	0	0	931.47	240	248
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	10	16	72	0.07%	38.4%	GPSSVEDIKAK	99.7%	80.2	25	66.1	9	0	0	1130.61	240	250
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	10	16	72	0.07%	38.4%	LLSISGKR	99.7%	49.4	25	37.8	4	0	0	873.55	135	142
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	10	16	72	0.07%	38.4%	MQASIEK	98.1%	32.7	25	13.9	1	0	0	806.41	251	257
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	10	16	72	0.07%	38.4%	MSVQPTVSLGGFEITPPVVLR	99.7%	88.4	25	88.4	12	4	0	2227.22	81	101
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	10	16	72	0.07%	38.4%	MTDQEAIQDLWQWR	99.7%	83.5	25	79.6	10	0	0	1835.84	278	291
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	10	16	72	0.07%	38.4%	SAPGGGSKVPQK	99.7%	40.9	25	40.9	1	0	0	1112.61	143	154
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	10	16	72	0.07%	38.4%	VDNDENEHQLSLR	99.7%	81.2	25	80.6	8	3	0	1568.73	33	45
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	6	6	9	0.01%	3.8%	ALLLVPASVNCLR	96.6%	30.2	25	30.2	2	0	0	1425.82	1142	1154
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	6	6	9	0.01%	3.8%	CTLLLILLR	99.7%	44.7	25	44.7	1	0	0	1114.70	1160	1168
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	6	6	9	0.01%	3.8%	ELSQIEAELNK	99.7%	44.6	25	39.2	1	0	0	1273.66	28	38
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	6	6	9	0.01%	3.8%	LAFSVTNNVIR	99.7%	57.7	25	53.2	2	0	0	1233.69	816	826
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	6	6	9	0.01%	3.8%	LLYPLGGQTNLR	99.7%	59.2	25	51.1	2	0	0	1344.76	501	512
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	6	6	9	0.01%	3.8%	QLFLDVLDGTK	98.8%	34.8	25	24.8	1	0	0	1248.68	1131	1141
Nucleoside diphosphate kinase 6	NME6	NDK6_HUMAN	21.1	100.0%	4	4	6	0.01%	23.7%	GSFGLTDTR	99.7%	61.7	25	41.6	1	0	0	953.47	117	125
Nucleoside diphosphate kinase 6	NME6	NDK6_HUMAN	21.1	100.0%	4	4	6	0.01%	23.7%	LVEFMASGPIR	99.7%	44.9	25	40.7	1	0	0	1235.65	72	82
Nucleoside diphosphate kinase 6	NME6	NDK6_HUMAN	21.1	100.0%	4	4	6	0.01%	23.7%	NTTHGSDSVVSASR	99.7%	49.7	25	48.8	3	0	0	1417.67	126	139
Nucleoside diphosphate kinase 6	NME6	NDK6_HUMAN	21.1	100.0%	4	4	6	0.01%	23.7%	WYEEEEPQLR	96.6%	30.1	25	30.1	1	0	0	1378.63	153	162
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	12	38	0.04%	46.7%	DRPFFAGLVK	99.4%	38	25	27.2	2	0	0	1149.64	57	66
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	12	38	0.04%	46.7%	GDFCIQVGR	99.7%	69.5	25	61.6	4	0	0	1051.50	106	114
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	12	38	0.04%	46.7%	GLVGEIIK	99.7%	45.2	25	35.2	4	0	0	828.52	19	26
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	12	38	0.04%	46.7%	GLVGEIIKR	99.7%	43.7	25	38.8	4	0	0	984.62	19	27
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	12	38	0.04%	46.7%	NIIHGSDSVESAEK	99.7%	56.4	25	50.1	1	2	0	1485.72	115	128
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	12	38	0.04%	46.7%	TFIAIKPDGVQR	99.7%	56.8	25	56.5	4	2	0	1344.76	7	18
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	12	38	0.04%	46.7%	VMLGETNPADSKPGTIR	99.7%	76.8	25	64.9	8	7	0	1785.92	89	105
Nucleoside diphosphate kinase, mitochondrial	NME4	NDKM_HUMAN	20.7	100.0%	5	7	11	0.01%	32.1%	AMIGHTDSAEAAPGTIR	99.6%	32.5	25	28.1	2	2	0	1713.82	122	138
Nucleoside diphosphate kinase, mitochondrial	NME4	NDKM_HUMAN	20.7	100.0%	5	7	11	0.01%	32.1%	GDFSVHISR	96.1%	29.6	25	15.6	1	0	0	1017.51	139	147
Nucleoside diphosphate kinase, mitochondrial	NME4	NDKM_HUMAN	20.7	100.0%	5	7	11	0.01%	32.1%	LVGDVIQR	98.5%	33.7	25	17.2	1	0	0	899.53	53	60
Nucleoside diphosphate kinase, mitochondrial	NME4	NDKM_HUMAN	20.7	100.0%	5	7	11	0.01%	32.1%	NVIHASDSVEGAQR	99.7%	46.4	25	44.7	1	2	0	1482.73	148	161

Nucleoside diphosphate kinase, mitochondrial	NME4	NDKM_HUMAN	20.7	100.0%	5	7	11	0.01%	32.1%	TLVAVKPDGVQR	99.7%	47.3	25	39.1	2	0	0	1282.75	40	51
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	5	5	15	0.01%	17.4%	FYEEVHDLER	99.7%	53.2	25	48.1	6	0	0	1336.62	95	104
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	5	5	15	0.01%	17.4%	GIPEFWLTVFK	99.7%	65.2	25	57	5	0	0	1336.73	166	176
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	5	5	15	0.01%	17.4%	LDGLVETPTGYIESLPR	99.7%	71.1	25	71.1	5	0	0	1859.98	56	72
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	5	5	15	0.01%	17.4%	NVDLLSDMVQEHDEPILK	94.7%	22.5	25	13.1	0	1	0	2095.04	177	194
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	5	5	15	0.01%	17.4%	YAVLYQPLFDK	99.7%	51	25	51	3	0	0	1356.72	106	116
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	5	5	15	0.01%	17.4%	YAVLYQPLFDKR	99.7%	41.7	25	41.7	1	0	0	1512.82	106	117
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	7	7	18	0.02%	21.9%	AAATAEEPDPK	99.7%	57.1	25	53.2	4	0	0	1099.53	147	157
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	7	7	18	0.02%	21.9%	FYEEVHDLER	99.7%	53.2	25	48.1	6	0	0	1336.62	84	93
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	7	7	18	0.02%	21.9%	LDNVPHTPSSYIETLPK	98.8%	28.1	25	27.4	0	1	0	1910.99	45	61
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	7	7	18	0.02%	21.9%	LTDQVMQNPR	99.7%	67.8	25	53.6	1	0	0	1201.60	27	36
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	7	7	18	0.02%	21.9%	QVPNESFFNFFNPLK	99.7%	64.8	25	57.5	1	0	0	1827.91	283	297
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	7	7	18	0.02%	21.9%	VLAALQER	99.7%	54.2	25	37.3	4	0	0	899.53	37	44
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	7	7	18	0.02%	21.9%	YAALYQPLFDK	99.7%	49.9	25	46.2	1	0	0	1328.69	95	105
Oligosaccharyltransferase complex subunit OSTC	OSTC	OSTC_HUMAN	16.8	99.8%	2	2	7	0.01%	14.1%	MKLPGYLMG	98.2%	33	25	17.2	3	0	0	1025.52	141	149
Oligosaccharyltransferase complex subunit OSTC	OSTC	OSTC_HUMAN	16.8	99.8%	2	2	7	0.01%	14.1%	VPFLVLECPNLK	99.7%	63.7	25	60.7	4	0	0	1428.79	7	18
Origin recognition complex subunit 3	ORC3	ORC3_HUMAN	82.3	100.0%	3	4	5	0.00%	4.8%	ENVVNFIDCLVR	99.7%	51.5	25	51.5	1	0	0	1477.75	553	564
Origin recognition complex subunit 3	ORC3	ORC3_HUMAN	82.3	100.0%	3	4	5	0.00%	4.8%	LLLTTQFPFK	98.8%	34.8	25	29.2	1	0	0	1207.71	292	301
Origin recognition complex subunit 3	ORC3	ORC3_HUMAN	82.3	100.0%	3	4	5	0.00%	4.8%	SKEEESVHVTQR	99.7%	67.4	25	64.4	1	2	0	1428.71	164	175
Origin recognition complex subunit 4	ORC4	ORC4_HUMAN	50.4	100.0%	3	3	5	0.00%	7.1%	LDILELLEK	99.7%	52.1	25	18.6	2	0	0	1085.65	196	204
Origin recognition complex subunit 4	ORC4	ORC4_HUMAN	50.4	100.0%	3	3	5	0.00%	7.1%	LLLDNTQIMNALQK	99.7%	84.5	25	78.7	2	0	0	1614.89	404	417
Origin recognition complex subunit 4	ORC4	ORC4_HUMAN	50.4	100.0%	3	3	5	0.00%	7.1%	SVQEVLQK	97.2%	30.9	25	6.78	1	0	0	930.53	261	268
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	5	5	9	0.01%	12.2%	EISSSQWEK	99.7%	45.2	25	32.3	2	0	0	1093.52	272	280
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	5	5	9	0.01%	12.2%	ESQVSILQSLFGER	99.7%	94	25	87.4	2	0	0	1592.83	12	25
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	5	5	9	0.01%	12.2%	LLLEQILNK	99.7%	54.1	25	42	2	0	0	1083.68	71	79
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	5	5	9	0.01%	12.2%	LQKDDTDPGQLK	99.7%	42.4	25	32.1	1	0	0	1357.70	281	292
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	5	5	9	0.01%	12.2%	TYVTQTLLK	98.9%	35.2	25	28.4	2	0	0	1066.61	44	52
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	22	55	0.05%	47.6%	AFYNNVLGEYEEYITK	99.7%	79.3	25	77.1	6	0	0	1952.93	114	129
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	22	55	0.05%	47.6%	DNGLLAKPTHGDIIR	99.7%	52.5	25	52.5	0	2	0	1619.89	399	413
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	22	55	0.05%	47.6%	EDELRESIEIINK	99.7%	64.3	25	49.2	1	0	0	1587.82	422	434
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	22	55	0.05%	47.6%	FAPPLVIKEDELR	99.7%	55.7	25	55.7	2	0	0	1526.86	414	426
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	22	55	0.05%	47.6%	GIYLWDVEGR	99.7%	62.3	25	49.4	3	0	0	1207.61	67	76
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	22	55	0.05%	47.6%	GIYLWDVEGRK	99.7%	47.6	25	42.1	2	0	0	1335.71	67	77
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	22	55	0.05%	47.6%	GLLNAIVIK	99.7%	62	25	52.7	3	0	0	940.62	375	383
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	22	55	0.05%	47.6%	HQVLFIADEIQTGLAR	99.7%	80.2	25	72.3	1	2	0	1810.98	256	271
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	22	55	0.05%	47.6%	IVFAAGNFWGR	99.7%	73.8	25	73.8	6	0	0	1237.65	170	180
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	22	55	0.05%	47.6%	KTVQGPPTSDDIFER	99.7%	51.2	25	51.2	0	2	0	1689.84	32	46
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	22	55	0.05%	47.6%	LPSDVVTAVR	99.7%	75	25	66.4	4	0	0	1056.60	363	372
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	22	55	0.05%	47.6%	NELMKLPSDVVTAVR	99.7%	49.9	25	40.7	0	1	0	1687.90	358	372
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	22	55	0.05%	47.6%	SQVDKLTLTSR	99.7%	65.7	25	58.8	3	2	0	1247.70	103	113
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	22	55	0.05%	47.6%	TVQGPPTSDDIFER	99.7%	92.2	25	77.7	2	0	0	1561.75	33	46
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	22	55	0.05%	47.6%	VAIAALEVLEEENLAENADK	99.7%	115	25	112	2	0	0	2141.10	332	351
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	22	55	0.05%	47.6%	VLPMNTGVEAGETACK	99.7%	96.9	25	96.9	4	0	0	1676.80	136	151
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	22	55	0.05%	47.6%	WLAVDYENVRPDIVLLGK	99.7%	65.1	25	65.1	2	3	0	2100.15	275	292
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	22	55	0.05%	47.6%	YGAHNYHPLPVALER	99.7%	50.3	25	46.4	2	0	0	1736.89	50	64
Oxysterol-binding protein-related protein 8	OSBPL8	OSBL8_HUMAN	101.2	99.8%	2	2	5	0.00%	3.4%	GEAVGSITQPLPSSYLIIR	99.7%	45.9	25	45.9	1	0	0	2001.10	228	246
Oxysterol-binding protein-related protein 8	OSBPL8	OSBL8_HUMAN	101.2	99.8%	2	2	5	0.00%	3.4%	VVLPTFILEPR	99.7%	59.3	25	59.3	4	0	0	1283.77	423	433
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	14	15	28	0.03%	37.0%	AGTEPSDAIR	96.3%	29.8	25	18.7	1	0	0	1016.50	266	275
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	14	15	28	0.03%	37.0%	CQIIYPR	99.7%	43.1	25	26.5	2	0	0	949.49	341	347
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	14	15	28	0.03%	37.0%	ELEMIGFIENNVSK	99.7%	87.7	25	80.2	2	0	0	1622.81	355	368
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	14	15	28	0.03%	37.0%	HSNVVILTTSNITEK	99.7%	53.3	25	53.3	0	2	0	1655.90	290	304

Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	14	15	28	0.03%	37.0%	IDVAFVDR	99.7%	54.1	25	32.5	2	0	0	934.50	305	312
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	14	15	28	0.03%	37.0%	IYLSCLEELMK	99.7%	62.8	25	51.8	2	0	0	1398.70	330	340
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	14	15	28	0.03%	37.0%	LSLLLNDISR	99.7%	68.8	25	48.9	2	0	0	1143.67	369	378
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	14	15	28	0.03%	37.0%	NVNSNLITWNR	99.7%	82.5	25	72	2	0	0	1330.69	163	173
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	14	15	28	0.03%	37.0%	NVQSVSIIDTELK	99.7%	70.2	25	61.2	2	0	0	1445.78	69	81
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	14	15	28	0.03%	37.0%	QQLLTLR	99.7%	46.5	25	25.1	2	0	0	871.54	348	354
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	14	15	28	0.03%	37.0%	QYIGPPSAAAIFK	99.7%	61.3	25	50.2	2	0	0	1362.74	317	329
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	14	15	28	0.03%	37.0%	VVLLHGPPGTGK	99.7%	73.4	25	69	2	0	0	1174.69	174	185
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	14	15	28	0.03%	37.0%	VVNAVLTQIDQIKR	99.7%	82.8	25	82.8	2	2	0	1596.94	276	289
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	14	15	28	0.03%	37.0%	YGQLIEINSHSLFSK	99.7%	72.4	25	72.4	1	0	0	1735.90	206	220
Paired amphipathic helix protein Sin3a	SIN3A	SIN3A_HUMAN	145.2	100.0%	4	4	6	0.01%	3.2%	LLFSNTAAQK	99.7%	46	25	34.4	2	0	0	1092.60	866	875
Paired amphipathic helix protein Sin3a	SIN3A	SIN3A_HUMAN	145.2	100.0%	4	4	6	0.01%	3.2%	SAEAYENFLR	99.7%	67.8	25	48.3	1	0	0	1199.57	476	485
Paired amphipathic helix protein Sin3a	SIN3A	SIN3A_HUMAN	145.2	100.0%	4	4	6	0.01%	3.2%	SLLESTYQR	99.7%	46.7	25	37.8	2	0	0	1096.56	1044	1052
Paired amphipathic helix protein Sin3a	SIN3A	SIN3A_HUMAN	145.2	100.0%	4	4	6	0.01%	3.2%	SQSIDTPGVISR	98.7%	34.5	25	21.5	1	0	0	1259.66	156	167
Parafibromin	CDC73	CDC73_HUMAN	60.6	99.8%	2	2	3	0.00%	4.3%	GDEVIFGEFSWPK	99.6%	40.9	25	40.9	1	0	0	1510.72	22	34
Parafibromin	CDC73	CDC73_HUMAN	60.6	99.8%	2	2	3	0.00%	4.3%	NIFAILQSVK	99.7%	47.8	25	47.8	2	0	0	1132.67	248	257
PC4 and SFRS1-interacting protein	PSIP1	PSIP1_HUMAN	60.1	99.8%	2	2	5	0.00%	3.0%	GQEEKQPK	98.3%	33.1	25	22.9	2	0	0	943.48	221	228
PC4 and SFRS1-interacting protein	PSIP1	PSIP1_HUMAN	60.1	99.8%	2	2	5	0.00%	3.0%	IDNLDVNR	99.7%	46.8	25	6.13	3	0	0	958.50	365	372
PCI domain-containing protein 2	PCID2	PCID2_HUMAN	46.0	100.0%	4	4	7	0.01%	11.8%	AIDSSNLKDDYSTAQR	99.7%	37.1	25	34.1	0	1	0	1783.85	194	209
PCI domain-containing protein 2	PCID2	PCID2_HUMAN	46.0	100.0%	4	4	7	0.01%	11.8%	CGIFLILEK	97.4%	31.3	25	25.4	2	0	0	1092.61	308	316
PCI domain-containing protein 2	PCID2	PCID2_HUMAN	46.0	100.0%	4	4	7	0.01%	11.8%	MILIYLLPVK	99.7%	58	25	58	2	0	0	1202.76	250	259
PCI domain-containing protein 2	PCID2	PCID2_HUMAN	46.0	100.0%	4	4	7	0.01%	11.8%	VFANNADQQLVK	99.7%	44.5	25	44.5	2	0	0	1346.71	117	128
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	6	6	10	0.01%	9.4%	FIGPDQHR	99.7%	41.2	25	29.9	1	0	0	969.49	447	454
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	6	6	10	0.01%	9.4%	SAYESQPIR	99.7%	47.8	25	36.6	1	0	0	1050.52	557	565
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	6	6	10	0.01%	9.4%	SELLNELMDSAK	99.7%	72.8	25	72.8	2	0	0	1349.66	608	619
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	6	6	10	0.01%	9.4%	SPALQVLR	99.7%	59.5	25	53.5	2	0	0	883.54	351	358
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	6	6	10	0.01%	9.4%	VEGTDVTGIEEVVIPK	99.7%	100	25	94.4	2	0	0	1684.90	46	61
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	6	6	10	0.01%	9.4%	VMSDFAINQEQK	99.7%	96.8	25	91.6	2	0	0	1409.67	649	660
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	9	12	23	0.02%	47.3%	EGMNIVEAMER	99.7%	50.5	25	50.5	5	0	0	1278.58	134	144
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	9	12	23	0.02%	47.3%	IIPGFMCQGGDFTR	99.2%	36.4	25	33.6	3	0	0	1598.75	56	69
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	9	12	23	0.02%	47.3%	ITIADCGQLE	99.7%	44.8	25	44.8	2	0	0	1119.54	156	165
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	9	12	23	0.02%	47.3%	KITIADCGQLE	99.7%	66	25	57.7	2	0	0	1247.63	155	165
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	9	12	23	0.02%	47.3%	SIYGEKFEDENFILK	99.7%	60.9	25	54.9	2	0	0	1831.91	77	91
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	9	12	23	0.02%	47.3%	TEWLDGKHVVFGK	96.0%	23.4	25	21.9	0	2	0	1515.80	119	131
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	9	12	23	0.02%	47.3%	VKEGMNIVEAMER	99.7%	63.8	25	63.8	3	0	0	1505.75	132	144
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	9	12	23	0.02%	47.3%	VSFELFADK	99.7%	53.6	25	48.6	2	0	0	1055.54	20	28
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	9	12	23	0.02%	47.3%	VSFELFADKVPK	99.7%	60.5	25	50.5	2	0	0	1379.76	20	31
Peptidyl-prolyl cis-trans isomerase H	PPIH	PPIH_HUMAN	19.2	99.8%	2	3	6	0.01%	13.0%	IIDGLLVMR	99.7%	52.1	25	39.3	4	0	0	1029.61	144	152
Peptidyl-prolyl cis-trans isomerase H	PPIH	PPIH_HUMAN	19.2	99.8%	2	3	6	0.01%	13.0%	KIENVPTGPNNKPK	99.7%	40.7	25	38	0	2	0	1535.85	153	166
Peptidyl-prolyl cis-trans isomerase-like 1	PPIL1	PPIL1_HUMAN	18.2	100.0%	3	6	10	0.01%	26.5%	IIKDFMIQGGDPTGTGR	99.7%	93.3	25	91.9	3	2	0	1805.92	56	72
Peptidyl-prolyl cis-trans isomerase-like 1	PPIL1	PPIL1_HUMAN	18.2	100.0%	3	6	10	0.01%	26.5%	VCQGIGMVNR	99.7%	61	25	39.9	2	0	0	1149.55	132	141
Peptidyl-prolyl cis-trans isomerase-like 1	PPIL1	PPIL1_HUMAN	18.2	100.0%	3	6	10	0.01%	26.5%	VGMVETNSQDRPVDDVK	99.7%	40.6	25	37.5	2	1	0	1888.91	142	158
Peptidyl-prolyl cis-trans isomerase-like 3	PPIL3	PPIL3_HUMAN	18.2	99.8%	2	3	4	0.00%	15.5%	GFMVQTGDPTGTGR	99.7%	77.1	25	77	3	0	0	1439.66	48	61
Peptidyl-prolyl cis-trans isomerase-like 3	PPIL3	PPIL3_HUMAN	18.2	99.8%	2	3	4	0.00%	15.5%	KFEDEYSEYLK	99.7%	69.3	25	66.4	1	0	0	1450.67	70	80
Peptidyl-tRNA hydrolase ICT1, mitochondrial	ICT1	ICT1_HUMAN	23.6	100.0%	3	3	5	0.00%	12.6%	IRIENMNR	95.5%	29	25	18.4	1	0	0	1045.56	178	185
Peptidyl-tRNA hydrolase ICT1, mitochondrial	ICT1	ICT1_HUMAN	23.6	100.0%	3	3	5	0.00%	12.6%	NLADCLQK	97.8%	32.1	25	25.2	2	0	0	961.48	146	153
Peptidyl-tRNA hydrolase ICT1, mitochondrial	ICT1	ICT1_HUMAN	23.6	100.0%	3	3	5	0.00%	12.6%	QADSDIPLDR	99.7%	82.3	25	61.1	2	0	0	1129.55	67	76
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	10	11	22	0.02%	47.2%	ADEGISFR	98.4%	33.6	25	25.1	1	0	0	894.43	121	128
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	10	11	22	0.02%	47.2%	DISLSDYKGK	99.7%	44.2	25	34.5	2	0	0	1125.58	28	37
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	10	11	22	0.02%	47.2%	GLFIIDDKGILR	99.7%	57.2	25	57.2	4	2	0	1359.80	129	140
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	10	11	22	0.02%	47.2%	IGHPAPNFK	97.4%	31.2	25	28.3	1	0	0	980.53	8	16

Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	10	11	22	0.02%	47.2%	LVQAFQFTDK	99.7%	51.1	25	41.8	2	0	0	1196.63	159	168
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	10	11	22	0.02%	47.2%	QGGLGPMNIPLVSDPKR	99.5%	32	25	32	0	1	0	1794.95	94	110
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	10	11	22	0.02%	47.2%	QITVNDLPVGR	99.7%	81.8	25	74.8	4	0	0	1211.67	141	151
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	10	11	22	0.02%	47.2%	SVDETLR	99.3%	37.4	25	24.2	1	0	0	819.42	152	158
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	10	11	22	0.02%	47.2%	TIAQDYGVLK	99.7%	65.8	25	57.4	2	0	0	1107.60	111	120
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	10	11	22	0.02%	47.2%	TIAQDYGVLKADEGISFR	99.7%	38.9	25	36.6	0	2	0	1983.02	111	128
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	3	3	6	0.01%	20.7%	ATAVVDGAFKEVK	99.7%	68.9	25	57.7	2	0	0	1334.73	17	29
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	3	3	6	0.01%	20.7%	GLFIIDGK	99.5%	39.1	25	38.5	2	0	0	862.50	128	135
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	3	3	6	0.01%	20.7%	LSEDYGVLK	99.7%	50.5	25	43.4	2	0	0	1023.54	111	119
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	3	3	6	0.01%	20.7%	QITVNDLPVGR	99.7%	81.8	25	74.8	4	0	0	1211.67	140	150
Peroxiredoxin-4	PRDX4	PRDX4_HUMAN	30.5	99.8%	2	2	3	0.00%	15.9%	DYGVYLEDSGHTLR	99.7%	60	25	60	2	0	0	1624.76	187	200
Peroxiredoxin-4	PRDX4	PRDX4_HUMAN	30.5	99.8%	2	2	3	0.00%	15.9%	GLFIIDDKGILR	99.7%	57.2	25	57.2	4	2	0	1359.80	201	212
Peroxiredoxin-4	PRDX4	PRDX4_HUMAN	30.5	99.8%	2	2	3	0.00%	15.9%	LVQAFQYTDK	97.2%	30.9	25	30.9	1	0	0	1212.63	231	240
Peroxiredoxin-4	PRDX4	PRDX4_HUMAN	30.5	99.8%	2	2	3	0.00%	15.9%	SVDETLR	99.3%	37.4	25	24.2	1	0	0	819.42	224	230
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	7	7	14	0.01%	41.5%	DFTPVCTTELGR	99.7%	45.7	25	45.7	3	0	0	1395.66	42	53
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	7	7	14	0.01%	41.5%	DINAYNCEEPTEK	99.7%	68.5	25	68.5	2	0	0	1582.67	85	97
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	7	7	14	0.01%	41.5%	FHDFLGDSWGILFSHPR	99.7%	40.5	25	40.5	0	1	0	2030.99	25	41
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	7	7	14	0.01%	41.5%	LPFPIIDDR	99.7%	58.9	25	46	2	0	0	1085.60	98	106
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	7	7	14	0.01%	41.5%	LSILYPATTGR	99.7%	59	25	41.8	2	0	0	1191.67	145	155
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	7	7	14	0.01%	41.5%	PGGLLLGDVAPNFEANTTVGR	99.7%	97.4	25	95.5	2	0	0	2098.09	2	22
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	7	7	14	0.01%	41.5%	VVFVFGPDKK	99.7%	54.8	25	51.9	2	0	0	1135.65	133	142
Peroxisomal biogenesis factor 3	PEX3	PEX3_HUMAN	42.1	99.8%	2	2	4	0.00%	5.6%	EAAEYIAQAR	99.7%	58.5	25	51.7	2	0	0	1121.56	44	53
Peroxisomal biogenesis factor 3	PEX3	PEX3_HUMAN	42.1	99.8%	2	2	4	0.00%	5.6%	HSLSLLDLEQK	99.7%	56.7	25	48.6	2	0	0	1282.70	198	208
Peroxisomal membrane protein PEX16	PEX16	PEX16_HUMAN	38.6	100.0%	3	3	3	0.00%	10.1%	AGLQTSPPIVPLDR	97.1%	30.8	25	30.8	1	0	0	1463.82	133	146
Peroxisomal membrane protein PEX16	PEX16	PEX16_HUMAN	38.6	100.0%	3	3	3	0.00%	10.1%	GFSYLLAGR	99.7%	44.4	25	28.6	1	0	0	983.53	31	39
Peroxisomal membrane protein PEX16	PEX16	PEX16_HUMAN	38.6	100.0%	3	3	3	0.00%	10.1%	TLQNTPSLHSR	99.7%	49.5	25	44.2	1	0	0	1253.66	177	187
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	13	0.01%	9.5%	EALAFIIR	99.7%	49.7	25	34.2	2	0	0	932.56	341	348
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	13	0.01%	9.5%	GSATNYITR	99.7%	68.5	25	52.4	2	0	0	982.50	12	20
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	13	0.01%	9.5%	LAQEEESEAK	99.7%	53.1	25	52.8	2	0	0	1133.53	524	533
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	13	0.01%	9.5%	LAQEEESEAKR	99.7%	44	25	36.8	2	0	0	1289.63	524	534
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	13	0.01%	9.5%	LEGQAQAEAK	99.7%	66.5	25	51.4	2	0	0	1044.53	250	259
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	13	0.01%	9.5%	LQLSLADFR	99.7%	59.1	25	49.2	2	0	0	1062.59	27	35
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	13	0.01%	9.5%	YPTFIDALR	99.2%	36.7	25	28.9	1	0	0	1095.58	124	132
PHD finger protein 6	PHF6	PHF6_HUMAN	41.3	100.0%	4	4	6	0.01%	10.4%	AEFGDFDIK	99.5%	38.7	25	30.6	2	0	0	1041.49	258	266
PHD finger protein 6	PHF6	PHF6_HUMAN	41.3	100.0%	4	4	6	0.01%	10.4%	DKECGQLLISENQK	99.7%	57.6	25	45.4	1	0	0	1661.82	25	38
PHD finger protein 6	PHF6	PHF6_HUMAN	41.3	100.0%	4	4	6	0.01%	10.4%	LHIFNAK	97.9%	32.2	25	16.5	1	0	0	842.49	228	234
PHD finger protein 6	PHF6	PHF6_HUMAN	41.3	100.0%	4	4	6	0.01%	10.4%	TVLQEIKR	99.7%	44.2	25	17.6	2	0	0	986.60	267	274
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	12	13	29	0.03%	27.8%	GSAFSTSISK	99.7%	41.6	25	36.4	2	0	0	984.50	178	187
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	12	13	29	0.03%	27.8%	HWELTAEGEEIAR	99.6%	40.8	25	39.1	1	0	0	1540.74	60	72
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	12	13	29	0.03%	27.8%	KLLAEVTLK	99.7%	45.7	25	35.3	1	0	0	1014.66	163	171
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	12	13	29	0.03%	27.8%	LDAEPRPPPTQEAA	99.7%	49.9	25	49.9	2	0	0	1491.74	495	508
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	12	13	29	0.03%	27.8%	LGITQLR	99.7%	53.2	25	30.1	4	0	0	800.50	398	404
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	12	13	29	0.03%	27.8%	QETELSPEMISSGSWR	99.7%	77.7	25	77.7	1	0	0	1852.84	188	203
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	12	13	29	0.03%	27.8%	SIPPEGLAQSELMR	96.3%	29.8	25	29.8	1	0	0	1543.78	83	96
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	12	13	29	0.03%	27.8%	SLQALGEVIEAELR	99.7%	90.6	25	74.9	4	0	0	1527.84	43	56
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	12	13	29	0.03%	27.8%	THSQGGYGSQGYK	99.7%	68.4	25	67.4	2	0	0	1369.61	299	311
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	12	13	29	0.03%	27.8%	VNLQMVYDSPLCR	99.7%	76.7	25	76.7	2	0	0	1594.77	482	494
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	12	13	29	0.03%	27.8%	VVDSMEDEVQR	99.7%	89.4	25	89.4	6	0	0	1306.59	128	138
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	12	13	29	0.03%	27.8%	YGINNIR	99.3%	37.4	25	23.1	3	0	0	849.46	469	475
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	20	0.02%	17.3%	ASEGPAFFPGR	99.7%	70.1	25	52.6	2	0	0	1135.55	537	547
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	20	0.02%	17.3%	AVHISNPK	96.3%	29.8	25	29.8	1	0	0	865.49	436	443

Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	20	0.02%	17.3%	DLLFQALGR	99.7%	56.2	25	38	3	0	0	1032.58	9	17
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	20	0.02%	17.3%	DRYDSFIELQEK	99.7%	54.8	25	45.9	2	0	0	1542.74	134	145
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	20	0.02%	17.3%	HLCAVYYNK	97.7%	31.9	25	21.3	2	0	0	1167.56	496	504
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	20	0.02%	17.3%	LGVLHPDVITK	99.7%	48.9	25	45.8	2	0	0	1191.71	561	571
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	20	0.02%	17.3%	LIITEETAK	99.7%	49.2	25	37.8	2	0	0	1017.58	108	116
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	20	0.02%	17.3%	NIFIECTGTDFTK	99.7%	85.7	25	81.5	2	0	0	1545.73	250	262
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	20	0.02%	17.3%	TTLLPGLLK	98.1%	32.6	25	23.9	2	0	0	955.62	452	460
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	10	10	20	0.02%	17.3%	YDLLCLEGLVR	99.7%	69.4	25	63.1	2	0	0	1350.71	72	82
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	21	67	0.06%	36.7%	EKGSSASLVLK	99.2%	37	25	28.8	3	0	0	1118.64	294	304
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	21	67	0.06%	36.7%	FACFER	98.6%	34.2	25	28.8	3	0	0	829.37	235	240
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	21	67	0.06%	36.7%	FGFYEVFK	99.1%	36	25	28.3	4	0	0	1036.51	138	145
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	21	67	0.06%	36.7%	GIFNGFSVTLK	99.7%	77	25	65.7	4	0	0	1182.65	102	112
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	21	67	0.06%	36.7%	GIFNGFSVTLKEDGVR	99.7%	67.4	25	63	1	0	0	1738.91	102	117
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	21	67	0.06%	36.7%	GSSASLVLK	99.5%	39.5	25	23.6	4	0	0	861.50	296	304
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	21	67	0.06%	36.7%	GSSASLVLKR	99.7%	71.7	25	53.7	4	0	0	1017.61	296	305
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	21	67	0.06%	36.7%	GVAPLWMR	99.7%	49.6	25	17.7	6	0	0	929.50	219	226
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	21	67	0.06%	36.7%	GWAPTFLGYSMQGLCK	99.7%	76.9	25	76.9	6	0	0	1815.86	122	137
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	21	67	0.06%	36.7%	IQTQPGYANTLR	99.7%	74.2	25	58.6	13	0	0	1361.72	190	201
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	21	67	0.06%	36.7%	LPRPPPPEMPESLK	99.7%	34.4	25	29	0	1	0	1587.86	342	355
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	21	67	0.06%	36.7%	LPRPPPPEMPESLKK	97.3%	24.9	25	24.9	0	1	0	1715.95	342	356
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	21	67	0.06%	36.7%	MQVDPQK	99.7%	41.2	25	18.4	2	0	0	845.42	93	99
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	21	67	0.06%	36.7%	MQVDPQKYK	97.1%	30.9	25	5.25	1	0	0	1152.57	93	101
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	21	67	0.06%	36.7%	MYKEEGLK	99.7%	42.4	25	29.9	7	0	0	997.50	207	214
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	21	67	0.06%	36.7%	TVEALYK	98.9%	35.3	25	18.4	2	0	0	823.46	241	247
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	21	67	0.06%	36.7%	VLYSNMLGEENTYLWR	99.7%	97.7	25	97.7	5	0	0	1987.96	146	161
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	5	6	11	0.01%	26.4%	AATALLEAGLAR	99.7%	92.6	25	79.1	2	0	0	1156.67	2	13
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	5	6	11	0.01%	26.4%	GVITMNEEYETR	99.7%	62.6	25	62.6	3	0	0	1457.66	67	78
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	5	6	11	0.01%	26.4%	IDPTVLLGALPLR	99.7%	44.2	25	43.3	2	0	0	1377.85	41	53
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	5	6	11	0.01%	26.4%	LGVEQLR	99.7%	47.9	25	14.6	2	0	0	814.48	90	96
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	5	6	11	0.01%	26.4%	QLVQDENVR	99.7%	56.9	25	48	2	0	0	1100.57	58	66
Phosphatidylinositide phosphatase SAC1	SACM1L	SAC1_HUMAN	67.0	100.0%	3	3	5	0.00%	4.9%	ELSAQPEVHR	99.7%	41.2	25	31.5	1	0	0	1165.60	175	184
Phosphatidylinositide phosphatase SAC1	SACM1L	SAC1_HUMAN	67.0	100.0%	3	3	5	0.00%	4.9%	TNVIQSLLAR	99.7%	41.3	25	32.9	2	0	0	1114.66	396	405
Phosphatidylinositide phosphatase SAC1	SACM1L	SAC1_HUMAN	67.0	100.0%	3	3	5	0.00%	4.9%	YFDWILISR	99.0%	35.4	25	25.5	2	0	0	1212.64	205	213
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	16	16	35	0.03%	27.1%	AALQALGVAEGGER	99.7%	83.5	25	77.7	3	0	0	1341.71	36	49
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	16	16	35	0.03%	27.1%	ALGATFGPLLLR	99.7%	49.3	25	39.1	4	0	0	1228.74	245	256
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	16	16	35	0.03%	27.1%	APGPGPPPAAR	99.7%	44.9	25	36.6	2	0	0	987.54	718	728
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	16	16	35	0.03%	27.1%	DTPDGTFLVR	96.0%	29.5	25	26	1	0	0	1120.56	346	355
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	16	16	35	0.03%	27.1%	EDSVEAVGAQLK	99.7%	74.1	25	63.1	1	0	0	1245.63	436	447
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	16	16	35	0.03%	27.1%	EYDQLYEEYTR	99.7%	44.7	25	43.2	2	0	0	1508.65	459	469
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	16	16	35	0.03%	27.1%	FLLQHLGR	99.7%	49.1	25	47	2	0	0	983.58	224	231
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	16	16	35	0.03%	27.1%	GCYACSVVVDGDTK	99.7%	91.3	25	91.3	1	0	0	1530.66	653	666
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	16	16	35	0.03%	27.1%	HESLAQYNAK	99.7%	45.8	25	38	2	0	0	1160.57	407	416
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	16	16	35	0.03%	27.1%	IAEIHESR	99.7%	54.1	25	28.5	4	0	0	954.50	532	539
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	16	16	35	0.03%	27.1%	IFEEQGQTQEK	99.7%	70.8	25	64.9	2	0	0	1336.64	490	500
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	16	16	35	0.03%	27.1%	SFLLALPAPLVTPEASAEAR	99.7%	79.6	25	71	4	0	0	2053.13	176	195
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	16	16	35	0.03%	27.1%	TAIEAFNETIK	99.7%	67.9	25	64.6	2	0	0	1236.65	479	489
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	16	16	35	0.03%	27.1%	TATGFGFAEPYNLYGSLK	99.7%	60.5	25	53.7	2	0	0	1935.95	673	690
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	16	16	35	0.03%	27.1%	TGLDSESHYRPELPAPR	99.7%	46.4	25	45.3	0	2	0	1924.95	138	154
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	16	16	35	0.03%	27.1%	TQAEEMLSGK	99.7%	42.3	25	23	1	0	0	1093.52	630	639
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	100.0%	2	2	3	0.00%	4.5%	GVDASGETTYKK	99.7%	48.5	25	43.8	1	0	0	1255.62	62	73
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	100.0%	2	2	3	0.00%	4.5%	QAQGAQSTSDEKRPVGQK	99.7%	37.7	25	37.7	0	2	0	1914.96	334	351

Phosphatidylserine decarboxylase proenzyme	PISD	PISD_HUMAN	46.7	99.9%	2	2	3	0.00%	6.6%	GSYNDFSFVTHTNR	99.7%	60.7	25	60.7	1	0	0	1644.74	347	360
Phosphatidylserine decarboxylase proenzyme	PISD	PISD_HUMAN	46.7	99.9%	2	2	3	0.00%	6.6%	GVTYSLESFLGPR	99.7%	73	25	63.7	2	0	0	1425.74	210	222
Phosphatidylserine synthase 1	PTDSS1	PTSS1_HUMAN	55.5	100.0%	3	3	5	0.00%	7.8%	AVLQFTPASWTYVR	99.7%	47.2	25	47.2	2	0	0	1638.86	263	276
Phosphatidylserine synthase 1	PTDSS1	PTSS1_HUMAN	55.5	100.0%	3	3	5	0.00%	7.8%	ILFIGGITAPTVR	99.7%	82.3	25	80.9	2	0	0	1357.82	324	336
Phosphatidylserine synthase 1	PTDSS1	PTSS1_HUMAN	55.5	100.0%	3	3	5	0.00%	7.8%	TLSKDDVNYK	99.5%	39.5	25	29.2	1	0	0	1182.60	9	18
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	6	6	13	0.01%	12.2%	AFVRPSGTEDVVR	99.7%	59.5	25	58	0	3	0	1432.75	493	505
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	6	6	13	0.01%	12.2%	MGLLAVLR	99.7%	74.2	25	55.5	4	0	0	872.54	42	49
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	6	6	13	0.01%	12.2%	QAVTPPGLQEAINDLVK	97.8%	32.1	25	32.1	1	0	0	1792.98	470	486
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	6	6	13	0.01%	12.2%	VDCANGIGALK	99.7%	41.3	25	29.4	1	0	0	1117.57	210	220
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	6	6	13	0.01%	12.2%	VISTTDAER	99.3%	37.7	25	31.5	3	0	0	991.51	461	469
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	6	6	13	0.01%	12.2%	VLIDISEK	99.4%	37.8	25	17.9	1	0	0	916.54	105	112
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	14	14	31	0.03%	27.2%	AIDTTQLFSLPK	99.7%	88.3	25	75.4	2	0	0	1333.74	589	600
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	14	14	31	0.03%	27.2%	DFVEHSAR	98.3%	33.3	25	22.2	1	0	0	960.45	46	53
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	14	14	31	0.03%	27.2%	EGALDLSGLR	99.7%	47.8	25	38.5	3	0	0	1030.55	579	588
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	14	14	31	0.03%	27.2%	EIISFGSGYGGNSLLGK	99.7%	110	25	110	3	0	0	1698.87	245	261
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	14	14	31	0.03%	27.2%	EVLAELEALER	99.7%	80.8	25	66.5	2	0	0	1271.68	625	635
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	14	14	31	0.03%	27.2%	GQLGNWMSPADFQR	99.7%	51.4	25	51.4	1	0	0	1606.74	129	142
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	14	14	31	0.03%	27.2%	GVPLVYEAFNWR	99.7%	47.1	25	32.7	2	0	0	1450.75	458	469
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	14	14	31	0.03%	27.2%	LGTPVLQALGDGDFVK	99.7%	108	25	101	3	0	0	1629.89	194	209
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	14	14	31	0.03%	27.2%	SYLTEQVNQDLPK	99.7%	108	25	99.7	2	0	0	1534.77	612	624
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	14	14	31	0.03%	27.2%	TLIGHVPDQR	98.6%	34	25	25.3	2	0	0	1135.62	235	244
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	14	14	31	0.03%	27.2%	TMYVLPFSMGPVGSPLSR	99.7%	86.3	25	67.5	5	0	0	1954.98	156	173
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	14	14	31	0.03%	27.2%	VLDWICR	99.4%	38	25	28.6	2	0	0	961.49	554	560
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	14	14	31	0.03%	27.2%	VLSGDLGQLPTGIR	99.7%	98.1	25	92.6	2	0	0	1425.81	32	45
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	14	14	31	0.03%	27.2%	YVAAAFPSACGK	98.8%	34.8	25	34.8	1	0	0	1241.60	297	308
Phosphoglycerate kinase 1	PGK1	PGK1_HUMAN	44.6	99.9%	2	2	4	0.00%	6.2%	LGDVYVNDAFGTAHR	99.7%	60.6	25	60.2	0	2	0	1634.79	157	171
Phosphoglycerate kinase 1	PGK1	PGK1_HUMAN	44.6	99.9%	2	2	4	0.00%	6.2%	VLPGVDALSNI	99.7%	51.3	25	48.2	2	0	0	1097.62	407	417
Phosphoglycerate mutase 1	PGAM1	PGAM1_HUMAN	28.8	100.0%	4	4	7	0.01%	17.7%	ALPFWNEEIVPQIK	99.7%	42.2	25	37.9	1	0	0	1683.91	163	176
Phosphoglycerate mutase 1	PGAM1	PGAM1_HUMAN	28.8	100.0%	4	4	7	0.01%	17.7%	AMEAVAAQGK	99.5%	39	25	37.8	2	0	0	975.49	242	251
Phosphoglycerate mutase 1	PGAM1	PGAM1_HUMAN	28.8	100.0%	4	4	7	0.01%	17.7%	HYGGLTGLNK	99.6%	40.7	25	27	2	0	0	1059.56	91	100
Phosphoglycerate mutase 1	PGAM1	PGAM1_HUMAN	28.8	100.0%	4	4	7	0.01%	17.7%	VLIAAHGNSLR	99.7%	53.4	25	53.4	2	0	0	1150.67	181	191
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	8	9	17	0.02%	29.9%	AVEMAAQR	99.7%	50.7	25	28.9	2	0	0	875.44	221	228
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	8	9	17	0.02%	29.9%	AVVVGFDPHFSYMK	99.7%	53.3	25	53.3	3	0	0	1596.79	167	180
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	8	9	17	0.02%	29.9%	FIAGTGCLVR	99.7%	61.8	25	35.4	2	0	0	1093.58	211	220
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	8	9	17	0.02%	29.9%	FIFDCVSQEYGINPER	99.7%	79.4	25	74	2	0	0	1973.91	239	254
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	8	9	17	0.02%	29.9%	GETAVPGAPEALR	99.7%	59.4	25	41.8	2	0	0	1267.66	42	54
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	8	9	17	0.02%	29.9%	LGFITNNSSK	99.7%	50.9	25	39.9	2	0	0	1080.57	63	72
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	8	9	17	0.02%	29.9%	QADIIGKPSR	99.4%	38.3	25	21.8	2	0	0	1084.61	229	238
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	8	9	17	0.02%	29.9%	TILTLTGVSTLGDVK	99.7%	95.4	25	95.3	2	0	0	1517.88	276	290
Phosphoinositide 3-kinase regulatory subunit 4	PIK3R4	PI3R4_HUMAN	153.1	100.0%	3	3	3	0.00%	2.5%	FLELVQLK	96.8%	30.4	25	10.1	1	0	0	989.60	496	503
Phosphoinositide 3-kinase regulatory subunit 4	PIK3R4	PI3R4_HUMAN	153.1	100.0%	3	3	3	0.00%	2.5%	GVIDLAALGITGR	98.7%	34.5	25	34.5	1	0	0	1255.74	817	829
Phosphoinositide 3-kinase regulatory subunit 4	PIK3R4	PI3R4_HUMAN	153.1	100.0%	3	3	3	0.00%	2.5%	VVTLLSDPENIVK	99.7%	54.3	25	49	1	0	0	1426.82	541	553
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	6	12	0.01%	32.0%	AGLTHIITMDLHQK	99.7%	57.9	25	0	0	4	0	1577.85	125	138
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	6	12	0.01%	32.0%	EIQGFFSFPVDNLR	99.7%	43.7	25	43.7	3	0	0	1668.84	139	152
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	6	12	0.01%	32.0%	EKPPITVVGDVGGR	99.7%	54.2	25	52.3	2	2	0	1423.79	237	250
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	6	12	0.01%	32.0%	GQDIFIIQTIPR	99.7%	72.1	25	65	2	0	0	1400.79	57	68
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	6	12	0.01%	32.0%	IYVMATHGILSAEAPR	99.7%	37.3	25	34.5	0	1	0	1744.91	280	295
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	6	12	0.01%	32.0%	NATVHPGLELPLMMAK	99.7%	38.1	25	38.1	0	2	0	1753.90	221	236
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	6	12	0.01%	32.0%	NIIGVIPYFPYSK	99.7%	56.9	25	56.9	2	0	0	1510.83	91	103
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	6	12	0.01%	32.0%	VFSANSTAACTELAK	99.7%	85.4	25	83.8	2	0	0	1569.76	10	24
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	10	17	31	0.03%	35.8%	AGLTHLITMDLHQK	99.7%	57.9	25	0	0	4	0	1577.85	137	150

Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	10	17	31	0.03%	35.8%	EIQGFFNIPVDNLR	99.7%	67.9	25	59.7	2	0	0	1661.86	151	164
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	10	17	31	0.03%	35.8%	EKPPITVVGDVGGR	99.7%	54.2	25	52.3	2	2	0	1423.79	250	263
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	10	17	31	0.03%	35.8%	GGLVLFSANSNSSCMELSK	99.7%	103	25	103	2	0	0	2016.94	18	36
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	10	17	31	0.03%	35.8%	IFVMATHGLLSSDAPR	99.7%	75.2	25	70	4	4	0	1714.89	293	308
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	10	17	31	0.03%	35.8%	IHNGESMSYLFR	94.7%	22.5	25	19.8	0	1	0	1469.68	352	363
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	10	17	31	0.03%	35.8%	SIIGVIPYFPYSK	99.7%	46.4	25	39.5	2	0	0	1483.82	103	115
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	10	17	31	0.03%	35.8%	TVDISMILSEAIR	99.7%	80	25	73.8	4	0	0	1447.78	338	350
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	10	17	31	0.03%	35.8%	VQIQESVR	99.7%	59.8	25	38.8	2	0	0	958.53	61	68
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	10	17	31	0.03%	35.8%	VQVYQEPNR	99.7%	57.3	25	47	2	0	0	1132.57	49	57
Phosphoserine aminotransferase	PSAT1	SERC_HUMAN	40.4	99.8%	2	2	2	0.00%	6.8%	ASLYNAVTIEDVQK	99.7%	77.3	25	77.3	1	0	0	1550.81	343	356
Phosphoserine aminotransferase	PSAT1	SERC_HUMAN	40.4	99.8%	2	2	2	0.00%	6.8%	QVVNFGPGPAK	99.3%	37	25	35	1	0	0	1113.61	6	16
Pinin	PNN	PININ_HUMAN	81.6	100.0%	3	3	5	0.00%	4.9%	FKQESTVATER	99.7%	60.3	25	27.7	3	0	0	1295.66	156	166
Pinin	PNN	PININ_HUMAN	81.6	100.0%	3	3	5	0.00%	4.9%	GFSDSGGGPPAK	97.5%	31.5	25	21.1	1	0	0	1076.50	64	75
Pinin	PNN	PININ_HUMAN	81.6	100.0%	3	3	5	0.00%	4.9%	NEEQKAEQEEGK	99.7%	45	25	44.6	1	0	0	1418.64	300	311
Plakophilin-1	PKP1	PKP1_HUMAN	82.9	99.8%	2	2	3	0.00%	3.5%	LLQSGNSDVVR	99.7%	56.6	25	47.4	1	0	0	1187.64	603	613
Plakophilin-1	PKP1	PKP1_HUMAN	82.9	99.8%	2	2	3	0.00%	3.5%	SPNQNVQQAAAGALR	99.7%	80.9	25	61.2	2	0	0	1524.79	298	312
Plasma membrane calcium-transporting ATPase 1	ATP2B1	AT2B1_HUMAN	138.8	100.0%	3	3	4	0.00%	4.1%	EASDIILTDDNFTSIVK	99.7%	83.2	25	83.2	2	0	0	1880.95	824	840
Plasma membrane calcium-transporting ATPase 1	ATP2B1	AT2B1_HUMAN	138.8	100.0%	3	3	4	0.00%	4.1%	TSPNEGLSGNPADLER	99.7%	64.9	25	58.5	1	0	0	1656.78	65	80
Plasma membrane calcium-transporting ATPase 1	ATP2B1	AT2B1_HUMAN	138.8	100.0%	3	3	4	0.00%	4.1%	YGDLLPADGILIQGNDLK	99.0%	35.5	25	20.7	1	0	0	1915.02	220	237
Plasminogen activator inhibitor 1 RNA-binding protein	SERBP1	PAIRB_HUMAN	45.0	99.8%	2	2	3	0.00%	6.6%	EETQPPVALKK	99.5%	38.8	25	35.7	1	0	0	1239.69	93	103
Plasminogen activator inhibitor 1 RNA-binding protein	SERBP1	PAIRB_HUMAN	45.0	99.8%	2	2	3	0.00%	6.6%	SAAQAAAQTNSNAAGK	99.7%	98.2	25	88.8	2	0	0	1460.71	53	68
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	19	19	27	0.03%	4.3%	ALQALEELR	99.1%	36.1	25	23.5	1	0	0	1042.59	1671	1679
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	19	19	27	0.03%	4.3%	LAAEQELIR	99.7%	50.7	25	39.1	1	0	0	1042.59	1846	1854
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	19	19	27	0.03%	4.3%	LAAIGEATR	99.7%	42.8	25	20.8	2	0	0	901.51	1976	1984
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	19	19	27	0.03%	4.3%	LAQGHTTVDELAR	98.4%	26.9	25	13.5	0	1	0	1410.73	2809	2821
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	19	19	27	0.03%	4.3%	LKAEATEAAR	99.7%	41.2	25	35.4	2	0	0	1059.58	2349	2358
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	19	19	27	0.03%	4.3%	LQAEEVAQQK	99.7%	50.6	25	36.8	2	0	0	1143.60	1783	1792
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	19	19	27	0.03%	4.3%	LQEAGILSAEELQR	99.7%	80	25	80	1	0	0	1556.83	2795	2808
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	19	19	27	0.03%	4.3%	LQLEETDHQK	97.5%	31.4	25	25.9	1	0	0	1240.62	2330	2339
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	19	19	27	0.03%	4.3%	LRAETEQGEQQR	99.0%	35.8	25	30.8	2	0	0	1444.71	1855	1866
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	19	19	27	0.03%	4.3%	LSVAAQEAAR	99.7%	72.3	25	44.1	1	0	0	1015.55	2420	2429
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	19	19	27	0.03%	4.3%	LTVDEAVR	98.3%	33.2	25	20.5	1	0	0	902.49	3213	3220
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	19	19	27	0.03%	4.3%	SDEGQLSPATR	99.7%	51.8	25	42.5	1	0	0	1160.55	714	724
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	19	19	27	0.03%	4.3%	SIQEELQQLR	99.7%	49.5	25	30.9	2	0	0	1243.66	1554	1563
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	19	19	27	0.03%	4.3%	SLVPAAELLESR	99.7%	44.5	25	39.1	2	0	0	1284.72	3116	3127
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	19	19	27	0.03%	4.3%	SQVEEELFSVR	99.7%	59.8	25	51.5	1	0	0	1322.66	2361	2371
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	19	19	27	0.03%	4.3%	SSIAGLLLK	99.0%	35.6	25	25.5	1	0	0	901.57	2833	2841
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	19	19	27	0.03%	4.3%	VLADPSDDTK	99.1%	36	25	28.9	2	0	0	1060.52	2979	2988
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	19	19	27	0.03%	4.3%	VLALPEPSPAAPTLR	98.1%	32.7	25	32.7	1	0	0	1531.88	1187	1201
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	19	19	27	0.03%	4.3%	VPVDVAYR	99.7%	50.6	25	40.7	2	0	0	918.50	2961	2968
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	10	13	22	0.02%	26.8%	ASVHTLSGHTNAVATVR	99.7%	44.9	25	44.9	1	2	0	1720.91	321	337
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	10	13	22	0.02%	26.8%	CIAVEPGNQWFVTGSADR	99.7%	76.1	25	76.1	1	0	0	2006.94	209	226
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	10	13	22	0.02%	26.8%	CQAAEPQIITGSHDTTIR	99.7%	48.8	25	41.5	0	1	0	1997.97	338	355
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	10	13	22	0.02%	26.8%	GPQNATDSYVHK	99.7%	68	25	62.9	2	2	0	1316.62	69	80
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	10	13	22	0.02%	26.8%	HYTFASGSPDNIK	99.7%	68.4	25	62	2	0	0	1436.68	384	396
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	10	13	22	0.02%	26.8%	LRNEYGPVLHMPTSK	99.7%	36.7	25	33.1	0	1	0	1741.91	48	62
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	10	13	22	0.02%	26.8%	LWDLVAGK	99.7%	43.5	25	28.5	2	0	0	901.51	356	363
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	10	13	22	0.02%	26.8%	MPSESAAQSLAVALPLQTK	99.7%	94.8	25	93.8	4	0	0	1942.03	117	135
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	10	13	22	0.02%	26.8%	SPYLFSCGEDK	99.7%	53.6	25	53.6	2	0	0	1302.57	258	268
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	10	13	22	0.02%	26.8%	TGYNFQR	99.7%	56.3	25	46	2	0	0	885.42	443	449
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	18	19	44	0.04%	22.6%	AEPVEVVAPR	99.7%	45	25	39.3	2	0	0	1066.59	487	496

Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	18	19	44	0.04%	22.6%	AMVEYEIDLQK	99.7%	69.2	25	58.6	2	0	0	1338.66	685	695
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	18	19	44	0.04%	22.6%	ASLCISTK	99.7%	56.6	25	38	2	0	0	879.46	426	433
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	18	19	44	0.04%	22.6%	GGAAVDPDSGLEHSAHVLEK	98.7%	27.9	25	23.9	0	2	0	1988.97	529	548
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	18	19	44	0.04%	22.6%	GGSDDSSKDPIDVNYEK	99.7%	54.3	25	53.7	1	0	0	1825.81	780	796
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	18	19	44	0.04%	22.6%	GIYFADMVSK	99.0%	35.4	25	16	1	0	0	1130.56	894	903
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	18	19	44	0.04%	22.6%	HPDVEVDGFSELR	99.7%	56.8	25	42.4	2	0	0	1499.71	66	78
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	18	19	44	0.04%	22.6%	IAPPEAPVTGYMFGK	99.7%	56.5	25	4.89	2	0	0	1577.80	879	893
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	18	19	44	0.04%	22.6%	KGDEVDGVDEVAK	99.7%	82.2	25	71.1	2	0	0	1360.66	209	221
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	18	19	44	0.04%	22.6%	KPPLLNNADSVQAK	99.7%	69.6	25	67.7	4	0	0	1494.83	748	761
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	18	19	44	0.04%	22.6%	LQLLEDDKENR	99.7%	48.7	25	42.9	2	0	0	1372.71	572	582
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	18	19	44	0.04%	22.6%	MAIMVQSPMFDGK	99.7%	66.3	25	58.5	2	0	0	1454.68	35	47
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	18	19	44	0.04%	22.6%	QQVPSGESAILDR	99.7%	59.2	25	50.1	3	0	0	1399.72	270	282
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	18	19	44	0.04%	22.6%	TLGDFAAEYAK	99.7%	72.3	25	68.2	4	0	0	1185.58	109	119
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	18	19	44	0.04%	22.6%	TTNFAGILSQGLR	99.7%	94.2	25	85.3	4	0	0	1377.75	866	878
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	18	19	44	0.04%	22.6%	VFSATLGLVDIVK	99.7%	90.2	25	60.6	4	0	0	1361.80	552	564
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	18	19	44	0.04%	22.6%	VGTVIGSNK	96.7%	30.3	25	19.2	1	0	0	874.50	592	600
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	18	19	44	0.04%	22.6%	VVSEDFLQDVSASTK	99.7%	122	25	110	4	0	0	1624.81	453	467
Poly(A) RNA polymerase, mitochondrial	MTPAP	PAPD1_HUMAN	66.2	100.0%	3	3	4	0.00%	5.2%	NVSQSQLQK	95.9%	29.4	25	18.7	2	0	0	1031.55	489	497
Poly(A) RNA polymerase, mitochondrial	MTPAP	PAPD1_HUMAN	66.2	100.0%	3	3	4	0.00%	5.2%	SPPILPTLDSLK	99.0%	35.7	25	34.9	1	0	0	1280.75	392	403
Poly(A) RNA polymerase, mitochondrial	MTPAP	PAPD1_HUMAN	66.2	100.0%	3	3	4	0.00%	5.2%	TVLIHCPEK	98.6%	33.9	25	30.9	1	0	0	1096.58	77	85
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	6	8	24	0.02%	22.8%	AITIAGVPQSVTECVK	99.7%	63.2	25	62.5	2	0	0	1672.89	145	160
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	6	8	24	0.02%	22.8%	ESTGAQVQVAGDMLPNSTER	99.7%	103	25	103	8	1	0	2089.98	125	144
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	6	8	24	0.02%	22.8%	IANPVEGSSGR	99.7%	70.4	25	60.3	5	0	0	1086.55	315	325
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	6	8	24	0.02%	22.8%	INISEGNCPER	99.7%	51.6	25	51.6	4	0	0	1288.60	47	57
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	6	8	24	0.02%	22.8%	LVVPATQCGSLIGK	99.6%	39.8	25	29.3	2	0	0	1442.80	102	115
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	6	8	24	0.02%	22.8%	QGANINEIR	99.7%	72.6	25	62.4	2	0	0	1014.53	298	306
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	19	0.02%	23.3%	AITIAGIPQSIIECVK	99.7%	68.8	25	59.6	4	0	0	1712.96	145	160
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	19	0.02%	23.3%	ESTGAQVQVAGDMLPNSTER	99.7%	103	25	103	8	1	0	2089.98	125	144
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	19	0.02%	23.3%	IANPVEGSTDR	99.7%	60.8	25	60.8	4	0	0	1158.58	323	333
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	19	0.02%	23.3%	IITLAGPTNAIFK	99.7%	76.9	25	74.9	7	0	0	1358.80	58	70
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	19	0.02%	23.3%	INISEGNCPER	99.7%	51.6	25	51.6	4	0	0	1288.60	47	57
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	19	0.02%	23.3%	LVVPASQCGSLIGK	99.7%	99.6	25	99.6	4	0	0	1428.79	102	115
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	21	0.02%	19.3%	AQSSQDAVSSMNLFDLGGQYLR	99.7%	78.7	25	78.7	2	0	0	2403.12	277	298
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	21	0.02%	19.3%	GYGFIEYEK	99.7%	44.8	25	42.5	3	0	0	1105.52	268	276
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	21	0.02%	19.3%	KQESTVMVLR	99.7%	52	25	42.2	4	0	0	1206.65	458	467
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	21	0.02%	19.3%	KVVAEVYDQER	99.7%	85.4	25	85	2	0	0	1335.69	541	551
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	21	0.02%	19.3%	LGLPPLTPEQQEALQK	99.7%	62	25	62	4	0	0	1761.97	54	69
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	21	0.02%	19.3%	QGEEEDAEIIVK	95.1%	28.6	25	15.8	1	0	0	1359.66	503	514
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	21	0.02%	19.3%	SIDMSWDSVTMK	99.7%	54.7	25	54.7	1	0	0	1415.62	157	168
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	21	0.02%	19.3%	VVAEVYDQER	99.7%	65.6	25	60.1	2	0	0	1207.60	542	551
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	10	21	0.02%	19.3%	VYVGSIYYELGEDTIR	99.7%	99	25	98.5	2	0	0	1876.93	131	146
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	AKEFTNVYIK	99.7%	48.5	25	42.5	8	3	0	1212.66	187	196
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	ALDTMNFDVIK	99.7%	89.5	25	80.8	33	0	0	1266.64	68	78
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	ALYDTFSAFGNILSCK	99.7%	107	25	104	15	0	0	1806.87	114	129
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	EFSPFGTITSAK	99.7%	60.8	25	49.1	10	0	0	1284.65	313	324
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	EFTNVYIK	99.7%	48.3	25	33.2	3	0	0	1013.53	189	196
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	EREAELGAR	99.7%	41.9	25	18.9	4	0	0	1030.53	178	186
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	FGPALSVK	99.7%	52.6	25	13.4	11	0	0	818.48	214	221
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	FSPAGPILSIR	99.7%	79.8	25	66.2	11	0	0	1157.67	31	41
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	GFGFVCFSSPEEATK	99.7%	91.8	25	91.8	13	0	0	1662.75	334	348
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	GFGFVSFER	99.7%	53.6	25	38.2	12	0	0	1045.51	232	240

Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	GYGFVHFETQEAAER	99.7%	83.6	25	82	6	6	0	1740.80	139	153
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	IVATKPLYVALAQR	99.7%	94.4	25	91.5	10	12	0	1542.94	357	370
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	KEFSPFGTITSAK	99.7%	81.5	25	80.8	8	4	0	1412.74	312	324
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	KSGVGNIFIK	99.7%	41.6	25	36.2	3	0	0	1062.63	95	104
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	LFPLIQAMHPTLAGK	99.7%	83.7	25	76.9	6	0	0	1636.92	566	580
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	LKDLFGK	96.9%	30.5	25	18.1	1	0	0	820.49	207	213
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	MNGMLLNDR	99.7%	65.1	25	51.4	8	0	0	1095.49	158	166
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	MNGMLLNDRK	99.7%	58	25	49.3	4	0	0	1191.60	158	167
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	NFGEDMDDER	99.7%	57.9	25	54.9	4	0	0	1227.46	197	206
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	NFGEDMDDERLK	99.7%	53.2	25	46.2	2	0	0	1468.64	197	208
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	NLDDGIDDER	99.7%	61.1	25	47.8	8	0	0	1161.50	300	309
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	NLDDGIDDERLR	99.7%	57.4	25	44	6	3	0	1430.69	300	311
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	QAHLTNQYMQR	99.7%	57.5	25	57.5	8	8	0	1405.66	375	385
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	RSLGYAYVNFQQPADAER	99.7%	53	25	48.3	0	2	0	2085.01	50	67
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	SGVGNIFIK	99.7%	79.9	25	52.5	14	0	0	934.54	96	104
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	SKVDEAVAVLQAHQAK	99.7%	101	25	96.3	2	4	0	1693.92	605	620
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	SLGYAYVNFQQPADAER	99.7%	90.7	25	90.7	18	0	0	1928.91	51	67
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	VDEAVAVLQAHQAK	99.7%	77	25	77	2	0	0	1478.80	607	620
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	29	42	282	0.27%	39.2%	YQGVNLYVK	99.7%	56.7	25	49.3	10	0	0	1083.58	291	299
Polyadenylate-binding protein 2	PABPN1	PABP2_HUMAN	32.7	100.0%	8	10	27	0.03%	19.0%	ELQNEVEK	99.7%	45.6	25	26.6	3	0	0	988.49	138	145
Polyadenylate-binding protein 2	PABPN1	PABP2_HUMAN	32.7	100.0%	8	10	27	0.03%	19.0%	EMEEEAEKLK	99.7%	46.8	25	33	2	0	0	1235.58	128	137
Polyadenylate-binding protein 2	PABPN1	PABP2_HUMAN	32.7	100.0%	8	10	27	0.03%	19.0%	GFAYIEFSDK	99.7%	58.2	25	47.4	2	0	0	1176.56	214	223
Polyadenylate-binding protein 2	PABPN1	PABP2_HUMAN	32.7	100.0%	8	10	27	0.03%	19.0%	GFAYIEFSDKESVR	99.7%	79.7	25	67.5	4	2	0	1647.80	214	227
Polyadenylate-binding protein 2	PABPN1	PABP2_HUMAN	32.7	100.0%	8	10	27	0.03%	19.0%	LKELQNEVEK	99.7%	42.1	25	11.5	2	0	0	1229.67	136	145
Polyadenylate-binding protein 2	PABPN1	PABP2_HUMAN	32.7	100.0%	8	10	27	0.03%	19.0%	TSLALDESLFR	99.7%	75.3	25	69.5	5	0	0	1251.66	228	238
Polyadenylate-binding protein 2	PABPN1	PABP2_HUMAN	32.7	100.0%	8	10	27	0.03%	19.0%	VREMEEEAEK	99.7%	46.6	25	39.2	2	0	0	1249.57	126	135
Polyadenylate-binding protein 2	PABPN1	PABP2_HUMAN	32.7	100.0%	8	10	27	0.03%	19.0%	VTILCDKFSGHPK	99.7%	65.8	25	58.7	2	3	0	1501.78	201	213
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	23	64	0.06%	36.2%	AHLTNQYMQR	99.7%	43.8	25	37.3	3	0	0	1277.61	376	385
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	23	64	0.06%	36.2%	AKEFTNVYIK	99.7%	48.5	25	42.5	8	3	0	1212.66	187	196
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	23	64	0.06%	36.2%	ALDTMNFDVIK	99.7%	89.5	25	80.8	33	0	0	1266.64	68	78
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	23	64	0.06%	36.2%	ALYDTFSAFGNILSCK	99.7%	107	25	104	15	0	0	1806.87	114	129
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	23	64	0.06%	36.2%	AVEEMNGKEISGK	99.6%	39.7	25	34.1	2	0	0	1407.68	247	259
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	23	64	0.06%	36.2%	EFSPFGSITSAK	99.7%	69.3	25	68.7	8	0	0	1270.63	313	324
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	23	64	0.06%	36.2%	EFTNVYIK	99.7%	48.3	25	33.2	3	0	0	1013.53	189	196
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	23	64	0.06%	36.2%	FSPAGPVLSIR	99.7%	64	25	59	12	0	0	1143.65	31	41
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	23	64	0.06%	36.2%	GFGFVCFSSPEEATK	99.7%	91.8	25	91.8	13	0	0	1662.75	334	348
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	23	64	0.06%	36.2%	GFGFVSYEK	99.7%	50.2	25	28.8	2	0	0	1033.50	232	240
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	23	64	0.06%	36.2%	GFGFVSYEKHEDANK	99.7%	35.6	25	34.7	0	2	0	1727.80	232	246
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	23	64	0.06%	36.2%	GYAFVHFETQEAADK	99.7%	72	25	72	2	2	0	1712.79	139	153
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	23	64	0.06%	36.2%	IVGSKPLYVALAQR	99.7%	67.2	25	53.4	2	3	0	1514.91	357	370
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	23	64	0.06%	36.2%	KAHLTNQYMQR	99.7%	50.7	25	44	4	3	0	1405.70	375	385
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	23	64	0.06%	36.2%	KEFSPFGSITSAK	99.7%	63	25	56.2	2	0	0	1398.73	312	324
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	23	64	0.06%	36.2%	LFPLIQTMHSNLAGK	99.7%	77.5	25	70.6	4	0	0	1669.91	575	589
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	23	64	0.06%	36.2%	MNGMLLNDR	99.7%	65.1	25	51.4	8	0	0	1095.49	158	166
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	23	64	0.06%	36.2%	MNGMLLNDRK	99.7%	58	25	49.3	4	0	0	1191.60	158	167
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	23	64	0.06%	36.2%	NLDDTIDDEK	99.7%	60.3	25	51.9	2	0	0	1177.52	300	309
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	23	64	0.06%	36.2%	NLDDTIDDEKLR	99.7%	61.3	25	53.7	2	0	0	1446.71	300	311
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	23	64	0.06%	36.2%	RSLGYAYVNFQQPADAER	99.7%	53	25	48.3	0	2	0	2085.01	50	67
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	23	64	0.06%	36.2%	SGVGNVFIK	99.7%	68.9	25	31.1	2	0	0	920.52	96	104
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	23	64	0.06%	36.2%	SKVDEAVAVLQAHHAK	99.1%	29.5	25	29.5	0	1	0	1702.92	614	629
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	23	64	0.06%	36.2%	SLGYAYVNFQQPADAER	99.7%	90.7	25	90.7	18	0	0	1928.91	51	67

Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	23	64	0.06%	36.2%	YQGVNLYIK	99.7%	50.2	25	38.8	6	0	0	1097.60	291	299
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	5	5	8	0.01%	15.8%	GVVLFPWQAR	97.6%	31.6	25	16	1	0	0	1172.66	92	101
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	5	5	8	0.01%	15.8%	IFSLSGTLETVR	99.7%	103	25	81.8	2	0	0	1322.73	286	297
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	5	5	8	0.01%	15.8%	LENLDSDVVQLR	99.7%	99.5	25	92.2	2	0	0	1400.74	269	280
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	5	5	8	0.01%	15.8%	NHPWLELSDVHR	99.0%	28.8	25	28.8	0	1	0	1502.75	224	235
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	5	5	8	0.01%	15.8%	VLETVGVFEVPK	99.7%	73.5	25	63.7	2	0	0	1316.75	61	72
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	14	17	36	0.03%	40.5%	AQAALQAVNSVQSGNLALAASAAAVDAGMAMAGQSPVLR	99.7%	34.5	25	34.5	0	1	0	3712.87	147	185
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	14	17	36	0.03%	40.5%	DYGNSPLHR	99.7%	49.6	25	41.7	2	0	0	1058.50	429	437
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	14	17	36	0.03%	40.5%	EGQEDQGLTK	99.3%	37.7	25	37.7	1	0	0	1104.52	419	428
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	14	17	36	0.03%	40.5%	ELKTDSSPNQAR	99.7%	53.3	25	28.1	2	0	0	1345.67	135	146
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	14	17	36	0.03%	40.5%	GQPIYIQFSNHK	99.7%	80	25	68.7	2	0	0	1431.74	123	134
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	14	17	36	0.03%	40.5%	HQNVQLPR	99.7%	46.2	25	41.6	2	0	0	991.54	411	418
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	14	17	36	0.03%	40.5%	IAIPGLAGAGNSVLLVSNLNPER	99.7%	124	25	124	4	2	0	2275.28	326	348
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	14	17	36	0.03%	40.5%	KLPIDVTEGEVISLGLPFGK	99.7%	38.6	25	38.6	0	2	0	2112.20	65	84
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	14	17	36	0.03%	40.5%	LPIDVTEGEVISLGLPFGK	99.7%	131	25	131	2	0	0	1984.10	66	84
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	14	17	36	0.03%	40.5%	LSLDGQNIYNACCTLR	99.7%	110	25	110	2	0	0	1897.89	239	254
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	14	17	36	0.03%	40.5%	NFQNIFPPSATLHLSNIPPSVSEEDLK	99.7%	39.6	25	39.6	0	4	0	2994.52	445	471
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	14	17	36	0.03%	40.5%	NNQFQALLQYADPVSAQHAK	99.7%	84	25	84	2	2	0	2243.12	219	238
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	14	17	36	0.03%	40.5%	VLFSSNGGVVK	99.7%	60.7	25	53.3	2	0	0	1106.62	472	482
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	14	17	36	0.03%	40.5%	VTNLLMLK	99.7%	59.9	25	0	4	0	0	931.56	85	92
Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	FIP1_HUMAN	66.5	100.0%	5	6	10	0.01%	12.0%	AEFTSPPSLFK	99.7%	45.7	25	35.6	2	0	0	1223.63	255	265
Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	FIP1_HUMAN	66.5	100.0%	5	6	10	0.01%	12.0%	ANENSNIQVLSER	99.7%	51.4	25	47.6	2	0	0	1473.73	332	344
Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	FIP1_HUMAN	66.5	100.0%	5	6	10	0.01%	12.0%	MGLEVIPVTSTTNK	99.7%	60.1	25	54.7	3	0	0	1489.79	197	210
Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	FIP1_HUMAN	66.5	100.0%	5	6	10	0.01%	12.0%	TGAPQYGSYGTAPVNLNIK	99.7%	80.4	25	73.1	2	0	0	1950.99	105	123
Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	FIP1_HUMAN	66.5	100.0%	5	6	10	0.01%	12.0%	TGNSEKETALPSTK	99.7%	52.6	25	51.6	1	0	0	1462.74	241	254
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	5	7	16	0.02%	46.4%	GTAYVVYEDIFDAK	99.7%	70.8	25	68.6	4	0	0	1590.77	58	71
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	5	7	16	0.02%	46.4%	ITAEEMYDIFGK	99.7%	93.3	25	78.1	4	0	0	1432.67	30	41
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	5	7	16	0.02%	46.4%	LPPEVNR	98.0%	32.4	25	31.2	2	0	0	824.46	13	19
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	5	7	16	0.02%	46.4%	NACDHLSGFNVCNR	99.7%	56	25	56	2	2	0	1663.71	72	85
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	5	7	16	0.02%	46.4%	YLVVLYYNANR	99.7%	76.6	25	69.9	2	0	0	1387.74	86	96
Pre-mRNA-processing factor 17	CDC40	PRP17_HUMAN	65.5	100.0%	4	4	6	0.01%	9.2%	SGEIVQEYDR	99.7%	55.4	25	47.8	2	0	0	1195.56	407	416
Pre-mRNA-processing factor 17	CDC40	PRP17_HUMAN	65.5	100.0%	4	4	6	0.01%	9.2%	TFATYGYALDPSLDNHQVSAK	99.3%	30.6	25	23	0	1	0	2298.10	131	151
Pre-mRNA-processing factor 17	CDC40	PRP17_HUMAN	65.5	100.0%	4	4	6	0.01%	9.2%	VITCGWDGLIK	99.2%	36.6	25	29.8	1	0	0	1261.66	566	576
Pre-mRNA-processing factor 17	CDC40	PRP17_HUMAN	65.5	100.0%	4	4	6	0.01%	9.2%	VWEWDIPVDFK	99.7%	45.6	25	40.4	2	0	0	1433.71	444	454
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	14	18	34	0.03%	45.0%	ALQDEWDAVMLHSFTLR	99.7%	85.1	25	80.2	1	2	0	2032.00	77	93
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	14	18	34	0.03%	45.0%	ATVLTTER	99.7%	52.6	25	41.2	2	0	0	890.49	180	187
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	14	18	34	0.03%	45.0%	FIASTGMDR	99.7%	68.7	25	50	4	0	0	997.48	489	497
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	14	18	34	0.03%	45.0%	ILTGGADKNVVVFDK	99.7%	83.2	25	78.2	2	2	0	1575.87	237	251
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	14	18	34	0.03%	45.0%	IWDLKER	96.4%	30	25	13.2	2	0	0	959.53	376	382
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	14	18	34	0.03%	45.0%	IWSVPNASCVQVVR	99.7%	82.3	25	73.1	2	0	0	1614.84	290	303
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	14	18	34	0.03%	45.0%	QELSHALYQHDAACR	99.7%	65.9	25	61	0	2	0	1798.83	101	115
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	14	18	34	0.03%	45.0%	QVASHVGLHSASIPGILALDLCPSDTNK	99.7%	35.6	25	35.6	0	1	0	2900.49	209	236
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	14	18	34	0.03%	45.0%	SSEQILATLK	99.7%	55.8	25	34.2	2	0	0	1089.62	252	261
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	14	18	34	0.03%	45.0%	TLQLDNNFEVK	99.7%	65.1	25	52.4	2	0	0	1320.68	429	439
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	14	18	34	0.03%	45.0%	TVPEELVKPEELSK	99.7%	66.9	25	59.2	2	0	0	1597.87	193	206
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	14	18	34	0.03%	45.0%	VTDETSGCSLTCAQFHPDGLIFGTGTMDSQIK	99.7%	66.1	25	66.1	0	2	0	3473.57	344	375
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	14	18	34	0.03%	45.0%	VTSVVFHPSQDLVFSASPDATIR	99.7%	40.7	25	40.7	0	2	0	2473.27	267	289
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	14	18	34	0.03%	45.0%	YIAENGTDPINNQPLSEEQLIDIK	99.7%	66.1	25	66	2	2	0	2714.35	33	56
Pre-mRNA-processing factor 40 homolog A	PRPF40A	PR40A_HUMAN	108.8	100.0%	4	4	7	0.01%	6.3%	ELEDLEGYQNTIVAGSLITK	99.7%	96.8	25	96.8	2	0	0	2193.13	214	233
Pre-mRNA-processing factor 40 homolog A	PRPF40A	PR40A_HUMAN	108.8	100.0%	4	4	7	0.01%	6.3%	EPAFEDITLESER	99.7%	80.1	25	79.3	1	0	0	1535.72	777	789
Pre-mRNA-processing factor 40 homolog A	PRPF40A	PR40A_HUMAN	108.8	100.0%	4	4	7	0.01%	6.3%	FTNMLGQPGSTALDLFK	99.7%	68	25	53.7	2	0	0	1855.93	646	662

Pre-mRNA-processing factor 40 homolog A	PRPF40A	PR40A_HUMAN	108.8	100.0%	4	4	7	0.01%	6.3%	STTLDAGNIK	98.8%	34.6	25	26.5	2	0	0	1019.54	709	718
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	21	23	36	0.03%	24.0%	AAELETDIR	99.7%	57.7	25	20.3	1	0	0	1017.52	379	387
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	21	23	36	0.03%	24.0%	AAVELEEPEDAR	99.7%	67	25	66.5	2	0	0	1328.63	409	420
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	21	23	36	0.03%	24.0%	AEVLWLMGAK	99.7%	63.9	25	56.1	2	0	0	1117.61	607	616
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	21	23	36	0.03%	24.0%	AGSVATCQAVMR	99.7%	54.2	25	44.4	3	0	0	1250.60	516	527
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	21	23	36	0.03%	24.0%	AIYAYALQVFPSK	99.7%	51.5	25	39.9	1	0	0	1470.80	561	573
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	21	23	36	0.03%	24.0%	AVIGIGIEEEDRK	99.7%	67.8	25	67.5	2	0	0	1428.77	528	540
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	21	23	36	0.03%	24.0%	AVVAQAVR	99.7%	43.6	25	40.1	2	0	0	813.49	360	367
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	21	23	36	0.03%	24.0%	ESLEALLQR	99.7%	53.9	25	35.3	2	0	0	1058.58	591	599
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	21	23	36	0.03%	24.0%	ETNPHHPPAWIASAR	99.7%	39.6	25	39.6	0	2	0	1683.84	303	317
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	21	23	36	0.03%	24.0%	GQIEEQKEMMEK	97.5%	31.4	25	24.4	1	0	0	1511.67	716	727
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	21	23	36	0.03%	24.0%	HGELWCAVSK	99.7%	49.2	25	38.3	1	0	0	1186.57	908	917
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	21	23	36	0.03%	24.0%	HIWITAAK	97.1%	30.9	25	18.6	1	0	0	939.54	465	472
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	21	23	36	0.03%	24.0%	HYEDFPK	98.9%	35.3	25	34.1	1	0	0	935.43	704	710
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	21	23	36	0.03%	24.0%	IDSDLGDAWAFFYK	99.7%	95.4	25	95.4	2	0	0	1647.77	870	883
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	21	23	36	0.03%	24.0%	IQQQFSDLKR	99.6%	32.8	25	22.8	1	1	0	1262.69	138	147
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	21	23	36	0.03%	24.0%	LESENDEYER	99.7%	59.3	25	59.3	2	0	0	1283.54	651	660
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	21	23	36	0.03%	24.0%	LETYENAR	94.9%	28.5	25	18.6	1	0	0	995.48	443	450
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	21	23	36	0.03%	24.0%	LEWVQDNIR	99.7%	47.1	25	31.2	2	0	0	1172.61	684	692
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	21	23	36	0.03%	24.0%	LSQVSDSVSGQTVVDPK	99.7%	126	25	111	2	0	0	1745.89	255	271
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	21	23	36	0.03%	24.0%	NPGLWLESVR	99.7%	50.7	25	44.3	2	0	0	1170.63	776	785
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	21	23	36	0.03%	24.0%	WLAGDVPAAR	99.7%	41.6	25	40	2	0	0	1055.56	619	628
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	ADWWTNTAHYNR	99.7%	44.9	25	44.9	1	0	0	1534.68	747	758
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	AISAANLHLR	99.7%	52.8	25	43.8	2	0	0	1065.62	2077	2086
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	ALDIPLVK	99.7%	41.5	25	35.2	2	0	0	868.55	421	428
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	ALNMAIPGGPK	96.5%	30	25	16.2	1	0	0	1084.58	268	278
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	ANPALYVLR	99.7%	54.1	25	46.5	2	0	0	1016.59	1736	1744
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	AQIAGYLYGVSPPDNPQVK	99.7%	91.4	25	86.6	2	0	0	2017.04	2122	2140
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	AVFWDIK	99.7%	42.7	25	29.9	2	0	0	878.48	1152	1158
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	DINLQDEDWNEFNDINK	99.7%	104	25	104	2	0	0	2121.94	285	301
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	DLILADYGKK	99.6%	39.7	25	28.7	2	0	0	1135.64	1985	1994
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	DNPNLLFNMCGFECR	99.7%	80.8	25	72.6	4	0	0	1886.80	1181	1195
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	EAVVNTQELLDLLVK	99.7%	107	25	96.2	2	0	0	1683.95	1276	1290
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	EELGLIEQAYDNPHEALSR	99.7%	59.7	25	59.7	0	2	0	2184.06	862	880
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	EHCPAGQPVK	94.8%	28.4	25	22	1	0	0	1122.54	433	442
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	EQSQLTATQTR	99.7%	66.5	25	53	2	0	0	1262.63	2035	2045
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	FGDLILK	99.7%	43.9	25	26	2	0	0	805.48	1902	1908
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	FGNAFHLCR	99.7%	46.4	25	37.1	2	0	0	1121.53	540	548
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	FICISDLR	99.7%	53.5	25	44.1	2	0	0	1023.53	2114	2121
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	FNTGPVGK	98.4%	33.4	25	17.2	2	0	0	819.44	616	623
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	FPPVVFYTPK	99.7%	56.2	25	52.9	5	0	0	1194.66	1311	1320
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	FSPIPFPPLSYK	97.9%	32.2	25	32.2	2	0	0	1392.76	822	833
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	GSELQLPFQACLK	99.7%	66.2	25	44.6	2	0	0	1490.77	1886	1898
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	GYLPSHYER	99.5%	39	25	36.9	2	0	0	1121.54	2250	2258
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	HGDEIITSTTSNYETQTFSSK	99.7%	38	25	38	0	1	0	2346.07	2050	2070
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	IDLTLLNR	99.7%	58.4	25	41.1	3	0	0	957.57	988	995
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	IIHTSVWAGQK	99.7%	46.8	25	40.2	2	0	0	1239.68	1821	1831
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	IMADNPSWDGEK	99.7%	60.4	25	60.4	4	0	0	1378.59	2199	2210
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	ISLIQIFR	99.7%	64.2	25	59	4	0	0	989.61	1571	1578
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	LIVDHNIADYMTAK	99.7%	67	25	67	4	1	0	1603.82	999	1012
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	LKEAYSVK	98.8%	34.6	25	19.2	2	0	0	937.54	846	853

Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	LLENMPMPWEQIR	99.3%	37.1	25	37.1	1	0	0	1688.81	102	114
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	LLILALER	99.7%	59.7	25	59.7	3	0	0	940.62	838	845
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	LTLEDLEDSWDR	99.7%	52.4	25	52.4	2	0	0	1491.70	1403	1414
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	LVVDSHVQYR	99.7%	74.3	25	68	2	0	0	1215.65	556	565
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	NNVNVASLTQSEIR	99.7%	101	25	95.3	1	0	0	1544.80	1995	2008
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	NNVVINYK	99.7%	45.8	25	42.3	2	0	0	963.53	1013	1020
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	QILMASGSTTFTK	99.7%	61.4	25	54.5	4	0	0	1400.71	1246	1258
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	QQIAEIEK	99.4%	37.8	25	28.4	2	0	0	958.52	2024	2031
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	QTDVGITHFR	99.7%	62.9	25	50.5	2	0	0	1173.60	1345	1354
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	RALDIPLVK	99.6%	40.2	25	30.8	2	0	0	1024.65	420	428
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	SGLNQIPNR	97.9%	32.2	25	18	2	0	0	998.54	1524	1532
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	SGMSHEEDQLIPNLYR	98.9%	28.7	25	21.9	0	2	0	1904.88	1355	1370
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	SLPVEEQPK	97.8%	32	25	28.6	2	0	0	1026.55	1851	1859
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	SVTTVQWENSFVSVYSK	99.7%	61.8	25	61.8	1	0	0	1960.96	1164	1180
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	TAEEVAALIR	99.7%	68.5	25	53	2	0	0	1072.60	1841	1850
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	TAQCFLR	99.2%	36.6	25	22.9	1	0	0	895.45	1225	1231
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	TGQLFLK	98.8%	34.7	25	22.8	2	0	0	806.48	1814	1820
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	TIIITCSFTPGSCTLTAYK	99.7%	86.9	25	86.9	2	0	0	2134.06	2211	2229
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	TISSYTAFSR	99.7%	64.1	25	60.9	2	0	0	1132.56	1926	1935
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	TSYEEFTHK	97.0%	30.7	25	30.2	2	0	0	1141.52	1202	1210
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	VPGLPTPIENMILR	97.3%	31.1	25	31.1	3	0	0	1549.88	728	741
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	VQMLLSDR	99.7%	57	25	32.9	2	0	0	961.51	2259	2266
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	WGDYDSHDIER	98.3%	33.1	25	33.1	1	0	0	1392.58	1668	1678
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	WNVSRPSLLADSK	99.7%	69.2	25	48.3	2	0	0	1472.79	1637	1649
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	WQFTLPMMSTLYR	96.8%	30.4	25	30.4	1	0	0	1705.81	228	240
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	YIQPWESEFIDSQR	99.7%	61.4	25	60.9	2	0	0	1797.84	1371	1384
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	YLTEHPDPNNENIVGYNNK	99.6%	32.5	25	32.5	0	2	0	2231.04	1113	1131
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	YLTEHPDPNNENIVGYNNKK	99.7%	52.5	25	52.5	0	2	0	2359.13	1113	1132
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	58	64	123	0.12%	27.5%	YYVLNALK	98.4%	33.5	25	30.8	2	0	0	983.56	453	460
Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16	DHX38	PRP16_HUMAN	140.5	100.0%	3	3	4	0.00%	2.8%	DATSDLAIIAR	99.7%	64.1	25	47.7	1	0	0	1145.62	435	445
Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16	DHX38	PRP16_HUMAN	140.5	100.0%	3	3	4	0.00%	2.8%	SLNTDVLFGLLR	99.7%	56.1	25	49.3	1	0	0	1347.76	658	669
Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16	DHX38	PRP16_HUMAN	140.5	100.0%	3	3	4	0.00%	2.8%	TNLANVVLLLK	99.7%	44	25	38.8	2	0	0	1197.76	889	899
Pre-mRNA-splicing factor CWC22 homolog	CWC22	CWC22_HUMAN	105.5	100.0%	3	3	5	0.00%	3.2%	LSEETTTSSSR	99.7%	65.3	25	56.7	2	0	0	1197.56	570	580
Pre-mRNA-splicing factor CWC22 homolog	CWC22	CWC22_HUMAN	105.5	100.0%	3	3	5	0.00%	3.2%	LTQVSPR	98.8%	34.7	25	21.5	2	0	0	800.46	304	310
Pre-mRNA-splicing factor CWC22 homolog	CWC22	CWC22_HUMAN	105.5	100.0%	3	3	5	0.00%	3.2%	YTSDKDVPSER	98.4%	33.4	25	26.2	1	0	0	1296.61	784	794
Pre-mRNA-splicing factor ISY1 homolog	ISY1	ISY1_HUMAN	33.0	100.0%	4	4	6	0.01%	16.8%	IKELGGPDYGK	99.6%	40	25	33.8	1	0	0	1176.63	91	101
Pre-mRNA-splicing factor ISY1 homolog	ISY1	ISY1_HUMAN	33.0	100.0%	4	4	6	0.01%	16.8%	IRDLNDEINK	96.3%	29.8	25	14.4	1	0	0	1229.65	70	79
Pre-mRNA-splicing factor ISY1 homolog	ISY1	ISY1_HUMAN	33.0	100.0%	4	4	6	0.01%	16.8%	VAQIQNAGLGEFR	99.7%	76.6	25	76.6	2	0	0	1402.74	57	69
Pre-mRNA-splicing factor ISY1 homolog	ISY1	ISY1_HUMAN	33.0	100.0%	4	4	6	0.01%	16.8%	YASETLQAQSEEAR	99.7%	82.2	25	82.2	2	0	0	1582.73	267	280
Pre-mRNA-splicing factor SPF27	BCAS2	SPF27_HUMAN	26.1	100.0%	8	8	12	0.01%	32.9%	EAAAALVEEETR	99.7%	74.1	25	61.3	2	0	0	1288.64	30	41
Pre-mRNA-splicing factor SPF27	BCAS2	SPF27_HUMAN	26.1	100.0%	8	8	12	0.01%	32.9%	EAAAALVEEETRR	95.5%	29	25	19.6	1	0	0	1444.74	30	42
Pre-mRNA-splicing factor SPF27	BCAS2	SPF27_HUMAN	26.1	100.0%	8	8	12	0.01%	32.9%	EMESNWVSLVSK	99.7%	59.4	25	59.4	2	0	0	1408.68	180	191
Pre-mRNA-splicing factor SPF27	BCAS2	SPF27_HUMAN	26.1	100.0%	8	8	12	0.01%	32.9%	NMQLTAGSK	99.7%	45.4	25	15.1	2	0	0	949.48	169	177
Pre-mRNA-splicing factor SPF27	BCAS2	SPF27_HUMAN	26.1	100.0%	8	8	12	0.01%	32.9%	NYEIER	95.3%	28.8	25	5.33	1	0	0	823.39	192	197
Pre-mRNA-splicing factor SPF27	BCAS2	SPF27_HUMAN	26.1	100.0%	8	8	12	0.01%	32.9%	QPIELLSMK	98.0%	32.4	25	30.2	1	0	0	1058.59	77	85
Pre-mRNA-splicing factor SPF27	BCAS2	SPF27_HUMAN	26.1	100.0%	8	8	12	0.01%	32.9%	RYELPAPSSGQK	99.7%	69.9	25	64.4	1	0	0	1332.69	86	97
Pre-mRNA-splicing factor SPF27	BCAS2	SPF27_HUMAN	26.1	100.0%	8	8	12	0.01%	32.9%	TIVQLENEIYQIK	99.7%	63.8	25	48.3	2	0	0	1590.87	198	210
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	18	19	32	0.03%	23.0%	AEQLAAEAER	99.7%	63.8	25	49.4	2	0	0	1087.54	776	785
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	18	19	32	0.03%	23.0%	AEQLAAEAERDQPLR	99.7%	59.1	25	57.1	2	0	0	1696.86	776	790
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	18	19	32	0.03%	23.0%	AIEVLSDEHAR	99.7%	43.3	25	41.5	1	0	0	1239.63	655	665
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	18	19	32	0.03%	23.0%	ALPITQHSR	98.2%	33	25	30.2	2	0	0	1022.57	139	147

Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	18	19	32	0.03%	23.0%	AVEPAQQYDMFNIYIK	99.7%	72.3	25	68.4	2	0	0	1929.94	622	637
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	18	19	32	0.03%	23.0%	DLFEQALDGCPPK	99.7%	51.6	25	47.6	2	0	0	1489.70	578	590
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	18	19	32	0.03%	23.0%	EIINTYTEAVQTVDPFK	99.7%	113	25	113	2	0	0	1968.00	373	389
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	18	19	32	0.03%	23.0%	HAMAVYER	97.2%	31	25	21.8	2	0	0	976.47	611	618
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	18	19	32	0.03%	23.0%	HENYDEALR	99.7%	47.5	25	47.5	2	0	0	1146.52	446	454
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	18	19	32	0.03%	23.0%	KATALPAR	98.1%	32.7	25	15.9	2	0	0	827.51	458	465
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	18	19	32	0.03%	23.0%	LATVVNDER	99.2%	37	25	23.8	1	0	0	1016.54	200	208
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	18	19	32	0.03%	23.0%	LEQQSVPAAVFGSLKED	99.7%	56	25	56	2	0	0	1817.93	839	855
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	18	19	32	0.03%	23.0%	LNQLYER	99.7%	45.9	25	33.5	2	0	0	935.49	53	59
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	18	19	32	0.03%	23.0%	LSPESAEEYIEYLK	99.7%	67.2	25	64.1	2	0	0	1670.82	175	188
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	18	19	32	0.03%	23.0%	LWCSLADYYIR	99.6%	40.2	25	39.8	1	0	0	1459.70	258	268
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	18	19	32	0.03%	23.0%	RPLLLNSVLLR	98.6%	34.2	25	22.8	1	0	0	1293.84	341	351
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	18	19	32	0.03%	23.0%	SSDRLDEAAQR	99.6%	39.8	25	30.4	2	1	0	1247.60	189	199
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	18	19	32	0.03%	23.0%	VQSLNVDAIIR	99.7%	52.7	25	35.1	1	0	0	1227.71	235	245
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	5	5	7	0.01%	10.0%	IVVEFSSPNVAK	99.2%	36.9	25	30.3	1	0	0	1289.71	127	138
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	5	5	7	0.01%	10.0%	LELGDVQALSLWQK	99.7%	47.7	25	47.7	1	0	0	1599.87	230	243
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	5	5	7	0.01%	10.0%	SSQDFQPR	99.6%	39.8	25	25.9	1	0	0	964.45	512	519
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	5	5	7	0.01%	10.0%	TVLQQVIEDGSK	99.7%	45.3	25	44.2	2	0	0	1316.71	100	111
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	5	5	7	0.01%	10.0%	VGLAALIIQDFK	99.7%	58	25	58	2	0	0	1287.77	427	438
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	13	13	25	0.02%	31.1%	APILIATDVASR	99.7%	80.7	25	80.7	6	0	0	1226.71	469	480
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	13	13	25	0.02%	31.1%	APLPDLYPFGTMR	99.7%	41.6	25	41.6	1	0	0	1477.75	69	81
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	13	13	25	0.02%	31.1%	DMVGIAQTGSGK	99.7%	76.8	25	69.8	2	0	0	1179.57	210	221
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	13	13	25	0.02%	31.1%	DWVLNEFR	99.7%	41.2	25	36.8	2	0	0	1078.53	458	465
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	13	13	25	0.02%	31.1%	ELAQQVQQVADDYGK	99.7%	99.9	25	99.9	2	0	0	1691.82	255	269
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	13	13	25	0.02%	31.1%	GDGPICLVLAPTR	99.7%	47	25	44.7	2	0	0	1368.73	242	254
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	13	13	25	0.02%	31.1%	GLDVEDVK	99.7%	44.2	25	31.3	4	0	0	874.45	481	488
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	13	13	25	0.02%	31.1%	GTAYTFFTPGNLK	99.7%	55.2	25	43.2	3	0	0	1416.72	516	528
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	13	13	25	0.02%	31.1%	GVEICIATPGR	99.7%	64.7	25	45.7	4	0	0	1172.61	294	304
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	13	13	25	0.02%	31.1%	IVDQIRPDR	96.8%	30.4	25	14.4	3	0	0	1111.62	342	350
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	13	13	25	0.02%	31.1%	LIDFLESGK	99.7%	54.4	25	52.5	2	0	0	1021.56	305	313
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	13	13	25	0.02%	31.1%	LMQLVDHR	98.5%	33.7	25	23.9	2	0	0	1027.54	548	555
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	13	13	25	0.02%	31.1%	LTPYEVDELRR	97.4%	31.4	25	23.1	2	0	0	1390.73	144	154
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	13	13	25	0.02%	31.1%	MLDMGFEPQIR	99.7%	74.2	25	43.5	6	0	0	1352.63	330	340
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	13	13	25	0.02%	31.1%	NFYVEHPEVAR	99.7%	49.8	25	46.1	2	0	0	1360.66	133	143
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	13	13	25	0.02%	31.1%	QLAEDFLR	99.7%	58.6	25	29.4	2	0	0	991.52	365	372
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	13	13	25	0.02%	31.1%	QTLMWSATWPK	99.7%	59.1	25	50.2	1	0	0	1348.67	351	361
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	13	13	25	0.02%	31.1%	SSQSSSQQFSGIGR	99.7%	114	25	108	2	0	0	1455.68	671	684
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	13	13	25	0.02%	31.1%	STCIYGGAPK	99.7%	59.2	25	50.5	4	0	0	1053.50	275	284
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	13	13	25	0.02%	31.1%	TIIFVETK	98.9%	35.1	25	35.1	1	0	0	950.56	421	428
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	13	13	25	0.02%	31.1%	VLEEANQAINPK	99.7%	88.7	25	77.5	2	0	0	1325.71	536	547
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	100.0%	11	11	16	0.02%	13.5%	AQPLSLEELLAK	99.7%	64.3	25	57.8	2	0	0	1311.75	139	150
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	100.0%	11	11	16	0.02%	13.5%	DIIGVAETGSGK	99.7%	64.4	25	53.9	2	0	0	1146.60	430	441
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	100.0%	11	11	16	0.02%	13.5%	EDSAVFYELK	99.7%	50	25	44.5	1	0	0	1200.58	771	780
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	100.0%	11	11	16	0.02%	13.5%	ELAQQIEEETIK	99.7%	48.7	25	47.5	2	0	0	1430.74	479	490
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	100.0%	11	11	16	0.02%	13.5%	GFIAGIDLK	99.7%	47.4	25	42	1	0	0	933.54	302	310
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	100.0%	11	11	16	0.02%	13.5%	HQVQLLGR	99.7%	49.2	25	44.9	2	0	0	950.55	294	301
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	100.0%	11	11	16	0.02%	13.5%	IFREDYSITTK	95.2%	22.9	25	20.4	0	1	0	1372.71	372	382
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	100.0%	11	11	16	0.02%	13.5%	LIDVLENR	98.1%	32.8	25	32.8	1	0	0	971.55	529	536
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	100.0%	11	11	16	0.02%	13.5%	NIEDYIHR	98.9%	35.1	25	20.6	1	0	0	1059.52	744	751
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	100.0%	11	11	16	0.02%	13.5%	QAIPIGLQNR	98.1%	32.7	25	24.6	1	0	0	1109.64	420	429
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	100.0%	11	11	16	0.02%	13.5%	TLEEKEQEEAR	99.7%	47.9	25	43.8	2	0	0	1361.65	329	339

Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	8	8	12	0.01%	10.9%	ALQEFDLALR	98.9%	35.2	25	28.4	2	0	0	1175.64	667	676
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	8	8	12	0.01%	10.9%	EAIVAALLTR	99.7%	69.7	25	62.6	2	0	0	1056.64	451	460
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	8	8	12	0.01%	10.9%	EAVVQEPER	99.3%	37.1	25	34	1	0	0	1056.53	642	650
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	8	8	12	0.01%	10.9%	ELGIQVHSVTR	99.7%	42.5	25	28.9	2	0	0	1238.69	300	310
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	8	8	12	0.01%	10.9%	IFVNSNTDVAPFLR	99.7%	70.2	25	59.1	2	0	0	1592.84	423	436
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	8	8	12	0.01%	10.9%	SADFNPDFVFTEK	99.4%	38	25	32.4	1	0	0	1516.70	79	91
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	8	8	12	0.01%	10.9%	SVFDEELTNTSK	99.7%	57.8	25	57.2	1	0	0	1369.65	746	757
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	8	8	12	0.01%	10.9%	VLVLVPTR	99.0%	35.7	25	35.7	1	0	0	896.59	292	299
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	5	5	8	0.01%	11.1%	GSFADLGLEPR	99.7%	65.2	25	58	2	0	0	1161.59	126	136
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	5	5	8	0.01%	11.1%	LLGQPSLDSLPIPAPR	99.7%	42.6	25	42.6	2	0	0	1673.96	190	205
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	5	5	8	0.01%	11.1%	SPDEPLPVVR	98.6%	34.2	25	33.6	1	0	0	1108.60	28	37
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	5	5	8	0.01%	11.1%	VAELVHILK	97.5%	31.4	25	31.4	1	0	0	1021.64	378	386
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	5	5	8	0.01%	11.1%	VASPDAVTTITSSK	99.7%	46.1	25	43.3	2	0	0	1376.73	344	357
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	6	6	9	0.01%	11.4%	DVLVATDVASK	99.7%	55.1	25	38.8	2	0	0	1117.61	484	494
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	6	6	9	0.01%	11.4%	GVEAVAIHGGKDQEER	99.3%	30.1	25	28.2	0	1	0	1694.85	456	471
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	6	6	9	0.01%	11.4%	ILESVAEGR	96.3%	29.8	25	6.98	1	0	0	973.53	116	124
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	6	6	9	0.01%	11.4%	LLQEDSSPLLR	99.1%	36.2	25	32	2	0	0	1270.70	283	293
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	6	6	9	0.01%	11.4%	SALVKPVTINVGR	99.5%	32.1	25	32.1	0	2	0	1353.82	388	400
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	6	6	9	0.01%	11.4%	TPPPVLIFAEK	99.7%	45	25	45	1	0	0	1211.70	431	441
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	5	5	12	0.01%	13.4%	IQIEAIPLALQGR	99.7%	113	25	107	2	0	0	1421.85	50	62
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	5	5	12	0.01%	13.4%	LFALVLTPTR	99.3%	37.6	25	32.7	1	0	0	1130.69	93	102
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	5	5	12	0.01%	13.4%	LIDHLENTK	99.7%	43.7	25	43.7	3	0	0	1082.58	153	161
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	5	5	12	0.01%	13.4%	LQQYYIFIPSK	99.7%	49.2	25	33.8	4	0	0	1399.76	238	248
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	5	5	12	0.01%	13.4%	TGAFALPILNALLETPQR	99.7%	52.5	25	52.5	2	0	0	1925.09	75	92
Probable ATP-dependent RNA helicase DDX49	DDX49	DDX49_HUMAN	54.2	100.0%	3	3	6	0.01%	7.7%	ILIATDVASR	99.7%	72.5	25	46.1	2	0	0	1058.62	301	310
Probable ATP-dependent RNA helicase DDX49	DDX49	DDX49_HUMAN	54.2	100.0%	3	3	6	0.01%	7.7%	TAAFVLPILQK	99.7%	47.8	25	35.2	2	0	0	1200.74	53	63
Probable ATP-dependent RNA helicase DDX49	DDX49	DDX49_HUMAN	54.2	100.0%	3	3	6	0.01%	7.7%	TPSGSHSGPVPSQGLV	99.3%	37.4	25	37.3	2	0	0	1506.75	468	483
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	23	24	71	0.07%	36.8%	APILIATDVASR	99.7%	80.7	25	80.7	6	0	0	1226.71	392	403
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	23	24	71	0.07%	36.8%	DRGFGAPR	95.5%	29	25	11.7	1	0	0	875.45	13	20
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	23	24	71	0.07%	36.8%	ELAQQVQQVAAEYCR	99.7%	92.9	25	92.9	3	0	0	1792.86	178	192
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	23	24	71	0.07%	36.8%	FVINYDYPNSSEDYIHR	99.6%	33.3	25	33.3	0	2	0	2131.97	412	428
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	23	24	71	0.07%	36.8%	GDGPICLVLAPTR	99.7%	47	25	44.7	2	0	0	1368.73	165	177
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	23	24	71	0.07%	36.8%	GLDVEDVK	99.7%	44.2	25	31.3	4	0	0	874.45	404	411
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	23	24	71	0.07%	36.8%	GVEICIATPGR	99.7%	64.7	25	45.7	4	0	0	1172.61	217	227
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	23	24	71	0.07%	36.8%	IVDQIRPDR	96.8%	30.4	25	14.4	3	0	0	1111.62	265	273
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	23	24	71	0.07%	36.8%	LIDFLECGK	99.7%	64.5	25	62.2	4	0	0	1094.56	228	236
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	23	24	71	0.07%	36.8%	LLQLVEDR	99.7%	65.5	25	46.1	4	0	0	985.57	471	478
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	23	24	71	0.07%	36.8%	LMEEIMSEK	99.4%	38	25	28.2	2	0	0	1109.52	332	340
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	23	24	71	0.07%	36.8%	LMEEIMSEKENK	99.4%	38.4	25	31.6	2	0	0	1480.70	332	343
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	23	24	71	0.07%	36.8%	MLDMGFEPQIR	99.7%	74.2	25	43.5	6	0	0	1352.63	253	263
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	23	24	71	0.07%	36.8%	NFYQEHPDLAR	99.7%	55.8	25	43	3	0	0	1389.65	57	67
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	23	24	71	0.07%	36.8%	QTLMWSATWPK	99.7%	59.1	25	50.2	1	0	0	1348.67	274	284
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	23	24	71	0.07%	36.8%	QVSDLISVLR	99.7%	61.6	25	46.6	5	0	0	1129.66	452	461
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	23	24	71	0.07%	36.8%	STCIYGGAPK	99.7%	59.2	25	50.5	4	0	0	1053.50	198	207
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	23	24	71	0.07%	36.8%	TAQEVETYR	99.7%	70.5	25	58.2	4	0	0	1096.53	69	77
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	23	24	71	0.07%	36.8%	TGTAYTFFTPNNIK	99.7%	75.6	25	64	4	0	0	1574.79	438	451
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	23	24	71	0.07%	36.8%	TIVFVETK	99.4%	37.9	25	30.8	1	0	0	936.54	344	351
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	23	24	71	0.07%	36.8%	TIVFVETKR	99.7%	51.7	25	51.7	2	0	0	1092.64	344	352
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	23	24	71	0.07%	36.8%	TTYLVLDEADR	99.7%	78.4	25	69.6	2	0	0	1295.65	242	252
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	23	24	71	0.07%	36.8%	WNLDELPK	97.8%	32.1	25	12.7	2	0	0	1014.53	46	53
Probable ATP-dependent RNA helicase DDX52	DDX52	DDX52_HUMAN	67.5	100.0%	4	5	6	0.01%	8.0%	ELASQIHR	99.7%	49.7	25	33.9	2	0	0	953.52	245	252

Probable ATP-dependent RNA helicase DDX52	DDX52	DDX52_HUMAN	67.5	100.0%	4	5	6	0.01%	8.0%	ELLASAPTGSGK	98.3%	33.3	25	33.3	1	0	0	1130.61	204	215
Probable ATP-dependent RNA helicase DDX52	DDX52	DDX52_HUMAN	67.5	100.0%	4	5	6	0.01%	8.0%	GFNPPVLVFVQSIER	99.7%	66.1	25	66.1	1	0	0	1701.93	410	424
Probable ATP-dependent RNA helicase DDX52	DDX52	DDX52_HUMAN	67.5	100.0%	4	5	6	0.01%	8.0%	TLAFSIPILMQLK	99.7%	44.1	25	44.1	2	0	0	1474.87	216	228
Probable ATP-dependent RNA helicase DHX36	DHX36	DHX36_HUMAN	114.8	100.0%	4	4	7	0.01%	4.6%	ASLLDDYQLPEILR	99.7%	81.7	25	73.3	2	0	0	1645.88	620	633
Probable ATP-dependent RNA helicase DHX36	DHX36	DHX36_HUMAN	114.8	100.0%	4	4	7	0.01%	4.6%	AVICAGLYPK	98.9%	35	25	33.1	2	0	0	1091.59	833	842
Probable ATP-dependent RNA helicase DHX36	DHX36	DHX36_HUMAN	114.8	100.0%	4	4	7	0.01%	4.6%	LGGIAYFLSR	99.7%	76.8	25	75.3	2	0	0	1096.62	648	657
Probable ATP-dependent RNA helicase DHX36	DHX36	DHX36_HUMAN	114.8	100.0%	4	4	7	0.01%	4.6%	NLQSDVLMTVVK	99.4%	38.4	25	27.7	1	0	0	1346.73	340	351
Probable ATP-dependent RNA helicase DHX37	DHX37	DHX37_HUMAN	129.5	99.8%	2	2	3	0.00%	1.6%	FLLEGQVFR	99.3%	37	25	28.8	1	0	0	1108.62	1067	1075
Probable ATP-dependent RNA helicase DHX37	DHX37	DHX37_HUMAN	129.5	99.8%	2	2	3	0.00%	1.6%	VEDFTQNPR	99.7%	62.6	25	52.8	2	0	0	1105.53	413	421
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	10	11	16	0.02%	7.6%	APEPPPALIVR	99.7%	54.2	25	53.1	2	0	0	1159.68	797	807
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	10	11	16	0.02%	7.6%	EMFLEDILR	99.6%	40.1	25	28.1	2	0	0	1165.59	377	385
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	10	11	16	0.02%	7.6%	IAVNIALER	99.7%	61.5	25	58.9	1	0	0	998.60	47	55
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	10	11	16	0.02%	7.6%	LAAIAVAER	99.7%	48.9	25	34.2	2	0	0	913.55	251	259
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	10	11	16	0.02%	7.6%	LASNALQEPSSFR	99.7%	76.6	25	68.1	2	0	0	1419.72	1069	1081
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	10	11	16	0.02%	7.6%	LLAPVNCPIADFLMK	95.2%	28.7	25	28.2	1	0	0	1701.91	782	796
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	10	11	16	0.02%	7.6%	LSQSLGLVSK	99.7%	72.6	25	58.5	2	0	0	1031.61	81	90
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	10	11	16	0.02%	7.6%	SFDALNFVTMLK	99.7%	71.8	25	67.1	2	0	0	1401.71	713	724
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	10	11	16	0.02%	7.6%	TQLLGQLR	95.3%	28.9	25	15.1	1	0	0	928.56	938	945
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	10	11	16	0.02%	7.6%	VVLIVGETGSGK	99.7%	42.4	25	42.4	1	0	0	1158.67	211	222
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	7	7	12	0.01%	7.0%	DLEDESTPIVK	99.7%	52.4	25	35.3	2	0	0	1245.62	940	950
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	7	7	12	0.01%	7.0%	DSPTLSNSGIR	99.7%	54.5	25	48.6	2	0	0	1146.58	898	908
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	7	7	12	0.01%	7.0%	GFQEDSEIR	99.7%	43.9	25	24.9	2	0	0	1080.50	208	216
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	7	7	12	0.01%	7.0%	LGDASIAAPFTSK	99.7%	77.3	25	68.9	2	0	0	1277.67	951	963
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	7	7	12	0.01%	7.0%	LGSTDLCYIAAVK	99.7%	57.2	25	51.7	1	0	0	1410.73	642	654
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	7	7	12	0.01%	7.0%	SIDGSIVLPLAR	99.7%	56.5	25	46.5	2	0	0	1240.73	786	797
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	7	7	12	0.01%	7.0%	SPQENLVPCDVLLLR	99.7%	42.1	25	39.5	1	0	0	1752.93	328	342
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	6	7	12	0.01%	8.4%	IMDLIGIQTK	99.7%	61.7	25	52	3	0	0	1131.64	123	132
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	6	7	12	0.01%	8.4%	IVYSMYSR	99.3%	37.6	25	27.8	2	0	0	1018.50	587	594
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	6	7	12	0.01%	8.4%	LTEYPLVINTLK	99.7%	63.4	25	61.3	2	0	0	1403.81	92	103
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	6	7	12	0.01%	8.4%	TEMGLYYSYFK	99.7%	45.1	25	45.1	1	0	0	1401.64	62	72
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	6	7	12	0.01%	8.4%	TPLCNLLVK	99.7%	49.7	25	45.7	2	0	0	1057.61	644	652
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	6	7	12	0.01%	8.4%	VLEVVKE	99.7%	42.1	25	16.6	2	0	0	815.49	669	675
Probable cytosolic iron-sulfur protein assembly protein CIAO1	CIAO1	CIAO1_HUMAN	37.8	100.0%	3	3	5	0.00%	10.3%	MKDSLVLLGR	99.7%	65.8	25	60.3	2	0	0	1131.66	1	10
Probable cytosolic iron-sulfur protein assembly protein CIAO1	CIAO1	CIAO1_HUMAN	37.8	100.0%	3	3	5	0.00%	10.3%	SVAWAPSGNLLATCSR	99.7%	50.9	25	43.8	1	0	0	1689.84	110	125
Probable cytosolic iron-sulfur protein assembly protein CIAO1	CIAO1	CIAO1_HUMAN	37.8	100.0%	3	3	5	0.00%	10.3%	SVLSEGHQR	99.7%	48.1	25	33.4	2	0	0	1012.52	54	62
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	7	7	12	0.01%	22.4%	LLHGFNAEGIHFS	99.4%	37.8	25	35.8	2	0	0	1441.72	301	313
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	7	7	12	0.01%	22.4%	LQVLVGDVLK	99.7%	60.5	25	42.3	2	0	0	1083.68	107	116
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	7	7	12	0.01%	22.4%	LSINTQLLAR	99.7%	77.2	25	61.3	2	0	0	1128.67	175	184
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	7	7	12	0.01%	22.4%	NNFRPPPK	97.6%	31.6	25	23.5	1	0	0	969.53	194	201
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	7	7	12	0.01%	22.4%	NPLIINSIIDK	99.7%	66.4	25	66.4	2	0	0	1239.73	41	51
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	7	7	12	0.01%	22.4%	SMDIDDFIR	99.7%	47.9	25	37.5	2	0	0	1111.51	292	300
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	7	7	12	0.01%	22.4%	VVACELDPR	99.7%	42.8	25	32.7	1	0	0	1058.53	81	89
Probable glutamate--tRNA ligase, mitochondrial	EARS2	SYEM_HUMAN	58.7	100.0%	4	4	7	0.01%	8.8%	GGPAGPYQQSQR	99.7%	51.6	25	48.8	2	0	0	1245.60	109	120
Probable glutamate--tRNA ligase, mitochondrial	EARS2	SYEM_HUMAN	58.7	100.0%	4	4	7	0.01%	8.8%	HEVASVEGDPVIMK	99.7%	54.6	25	48.7	1	0	0	1510.76	208	221
Probable glutamate--tRNA ligase, mitochondrial	EARS2	SYEM_HUMAN	58.7	100.0%	4	4	7	0.01%	8.8%	NMSQEQVAQK	99.7%	60.4	25	59.2	2	0	0	1162.55	169	178
Probable glutamate--tRNA ligase, mitochondrial	EARS2	SYEM_HUMAN	58.7	100.0%	4	4	7	0.01%	8.8%	TALYNYIFAK	99.7%	54.2	25	36.9	2	0	0	1203.64	56	65
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	12	12	20	0.02%	14.4%	ADLEGSLDSK	99.5%	39.3	25	29.4	2	0	0	1034.50	364	373
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	12	12	20	0.02%	14.4%	AMQDALADLPEWYGIK	99.5%	38.9	25	30.4	1	0	0	1820.89	251	266
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	12	12	20	0.02%	14.4%	EEVDLTGSVPVHAK	99.7%	52	25	40.3	1	0	0	1480.76	615	628
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	12	12	20	0.02%	14.4%	FYVLSMFPYPSGK	99.7%	72.9	25	72.9	2	0	0	1535.76	84	96
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	12	12	20	0.02%	14.4%	IPVPQQVAR	98.5%	33.8	25	33.8	2	0	0	1007.60	853	861

Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	12	12	20	0.02%	14.4%	LLAQGLIK	95.1%	28.7	25	0	1	0	0	855.57	593	600
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	12	12	20	0.02%	14.4%	LPSGQYLQR	99.7%	70	25	59.5	2	0	0	1061.57	606	614
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	12	12	20	0.02%	14.4%	LSSSAEFTGMTR	99.7%	59.4	25	57.8	1	0	0	1286.60	408	419
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	12	12	20	0.02%	14.4%	QDAFLALTQK	99.7%	46.7	25	35.5	2	0	0	1134.62	420	429
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	12	12	20	0.02%	14.4%	TALINFLVQD	99.7%	57.8	25	53.5	2	0	0	1133.62	894	903
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	12	12	20	0.02%	14.4%	TDALPGVLR	99.7%	49.5	25	37.3	2	0	0	941.54	682	690
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	12	12	20	0.02%	14.4%	VYTISDTIAR	99.7%	48	25	37.4	2	0	0	1138.61	104	113
Probable proline--tRNA ligase, mitochondrial	PARS2	SYPM_HUMAN	53.3	99.9%	2	2	4	0.00%	4.6%	FGYPFVIIAGK	99.6%	40.9	25	37.2	2	0	0	1211.68	428	438
Probable proline--tRNA ligase, mitochondrial	PARS2	SYPM_HUMAN	53.3	99.9%	2	2	4	0.00%	4.6%	QLPFLLYQVTR	99.7%	53.1	25	51.8	2	0	0	1377.79	176	186
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	4	4	7	0.01%	13.1%	AVDPEDDFQR	99.7%	69	25	67.8	2	0	0	1191.53	95	104
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	4	4	7	0.01%	13.1%	ELQDAFSR	95.0%	28.6	25	19	1	0	0	965.47	22	29
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	4	4	7	0.01%	13.1%	ESYDDVSSFR	99.7%	51	25	51	2	0	0	1204.51	263	272
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	4	4	7	0.01%	13.1%	QAQAAVLAVLPR	99.7%	61.1	25	56.1	2	0	0	1236.74	111	122
Probable serine carboxypeptidase CPVL	CPVL	CPVL_HUMAN	54.2	100.0%	3	3	10	0.01%	6.7%	FLSLPEVR	99.5%	39.1	25	26.5	2	0	0	960.55	332	339
Probable serine carboxypeptidase CPVL	CPVL	CPVL_HUMAN	54.2	100.0%	3	3	10	0.01%	6.7%	NNDFYVTGESYAGK	99.7%	93.6	25	93.6	4	0	0	1564.69	195	208
Probable serine carboxypeptidase CPVL	CPVL	CPVL_HUMAN	54.2	100.0%	3	3	10	0.01%	6.7%	SDSEVAGYIR	99.7%	66.7	25	57.8	4	0	0	1096.53	424	433
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	7	8	12	0.01%	26.3%	GPGMGAPLVSVAVVAR	99.4%	38	25	26	2	0	0	1496.83	79	94
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	7	8	12	0.01%	26.3%	ISNDPSPGYNIEQMAK	99.7%	56.2	25	56.2	1	0	0	1763.83	170	185
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	7	8	12	0.01%	26.3%	LFATDER	95.7%	29.1	25	10.8	1	0	0	851.43	284	290
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	7	8	12	0.01%	26.3%	LVELPYTVK	98.9%	35.1	25	28.2	2	0	0	1061.62	190	198
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	7	8	12	0.01%	26.3%	PAVLGFEGSANK	99.7%	87.2	25	85.4	2	0	0	1189.62	2	13
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	7	8	12	0.01%	26.3%	TPLSDSGVTQR	99.7%	58	25	43.4	2	0	0	1160.59	313	323
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	7	8	12	0.01%	26.3%	TYVTPPGTGFLPGDTAR	99.7%	73.9	25	72.5	2	0	0	1749.88	31	47
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	21	22	34	0.03%	9.1%	CLAENAVYLCDR	99.7%	54.2	25	54.2	1	0	0	1483.67	683	694
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	21	22	34	0.03%	9.1%	DGQLWLCAPQAK	99.7%	52	25	49.8	2	0	0	1386.68	667	678
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	21	22	34	0.03%	9.1%	DHEDYDPQTVR	97.5%	31.5	25	30.8	1	0	0	1374.59	633	643
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	21	22	34	0.03%	9.1%	EIYTNLGPR	99.7%	52	25	47	2	0	0	1062.56	795	803
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	21	22	34	0.03%	9.1%	ELDMEPYTVAGVAK	99.7%	41.6	25	40.6	1	0	0	1522.75	1821	1834
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	21	22	34	0.03%	9.1%	ELLAFQTSEK	99.7%	42	25	33.7	2	0	0	1165.61	1436	1445
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	21	22	34	0.03%	9.1%	EYNIGVLR	97.7%	31.8	25	25.3	1	0	0	963.53	1638	1645
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	21	22	34	0.03%	9.1%	FNDYFEFPR	99.7%	48.1	25	41.4	2	0	0	1234.55	1812	1820
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	21	22	34	0.03%	9.1%	FSEYLLECPSAEVR	99.7%	72.7	25	66.8	2	0	0	1699.80	2100	2113
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	21	22	34	0.03%	9.1%	GDLLEGANAYHCEK	99.7%	52.8	25	52.8	1	0	0	1576.71	1760	1773
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	21	22	34	0.03%	9.1%	IIEDCSNSEETVK	99.7%	56.4	25	12.2	1	0	0	1523.69	2289	2301
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	21	22	34	0.03%	9.1%	LAQQISDEASR	99.7%	62.9	25	61.1	2	0	0	1217.61	1221	1231
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	21	22	34	0.03%	9.1%	LPPVLAIQLK	95.3%	28.9	25	28.9	1	0	0	1091.72	1789	1798
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	21	22	34	0.03%	9.1%	LYSVVSQLIR	99.7%	64.3	25	51	2	0	0	1177.69	2228	2237
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	21	22	34	0.03%	9.1%	MDTIDQDDELIR	99.7%	45.9	25	41.7	1	0	0	1463.67	1956	1967
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	21	22	34	0.03%	9.1%	MNALNEVNK	99.2%	36.5	25	27.1	1	0	0	1048.51	352	360
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	21	22	34	0.03%	9.1%	NDALSMIIK	97.2%	31	25	8.51	1	0	0	1020.54	304	312
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	21	22	34	0.03%	9.1%	SGGLPLVLSMLTR	99.7%	58.8	25	58.8	4	0	0	1343.77	1120	1132
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	21	22	34	0.03%	9.1%	VISSVSYYTHR	99.7%	61.4	25	51.8	2	0	0	1311.67	361	371
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	21	22	34	0.03%	9.1%	VLGGSFADQK	99.3%	37.4	25	33	2	0	0	1021.53	1713	1722
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	21	22	34	0.03%	9.1%	VVIQSNDDIASR	99.7%	68.9	25	66.3	2	0	0	1316.68	777	788
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	100.0%	6	7	13	0.01%	10.6%	FLGSGGFIGYAPNLSK	99.7%	133	25	128	2	0	0	1627.85	151	166
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	100.0%	6	7	13	0.01%	10.6%	FLLEYIAPMTEK	99.7%	63.7	25	60.7	4	0	0	1454.76	615	626
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	100.0%	6	7	13	0.01%	10.6%	IFQNLDGALDEVVLK	99.7%	62.4	25	52.7	2	0	0	1673.91	206	220
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	100.0%	6	7	13	0.01%	10.6%	LQLNYLGNYIPR	99.7%	55.2	25	55.2	1	0	0	1463.80	248	259
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	100.0%	6	7	13	0.01%	10.6%	SEDYVDIVQGR	99.7%	70.8	25	63.9	2	0	0	1280.61	431	441
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	100.0%	6	7	13	0.01%	10.6%	VGVDYEGGGCR	99.7%	97.4	25	90.3	2	0	0	1168.51	671	681
Profilin-1	PFN1	PROF1_HUMAN	15.1	100.0%	3	4	7	0.01%	27.9%	DSLLQDGEFSMDLR	99.7%	75.2	25	69.2	4	0	0	1625.75	76	89

Profilin-1	PFN1	PROF1_HUMAN	15.1	100.0%	3	4	7	0.01%	27.9%	STGGAPTFNVTVTK	99.7%	61.9	25	55.6	2	0	0	1379.72	92	105
Profilin-1	PFN1	PROF1_HUMAN	15.1	100.0%	3	4	7	0.01%	27.9%	TDKTLVLLMGK	99.7%	55.9	25	55.9	1	0	0	1234.71	106	116
Profilin-2	PFN2	PROF2_HUMAN	15.0	99.8%	2	2	4	0.00%	19.3%	EGFFTNGLTLGAK	97.2%	31	25	18.4	2	0	0	1354.70	57	69
Profilin-2	PFN2	PROF2_HUMAN	15.0	99.8%	2	2	4	0.00%	19.3%	SQGGEPTYNVAVGR	99.7%	67.8	25	66.4	2	0	0	1434.70	92	105
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	10	10	18	0.02%	14.6%	DTIVLLCKPEPELNAAIPSANPAK	98.1%	26.2	25	26.2	0	1	0	2561.36	518	541
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	10	10	18	0.02%	14.6%	ELPELLQR	99.4%	37.8	25	37.8	2	0	0	997.57	439	446
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	10	10	18	0.02%	14.6%	FYNELTEILVR	99.7%	76.4	25	68.7	2	0	0	1396.75	676	686
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	10	10	18	0.02%	14.6%	LANQAADYFGDAFK	99.7%	67.9	25	58.7	2	0	0	1530.72	216	229
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	10	10	18	0.02%	14.6%	LQHAAELIK	99.3%	37.1	25	21.7	1	0	0	1022.60	277	285
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	10	10	18	0.02%	14.6%	NIQVSHQEFSK	99.4%	37.9	25	31.8	2	0	0	1316.66	628	638
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	10	10	18	0.02%	14.6%	SLLSNLDEVKK	99.7%	51.1	25	25.7	2	0	0	1245.71	554	564
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	10	10	18	0.02%	14.6%	STPVNVPISQK	98.9%	35.2	25	35.2	2	0	0	1169.65	340	350
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	10	10	18	0.02%	14.6%	SVIEQGGIQTVDQLIK	99.7%	106	25	89.2	2	0	0	1727.95	423	438
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	10	10	18	0.02%	14.6%	TSEVDLAKPLVK	99.7%	44.1	25	36.2	2	0	0	1299.75	12	23
Programmed cell death protein 10	PDCD10	PDC10_HUMAN	24.7	100.0%	3	3	5	0.00%	14.2%	AINVFVSANR	99.7%	62.5	25	47.1	2	0	0	1090.60	187	196
Programmed cell death protein 10	PDCD10	PDC10_HUMAN	24.7	100.0%	3	3	5	0.00%	14.2%	IPDEINDR	99.6%	40.1	25	33.2	1	0	0	971.48	117	124
Programmed cell death protein 10	PDCD10	PDC10_HUMAN	24.7	100.0%	3	3	5	0.00%	14.2%	SVEVNFTESLLR	99.7%	65.2	25	60.9	2	0	0	1393.73	71	82
Programmed cell death protein 6	PDCD6	PDCD6_HUMAN	21.9	100.0%	6	8	14	0.01%	28.3%	AGVNFSEFTGVWK	99.7%	72.8	25	64.7	2	0	0	1441.71	78	90
Programmed cell death protein 6	PDCD6	PDCD6_HUMAN	21.9	100.0%	6	8	14	0.01%	28.3%	LSDQFHDILIR	99.7%	60.9	25	49.8	2	2	0	1356.73	126	136
Programmed cell death protein 6	PDCD6	PDCD6_HUMAN	21.9	100.0%	6	8	14	0.01%	28.3%	QALSGFGYR	99.7%	79.5	25	64.6	2	0	0	998.51	117	125
Programmed cell death protein 6	PDCD6	PDCD6_HUMAN	21.9	100.0%	6	8	14	0.01%	28.3%	SIISMFDR	99.4%	38.5	25	17.5	2	0	0	984.48	67	74
Programmed cell death protein 6	PDCD6	PDCD6_HUMAN	21.9	100.0%	6	8	14	0.01%	28.3%	SIISMFDRENK	99.7%	51.7	25	51.7	2	0	0	1339.67	67	77
Programmed cell death protein 6	PDCD6	PDCD6_HUMAN	21.9	100.0%	6	8	14	0.01%	28.3%	YITDWQNVFR	99.7%	55.4	25	48.3	2	0	0	1341.66	91	100
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	66	0.06%	59.9%	AAELIANSLATAGDGLIELR	99.7%	99.9	25	87.8	6	2	0	1998.09	220	239
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	66	0.06%	59.9%	AAIISAEGDSK	99.7%	71.9	25	66.9	6	0	0	1061.55	209	219
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	66	0.06%	59.9%	AVIFDRFR	97.7%	31.8	25	31.8	1	0	0	1023.57	36	43
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	66	0.06%	59.9%	DLQNVNITLR	99.7%	74.8	25	59.4	2	0	0	1185.66	84	93
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	66	0.06%	59.9%	EFTEAVEAK	99.7%	59.2	25	47.1	2	0	0	1023.50	178	186
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	66	0.06%	59.9%	FDAGELITQR	99.7%	77.2	25	72.2	12	0	0	1149.59	134	143
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	66	0.06%	59.9%	FVVEKAEQQK	99.7%	43	25	39.2	2	0	0	1205.65	198	207
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	66	0.06%	59.9%	IFTSIGEDYDER	99.7%	85.2	25	77.1	7	0	0	1444.66	106	117
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	66	0.06%	59.9%	ILFRPVASQLPR	99.7%	58.8	25	48.2	4	7	0	1396.84	94	105
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	66	0.06%	59.9%	KAAIISAEGDSK	99.7%	73.4	25	66	2	0	0	1189.64	208	219
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	66	0.06%	59.9%	KLEAAEDIAYQLSR	99.7%	131	25	125	3	0	0	1606.84	240	253
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	66	0.06%	59.9%	NITYLPAGQSVLLQLPQ	99.3%	37.5	25	37.5	3	0	0	1855.03	256	272
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	66	0.06%	59.9%	QVAQQEAER	99.2%	36.8	25	28.5	1	0	0	1058.52	187	195
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	66	0.06%	59.9%	QVSDDLTER	99.7%	60.4	25	53.1	2	0	0	1062.51	149	157
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	17	66	0.06%	59.9%	VLPSITTEILK	99.7%	65.3	25	52.8	4	0	0	1213.74	118	128
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	102	0.10%	57.5%	AQFLVEK	99.7%	42.6	25	23.2	4	0	0	834.47	210	216
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	102	0.10%	57.5%	AQVSLLIR	99.7%	53.6	25	39.6	5	0	0	899.57	158	165
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	102	0.10%	57.5%	DLQMVNISLR	99.7%	71.4	25	55.3	8	0	0	1188.64	98	107
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	102	0.10%	57.5%	ESVFTVEGGHR	99.7%	74.6	25	57.4	4	4	0	1217.59	38	48
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	102	0.10%	57.5%	EYTAAVEAK	99.7%	60.8	25	49.4	4	0	0	981.49	192	200
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	102	0.10%	57.5%	FNASQLITQR	99.7%	77.4	25	65.8	8	0	0	1177.63	148	157
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	102	0.10%	57.5%	IGGVQQDTILAEGLHFR	99.7%	98.3	25	98.3	4	6	0	1853.99	55	71
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	102	0.10%	57.5%	IPWFQYPIIYDIR	99.7%	63.8	25	56.6	4	0	0	1723.92	72	84
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	102	0.10%	57.5%	IVQAEGEAEAAK	99.7%	93.1	25	80.6	4	0	0	1215.62	225	236
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	102	0.10%	57.5%	IYLTADNLVLNLQDESFTR	99.7%	91.9	25	91.9	4	2	0	2225.15	271	289
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	102	0.10%	57.5%	LGLDYEER	99.7%	59.3	25	46.9	8	0	0	994.48	124	131
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	102	0.10%	57.5%	LLLGAGAVAYGVR	99.7%	104	25	87.3	9	0	0	1259.75	25	37
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	102	0.10%	57.5%	MLGEALSK	99.6%	40.7	25	16	6	0	0	864.45	237	244

Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	102	0.10%	57.5%	VLPSIVNEVLK	99.7%	54.5	25	46.6	4	0	0	1210.74	132	142
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	102	0.10%	57.5%	VLSRPNAQELPSMYQR	99.7%	57.6	25	50	6	8	0	1888.97	108	123
Prolactin-inducible protein	PIP	PIP_HUMAN	16.6	100.0%	4	4	14	0.01%	32.9%	ELGICPDDAAVIPIK	99.7%	41.5	25	41.5	2	0	0	1610.85	119	133
Prolactin-inducible protein	PIP	PIP_HUMAN	16.6	100.0%	4	4	14	0.01%	32.9%	FYTIEILKVE	99.7%	45.8	25	41	4	0	0	1254.70	137	146
Prolactin-inducible protein	PIP	PIP_HUMAN	16.6	100.0%	4	4	14	0.01%	32.9%	TVQIAAVVDVIR	99.7%	69.4	25	61.7	4	0	0	1283.77	107	118
Prolactin-inducible protein	PIP	PIP_HUMAN	16.6	100.0%	4	4	14	0.01%	32.9%	YTACLCDDNPK	99.7%	55	25	55	4	0	0	1356.56	86	96
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	13	17	32	0.03%	57.9%	AEDNADTLALVFEAPNQEK	99.7%	90.7	25	90.7	2	0	0	2074.99	92	110
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	13	17	32	0.03%	57.9%	ATPLSSTVTLSMSADVPLVVEYK	99.7%	76.1	25	76.1	2	2	0	2424.26	218	240
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	13	17	32	0.03%	57.9%	DLSHIGDAVVISCAK	99.7%	78.2	25	75.1	2	0	0	1584.81	150	164
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	13	17	32	0.03%	57.9%	FSASGELGNGNIK	99.7%	98.3	25	91.8	2	0	0	1293.64	169	181
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	13	17	32	0.03%	57.9%	IADMGHLK	99.7%	48.5	25	45.6	2	0	0	884.47	241	248
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	13	17	32	0.03%	57.9%	LMDLDVEQLGIPEQEYSCVVK	99.7%	78.4	25	78.4	4	0	0	2465.19	118	138
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	13	17	32	0.03%	57.9%	LVQGSILK	99.7%	47.9	25	17.1	1	0	0	857.55	6	13
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	13	17	32	0.03%	57.9%	LVQGSILKK	99.7%	58.2	25	34.8	2	0	0	985.64	6	14
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	13	17	32	0.03%	57.9%	MPSGEFAR	99.6%	40.6	25	32.2	2	0	0	910.41	139	146
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	13	17	32	0.03%	57.9%	NLAMGVNLTSMSK	99.7%	115	25	110	6	0	0	1365.69	65	77
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	13	17	32	0.03%	57.9%	SEGFDTYR	99.7%	46.7	25	38.2	2	0	0	974.42	54	61
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	13	17	32	0.03%	57.9%	VSDYEMK	95.1%	28.7	25	28.7	1	0	0	871.39	111	117
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	13	17	32	0.03%	57.9%	YLNFFTK	99.7%	43.7	25	26.9	2	0	0	932.49	211	217
Prolyl 3-hydroxylase 1	LEPRE1	P3H1_HUMAN	83.4	99.8%	2	2	3	0.00%	3.1%	DLSFFGGLLR	99.7%	66	25	52	2	0	0	1124.61	106	115
Prolyl 3-hydroxylase 1	LEPRE1	P3H1_HUMAN	83.4	99.8%	2	2	3	0.00%	3.1%	LTNVAATSGDGYR	99.7%	64	25	60.3	1	0	0	1324.65	489	501
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	8	8	15	0.01%	18.9%	DPEGFVGHPVNAFK	99.7%	58.4	25	47.6	2	0	0	1513.74	73	86
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	8	8	15	0.01%	18.9%	FHDIISDAEIEIVK	99.7%	59.9	25	59.9	2	0	0	1628.85	340	353
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	8	8	15	0.01%	18.9%	GVAVDYLPER	99.7%	53	25	47.3	2	0	0	1118.58	277	286
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	8	8	15	0.01%	18.9%	HAACPVLVGNK	99.7%	50.7	25	39.6	2	0	0	1165.61	500	510
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	8	8	15	0.01%	18.9%	LLELDPEHQR	99.7%	41.8	25	38	1	0	0	1249.65	231	240
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	8	8	15	0.01%	18.9%	LNTEWSELENLVLK	99.7%	44.6	25	32.4	2	0	0	1687.89	91	104
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	8	8	15	0.01%	18.9%	LQDTYNLDTDTISK	99.7%	101	25	97.1	2	0	0	1626.79	137	150
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	8	8	15	0.01%	18.9%	SAWLSGYENPVVSR	99.7%	82.7	25	80.2	2	0	0	1564.78	383	396
Proteasomal ATPase-associated factor 1	PAAF1	PAAF1_HUMAN	42.2	100.0%	3	3	5	0.00%	8.4%	FLAPYTTFSR	96.4%	29.9	25	17.8	1	0	0	1202.62	80	89
Proteasomal ATPase-associated factor 1	PAAF1	PAAF1_HUMAN	42.2	100.0%	3	3	5	0.00%	8.4%	GGILDTAIVDR	99.7%	74.1	25	63.3	2	0	0	1129.62	177	187
Proteasomal ATPase-associated factor 1	PAAF1	PAAF1_HUMAN	42.2	100.0%	3	3	5	0.00%	8.4%	SGAPVLSLLSVR	99.7%	98.7	25	94	2	0	0	1198.72	321	332
Proteasomal ubiquitin receptor ADRM1	ADRM1	ADRM1_HUMAN	42.2	100.0%	2	2	3	0.00%	6.1%	LFFWMQEPK	99.1%	36.1	25	25.1	1	0	0	1225.61	105	113
Proteasomal ubiquitin receptor ADRM1	ADRM1	ADRM1_HUMAN	42.2	100.0%	2	2	3	0.00%	6.1%	SQSAAVTPSSTTSSTR	99.7%	87.3	25	83.9	2	0	0	1567.76	211	226
Proteasome activator complex subunit 3	PSME3	PSME3_HUMAN	29.5	100.0%	3	3	5	0.00%	16.1%	ITSEAEDLVANFFPK	99.7%	80.4	25	80.3	2	0	0	1680.85	22	36
Proteasome activator complex subunit 3	PSME3	PSME3_HUMAN	29.5	100.0%	3	3	5	0.00%	16.1%	SNQQLVDIIEK	99.7%	61.6	25	56.2	1	0	0	1286.70	111	121
Proteasome activator complex subunit 3	PSME3	PSME3_HUMAN	29.5	100.0%	3	3	5	0.00%	16.1%	TVESEAASYLDQISR	99.7%	94.4	25	68.2	2	0	0	1668.81	167	181
Proteasome subunit alpha type-1	PSMA1	PSA1_HUMAN	29.6	99.8%	2	2	3	0.00%	8.8%	LVSLIGSK	98.1%	32.7	25	13.4	1	0	0	816.52	108	115
Proteasome subunit alpha type-1	PSMA1	PSA1_HUMAN	29.6	99.8%	2	2	3	0.00%	8.8%	NQYDNDVTVWSPQGR	99.7%	58.6	25	58.6	2	0	0	1778.81	4	18
Proteasome subunit alpha type-3	PSMA3	PSA3_HUMAN	28.4	100.0%	3	3	6	0.01%	12.2%	AVENSSTAIGIR	99.7%	58.8	25	45.4	2	0	0	1217.65	30	41
Proteasome subunit alpha type-3	PSMA3	PSA3_HUMAN	28.4	100.0%	3	3	6	0.01%	12.2%	SNFGYNIPLK	99.3%	37	25	36.1	2	0	0	1152.60	101	110
Proteasome subunit alpha type-3	PSMA3	PSA3_HUMAN	28.4	100.0%	3	3	6	0.01%	12.2%	VFQVEYAMK	99.7%	60.5	25	56.3	2	0	0	1114.56	21	29
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	7	9	21	0.02%	26.1%	ATCIGNNSAAAVSMLK	99.7%	114	25	98.2	4	0	0	1607.79	161	176
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	7	9	21	0.02%	26.1%	LLDEVFFSEK	99.7%	57.2	25	52.6	4	0	0	1226.63	55	64
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	7	9	21	0.02%	26.1%	LSAEKVEIATLTR	99.7%	74.7	25	60.7	2	2	0	1430.82	206	218
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	7	9	21	0.02%	26.1%	QAYTQFGGK	99.6%	40	25	32.2	2	0	0	999.49	119	127
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	7	9	21	0.02%	26.1%	QDYKEGEMTLK	98.4%	33.5	25	25.5	1	0	0	1341.64	177	187
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	7	9	21	0.02%	26.1%	TTIFSPEGR	99.5%	38.7	25	22.9	2	0	0	1007.52	9	17
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	7	9	21	0.02%	26.1%	VEIATLTR	99.7%	56.8	25	41	4	0	0	902.53	211	218
Proteasome subunit alpha type-5	PSMA5	PSA5_HUMAN	26.4	100.0%	3	4	8	0.01%	14.5%	GVNTFSPEGR	99.7%	45.4	25	30.5	2	0	0	1063.52	11	20
Proteasome subunit alpha type-5	PSMA5	PSA5_HUMAN	26.4	100.0%	3	4	8	0.01%	14.5%	ITSPLMEPSSIEK	99.7%	66	25	60.4	4	0	0	1431.74	54	66

Proteasome subunit alpha type-5	PSMA5	PSA5_HUMAN	26.4	100.0%	3	4	8	0.01%	14.5%	LFQVEYAIEAIK	99.7%	80.8	25	69.3	2	0	0	1423.78	21	32
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	6	6	11	0.01%	29.4%	ALLEVVQSGGK	99.7%	76.1	25	69.4	2	0	0	1100.63	194	204
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	6	6	11	0.01%	29.4%	GRDIVVLGVEK	99.7%	56.5	25	47.9	2	0	0	1184.70	37	47
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	6	6	11	0.01%	29.4%	LTVEDPVTVEYITR	99.7%	103	25	91.3	2	0	0	1634.86	96	109
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	6	6	11	0.01%	29.4%	LYQTDPSGTYHAWK	99.7%	53.3	25	45.3	1	0	0	1666.79	144	157
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	6	6	11	0.01%	29.4%	NIELAVMR	99.3%	37	25	24.5	2	0	0	945.52	205	212
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	6	6	11	0.01%	29.4%	NYTDEAIETDDLTIK	99.7%	130	25	125	2	0	0	1740.82	175	189
Proteasome subunit beta type-5	PSMB5	PSB5_HUMAN	28.5	100.0%	2	2	4	0.00%	8.8%	ATAGAYIASQTVK	99.7%	75.9	25	71.1	2	0	0	1280.68	79	91
Proteasome subunit beta type-5	PSMB5	PSB5_HUMAN	28.5	100.0%	2	2	4	0.00%	8.8%	LLANMVYQYK	99.7%	41.2	25	41.2	2	0	0	1242.66	141	150
Proteasome subunit beta type-6	PSMB6	PSB6_HUMAN	25.4	100.0%	3	3	4	0.00%	13.0%	LAAIAESGVER	99.7%	73.4	25	60.1	2	0	0	1115.61	210	220
Proteasome subunit beta type-6	PSMB6	PSB6_HUMAN	25.4	100.0%	3	3	4	0.00%	13.0%	QVLLGDQIPK	99.0%	35.8	25	22.7	1	0	0	1110.65	221	230
Proteasome subunit beta type-6	PSMB6	PSB6_HUMAN	25.4	100.0%	3	3	4	0.00%	13.0%	TTTGSYIANR	95.9%	29.4	25	19.6	1	0	0	1083.54	54	63
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	35	0.03%	13.8%	AGEQLAPFLPQLVPR	98.5%	33.7	25	33	1	0	0	1635.92	1112	1126
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	35	0.03%	13.8%	AIACVVTACSAELEK	99.7%	95.3	25	90.9	1	0	0	1621.79	1591	1605
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	35	0.03%	13.8%	ALSINTLVK	94.9%	28.5	25	14.5	1	0	0	958.59	1272	1280
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	35	0.03%	13.8%	ESSCLALNDLLR	99.7%	55.3	25	43.6	1	0	0	1390.70	1180	1191
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	35	0.03%	13.8%	HSVATAADLELK	95.4%	28.9	25	22.1	1	0	0	1254.67	274	285
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	35	0.03%	13.8%	IVAISCAADILK	99.7%	71.2	25	62.1	2	0	0	1273.72	1633	1644
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	35	0.03%	13.8%	LCELIR	96.0%	29.5	25	11.3	1	0	0	803.44	1363	1368
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	35	0.03%	13.8%	LLLQGLMDSVEAK	95.3%	28.8	25	24.7	1	0	0	1432.77	880	892
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	35	0.03%	13.8%	LLSMAYSAVGK	99.7%	74.1	25	66.8	4	0	0	1139.61	415	425
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	35	0.03%	13.8%	LMSALLSGLTDR	99.7%	84.3	25	76.5	2	0	0	1276.69	1401	1412
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	35	0.03%	13.8%	LSSTQEGVR	99.7%	51.4	25	32.9	2	0	0	976.51	47	55
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	35	0.03%	13.8%	MSEQQDLER	99.7%	41.6	25	33.7	2	0	0	1151.50	771	779
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	35	0.03%	13.8%	NGPLPIPSEGSGFTK	97.4%	31.3	25	31.3	1	0	0	1500.77	823	837
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	35	0.03%	13.8%	SASPFNLAEKPK	99.7%	45.8	25	45.7	2	0	0	1288.69	157	168
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	35	0.03%	13.8%	TEALSVIELLLK	99.7%	83.2	25	75.2	2	0	0	1328.80	1785	1796
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	35	0.03%	13.8%	TIAALLPCLLDK	99.7%	43	25	37	2	0	0	1327.77	1250	1261
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	35	0.03%	13.8%	TLMSSGQMAPSSSNK	99.7%	71.7	25	71.7	2	0	0	1557.69	632	646
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	35	0.03%	13.8%	TPDGQGLSTYK	99.7%	44.3	25	44.3	2	0	0	1166.57	1057	1067
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	35	0.03%	13.8%	TSCALTIHAIGR	99.7%	51.7	25	47.1	1	0	0	1299.68	1457	1468
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	35	0.03%	13.8%	VQDDIKESVR	98.8%	34.7	25	22.4	1	0	0	1188.62	1212	1221
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	35	0.03%	13.8%	VYLGDIPLK	95.9%	29.4	25	26.7	1	0	0	1017.60	305	313
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	35	0.03%	13.8%	YLLLLAAGDPR	99.7%	72.8	25	70.8	2	0	0	1201.69	517	527
Protein AAR2 homolog	AAR2	AAR2_HUMAN	43.5	100.0%	3	4	5	0.00%	12.0%	GTEFGIDYNSWEVGPK	99.7%	57.9	25	57.9	1	0	0	1798.83	29	44
Protein AAR2 homolog	AAR2	AAR2_HUMAN	43.5	100.0%	3	4	5	0.00%	12.0%	QICAFSDVLPVLSMK	99.6%	40.2	25	35.5	3	0	0	1707.88	154	168
Protein AAR2 homolog	AAR2	AAR2_HUMAN	43.5	100.0%	3	4	5	0.00%	12.0%	WISLTNFISEATVEK	99.7%	56.7	25	54.3	1	0	0	1737.91	133	147
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	AAILPTSIFLTNK	99.7%	101	25	101	31	0	0	1388.81	228	240
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	AAILPTSIFLTNKK	99.7%	61.8	25	61.8	4	4	0	1516.91	228	241
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	DDGVSIPGEYTSFLAPISSSK	99.7%	98.7	25	98.7	16	0	0	2170.06	459	479
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	DDIIENAPTTHTEEYSGEEK	99.7%	88.7	25	88.7	4	4	0	2278.00	165	184
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	DLNCVPEIADTLGAVAK	99.7%	112	25	106	29	2	0	1785.91	19	35
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	DPEAQFEMPYVVR	99.7%	71.5	25	71.5	4	0	0	1580.74	493	505
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	DPIKYSQYQQAIYK	99.0%	35.5	25	34.3	1	0	0	1744.89	330	343
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	DPMIDNNR	99.7%	52	25	42.9	4	0	0	974.44	527	534
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	DRDPEAQFEMPYVVR	99.7%	60.6	25	60.6	3	4	0	1867.86	491	505
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	DTNVQVLMVLGAGR	99.7%	93.4	25	81.7	2	0	0	1488.78	355	368
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	DWNTLIVGK	99.7%	64.8	25	49.8	11	0	0	1045.57	77	85
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	EFIQEPAK	99.7%	47.3	25	32	14	0	0	961.50	53	60
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	EGQTICVR	99.7%	43.7	25	37.3	21	0	0	962.47	594	601
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	GPLVNASLR	99.7%	64.4	25	55.5	10	0	0	926.54	369	377

Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	IAVALEIGADLPSNHVIDR	99.7%	111	25	111	3	5	0	2003.09	202	220
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	IKLYAVEK	95.8%	29.3	25	11.1	1	0	0	963.59	386	393
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	KGFPVLSK	99.7%	52.9	25	30.4	10	0	0	875.54	241	248
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	LSPWIRPDSK	97.4%	31.3	25	28.5	4	0	0	1198.66	86	95
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	QGFDFLCMPVFHPR	99.7%	49.4	25	49.4	4	10	0	1766.81	36	49
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	REFIQEPAK	98.6%	34	25	18.7	2	0	0	1117.60	52	60
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	SDLLLSGR	99.7%	54.8	25	33.9	5	0	0	860.48	69	76
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	SDLLLSGRDWNTLIVGK	99.3%	30.5	25	30.5	0	1	0	1887.03	69	85
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	TLCDYSKR	99.7%	47.7	25	33.2	3	0	0	1042.50	194	201
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	TWMWWHNFR	95.5%	29	25	21.4	1	0	0	1379.61	185	193
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	VPEEEKDTNVQVLMVLGAGR	99.7%	113	25	113	4	10	0	2184.13	349	368
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	VPLVAPEDLR	99.7%	58.9	25	48.1	13	0	0	1108.64	155	164
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	VPLVAPEDLRDDIIENAPTTHTEEYSGEEK	99.7%	85.3	25	85.3	0	3	0	3367.62	155	184
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	VWYEWAVTAPVCSAIHNPTGR	99.4%	30.9	25	30.9	0	1	0	2414.17	611	631
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	WLGEPIK	99.3%	37.1	25	17.2	3	0	0	842.48	221	227
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	30	45	266	0.25%	44.7%	YSQYQQAIYK	99.7%	66.2	25	59.8	15	0	0	1291.63	334	343
Protein argonaute-2	AGO2	AGO2_HUMAN	97.2	99.8%	2	2	2	0.00%	2.4%	AVQVHQDTLR	99.0%	35.8	25	24.6	1	0	0	1166.63	845	854
Protein argonaute-2	AGO2	AGO2_HUMAN	97.2	99.8%	2	2	2	0.00%	2.4%	SAPDRQEEISK	96.0%	29.5	25	29.5	1	0	0	1259.62	371	381
Protein BUD31 homolog	BUD31	BUD31_HUMAN	17.0	100.0%	4	4	7	0.01%	28.5%	DTNFGTNCICR	99.7%	55.8	25	52.1	2	0	0	1357.56	110	120
Protein BUD31 homolog	BUD31	BUD31_HUMAN	17.0	100.0%	4	4	7	0.01%	28.5%	IIECTHCGCR	99.7%	43.9	25	43.9	1	0	0	1305.55	131	140
Protein BUD31 homolog	BUD31	BUD31_HUMAN	17.0	100.0%	4	4	7	0.01%	28.5%	KVESLWPIFR	99.7%	46	25	40.8	2	0	0	1274.73	42	51
Protein BUD31 homolog	BUD31	BUD31_HUMAN	17.0	100.0%	4	4	7	0.01%	28.5%	QGYENLCCLR	98.9%	35.1	25	28.7	2	0	0	1312.58	95	104
Protein CIP2A	KIAA1524	CIP2A_HUMAN	102.2	100.0%	5	5	8	0.01%	6.2%	ALALAQADR	99.7%	61.6	25	54.1	2	0	0	928.52	648	656
Protein CIP2A	KIAA1524	CIP2A_HUMAN	102.2	100.0%	5	5	8	0.01%	6.2%	EVQNQLVDR	99.4%	38.2	25	17.5	1	0	0	1100.57	789	797
Protein CIP2A	KIAA1524	CIP2A_HUMAN	102.2	100.0%	5	5	8	0.01%	6.2%	KLESVAEEHEILTK	99.7%	34.3	25	34.3	0	2	0	1625.87	716	729
Protein CIP2A	KIAA1524	CIP2A_HUMAN	102.2	100.0%	5	5	8	0.01%	6.2%	LITPLAFALTSDNR	99.7%	70.7	25	70.7	2	0	0	1531.85	509	522
Protein CIP2A	KIAA1524	CIP2A_HUMAN	102.2	100.0%	5	5	8	0.01%	6.2%	SLLLTVSQYK	99.7%	57.6	25	51	1	0	0	1151.67	9	18
Protein CMSS1	CMSS1	CMS1_HUMAN	31.9	100.0%	3	3	6	0.01%	12.2%	ANDLTHSLSSYLK	99.7%	52.5	25	44.9	2	0	0	1448.74	125	137
Protein CMSS1	CMSS1	CMS1_HUMAN	31.9	100.0%	3	3	6	0.01%	12.2%	QGGLNLSPLK	99.7%	60.1	25	49.5	2	0	0	1026.59	222	231
Protein CMSS1	CMSS1	CMS1_HUMAN	31.9	100.0%	3	3	6	0.01%	12.2%	VVHLGVGTPGR	99.7%	67.5	25	63.6	2	0	0	1091.63	205	215
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	8	9	18	0.02%	19.5%	EPFTIAQGK	97.5%	31.5	25	16.3	1	0	0	990.53	76	84
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	8	9	18	0.02%	19.5%	LCEIER	95.6%	29.1	25	10.5	2	0	0	819.40	88	93
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	8	9	18	0.02%	19.5%	LLASANLEEVTMK	99.7%	100	25	91.7	4	0	0	1434.75	332	344
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	8	9	18	0.02%	19.5%	LLYNRPGTVSSLK	99.7%	48.7	25	39.2	1	0	0	1447.83	112	124
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	8	9	18	0.02%	19.5%	NVGQFSGFPFEK	99.7%	42.9	25	41.6	4	0	0	1356.66	126	137
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	8	9	18	0.02%	19.5%	SGVNSELVK	99.7%	67	25	48.2	2	0	0	932.50	169	177
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	8	9	18	0.02%	19.5%	SGVNSELVKR	99.7%	51	25	29.9	2	0	0	1088.61	169	178
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	8	9	18	0.02%	19.5%	SICEVLDLER	99.7%	66.4	25	49.7	2	0	0	1233.61	159	168
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	7	7	10	0.01%	6.7%	ELGEYFLFDPK	99.7%	64.3	25	61.9	2	0	0	1357.67	1117	1127
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	7	7	10	0.01%	6.7%	KLDSELTAR	99.5%	38.7	25	30.7	2	0	0	1032.57	487	495
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	7	7	10	0.01%	6.7%	LNAILFK	99.3%	37.5	25	19.1	1	0	0	818.51	937	943
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	7	7	10	0.01%	6.7%	LQDLQGEKDALHSEK	99.1%	29.2	25	26.5	0	1	0	1710.87	513	527
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	7	7	10	0.01%	6.7%	QDLEAEVSQLTGEVAK	99.7%	60.9	25	56.5	1	0	0	1716.87	535	550
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	7	7	10	0.01%	6.7%	SPDELPSAGGDGGK	99.3%	37.6	25	37.6	1	0	0	1286.59	22	35
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	7	7	10	0.01%	6.7%	TAQNLSIFLGSFR	99.7%	68.1	25	68.1	2	0	0	1453.78	856	868
Protein disulfide-isomerase	P4HB	PDIA1_HUMAN	57.1	100.0%	2	2	2	0.00%	4.1%	EADDIVNWLK	98.3%	33.1	25	22.5	1	0	0	1202.61	121	130
Protein disulfide-isomerase	P4HB	PDIA1_HUMAN	57.1	100.0%	2	2	2	0.00%	4.1%	NFEDVAFDEKK	95.9%	29.4	25	27	1	0	0	1341.63	376	386
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	9	9	14	0.01%	8.6%	ADLTALFLPR	99.7%	80.9	25	73	2	0	0	1116.64	875	884
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	9	9	14	0.01%	8.6%	AVQGAQQPSLYQIR	99.7%	62.6	25	59.5	2	0	0	1558.83	1047	1060
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	9	9	14	0.01%	8.6%	GLDIYVWR	99.7%	52.1	25	34.4	1	0	0	1021.55	653	660
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	9	9	14	0.01%	8.6%	GVDLSGNDFK	97.7%	31.9	25	24.6	1	0	0	1051.51	12	21

Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	9	9	14	0.01%	8.6%	LAEDILNTMFDTSYSK	99.7%	48.3	25	48.3	1	0	0	1847.87	1116	1131
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	9	9	14	0.01%	8.6%	LLQSLLDTR	99.7%	62.6	25	51.1	2	0	0	1058.62	765	773
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	9	9	14	0.01%	8.6%	NAEAVLQSPGLSGK	99.7%	63.9	25	61.9	1	0	0	1370.73	849	862
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	9	9	14	0.01%	8.6%	VGLGLGYLELPQINYK	99.7%	47.1	25	47.1	2	0	0	1776.99	731	746
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	9	9	14	0.01%	8.6%	VPECLYTLPSLR	99.7%	66.4	25	52	2	0	0	1447.76	238	249
Protein jagunal homolog 1	JAGN1	JAGN1_HUMAN	21.1	100.0%	4	4	8	0.01%	17.5%	AAGTDGSDFQHR	99.7%	71.1	25	64.5	2	0	0	1261.56	9	20
Protein jagunal homolog 1	JAGN1	JAGN1_HUMAN	21.1	100.0%	4	4	8	0.01%	17.5%	LLDSWFTSTQEK	99.7%	105	25	105	2	0	0	1454.72	169	180
Protein jagunal homolog 1	JAGN1	JAGN1_HUMAN	21.1	100.0%	4	4	8	0.01%	17.5%	LLDSWFTSTQEKK	99.7%	78.8	25	77.6	2	0	0	1582.81	169	181
Protein jagunal homolog 1	JAGN1	JAGN1_HUMAN	21.1	100.0%	4	4	8	0.01%	17.5%	MSVGHLR	99.6%	40.2	25	28.7	2	0	0	799.42	55	61
Protein KRI1 homolog	KRI1	KRI1_HUMAN	82.6	100.0%	5	5	6	0.01%	10.0%	AFVEDSEDEDGAGEGGSSLLQK	99.7%	68.1	25	52.3	1	0	0	2239.98	166	187
Protein KRI1 homolog	KRI1	KRI1_HUMAN	82.6	100.0%	5	5	6	0.01%	10.0%	FEEPDSASVK	99.0%	35.8	25	27.4	1	0	0	1108.52	302	311
Protein KRI1 homolog	KRI1	KRI1_HUMAN	82.6	100.0%	5	5	6	0.01%	10.0%	LLGPTVMLGGCEFSR	99.7%	61.6	25	61.6	2	0	0	1636.82	657	671
Protein KRI1 homolog	KRI1	KRI1_HUMAN	82.6	100.0%	5	5	6	0.01%	10.0%	LQAFGLNPK	99.5%	38.9	25	23.5	1	0	0	987.56	674	682
Protein KRI1 homolog	KRI1	KRI1_HUMAN	82.6	100.0%	5	5	6	0.01%	10.0%	LQETSSQSYVEEQK	99.7%	95.6	25	91.8	1	0	0	1655.78	145	158
Protein lin-28 homolog B	LIN28B	LN28B_HUMAN	27.1	100.0%	5	5	12	0.01%	27.2%	EGSPLDIPVDVFVHQSK	99.4%	37.8	25	37.7	2	0	0	1866.96	52	68
Protein lin-28 homolog B	LIN28B	LN28B_HUMAN	27.1	100.0%	5	5	12	0.01%	27.2%	GGGEEPGKLPEPAEEESQVLR	96.8%	24.3	25	24.3	0	1	0	2208.08	9	29
Protein lin-28 homolog B	LIN28B	LN28B_HUMAN	27.1	100.0%	5	5	12	0.01%	27.2%	LFMEGFR	99.3%	37.7	25	24.2	1	0	0	899.44	69	75
Protein lin-28 homolog B	LIN28B	LN28B_HUMAN	27.1	100.0%	5	5	12	0.01%	27.2%	MGFGFISMINR	99.7%	56.7	25	56.7	4	0	0	1272.62	41	51
Protein lin-28 homolog B	LIN28B	LN28B_HUMAN	27.1	100.0%	5	5	12	0.01%	27.2%	NVAQPPASSQGR	99.7%	44.7	25	44.7	4	0	0	1211.61	168	179
Protein LYRIC	MTDH	LYRIC_HUMAN	63.8	100.0%	3	3	5	0.00%	6.0%	LSSQISAGEEK	99.7%	54.1	25	29.8	2	0	0	1148.58	293	303
Protein LYRIC	MTDH	LYRIC_HUMAN	63.8	100.0%	3	3	5	0.00%	6.0%	TISTSDPAEVLVK	99.7%	66.2	25	54.3	2	0	0	1359.74	492	504
Protein LYRIC	MTDH	LYRIC_HUMAN	63.8	100.0%	3	3	5	0.00%	6.0%	TVEVAEGEAVR	99.7%	73.5	25	66.6	1	0	0	1159.60	132	142
Protein mago nashi homolog 2	MAGOHB	MGN2_HUMAN	17.3	100.0%	4	5	7	0.01%	23.6%	IGSLIDVNQSK	99.7%	77.2	25	61.7	2	0	0	1173.65	106	116
Protein mago nashi homolog 2	MAGOHB	MGN2_HUMAN	17.3	100.0%	4	5	7	0.01%	23.6%	IGSLIDVNQSKDPEGLR	99.0%	35.6	25	35.6	1	1	0	1840.98	106	122
Protein mago nashi homolog 2	MAGOHB	MGN2_HUMAN	17.3	100.0%	4	5	7	0.01%	23.6%	SVMEELKR	97.5%	31.5	25	23.4	1	0	0	991.52	57	64
Protein mago nashi homolog 2	MAGOHB	MGN2_HUMAN	17.3	100.0%	4	5	7	0.01%	23.6%	VFYYLVQDLK	99.7%	61.7	25	50.5	2	0	0	1287.70	123	132
Protein NipSnap homolog 1	NIPSNAP1	NIPS1_HUMAN	33.3	100.0%	5	6	9	0.01%	16.5%	DAHSTLLSK	98.7%	34.3	25	27.9	1	0	0	971.52	57	65
Protein NipSnap homolog 1	NIPSNAP1	NIPS1_HUMAN	33.3	100.0%	5	6	9	0.01%	16.5%	FSGGYPALMDCMNK	99.7%	51.3	25	51.3	1	0	0	1590.68	128	141
Protein NipSnap homolog 1	NIPSNAP1	NIPS1_HUMAN	33.3	100.0%	5	6	9	0.01%	16.5%	GWDENVYYTVPLVR	99.7%	60.7	25	54.5	2	0	0	1710.85	255	268
Protein NipSnap homolog 1	NIPSNAP1	NIPS1_HUMAN	33.3	100.0%	5	6	9	0.01%	16.5%	KDAHSTLLSK	99.7%	49.8	25	37.3	2	0	0	1099.61	56	65
Protein NipSnap homolog 1	NIPSNAP1	NIPS1_HUMAN	33.3	100.0%	5	6	9	0.01%	16.5%	MGPNIYELR	99.7%	52.8	25	44.5	3	0	0	1108.55	180	188
Protein NipSnap homolog 2	GBAS	NIPS2_HUMAN	33.7	100.0%	4	4	6	0.01%	14.0%	DAHSNLLAK	98.0%	32.4	25	27.8	1	0	0	968.52	59	67
Protein NipSnap homolog 2	GBAS	NIPS2_HUMAN	33.7	100.0%	4	4	6	0.01%	14.0%	ICQEVLPK	99.7%	43.5	25	24.5	2	0	0	986.53	92	99
Protein NipSnap homolog 2	GBAS	NIPS2_HUMAN	33.7	100.0%	4	4	6	0.01%	14.0%	SGPNIYELR	99.7%	66.2	25	59	2	0	0	1048.54	182	190
Protein NipSnap homolog 2	GBAS	NIPS2_HUMAN	33.7	100.0%	4	4	6	0.01%	14.0%	YEGGYPALTEVMNK	99.7%	52.7	25	52.7	1	0	0	1571.74	130	143
Protein Njmu-R1	C17orf75	NJMU_HUMAN	44.6	99.8%	2	2	3	0.00%	4.8%	GGNPFLFR	99.7%	43.3	25	19.8	2	0	0	907.48	309	316
Protein Njmu-R1	C17orf75	NJMU_HUMAN	44.6	99.8%	2	2	3	0.00%	4.8%	NVIAVLEEFMK	99.7%	56	25	49.8	1	0	0	1292.69	379	389
Protein O-linked-mannose beta-1,4-N-acetylglucosaminyltransferase 2	POMGNT2	PMGT2_HUMAN	66.6	99.8%	2	2	2	0.00%	4.5%	CQASVHGASEAR	99.7%	44.7	25	37.8	1	0	0	1272.57	490	501
Protein O-linked-mannose beta-1,4-N-acetylglucosaminyltransferase 2	POMGNT2	PMGT2_HUMAN	66.6	99.8%	2	2	2	0.00%	4.5%	ILLGPFADVLVCNT	99.1%	36.3	25	36.3	1	0	0	1531.82	567	580
Protein PBDC1	PBDC1	PBDC1_HUMAN	26.1	99.8%	2	2	2	0.00%	10.7%	FNGIVEDFNYGTLLR	99.7%	61	25	50	1	0	0	1757.89	108	122
Protein PBDC1	PBDC1	PBDC1_HUMAN	26.1	99.8%	2	2	2	0.00%	10.7%	IQFFAIEIAR	97.7%	31.8	25	26.5	1	0	0	1207.68	140	149
Protein pelota homolog	PELO	PELO_HUMAN	43.4	100.0%	5	6	9	0.01%	12.2%	FYEQVVQAIQR	99.7%	59	25	49.5	2	0	0	1380.73	185	195
Protein pelota homolog	PELO	PELO_HUMAN	43.4	100.0%	5	6	9	0.01%	12.2%	GTNIQENEYVK	99.7%	49.1	25	41	1	0	0	1294.63	85	95
Protein pelota homolog	PELO	PELO_HUMAN	43.4	100.0%	5	6	9	0.01%	12.2%	KQWDSVVLER	99.7%	53.1	25	48	1	0	0	1259.67	115	124
Protein pelota homolog	PELO	PELO_HUMAN	43.4	100.0%	5	6	9	0.01%	12.2%	KVQTESSTGSVGSNR	99.7%	83.3	25	78.6	2	2	0	1536.76	46	60
Protein pelota homolog	PELO	PELO_HUMAN	43.4	100.0%	5	6	9	0.01%	12.2%	VQTESSTGSVGSNR	99.7%	72	25	67.4	1	0	0	1408.67	47	60
Protein phosphatase 1F	PPM1F	PPM1F_HUMAN	49.8	99.8%	2	2	3	0.00%	5.5%	QPELPTDPEGALR	98.5%	33.8	25	25.4	1	0	0	1422.72	220	232
Protein phosphatase 1F	PPM1F	PPM1F_HUMAN	49.8	99.8%	2	2	3	0.00%	5.5%	YAAVHVHTNAAR	97.9%	25.9	25	24.5	0	2	0	1309.68	208	219
Protein PRRC2A	PRRC2A	PRC2A_HUMAN	228.9	100.0%	5	6	8	0.01%	3.4%	GGGTGGPNHPPAPR	98.8%	34.7	25	30.8	1	2	0	1271.62	1067	1080
Protein PRRC2A	PRRC2A	PRC2A_HUMAN	228.9	100.0%	5	6	8	0.01%	3.4%	GVGSGGQGPPPPR	99.7%	88.7	25	80.6	2	0	0	1162.60	905	917
Protein PRRC2A	PRRC2A	PRC2A_HUMAN	228.9	100.0%	5	6	8	0.01%	3.4%	LIPGPLSPVAR	97.4%	31.3	25	27.9	1	0	0	1119.69	1213	1223

Protein PRRC2A	PRRC2A	PRC2A_HUMAN	228.9	100.0%	5	6	8	0.01%	3.4%	LKAEPAAPPAAPSTPAPPPAVPK	99.3%	30.1	25	30.1	0	1	0	2175.22	504	526
Protein PRRC2A	PRRC2A	PRC2A_HUMAN	228.9	100.0%	5	6	8	0.01%	3.4%	QSSSEISLAVER	99.7%	44.5	25	41.7	1	0	0	1305.66	455	466
Protein PRRC2C	PRRC2C	PRC2C_HUMAN	316.9	99.8%	2	2	3	0.00%	0.7%	DHAISLSEPR	99.7%	52	25	47	1	0	0	1124.57	795	804
Protein PRRC2C	PRRC2C	PRC2C_HUMAN	316.9	99.8%	2	2	3	0.00%	0.7%	NADLNAQTVVK	99.5%	39.4	25	30.9	2	0	0	1172.63	1516	1526
Protein QIL1	QIL1	QIL1_HUMAN	13.1	99.9%	2	2	4	0.00%	9.3%	EGWEYVK	95.4%	28.9	25	21.6	2	0	0	910.43	108	114
Protein QIL1	QIL1	QIL1_HUMAN	13.1	99.9%	2	2	4	0.00%	9.3%	EYSKEGWEYVK	99.7%	45.9	25	38.6	2	0	0	1417.66	104	114
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	21	21	39	0.04%	13.0%	ACILCVHPR	99.7%	45	25	26.1	2	0	0	1125.57	329	337
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	21	21	39	0.04%	13.0%	AIFENTLSTYPK	99.7%	58.7	25	48.6	2	0	0	1383.72	1782	1793
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	21	21	39	0.04%	13.0%	AINIGQLVDVK	99.7%	73.8	25	57.3	2	0	0	1169.69	632	642
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	21	21	39	0.04%	13.0%	FAQLEFQLGDAER	99.7%	94.1	25	84.2	2	0	0	1523.75	1767	1779
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	21	21	39	0.04%	13.0%	FYNNVQGLVPK	99.5%	39.3	25	34.6	2	0	0	1278.68	561	571
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	21	21	39	0.04%	13.0%	GQEEVEMPSKEK	99.7%	56.6	25	47.8	2	0	0	1406.65	1446	1457
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	21	21	39	0.04%	13.0%	IPLLLTSLSFK	99.7%	59.3	25	59.3	4	0	0	1231.77	1178	1188
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	21	21	39	0.04%	13.0%	KPALVSTVEGGQDPK	99.7%	57.9	25	56.5	1	0	0	1525.82	707	721
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	21	21	39	0.04%	13.0%	LGPSVVGLAR	99.7%	74.7	25	68.3	2	0	0	968.59	1343	1352
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	21	21	39	0.04%	13.0%	LKDGVLAYAR	99.7%	56.4	25	49.6	2	0	0	1105.64	386	395
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	21	21	39	0.04%	13.0%	QYQAGQTVTCFLK	95.1%	28.6	25	28.6	1	0	0	1543.76	1145	1157
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	21	21	39	0.04%	13.0%	TSIIEAQYLR	99.7%	67	25	58.6	2	0	0	1193.65	437	446
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	21	21	39	0.04%	13.0%	TTEPGVTGLLLAVEGPAAK	99.7%	88.3	25	88.3	2	0	0	1824.01	982	1000
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	21	21	39	0.04%	13.0%	VGQYLNCIVEK	99.3%	37.1	25	32.6	2	0	0	1322.68	235	245
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	21	21	39	0.04%	13.0%	VKDYGCIVK	95.7%	29.1	25	15	1	0	0	1081.57	552	560
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	21	21	39	0.04%	13.0%	VLCLSQSEGR	99.1%	36	25	30.5	2	0	0	1148.57	692	701
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	21	21	39	0.04%	13.0%	VLLCDPEAK	97.8%	31.9	25	30.2	2	0	0	1044.54	507	515
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	21	21	39	0.04%	13.0%	VTPNEGLTVSFPFGK	98.3%	33.1	25	26.9	1	0	0	1592.83	1240	1254
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	21	21	39	0.04%	13.0%	VVVLNCEPSKER	99.7%	56.7	25	56	1	0	0	1429.75	594	605
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	21	21	39	0.04%	13.0%	WLEVEIAPDIR	99.7%	41.8	25	20.9	2	0	0	1340.72	1165	1175
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	21	21	39	0.04%	13.0%	YHDIEPGAVVK	99.7%	60.7	25	54.5	2	0	0	1227.64	447	457
Protein S100-A8	S100A8	S10A8_HUMAN	10.8	99.8%	2	2	8	0.01%	23.7%	ALNSIIDVYHK	98.9%	35.4	25	31.5	2	0	0	1272.69	8	18
Protein S100-A8	S100A8	S10A8_HUMAN	10.8	99.8%	2	2	8	0.01%	23.7%	LLETECPQYIR	99.7%	52.4	25	45.8	6	0	0	1421.71	37	47
Protein SAAL1	SAAL1	SAAL1_HUMAN	53.6	100.0%	3	4	6	0.01%	7.6%	KPENSAESNTEETKR	99.7%	49.3	25	49.3	0	2	0	1719.81	369	383
Protein SAAL1	SAAL1	SAAL1_HUMAN	53.6	100.0%	3	4	6	0.01%	7.6%	VDLPLIDSLIR	99.7%	51.2	25	48.9	1	0	0	1253.75	348	358
Protein SAAL1	SAAL1	SAAL1_HUMAN	53.6	100.0%	3	4	6	0.01%	7.6%	VLQNMEQCQK	99.7%	42.5	25	39.1	3	0	0	1277.60	359	368
Protein SCO2 homolog, mitochondrial	SCO2	SCO2_HUMAN	29.8	99.8%	2	2	2	0.00%	7.5%	QVAQASHSYR	99.7%	54.5	25	48.8	1	0	0	1146.56	197	206
Protein SCO2 homolog, mitochondrial	SCO2	SCO2_HUMAN	29.8	99.8%	2	2	2	0.00%	7.5%	SAEQISDSVR	99.7%	48.4	25	24.4	1	0	0	1091.53	246	255
Protein SET	SET	SET_HUMAN	33.5	100.0%	4	4	7	0.01%	16.6%	EFHLNESGDPSSK	99.7%	68.3	25	64.1	2	0	0	1446.65	155	167
Protein SET	SET	SET_HUMAN	33.5	100.0%	4	4	7	0.01%	16.6%	IDFYFDENPYFENK	99.7%	64	25	64	2	0	0	1840.81	137	150
Protein SET	SET	SET_HUMAN	33.5	100.0%	4	4	7	0.01%	16.6%	LNEQASEEILK	99.7%	52.9	25	43.1	1	0	0	1273.66	58	68
Protein SET	SET	SET_HUMAN	33.5	100.0%	4	4	7	0.01%	16.6%	VEVTEFEDIK	99.7%	80.1	25	73.3	2	0	0	1208.60	123	132
Protein SON	SON	SON_HUMAN	263.8	100.0%	3	3	5	0.00%	1.8%	AGIEGPLLASDVGR	99.7%	73.4	25	69.2	1	0	0	1354.73	1750	1763
Protein SON	SON	SON_HUMAN	263.8	100.0%	3	3	5	0.00%	1.8%	ILDSFAAAPVPTTTLVLK	99.7%	43.2	25	43.2	2	0	0	1857.07	241	258
Protein SON	SON	SON_HUMAN	263.8	100.0%	3	3	5	0.00%	1.8%	SVESTSPEPSK	99.4%	37.8	25	28.8	2	0	0	1147.55	278	288
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	5	6	11	0.01%	9.0%	DVLLDVAYAYGK	99.7%	89.1	25	85.5	2	0	0	1326.69	293	304
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	5	6	11	0.01%	9.0%	LLGSLYALGIPK	99.7%	76.1	25	76.1	2	0	0	1244.76	149	160
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	5	6	11	0.01%	9.0%	LSFHQTQVSQR	99.7%	53.6	25	40.2	2	0	0	1330.69	305	315
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	5	6	11	0.01%	9.0%	LSHLLSEKPEDK	99.7%	54.5	25	43.4	1	0	0	1395.75	107	118
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	5	6	11	0.01%	9.0%	VLVMLAAQSR	99.7%	75.9	25	68	4	0	0	1087.63	261	270
Protein THEM6	THEM6	THEM6_HUMAN	23.9	99.8%	2	2	2	0.00%	8.2%	DGFVCALLR	98.7%	34.3	25	2.84	1	0	0	1050.54	142	150
Protein THEM6	THEM6	THEM6_HUMAN	23.9	99.8%	2	2	2	0.00%	8.2%	LLEPFEVR	98.5%	33.8	25	16.2	1	0	0	1002.56	113	120
Protein transport protein Sec23A	SEC23A	SC23A_HUMAN	86.2	99.8%	2	2	3	0.00%	3.3%	MVVPVAALFTPLK	99.7%	47.2	25	47.2	1	0	0	1385.82	34	46
Protein transport protein Sec23A	SEC23A	SC23A_HUMAN	86.2	99.8%	2	2	3	0.00%	3.3%	YIDTEHGGSQAR	99.7%	47.2	25	39	2	0	0	1333.61	705	716
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	7	22	0.02%	10.9%	AFSPTTVNTGR	99.7%	69.5	25	52	4	0	0	1150.59	195	205

Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	7	22	0.02%	10.9%	ETSMVHELNR	99.7%	57.3	25	48.5	5	0	0	1215.58	406	415
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	7	22	0.02%	10.9%	GQYNTYPIK	99.7%	53.1	25	43.7	4	0	0	1083.55	274	282
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	7	22	0.02%	10.9%	IIEVGDTPK	99.7%	49.4	25	38.5	4	0	0	971.54	99	107
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	7	22	0.02%	10.9%	IIEVGDTPKDR	99.7%	57.3	25	40.2	2	0	0	1242.67	99	109
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	7	22	0.02%	10.9%	TWIEVSGSSAK	99.7%	41.5	25	33.6	3	0	0	1164.59	378	388
Protein tyrosine phosphatase type IVA 1	PTP4A1	TP4A1_HUMAN	19.8	99.8%	2	2	3	0.00%	15.6%	FLITHNPTNATLNK	99.7%	62.8	25	60.2	1	0	0	1583.85	19	32
Protein tyrosine phosphatase type IVA 1	PTP4A1	TP4A1_HUMAN	19.8	99.8%	2	2	3	0.00%	15.6%	VCEATYDTTLVEK	99.7%	76.4	25	72	2	0	0	1528.72	48	60
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	12	12	18	0.02%	15.8%	ALIPLALEGTDVGQTK	99.7%	93.4	25	93.4	2	0	0	1625.91	692	707
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	12	12	18	0.02%	15.8%	DNALTLLIK	98.7%	34.2	25	11.7	1	0	0	1000.60	313	321
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	12	12	18	0.02%	15.8%	EVQDLFEAQGNDR	99.7%	61.3	25	61.3	1	0	0	1520.70	807	819
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	12	12	18	0.02%	15.8%	LDQAVLDLQR	99.7%	59.1	25	41.8	2	0	0	1170.65	108	117
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	12	12	18	0.02%	15.8%	LGSAGGTDFSMK	99.3%	37.6	25	27.6	1	0	0	1170.55	505	516
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	12	12	18	0.02%	15.8%	LLDMGETDLMLAALR	99.7%	60.6	25	57.2	1	0	0	1661.86	203	217
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	12	12	18	0.02%	15.8%	LLVLYSGEDDELLQR	99.7%	71.6	25	66.9	2	0	0	1762.92	822	836
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	12	12	18	0.02%	15.8%	LTITSNPEMTFPGER	99.7%	43	25	43	1	0	0	1708.82	715	729
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	12	12	18	0.02%	15.8%	TVATLSILGTR	99.7%	71.3	25	69.9	2	0	0	1131.67	230	240
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	12	12	18	0.02%	15.8%	VEQMFQILLDPEEK	99.7%	59.9	25	42.7	2	0	0	1718.87	153	166
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	12	12	18	0.02%	15.8%	VFLALVEEVEDR	99.7%	53.2	25	49.7	2	0	0	1418.75	670	681
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	12	12	18	0.02%	15.8%	VFQEALR	98.4%	33.3	25	16	1	0	0	862.48	127	133
Protein virilizer homolog	KIAA1429	VIR_HUMAN	202.0	100.0%	2	2	3	0.00%	1.4%	DTGELASSFLEFMR	99.6%	40.5	25	40.5	1	0	0	1602.75	1389	1402
Protein virilizer homolog	KIAA1429	VIR_HUMAN	202.0	100.0%	2	2	3	0.00%	1.4%	LLELILLDQTVR	99.7%	50.7	25	50.7	2	0	0	1425.87	534	545
Protein YIPF5	YIPF5	YIPF5_HUMAN	28.0	99.8%	2	2	4	0.00%	8.2%	QYAGYDYSQQGR	99.7%	65.5	25	57.2	2	0	0	1435.62	38	49
Protein YIPF5	YIPF5	YIPF5_HUMAN	28.0	99.8%	2	2	4	0.00%	8.2%	TLTVLHPLK	99.7%	48.7	25	48.1	2	0	0	1021.64	107	115
Pumilio homolog 1	PUM1	PUM1_HUMAN	126.5	100.0%	4	4	6	0.01%	4.3%	FFEFGSLEQK	99.7%	47.4	25	33.2	2	0	0	1231.60	905	914
Pumilio homolog 1	PUM1	PUM1_HUMAN	126.5	100.0%	4	4	6	0.01%	4.3%	GNVLVLSQHK	99.7%	47.6	25	39.4	1	0	0	1094.63	1067	1076
Pumilio homolog 1	PUM1	PUM1_HUMAN	126.5	100.0%	4	4	6	0.01%	4.3%	SASSASSLFSPSSTLFSSSR	99.7%	57.6	25	53.4	2	0	0	1992.95	797	816
Pumilio homolog 1	PUM1	PUM1_HUMAN	126.5	100.0%	4	4	6	0.01%	4.3%	YISAAPGAEAK	96.7%	30.2	25	24.2	1	0	0	1077.56	784	794
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	AFFESHPAPSAER	99.7%	46.5	25	46.4	2	2	0	1445.68	870	882
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	AGIISTVEVLK	99.7%	67.8	25	53.7	4	0	0	1129.68	628	638
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	ATFDISLVVPK	99.7%	72.8	25	67.4	2	0	0	1189.68	198	208
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	DAESIHQYLLQR	99.7%	64.3	25	59	2	0	0	1472.75	901	912
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	DYFNVPYPLPK	99.7%	55.5	25	52.9	5	0	0	1352.69	294	304
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	ETALLIDPK	99.7%	50.5	25	36.5	2	0	0	999.57	328	336
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	FALEVAAK	99.7%	41.4	25	25.7	2	0	0	848.49	280	287
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	FIKDNWEELYNR	99.7%	56.2	25	47.4	1	0	0	1626.79	830	841
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	GMNMYLTK	99.2%	36.7	25	30.1	2	0	0	957.45	460	467
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	HGDGTTLDIMLK	99.7%	50.9	25	43.2	2	0	0	1316.65	754	765
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	IDFVGELNDK	99.7%	64.6	25	47.7	2	0	0	1149.58	146	155
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	KPYPDDENLVEVK	99.7%	78.1	25	67.1	2	1	0	1545.78	222	234
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	LEAAAQVR	99.5%	38.6	25	23.9	2	0	0	857.48	80	87
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	LGLQNDLFSLAR	99.7%	92.6	25	74.1	4	0	0	1346.74	616	627
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	LNLGTVGFYR	99.7%	63.3	25	56	6	0	0	1139.62	581	590
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	LSVEGFAVDK	98.9%	35.1	25	7.57	1	0	0	1064.56	854	863
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	NVKPDQWVK	96.2%	29.7	25	16.1	1	0	0	1113.61	572	580
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	QILSADLR	99.7%	51.5	25	38.9	2	0	0	915.53	737	744
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	SKYTTPSGEVR	95.9%	29.4	25	23.8	1	0	0	1224.62	162	172
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	SPVYLTVLK	99.7%	51.4	25	47.3	3	0	0	1019.61	745	753
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	TIQQCCENILLNAAWLK	99.7%	56.6	25	49.8	2	0	0	2075.04	883	899
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	TQYSSAMLESLLPGIR	99.7%	67.6	25	57.9	4	0	0	1781.91	591	606
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	VALSNMNVIDR	99.7%	69.1	25	57.1	4	0	0	1231.65	211	221
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	VLGATLLPDLIQK	99.7%	90.8	25	90.8	4	0	0	1380.85	782	794

Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	VTLSFPSTLQTGTGTLK	99.7%	77.4	25	77.4	2	0	0	1750.96	129	145
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	YAAVTQFEATDAR	99.7%	105	25	105	4	0	0	1442.69	173	185
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	YQGGFLISR	99.7%	59.7	25	53	2	0	0	1040.55	842	850
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	28	33	74	0.07%	33.0%	YTTPSGEVR	99.6%	39.8	25	31.8	1	0	0	1009.49	164	172
Putative ataxin-7-like protein 3B	ATXN7L3B	A7L3B_HUMAN	10.8	99.8%	2	2	3	0.00%	30.9%	DFGIQPVEDK	99.7%	43.8	25	38.4	2	0	0	1147.56	58	67
Putative ataxin-7-like protein 3B	ATXN7L3B	A7L3B_HUMAN	10.8	99.8%	2	2	3	0.00%	30.9%	LPLCSLPGEPGNGPDQQLQR	99.7%	43.2	25	42.3	1	0	0	2176.08	72	91
Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial	CLPP	CLPP_HUMAN	30.2	99.8%	2	3	6	0.01%	7.9%	AYDIYSR	99.7%	42.3	25	24.4	2	0	0	887.43	72	78
Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial	CLPP	CLPP_HUMAN	30.2	99.8%	2	3	6	0.01%	7.9%	GQATDIAIQAEEIMK	99.7%	74.4	25	72.5	4	0	0	1617.82	186	200
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	AIFQQPPVGVR	99.7%	51.1	25	46.2	4	0	0	1211.69	715	725
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	AIVLAAIFR	99.7%	74.6	25	74.6	4	0	0	973.62	886	894
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	ALLSHDSGSDHLAFVR	99.7%	36.2	25	36.2	0	1	0	1724.87	926	941
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	ALTQFPLPK	98.6%	34.1	25	24.1	1	0	0	1014.60	238	246
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	ATISLSDSDLLR	99.7%	73.7	25	65.3	2	0	0	1290.69	1116	1127
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	AVAGWEEVLR	99.7%	65.4	25	51.4	2	0	0	1129.60	942	951
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	CNVIITQPR	99.7%	50	25	29.1	2	0	0	1100.59	484	492
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	DPFSSSLQNR	99.7%	67.9	25	56.6	4	0	0	1150.55	909	918
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	DSGPLSDPITGKPYVPLLEAEEVR	99.7%	38.3	25	38.3	0	2	0	2582.34	389	412
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	DVNTDFLLILLK	99.7%	86.6	25	64.4	3	0	0	1403.81	565	576
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	EHYLEDILAK	97.8%	32	25	24.2	1	0	0	1230.64	620	629
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	ENYLEENLLYAPSLR	99.7%	69.9	25	65.3	4	0	0	1823.92	959	973
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	EYLTTLGQR	99.7%	51.6	25	45.5	2	0	0	1080.57	865	873
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	GEPGGILCFLPGWQEIK	99.7%	42.3	25	34.5	1	0	0	1900.96	666	682
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	GGALLFCTVGILLR	99.7%	63.8	25	56.2	3	0	0	1489.86	529	542
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	GSSFEMTDDDSAIR	99.7%	69.8	25	66.8	2	0	0	1530.64	224	237
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	GVLMAGLYPNLIQVR	99.7%	60.7	25	60.7	5	0	0	1659.93	1017	1031
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	IPQLLLER	99.7%	62.3	25	45.7	4	0	0	981.61	467	474
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	ISAVSVAQR	99.7%	72.9	25	30.2	2	0	0	930.54	494	502
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	LQEALGMHESK	99.7%	69.8	25	61	4	0	0	1242.61	688	698
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	LQSDDILPLGK	99.7%	47.3	25	36.8	2	0	0	1198.67	378	388
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	LSQSLLELWR	99.7%	84.4	25	79.1	2	0	0	1244.70	413	422
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	LVLMSATGDNER	99.7%	83.6	25	74.8	5	0	0	1305.65	587	598
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	MVPFQVPEILR	98.8%	34.9	25	26.5	2	0	0	1328.74	803	813
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	NLLNSVIGR	99.7%	64.5	25	52.9	2	0	0	985.58	55	63
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	NLMQFHTVGTK	99.7%	42.4	25	36.4	4	0	0	1291.65	264	274
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	NVGFQVR	99.0%	35.8	25	25	2	0	0	819.45	514	520
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	QAAAAACQLFK	99.7%	68.1	25	65.4	2	0	0	1178.60	112	122
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	RISAVSVAQR	99.7%	48.8	25	18.9	2	0	0	1086.64	493	502
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	RPCTIQVPEPILR	99.5%	32.2	25	32.2	0	2	0	1578.88	344	356
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	SGNILLHK	99.4%	37.8	25	22.8	2	0	0	881.52	1052	1059
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	SVEVEGYGSK	99.7%	64.2	25	55.4	2	0	0	1054.51	96	105
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	TPLENLVLQAK	99.7%	78.3	25	78.3	4	0	0	1225.72	814	824
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	VIQIATSSSTAK	99.7%	84.3	25	75.2	3	0	0	1205.67	252	263
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	VSCLETVWVSR	99.7%	77.4	25	67.9	2	0	0	1335.67	763	773
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	VSHELGPSLR	96.5%	30	25	23.1	1	0	0	1094.60	503	512
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	37	41	93	0.09%	34.4%	WLTYFMAVK	99.7%	42.6	25	27.5	1	0	0	1158.60	1073	1081
Putative ATP-dependent RNA helicase DHX57	DHX57	DHX57_HUMAN	155.6	100.0%	6	6	7	0.01%	4.9%	CLDPALTIAASLAFK	96.8%	30.4	25	30.4	1	0	0	1590.86	1080	1094
Putative ATP-dependent RNA helicase DHX57	DHX57	DHX57_HUMAN	155.6	100.0%	6	6	7	0.01%	4.9%	ETILNLLR	98.0%	32.5	25	10.9	1	0	0	971.59	551	558
Putative ATP-dependent RNA helicase DHX57	DHX57	DHX57_HUMAN	155.6	100.0%	6	6	7	0.01%	4.9%	LLYCTTGVLLR	99.7%	48.5	25	39	1	0	0	1308.73	641	651
Putative ATP-dependent RNA helicase DHX57	DHX57	DHX57_HUMAN	155.6	100.0%	6	6	7	0.01%	4.9%	QFTELLSDIGFAR	99.7%	41.5	25	37.3	1	0	0	1496.77	1165	1177
Putative ATP-dependent RNA helicase DHX57	DHX57	DHX57_HUMAN	155.6	100.0%	6	6	7	0.01%	4.9%	TEESDFLLLVLK	99.7%	60.3	25	53.3	2	0	0	1406.78	674	685
Putative ATP-dependent RNA helicase DHX57	DHX57	DHX57_HUMAN	155.6	100.0%	6	6	7	0.01%	4.9%	VPLEQLCLR	99.4%	38.4	25	33	1	0	0	1127.62	997	1005

Putative deoxyribose-phosphate aldolase	DERA	DEOC_HUMAN	35.2	100.0%	7	7	13	0.01%	29.6%	AVTFIDLTTLSGDDTSSNIQR	99.7%	70.3	25	70.3	1	0	0	2254.12	50	70
Putative deoxyribose-phosphate aldolase	DERA	DEOC_HUMAN	35.2	100.0%	7	7	13	0.01%	29.6%	DSLAWLSLVK	99.7%	84.5	25	75.9	2	0	0	1131.64	264	273
Putative deoxyribose-phosphate aldolase	DERA	DEOC_HUMAN	35.2	100.0%	7	7	13	0.01%	29.6%	ETVNATFPVAIVMLR	99.7%	60.5	25	55.6	2	0	0	1660.91	224	238
Putative deoxyribose-phosphate aldolase	DERA	DEOC_HUMAN	35.2	100.0%	7	7	13	0.01%	29.6%	EWQAAWLLK	99.7%	41.5	25	30	2	0	0	1144.62	41	49
Putative deoxyribose-phosphate aldolase	DERA	DEOC_HUMAN	35.2	100.0%	7	7	13	0.01%	29.6%	GTELDLSWISK	99.7%	56.7	25	44.1	2	0	0	1248.65	7	17
Putative deoxyribose-phosphate aldolase	DERA	DEOC_HUMAN	35.2	100.0%	7	7	13	0.01%	29.6%	IGASTLLSDIER	99.7%	87.4	25	76.3	2	0	0	1274.70	288	299
Putative deoxyribose-phosphate aldolase	DERA	DEOC_HUMAN	35.2	100.0%	7	7	13	0.01%	29.6%	TILATGELGTLTNVYK	99.7%	107	25	107	2	0	0	1693.94	189	204
Putative GTP-binding protein 6	GTPBP6	GTPB6_HUMAN	56.9	99.9%	2	2	2	0.00%	4.3%	ALTGDAAIQPR	99.6%	40.7	25	30	1	0	0	1112.61	313	323
Putative GTP-binding protein 6	GTPBP6	GTPB6_HUMAN	56.9	99.9%	2	2	2	0.00%	4.3%	DVSHPEAELQK	99.0%	35.6	25	34.6	1	0	0	1252.62	383	393
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	28.8%	AHILACAPSNSGADLLCQR	99.7%	34.5	25	29.9	0	1	0	2053.99	548	566
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	28.8%	DGQLLIR	98.8%	34.7	25	5.65	2	0	0	814.48	136	142
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	28.8%	EAGQCFESFLVVR	99.7%	75	25	75	4	0	0	1541.74	12	24
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	28.8%	EGNSPSFFNPEEAATVTSYLK	99.7%	106	25	106	4	0	0	2288.07	788	808
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	28.8%	ETGDPGGQLVLAGDPR	99.7%	114	25	113	4	0	0	1581.79	667	682
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	28.8%	GLDDIKDLK	97.7%	31.9	25	18.2	1	0	0	1016.56	853	861
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	28.8%	GPDGYDPQFITK	99.7%	62.6	25	54.4	2	0	0	1337.64	716	727
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	28.8%	HGLGYSLLER	99.7%	41.4	25	35.6	2	0	0	1144.61	696	705
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	28.8%	HGVDVEVQGPHEAR	99.7%	69.9	25	69.9	0	5	0	1529.75	122	135
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	28.8%	IANLAYVTK	99.7%	43	25	35.8	2	0	0	992.58	63	71
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	28.8%	ISFGTPAPGFSSMLYGMK	99.7%	43.3	25	32.8	2	0	0	1890.91	45	62
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	28.8%	ITGNPVVTNR	99.7%	58.2	25	52.4	1	0	0	1070.60	261	270
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	28.8%	KGEYVFPAK	99.7%	44.2	25	32.6	2	0	0	1038.56	602	610
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	28.8%	KGPDGYDPQFITK	98.9%	35.1	25	28.9	1	0	0	1465.73	715	727
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	28.8%	LDLQQGQNLLQGLSK	99.7%	78.4	25	66.1	5	0	0	1654.91	953	967
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	28.8%	LLTLEVPGVTESRPSVLR	96.6%	24.1	25	24.1	0	1	0	1966.13	376	393
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	28.8%	LLTYNSLYK	96.7%	30.3	25	23.3	2	0	0	1114.61	706	714
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	28.8%	RFNVAVTR	99.7%	42.2	25	35.9	3	0	0	962.55	904	911
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	28.8%	SLESNPEQLQAMR	99.7%	84.7	25	79.8	7	0	0	1502.73	496	508
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	28.8%	SVGVISPYR	99.7%	43.3	25	22.1	4	0	0	977.54	826	834
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	28.8%	SVGVISPYRK	98.2%	32.8	25	22.1	2	0	0	1105.64	826	835
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	28.8%	SVILISTVR	99.7%	64.6	25	54.8	4	0	0	987.62	874	882
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	28.8%	TVTLVEAIK	99.7%	47.5	25	40.9	4	0	0	973.59	531	539
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	28.8%	VGSVEEFQGQER	99.7%	72.8	25	64.6	3	0	0	1364.64	862	873
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	28.8%	VLITTLITAGR	99.7%	91.3	25	85.7	5	0	0	1157.73	618	628
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	28.8%	VNFTFNR	98.7%	34.5	25	26.9	2	0	0	897.46	445	451
Putative mitochondrial import inner membrane translocase subunit Tim23B	TIMM23B	TI23B_HUMAN	21.9	100.0%	3	4	7	0.01%	18.3%	GAEDDLNTVAAGTMTGMLYK	99.7%	43.1	25	43.1	1	0	0	2089.94	150	169
Putative mitochondrial import inner membrane translocase subunit Tim23B	TIMM23B	TI23B_HUMAN	21.9	100.0%	3	4	7	0.01%	18.3%	NVQILNMVTR	99.7%	70.9	25	37.3	4	0	0	1187.66	113	122
Putative mitochondrial import inner membrane translocase subunit Tim23B	TIMM23B	TI23B_HUMAN	21.9	100.0%	3	4	7	0.01%	18.3%	YLVQDTDEFILPTGANK	99.7%	69.1	25	65.2	2	0	0	1923.97	52	68
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	5	6	11	0.01%	13.0%	ALDQSDNDMSAVYR	99.7%	81.5	25	81.5	3	0	0	1600.69	536	549
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	5	6	11	0.01%	13.0%	DLVLGPSGVLQGIRPGK	99.7%	65	25	65	2	0	0	1706.00	339	355
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	5	6	11	0.01%	13.0%	FQQAVDAVEEFLR	99.7%	90.8	25	81.6	2	0	0	1551.78	79	91
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	5	6	11	0.01%	13.0%	GLYEDCSSCFQAMGK	99.7%	80.3	25	80.3	2	0	0	1768.70	408	422
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	5	6	11	0.01%	13.0%	TSFFLGEVGNAAK	99.7%	96	25	92.9	2	0	0	1340.68	423	435
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	17	21	48	0.05%	23.1%	ASTNAMLISAGLPPLK	99.7%	51.1	25	51.1	2	0	0	1583.88	63	78
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	17	21	48	0.05%	23.1%	EAMNDPLLER	99.7%	43.6	25	32.7	4	0	0	1187.57	244	253
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	17	21	48	0.05%	23.1%	EVDDLGPEVGDIK	99.7%	64.4	25	56.7	1	0	0	1385.68	372	384
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	17	21	48	0.05%	23.1%	FTDILVR	99.7%	44.3	25	27.2	2	0	0	863.50	146	152
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	17	21	48	0.05%	23.1%	HQSFVLVGETGSGK	99.7%	84.5	25	84.2	2	2	0	1445.74	153	166
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	17	21	48	0.05%	23.1%	HRLDLGEDYPSGK	99.6%	32.7	25	27.4	0	1	0	1486.73	5	17
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	17	21	48	0.05%	23.1%	IIPLYSTLPPQQQQR	99.7%	41.4	25	39.9	2	0	0	1781.99	385	399
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	17	21	48	0.05%	23.1%	RVAAMSVAQR	99.7%	49.4	25	28.6	2	0	0	1088.60	195	204

Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	17	21	48	0.05%	23.1%	SLMSADNVR	99.7%	44	25	27.6	2	0	0	992.48	653	661
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	17	21	48	0.05%	23.1%	SNLGSVVLQLK	99.7%	86.8	25	76.8	6	0	0	1157.69	505	515
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	17	21	48	0.05%	23.1%	TCTDIKPEWLVK	99.5%	39.2	25	38	1	0	0	1489.77	749	760
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	17	21	48	0.05%	23.1%	TEMQDNTYPEILR	99.7%	51.2	25	47	1	0	0	1609.75	492	504
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	17	21	48	0.05%	23.1%	TGHYLTVK	95.4%	28.9	25	18.5	1	0	0	918.50	707	714
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	17	21	48	0.05%	23.1%	TLATDILMGVLK	99.7%	104	25	89.1	10	0	0	1290.73	266	277
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	17	21	48	0.05%	23.1%	VAAMSVAQR	99.7%	70.4	25	13.1	2	0	0	948.49	196	204
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	17	21	48	0.05%	23.1%	YGVIILDEAHER	99.7%	63.3	25	57.9	4	2	0	1414.73	254	265
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	17	21	48	0.05%	23.1%	YMTDGMLLR	99.7%	52.5	25	47.2	1	0	0	1099.53	235	243
Putative ribonuclease	YBEY	YBEY_HUMAN	19.3	99.8%	2	2	3	0.00%	12.0%	AVLDELGRR	95.5%	29	25	24.1	1	0	0	1028.58	143	151
Putative ribonuclease	YBEY	YBEY_HUMAN	19.3	99.8%	2	2	3	0.00%	12.0%	FDLGIICVDNK	99.7%	84.6	25	72.6	2	0	0	1293.65	35	45
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	12	12	30	0.03%	17.9%	DLAQALINR	98.6%	34.1	25	34.1	1	0	0	1013.57	323	331
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	12	12	30	0.03%	17.9%	ELLLSAIDSVNATSK	99.7%	110	25	110	4	0	0	1560.85	493	507
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	12	12	30	0.03%	17.9%	GADSELSTVPSVTK	99.7%	85.1	25	71.1	4	0	0	1390.71	656	669
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	12	12	30	0.03%	17.9%	GISAGAVQTAGK	99.7%	88.4	25	79.3	2	0	0	1059.58	80	91
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	12	12	30	0.03%	17.9%	GVNLDPLGK	98.2%	32.9	25	26.6	1	0	0	912.52	332	340
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	12	12	30	0.03%	17.9%	IQDIVGILR	99.7%	70.1	25	50.4	3	0	0	1026.63	243	251
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	12	12	30	0.03%	17.9%	LGVTNTIISHYDGR	99.7%	43.7	25	42.8	1	0	0	1545.80	432	445
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	12	12	30	0.03%	17.9%	LVPTGLDFGQEGFTR	99.7%	86.8	25	84.2	4	0	0	1636.83	539	553
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	12	12	30	0.03%	17.9%	NTGVILANDANAER	99.7%	76.8	25	75.1	1	0	0	1457.73	408	421
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	12	12	30	0.03%	17.9%	SPEAKPLPGK	99.7%	41	25	34.1	3	0	0	1023.58	67	76
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	12	12	30	0.03%	17.9%	SVVGNLHR	99.3%	37.6	25	27.9	4	0	0	881.50	424	431
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	12	12	30	0.03%	17.9%	TQASSSFQDSSQPAGK	99.7%	101	25	89.6	2	0	0	1625.74	670	685
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	9	11	14	0.01%	12.1%	FGVITEVDIK	99.7%	46.8	25	41	1	0	0	1120.63	397	406
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	9	11	14	0.01%	12.1%	ISHLSGSGSGDER	99.7%	46	25	36.8	2	1	0	1301.61	204	216
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	9	11	14	0.01%	12.1%	LPPPPPPPLPR	99.7%	46.7	25	46.7	1	0	0	1177.71	315	325
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	9	11	14	0.01%	12.1%	LQQLALGR	99.7%	53.2	25	24.7	1	0	0	898.55	307	314
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	9	11	14	0.01%	12.1%	QDGGTAPVASASPK	99.7%	54.5	25	45	2	0	0	1285.64	770	783
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	9	11	14	0.01%	12.1%	SDGSAPSTSTASSK	94.6%	28.3	25	28.3	1	0	0	1282.58	749	762
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	9	11	14	0.01%	12.1%	SSGAASSAPGGGDGAEYK	99.7%	59.3	25	49.3	1	0	0	1568.68	153	170
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	9	11	14	0.01%	12.1%	SSSSSAASDTATSTQRPLR	98.0%	26	25	23.5	1	1	0	1909.92	871	889
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	9	11	14	0.01%	12.1%	VGAGAGAAPFR	99.7%	61.5	25	48	2	0	0	973.52	349	359
Putative RNA-binding protein 3	RBM3	RBM3_HUMAN	17.2	99.8%	2	2	3	0.00%	17.2%	YSGGNYRDNYDN	98.8%	34.8	25	34.8	2	0	0	1437.57	146	157
Putative RNA-binding protein 3	RBM3	RBM3_HUMAN	17.2	99.8%	2	2	3	0.00%	17.2%	YYDSRPGGYGYGYGR	98.1%	26.3	25	24.6	0	1	0	1730.76	117	131
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	9	10	25	0.02%	27.0%	AMLDQLMGTSR	99.7%	66.8	25	59	4	0	0	1254.58	9	19
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	9	10	25	0.02%	27.0%	LADHFGGK	99.6%	39.9	25	29.8	4	0	0	844.43	206	213
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	9	10	25	0.02%	27.0%	LAETQEEISAEVAAK	99.7%	109	25	105	3	0	0	1588.81	108	122
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	9	10	25	0.02%	27.0%	LHLGFIEIR	99.2%	36.7	25	33.6	1	0	0	1097.65	214	222
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	9	10	25	0.02%	27.0%	NSMPASSFQQQK	99.7%	58.2	25	52	3	0	0	1352.63	175	186
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	9	10	25	0.02%	27.0%	SHLLNCCPHDVLSGTR	99.1%	29.2	25	28.9	0	1	0	1865.87	38	53
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	9	10	25	0.02%	27.0%	SSEEREAGEI	97.8%	31.9	25	31.9	1	0	0	1106.50	383	392
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	9	10	25	0.02%	27.0%	VEQLGAEGNVEESQK	99.7%	110	25	106	6	0	0	1616.78	140	154
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	9	10	25	0.02%	27.0%	VHELNEEIGK	99.7%	59.3	25	51.8	2	0	0	1167.60	126	135
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	21	39	0.04%	51.1%	CMTNTPVVVR	99.7%	63.5	25	51.7	2	0	0	1192.58	120	129
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	21	39	0.04%	51.1%	DNVSSPGGATIHALHVLESGGFR	99.7%	35.1	25	35.1	0	2	0	2321.16	229	251
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	21	39	0.04%	51.1%	EGATVYATGTHAQVEDGR	99.7%	99.1	25	99.1	2	2	0	1861.87	130	147
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	21	39	0.04%	51.1%	ELQSMADQEQVSPAAIK	99.7%	112	25	109	4	0	0	1844.91	267	283
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	21	39	0.04%	51.1%	ELQSMADQEQVSPAAIKK	99.7%	76	25	65.7	1	4	0	1973.00	267	284
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	21	39	0.04%	51.1%	GFTAAGVLAAHK	99.7%	69.8	25	58.9	2	0	0	1142.63	18	29
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	21	39	0.04%	51.1%	IMASSPDMDLATVSALR	99.7%	116	25	116	4	0	0	1777.88	30	46
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	21	39	0.04%	51.1%	IMASSPDMDLATVSALRK	98.3%	26.8	25	26.3	0	1	0	1921.97	30	47

Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	21	39	0.04%	51.1%	LDSPAGTALSPSGHTK	99.7%	81.1	25	74.7	2	2	0	1538.78	292	307
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	21	39	0.04%	51.1%	LGAQALLGAAK	99.7%	89.7	25	82	3	0	0	1012.62	205	215
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	21	39	0.04%	51.1%	LSAFRPAPR	98.7%	34.3	25	27.9	1	0	0	1014.58	108	116
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	21	39	0.04%	51.1%	MLLHSEQHPGQLK	99.7%	34.5	25	25.4	2	3	0	1517.79	216	228
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	21	39	0.04%	51.1%	SLLINAVEASCIR	99.7%	84.9	25	72	6	0	0	1445.78	252	264
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	21	39	0.04%	51.1%	VKLDSPAGTALSPSGHTK	99.7%	41.5	25	30.7	0	2	0	1765.94	290	307
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	14	17	39	0.04%	44.1%	ELQSMADQEK	99.7%	67.4	25	56.4	5	0	0	1194.53	267	276
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	14	17	39	0.04%	44.1%	GFTAAGILSAHK	99.7%	66.2	25	62.2	4	0	0	1172.64	18	29
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	14	17	39	0.04%	44.1%	HIVVSCAAGVTISSVEK	99.7%	43.8	25	43.8	0	2	0	1756.93	90	106
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	14	17	39	0.04%	44.1%	IIASSPEMNLPTVSALR	99.7%	136	25	117	4	0	0	1814.97	30	46
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	14	17	39	0.04%	44.1%	ISPAALKK	99.7%	41.2	25	35.8	2	0	0	827.54	277	284
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	14	17	39	0.04%	44.1%	KLMAFQPAPK	99.7%	52.7	25	38.5	1	0	0	1130.64	107	116
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	14	17	39	0.04%	44.1%	KMGVNLTR	98.1%	32.6	25	15.4	1	0	0	918.52	47	54
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	14	17	39	0.04%	44.1%	LAIQLGAQALLGAAK	99.7%	92.3	25	92.3	2	0	0	1437.88	201	215
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	14	17	39	0.04%	44.1%	LESPTVSTLTPSSPGK	99.7%	89.8	25	66.3	2	0	0	1600.84	292	307
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	14	17	39	0.04%	44.1%	LMAFQPAPK	99.7%	60.5	25	52.6	2	0	0	1002.54	108	116
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	14	17	39	0.04%	44.1%	MGVNLTR	99.7%	46.4	25	10.2	2	0	0	806.42	48	54
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	14	17	39	0.04%	44.1%	MLLDSEQHPCQLK	99.7%	71.6	25	62.2	4	0	0	1598.77	216	228
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	14	17	39	0.04%	44.1%	SLLINAVEASCIR	99.7%	84.9	25	72	6	0	0	1445.78	252	264
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	14	17	39	0.04%	44.1%	VKLESPTVSTLTPSSPGK	99.7%	80	25	74.7	2	0	0	1828.01	290	307
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	5	8	12	0.01%	21.5%	AATMSAVEAATCR	99.7%	85.9	25	84.4	3	0	0	1354.61	255	267
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	5	8	12	0.01%	21.5%	IAAQTLLGTAK	99.7%	87.9	25	87.3	2	0	0	1086.65	208	218
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	5	8	12	0.01%	21.5%	MAGAIAQGLIR	99.7%	92.2	25	84.3	4	0	0	1116.62	19	29
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	5	8	12	0.01%	21.5%	MGMPSSLAHR	99.7%	42.2	25	31.2	2	0	0	1086.52	198	207
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	5	8	12	0.01%	21.5%	VEAQHILASAPTDR	98.5%	27.2	25	22.1	0	1	0	1507.79	33	46
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	4	4	4	0.00%	4.0%	DAHQSLLATR	97.2%	31	25	25.7	1	0	0	1111.59	572	581
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	4	4	4	0.00%	4.0%	DFTATFGPLDSLNTR	99.7%	61.5	25	59.2	1	0	0	1654.81	1022	1036
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	4	4	4	0.00%	4.0%	FIGPSPEVVR	98.2%	33	25	26.5	1	0	0	1100.61	138	147
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	4	4	4	0.00%	4.0%	TSTAPAASPNVR	96.1%	29.6	25	17.8	1	0	0	1171.61	19	30
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	11	12	28	0.03%	31.3%	AAASTDYYK	97.8%	32	25	26.6	2	0	0	989.46	236	244
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	11	12	28	0.03%	31.3%	AHGFTFTR	95.3%	28.9	25	25	1	0	0	936.47	120	127
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	11	12	28	0.03%	31.3%	EILAELTGR	99.7%	55.2	25	41.5	3	0	0	1001.56	133	141
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	11	12	28	0.03%	31.3%	GPILMELQTYR	99.7%	57.8	25	57.8	2	0	0	1320.70	278	288
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	11	12	28	0.03%	31.3%	LEEGPPVTTVLTR	99.7%	83.5	25	79.6	6	0	0	1411.78	46	58
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	11	12	28	0.03%	31.3%	LPCIFICENNR	99.7%	57.8	25	53.2	2	0	0	1435.68	216	226
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	11	12	28	0.03%	31.3%	NFYGGNGIVGAQVPLGAGIALACK	99.7%	47.7	25	47.7	0	2	0	2347.22	159	182
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	11	12	28	0.03%	31.3%	RGDFIPGLR	97.2%	31	25	9.83	1	0	0	1030.58	245	253
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	11	12	28	0.03%	31.3%	TREEIQEVR	99.0%	35.7	25	12.1	3	0	0	1159.61	303	311
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	11	12	28	0.03%	31.3%	VDGMDILCVR	99.1%	36.3	25	30.2	1	0	0	1177.57	254	263
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	11	12	28	0.03%	31.3%	YGMGTSVER	99.7%	56.8	25	51.1	5	0	0	1015.45	227	235
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	18	31	0.03%	39.3%	DAINQGMDEELER	96.9%	30.5	25	30.5	1	0	0	1519.67	37	49
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	18	31	0.03%	39.3%	DAINQGMDEELERDEK	99.7%	66	25	64	2	2	0	1891.83	37	52
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	18	31	0.03%	39.3%	DFLIPIGK	99.7%	51.6	25	31.5	2	0	0	902.53	220	227
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	18	31	0.03%	39.3%	DIIFAIKK	98.8%	34.7	25	24	2	0	0	947.59	348	355
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	18	31	0.03%	39.3%	EGVECEVINMR	99.7%	60.2	25	60.2	4	0	0	1351.60	259	269
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	18	31	0.03%	39.3%	ILEDNSIPQVK	99.7%	59.4	25	47	2	0	0	1255.69	337	347
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	18	31	0.03%	39.3%	IMEGPAFNFLDAPAVR	99.7%	110	25	110	4	0	0	1747.88	309	324
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	18	31	0.03%	39.3%	TIRPMDMETIEASVMK	96.1%	23.6	25	23.6	0	1	0	1883.89	270	285
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	18	31	0.03%	39.3%	TYYMSGGLQPVPIVFR	99.7%	106	25	100	4	0	0	1827.95	130	145
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	18	31	0.03%	39.3%	VFLLGEEVAQYDGAYK	99.7%	132	25	131	2	0	0	1801.90	53	68
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	18	31	0.03%	39.3%	VTGADVPMPYAK	99.7%	60.7	25	60.7	4	0	0	1264.62	325	336

Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	18	31	0.03%	39.3%	VVSPWNSEDAK	99.1%	36.3	25	26	1	0	0	1231.60	174	184
Pyruvate dehydrogenase protein X component, mitochondrial	PDHX	ODPX_HUMAN	54.1	99.8%	2	2	4	0.00%	4.6%	HSLDASQGTATGPR	99.7%	69.6	25	69.2	2	0	0	1397.68	195	208
Pyruvate dehydrogenase protein X component, mitochondrial	PDHX	ODPX_HUMAN	54.1	99.8%	2	2	4	0.00%	4.6%	VVDDELATR	99.7%	61.3	25	51.9	2	0	0	1017.52	477	485
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	AEGSDVANAVLDGADCIMLSGETAK	99.7%	115	25	115	4	4	0	2494.14	343	367
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	AGKPVICATQMLESMIK	99.7%	53.6	25	53.6	5	7	0	1908.96	320	336
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	CCSGAIIVLTK	99.7%	72.2	25	66.6	3	0	0	1221.63	423	433
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	CDENILWLDYK	99.7%	75.6	25	74.5	5	0	0	1468.68	152	162
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	DPVQEAWAEDVDLR	99.7%	96.2	25	91.5	2	0	0	1642.77	476	489
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	EAEAAIYHLQLFEELR	99.5%	39.1	25	39.1	1	0	0	1931.99	384	399
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	EAEAAIYHLQLFEELRR	97.5%	25.2	25	25.2	0	1	0	2088.09	384	400
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	FGVEQDVDMVFASFIR	99.7%	114	25	111	7	1	0	1875.89	231	246
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	GADFLVTEVENGGSLGSK	99.7%	113	25	108	9	0	0	1779.88	189	206
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	GADFLVTEVENGGSLGSKK	96.9%	24.5	25	22.2	0	2	0	1907.97	189	207
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	GDLGIEIPAEK	99.7%	64.4	25	45.3	16	0	0	1141.61	295	305
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	GDYPLEAVR	99.7%	59.3	25	51.6	16	0	0	1019.52	368	376
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	GIFPVLCK	97.7%	31.9	25	14.8	1	0	0	933.52	468	475
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	GSGTAEVELK	99.7%	70.3	25	43.7	2	0	0	990.51	126	135
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	GSGTAEVELKK	99.7%	66.9	25	47.4	13	0	0	1118.61	126	136
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	GVNLPGAAVDLPAVSEK	99.7%	127	25	117	3	0	0	1636.89	208	224
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	GVNLPGAAVDLPAVSEKDIQDLK	99.7%	41.1	25	40.2	0	3	0	2349.27	208	230
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	ITLDNAYMEK	99.7%	62.3	25	50	6	0	0	1197.58	142	151
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	IYVDDGLISLQVK	99.7%	107	25	107	10	0	0	1462.82	174	186
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	KGVNLPGAAVDLPAVSEK	99.7%	97.9	25	97.9	2	2	0	1764.99	207	224
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	LAPITSDPTEATAVGAVEASFK	99.7%	141	25	141	8	4	0	2175.12	401	422
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	LDIDSPPITAR	99.7%	76.3	25	67.3	16	0	0	1197.65	33	43
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	LNFSHGTHEYHAETIK	99.7%	81.7	25	70	2	3	0	1883.90	74	89
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	MQHLIAR	99.5%	39.3	25	28.2	10	0	0	868.48	377	383
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	NTGIICTIGPASR	99.7%	98.6	25	98	13	0	0	1359.71	44	56
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	RFDEILEASDGIMVAR	99.7%	88.4	25	82.6	4	4	0	1821.92	279	294
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	SVETLKEMIK	99.7%	57.1	25	50.4	4	0	0	1193.64	57	66
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	TATESFASDPILYRPVAVALDTK	99.7%	52.5	25	52.5	2	5	0	2465.29	93	115
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	29	46	207	0.20%	64.4%	VNFAMNVGK	99.7%	60.1	25	50.6	7	0	0	979.50	490	498
Queuine tRNA-ribosyltransferase subunit QTRTD1	QTRTD1	QTRD1_HUMAN	46.7	100.0%	4	4	7	0.01%	11.1%	GVDLFESFFPYQVTER	99.7%	81	25	79.2	2	0	0	1933.93	267	282
Queuine tRNA-ribosyltransferase subunit QTRTD1	QTRTD1	QTRD1_HUMAN	46.7	100.0%	4	4	7	0.01%	11.1%	LQEESEVLQK	99.7%	48.4	25	32.7	2	0	0	1202.63	177	186
Queuine tRNA-ribosyltransferase subunit QTRTD1	QTRTD1	QTRD1_HUMAN	46.7	100.0%	4	4	7	0.01%	11.1%	SLLFLDNCLR	99.7%	41.5	25	29.8	2	0	0	1250.66	167	176
Queuine tRNA-ribosyltransferase subunit QTRTD1	QTRTD1	QTRD1_HUMAN	46.7	100.0%	4	4	7	0.01%	11.1%	SVSVWSVAGR	99.7%	61.9	25	55.7	1	0	0	1047.56	112	121
Rab-like protein 3	RABL3	RABL3_HUMAN	26.4	100.0%	4	5	8	0.01%	16.5%	LDQIHETK	98.1%	32.6	25	24	2	0	0	983.52	149	156
Rab-like protein 3	RABL3	RABL3_HUMAN	26.4	100.0%	4	5	8	0.01%	16.5%	VHDYKEGTPEEK	97.9%	32.3	25	32.3	1	1	0	1431.68	47	58
Rab-like protein 3	RABL3	RABL3_HUMAN	26.4	100.0%	4	5	8	0.01%	16.5%	WSLEALNR	99.7%	41.9	25	30.6	2	0	0	988.52	109	116
Rab-like protein 3	RABL3	RABL3_HUMAN	26.4	100.0%	4	5	8	0.01%	16.5%	YLAAGSSNAVK	99.7%	53.3	25	32.3	2	0	0	1080.57	185	195
Ragulator complex protein LAMTOR1	LAMTOR1	LTOR1_HUMAN	17.7	100.0%	3	3	4	0.00%	23.6%	IAAYAYSALSQIR	99.7%	53.6	25	45.9	2	0	0	1426.77	135	147
Ragulator complex protein LAMTOR1	LAMTOR1	LTOR1_HUMAN	17.7	100.0%	3	3	4	0.00%	23.6%	LAVLSSSLTHWK	99.3%	37.4	25	37.4	1	0	0	1341.75	92	103
Ragulator complex protein LAMTOR1	LAMTOR1	LTOR1_HUMAN	17.7	100.0%	3	3	4	0.00%	23.6%	TDEQALLSSILAK	99.7%	65.9	25	59.8	1	0	0	1388.76	48	60
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	11	11	23	0.02%	22.7%	AFNSSSFNSNTFLTR	99.7%	84.5	25	71.2	2	0	0	1692.80	501	515
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	11	11	23	0.02%	22.7%	GAVAIADAIR	99.7%	72.8	25	59.5	4	0	0	956.55	280	289
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	11	11	23	0.02%	22.7%	GAVAMAETLK	99.7%	43.5	25	12.8	2	0	0	990.53	252	261
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	11	11	23	0.02%	22.7%	ILAAALTECHR	99.7%	58	25	56.8	2	0	0	1254.66	161	171
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	11	11	23	0.02%	22.7%	LNTAEDAKDVIK	99.5%	39.4	25	22.6	1	0	0	1316.71	32	43
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	11	11	23	0.02%	22.7%	QVEVINFGDCLVR	99.7%	64.7	25	64.2	1	0	0	1548.78	265	277
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	11	11	23	0.02%	22.7%	SSAQGKPLALK	97.3%	31.1	25	24.1	2	0	0	1099.65	173	183
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	11	11	23	0.02%	22.7%	SSVLIAQQTDTSDPEK	99.7%	96.6	25	93.5	2	0	0	1718.84	453	468

Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	11	11	23	0.02%	22.7%	TQVAGGQLSFK	99.7%	63.7	25	56.6	3	0	0	1135.61	16	26
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	11	11	23	0.02%	22.7%	VINLNDNTFTEK	99.7%	61.5	25	54.4	2	0	0	1407.71	240	251
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	11	11	23	0.02%	22.7%	VSSVFKDEATVR	99.7%	68.3	25	52.8	2	0	0	1337.71	476	487
Ran-specific GTPase-activating protein	RANBP1	RANG_HUMAN	23.3	99.8%	2	2	4	0.00%	10.0%	FLNAENAQK	99.7%	51	25	35.4	2	0	0	1034.53	142	150
Ran-specific GTPase-activating protein	RANBP1	RANG_HUMAN	23.3	99.8%	2	2	4	0.00%	10.0%	TLEEDEEELFK	99.6%	40	25	40	2	0	0	1381.64	40	50
Ras GTPase-activating protein-binding protein 1	G3BP1	G3BP1_HUMAN	52.2	100.0%	3	3	5	0.00%	8.2%	EAGEQGDIEPR	99.7%	66.2	25	66.2	2	0	0	1200.55	321	331
Ras GTPase-activating protein-binding protein 1	G3BP1	G3BP1_HUMAN	52.2	100.0%	3	3	5	0.00%	8.2%	LPNFGFVVFDDSEPVQK	99.7%	48.3	25	48.3	2	0	0	1937.96	377	393
Ras GTPase-activating protein-binding protein 1	G3BP1	G3BP1_HUMAN	52.2	100.0%	3	3	5	0.00%	8.2%	TFSWASVTSK	95.5%	29	25	28.9	1	0	0	1113.56	248	257
Ras GTPase-activating protein-binding protein 2	G3BP2	G3BP2_HUMAN	54.1	100.0%	3	4	8	0.01%	8.5%	LPNFGFVVFDDSEPVQR	99.7%	45	25	45	2	0	0	1965.97	371	387
Ras GTPase-activating protein-binding protein 2	G3BP2	G3BP2_HUMAN	54.1	100.0%	3	4	8	0.01%	8.5%	TEELKPQVEEK	99.7%	47.1	25	33.8	2	0	0	1329.69	206	216
Ras GTPase-activating protein-binding protein 2	G3BP2	G3BP2_HUMAN	54.1	100.0%	3	4	8	0.01%	8.5%	VEAKPEVQSQPPR	99.7%	34.9	25	34.9	2	2	0	1464.78	278	290
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	18	18	30	0.03%	13.1%	ALESGDVNTVWK	99.7%	45.1	25	40.9	1	0	0	1318.66	466	477
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	18	18	30	0.03%	13.1%	ALQSPALGLR	99.3%	37.2	25	34	2	0	0	1025.61	327	336
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	18	18	30	0.03%	13.1%	ATFYGEQVDYYK	99.7%	55.3	25	55.3	2	0	0	1483.67	1517	1528
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	18	18	30	0.03%	13.1%	ATGLHFR	97.5%	31.4	25	13.3	1	0	0	801.44	105	111
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	18	18	30	0.03%	13.1%	DHINDIIK	95.1%	28.7	25	23.5	1	0	0	967.52	834	841
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	18	18	30	0.03%	13.1%	EEIQSSISGVTAAYNR	99.7%	106	25	106	1	0	0	1724.84	723	738
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	18	18	30	0.03%	13.1%	FALGIFAINEAVESGDVGK	99.7%	54.6	25	46.5	1	0	0	1937.00	623	641
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	18	18	30	0.03%	13.1%	ILAIGLINEALDEGDAQK	99.7%	75.6	25	69.9	2	0	0	1883.01	539	556
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	18	18	30	0.03%	13.1%	ITLQDVVSHSK	99.7%	49.7	25	44.5	2	0	0	1226.67	925	935
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	18	18	30	0.03%	13.1%	LAAVALINAAIQK	99.7%	60.8	25	48.1	2	0	0	1295.80	389	401
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	18	18	30	0.03%	13.1%	LGNFFSPK	99.6%	40.3	25	32	2	0	0	909.48	81	88
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	18	18	30	0.03%	13.1%	LIFQMPQNK	98.5%	33.7	25	20.6	2	0	0	1118.60	989	997
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	18	18	30	0.03%	13.1%	LIVDVIR	97.0%	30.7	25	4.35	1	0	0	827.54	1391	1397
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	18	18	30	0.03%	13.1%	LPYDVTPEQALAHEEVK	99.7%	45.1	25	41.2	0	2	0	1938.98	1112	1128
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	18	18	30	0.03%	13.1%	LQQTYAALNSK	99.7%	61.9	25	51.8	2	0	0	1236.66	1506	1516
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	18	18	30	0.03%	13.1%	NVIFEISPTEEVGDFEVK	99.7%	75.6	25	73.7	2	0	0	2052.02	1587	1604
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	18	18	30	0.03%	13.1%	TLQALQIPAAK	99.7%	69.6	25	60.8	2	0	0	1153.69	557	567
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	18	18	30	0.03%	13.1%	YQELINDIAR	99.7%	53.4	25	46.3	2	0	0	1234.64	1478	1487
Ras suppressor protein 1	RSU1	RSU1_HUMAN	31.5	100.0%	2	2	2	0.00%	9.4%	DNDLISLPK	99.3%	37.4	25	34	1	0	0	1014.55	166	174
Ras suppressor protein 1	RSU1	RSU1_HUMAN	31.5	100.0%	2	2	2	0.00%	9.4%	LTVLPPELGNLDLTGQK	99.7%	44.6	25	44.6	1	0	0	1808.02	192	208
Ras-related protein Rab-10	RAB10	RAB10_HUMAN	22.5	99.8%	2	2	2	0.00%	22.0%	FHTITTSYYR	99.7%	43.1	25	38	1	0	0	1288.63	71	80
Ras-related protein Rab-10	RAB10	RAB10_HUMAN	22.5	99.8%	2	2	2	0.00%	22.0%	LLLIGDSGVGK	99.7%	59.1	25	0	1	0	0	1071.64	12	22
Ras-related protein Rab-10	RAB10	RAB10_HUMAN	22.5	99.8%	2	2	2	0.00%	22.0%	LQIWDTAGQER	99.7%	69.9	25	0	5	0	0	1316.66	60	70
Ras-related protein Rab-10	RAB10	RAB10_HUMAN	22.5	99.8%	2	2	2	0.00%	22.0%	NIDEHANEDVER	99.7%	50.9	25	47.2	1	0	0	1440.64	106	117
Ras-related protein Rab-13	RAB13	RAB13_HUMAN	22.8	100.0%	3	3	5	0.00%	22.2%	LLLIGDSGVGK	99.7%	59.1	25	0	1	0	0	1071.64	11	21
Ras-related protein Rab-13	RAB13	RAB13_HUMAN	22.8	100.0%	3	3	5	0.00%	22.2%	SIKENASAGVER	99.7%	69.1	25	52.8	2	0	0	1260.65	105	116
Ras-related protein Rab-13	RAB13	RAB13_HUMAN	22.8	100.0%	3	3	5	0.00%	22.2%	SSMNVDEAFSSLAR	99.7%	95.5	25	87.6	2	0	0	1529.69	154	167
Ras-related protein Rab-13	RAB13	RAB13_HUMAN	22.8	100.0%	3	3	5	0.00%	22.2%	TITTAYYR	97.7%	31.9	25	17.8	1	0	0	988.51	72	79
Ras-related protein Rab-18	RAB18	RAB18_HUMAN	23.0	100.0%	3	3	5	0.00%	18.0%	IIQTPGLWESENQNK	99.7%	56.8	25	52.5	1	0	0	1756.89	169	183
Ras-related protein Rab-18	RAB18	RAB18_HUMAN	23.0	100.0%	3	3	5	0.00%	18.0%	ILIIGESGVGK	99.7%	57.1	25	27	2	0	0	1085.66	11	21
Ras-related protein Rab-18	RAB18	RAB18_HUMAN	23.0	100.0%	3	3	5	0.00%	18.0%	LAIWDTAGQER	99.7%	61.6	25	54	2	0	0	1259.64	59	69
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	6	6	11	0.01%	44.3%	FADDTYTESYISTIGVDFK	99.7%	120	25	120	2	0	0	2172.00	28	46
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	6	6	11	0.01%	44.3%	LLLIGDSGVGK	99.7%	59.1	25	0	1	0	0	1071.64	11	21
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	6	6	11	0.01%	44.3%	LQIWDTAGQER	99.7%	69.9	25	0	5	0	0	1316.66	59	69
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	6	6	11	0.01%	44.3%	MGPGAASGGERPNLK	99.0%	28.9	25	25	0	1	0	1457.72	173	187
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	6	6	11	0.01%	44.3%	NATNVEQAFMTMAAEIK	99.7%	51	25	15.6	1	0	0	1884.88	154	170
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	6	6	11	0.01%	44.3%	QWLQEIDRYASENVNK	99.7%	39.1	25	39.1	0	1	0	1992.98	101	116
Ras-related protein Rab-2A	RAB2A	RAB2A_HUMAN	23.5	99.8%	2	2	3	0.00%	14.2%	IQEGVFDINNEANGIK	99.7%	67.2	25	67.2	1	0	0	1760.88	171	186
Ras-related protein Rab-2A	RAB2A	RAB2A_HUMAN	23.5	99.8%	2	2	3	0.00%	14.2%	TASNVEEAFINTAK	99.7%	85.2	25	80.2	2	0	0	1494.74	152	165
Ras-related protein Rab-32	RAB32	RAB32_HUMAN	25.0	99.8%	2	2	4	0.00%	9.3%	DNINIEEAAR	99.7%	63.1	25	52.7	2	0	0	1144.56	177	186

Ras-related protein Rab-32	RAB32	RAB32_HUMAN	25.0	99.8%	2	2	4	0.00%	9.3%	LQLWDIAGQER	99.7%	52.4	25	39.2	2	0	0	1328.70	77	87
Ras-related protein Rab-5A	RAB5A	RAB5A_HUMAN	23.7	100.0%	3	3	5	0.00%	22.3%	GVDLTEPTQPTR	99.7%	58.2	25	45.7	1	0	0	1313.67	198	209
Ras-related protein Rab-5A	RAB5A	RAB5A_HUMAN	23.7	100.0%	3	3	5	0.00%	22.3%	NEPQNPGANSAR	98.3%	33.1	25	26.8	2	0	0	1254.58	184	195
Ras-related protein Rab-5A	RAB5A	RAB5A_HUMAN	23.7	100.0%	3	3	5	0.00%	22.3%	TSMNVNEIFMAIAK	99.7%	59.7	25	0.77	2	0	0	1568.78	166	179
Ras-related protein Rab-5A	RAB5A	RAB5A_HUMAN	23.7	100.0%	3	3	5	0.00%	22.3%	YHSLAPMYYR	94.7%	22.5	25	22.5	0	1	0	1300.61	82	91
Ras-related protein Rab-5C	RAB5C	RAB5C_HUMAN	23.5	99.7%	2	2	3	0.00%	11.1%	QASPNIVIALAGNK	99.7%	42.6	25	42.6	2	0	0	1395.80	122	135
Ras-related protein Rab-5C	RAB5C	RAB5C_HUMAN	23.5	99.7%	2	2	3	0.00%	11.1%	YHSLAPMYYR	94.7%	22.5	25	22.5	0	1	0	1300.61	83	92
Ras-related protein Rab-7a	RAB7A	RAB7A_HUMAN	23.5	99.8%	2	2	3	0.00%	13.0%	DPENFPFVVLGNK	97.5%	31.4	25	29.9	1	0	0	1475.75	114	126
Ras-related protein Rab-7a	RAB7A	RAB7A_HUMAN	23.5	99.8%	2	2	3	0.00%	13.0%	EAINVEQAFQTIAR	99.7%	61.5	25	61.5	2	0	0	1589.83	158	171
Ras-related protein Rab-9A	RAB9A	RAB9A_HUMAN	22.8	99.8%	2	2	4	0.00%	12.4%	DATNVAAAFEEAVR	99.7%	61.8	25	61.8	2	0	0	1463.71	157	170
Ras-related protein Rab-9A	RAB9A	RAB9A_HUMAN	22.8	99.8%	2	2	4	0.00%	12.4%	VILLGDGGVGK	99.7%	61.1	25	32.5	2	0	0	1027.61	10	20
Ras-related protein R-Ras2	RRAS2	RRAS2_HUMAN	23.4	100.0%	2	2	4	0.00%	11.3%	LVVVGGGGVGK	98.1%	32.7	25	32.2	2	0	0	941.58	17	27
Ras-related protein R-Ras2	RRAS2	RRAS2_HUMAN	23.4	100.0%	2	2	4	0.00%	11.3%	QVTQEEGQQLAR	99.7%	61.3	25	49.1	2	0	0	1386.70	136	147
Regulation of nuclear pre-mRNA domain-containing protein 1A	RPRD1A	RPR1A_HUMAN	35.7	100.0%	3	3	6	0.01%	13.5%	DFAPVIVEAFK	99.7%	56.2	25	47.7	2	0	0	1235.67	80	90
Regulation of nuclear pre-mRNA domain-containing protein 1A	RPRD1A	RPR1A_HUMAN	35.7	100.0%	3	3	6	0.01%	13.5%	IASLPVEVQEVSLLDK	99.7%	87.2	25	78.7	2	0	0	1739.98	187	202
Regulation of nuclear pre-mRNA domain-containing protein 1A	RPRD1A	RPR1A_HUMAN	35.7	100.0%	3	3	6	0.01%	13.5%	LTFLYLANDVIQNSK	99.7%	60.2	25	58.9	2	0	0	1738.94	57	71
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	ADSVVVLLCR	99.7%	59.5	25	53	2	0	0	1131.62	201	210
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	AGAKPDQIGIITPYEGQR	99.7%	36.3	25	28.2	0	2	0	1914.01	794	811
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	AGLSQSLFER	99.7%	87.2	25	63.5	2	0	0	1107.58	689	698
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	AYQHGGVTGLSQY	99.7%	47.4	25	47.4	2	0	0	1380.65	1117	1129
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	CFLSWLVK	97.9%	32.2	25	21.6	1	0	0	1052.56	237	244
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	DETGELSSADEKR	99.7%	68.9	25	64.1	1	0	0	1436.65	593	605
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	DGPLGETVLECYNCGCR	99.7%	103	25	103	2	0	0	1999.83	173	189
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	EAIDSPVSFLALHNQIR	99.7%	66.1	25	55.4	2	0	0	1910.01	561	577
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	EAIIPGSVYDR	99.4%	37.7	25	35	2	0	0	1219.63	950	960
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	EKDFIILSCVR	99.7%	55.8	25	53.8	2	0	0	1379.74	844	854
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	ESQTQDNITVR	98.8%	34.6	25	29.3	2	0	0	1290.63	322	332
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	FMTTAMYDAR	99.7%	53.6	25	49.4	1	0	0	1206.53	940	949
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	IAYFTLPK	99.7%	43.4	25	40.3	2	0	0	952.55	342	349
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	IPSEQEQLR	99.7%	53.8	25	38	3	0	0	1099.57	245	253
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	KLVNTINPGAR	99.7%	64.6	25	60.4	2	0	0	1182.70	929	939
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	LEADYDKK	99.0%	35.4	25	15.5	2	0	0	981.49	312	319
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	LKESQTQDNITVR	99.7%	71.6	25	56.6	1	0	0	1531.81	320	332
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	LLGHEVEDVIIK	99.7%	63.4	25	59.1	2	1	0	1364.78	456	467
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	LMQGDEICLR	99.7%	53.1	25	35.9	2	0	0	1234.59	367	376
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	LQVQYR	96.8%	30.5	25	0	1	0	0	806.45	709	714
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	LVNTINPGAR	99.2%	36.9	25	29.5	2	0	0	1054.60	930	939
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	LYQEVEIASVDAFQGR	99.7%	72.1	25	68.7	2	0	0	1824.91	828	843
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	QITAQQINK	99.2%	36.9	25	31.4	2	0	0	1043.58	256	264
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	QPCASQSSLK	99.7%	47.1	25	33.5	1	0	0	1105.53	211	220
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	SILIDESTQATEPECMVPVVLGAK	99.7%	41.6	25	41.6	1	0	0	2587.30	643	666
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	SQIDVALSQDSTYQGER	99.7%	84.7	25	78.8	2	0	0	1896.89	1100	1116
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	TFAVDETSVSGYIYHK	99.7%	81.7	25	75.2	1	0	0	1816.88	440	455
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	TVLQRPLSLIQGPPGTGK	99.7%	36.9	25	36.9	0	2	0	1862.09	492	509
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	TVTSATIVYHLAR	99.7%	95.9	25	90.1	2	1	0	1431.80	510	522
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	VLVEGPLNNLR	99.7%	53.2	25	44.2	2	0	0	1223.71	908	918
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	VPDNYGDEIAIELR	99.7%	92.5	25	92.5	2	0	0	1603.80	394	407
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	YEDAYQYQNIFGPLVK	99.7%	87	25	87	2	0	0	1947.95	296	311
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	35	61	0.06%	34.5%	YGVIIVGNPK	99.7%	61.6	25	61.6	2	0	0	1059.62	879	888
Regulator of nonsense transcripts 3B	UPF3B	REN3B_HUMAN	57.8	100.0%	4	5	9	0.01%	9.9%	FLESYATDNEK	99.7%	52.7	25	41.7	1	0	0	1316.60	163	173
Regulator of nonsense transcripts 3B	UPF3B	REN3B_HUMAN	57.8	100.0%	4	5	9	0.01%	9.9%	KAESTESIGSSEK	99.7%	74	25	69.8	2	0	0	1352.65	406	418

Regulator of nonsense transcripts 3B	UPF3B	REN3B_HUMAN	57.8	100.0%	4	5	9	0.01%	9.9%	MTSTPETLLEEIEAK	99.7%	67.5	25	67.5	4	0	0	1691.84	174	188
Regulator of nonsense transcripts 3B	UPF3B	REN3B_HUMAN	57.8	100.0%	4	5	9	0.01%	9.9%	NQEDIILFR	99.7%	61.2	25	49.9	2	0	0	1147.61	103	111
Regulatory-associated protein of mTOR	RPTOR	RPTOR_HUMAN	149.0	100.0%	4	4	5	0.00%	2.9%	ALETIGANLQK	98.2%	32.9	25	25.1	1	0	0	1157.65	98	108
Regulatory-associated protein of mTOR	RPTOR	RPTOR_HUMAN	149.0	100.0%	4	4	5	0.00%	2.9%	LDDQIFLNR	99.7%	41	25	35.7	1	0	0	1133.60	1013	1021
Regulatory-associated protein of mTOR	RPTOR	RPTOR_HUMAN	149.0	100.0%	4	4	5	0.00%	2.9%	QDLLVASLFR	99.7%	44.2	25	28.5	1	0	0	1161.66	339	348
Regulatory-associated protein of mTOR	RPTOR	RPTOR_HUMAN	149.0	100.0%	4	4	5	0.00%	2.9%	SVSSYGNIR	98.9%	35.2	25	30	2	0	0	982.50	719	727
Renin receptor	ATP6AP2	RENR_HUMAN	39.0	100.0%	4	4	6	0.01%	15.1%	ANSVFEDLSVTLR	99.7%	64	25	58.9	2	0	0	1450.75	140	152
Renin receptor	ATP6AP2	RENR_HUMAN	39.0	100.0%	4	4	6	0.01%	15.1%	ILVDALQK	95.5%	29	25	20.4	1	0	0	899.56	239	246
Renin receptor	ATP6AP2	RENR_HUMAN	39.0	100.0%	4	4	6	0.01%	15.1%	IPDVAALSMGFSVK	99.7%	51	25	44.1	1	0	0	1434.77	42	55
Renin receptor	ATP6AP2	RENR_HUMAN	39.0	100.0%	4	4	6	0.01%	15.1%	LFQENSVLSSLPLNSLSR	99.7%	81.9	25	81.9	2	0	0	2004.08	158	175
Replication factor C subunit 1	RFC1	RFC1_HUMAN	128.3	100.0%	6	6	11	0.01%	6.9%	AALLSGPPGVGK	99.7%	43.3	25	35.2	1	0	0	1066.63	646	657
Replication factor C subunit 1	RFC1	RFC1_HUMAN	128.3	100.0%	6	6	11	0.01%	6.9%	AIVAESLNNTSIK	99.7%	74	25	62.4	2	0	0	1359.75	688	700
Replication factor C subunit 1	RFC1	RFC1_HUMAN	128.3	100.0%	6	6	11	0.01%	6.9%	ELSQNTDESGLNDEAIAK	99.7%	60.1	25	60.1	1	0	0	1933.90	188	205
Replication factor C subunit 1	RFC1	RFC1_HUMAN	128.3	100.0%	6	6	11	0.01%	6.9%	GGIQELIGLIK	99.7%	47	25	37.2	4	0	0	1140.70	732	742
Replication factor C subunit 1	RFC1	RFC1_HUMAN	128.3	100.0%	6	6	11	0.01%	6.9%	TIIGQQGDQSCANK	99.7%	51.8	25	51.8	1	0	0	1519.72	597	610
Replication factor C subunit 1	RFC1	RFC1_HUMAN	128.3	100.0%	6	6	11	0.01%	6.9%	TVNMDYLSLLR	99.7%	62.1	25	60.4	2	0	0	1324.69	993	1003
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	13	15	28	0.03%	42.1%	APGSAGHYELPWVEK	99.7%	51.9	25	51.9	1	0	0	1640.81	27	41
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	13	15	28	0.03%	42.1%	DAMLELNASNDR	99.7%	58.5	25	58.5	2	0	0	1348.62	100	111
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	13	15	28	0.03%	42.1%	EGNVPNIIIAGPPGTGK	99.7%	89.5	25	83.4	2	0	0	1633.89	66	82
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	13	15	28	0.03%	42.1%	FALACNASDK	99.7%	58.4	25	49.6	2	0	0	1096.51	167	176
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	13	15	28	0.03%	42.1%	FALACNASDKIIEPIQSR	99.6%	33.1	25	33.1	0	2	0	2033.05	167	184
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	13	15	28	0.03%	42.1%	IAEGVNSLLQMAGLLAR	99.7%	72.3	25	72.3	2	0	0	1771.97	327	343
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	13	15	28	0.03%	42.1%	IIEPIQSR	98.9%	35.4	25	17.8	1	0	0	955.56	177	184
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	13	15	28	0.03%	42.1%	IIILDEADSMTDGAQQALR	99.7%	117	25	114	3	0	0	2076.03	137	155
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	13	15	28	0.03%	42.1%	LNEIVGNEDTVSR	99.7%	87	25	87	2	0	0	1445.72	47	59
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	13	15	28	0.03%	42.1%	LTDAQILTR	99.7%	72.7	25	63	4	0	0	1030.59	193	201
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	13	15	28	0.03%	42.1%	TFQMAEYLK	98.7%	34.5	25	26.4	4	0	0	1146.55	305	313
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	13	15	28	0.03%	42.1%	TTSILCLAR	99.7%	45.3	25	30.4	2	0	0	1034.57	83	91
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	13	15	28	0.03%	42.1%	VCDEPHPLLVK	98.6%	33.9	25	30.4	1	0	0	1306.68	254	264
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	12	14	24	0.02%	31.2%	AIYHLEAFVAK	99.7%	66.5	25	44.3	2	0	0	1261.69	328	338
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	12	14	24	0.02%	31.2%	ALLMCEACR	99.7%	45.8	25	38.1	4	0	0	1123.51	226	234
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	12	14	24	0.02%	31.2%	EGLNLPSQLAHR	99.5%	38.8	25	36.6	2	0	0	1334.72	203	214
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	12	14	24	0.02%	31.2%	ETANAIVSQQTPQR	99.7%	108	25	102	2	0	0	1542.79	257	270
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	12	14	24	0.02%	31.2%	IEHQTITTPSK	99.7%	45.4	25	39.5	2	0	0	1254.67	69	79
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	12	14	24	0.02%	31.2%	IMCILR	94.8%	28.4	25	15.5	1	0	0	821.44	52	57
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	12	14	24	0.02%	31.2%	LDYHKEQAAQLR	99.2%	29.7	25	29.7	0	1	0	1471.77	16	27
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	12	14	24	0.02%	31.2%	LRIEHQTITTPSK	98.7%	27.7	25	23.5	0	1	0	1523.85	67	79
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	12	14	24	0.02%	31.2%	TVAQSQQLETNSQR	99.7%	111	25	103	2	0	0	1589.79	114	127
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	12	14	24	0.02%	31.2%	VVIQEMLK	99.7%	55.4	25	38.8	3	0	0	959.56	106	113
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	12	14	24	0.02%	31.2%	VVLLTEVDK	99.2%	36.8	25	36.8	2	0	0	1015.60	131	139
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	12	14	24	0.02%	31.2%	VVLLTEVDKLTK	99.7%	71	25	71	2	0	0	1357.83	131	142
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	17	0.02%	30.9%	AITFLQSATR	99.7%	83.7	25	69.2	2	0	0	1107.62	241	250
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	17	0.02%	30.9%	ELFGPELFR	99.7%	60.3	25	40.8	2	0	0	1107.58	94	102
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	17	0.02%	30.9%	ISDEGIAYLVK	99.7%	76.6	25	70.6	2	0	0	1207.66	222	232
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	17	0.02%	30.9%	IVILDEADSMTSAAQAALR	99.7%	77.6	25	73.5	2	0	0	1975.02	146	164
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	17	0.02%	30.9%	NFAQLTVSGSR	99.7%	45.5	25	5.46	1	0	0	1179.61	125	135
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	17	0.02%	30.9%	SLEGADLPNLLFYGPPGTGK	99.7%	80.7	25	80.7	2	0	0	2046.05	65	84
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	17	0.02%	30.9%	TSTILAAAR	99.7%	48.9	25	41.7	2	0	0	903.53	85	93
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	17	0.02%	30.9%	VITDIAGVIPAEK	99.7%	98.4	25	90.1	2	0	0	1325.77	261	273
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	17	0.02%	30.9%	VLELNASDER	99.7%	65.6	25	60.7	2	0	0	1145.58	105	114
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	12	17	31	0.03%	40.3%	ALNILQSTNMAFGK	99.7%	99.7	25	87.7	4	0	0	1523.79	216	229

Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	12	17	31	0.03%	40.3%	ALVTLSSGDMR	99.7%	83.7	25	73.6	4	0	0	1149.59	204	214
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	12	17	31	0.03%	40.3%	FCLICNYLSK	99.7%	56.8	25	55.6	2	0	0	1317.63	151	160
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	12	17	31	0.03%	40.3%	FGPLTPELMVPR	99.7%	44.4	25	41.8	3	0	0	1356.73	174	185
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	12	17	31	0.03%	40.3%	GPILSFASTR	99.7%	69.6	25	68.6	3	0	0	1048.58	103	112
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	12	17	31	0.03%	40.3%	IQLSSLIAAFQVTR	99.7%	97.2	25	92.6	2	0	0	1546.90	320	333
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	12	17	31	0.03%	40.3%	LSVGTNEK	95.7%	29.2	25	21.3	2	0	0	847.45	312	319
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	12	17	31	0.03%	40.3%	LVILDEADAMTQDAQNALR	99.7%	120	25	113	4	0	0	2103.04	121	139
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	12	17	31	0.03%	40.3%	MADIEYR	99.7%	51.7	25	38.8	3	0	0	897.41	305	311
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	12	17	31	0.03%	40.3%	TSTILACAK	99.7%	45.2	25	35.9	2	0	0	964.51	67	75
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	12	17	31	0.03%	40.3%	VDFPSSVR	99.7%	45.8	25	34	1	0	0	906.47	291	298
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	12	17	31	0.03%	40.3%	VTEETVYTCTGHPLK	97.6%	25.3	25	24.5	0	1	0	1734.84	230	244
Required for meiotic nuclear division protein 1 homolog	RMND1	RMND1_HUMAN	51.6	100.0%	4	4	7	0.01%	9.8%	DAANILVMGVENSAK	99.7%	105	25	105	2	0	0	1531.78	205	219
Required for meiotic nuclear division protein 1 homolog	RMND1	RMND1_HUMAN	51.6	100.0%	4	4	7	0.01%	9.8%	EGAAVFWNVK	97.7%	31.9	25	29.8	1	0	0	1120.58	231	240
Required for meiotic nuclear division protein 1 homolog	RMND1	RMND1_HUMAN	51.6	100.0%	4	4	7	0.01%	9.8%	EGDPGTIFFFR	99.7%	52.2	25	43.8	2	0	0	1285.62	220	230
Required for meiotic nuclear division protein 1 homolog	RMND1	RMND1_HUMAN	51.6	100.0%	4	4	7	0.01%	9.8%	IGELFALR	99.7%	66.6	25	49.5	2	0	0	918.54	353	360
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	7	10	0.01%	23.3%	AEELHYPLGER	99.2%	36.5	25	36.5	1	1	0	1313.65	25	35
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	7	10	0.01%	23.3%	EALLGVQEDVDEYVK	99.7%	101	25	101	2	0	0	1706.85	42	56
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	7	10	0.01%	23.3%	QLHDDYFYHDEL	98.8%	34.8	25	32.7	2	0	0	1594.68	306	317
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	7	10	0.01%	23.3%	VIDFDENTALDDAEEESFR	99.7%	85.1	25	85.1	1	0	0	2214.97	130	148
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	7	10	0.01%	23.3%	VIDFDENTALDDAEEESFRK	99.7%	51.9	25	51.9	0	1	0	2343.06	130	149
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	7	10	0.01%	23.3%	WDPTANEDPEWILVEK	99.7%	81.1	25	79.1	2	0	0	1941.92	217	232
Retinoid-inducible serine carboxypeptidase	SCPEP1	RISC_HUMAN	50.8	100.0%	4	4	6	0.01%	9.5%	DLAMVASDMMVLLK	99.7%	55.3	25	42.7	1	0	0	1536.78	134	147
Retinoid-inducible serine carboxypeptidase	SCPEP1	RISC_HUMAN	50.8	100.0%	4	4	6	0.01%	9.5%	NLAFYWILK	99.3%	37.3	25	21	2	0	0	1167.66	420	428
Retinoid-inducible serine carboxypeptidase	SCPEP1	RISC_HUMAN	50.8	100.0%	4	4	6	0.01%	9.5%	SLETSAFVK	97.9%	32.3	25	25.2	2	0	0	981.53	408	416
Retinoid-inducible serine carboxypeptidase	SCPEP1	RISC_HUMAN	50.8	100.0%	4	4	6	0.01%	9.5%	VAEQVLNAVNK	99.7%	75.9	25	73	1	0	0	1184.66	233	243
Rho guanine nucleotide exchange factor 7	ARHGEF7	ARHG7_HUMAN	90.0	99.8%	2	2	2	0.00%	2.2%	GDVIHVTR	98.2%	32.9	25	32.9	1	0	0	896.49	208	215
Rho guanine nucleotide exchange factor 7	ARHGEF7	ARHG7_HUMAN	90.0	99.8%	2	2	2	0.00%	2.2%	KPSDEEFASR	99.6%	40	25	33.7	1	0	0	1165.55	692	701
Rho-related GTP-binding protein RhoG	RHOG	RHOG_HUMAN	21.3	100.0%	4	4	6	0.01%	29.3%	AVLNPTPIKR	98.9%	35.1	25	19.7	2	0	0	1108.68	175	184
Rho-related GTP-binding protein RhoG	RHOG	RHOG_HUMAN	21.3	100.0%	4	4	6	0.01%	29.3%	LKEQGQAPITPQQGQALAK	98.4%	27	25	27	0	1	0	2006.10	129	147
Rho-related GTP-binding protein RhoG	RHOG	RHOG_HUMAN	21.3	100.0%	4	4	6	0.01%	29.3%	TCLLICYTTNAFPK	99.7%	46.8	25	44.6	2	0	0	1701.83	17	30
Rho-related GTP-binding protein RhoG	RHOG	RHOG_HUMAN	21.3	100.0%	4	4	6	0.01%	29.3%	YLECSALQQDGVK	99.7%	59.9	25	58.3	1	0	0	1510.72	154	166
Ribonuclease P protein subunit p14	RPP14	RPP14_HUMAN	13.7	99.8%	2	2	2	0.00%	20.2%	PAPAATYER	99.3%	37.1	25	36.6	1	0	0	975.49	2	10
Ribonuclease P protein subunit p14	RPP14	RPP14_HUMAN	13.7	99.8%	2	2	2	0.00%	20.2%	VIQVSPFLLALSGNSR	99.0%	35.8	25	33.3	1	0	0	1700.97	104	119
Ribonuclease P protein subunit p20	POP7	POP7_HUMAN	15.7	99.8%	2	2	3	0.00%	17.9%	GAVEAELDPVEYTLR	99.7%	100	25	87.9	2	0	0	1661.84	9	23
Ribonuclease P protein subunit p20	POP7	POP7_HUMAN	15.7	99.8%	2	2	3	0.00%	17.9%	RPNDIYVNMK	98.2%	32.9	25	30.5	1	0	0	1265.63	33	42
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	5	5	9	0.01%	26.8%	AVVLEYFTR	98.5%	33.8	25	27.9	1	0	0	1097.60	55	63
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	5	5	9	0.01%	26.8%	CPSYVGITGILLQETK	99.7%	44.7	25	44.7	2	0	0	1778.94	147	162
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	5	5	9	0.01%	26.8%	EANDSDVQPSGAQR	99.7%	65.9	25	57.9	2	0	0	1473.66	13	26
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	5	5	9	0.01%	26.8%	LFDIKPEQQR	99.7%	48.3	25	43.8	2	0	0	1273.69	86	95
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	5	5	9	0.01%	26.8%	SVIYHALSQK	99.7%	53.2	25	42.1	2	0	0	1145.63	3	12
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	8	9	17	0.02%	38.1%	AALLHGETR	99.6%	39.6	25	33.8	2	0	0	967.53	227	235
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	8	9	17	0.02%	38.1%	GLAFELVYSPAIK	99.7%	73.9	25	72	2	0	0	1407.79	149	161
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	8	9	17	0.02%	38.1%	GPYDVANLGLLFGLSESDAK	99.7%	48.3	25	48.3	1	0	0	2066.04	199	218
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	8	9	17	0.02%	38.1%	KTAFGIISTVK	99.5%	39.4	25	39.4	2	0	0	1164.70	236	246
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	8	9	17	0.02%	38.1%	LYDVVAVFPK	99.7%	69.3	25	65.9	4	0	0	1150.65	99	108
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	8	9	17	0.02%	38.1%	NVIISSAAERPLEIR	99.7%	46.6	25	36	2	0	0	1667.94	184	198
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	8	9	17	0.02%	38.1%	RPPINVAIDR	99.7%	46	25	28.5	2	0	0	1150.67	139	148
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	8	9	17	0.02%	38.1%	YTISSALNLMQICK	99.7%	77.4	25	70.3	2	0	0	1657.83	168	181
Ribonuclease P protein subunit p38	RPP38	RPP38_HUMAN	31.8	100.0%	6	6	9	0.01%	21.9%	ELLLVLVCK	99.7%	44.5	25	44.5	2	0	0	1086.66	128	136
Ribonuclease P protein subunit p38	RPP38	RPP38_HUMAN	31.8	100.0%	6	6	9	0.01%	21.9%	NTTDFVDEVR	99.7%	44.2	25	37	2	0	0	1195.56	185	194
Ribonuclease P protein subunit p38	RPP38	RPP38_HUMAN	31.8	100.0%	6	6	9	0.01%	21.9%	QASVTLQPLK	98.9%	35.3	25	28.4	1	0	0	1084.64	251	260

Ribonuclease P protein subunit p38	RPP38	RPP38_HUMAN	31.8	100.0%	6	6	9	0.01%	21.9%	QLAIGVNEVTR	99.7%	61.2	25	43.8	2	0	0	1199.67	112	122
Ribonuclease P protein subunit p38	RPP38	RPP38_HUMAN	31.8	100.0%	6	6	9	0.01%	21.9%	TSLNNPYIIR	99.7%	56.4	25	49.4	1	0	0	1190.65	23	32
Ribonuclease P protein subunit p38	RPP38	RPP38_HUMAN	31.8	100.0%	6	6	9	0.01%	21.9%	VPSLSVPWLQDR	98.7%	34.5	25	34.2	1	0	0	1396.76	200	211
Ribonuclease P/MRP protein subunit POP5	POP5	POP5_HUMAN	18.8	100.0%	3	3	5	0.00%	19.0%	FLIQYNR	96.8%	30.4	25	18.3	1	0	0	953.52	113	119
Ribonuclease P/MRP protein subunit POP5	POP5	POP5_HUMAN	18.8	100.0%	3	3	5	0.00%	19.0%	YLLCELVSDDPR	99.7%	60.5	25	58.5	2	0	0	1479.72	8	19
Ribonuclease P/MRP protein subunit POP5	POP5	POP5_HUMAN	18.8	100.0%	3	3	5	0.00%	19.0%	YLNAYTGIVLLR	99.7%	54.8	25	48.4	2	0	0	1395.80	57	68
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	7	7	12	0.01%	8.4%	AACQCVEPIK	99.1%	36.4	25	27.5	1	0	0	1175.55	345	354
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	7	7	12	0.01%	8.4%	AASVHTVGEDTEETPHR	99.7%	35.5	25	35.5	0	2	0	1835.85	449	465
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	7	7	12	0.01%	8.4%	AGPEGTSQEIPK	99.7%	58.5	25	49.9	2	0	0	1213.61	89	100
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	7	7	12	0.01%	8.4%	ISDQDLNR	99.7%	46.5	25	35.3	2	0	0	960.47	567	574
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	7	7	12	0.01%	8.4%	NQPTNVTLSSGFVADR	99.7%	71.7	25	71.7	1	0	0	1705.85	15	30
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	7	7	12	0.01%	8.4%	SSNSLVFQTLPR	99.7%	60.4	25	43.2	2	0	0	1348.72	126	137
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	7	7	12	0.01%	8.4%	YITASTFAQAR	99.7%	47.7	25	45.6	2	0	0	1228.63	101	111
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	9	12	25	0.02%	35.8%	IFSGSSHQDLSQK	99.7%	74.1	25	66.7	2	0	0	1433.70	6	18
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	9	12	25	0.02%	35.8%	INNACFEAVVVTNTIPQEDK	99.7%	57.8	25	57.8	1	0	0	2262.11	261	280
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	9	12	25	0.02%	35.8%	MVLVGDVK	99.7%	43.9	25	34.2	2	0	0	876.49	205	212
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	9	12	25	0.02%	35.8%	MVLVGDVKDR	99.7%	73	25	55.9	4	0	0	1147.61	205	214
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	9	12	25	0.02%	35.8%	NCTIVSPDAGGAK	99.7%	58.6	25	48.5	3	0	0	1289.62	164	176
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	9	12	25	0.02%	35.8%	RVTSIADR	99.7%	48.7	25	29.4	2	0	0	917.52	177	184
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	9	12	25	0.02%	35.8%	VAILVDDMADTCGTICHAADK	99.7%	44.2	25	44.2	0	4	0	2276.04	215	235
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	9	12	25	0.02%	35.8%	VTAVIPCFPYAR	99.7%	48.7	25	45.2	3	0	0	1393.73	85	96
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	9	12	25	0.02%	35.8%	VYAILTHGIFSGPAISR	99.7%	74.6	25	74.3	2	2	0	1802.00	244	260
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	4	4	7	0.01%	38.7%	FSNQETSVEIGESVR	99.7%	99.9	25	99.1	2	0	0	1681.80	35	49
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	4	4	7	0.01%	38.7%	LNVEFALIHK	99.7%	59.6	25	51.7	2	0	0	1183.68	185	194
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	4	4	7	0.01%	38.7%	MVLVGDVK	99.7%	43.9	25	34.2	2	0	0	876.49	205	212
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	4	4	7	0.01%	38.7%	MVLVGDVKDR	99.7%	73	25	55.9	4	0	0	1147.61	205	214
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	4	4	7	0.01%	38.7%	NCIIVSPDAGGAK	99.3%	37.7	25	35.5	1	0	0	1301.65	164	176
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	4	4	7	0.01%	38.7%	PNIVLFSGSSHQDLSQR	99.7%	44.8	25	44.7	0	2	0	1884.96	2	18
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	4	4	7	0.01%	38.7%	RVTSIADR	99.7%	48.7	25	29.4	2	0	0	917.52	177	184
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	4	4	7	0.01%	38.7%	VAILVDDMADTCGTICHAADK	99.7%	44.2	25	44.2	0	4	0	2276.04	215	235
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	4	4	7	0.01%	38.7%	VTAVIPCFPYAR	99.7%	48.7	25	45.2	3	0	0	1393.73	85	96
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	4	4	7	0.01%	38.7%	VYAILTHGIFSGPAISR	99.7%	74.6	25	74.3	2	2	0	1802.00	244	260
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	5	5	9	0.01%	8.0%	FVNLISER	99.7%	53.9	25	37.5	2	0	0	977.54	122	129
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	5	5	9	0.01%	8.0%	GCYFVLDWLQK	99.7%	41.4	25	41.4	2	0	0	1428.70	172	182
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	5	5	9	0.01%	8.0%	LLDVTGGLGTDELR	99.7%	79.4	25	72.6	2	0	0	1458.78	99	112
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	5	5	9	0.01%	8.0%	SGNELPLAVASTADLIR	99.7%	107	25	103	2	0	0	1726.93	80	96
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	5	5	9	0.01%	8.0%	VECVLAELK	98.3%	33	25	7.27	1	0	0	1060.57	304	312
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	28	0.03%	30.4%	AAESETPGKSPEK	99.6%	40.5	25	31.5	2	0	0	1330.65	418	430
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	28	0.03%	30.4%	ATNESEDEIPQLVPIGK	99.1%	36	25	32.4	2	0	0	1839.93	357	373
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	28	0.03%	30.4%	AVDALLTHCK	99.7%	57.7	25	52.6	2	0	0	1127.59	39	48
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	28	0.03%	30.4%	DDVAPESGDTTVK	99.7%	65.5	25	65.5	2	0	0	1333.61	319	331
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	28	0.03%	30.4%	EINDCIGGTVLNISK	99.7%	90.6	25	84	2	0	0	1632.83	193	207
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	28	0.03%	30.4%	KALPASETPK	99.4%	38	25	34	2	0	0	1041.59	408	417
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	28	0.03%	30.4%	KVPVSVNLLSK	99.7%	48.3	25	47.8	2	0	0	1183.74	178	188
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	28	0.03%	30.4%	LLPSLIGR	99.7%	49.6	25	30.4	2	0	0	868.56	164	171
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	28	0.03%	30.4%	LLSSFDFFLTDAR	99.7%	112	25	108	2	0	0	1531.78	148	160
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	28	0.03%	30.4%	LTLPHSIR	99.6%	40.2	25	40.2	2	0	0	936.56	82	89
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	28	0.03%	30.4%	TASVLSKDDVAPESGDTTVK	99.5%	32	25	30	0	1	0	2020.01	312	331
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	28	0.03%	30.4%	TPANEKVEIQK	99.7%	44.5	25	39	2	0	0	1256.68	375	385
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	28	0.03%	30.4%	TVSQIISLQTLK	99.7%	86.4	25	86.4	2	0	0	1330.79	125	136
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	28	0.03%	30.4%	TVSQIISLQTLKK	99.4%	37.7	25	37.7	1	0	0	1458.89	125	137

Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	15	15	28	0.03%	30.4%	VPVSVNLLSK	99.7%	50.7	25	45	2	0	0	1055.65	179	188
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	5	5	6	0.01%	8.1%	DLKPENILLDEEGHIK	99.6%	32.4	25	29	0	1	0	1862.99	193	208
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	5	5	6	0.01%	8.1%	EASAVLFTITK	99.7%	48.4	25	44	1	0	0	1179.66	515	525
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	5	5	6	0.01%	8.1%	GAMAATYSALNR	99.7%	64.8	25	58.9	1	0	0	1241.59	701	712
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	5	5	6	0.01%	8.1%	ICDFGFAK	99.5%	38.9	25	0	2	0	0	957.45	559	566
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	5	5	6	0.01%	8.1%	LGAGPDGVEEIKR	98.9%	28.5	25	28.5	0	1	0	1340.72	311	323
Ribosomal RNA processing protein 1 homolog A	RRP1	RRP1_HUMAN	52.8	100.0%	6	6	10	0.01%	12.8%	AANVQEPEK	99.3%	37.2	25	32.5	2	0	0	985.49	447	455
Ribosomal RNA processing protein 1 homolog A	RRP1	RRP1_HUMAN	52.8	100.0%	6	6	10	0.01%	12.8%	FIDPFCR	95.1%	28.7	25	23	1	0	0	954.45	193	199
Ribosomal RNA processing protein 1 homolog A	RRP1	RRP1_HUMAN	52.8	100.0%	6	6	10	0.01%	12.8%	GVGADPEAR	95.6%	29.1	25	25.8	1	0	0	871.43	395	403
Ribosomal RNA processing protein 1 homolog A	RRP1	RRP1_HUMAN	52.8	100.0%	6	6	10	0.01%	12.8%	LAGNEQVTR	99.7%	77.7	25	61.4	2	0	0	987.52	17	25
Ribosomal RNA processing protein 1 homolog A	RRP1	RRP1_HUMAN	52.8	100.0%	6	6	10	0.01%	12.8%	TKDSLVLNNITR	99.7%	68.8	25	60.5	2	0	0	1373.77	204	215
Ribosomal RNA processing protein 1 homolog A	RRP1	RRP1_HUMAN	52.8	100.0%	6	6	10	0.01%	12.8%	VGAEELTADQNLK	99.7%	75.5	25	59.5	2	0	0	1387.71	180	192
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	9	10	17	0.02%	16.9%	ELLADQNLK	98.6%	34.1	25	28.3	2	0	0	1043.57	183	191
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	9	10	17	0.02%	16.9%	ETGGFSQEELLK	98.4%	33.5	25	24	1	0	0	1337.66	42	53
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	9	10	17	0.02%	16.9%	GVFEAIVDQSPFVPEETMEEQK	99.7%	40.9	25	40.9	0	4	0	2525.18	215	236
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	9	10	17	0.02%	16.9%	HHLQPENPGPGGAAPSLEQNR	99.7%	43.3	25	34.7	0	1	0	2206.08	407	427
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	9	10	17	0.02%	16.9%	SILVSPTGPSR	97.3%	31.1	25	17.8	2	0	0	1113.63	702	712
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	9	10	17	0.02%	16.9%	SSTATHPPGPAVQLNK	99.7%	45.8	25	44.5	2	0	0	1604.84	661	676
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	9	10	17	0.02%	16.9%	TPTSSPASSPLVAK	99.7%	61.7	25	60.7	2	0	0	1342.72	728	741
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	9	10	17	0.02%	16.9%	VFCVEEEDSESSLQK	99.7%	97	25	81.6	2	0	0	1785.78	384	398
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	9	10	17	0.02%	16.9%	VFLDVLMK	97.7%	31.9	25	28.7	1	0	0	964.55	144	151
Ribosome biogenesis protein BMS1 homolog	BMS1	BMS1_HUMAN	145.8	100.0%	2	2	2	0.00%	1.6%	AFAVQSAVR	99.7%	50.4	25	33	1	0	0	948.53	44	52
Ribosome biogenesis protein BMS1 homolog	BMS1	BMS1_HUMAN	145.8	100.0%	2	2	2	0.00%	1.6%	IAATGVVLDLDK	99.7%	97	25	92.2	1	0	0	1214.70	1008	1019
Ribosome biogenesis protein BRX1 homolog	BRIX1	BRX1_HUMAN	41.4	100.0%	3	3	4	0.00%	8.8%	ELLIQIFSTPR	99.7%	51.2	25	51.2	2	0	0	1316.76	183	193
Ribosome biogenesis protein BRX1 homolog	BRIX1	BRX1_HUMAN	41.4	100.0%	3	3	4	0.00%	8.8%	FLVQNIHTLAELK	99.7%	60.5	25	50.7	1	0	0	1525.87	141	153
Ribosome biogenesis protein BRX1 homolog	BRIX1	BRX1_HUMAN	41.4	100.0%	3	3	4	0.00%	8.8%	FVLNLIK	95.2%	28.8	25	28.8	1	0	0	846.54	236	242
Ribosome biogenesis regulatory protein homolog	RRS1	RRS1_HUMAN	41.2	100.0%	2	2	2	0.00%	7.7%	AEQDEAEKLQR	97.8%	31.9	25	31.9	1	0	0	1316.64	13	23
Ribosome biogenesis regulatory protein homolog	RRS1	RRS1_HUMAN	41.2	100.0%	2	2	2	0.00%	7.7%	DNTQLLINQLWQLPTER	99.7%	41.3	25	30	1	0	0	2082.10	67	83
Ribosome maturation protein SBDS	SBDS	SBDS_HUMAN	28.8	99.8%	2	2	3	0.00%	7.2%	GEVQVSDKER	99.7%	58.1	25	45.4	2	0	0	1146.58	91	100
Ribosome maturation protein SBDS	SBDS	SBDS_HUMAN	28.8	99.8%	2	2	3	0.00%	7.2%	LTNVAVVR	99.7%	61.4	25	41.8	1	0	0	871.54	12	19
Ribosome production factor 2 homolog	RPF2	RPF2_HUMAN	35.6	100.0%	4	5	9	0.01%	13.4%	GPTVSNIR	99.5%	38.9	25	29.9	2	0	0	843.47	169	176
Ribosome production factor 2 homolog	RPF2	RPF2_HUMAN	35.6	100.0%	4	5	9	0.01%	13.4%	IELEEMGPSLDLVLR	99.7%	74.4	25	66.2	4	0	0	1713.91	212	226
Ribosome production factor 2 homolog	RPF2	RPF2_HUMAN	35.6	100.0%	4	5	9	0.01%	13.4%	KPYGVLYK	98.5%	33.6	25	19.8	1	0	0	967.56	57	64
Ribosome production factor 2 homolog	RPF2	RPF2_HUMAN	35.6	100.0%	4	5	9	0.01%	13.4%	THLASDDLYK	99.6%	39.9	25	38.8	2	0	0	1162.57	228	237
Ribosome-binding protein 1	RRBP1	RRBP1_HUMAN	152.5	100.0%	6	6	10	0.01%	5.3%	DALNQATSQVESK	99.7%	63.6	25	63.6	1	0	0	1390.68	807	819
Ribosome-binding protein 1	RRBP1	RRBP1_HUMAN	152.5	100.0%	6	6	10	0.01%	5.3%	EQEITAVQAR	99.7%	53.3	25	48.7	2	0	0	1144.60	752	761
Ribosome-binding protein 1	RRBP1	RRBP1_HUMAN	152.5	100.0%	6	6	10	0.01%	5.3%	LQQENSILR	97.0%	30.7	25	21.2	1	0	0	1100.61	798	806
Ribosome-binding protein 1	RRBP1	RRBP1_HUMAN	152.5	100.0%	6	6	10	0.01%	5.3%	NTDVAQSPEAPK	99.7%	74.4	25	54.8	2	0	0	1256.61	609	620
Ribosome-binding protein 1	RRBP1	RRBP1_HUMAN	152.5	100.0%	6	6	10	0.01%	5.3%	SIEALLEAGQAR	99.7%	51.7	25	32.3	2	0	0	1257.68	959	970
Ribosome-binding protein 1	RRBP1	RRBP1_HUMAN	152.5	100.0%	6	6	10	0.01%	5.3%	VEPAVSSVVNSIQVLTSK	99.7%	64.4	25	64.4	2	0	0	1857.03	149	166
RING finger protein 219	RNF219	RN219_HUMAN	81.1	100.0%	4	4	5	0.00%	6.1%	FAVAALQSK	99.7%	44.2	25	24.6	2	0	0	934.54	217	225
RING finger protein 219	RNF219	RN219_HUMAN	81.1	100.0%	4	4	5	0.00%	6.1%	GSEEDVVSK	99.6%	39.8	25	30.6	1	0	0	949.45	284	292
RING finger protein 219	RNF219	RN219_HUMAN	81.1	100.0%	4	4	5	0.00%	6.1%	NLSLESQIK	95.1%	28.7	25	8.64	1	0	0	1031.57	117	125
RING finger protein 219	RNF219	RN219_HUMAN	81.1	100.0%	4	4	5	0.00%	6.1%	TILDPLTLVQGNQNEDK	99.6%	40.1	25	22.4	1	0	0	1897.99	126	142
RISC-loading complex subunit TARBP2	TARBP2	TRBP2_HUMAN	39.0	100.0%	2	2	3	0.00%	7.7%	SCSLGSLGALGPACCR	99.7%	56.7	25	51	1	0	0	1665.75	281	296
RISC-loading complex subunit TARBP2	TARBP2	TRBP2_HUMAN	39.0	100.0%	2	2	3	0.00%	7.7%	TPISLLQEYGTR	99.7%	85.3	25	72.3	2	0	0	1377.74	30	41
RNA 3'-terminal phosphate cyclase	RTCA	RTCA_HUMAN	39.3	100.0%	3	3	6	0.01%	9.3%	AFVAGVLPFK	99.7%	53.2	25	48	2	0	0	1048.62	196	205
RNA 3'-terminal phosphate cyclase	RTCA	RTCA_HUMAN	39.3	100.0%	3	3	6	0.01%	9.3%	FGFIFNCDIK	99.7%	48.5	25	46.3	2	0	0	1260.61	147	156
RNA 3'-terminal phosphate cyclase	RTCA	RTCA_HUMAN	39.3	100.0%	3	3	6	0.01%	9.3%	VSTALSCLLGLPLR	99.7%	42.2	25	36.4	2	0	0	1499.86	22	35
RNA 3'-terminal phosphate cyclase-like protein	RCL1	RCL1_HUMAN	40.8	100.0%	3	3	5	0.00%	9.4%	LLLEEIYR	99.7%	49.3	25	48.4	2	0	0	1048.60	282	289
RNA 3'-terminal phosphate cyclase-like protein	RCL1	RCL1_HUMAN	40.8	100.0%	3	3	5	0.00%	9.4%	LVLSTLSGRPVK	99.5%	39.4	25	39.1	2	0	0	1269.79	20	31

RNA 3'-terminal phosphate cyclase-like protein	RCL1	RCL1_HUMAN	40.8	100.0%	3	3	5	0.00%	9.4%	VLLGPLSPYTIEFLR	99.0%	35.7	25	35.7	1	0	0	1717.99	315	329
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	100.0%	2	2	3	0.00%	41.8%	ALETVFGK	97.0%	30.7	25	14.5	1	0	0	864.48	23	30
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	100.0%	2	2	3	0.00%	41.8%	DRDYSDHPSGGSYR	99.7%	58.5	25	58.5	2	1	0	1611.68	269	282
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	100.0%	2	2	3	0.00%	41.8%	DSYESYGNSR	99.7%	73.3	25	73.2	5	0	0	1177.48	283	292
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	100.0%	2	2	3	0.00%	41.8%	DSYGGPPR	98.1%	32.7	25	17.5	2	0	0	848.39	188	195
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	100.0%	2	2	3	0.00%	41.8%	DVYLSPR	99.0%	35.8	25	31.3	1	0	0	849.45	204	210
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	100.0%	2	2	3	0.00%	41.8%	DYAPPPRDYTYR	98.5%	33.8	25	26.8	2	0	0	1513.71	233	244
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	100.0%	2	2	3	0.00%	41.8%	DYGHSSSRDDYPSR	99.7%	54.8	25	54.8	2	1	0	1641.69	245	258
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	100.0%	2	2	3	0.00%	41.8%	DYSDHPSGGSYR	99.7%	58.4	25	57.5	2	0	0	1340.55	271	282
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	100.0%	2	2	3	0.00%	41.8%	GFAFVTFESPADAK	99.7%	103	25	68.8	14	0	0	1486.72	50	63
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	100.0%	2	2	3	0.00%	41.8%	GFAFVTFESPADAKDAAR	99.7%	104	25	104	2	2	0	1899.92	50	67
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	100.0%	2	2	3	0.00%	41.8%	GGHMDDGGYSMNFNMSSSR	99.7%	93.4	25	93.4	2	13	0	2097.77	126	144
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	100.0%	2	2	3	0.00%	41.8%	GPPPSYGGSSR	99.7%	70.5	25	62.1	7	0	0	1061.50	299	309
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	100.0%	2	2	3	0.00%	41.8%	GRDSYGGPPR	99.7%	46.8	25	10.1	2	0	0	1061.51	186	195
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	100.0%	2	2	3	0.00%	41.8%	LFIGGLNTETNEK	99.7%	102	25	89.4	12	0	0	1435.74	10	22
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	100.0%	2	2	3	0.00%	41.8%	RDVYLSPR	99.7%	46.8	25	27.6	2	0	0	1005.55	203	210
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	100.0%	2	2	3	0.00%	41.8%	REPLPSR	98.6%	34.2	25	16	2	0	0	854.48	196	202
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	100.0%	2	2	3	0.00%	41.8%	VEQATKPSFER	99.7%	46.2	25	42.7	2	0	0	1291.66	81	91
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	100.0%	2	2	3	0.00%	41.8%	YDDYSSSR	99.7%	50.9	25	50.9	2	0	0	992.40	310	317
RNA binding protein fox-1 homolog 1	RBFOX1	RFOX1_HUMAN	42.8	100.0%	2	2	6	0.01%	6.3%	GFGFVTFENSADADR	99.7%	98.5	25	94.6	3	0	0	1632.73	157	171
RNA binding protein fox-1 homolog 1	RBFOX1	RFOX1_HUMAN	42.8	100.0%	2	2	6	0.01%	6.3%	KIEVNNATAR	99.7%	41.1	25	30.2	3	0	0	1115.62	185	194
RNA methyltransferase-like protein 1	RNMTL1	RMTL1_HUMAN	47.0	100.0%	4	4	6	0.01%	11.0%	APSTWEESGLR	99.7%	67.7	25	62.3	2	0	0	1232.59	83	93
RNA methyltransferase-like protein 1	RNMTL1	RMTL1_HUMAN	47.0	100.0%	4	4	6	0.01%	11.0%	EKQPLEESASR	99.6%	40.4	25	28.8	1	0	0	1273.64	72	82
RNA methyltransferase-like protein 1	RNMTL1	RMTL1_HUMAN	47.0	100.0%	4	4	6	0.01%	11.0%	KAPSEASAQEQR	99.7%	55.2	25	44.9	2	0	0	1301.64	60	71
RNA methyltransferase-like protein 1	RNMTL1	RMTL1_HUMAN	47.0	100.0%	4	4	6	0.01%	11.0%	VVFPSGEVVEQK	99.0%	35.4	25	34.9	1	0	0	1317.70	40	51
RNA polymerase II-associated factor 1 homolog	PAF1	PAF1_HUMAN	60.0	99.8%	2	2	2	0.00%	4.7%	VTPVEVMPVFPDFK	98.7%	34.3	25	33.6	1	0	0	1604.84	199	212
RNA polymerase II-associated factor 1 homolog	PAF1	PAF1_HUMAN	60.0	99.8%	2	2	2	0.00%	4.7%	YGISNEKPEVK	99.4%	38.2	25	32.7	1	0	0	1263.66	144	154
RNA pseudouridylate synthase domain-containing protein 3	RPUSD3	RUSD3_HUMAN	38.5	100.0%	4	4	6	0.01%	13.7%	DTPVELLAPLPPYFSR	94.6%	28.2	25	22.5	1	0	0	1814.97	326	341
RNA pseudouridylate synthase domain-containing protein 3	RPUSD3	RUSD3_HUMAN	38.5	100.0%	4	4	6	0.01%	13.7%	QVLDEALLR	99.7%	46.2	25	32.8	1	0	0	1056.60	288	296
RNA pseudouridylate synthase domain-containing protein 3	RPUSD3	RUSD3_HUMAN	38.5	100.0%	4	4	6	0.01%	13.7%	SGPLGDQPFAGLLPK	99.7%	59	25	59	2	0	0	1496.81	54	68
RNA pseudouridylate synthase domain-containing protein 3	RPUSD3	RUSD3_HUMAN	38.5	100.0%	4	4	6	0.01%	13.7%	TLQCLGLR	98.3%	33.2	25	8.88	2	0	0	960.53	342	349
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	23	31	126	0.12%	47.6%	AIKVEQATKPSFESGR	99.7%	79.2	25	78.4	2	2	0	1747.93	78	93
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	23	31	126	0.12%	47.6%	ALEAVFGK	99.7%	57.2	25	41.2	2	0	0	834.47	23	30
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	23	31	126	0.12%	47.6%	DRDYSDHPSGGSYR	99.7%	58.5	25	58.5	2	1	0	1611.68	269	282
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	23	31	126	0.12%	47.6%	DSYESYGNSR	99.7%	73.3	25	73.2	5	0	0	1177.48	283	292
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	23	31	126	0.12%	47.6%	DSYGGPPR	98.1%	32.7	25	17.5	2	0	0	848.39	188	195
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	23	31	126	0.12%	47.6%	DVYLSPR	99.0%	35.8	25	31.3	1	0	0	849.45	204	210
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	23	31	126	0.12%	47.6%	DYAPPPRDYTYR	98.5%	33.8	25	26.8	2	0	0	1513.71	233	244
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	23	31	126	0.12%	47.6%	DYGHSSSRDDYPSR	99.7%	54.8	25	54.8	2	1	0	1641.69	245	258
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	23	31	126	0.12%	47.6%	DYSDHPSGGSYR	99.7%	58.4	25	57.5	2	0	0	1340.55	271	282
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	23	31	126	0.12%	47.6%	GFAFVTFESPADAK	99.7%	103	25	68.8	14	0	0	1486.72	50	63
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	23	31	126	0.12%	47.6%	GFAFVTFESPADAKDAAR	99.7%	104	25	104	2	2	0	1899.92	50	67
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	23	31	126	0.12%	47.6%	GGHMDDGGYSMNFNMSSSR	99.7%	93.4	25	93.4	2	13	0	2097.77	126	144
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	23	31	126	0.12%	47.6%	GPPPSYGGSSR	99.7%	70.5	25	62.1	7	0	0	1061.50	299	309
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	23	31	126	0.12%	47.6%	GRDSYGGPPR	99.7%	46.8	25	10.1	2	0	0	1061.51	186	195
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	23	31	126	0.12%	47.6%	IVEVLLMK	99.7%	57.8	25	37.5	6	0	0	960.58	34	41
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	23	31	126	0.12%	47.6%	IVEVLLMKDR	99.7%	65.6	25	65.2	2	0	0	1231.71	34	43
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	23	31	126	0.12%	47.6%	LFIGGLNTETNEK	99.7%	102	25	89.4	12	0	0	1435.74	10	22
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	23	31	126	0.12%	47.6%	RDVYLSPR	99.7%	46.8	25	27.6	2	0	0	1005.55	203	210
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	23	31	126	0.12%	47.6%	REPLPSR	98.6%	34.2	25	16	2	0	0	854.48	196	202
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	23	31	126	0.12%	47.6%	RGPPPPPR	99.7%	53.4	25	47.9	17	0	0	873.51	94	101

RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	23	31	126	0.12%	47.6%	VEQATKPSFESGR	99.7%	73.6	25	67.9	10	6	0	1435.72	81	93
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	23	31	126	0.12%	47.6%	VEQATKPSFESGRR	95.7%	29.2	25	28.6	1	0	0	1591.82	81	94
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	23	31	126	0.12%	47.6%	YDDYSSSR	99.7%	50.9	25	50.9	2	0	0	992.40	310	317
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	24	25	70	0.07%	29.7%	AHLSENELEALEK	99.7%	60	25	60	1	0	0	1482.74	794	806
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	24	25	70	0.07%	29.7%	DGDYRDQDYR	99.6%	40.7	25	40.7	1	0	0	1302.53	99	108
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	24	25	70	0.07%	29.7%	DGLGSDNIGSR	99.7%	54.7	25	47.7	2	0	0	1090.51	854	864
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	24	25	70	0.07%	29.7%	EKYGIPEPPEPK	99.7%	43.8	25	35	2	0	0	1383.72	823	834
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	24	25	70	0.07%	29.7%	ESATADAGYAILEK	99.7%	111	25	105	4	0	0	1438.71	686	699
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	24	25	70	0.07%	29.7%	GDPTGAGPEASLEPGADSVSMQAFSR	99.7%	45.9	25	45.9	0	2	0	2550.14	473	498
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	24	25	70	0.07%	29.7%	GLVAAYSGESDSEEEQER	99.7%	113	25	107	2	0	0	1955.85	727	744
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	24	25	70	0.07%	29.7%	GQLQSHGVQAR	99.7%	75.1	25	64.8	10	0	0	1180.62	147	157
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	24	25	70	0.07%	29.7%	GSSYGVTSTESYK	99.7%	53.5	25	53.5	2	0	0	1365.62	903	915
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	24	25	70	0.07%	29.7%	HQQLSGLHK	97.1%	30.9	25	28.4	1	0	0	1047.57	777	785
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	24	25	70	0.07%	29.7%	INEDWLCNK	99.7%	61.2	25	35.1	4	0	0	1191.55	213	221
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	24	25	70	0.07%	29.7%	KYGGISTASVDFEQPTR	99.7%	40.5	25	40.5	0	2	0	1855.92	837	853
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	24	25	70	0.07%	29.7%	LACLLCR	99.7%	46.4	25	35	2	0	0	905.47	759	765
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	24	25	70	0.07%	29.7%	LDQQTLPLGGR	99.7%	80.4	25	71.7	6	0	0	1197.66	253	263
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	24	25	70	0.07%	29.7%	MLPQAATEDDIR	99.7%	84.1	25	70	6	0	0	1359.66	135	146
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	24	25	70	0.07%	29.7%	NSFQPISSLR	99.7%	44.8	25	16.3	4	0	0	1148.61	671	680
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	24	25	70	0.07%	29.7%	QGIVTPIEAQTR	99.7%	57	25	44	2	0	0	1312.72	882	893
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	24	25	70	0.07%	29.7%	RTYVPALEQSADGHK	98.9%	28.3	25	28.3	0	1	0	1671.85	613	627
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	24	25	70	0.07%	29.7%	SEAEQKLPLGTR	99.7%	47.4	25	38.9	4	0	0	1328.72	241	252
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	24	25	70	0.07%	29.7%	TINVEFAK	99.4%	37.9	25	27.2	2	0	0	921.50	376	383
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	24	25	70	0.07%	29.7%	TYVPALEQSADGHK	99.7%	63.7	25	58.9	2	0	0	1515.74	614	627
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	24	25	70	0.07%	29.7%	VSMHYSDPKPK	99.7%	35.7	25	32.3	0	5	0	1304.63	202	212
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	24	25	70	0.07%	29.7%	WMEANQHSLNILGQK	99.5%	31.7	25	31.7	0	1	0	1768.88	187	201
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	24	25	70	0.07%	29.7%	YGGISTASVDFEQPTR	99.7%	97	25	96.3	2	0	0	1727.82	838	853
RNA-binding protein 12B	RBM12B	RB12B_HUMAN	118.1	99.8%	2	2	3	0.00%	2.3%	FLGTEVLLR	99.7%	65.2	25	53.3	2	0	0	1047.62	465	473
RNA-binding protein 12B	RBM12B	RB12B_HUMAN	118.1	99.8%	2	2	3	0.00%	2.3%	LLGLPFIAGPVDIR	99.7%	55.8	25	55.8	1	0	0	1480.89	7	20
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	11	11	22	0.02%	20.8%	AQPSASLGVGYR	99.7%	42.6	25	34.4	2	0	0	1205.63	251	262
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	11	11	22	0.02%	20.8%	AQPSVSLGAPYR	99.3%	37.2	25	27	2	0	0	1245.66	275	286
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	11	11	22	0.02%	20.8%	ASYDDPYKK	99.2%	36.6	25	31	2	0	0	1086.51	586	594
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	11	11	22	0.02%	20.8%	ASYVAPLTAQPATYR	99.7%	93.1	25	75.8	2	0	0	1608.84	224	238
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	11	11	22	0.02%	20.8%	IFVGNVSAACTSQELR	99.7%	117	25	105	3	0	0	1751.87	81	96
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	11	11	22	0.02%	20.8%	INVELSTK	99.7%	41.1	25	33.4	3	0	0	903.51	142	149
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	11	11	22	0.02%	20.8%	KGPGLAVQSGDK	99.7%	56.9	25	56.9	1	0	0	1156.63	153	164
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	11	11	22	0.02%	20.8%	QPTPPFFGR	95.0%	28.6	25	26.2	1	0	0	1046.54	204	212
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	11	11	22	0.02%	20.8%	TQPMTAQAASYR	99.6%	39.7	25	36.3	2	0	0	1340.63	263	274
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	11	11	22	0.02%	20.8%	TQSSASLAASYAAQQHPQAAASYR	99.7%	70.9	25	70.9	0	2	0	2465.18	518	541
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	11	11	22	0.02%	20.8%	YSGSYNDYLR	99.7%	57.6	25	57.6	2	0	0	1237.55	648	657
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	10	18	0.02%	12.0%	EDINAIEMEEDKR	98.9%	35	25	29.3	2	0	0	1591.73	262	274
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	10	18	0.02%	12.0%	EKEELEEIR	99.7%	59.1	25	34.5	2	0	0	1174.60	539	547
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	10	18	0.02%	12.0%	EYSSELNAPSQESDSHPR	99.7%	40	25	40	0	2	0	2032.88	217	234
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	10	18	0.02%	12.0%	FPVAPLIPYPLITK	99.7%	52.2	25	52.2	2	0	0	1568.95	248	261
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	10	18	0.02%	12.0%	GAIEVLIR	99.7%	53.8	25	29.7	2	0	0	870.54	209	216
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	10	18	0.02%	12.0%	LGASNSPGQPNSVK	99.7%	54.5	25	54.4	2	0	0	1355.69	672	685
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	10	18	0.02%	12.0%	LLAEGHPDPDAELQR	99.7%	57.1	25	54.9	2	2	0	1660.83	550	564
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	10	18	0.02%	12.0%	LLHDLQIGEK	99.3%	37.5	25	34.5	2	0	0	1165.66	146	155
RNA-binding protein 26	RBM26	RBM26_HUMAN	113.6	100.0%	4	4	6	0.01%	5.0%	AEAEAAAVHGAR	99.7%	60	25	43	2	0	0	1152.58	936	947
RNA-binding protein 26	RBM26	RBM26_HUMAN	113.6	100.0%	4	4	6	0.01%	5.0%	AISSTEAVLNNR	99.7%	54.4	25	45.6	1	0	0	1274.67	586	597
RNA-binding protein 26	RBM26	RBM26_HUMAN	113.6	100.0%	4	4	6	0.01%	5.0%	EGSTQQLQTTSPK	99.7%	46.9	25	42.9	2	0	0	1404.70	606	618

RNA-binding protein 26	RBM26	RBM26_HUMAN	113.6	100.0%	4	4	6	0.01%	5.0%	TIGSGEPGVPTKK	96.4%	29.9	25	29	1	0	0	1270.70	493	505
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	7	8	13	0.01%	10.3%	AAEGVSAADMAK	99.7%	64.7	25	60.8	3	0	0	1136.53	454	465
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	7	8	13	0.01%	10.3%	FNQLVEQYK	99.7%	43.9	25	23.4	2	0	0	1168.60	730	738
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	7	8	13	0.01%	10.3%	GFGFVQFK	99.6%	40.3	25	32.1	2	0	0	929.49	155	162
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	7	8	13	0.01%	10.3%	IVLHPDTEHSK	98.1%	26.3	25	21.8	0	1	0	1275.67	366	376
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	7	8	13	0.01%	10.3%	LINNNPEIFGPLK	99.7%	51.1	25	47.2	2	0	0	1468.82	559	571
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	7	8	13	0.01%	10.3%	LLLSATSGEK	95.3%	28.8	25	25.3	1	0	0	1018.58	506	515
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	7	8	13	0.01%	10.3%	SEQLEELFSQVGPVK	99.7%	103	25	95	2	0	0	1689.87	17	31
RNA-binding protein 34	RBM34	RBM34_HUMAN	48.6	100.0%	4	4	6	0.01%	9.5%	EYGQIESVR	98.1%	32.8	25	26.3	1	0	0	1080.53	207	215
RNA-binding protein 34	RBM34	RBM34_HUMAN	48.6	100.0%	4	4	6	0.01%	9.5%	ILDDTEDTVVSQR	99.2%	36.8	25	33.1	1	0	0	1490.73	157	169
RNA-binding protein 34	RBM34	RBM34_HUMAN	48.6	100.0%	4	4	6	0.01%	9.5%	IQINQEEER	99.7%	50.1	25	50.1	2	0	0	1158.58	172	180
RNA-binding protein 34	RBM34	RBM34_HUMAN	48.6	100.0%	4	4	6	0.01%	9.5%	LGQVASSLFR	99.7%	63.4	25	57.3	2	0	0	1077.61	35	44
RNA-binding protein 39	RBM39	RBM39_HUMAN	59.4	100.0%	5	5	15	0.01%	11.9%	AAAMANNLQK	99.7%	49.1	25	33.9	2	0	0	1031.53	235	244
RNA-binding protein 39	RBM39	RBM39_HUMAN	59.4	100.0%	5	5	15	0.01%	11.9%	DLEEFFSTVGK	99.7%	67.3	25	56.3	4	0	0	1271.62	168	178
RNA-binding protein 39	RBM39	RBM39_HUMAN	59.4	100.0%	5	5	15	0.01%	11.9%	TDASSASSFLDSDELER	99.7%	108	25	108	2	0	0	1829.80	330	346
RNA-binding protein 39	RBM39	RBM39_HUMAN	59.4	100.0%	5	5	15	0.01%	11.9%	TGIDLGTTGR	99.7%	46	25	7	3	0	0	990.52	347	356
RNA-binding protein 39	RBM39	RBM39_HUMAN	59.4	100.0%	5	5	15	0.01%	11.9%	VLGVPIIVQASQAEK	99.7%	80.3	25	80.3	4	0	0	1551.91	218	232
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	9	10	18	0.02%	30.8%	AEDAVEAIR	99.7%	52	25	21.6	1	0	0	973.49	121	129
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	9	10	18	0.02%	30.8%	ATAPVPTVGEGYGYGHESELSQASAAAR	99.7%	51.7	25	51.7	0	2	0	2776.32	314	341
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	9	10	18	0.02%	30.8%	GLDNTEFQGK	99.7%	68.7	25	57	2	0	0	1108.53	130	139
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	9	10	18	0.02%	30.8%	LFIGNLPR	99.7%	45.1	25	19.6	2	0	0	929.56	4	11
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	9	10	18	0.02%	30.8%	LHGVNINVEASK	99.7%	56.3	25	49.8	2	2	0	1280.70	60	71
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	9	10	18	0.02%	30.8%	LHVGNISPTCTNK	99.7%	46.3	25	42.5	2	0	0	1440.73	80	92
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	9	10	18	0.02%	30.8%	TAAEDAIR	99.5%	39.3	25	31.8	1	0	0	846.43	46	53
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	9	10	18	0.02%	30.8%	VADLTEQYNEQYGAVR	99.7%	121	25	120	2	0	0	1855.88	183	198
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	9	10	18	0.02%	30.8%	VLECDIIK	99.7%	41.5	25	25.5	2	0	0	989.53	28	35
RNA-binding protein FUS	FUS	FUS_HUMAN	53.4	99.8%	2	2	3	0.00%	3.0%	GEATVSFDDPPSAK	99.7%	108	25	101	2	0	0	1420.66	335	348
RNA-binding protein FUS	FUS	FUS_HUMAN	53.4	99.8%	2	2	3	0.00%	3.0%	LKGEATVSFDDPPSAK	99.7%	43.3	25	43.3	0	1	0	1661.84	333	348
RNA-binding protein Musashi homolog 1	MSI1	MSI1H_HUMAN	39.1	100.0%	3	4	8	0.01%	9.1%	EYFGQFGEVK	99.7%	48.6	25	43.5	2	0	0	1203.57	38	47
RNA-binding protein Musashi homolog 1	MSI1	MSI1H_HUMAN	39.1	100.0%	3	4	8	0.01%	9.1%	GFGFVTFMDQAGVDK	99.7%	94.7	25	85.3	5	0	0	1634.75	62	76
RNA-binding protein Musashi homolog 1	MSI1	MSI1H_HUMAN	39.1	100.0%	3	4	8	0.01%	9.1%	QYFEQFGK	95.9%	29.3	25	20.2	1	0	0	1046.49	127	134
RNA-binding protein Musashi homolog 2	MSI2	MSI2H_HUMAN	35.2	100.0%	3	3	12	0.01%	16.5%	GFGFVTFADPASVDK	99.7%	84.7	25	81.2	6	0	0	1557.76	63	77
RNA-binding protein Musashi homolog 2	MSI2	MSI2H_HUMAN	35.2	100.0%	3	3	12	0.01%	16.5%	GFGFVTFENEDVVEK	99.7%	85.2	25	77.5	2	0	0	1716.81	152	166
RNA-binding protein Musashi homolog 2	MSI2	MSI2H_HUMAN	35.2	100.0%	3	3	12	0.01%	16.5%	IFVGGLSANTVVEDVK	99.7%	94.9	25	92	4	0	0	1647.90	112	127
RNA-binding protein Musashi homolog 2	MSI2	MSI2H_HUMAN	35.2	100.0%	3	3	12	0.01%	16.5%	QYFEQFGK	95.9%	29.3	25	20.2	1	0	0	1046.49	128	135
RNA-binding protein PNO1	PNO1	PNO1_HUMAN	27.9	100.0%	4	4	7	0.01%	17.5%	AEEGFTQVTR	99.7%	68.4	25	55.8	2	0	0	1137.55	12	21
RNA-binding protein PNO1	PNO1	PNO1_HUMAN	27.9	100.0%	4	4	7	0.01%	17.5%	FTIENVTR	98.8%	34.6	25	19.3	1	0	0	979.52	192	199
RNA-binding protein PNO1	PNO1	PNO1_HUMAN	27.9	100.0%	4	4	7	0.01%	17.5%	MDTEEARPAK	99.5%	39	25	39	2	0	0	1147.54	47	56
RNA-binding protein PNO1	PNO1	PNO1_HUMAN	27.9	100.0%	4	4	7	0.01%	17.5%	QAEQLSAAGEGGDAGR	99.7%	88.2	25	88.2	2	0	0	1516.70	31	46
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	13	13	48	0.05%	38.2%	AAVLGENGR	99.6%	40.2	25	40.2	1	0	0	886.47	70	78
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	13	13	48	0.05%	38.2%	GYAFVQYSNER	99.7%	73.7	25	66.3	4	0	0	1333.62	56	66
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	13	13	48	0.05%	38.2%	KSDVETIFSK	99.7%	71.5	25	56.4	2	0	0	1153.61	35	44
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	13	13	48	0.05%	38.2%	LEQIAAEQK	99.7%	61.8	25	52.7	6	0	0	1029.56	208	216
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	13	13	48	0.05%	38.2%	LQASNVTNK	99.7%	47.4	25	35.3	3	0	0	974.53	5	13
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	13	13	48	0.05%	38.2%	LQASNVTNKNDPK	99.7%	47.8	25	37.4	4	0	0	1428.74	5	17
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	13	13	48	0.05%	38.2%	LSPVPVPR	96.7%	30.3	25	24.1	1	0	0	864.53	134	141
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	13	13	48	0.05%	38.2%	SDVETIFSK	99.7%	52.8	25	44	3	0	0	1025.52	36	44
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	13	13	48	0.05%	38.2%	SNIDALLSR	99.7%	82	25	54.5	6	0	0	988.54	199	207
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	13	13	48	0.05%	38.2%	SSELQAIK	99.7%	79.2	25	48.5	4	0	0	875.48	184	191
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	13	13	48	0.05%	38.2%	TELTQIK	97.7%	31.8	25	4.18	1	0	0	832.48	192	198
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	13	13	48	0.05%	38.2%	VFIGNLNTALVK	99.7%	97.8	25	0	9	0	0	1288.76	23	34

RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	13	13	48	0.05%	38.2%	VLAGQTLDINMAGEPKPDRPK	99.7%	66.4	25	66.4	0	4	0	2266.19	79	99
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	13	16	27	0.03%	45.2%	ANCIDSTASAEAVFASEVK	99.7%	144	25	144	2	1	0	1969.92	266	284
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	13	16	27	0.03%	45.2%	ANCIDSTASAEAVFASEVKK	99.7%	33.7	25	33.7	0	2	0	2098.01	266	285
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	13	16	27	0.03%	45.2%	DHAVVVGVYRPPPK	99.7%	84.9	25	81.1	2	2	0	1533.85	305	318
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	13	16	27	0.03%	45.2%	GKEDALVTK	99.7%	42.3	25	34.3	2	0	0	960.54	101	109
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	13	16	27	0.03%	45.2%	HEGVFICR	98.3%	33.2	25	29.1	2	0	0	1017.49	93	100
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	13	16	27	0.03%	45.2%	IVALNAHTFLR	99.7%	68.8	25	63.5	2	2	0	1254.73	245	255
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	13	16	27	0.03%	45.2%	LAAAILGGVDQIHIKPGAK	99.7%	51.7	25	46.4	0	1	0	1872.11	144	162
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	13	16	27	0.03%	45.2%	MQQENMKPQEQLTLEPYER	99.7%	56.3	25	56.3	0	1	0	2424.12	286	304
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	13	16	27	0.03%	45.2%	NLVPGESVYGEK	97.4%	31.3	25	27.1	1	0	0	1291.65	110	121
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	13	16	27	0.03%	45.2%	NLVPGESVYGEKR	99.7%	49.9	25	42	2	0	0	1447.75	110	122
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	13	16	27	0.03%	45.2%	NVMVEPHR	99.5%	38.8	25	34.9	1	0	0	997.49	85	92
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	13	16	27	0.03%	45.2%	TNIIPVIEDAR	99.7%	54.5	25	0	2	0	0	1240.69	208	218
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	13	16	27	0.03%	45.2%	VSISEGDDKIEYR	99.7%	71.2	25	71.2	2	0	0	1510.74	123	135
RRP12-like protein	RRP12	RRP12_HUMAN	143.7	100.0%	3	3	4	0.00%	2.5%	EGGGDEPLNFLDPK	99.7%	42.1	25	38.3	1	0	0	1487.70	1111	1124
RRP12-like protein	RRP12	RRP12_HUMAN	143.7	100.0%	3	3	4	0.00%	2.5%	SWLLPVIR	98.5%	33.6	25	10.6	1	0	0	983.60	567	574
RRP12-like protein	RRP12	RRP12_HUMAN	143.7	100.0%	3	3	4	0.00%	2.5%	VLATQPGPGR	99.7%	54.8	25	47	2	0	0	995.56	1129	1138
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	13	0.01%	19.3%	ALESSIAPIVIFASNR	99.7%	75.9	25	75.9	2	1	0	1687.94	318	333
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	13	0.01%	19.3%	AVLLAGPPGTGK	99.7%	59.2	25	52	1	0	0	1080.64	65	76
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	13	0.01%	19.3%	EACGVIVELIK	99.1%	36.1	25	22.3	1	0	0	1230.68	47	57
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	13	0.01%	19.3%	GLGLDESGLAK	99.4%	38.4	25	30.3	2	0	0	1059.57	23	33
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	13	0.01%	19.3%	LDPSIFESLQK	99.7%	53.6	25	43	2	0	0	1276.68	172	182
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	13	0.01%	19.3%	QAASGLVGQENAR	99.7%	94.6	25	82.7	2	0	0	1300.66	34	46
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	13	0.01%	19.3%	TALALAIAQELGSK	99.7%	98.2	25	98.2	2	0	0	1385.80	77	90
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	13	23	0.02%	33.0%	ALESDMAPVLIMATNR	99.7%	87	25	78.9	2	0	0	1731.88	315	330
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	13	23	0.02%	33.0%	AVLIAGQPGTGK	99.7%	63.8	25	55.7	2	0	0	1111.65	72	83
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	13	23	0.02%	33.0%	DKVQAGDVITIDK	99.7%	67.7	25	57.7	2	0	0	1401.76	185	197
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	13	23	0.02%	33.0%	EVVHTVSLHEIDVINSR	99.7%	35.9	25	35.9	0	2	0	1947.03	237	253
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	13	23	0.02%	33.0%	FVQCPDGELQK	99.7%	43.2	25	35.4	2	0	0	1320.63	224	234
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	13	23	0.02%	33.0%	GTEVQVDDIKR	99.7%	59.3	25	41.2	2	0	0	1259.66	418	428
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	13	23	0.02%	33.0%	LLIVSTTPYSEK	99.7%	41	25	39	2	0	0	1350.75	354	365
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	13	23	0.02%	33.0%	QASQGMVGQLAAR	99.7%	75.7	25	66.4	1	0	0	1316.67	41	53
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	13	23	0.02%	33.0%	TEALTQAFR	99.7%	46.2	25	37.5	2	0	0	1036.54	116	124
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	13	23	0.02%	33.0%	TQGFLALFSGDTGEIK	99.7%	122	25	113	2	0	0	1683.86	254	269
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	13	23	0.02%	33.0%	TTEMETIYDLGTK	99.7%	45.1	25	45.1	3	0	0	1517.70	165	177
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	12	13	23	0.02%	33.0%	VYSLFLDESR	99.7%	55.7	25	46.4	1	0	0	1228.62	429	438
S1 RNA-binding domain-containing protein 1	SRBD1	SRBD1_HUMAN	111.8	99.9%	2	2	2	0.00%	2.5%	ETEAYFADLIMK	99.6%	39.7	25	39.7	1	0	0	1430.69	603	614
S1 RNA-binding domain-containing protein 1	SRBD1	SRBD1_HUMAN	111.8	99.9%	2	2	2	0.00%	2.5%	LFNDDNTIPFIIR	97.7%	31.8	25	23.9	1	0	0	1577.83	235	247
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	4	6	13	0.01%	13.7%	FVIGGPQGDAGLTGR	99.7%	100	25	91.1	3	0	0	1444.75	250	264
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	4	6	13	0.01%	13.7%	TGMILLAGEITSR	99.7%	82.3	25	72.2	4	0	0	1377.74	62	74
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	4	6	13	0.01%	13.7%	TQVTVQYMQDR	99.6%	40.7	25	35.5	2	0	0	1384.65	182	192
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	4	6	13	0.01%	13.7%	YLDEDTIYHLQPSGR	99.7%	73.3	25	73.3	2	2	0	1806.87	235	249
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	35	70	0.07%	27.2%	AEIGIAMGSGTAVAK	99.7%	55.5	25	49	2	0	0	1391.72	713	727
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	35	70	0.07%	27.2%	AMGVVVATGVNTEIGK	99.7%	79.3	25	69.2	1	0	0	1561.83	219	234
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	35	70	0.07%	27.2%	ANACNSVIK	98.3%	33.3	25	22.3	2	0	0	976.49	468	476
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	35	70	0.07%	27.2%	DIVPGDIVEIAVGDK	99.7%	43.1	25	41.9	2	0	0	1539.83	144	158
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	35	70	0.07%	27.2%	EFDELNPSAQR	99.7%	66.2	25	58.2	2	0	0	1305.61	656	666
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	35	70	0.07%	27.2%	EFTLEFSR	99.7%	50	25	34.9	3	0	0	1028.50	482	489
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	35	70	0.07%	27.2%	EWGSGSDTLR	99.7%	48.8	25	33.7	2	0	0	1107.51	550	559
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	35	70	0.07%	27.2%	GTAVAICR	99.7%	42.4	25	25.1	2	0	0	847.45	629	636
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	35	70	0.07%	27.2%	HTDPVPDPR	98.5%	33.8	25	21	1	0	0	1033.51	190	198

Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	35	70	0.07%	27.2%	IGIFGQDEDVTSK	99.7%	80.6	25	75.4	4	0	0	1408.70	638	650
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	35	70	0.07%	27.2%	IRDEMVATEQER	99.7%	62.7	25	53.3	4	2	0	1476.71	235	246
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	35	70	0.07%	27.2%	ISLPVILMDETLK	99.7%	85.3	25	72.3	5	0	0	1471.84	972	984
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	35	70	0.07%	27.2%	KAEIGIAMGSGTAVAK	99.7%	65	25	59	2	1	0	1519.82	712	727
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	35	70	0.07%	27.2%	LDEFGEQLSK	99.7%	62.6	25	38.5	3	0	0	1165.57	253	262
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	35	70	0.07%	27.2%	MNVFDTELK	99.7%	44.5	25	27.1	3	0	0	1112.53	452	460
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	35	70	0.07%	27.2%	NMLFSGTNIAAGK	99.7%	83.6	25	81.5	4	0	0	1323.67	206	218
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	35	70	0.07%	27.2%	NYLEPGKECVQPATK	99.4%	37.8	25	31	2	0	0	1733.85	989	1003
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	35	70	0.07%	27.2%	RIGIFGQDEDVTSK	98.1%	32.6	25	32.6	1	0	0	1564.80	637	650
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	35	70	0.07%	27.2%	SLPSVETLGCTSVICSDK	99.7%	100	25	98.6	2	0	0	1952.93	335	352
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	35	70	0.07%	27.2%	SMSVYCTPNKPSR	99.7%	56.5	25	54.4	4	0	0	1542.70	493	505
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	35	70	0.07%	27.2%	TGTLTTNQMSVCR	99.7%	85.4	25	81.1	4	0	0	1468.69	353	365
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	35	70	0.07%	27.2%	VDQSILTGESVSVIK	99.7%	76.3	25	71.8	3	0	0	1574.86	175	189
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	35	70	0.07%	27.2%	VGEATETALTCLVEK	99.7%	107	25	97.4	4	0	0	1620.82	437	451
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	35	70	0.07%	27.2%	VIMITGDNK	99.3%	37.5	25	24.1	3	0	0	1006.52	620	628
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	25	35	70	0.07%	27.2%	WGSNELPAEEGK	99.7%	91.9	25	87.3	2	0	0	1316.61	36	47
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	24	63	0.06%	22.4%	ADSLLAVVK	99.7%	82	25	65.6	4	0	0	915.55	286	294
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	24	63	0.06%	22.4%	AIEDEGGNPDEIEITSEGNKK	99.7%	89.3	25	89.3	2	4	0	2245.05	64	84
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	24	63	0.06%	22.4%	CYGFVTMSTAEEATK	99.7%	97.8	25	95.7	6	0	0	1710.74	448	462
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	24	63	0.06%	22.4%	DDAYWPEAK	98.6%	34.2	25	32.5	1	0	0	1094.48	720	728
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	24	63	0.06%	22.4%	DGWGGYGSDKR	99.7%	42.4	25	32.9	2	0	0	1197.53	796	806
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	24	63	0.06%	22.4%	ELVEGEMK	99.3%	37.6	25	32.2	3	0	0	950.45	165	172
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	24	63	0.06%	22.4%	EPAEQPGDGER	96.7%	30.2	25	30.2	2	0	0	1184.52	296	306
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	24	63	0.06%	22.4%	FHDFDHR	99.2%	36.9	25	29.7	1	0	0	973.43	746	752
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	24	63	0.06%	22.4%	GRYPDHSVDR	98.7%	27.6	25	27.6	0	2	0	1201.57	755	764
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	24	63	0.06%	22.4%	ILDILGETCK	99.7%	77.5	25	66.4	5	0	0	1161.62	217	226
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	24	63	0.06%	22.4%	KFDFDACNEVPPAPK	99.7%	78.2	25	72.8	1	0	0	1734.82	356	370
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	24	63	0.06%	22.4%	MQAQWER	96.4%	29.9	25	19.7	2	0	0	948.44	633	639
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	24	63	0.06%	22.4%	MSSPEDDSDTKR	99.7%	55.6	25	55.6	4	1	0	1383.57	382	393
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	24	63	0.06%	22.4%	NFWVSGLSSTTR	99.7%	70	25	60.8	7	0	0	1354.67	407	418
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	24	63	0.06%	22.4%	REPAEQPGDGER	99.7%	48.8	25	47.9	6	0	0	1340.62	295	306
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	24	63	0.06%	22.4%	RPYDLDR	95.3%	28.8	25	12.1	1	0	0	934.47	712	718
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	24	63	0.06%	22.4%	SEPVKEESSELEQPFAQDTSSVGPDR	99.7%	79.7	25	79.7	0	4	0	2848.31	227	252
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	24	63	0.06%	22.4%	SKDQDDQKPGPSER	99.7%	45.4	25	45.2	2	3	0	1586.74	536	549
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.5%	ADSLLAVVK	99.7%	82	25	65.6	4	0	0	915.55	285	293
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.5%	DGWGGYGSDKR	99.7%	42.4	25	32.9	2	0	0	1197.53	820	830
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.5%	DIKPIIKDEK	99.2%	36.6	25	30	2	2	0	1198.70	389	398
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.5%	EPAEQPGDGER	96.7%	30.2	25	30.2	2	0	0	1184.52	295	305
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.5%	EYVAAQLR	99.7%	42	25	15.4	3	0	0	949.51	164	171
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.5%	FHDFDHR	99.2%	36.9	25	29.7	1	0	0	973.43	765	771
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.5%	GLSGPSGPGHMASR	98.6%	33.9	25	33.9	2	0	0	1326.62	884	897
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.5%	GQYQDHAIDR	99.1%	36.4	25	29.2	1	0	0	1202.56	774	783
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.5%	ILDILGETCK	99.7%	77.5	25	66.4	5	0	0	1161.62	216	225
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.5%	KFDFDACNEVPPAPK	99.7%	78.2	25	72.8	1	0	0	1734.82	355	369
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.5%	LEAFHER	99.7%	50.4	25	39	4	0	0	901.45	651	657
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.5%	NLWVSGLSSTTR	99.7%	79.5	25	74.5	3	0	0	1320.69	408	419
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.5%	NTLETSSLNFK	99.7%	76.5	25	70.7	4	0	0	1253.64	189	199
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.5%	REPAEQPGDGER	99.7%	48.8	25	47.9	6	0	0	1340.62	294	305
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.5%	RPYDLDR	95.3%	28.8	25	12.1	1	0	0	934.47	730	736
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.5%	SEPVKEESSELEQPFAQDTSSVGPDR	99.7%	79.7	25	79.7	0	4	0	2848.31	226	251
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.5%	SKGEPVISVK	99.7%	45.1	25	33.7	4	0	0	1043.61	577	586

Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.5%	VTPDIEESLLEPENEK	99.7%	96.7	25	93.7	4	0	0	1841.90	200	215
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	9	10	20	0.02%	11.5%	DQIIDSLKR	99.4%	38.4	25	24.8	1	0	0	1087.61	80	88
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	9	10	20	0.02%	11.5%	EPAVLMGILGIYK	99.7%	49.3	25	49.3	2	0	0	1403.80	539	551
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	9	10	20	0.02%	11.5%	LGSSSLTNIPEEVR	99.7%	72.8	25	59	2	0	0	1501.79	288	301
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	9	10	20	0.02%	11.5%	LILPELGPVFK	99.7%	50.2	25	38	2	0	0	1225.76	408	418
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	9	10	20	0.02%	11.5%	LLTVQHPLEESR	99.7%	49.8	25	41	2	0	0	1421.77	101	112
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	9	10	20	0.02%	11.5%	NACLQTSSLAVR	99.7%	89.9	25	77.9	4	0	0	1319.67	494	505
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	9	10	20	0.02%	11.5%	VNSLVCLGK	97.9%	32.3	25	19.3	1	0	0	989.54	506	514
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	9	10	20	0.02%	11.5%	VTADVTSAVMGNPVTR	99.7%	107	25	99	2	0	0	1633.82	15	30
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	9	10	20	0.02%	11.5%	VTNIGNQQIDK	99.7%	57.4	25	43.7	4	0	0	1229.65	637	647
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	5	5	9	0.01%	9.8%	FGQDIISPLLSVK	99.7%	64.4	25	64.4	2	0	0	1416.81	51	63
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	5	5	9	0.01%	9.8%	GTAAEMVAVK	99.7%	60.3	25	43.9	2	0	0	976.51	215	224
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	5	5	9	0.01%	9.8%	LTSAVSSLPELLEK	99.7%	79.2	25	63.2	2	0	0	1486.84	382	395
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	5	5	9	0.01%	9.8%	SLLDIISDPDAGTPEDK	99.7%	91.2	25	86	2	0	0	1785.88	437	453
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	5	5	9	0.01%	9.8%	SNPETDDYR	97.3%	31.2	25	31.2	1	0	0	1096.45	559	567
Septin-2	2-Sep	SEPT2_HUMAN	41.5	99.9%	2	2	2	0.00%	5.8%	TIISYIDEQFER	99.7%	44	25	40.3	1	0	0	1513.75	117	128
Septin-2	2-Sep	SEPT2_HUMAN	41.5	99.9%	2	2	2	0.00%	5.8%	VNIVPVIAK	97.8%	31.9	25	12.1	1	0	0	952.62	175	183
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	6	6	12	0.01%	12.1%	LEPKPQPPVAEATPR	99.7%	49.5	25	48.2	0	2	0	1629.90	223	237
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	6	6	12	0.01%	12.1%	QVENAGAIGPSR	99.7%	52.3	25	42.4	2	0	0	1198.62	118	129
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	6	6	12	0.01%	12.1%	STLINTLFK	98.0%	32.4	25	16.1	2	0	0	1036.60	312	320
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	6	6	12	0.01%	12.1%	VPEVPTAPATDAAPK	99.7%	66.3	25	61.3	2	0	0	1463.77	172	186
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	6	6	12	0.01%	12.1%	VVNIVPVIAK	99.5%	39	25	39	2	0	0	1051.69	436	445
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	6	6	12	0.01%	12.1%	YLQEEVNINR	99.7%	59.2	25	50.5	2	0	0	1277.65	390	399
Serine hydroxymethyltransferase, mitochondrial	SHMT2	GLYM_HUMAN	56.0	100.0%	3	3	3	0.00%	7.1%	AALEALGSCLNNK	99.7%	49.8	25	49.7	1	0	0	1360.69	83	95
Serine hydroxymethyltransferase, mitochondrial	SHMT2	GLYM_HUMAN	56.0	100.0%	3	3	3	0.00%	7.1%	AMADALLER	99.7%	75.5	25	61.4	1	0	0	989.51	360	368
Serine hydroxymethyltransferase, mitochondrial	SHMT2	GLYM_HUMAN	56.0	100.0%	3	3	3	0.00%	7.1%	TGLIDYNQLALTAR	99.7%	68.3	25	60.8	1	0	0	1548.84	201	214
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	7	8	16	0.02%	15.9%	AACFAIQK	99.7%	43.9	25	30.6	2	0	0	908.47	190	197
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	7	8	16	0.02%	15.9%	DHPALNYNIVSGPPSHK	99.7%	35	25	35	0	2	0	1845.92	76	92
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	7	8	16	0.02%	15.9%	EQEIEDQKNPR	99.7%	65.4	25	51.8	2	0	0	1385.67	223	233
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	7	8	16	0.02%	15.9%	HNDMADLER	99.7%	51.5	25	51.5	4	0	0	1100.48	211	219
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	7	8	16	0.02%	15.9%	LLQEIVDQCMNR	99.7%	70.8	25	70.8	2	0	0	1518.74	411	422
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	7	8	16	0.02%	15.9%	RGDIVFVDR	99.4%	38.2	25	17.1	2	0	0	1076.58	181	189
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	7	8	16	0.02%	15.9%	YGVGTCGPR	99.7%	58.5	25	50.4	2	0	0	966.45	128	136
Serine racemase	SRR	SRR_HUMAN	36.6	99.8%	2	2	2	0.00%	10.0%	AVVTHSSGNHGQALTYAAK	99.6%	32.4	25	32.4	0	1	0	1911.97	78	96
Serine racemase	SRR	SRR_HUMAN	36.6	99.8%	2	2	2	0.00%	10.0%	DLVDDIFTVTEDEIK	99.7%	67.1	25	65.5	1	0	0	1751.86	254	268
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	10	12	63	0.06%	40.7%	DAEDAVYGR	99.7%	49.8	25	45.8	2	0	0	995.44	66	74
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	10	12	63	0.06%	40.7%	DGTGVVEFVR	99.7%	63.9	25	49.1	7	0	0	1078.55	155	164
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	10	12	63	0.06%	40.7%	DGYDYDGYR	99.7%	63.5	25	61.8	6	0	0	1123.43	75	83
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	10	12	63	0.06%	40.7%	EAGDVCYADVYR	99.7%	68.8	25	68.8	7	0	0	1417.61	143	154
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	10	12	63	0.06%	40.7%	GGPPFAFVEFEDPR	99.7%	61.8	25	61.8	2	0	0	1564.74	52	65
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	10	12	63	0.06%	40.7%	GGPPFAFVEFEDPRDAEDAVYGR	99.7%	43.7	25	43.1	0	2	0	2541.17	52	74
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	10	12	63	0.06%	40.7%	IYVGNLPPDIR	99.7%	71	25	58.7	8	0	0	1256.70	18	28
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	10	12	63	0.06%	40.7%	KEDMTYAVR	99.7%	67.9	25	60.1	12	0	0	1112.54	165	173
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	10	12	63	0.06%	40.7%	LRVEFPR	99.2%	36.8	25	17.7	10	0	0	916.54	84	90
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	10	12	63	0.06%	40.7%	SHEGETAYIR	99.7%	51.5	25	51.5	9	0	0	1162.55	182	191
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	10	12	63	0.06%	40.7%	TKDIEDVFYK	99.7%	55.6	25	52.2	6	2	0	1257.64	29	38
Serine/arginine-rich splicing factor 10	SRSF10	SRS10_HUMAN	31.3	100.0%	4	6	12	0.01%	13.4%	GFAYVQFEDVR	99.7%	58.7	25	47.5	4	0	0	1330.64	52	62
Serine/arginine-rich splicing factor 10	SRSF10	SRS10_HUMAN	31.3	100.0%	4	6	12	0.01%	13.4%	QIEIQFAQGDR	99.7%	41.6	25	40.7	1	0	0	1304.66	80	90
Serine/arginine-rich splicing factor 10	SRSF10	SRS10_HUMAN	31.3	100.0%	4	6	12	0.01%	13.4%	QIEIQFAQGDRK	99.7%	60	25	40.5	2	2	0	1432.75	80	91
Serine/arginine-rich splicing factor 10	SRSF10	SRS10_HUMAN	31.3	100.0%	4	6	12	0.01%	13.4%	YLRPPNTSLFVR	99.7%	40.8	25	40.8	1	2	0	1462.82	4	15
Serine/arginine-rich splicing factor 2	SRSF2	SRSF2_HUMAN	25.5	99.8%	2	2	3	0.00%	12.7%	DAEDAMDAMDGAVLDGR	99.7%	87.4	25	87.4	1	0	0	1751.72	67	83

Serine/arginine-rich splicing factor 2	SRSF2	SRSF2_HUMAN	25.5	99.8%	2	2	3	0.00%	12.7%	YGRPPDSHHSR	99.7%	35.7	25	30.5	0	2	0	1308.62	92	102
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	10	11	45	0.04%	46.3%	AFGYYGPLR	99.7%	55.5	25	50.4	8	0	0	1043.53	29	37
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	10	11	45	0.04%	46.3%	DSCPLDCK	99.2%	36.5	25	35.5	3	0	0	994.40	4	11
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	10	11	45	0.04%	46.3%	GPPPSWGR	99.5%	38.9	25	32.8	3	0	0	853.43	91	98
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	10	11	45	0.04%	46.3%	NPPGFAFVEFEDPR	99.7%	70.2	25	70.2	5	0	0	1621.76	44	57
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	10	11	45	0.04%	46.3%	NPPGFAFVEFEDPRDAADAVR	97.1%	24.7	25	24.7	0	2	0	2320.10	44	64
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	10	11	45	0.04%	46.3%	NRGPPPSWGR	99.7%	47.5	25	43.9	6	0	0	1123.58	89	98
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	10	11	45	0.04%	46.3%	VELSNGEKR	99.7%	42	25	26.5	1	0	0	1031.55	78	86
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	10	11	45	0.04%	46.3%	VRVELSNGEK	99.7%	63.2	25	53.8	5	0	0	1130.62	76	85
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	10	11	45	0.04%	46.3%	VYVGNLGNNGNK	99.7%	58.5	25	50.8	4	0	0	1248.63	12	23
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	10	11	45	0.04%	46.3%	VYVGNLGNNGNKTELER	99.7%	77.1	25	62.6	4	4	0	1876.95	12	28
Serine/arginine-rich splicing factor 5	SRSF5	SRSF5_HUMAN	31.3	100.0%	6	7	10	0.01%	24.6%	GFGFVEFEDPR	99.7%	43.7	25	41	1	0	0	1299.60	38	48
Serine/arginine-rich splicing factor 5	SRSF5	SRSF5_HUMAN	31.3	100.0%	6	7	10	0.01%	24.6%	LIVENLSSR	99.7%	41.3	25	41.3	1	0	0	1030.59	110	118
Serine/arginine-rich splicing factor 5	SRSF5	SRSF5_HUMAN	31.3	100.0%	6	7	10	0.01%	24.6%	LNEGVVEFASYGDLK	99.7%	110	25	106	2	0	0	1640.82	144	158
Serine/arginine-rich splicing factor 5	SRSF5	SRSF5_HUMAN	31.3	100.0%	6	7	10	0.01%	24.6%	QAGEVTFADAHRPK	99.7%	49.1	25	47.1	1	2	0	1526.77	130	143
Serine/arginine-rich splicing factor 5	SRSF5	SRSF5_HUMAN	31.3	100.0%	6	7	10	0.01%	24.6%	VSWQDLKDFMR	98.8%	34.7	25	29.5	1	0	0	1424.70	119	129
Serine/arginine-rich splicing factor 5	SRSF5	SRSF5_HUMAN	31.3	100.0%	6	7	10	0.01%	24.6%	VTIEHAR	99.6%	40.1	25	22	2	0	0	825.46	67	73
Serine/arginine-rich splicing factor 6	SRSF6	SRSF6_HUMAN	39.6	99.8%	2	2	2	0.00%	7.3%	LIEDKPR	98.6%	34.1	25	16.1	1	0	0	870.50	178	184
Serine/arginine-rich splicing factor 6	SRSF6	SRSF6_HUMAN	39.6	99.8%	2	2	2	0.00%	7.3%	LIVENLSSR	99.7%	41.3	25	41.3	1	0	0	1030.59	112	120
Serine/arginine-rich splicing factor 6	SRSF6	SRSF6_HUMAN	39.6	99.8%	2	2	2	0.00%	7.3%	TNEGVIEFR	99.7%	47.8	25	34.5	1	0	0	1064.54	146	154
Serine/arginine-rich splicing factor 7	SRSF7	SRSF7_HUMAN	27.4	100.0%	7	8	19	0.02%	28.2%	AFSYYGPLR	99.7%	52.2	25	39.5	2	0	0	1073.54	30	38
Serine/arginine-rich splicing factor 7	SRSF7	SRSF7_HUMAN	27.4	100.0%	7	8	19	0.02%	28.2%	GHYAYDCHR	99.5%	39.3	25	39.3	2	0	0	1178.48	113	121
Serine/arginine-rich splicing factor 7	SRSF7	SRSF7_HUMAN	27.4	100.0%	7	8	19	0.02%	28.2%	NPPGFAFVEFEDPR	99.7%	70.2	25	70.2	5	0	0	1621.76	45	58
Serine/arginine-rich splicing factor 7	SRSF7	SRSF7_HUMAN	27.4	100.0%	7	8	19	0.02%	28.2%	NPPGFAFVEFEDPRDAEDAVR	99.7%	37.7	25	37.7	0	2	0	2378.10	45	65
Serine/arginine-rich splicing factor 7	SRSF7	SRSF7_HUMAN	27.4	100.0%	7	8	19	0.02%	28.2%	VELSTGMPR	99.7%	47.9	25	36.8	4	0	0	989.51	79	87
Serine/arginine-rich splicing factor 7	SRSF7	SRSF7_HUMAN	27.4	100.0%	7	8	19	0.02%	28.2%	VRVELSTGMPR	99.7%	46.4	25	46.4	2	0	0	1244.68	77	87
Serine/arginine-rich splicing factor 7	SRSF7	SRSF7_HUMAN	27.4	100.0%	7	8	19	0.02%	28.2%	VYVGNLGTGAGK	99.7%	82.8	25	80.4	6	0	0	1135.61	13	24
Serine/arginine-rich splicing factor 7	SRSF7	SRSF7_HUMAN	27.4	100.0%	7	8	19	0.02%	28.2%	VYVGNLGTGAGKGELER	99.5%	32	25	31.6	0	1	0	1719.90	13	29
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	64	0.06%	55.2%	DAEDAIYGR	99.2%	36.4	25	27.2	2	0	0	1009.46	64	72
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	64	0.06%	55.2%	DGVGMVEYLR	99.7%	61.5	25	46.1	8	0	0	1138.56	145	154
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	64	0.06%	55.2%	EAGDVCYADVQK	99.7%	73.7	25	73.7	4	0	0	1354.59	133	144
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	64	0.06%	55.2%	EDMEYALR	99.5%	38.9	25	26.3	2	0	0	1026.46	156	163
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	64	0.06%	55.2%	EKDLEDLFYK	99.7%	53.2	25	44.8	2	1	0	1299.65	27	36
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	64	0.06%	55.2%	FEDPRDAEDAIYGR	99.4%	38	25	38	3	3	0	1653.75	59	72
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	64	0.06%	55.2%	GSPHYFSPFRPY	99.6%	39.6	25	39.6	1	2	0	1454.69	210	221
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	64	0.06%	55.2%	HGLVPFAFVR	99.7%	41.6	25	40.8	6	0	0	1142.65	49	58
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	64	0.06%	55.2%	IYVGNLPTDVR	99.7%	62.9	25	46.3	2	0	0	1246.68	16	26
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	64	0.06%	55.2%	KEDMEYALR	99.7%	65.8	25	57.9	6	0	0	1170.55	155	163
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	64	0.06%	55.2%	LRVEFPR	99.2%	36.8	25	17.7	10	0	0	916.54	82	88
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	64	0.06%	55.2%	NGYDYGQCR	99.7%	70.1	25	64.9	4	0	0	1132.45	73	81
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	64	0.06%	55.2%	SHEGETSYIR	99.7%	51.8	25	45.1	6	0	0	1178.54	172	181
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	64	0.06%	55.2%	STSYGYSR	99.7%	41.6	25	40.9	2	0	0	920.41	187	194
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	9	10	16	0.02%	27.3%	AKDLILR	98.1%	32.8	25	17.3	3	0	0	828.53	353	359
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	9	10	16	0.02%	27.3%	DIKPDNLLLDSK	99.7%	41.3	25	34.7	2	1	0	1370.75	212	223
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	9	10	16	0.02%	27.3%	DTGHVYAMK	99.3%	37.1	25	26.9	2	0	0	1021.48	110	118
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	9	10	16	0.02%	27.3%	DWVFINYTYK	99.7%	51.6	25	0	2	0	0	1348.66	437	446
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	9	10	16	0.02%	27.3%	ERPAAISIEIK	99.7%	41.5	25	19.1	1	0	0	1226.71	392	402
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	9	10	16	0.02%	27.3%	GAIPSYMK	94.6%	28.3	25	12.7	1	0	0	882.44	455	462
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	9	10	16	0.02%	27.3%	IGAPGVEEIK	99.7%	71.1	25	56.3	2	0	0	1012.57	368	377
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	9	10	16	0.02%	27.3%	LGLEDFESLK	99.7%	54.2	25	52.3	2	0	0	1150.60	84	93
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	9	10	16	0.02%	27.3%	LSDFGLCTGLK	99.7%	79.1	25	72.2	2	0	0	1210.61	228	238

Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	9	10	16	0.02%	27.3%	LSDFGLCTGLKK	99.7%	66.6	25	59	3	0	0	1338.71	228	239
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	9	10	16	0.02%	27.3%	NLNHSLPSDFTFQNMNSK	99.7%	55.1	25	50.7	0	1	0	2093.97	248	265
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	9	10	16	0.02%	27.3%	RFEGLTAR	99.7%	47.8	25	41.6	2	0	0	949.52	447	454
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	9	10	16	0.02%	27.3%	VMEEEGLKDEEK	99.7%	65	25	48.4	2	0	0	1435.66	51	62
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	15	41	0.04%	29.5%	AKDLILR	98.1%	32.8	25	17.3	3	0	0	828.53	354	360
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	15	41	0.04%	29.5%	DIKPDNLLLDAK	99.7%	47.2	25	46.7	4	0	0	1354.76	213	224
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	15	41	0.04%	29.5%	DTGHIYAMK	99.1%	36.1	25	30.1	2	0	0	1035.49	111	119
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	15	41	0.04%	29.5%	DWVFLNYTYK	99.7%	51.6	25	0	2	0	0	1348.66	435	444
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	15	41	0.04%	29.5%	ERPAAIPIEIK	99.5%	38.7	25	27.7	3	0	0	1236.73	393	403
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	15	41	0.04%	29.5%	ETLVFPPEVPISEK	99.7%	55.6	25	50.5	2	0	0	1584.85	340	353
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	15	41	0.04%	29.5%	FCIDSENR	99.5%	38.8	25	33	4	0	0	1040.45	361	368
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	15	41	0.04%	29.5%	FEGLTQR	98.8%	34.9	25	16.9	2	0	0	850.44	446	452
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	15	41	0.04%	29.5%	KLEVAMEEEGLADEEK	99.7%	55.5	25	55.5	1	0	0	1835.86	48	63
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	15	41	0.04%	29.5%	LGLDDFESLK	99.7%	65.2	25	65.2	3	0	0	1136.58	85	94
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	15	41	0.04%	29.5%	LSDFGLCTGLK	99.7%	79.1	25	72.2	2	0	0	1210.61	229	239
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	15	41	0.04%	29.5%	LSDFGLCTGLKK	99.7%	66.6	25	59	3	0	0	1338.71	229	240
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	15	41	0.04%	29.5%	NLTHNPPSDFSFQNMNSK	99.7%	49.9	25	49.9	0	4	0	2093.93	249	266
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	15	41	0.04%	29.5%	RFEGLTQR	99.0%	35.4	25	21.8	4	0	0	1006.54	445	452
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	15	41	0.04%	29.5%	SKDWVFLNYTYK	99.7%	53.9	25	42.3	2	0	0	1563.78	433	444
Serine/threonine-protein kinase Chk1	CHEK1	CHK1_HUMAN	54.4	100.0%	3	3	3	0.00%	6.9%	ILVENPSAR	98.5%	33.6	25	12	1	0	0	998.56	245	253
Serine/threonine-protein kinase Chk1	CHEK1	CHK1_HUMAN	54.4	100.0%	3	3	3	0.00%	6.9%	VTSGGVSESPSGFSK	99.7%	44.7	25	44.7	1	0	0	1425.69	278	292
Serine/threonine-protein kinase Chk1	CHEK1	CHK1_HUMAN	54.4	100.0%	3	3	3	0.00%	6.9%	YSSSQPEPR	99.3%	37.6	25	37.6	1	0	0	1050.49	314	322
Serine/threonine-protein kinase MST4	MST4	MST4_HUMAN	46.5	100.0%	3	3	8	0.01%	10.1%	AANVLLSEQGDVK	99.7%	67.3	25	67.3	4	0	0	1343.72	147	159
Serine/threonine-protein kinase MST4	MST4	MST4_HUMAN	46.5	100.0%	3	3	8	0.01%	10.1%	ADIWSLGITAIELAK	99.7%	85.1	25	58.9	2	0	0	1600.89	200	214
Serine/threonine-protein kinase MST4	MST4	MST4_HUMAN	46.5	100.0%	3	3	8	0.01%	10.1%	AGPFDEFQIATMLK	99.7%	46.7	25	41.7	2	0	0	1567.78	113	126
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	6	6	9	0.01%	2.9%	DASAVSLSESK	99.7%	60.6	25	50.6	2	0	0	1093.54	911	921
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	6	6	9	0.01%	2.9%	DLELAVPGTYDPNQPIIR	98.5%	33.9	25	32	1	0	0	2011.05	2135	2152
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	6	6	9	0.01%	2.9%	LFDAPEAPLPSR	99.7%	54	25	37.9	2	0	0	1312.69	1121	1132
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	6	6	9	0.01%	2.9%	TLDQSPELR	97.6%	31.7	25	26.2	1	0	0	1058.55	1162	1170
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	6	6	9	0.01%	2.9%	TLVLLLGVDPSR	99.7%	65.4	25	52.1	1	0	0	1282.77	1672	1683
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	6	6	9	0.01%	2.9%	VLGLLGALDPYK	99.7%	47.8	25	47.8	2	0	0	1258.74	887	898
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	5	5	9	0.01%	12.9%	DTAEGVSQELISAGLVDGR	99.7%	72.1	25	69.5	1	0	0	1916.96	459	477
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	5	5	9	0.01%	12.9%	IPISLVLR	99.7%	45.8	25	45.8	2	0	0	910.61	432	439
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	5	5	9	0.01%	12.9%	LLSGGSVLDIIK	99.7%	79.6	25	59.2	2	0	0	1214.74	94	105
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	5	5	9	0.01%	12.9%	SGVLDESTIATILR	99.7%	59.6	25	51	2	0	0	1474.81	115	128
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	5	5	9	0.01%	12.9%	TAQALSSGSGSQETK	99.7%	83.3	25	73.8	2	0	0	1451.70	417	431
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	22	80	0.08%	34.3%	AMEIASQR	99.7%	51.1	25	27.7	5	0	0	905.45	402	409
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	22	80	0.08%	34.3%	ATVEQVLDPR	99.7%	73.3	25	68.6	8	0	0	1127.61	156	165
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	22	80	0.08%	34.3%	DCANVNDFFMR	99.7%	72.6	25	72.6	6	0	0	1404.57	360	370
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	22	80	0.08%	34.3%	DKYVSGEFR	96.5%	30	25	20.1	1	0	0	1100.54	221	229
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	22	80	0.08%	34.3%	EANVYHASTANGESR	99.7%	91.9	25	91.9	5	0	0	1605.73	191	205
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	22	80	0.08%	34.3%	ELFEFVTDPSITHENMDAYLSK	97.9%	25.9	25	25.9	0	3	0	2602.20	380	401
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	22	80	0.08%	34.3%	ELYLQVIQYMR	99.7%	85	25	75.4	8	0	0	1455.77	302	312
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	22	80	0.08%	34.3%	GIITEINGCISTGK	99.7%	59.6	25	59.6	2	0	0	1462.76	177	190
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	22	80	0.08%	34.3%	GYVWNGGSNPQANR	99.7%	70.4	25	67.7	2	0	0	1519.70	82	95
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	22	80	0.08%	34.3%	HSVAVMTVR	99.7%	50	25	37.3	7	0	0	999.54	371	379
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	22	80	0.08%	34.3%	INLDKLNVTDSVINK	99.7%	84.9	25	82.3	4	4	0	1685.94	120	134
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	22	80	0.08%	34.3%	LNTAEIPCPEPIMLR	99.7%	51.7	25	39	4	0	0	1753.90	257	271
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	22	80	0.08%	34.3%	LNVTDSVINK	99.7%	68.7	25	52.6	6	0	0	1102.61	125	134
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	22	80	0.08%	34.3%	SSQDHVDEEVFKR	99.7%	68.4	25	56.1	2	4	0	1575.74	415	427
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	22	80	0.08%	34.3%	VPALLENQVEER	99.7%	82.6	25	82.6	6	0	0	1396.74	482	493

Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	22	80	0.08%	34.3%	VVPGQFDDADSSDSENR	99.7%	76.7	25	76.7	2	0	0	1837.78	11	27
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	22	80	0.08%	34.3%	YVSGEFR	96.6%	30.2	25	22	1	0	0	857.42	223	229
Serine/threonine-protein kinase VRK1	VRK1	VRK1_HUMAN	45.5	100.0%	4	4	7	0.01%	11.6%	ASNLLLNYK	99.7%	67.8	25	54.1	2	0	0	1035.58	180	188
Serine/threonine-protein kinase VRK1	VRK1	VRK1_HUMAN	45.5	100.0%	4	4	7	0.01%	11.6%	NPDQVYLVDYGLAYR	99.7%	87.8	25	84.3	2	0	0	1785.88	189	203
Serine/threonine-protein kinase VRK1	VRK1	VRK1_HUMAN	45.5	100.0%	4	4	7	0.01%	11.6%	TVLQLSLR	99.7%	41.5	25	23.2	1	0	0	929.58	153	160
Serine/threonine-protein kinase VRK1	VRK1	VRK1_HUMAN	45.5	100.0%	4	4	7	0.01%	11.6%	VEPSDNGPLFTELK	99.7%	57.1	25	45.9	2	0	0	1545.78	72	85
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	5	5	8	0.01%	9.6%	ESSLTEPVIVGLLK	99.4%	37.9	25	37.9	2	0	0	1484.86	354	367
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	5	5	8	0.01%	9.6%	FLESPDFQPNIAK	99.7%	66	25	58.4	2	0	0	1505.76	220	232
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	5	5	8	0.01%	9.6%	TVETEAVQMLK	99.7%	46.5	25	35.3	2	0	0	1248.65	550	560
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	5	5	8	0.01%	9.6%	VLPIMFPALYR	98.8%	34.9	25	34.9	1	0	0	1319.75	442	452
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	5	5	8	0.01%	9.6%	YSGGPQIVK	98.6%	34.2	25	25.2	1	0	0	948.52	74	82
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	3	3	5	0.00%	5.3%	ELVSDANQHVK	99.7%	43.5	25	33.7	1	0	0	1239.63	332	342
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	3	3	5	0.00%	5.3%	LAGGDWFTSR	96.6%	30.1	25	11.3	2	0	0	1109.54	135	144
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	3	3	5	0.00%	5.3%	LTQDQDVDVK	99.7%	44.3	25	31.8	2	0	0	1160.58	567	576
Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	PPP2CA	PP2AA_HUMAN	35.6	99.8%	2	2	4	0.00%	8.4%	SPDTNYLFMGDYVDR	99.7%	71.9	25	71.9	2	0	0	1792.78	75	89
Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	PPP2CA	PP2AA_HUMAN	35.6	99.8%	2	2	4	0.00%	8.4%	YSFLQFDPAPR	99.7%	44	25	43.5	2	0	0	1340.66	284	294
Serine/threonine-protein phosphatase 4 regulatory subunit 3A	SMEK1	P4R3A_HUMAN	95.4	99.8%	2	2	3	0.00%	2.2%	INPNTAYQK	97.0%	30.7	25	28.1	1	0	0	1048.54	56	64
Serine/threonine-protein phosphatase 4 regulatory subunit 3A	SMEK1	P4R3A_HUMAN	95.4	99.8%	2	2	3	0.00%	2.2%	SFLFEPVVK	99.2%	36.5	25	33.7	2	0	0	1065.60	577	585
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	6	7	18	0.02%	24.9%	AHQLVHEGYK	99.7%	50.8	25	50.4	1	0	0	1181.61	236	245
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	6	7	18	0.02%	24.9%	APLDLDKYVEIAR	99.7%	77.5	25	69.6	4	1	0	1502.82	2	14
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	6	7	18	0.02%	24.9%	GAGWLFGAK	99.7%	56.3	25	33.1	2	0	0	906.48	211	219
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	6	7	18	0.02%	24.9%	LVTVWSAPNYCYR	99.7%	53.8	25	51.4	3	0	0	1628.79	252	264
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	6	7	18	0.02%	24.9%	TGGQVPDTNYIFMGDFVDR	99.7%	75.2	25	71.5	3	0	0	2131.98	67	85
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	6	7	18	0.02%	24.9%	VTNEFVHINNLK	99.7%	63.4	25	63.4	4	0	0	1427.76	220	231
Serine/threonine-protein phosphatase 6 regulatory subunit 3	PPP6R3	PP6R3_HUMAN	97.7	99.8%	2	2	3	0.00%	2.3%	GPNSALVQQLIK	99.7%	47.1	25	29	2	0	0	1267.74	475	486
Serine/threonine-protein phosphatase 6 regulatory subunit 3	PPP6R3	PP6R3_HUMAN	97.7	99.8%	2	2	3	0.00%	2.3%	VLSILISR	99.6%	39.9	25	39.9	1	0	0	900.59	127	134
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	12	13	40	0.04%	35.6%	AIETTDIISR	99.7%	75.2	25	61.8	5	0	0	1118.61	153	162
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	12	13	40	0.04%	35.6%	ALQFPPEGWLR	99.4%	38.3	25	24	6	0	0	1313.70	241	251
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	12	13	40	0.04%	35.6%	EPLSLINVR	99.7%	48.3	25	45.6	2	0	0	1040.61	66	74
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	12	13	40	0.04%	35.6%	EQAELTGLR	99.7%	50.5	25	35.7	7	0	0	1016.54	126	134
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	12	13	40	0.04%	35.6%	HSQYHVDGSLEK	99.7%	37.9	25	31.3	1	2	0	1399.66	105	116
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	12	13	40	0.04%	35.6%	HSQYHVDGSLEKDR	99.7%	44.8	25	36.4	0	2	0	1670.79	105	118
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	12	13	40	0.04%	35.6%	NVESGEEELASK	99.7%	86.8	25	78.8	4	0	0	1291.60	77	88
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	12	13	40	0.04%	35.6%	QEEDSYEIFICHANVIR	99.7%	55.2	25	55.2	0	2	0	2122.99	219	235
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	12	13	40	0.04%	35.6%	REPLSLINVR	99.3%	37.6	25	37.6	2	0	0	1196.71	65	74
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	12	13	40	0.04%	35.6%	RNVESGEEELASK	99.0%	35.6	25	34.8	1	0	0	1447.70	76	88
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	12	13	40	0.04%	35.6%	TLGDTGFMPPDK	99.7%	54.8	25	48.4	2	0	0	1278.60	274	285
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	12	13	40	0.04%	35.6%	VSTDLLR	99.5%	38.9	25	24.9	4	0	0	803.46	170	176
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	PP1G_HUMAN	37.0	100.0%	6	7	15	0.01%	24.1%	AHQVVEDGYEFFAK	99.7%	66.6	25	66.6	2	2	0	1639.78	247	260
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	PP1G_HUMAN	37.0	100.0%	6	7	15	0.01%	24.1%	ICGDIHGQYYDLLR	98.9%	28.5	25	26.9	0	2	0	1722.83	61	74
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	PP1G_HUMAN	37.0	100.0%	6	7	15	0.01%	24.1%	NVQLQENEIR	99.7%	52.3	25	46.4	2	0	0	1242.64	27	36
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	PP1G_HUMAN	37.0	100.0%	6	7	15	0.01%	24.1%	QSLETICLLLAYK	99.7%	49.1	25	45.4	2	0	0	1551.85	99	111
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	PP1G_HUMAN	37.0	100.0%	6	7	15	0.01%	24.1%	TFTDCFNCLPIAAIVDEK	99.7%	81.1	25	67.5	3	0	0	2113.99	151	168
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	PP1G_HUMAN	37.0	100.0%	6	7	15	0.01%	24.1%	YPENFFLLR	99.7%	53.9	25	33.9	2	0	0	1198.63	114	122
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	6	6	10	0.01%	22.9%	EFLVAGGEDFK	99.2%	37	25	33.6	1	0	0	1211.59	236	246
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	6	6	10	0.01%	22.9%	FSPDGELYASGSEDGTLR	99.7%	75.1	25	74.5	1	0	0	1900.86	273	290
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	6	6	10	0.01%	22.9%	IYDLNKPEAEPK	99.7%	64.3	25	59.2	2	0	0	1416.74	126	137
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	6	6	10	0.01%	22.9%	LWQTVVGK	99.7%	42.3	25	32.9	2	0	0	930.54	291	298
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	6	6	10	0.01%	22.9%	TVDFTQDSNYLLTGGQDK	99.7%	82.8	25	82.8	2	0	0	2001.94	105	122
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	6	6	10	0.01%	22.9%	YDYNSGEELESYK	99.7%	80.2	25	80.2	2	0	0	1596.67	250	262
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	12	12	23	0.02%	36.8%	DQAVENILVSPVVVASSLGLVSLGGK	99.7%	52.4	25	52.4	0	1	0	2551.43	61	86

Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	12	12	23	0.02%	36.8%	DTQSGSLLFIGR	99.7%	93.5	25	78.4	4	0	0	1293.68	394	405
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	12	12	23	0.02%	36.8%	GVVEVTHDLQK	99.7%	55.5	25	43.1	2	0	0	1224.66	309	319
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	12	12	23	0.02%	36.8%	HLAGLGLTEAIDK	99.7%	56.3	25	54.7	1	0	0	1337.74	320	332
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	12	12	23	0.02%	36.8%	HLAGLGLTEAIDKNK	99.7%	62.9	25	62.9	0	2	0	1579.88	320	334
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	12	12	23	0.02%	36.8%	KPAAAAAPGTAEK	99.7%	65.2	25	56.8	2	0	0	1182.65	23	35
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	12	12	23	0.02%	36.8%	LFYADHPFIFLVR	99.7%	53.4	25	53.4	2	0	0	1637.88	381	393
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	12	12	23	0.02%	36.8%	LQIVEMPLAHK	99.7%	50.4	25	39.5	2	0	0	1294.72	253	263
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	12	12	23	0.02%	36.8%	LYGPSSVSFADDFVR	99.7%	87.1	25	82.9	3	0	0	1659.80	134	148
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	12	12	23	0.02%	36.8%	SAGLAFSLYQAMAK	99.7%	79.2	25	78.4	2	0	0	1457.75	47	60
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	12	12	23	0.02%	36.8%	SYTVGVMMMHR	96.3%	29.9	25	23.3	1	0	0	1311.60	229	239
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	12	12	23	0.02%	36.8%	TGLYNYYDDEKEK	99.4%	31.1	25	31.1	0	1	0	1637.73	240	252
Serum albumin	ALB	ALBU_HUMAN	69.4	100.0%	4	4	7	0.01%	7.9%	KVPQVSTPTLVEVSR	96.6%	30.2	25	30.2	1	0	0	1639.94	438	452
Serum albumin	ALB	ALBU_HUMAN	69.4	100.0%	4	4	7	0.01%	7.9%	LVAASQAALGL	97.4%	31.2	25	31.2	2	0	0	1013.60	599	609
Serum albumin	ALB	ALBU_HUMAN	69.4	100.0%	4	4	7	0.01%	7.9%	LVNEVTEFAK	98.7%	34.4	25	34.4	2	0	0	1149.62	66	75
Serum albumin	ALB	ALBU_HUMAN	69.4	100.0%	4	4	7	0.01%	7.9%	YICENQDSISSK	99.7%	53.9	25	51.6	2	0	0	1443.64	287	298
Sestrin-2	SESN2	SESN2_HUMAN	54.5	99.8%	2	2	3	0.00%	6.0%	FAPGGVGDSGPGEEQR	99.7%	74.2	25	74.2	1	0	0	1559.71	18	33
Sestrin-2	SESN2	SESN2_HUMAN	54.5	99.8%	2	2	3	0.00%	6.0%	GPSAFIPVEEVLR	99.7%	46	25	37.6	2	0	0	1413.77	43	55
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	9	10	20	0.02%	27.1%	ASSTCPLTFENVK	99.7%	71.9	25	60.5	2	0	0	1453.70	257	269
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	9	10	20	0.02%	27.1%	ATYLPQLTTEK	99.7%	60.1	25	53.8	2	0	0	1264.68	160	170
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	9	10	20	0.02%	27.1%	FAQEQIAPLVSTMDENSK	99.7%	72.9	25	72.9	2	0	0	2023.96	71	88
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	9	10	20	0.02%	27.1%	GITSFLVDR	96.7%	30.2	25	14.7	2	0	0	1007.55	231	239
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	9	10	20	0.02%	27.1%	IGTIYEGASNIQLNTIAK	99.7%	97.7	25	95.4	2	0	0	1906.03	409	426
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	9	10	20	0.02%	27.1%	LLEAGKPFIK	99.7%	44.5	25	33.4	2	0	0	1115.68	356	365
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	9	10	20	0.02%	27.1%	VPEANILGQIGHGYK	99.7%	78.7	25	76.6	2	2	0	1595.85	270	284
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	9	10	20	0.02%	27.1%	YAIGSLNEGR	99.7%	74.9	25	60.4	2	0	0	1079.55	285	294
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	9	10	20	0.02%	27.1%	YYASEIAGQTTSK	99.7%	105	25	96.3	2	0	0	1418.68	372	384
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	13	18	34	0.03%	48.4%	ANHFFTVTDPR	99.7%	56.7	25	44.1	2	1	0	1304.64	25	35
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	13	18	34	0.03%	48.4%	FVPFAAVAAANCINIPLMR	99.7%	44.4	25	44.4	0	3	0	2091.09	179	197
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	13	18	34	0.03%	48.4%	HVSPLIGR	97.8%	32	25	28.9	2	0	0	878.52	171	178
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	13	18	34	0.03%	48.4%	ILMAAPGMAIPPFIMNTLEK	99.7%	56.3	25	35.5	4	1	0	2190.14	234	253
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	13	18	34	0.03%	48.4%	IQESHPELR	99.7%	63.4	25	45.8	2	0	0	1108.57	306	314
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	13	18	34	0.03%	48.4%	IQESHPELRR	99.4%	31.2	25	20.6	0	2	0	1264.68	306	315
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	13	18	34	0.03%	48.4%	NILLTNEQLESAR	99.7%	101	25	97.2	2	0	0	1500.80	36	48
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	13	18	34	0.03%	48.4%	QAITQVVVSR	99.7%	95.5	25	87.8	2	0	0	1100.64	224	233
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	13	18	34	0.03%	48.4%	QGIVPPGLTENELWR	99.7%	67.9	25	65.1	2	0	0	1708.90	56	70
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	13	18	34	0.03%	48.4%	SSMSVTSLEAELQAK	99.7%	77.5	25	77.5	3	0	0	1596.78	291	305
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	13	18	34	0.03%	48.4%	VGIPVTDENGNR	99.7%	59.2	25	59.2	2	0	0	1270.64	203	214
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	13	18	34	0.03%	48.4%	WDQSTFIGR	99.7%	54.1	25	0	2	0	0	1109.54	16	24
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	13	18	34	0.03%	48.4%	YIYDSAFHPDTGEK	99.7%	69.8	25	66.5	2	2	0	1642.74	73	86
Sideroflexin-2	SFXN2	SFXN2_HUMAN	36.2	99.9%	2	2	6	0.01%	7.8%	AAAIGITQVVISR	99.7%	66.6	25	54.3	2	0	0	1298.78	220	232
Sideroflexin-2	SFXN2	SFXN2_HUMAN	36.2	99.9%	2	2	6	0.01%	7.8%	YGELEPYVYFNK	99.7%	51.9	25	44.8	4	0	0	1521.73	309	320
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	100.0%	7	7	12	0.01%	22.0%	DAVPAFIEPNVR	99.7%	45.7	25	40	2	0	0	1327.70	19	30
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	100.0%	7	7	12	0.01%	22.0%	EGNVLGHSR	99.7%	47.3	25	35	2	0	0	968.49	231	239
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	100.0%	7	7	12	0.01%	22.0%	FWITER	98.5%	33.9	25	23.3	1	0	0	851.44	31	36
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	100.0%	7	7	12	0.01%	22.0%	IQSPTEETEIFYHR	99.7%	36.4	25	35.8	0	2	0	1749.84	322	335
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	100.0%	7	7	12	0.01%	22.0%	SLATVHPDSSNLIPK	98.9%	35	25	31.5	2	0	0	1578.85	92	106
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	100.0%	7	7	12	0.01%	22.0%	SYTCKPLER	96.8%	30.4	25	18.5	1	0	0	1153.57	156	164
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	100.0%	7	7	12	0.01%	22.0%	YGLTGPWIK	99.6%	40.3	25	29.9	2	0	0	1034.57	189	197
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	6	7	17	0.02%	30.7%	EIPIVHR	97.9%	32.3	25	15.9	2	0	0	863.51	91	97
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	6	7	17	0.02%	30.7%	GDLLFLTNR	99.7%	73.6	25	52.1	4	0	0	1048.58	64	72
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	6	7	17	0.02%	30.7%	GDLLFLTNRVEDPIR	95.7%	23.2	25	19.1	0	1	0	1757.95	64	78

Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	6	7	17	0.02%	30.7%	GDNNAVDDRGLYK	99.7%	49.9	25	47.3	2	0	0	1436.68	115	127
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	6	7	17	0.02%	30.7%	MLSLDFLDDVRR	99.6%	33.4	25	29.9	1	2	0	1495.76	1	12
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	6	7	17	0.02%	30.7%	VGEIVVFR	99.7%	71.6	25	66.9	5	0	0	918.54	79	86
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	9	9	17	0.02%	45.1%	FDDKYTLK	99.2%	36.6	25	29	2	0	0	1029.53	166	173
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	9	9	17	0.02%	45.1%	FFDHSGTLVMDAYEPEISR	99.7%	38.9	25	35.5	0	2	0	2230.01	196	214
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	9	9	17	0.02%	45.1%	IDDKPVKIDK	99.7%	43.5	25	32.3	2	0	0	1170.67	41	50
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	9	9	17	0.02%	45.1%	IDKWDGSAVK	99.7%	42.9	25	24.3	2	0	0	1118.58	48	57
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	9	9	17	0.02%	45.1%	LHDSLAIER	99.7%	55.9	25	47.3	2	0	0	1053.57	215	223
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	9	9	17	0.02%	45.1%	SGGSGGCSGAGGASNCGTGSGR	99.7%	54.7	25	54.7	1	0	0	1857.72	11	32
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	9	9	17	0.02%	45.1%	SGLLDKWK	99.7%	49.8	25	27.9	2	0	0	946.54	33	40
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	9	9	17	0.02%	45.1%	SIFLVAHR	99.4%	38.1	25	28.1	2	0	0	942.55	138	145
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	9	9	17	0.02%	45.1%	YVENFGLIDGR	99.7%	70	25	65.5	2	0	0	1282.64	74	84
Signal peptidase complex subunit 3	SPCS3	SPCS3_HUMAN	20.3	100.0%	3	3	6	0.01%	17.8%	NNALNQVVLWDK	99.7%	67.9	25	60.3	2	0	0	1413.75	97	108
Signal peptidase complex subunit 3	SPCS3	SPCS3_HUMAN	20.3	100.0%	3	3	6	0.01%	17.8%	NVEDFTGPR	99.7%	48.3	25	44	2	0	0	1034.49	50	58
Signal peptidase complex subunit 3	SPCS3	SPCS3_HUMAN	20.3	100.0%	3	3	6	0.01%	17.8%	YFFFDDGNGLK	99.3%	37.4	25	33.9	2	0	0	1322.61	127	137
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	9	14	38	0.04%	47.8%	EVNKFQMAYSNLLR	99.7%	52.1	25	39.4	4	4	0	1712.88	75	88
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	9	14	38	0.04%	47.8%	FQMAYSNLLR	99.7%	76.7	25	62.8	6	0	0	1242.63	79	88
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	9	14	38	0.04%	47.8%	GTVEGFEPADNK	99.7%	83.3	25	79.3	3	0	0	1263.59	44	55
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	9	14	38	0.04%	47.8%	GTVEGFEPADNKCLLR	98.0%	26.1	25	26.1	0	1	0	1805.89	44	59
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	9	14	38	0.04%	47.8%	ISTVVSSK	99.0%	35.8	25	29	2	0	0	820.48	67	74
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	9	14	38	0.04%	47.8%	KGTVEGFEPADNK	99.6%	40.6	25	35.2	4	1	0	1391.68	43	55
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	9	14	38	0.04%	47.8%	KISTVVSSK	99.7%	49.2	25	37.8	3	0	0	948.57	66	74
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	9	14	38	0.04%	47.8%	TSGSVYITLKK	99.7%	61	25	61	4	0	0	1196.69	22	32
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	9	14	38	0.04%	47.8%	VLLESEQFLTELTR	99.7%	83.5	25	74.6	6	0	0	1677.91	2	15
Signal recognition particle 19 kDa protein	SRP19	SRP19_HUMAN	16.2	100.0%	2	3	6	0.01%	18.8%	SVMLYAAEMIPK	99.7%	51.6	25	41	4	0	0	1384.69	103	114
Signal recognition particle 19 kDa protein	SRP19	SRP19_HUMAN	16.2	100.0%	2	3	6	0.01%	18.8%	TGGADQSLQQGEGSK	99.7%	63.5	25	53.5	2	0	0	1462.68	122	136
Signal recognition particle 9 kDa protein	SRP9	SRP09_HUMAN	10.1	100.0%	4	5	12	0.01%	43.0%	FHSQLMR	97.9%	32.3	25	23.7	1	0	0	934.46	65	71
Signal recognition particle 9 kDa protein	SRP9	SRP09_HUMAN	10.1	100.0%	4	5	12	0.01%	43.0%	LYLADPMK	99.7%	42.8	25	25.4	5	0	0	966.50	17	24
Signal recognition particle 9 kDa protein	SRP9	SRP09_HUMAN	10.1	100.0%	4	5	12	0.01%	43.0%	PQYQTWEEFSR	99.7%	70.4	25	70.4	2	0	0	1470.66	2	12
Signal recognition particle 9 kDa protein	SRP9	SRP09_HUMAN	10.1	100.0%	4	5	12	0.01%	43.0%	VTDDLVCLVYK	99.7%	70.9	25	60.1	4	0	0	1324.68	42	52
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	7	9	11	0.01%	12.5%	AGAVEQLR	99.7%	46.7	25	25.2	2	0	0	843.47	459	466
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	7	9	11	0.01%	12.5%	DAAGIAMEAIAFAR	99.7%	87.8	25	78.5	3	0	0	1406.71	497	510
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	7	9	11	0.01%	12.5%	GGNNSFTHEALTLK	99.7%	51.9	25	45	1	0	0	1488.74	42	55
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	7	9	11	0.01%	12.5%	KEGSDGPLATSKPVPAEK	99.6%	33.1	25	29.5	0	1	0	1810.95	174	191
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	7	9	11	0.01%	12.5%	LIDGIVLTK	99.7%	42	25	27	1	0	0	971.61	581	589
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	7	9	11	0.01%	12.5%	MLDFFTIFSK	99.7%	43.2	25	43.2	2	0	0	1264.63	1	10
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	7	9	11	0.01%	12.5%	SVLLQER	98.9%	35	25	0	1	0	0	844.49	35	41
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	10	10	26	0.02%	48.3%	AIVFVVDSAAFQR	99.7%	49.6	25	44.2	2	0	0	1422.77	138	150
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	10	10	26	0.02%	48.3%	AVLLVGLCDSGK	99.7%	84.5	25	73.9	2	0	0	1231.67	66	77
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	10	10	26	0.02%	48.3%	DTQTSITDSCAVYR	99.7%	76.5	25	76.5	4	0	0	1616.72	91	104
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	10	10	26	0.02%	48.3%	GDVGSADIQDLEK	99.7%	90.4	25	79.5	4	0	0	1346.64	253	265
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	10	10	26	0.02%	48.3%	GNSLTLIDLPGHESLR	99.7%	33.5	25	33.5	0	2	0	1721.92	110	125
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	10	10	26	0.02%	48.3%	LIQQQLEK	99.7%	42.4	25	20.2	2	0	0	999.58	192	199
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	10	10	26	0.02%	48.3%	LQFLER	99.6%	40.5	25	0	2	0	0	805.46	126	131
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	10	10	26	0.02%	48.3%	NTPSFLIACNK	99.5%	39.2	25	29.4	3	0	0	1264.64	171	181
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	10	10	26	0.02%	48.3%	SAAPSTLDSSSTAPAQLGK	99.7%	103	25	103	2	0	0	1788.90	209	227
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	10	10	26	0.02%	48.3%	VADGGGAGGTFQPYLDTLR	99.7%	88.4	25	88.4	3	0	0	1894.93	9	27
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	12	12	24	0.02%	23.8%	AAIEAFNK	99.4%	38.3	25	27.7	1	0	0	863.46	206	213
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	12	12	24	0.02%	23.8%	ALLQQQPEDDSKR	99.2%	29.9	25	25.6	0	1	0	1527.78	405	417
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	12	12	24	0.02%	23.8%	DLPDVQELITQVR	99.7%	48.1	25	44.8	4	0	0	1525.82	509	521
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	12	12	24	0.02%	23.8%	FETFCLDPSLVTK	99.7%	73.3	25	70	2	0	0	1556.77	558	570

Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	12	12	24	0.02%	23.8%	LASAFTEEQAVLYNQR	99.7%	85.9	25	80.4	2	0	0	1839.92	221	236
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	12	12	24	0.02%	23.8%	LEALITQTR	99.7%	48.5	25	34.7	2	0	0	1044.60	278	286
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	12	12	24	0.02%	23.8%	LFESMLSECR	99.7%	55.7	25	46.4	2	0	0	1271.58	336	345
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	12	12	24	0.02%	23.8%	QVPGGGGGGGSGGGGGSGGGGSGGGR	99.7%	51.7	25	51.7	1	0	0	1843.80	6	31
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	12	12	24	0.02%	23.8%	SPRPQDLIR	95.8%	29.3	25	21.4	1	0	0	1081.61	418	426
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	12	12	24	0.02%	23.8%	VEEISPNIR	99.7%	45.8	25	41.9	4	0	0	1056.57	237	245
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	12	12	24	0.02%	23.8%	VTEELLTDNR	99.7%	72.3	25	53.7	2	0	0	1189.61	113	122
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	12	12	24	0.02%	23.8%	YANEVNSDAGAFK	99.7%	64.2	25	49.7	2	0	0	1385.63	492	504
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	11	11	20	0.02%	20.3%	AIELLQEFSDQHPENAAEIK	99.7%	40	25	40	0	2	0	2282.13	357	376
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	11	11	20	0.02%	20.3%	EALNVINTHTK	99.7%	44	25	37.2	2	0	0	1239.67	63	73
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	11	11	20	0.02%	20.3%	GTQGATAGASSELDASK	99.7%	90.4	25	87	2	0	0	1550.73	601	617
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	11	11	20	0.02%	20.3%	ISQGNISK	99.4%	37.8	25	24.5	1	0	0	846.47	384	391
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	11	11	20	0.02%	20.3%	SPAHLSLIR	99.7%	57.3	25	46.3	2	0	0	993.58	443	451
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	11	11	20	0.02%	20.3%	TEEALQLYNQIIK	99.7%	99.9	25	91.3	2	0	0	1562.84	242	254
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	11	11	20	0.02%	20.3%	TIESANQQTDKLK	99.7%	66.7	25	56.6	2	0	0	1475.77	100	112
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	11	11	20	0.02%	20.3%	VDVEALENSAGATYIR	99.7%	119	25	114	2	0	0	1707.85	516	531
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	11	11	20	0.02%	20.3%	VLANNSLSFEK	99.7%	55.4	25	43.3	2	0	0	1221.65	74	84
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	11	11	20	0.02%	20.3%	YDECLAVYR	99.7%	50.4	25	48.7	1	0	0	1188.54	125	133
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	11	11	20	0.02%	20.3%	YGQNGDFTR	99.7%	56.4	25	43.8	2	0	0	1057.47	21	29
Signal transducer and activator of transcription 1-alpha/beta	STAT1	STAT1_HUMAN	87.3	100.0%	3	3	3	0.00%	5.1%	NLSFFLTPPCAR	99.6%	39.8	25	39.8	1	0	0	1422.72	483	494
Signal transducer and activator of transcription 1-alpha/beta	STAT1	STAT1_HUMAN	87.3	100.0%	3	3	3	0.00%	5.1%	TELISVSEVHPSR	99.7%	64.2	25	52.5	1	0	0	1453.76	704	716
Signal transducer and activator of transcription 1-alpha/beta	STAT1	STAT1_HUMAN	87.3	100.0%	3	3	3	0.00%	5.1%	VMAAENIPENPLK	99.7%	46	25	41.4	1	0	0	1425.74	653	665
Signal transducer and activator of transcription 3	STAT3	STAT3_HUMAN	88.1	100.0%	4	4	7	0.01%	8.3%	FLQESNVLYQHNLR	98.9%	28.5	25	27.4	0	1	0	1760.91	71	84
Signal transducer and activator of transcription 3	STAT3	STAT3_HUMAN	88.1	100.0%	4	4	7	0.01%	8.3%	GLSIEQLTTLAEK	99.7%	92.2	25	78.1	2	0	0	1402.78	519	531
Signal transducer and activator of transcription 3	STAT3	STAT3_HUMAN	88.1	100.0%	4	4	7	0.01%	8.3%	LLQTAATAAQQGGQANHPTAAVVTEK	99.7%	87.3	25	87.3	0	3	0	2576.34	115	140
Signal transducer and activator of transcription 3	STAT3	STAT3_HUMAN	88.1	100.0%	4	4	7	0.01%	8.3%	TQIQSVEPYTK	94.7%	28.4	25	0.24	1	0	0	1293.67	632	642
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	7	9	16	0.02%	58.1%	DVAYQYVK	99.6%	40.8	25	34.2	2	0	0	985.50	96	103
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	7	9	16	0.02%	58.1%	IDYGEYMDKNNVR	99.4%	38.5	25	37.2	2	0	0	1616.74	114	126
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	7	9	16	0.02%	58.1%	ISVFRPGLR	97.9%	32.1	25	25.4	2	0	0	1044.63	87	95
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	7	9	16	0.02%	58.1%	NPVTIFSLATNEMWR	99.7%	76.6	25	76.6	4	0	0	1778.89	52	66
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	7	9	16	0.02%	58.1%	QATTIIADNIIFLSDQTK	99.7%	51.8	25	51.8	2	0	0	1992.07	128	145
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	7	9	16	0.02%	58.1%	SGDSEVYQLGDVSQK	99.7%	108	25	105	2	0	0	1611.75	67	81
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	7	9	16	0.02%	58.1%	VGQDPVLR	99.7%	56.7	25	49.4	2	0	0	883.50	39	46
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	12	12	22	0.02%	11.7%	DLALVNDQLLGFVR	99.7%	65.7	25	65.7	2	0	0	1572.87	391	404
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	12	12	22	0.02%	11.7%	EINSDQATQGNISSDR	99.7%	84.3	25	84.3	1	0	0	1734.79	1220	1235
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	12	12	22	0.02%	11.7%	EVQLAQIFEPLSR	99.7%	94.5	25	87.1	2	0	0	1529.83	751	763
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	12	12	22	0.02%	11.7%	FNDIHVPVR	99.7%	44.6	25	31.6	2	0	0	1096.59	332	340
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	12	12	22	0.02%	11.7%	IAPVHIDSEAISALVK	98.7%	27.8	25	27.8	0	2	0	1662.94	618	633
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	12	12	22	0.02%	11.7%	IETDLPQIR	99.6%	39.7	25	33.5	2	0	0	1084.60	709	717
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	12	12	22	0.02%	11.7%	LLVACCLADIFR	99.7%	80.6	25	80.6	2	0	0	1450.75	88	99
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	12	12	22	0.02%	11.7%	LYTVCDVALCVINSK	99.7%	59.7	25	54.5	2	0	0	1754.88	1075	1089
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	12	12	22	0.02%	11.7%	NDDLNKPINK	99.5%	38.8	25	34	2	0	0	1170.61	1285	1294
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	12	12	22	0.02%	11.7%	SIEGTADDEEEGVSPDTAIR	99.7%	81.4	25	73.1	2	0	0	2090.94	638	657
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	12	12	22	0.02%	11.7%	STLIPILHQK	99.1%	36.3	25	19.1	1	0	0	1149.70	718	727
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	12	12	22	0.02%	11.7%	TVTAAGAENIQQK	99.7%	91.7	25	80.3	2	0	0	1330.70	1240	1252
Sister chromatid cohesion protein PDS5 homolog B	PDS5B	PDS5B_HUMAN	164.7	100.0%	2	2	2	0.00%	2.1%	IEEDFPHIR	99.7%	54.4	25	45	1	0	0	1155.58	699	707
Sister chromatid cohesion protein PDS5 homolog B	PDS5B	PDS5B_HUMAN	164.7	100.0%	2	2	2	0.00%	2.1%	LLVACCLADIFR	99.7%	80.6	25	80.6	2	0	0	1450.75	78	89
Sister chromatid cohesion protein PDS5 homolog B	PDS5B	PDS5B_HUMAN	164.7	100.0%	2	2	2	0.00%	2.1%	VAEAALQIFK	99.7%	55.5	25	49.6	1	0	0	1089.63	684	693
Small nuclear ribonucleoprotein E	SNRPE	RUXE_HUMAN	10.8	100.0%	4	6	17	0.02%	42.4%	GDNITLLQSVSN	99.7%	43.9	25	43.2	4	0	0	1260.64	81	92
Small nuclear ribonucleoprotein E	SNRPE	RUXE_HUMAN	10.8	100.0%	4	6	17	0.02%	42.4%	IMLKGDNITLLQSVSN	99.7%	48.2	25	48.2	4	0	0	1761.94	77	92
Small nuclear ribonucleoprotein E	SNRPE	RUXE_HUMAN	10.8	100.0%	4	6	17	0.02%	42.4%	IQVWLYEQVNMR	99.7%	54.4	25	49.5	2	0	0	1594.80	31	42

Small nuclear ribonucleoprotein E	SNRPE	RUXE_HUMAN	10.8	100.0%	4	6	17	0.02%	42.4%	VMVQPINLIFR	99.7%	60.9	25	48.6	7	0	0	1345.77	13	23
Small nuclear ribonucleoprotein F	SNRPF	RUXF_HUMAN	9.7	100.0%	2	3	7	0.01%	24.4%	CNNVLYIR	99.7%	57.8	25	39.8	5	0	0	1051.54	66	73
Small nuclear ribonucleoprotein F	SNRPF	RUXF_HUMAN	9.7	100.0%	2	3	7	0.01%	24.4%	GVEEEEEDGEMRE	99.7%	52.5	25	52.5	2	0	0	1553.59	74	86
Small nuclear ribonucleoprotein G-like protein	SNRPG	RUXG_HUMAN	8.5	99.8%	2	2	3	0.00%	26.3%	GNSIIMLEALERV	99.7%	58.4	25	53.1	2	0	0	1460.78	64	76
Small nuclear ribonucleoprotein G-like protein	SNRPG	RUXG_HUMAN	8.5	99.8%	2	2	3	0.00%	26.3%	HVQGILR	95.2%	28.7	25	7.42	1	0	0	822.49	26	32
Small nuclear ribonucleoprotein Sm D1	SNRPD1	SMD1_HUMAN	13.3	100.0%	4	6	21	0.02%	37.8%	EPVQLETLSIR	99.7%	44.2	25	30.4	2	0	0	1284.72	51	61
Small nuclear ribonucleoprotein Sm D1	SNRPD1	SMD1_HUMAN	13.3	100.0%	4	6	21	0.02%	37.8%	LSHETVTIELK	99.7%	56	25	44.1	6	0	0	1269.71	10	20
Small nuclear ribonucleoprotein Sm D1	SNRPD1	SMD1_HUMAN	13.3	100.0%	4	6	21	0.02%	37.8%	NGTQVHGTITGVDVSMNTHLK	99.7%	51.6	25	51.6	0	6	0	2209.10	21	41
Small nuclear ribonucleoprotein Sm D1	SNRPD1	SMD1_HUMAN	13.3	100.0%	4	6	21	0.02%	37.8%	NREPVQLETLSIR	99.7%	62.8	25	62.8	5	2	0	1554.86	49	61
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	8	12	30	0.03%	55.9%	EEEEFNTGPLSVLTQSVK	99.7%	94.8	25	94.5	2	0	0	2006.99	20	37
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	8	12	30	0.03%	55.9%	EMWTEVPK	98.8%	34.9	25	25.5	2	0	0	1019.49	72	79
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	8	12	30	0.03%	55.9%	GDSVIVVLR	99.7%	67.5	25	52.2	7	0	0	957.57	103	111
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	8	12	30	0.03%	55.9%	HCNMVLENVK	99.7%	52.6	25	52.6	4	0	0	1243.59	62	71
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	8	12	30	0.03%	55.9%	NNTQVLINCR	99.7%	62	25	54.7	4	0	0	1231.62	38	47
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	8	12	30	0.03%	55.9%	REEEEFNTGPLSVLTQSVK	99.7%	66.5	25	66.5	1	2	0	2163.09	19	37
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	8	12	30	0.03%	55.9%	SEMTPEELQK	99.7%	52.7	25	39.3	4	0	0	1191.56	9	18
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	8	12	30	0.03%	55.9%	SEMTPEELQKR	99.7%	41.1	25	33.2	4	0	0	1363.65	9	19
Small nuclear ribonucleoprotein Sm D3	SNRPD3	SMD3_HUMAN	13.9	100.0%	4	5	8	0.01%	47.6%	FLILPDMLK	99.7%	55.6	25	35.4	3	0	0	1105.63	70	78
Small nuclear ribonucleoprotein Sm D3	SNRPD3	SMD3_HUMAN	13.9	100.0%	4	5	8	0.01%	47.6%	LIEAEDNMNCQMSNITVTYR	99.7%	87.1	25	87.1	1	0	0	2402.08	32	51
Small nuclear ribonucleoprotein Sm D3	SNRPD3	SMD3_HUMAN	13.9	100.0%	4	5	8	0.01%	47.6%	VAQLEQVYIR	99.7%	77.6	25	67.6	2	0	0	1218.68	55	64
Small nuclear ribonucleoprotein Sm D3	SNRPD3	SMD3_HUMAN	13.9	100.0%	4	5	8	0.01%	47.6%	VLHEAEGHIVTCETNTGEVYR	99.7%	71.8	25	71.8	0	2	0	2414.14	9	29
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN	24.6	100.0%	8	12	27	0.03%	27.5%	CILQDGR	97.2%	30.9	25	21.2	1	0	0	861.42	19	25
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN	24.6	100.0%	8	12	27	0.03%	27.5%	GENLVSMTVEGPPPK	99.7%	80	25	77.4	4	0	0	1570.78	74	88
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN	24.6	100.0%	8	12	27	0.03%	27.5%	GENLVSMTVEGPPPKDTGIAR	99.7%	95.1	25	95.1	1	4	0	2168.10	74	94
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN	24.6	100.0%	8	12	27	0.03%	27.5%	HMNLILCDCDEFRK	99.7%	41.3	25	41.3	0	1	0	1850.83	37	50
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN	24.6	100.0%	8	12	27	0.03%	27.5%	IFIGTFK	99.1%	36.2	25	22.5	2	0	0	825.49	26	32
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN	24.6	100.0%	8	12	27	0.03%	27.5%	MLQHIDYR	99.7%	41.8	25	36.2	3	0	0	1075.54	9	16
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN	24.6	100.0%	8	12	27	0.03%	27.5%	RVLGLVLLR	99.6%	39.8	25	25.5	2	0	0	1038.71	65	73
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN	24.6	100.0%	8	12	27	0.03%	27.5%	VLGLVLLR	99.7%	64.8	25	64.8	9	0	0	882.61	66	73
SNW domain-containing protein 1	SNW1	SNW1_HUMAN	61.5	100.0%	8	9	14	0.01%	15.3%	DMAQSIYRPSK	99.7%	41.5	25	41.5	2	0	0	1295.64	442	452
SNW domain-containing protein 1	SNW1	SNW1_HUMAN	61.5	100.0%	8	9	14	0.01%	15.3%	GLQTVHINENFAK	99.7%	64	25	61.8	1	0	0	1470.77	274	286
SNW domain-containing protein 1	SNW1	SNW1_HUMAN	61.5	100.0%	8	9	14	0.01%	15.3%	GYTIPLDKR	96.7%	30.4	25	12.7	1	0	0	1062.59	259	267
SNW domain-containing protein 1	SNW1	SNW1_HUMAN	61.5	100.0%	8	9	14	0.01%	15.3%	IKYDAIAR	99.7%	41.5	25	31.8	2	0	0	949.55	96	103
SNW domain-containing protein 1	SNW1	SNW1_HUMAN	61.5	100.0%	8	9	14	0.01%	15.3%	LAEALYIADR	99.7%	93.5	25	84.7	2	0	0	1134.62	287	296
SNW domain-containing protein 1	SNW1	SNW1_HUMAN	61.5	100.0%	8	9	14	0.01%	15.3%	LAPAQYIR	97.5%	31.5	25	14.4	1	0	0	931.54	171	178
SNW domain-containing protein 1	SNW1	SNW1_HUMAN	61.5	100.0%	8	9	14	0.01%	15.3%	VAAAMPVR	99.7%	49.2	25.8	37.3	4	0	0	830.46	159	166
SNW domain-containing protein 1	SNW1	SNW1_HUMAN	61.5	100.0%	8	9	14	0.01%	15.3%	YTPSQQGVAFNSGAK	99.7%	60.5	25	58	1	0	0	1554.75	179	193
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	30	75	0.07%	29.9%	ADIGVAMGIAGSDVSK	99.7%	131	25	124	4	0	0	1490.75	728	743
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	30	75	0.07%	29.9%	AVAGDASESALLK	99.7%	100	25	91.5	5	0	0	1231.65	446	458
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	30	75	0.07%	29.9%	AVFQANQENLPILK	99.7%	71.9	25	38	4	0	0	1584.87	431	444
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	30	75	0.07%	29.9%	CIELCCGSVK	99.7%	48.3	25	34.1	2	0	0	1225.54	459	468
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	30	75	0.07%	29.9%	DGPNALTPPPTTPEWIK	99.7%	46.5	25	43.5	2	0	0	1833.94	75	91
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	30	75	0.07%	29.9%	GIVVYTGDR	99.7%	52.3	25	52.3	4	0	0	979.52	256	264
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	30	75	0.07%	29.9%	GVGIISEGNETVEDIAAR	99.7%	130	25	130	2	0	0	1829.92	630	647
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	30	75	0.07%	29.9%	IAGLCNR	98.4%	34	25.5	21.4	2	0	0	803.42	424	430
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	30	75	0.07%	29.9%	IVEIPFNSTNK	99.7%	43.9	25	36.9	2	0	0	1261.68	477	487
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	30	75	0.07%	29.9%	LIFDNLKK	99.0%	35.5	25	19.4	2	0	0	990.60	767	774
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	30	75	0.07%	29.9%	LIIVEGCQR	99.7%	53.9	25	47.1	4	0	0	1087.59	699	707
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	30	75	0.07%	29.9%	LNIPVSQVNPR	99.7%	70.5	25	63.6	6	0	0	1236.71	648	658
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	30	75	0.07%	29.9%	LSLDELHR	99.7%	55.2	25	51.1	2	0	0	982.53	46	53
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	30	75	0.07%	29.9%	MSINAEEVVVGDLVEVK	99.7%	83.9	25	77.6	2	0	0	1846.95	178	194

Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	30	75	0.07%	29.9%	NIAFFSTNCVEGTAR	99.7%	86	25	86	2	0	0	1686.79	241	255
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	30	75	0.07%	29.9%	NLEAVETLGSTSTICSDK	99.7%	65.2	25	65.2	2	0	0	1924.92	360	377
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	30	75	0.07%	29.9%	NMVPQQALVIR	99.7%	48.8	25	48.8	4	0	0	1268.71	163	173
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	30	75	0.07%	29.9%	NPNTSEPQHLLVMK	99.7%	76	25	68.7	4	0	0	1607.82	495	508
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	30	75	0.07%	29.9%	QGAIVAVTGDGVNDSPALK	99.7%	97.8	25	97.8	2	0	0	1811.95	708	726
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	30	75	0.07%	29.9%	QGAIVAVTGDGVNDSPALKK	99.7%	48.1	25	48.1	0	2	0	1940.05	708	727
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	30	75	0.07%	29.9%	SPDFTNENPLETR	99.7%	96.4	25	89.8	4	0	0	1519.70	228	240
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	30	75	0.07%	29.9%	TSATWLALSR	99.7%	87	25	74.1	4	0	0	1105.60	414	423
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	30	75	0.07%	29.9%	VDNSSLTGESEPQTR	99.7%	82.6	25	71	3	0	0	1619.75	213	227
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	30	75	0.07%	29.9%	VIMVTGDHPITAK	99.7%	72.5	25	68.5	4	0	0	1381.75	613	625
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	30	75	0.07%	29.9%	YHTEIVFAR	95.7%	29.2	25	19.4	1	0	0	1135.59	684	692
Sorting and assembly machinery component 50 homolog	SAMM50	SAM50_HUMAN	52.0	100.0%	4	4	8	0.01%	9.6%	ICDGVQFGAGIR	99.7%	66.1	25	55.1	2	0	0	1292.64	456	467
Sorting and assembly machinery component 50 homolog	SAMM50	SAM50_HUMAN	52.0	100.0%	4	4	8	0.01%	9.6%	SSLSHAMVIDSR	99.7%	60.8	25	45	2	0	0	1302.65	256	267
Sorting and assembly machinery component 50 homolog	SAMM50	SAM50_HUMAN	52.0	100.0%	4	4	8	0.01%	9.6%	VTFQFSYGTK	99.7%	50.3	25	45.8	2	0	0	1177.59	159	168
Sorting and assembly machinery component 50 homolog	SAMM50	SAM50_HUMAN	52.0	100.0%	4	4	8	0.01%	9.6%	VTGQFPWSSLR	99.7%	48.7	25	36	2	0	0	1277.66	195	205
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	3	3	3	0.00%	2.0%	ALVADSHPESER	99.7%	43.8	25	39.9	1	0	0	1310.63	1657	1668
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	3	3	3	0.00%	2.0%	LQQFLR	95.8%	29.3	25	0	1	0	0	804.47	1064	1069
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	3	3	3	0.00%	2.0%	LVSQDNFGFDLPAVEAATK	98.9%	35.3	25	35.3	1	0	0	2022.02	444	462
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	3	3	3	0.00%	2.0%	VLDNAIETEK	95.1%	28.7	25	25.3	1	0	0	1131.59	293	302
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	14	16	27	0.03%	30.4%	AIDLMNALMR	99.7%	60.6	25	51.1	4	0	0	1147.60	385	394
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	14	16	27	0.03%	30.4%	ASAALAALEK	99.7%	96.2	25	65.7	2	0	0	944.54	564	573
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	14	16	27	0.03%	30.4%	DKPTETLLNTVK	99.7%	41.7	25	36.8	1	0	0	1358.75	111	122
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	14	16	27	0.03%	30.4%	DNLPIQIQK	99.7%	48.5	25	40	1	0	0	1068.61	123	131
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	14	16	27	0.03%	30.4%	EDITHSAQHALR	98.8%	28.3	25	24.6	0	1	0	1377.69	304	315
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	14	16	27	0.03%	30.4%	FPTYPVPHYSFF	99.7%	48.5	25	48.5	2	0	0	1501.72	661	672
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	14	16	27	0.03%	30.4%	FVMEVEVDGQK	99.7%	71.1	25	64.3	11	0	0	1296.61	541	551
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	14	16	27	0.03%	30.4%	GWPLELICEK	99.7%	60.2	25	0	13	0	0	1244.63	240	249
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	14	16	27	0.03%	30.4%	LFSGPNAANNK	99.7%	44	25	28.4	3	0	0	1132.57	574	584
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	14	16	27	0.03%	30.4%	LFSGPNAANNKK	99.7%	42	25	21.9	2	0	0	1260.67	574	585
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	14	16	27	0.03%	30.4%	LNQIRPGLQYK	99.7%	52.6	25	49.4	2	1	0	1329.76	395	405
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	14	16	27	0.03%	30.4%	LSAFGQIYK	99.6%	40.7	25	34.2	2	0	0	1026.56	316	324
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	14	16	27	0.03%	30.4%	NPVMELNEK	99.7%	59.3	25	50.1	10	0	0	1089.52	513	521
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	14	16	27	0.03%	30.4%	NPVMELNEKR	99.7%	57.2	25	48.1	4	0	0	1229.63	513	522
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	14	16	27	0.03%	30.4%	NTKEPTLTLK	97.1%	30.9	25	17.3	2	0	0	1144.66	152	161
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	14	16	27	0.03%	30.4%	SCVIVLR	99.7%	46.8	25	0	2	0	0	846.49	217	223
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	14	16	27	0.03%	30.4%	SIGTCNRPLGAGEALR	99.2%	29.8	25	28.5	0	2	0	1671.86	250	265
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	14	16	27	0.03%	30.4%	VILTSPLIRDELEK	99.6%	40.9	25	40.9	1	0	0	1625.95	162	175
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	14	16	27	0.03%	30.4%	VLEMDPLPSSKPFQK	97.0%	24.5	25	17.4	0	1	0	1731.90	325	339
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	14	16	27	0.03%	30.4%	YELISETGGSHDK	99.7%	76.9	25	65.3	2	0	0	1435.67	527	539
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	14	16	27	0.03%	30.4%	YELISETGGSHDKR	99.7%	77.6	25	74	6	3	0	1591.77	527	540
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	5	5	7	0.01%	17.2%	AAFVLPEFAR	98.8%	34.8	25	30.8	1	0	0	1120.61	286	295
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	5	5	7	0.01%	17.2%	FLPGMAIGYSSSK	99.7%	55.6	25	39.8	1	0	0	1357.68	136	148
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	5	5	7	0.01%	17.2%	VLIIGGGDGGVLR	99.7%	54	25	54	2	0	0	1225.73	97	109
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	5	5	7	0.01%	17.2%	YQDILVFR	99.7%	62.6	25	62.6	2	0	0	1053.57	48	55
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	5	5	7	0.01%	17.2%	YYNSDVHR	98.9%	35.3	25	33.8	1	0	0	1053.47	278	285
Sphingomyelin phosphodiesterase 4	SMPD4	NSMA3_HUMAN	93.4	100.0%	3	3	3	0.00%	3.9%	FDFPVSYLPGPVK	99.6%	39.7	25	39	1	0	0	1465.77	107	119
Sphingomyelin phosphodiesterase 4	SMPD4	NSMA3_HUMAN	93.4	100.0%	3	3	3	0.00%	3.9%	LFVGFLNR	99.7%	46	25	43	1	0	0	965.56	444	451
Sphingomyelin phosphodiesterase 4	SMPD4	NSMA3_HUMAN	93.4	100.0%	3	3	3	0.00%	3.9%	YHLTEPGLASR	98.1%	32.8	25	28.6	1	0	0	1243.64	739	749
Sphingosine-1-phosphate lyase 1	SGPL1	SGPL1_HUMAN	63.5	100.0%	3	3	5	0.00%	7.2%	AFEPYLEILEVYSTK	99.7%	46.5	25	37	1	0	0	1801.93	11	25
Sphingosine-1-phosphate lyase 1	SGPL1	SGPL1_HUMAN	63.5	100.0%	3	3	5	0.00%	7.2%	ALPSQGLSSSAVLEK	99.7%	72.9	25	69.6	2	0	0	1486.81	115	129
Sphingosine-1-phosphate lyase 1	SGPL1	SGPL1_HUMAN	63.5	100.0%	3	3	5	0.00%	7.2%	ASGTVYSGEEK	99.7%	48.6	25	46.6	2	0	0	1127.52	145	155

Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	6	7	15	0.01%	30.2%	EGNGPVTQWK	97.7%	31.9	25	19	1	0	0	1115.55	64	73
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	6	7	15	0.01%	30.2%	GTVLDQVPVNPSLYLIK	99.7%	80.3	25	61.4	3	0	0	1856.05	74	90
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	6	7	15	0.01%	30.2%	ISDAHLADTMIGK	99.7%	53.1	25	48.7	1	0	0	1371.69	123	135
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	6	7	15	0.01%	30.2%	SRADAGHAGVSANMMK	98.2%	26.6	25	26.6	0	1	0	1634.74	13	28
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	6	7	15	0.01%	30.2%	SSVGPSKPVSQPR	99.7%	63.3	25	42.7	3	4	0	1325.72	38	50
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	6	7	15	0.01%	30.2%	VSALEVLPDR	99.7%	78.4	25	68.8	2	0	0	1098.62	108	117
Spliceosome RNA helicase DDX39B	DDX39B	DX39B_HUMAN	49.0	99.8%	2	3	4	0.00%	19.2%	DVQEIFR	98.4%	33.3	25	14.2	2	0	0	906.47	210	216
Spliceosome RNA helicase DDX39B	DDX39B	DX39B_HUMAN	49.0	99.8%	2	3	4	0.00%	19.2%	ELAFQISK	99.6%	40.2	25	31.8	2	0	0	935.52	124	131
Spliceosome RNA helicase DDX39B	DDX39B	DX39B_HUMAN	49.0	99.8%	2	3	4	0.00%	19.2%	GLAITFVSDENDAK	99.7%	73.5	25	64.9	2	0	0	1479.73	385	398
Spliceosome RNA helicase DDX39B	DDX39B	DX39B_HUMAN	49.0	99.8%	2	3	4	0.00%	19.2%	GSYVSIHSSGFR	99.7%	71.8	25	70.4	2	0	0	1296.63	37	48
Spliceosome RNA helicase DDX39B	DDX39B	DX39B_HUMAN	49.0	99.8%	2	3	4	0.00%	19.2%	ILNDVQDR	99.7%	55.1	25	44.5	2	0	0	972.51	399	406
Spliceosome RNA helicase DDX39B	DDX39B	DX39B_HUMAN	49.0	99.8%	2	3	4	0.00%	19.2%	ILVATNLFGR	99.7%	73.9	25	56.8	5	0	0	1103.66	340	349
Spliceosome RNA helicase DDX39B	DDX39B	DX39B_HUMAN	49.0	99.8%	2	3	4	0.00%	19.2%	NCPHIVVGTPGR	99.7%	63.5	25	55.5	1	1	0	1306.67	164	175
Spliceosome RNA helicase DDX39B	DDX39B	DX39B_HUMAN	49.0	99.8%	2	3	4	0.00%	19.2%	VAVFFGGLSIK	99.7%	52.8	25	43.6	2	0	0	1137.67	145	155
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	AAGLATMISTMRPDIDNMDEYVR	99.7%	39.8	25	39.8	0	1	0	2618.19	603	625
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	AIVNVIGMHK	99.7%	43.7	25	40.7	2	0	0	1097.61	999	1008
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	ATVNTFGYIAK	99.7%	73	25	67.1	2	0	0	1184.63	1076	1086
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	DTPGHGSGWAETPR	99.7%	61.2	25	54.8	1	2	0	1467.66	302	315
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	EFQSPDEEMKK	99.7%	47.1	25	44	1	0	0	1367.61	776	786
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	EVMLILIR	99.7%	55	25	36.5	4	0	0	986.61	768	775
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	GDTPGHATPGHGGATSSAR	99.7%	64.4	25	64.4	2	2	0	1733.80	271	289
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	GGDSIGETPTPGASK	99.7%	68.5	25	61.9	2	0	0	1373.65	319	333
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	GSETPGATPGSK	99.7%	44	25	41.3	1	0	0	1088.52	241	252
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	ICFELLELLK	99.7%	50.2	25	46.4	1	0	0	1277.72	1058	1067
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	ILVVIEPLLIDEDYYAR	99.7%	62.5	25	62.5	1	0	0	2034.12	574	590
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	IWDPTPSHTPAGAATPGR	99.7%	42.8	25	42.3	0	1	0	1831.91	253	270
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	IYNDDKNTYIR	99.7%	52.2	25	48.1	2	2	0	1414.70	1287	1297
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	LLVDVDESTLSPEEQKER	99.7%	111	25	104	1	2	0	2087.05	478	495
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	QCCGTDGVEANYIK	99.7%	79.8	25	69.3	2	0	0	1614.69	794	807
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	QLVDTTVELANK	99.7%	89.4	25	82.5	2	0	0	1330.72	832	843
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	QQAADLISR	99.7%	47.7	25	33.1	2	0	0	1001.54	949	957
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	SLVEIIEHGLVDEQQK	99.7%	49.8	25	47.6	2	0	0	1836.97	685	700
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	SVNDQPSGNLPFLKPDDIQYFDK	99.7%	48.2	25	40.9	0	2	0	2637.28	455	477
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	TEILPPFFK	99.7%	47.4	25	37.3	2	0	0	1091.61	808	816
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	THEDIEAQIR	99.7%	62.4	25	56.5	2	0	0	1211.60	7	16
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	TMIISPER	99.7%	43.1	25	35.8	1	0	0	962.50	125	132
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	VGAAEIISR	99.7%	78.2	25	34.6	2	0	0	915.53	844	852
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	VPELNVQNGVLK	99.7%	60.6	25	53.4	2	0	0	1309.75	1138	1149
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	VQENCIDLVGR	99.7%	67	25	61.8	2	0	0	1302.65	1031	1041
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	VVNGAAASQPPSK	99.6%	40.1	25	26.8	1	0	0	1225.65	183	195
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	VVNGAAASQPPSKR	99.7%	48.1	25	48.1	2	0	0	1381.75	183	196
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	WDETPASQMGGSTPVLTPGK	99.7%	98.8	25	98.8	2	0	0	2074.98	338	357
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	58	0.06%	29.0%	WDQTADQTPGATPK	99.7%	74	25	68.2	2	0	0	1515.71	200	213
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	12	14	20	0.02%	14.6%	AAVLLEQER	99.7%	75.8	25	62.3	2	0	0	1028.57	184	192
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	12	14	20	0.02%	14.6%	EALQEKEEQK	96.9%	30.6	25	22.5	1	0	0	1231.62	538	547
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	12	14	20	0.02%	14.6%	FTVAELK	97.7%	31.9	25	22.2	1	0	0	807.46	460	466
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	12	14	20	0.02%	14.6%	IDIDYQK	96.9%	30.6	25	19.9	1	0	0	894.46	564	570
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	12	14	20	0.02%	14.6%	ISLGMPVGPNAHK	99.7%	46.9	25	30.6	1	1	0	1320.71	615	627
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	12	14	20	0.02%	14.6%	KPGDLSDELR	99.7%	59.1	25	38	2	0	0	1129.59	605	614
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	12	14	20	0.02%	14.6%	LAEIGAPIQGNR	99.7%	54.7	25	52.8	2	0	0	1238.69	36	47
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	12	14	20	0.02%	14.6%	LAEIGAPIQGNREELVER	98.6%	27.5	25	17.9	0	2	0	1994.07	36	53

Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	12	14	20	0.02%	14.6%	LAQQQAALLMQQEER	99.7%	84.5	25	81	2	0	0	1772.90	149	163
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	12	14	20	0.02%	14.6%	SSLGQSASETEEDTVSVSK	99.7%	86.6	25	83.8	1	0	0	1940.89	302	320
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	12	14	20	0.02%	14.6%	VGEPVALSEEER	99.7%	72.8	25	64.3	2	0	0	1314.65	135	146
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	12	14	20	0.02%	14.6%	YGPPPSYPNLK	99.2%	36.5	25	26.5	2	0	0	1232.63	639	649
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	13	14	32	0.03%	13.5%	DYIVVGSDSGR	99.7%	56	25	50	1	0	0	1167.56	76	86
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	13	14	32	0.03%	13.5%	FGNICVVR	99.7%	54.7	25	44.9	2	0	0	964.50	1050	1057
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	13	14	32	0.03%	13.5%	FLAVGLVDNTVR	99.7%	85.2	25	68.1	3	0	0	1303.74	604	615
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	13	14	32	0.03%	13.5%	FSNTGEDWYVLVGVAK	99.7%	64.1	25	64.1	2	0	0	1784.89	896	911
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	13	14	32	0.03%	13.5%	IVILEYQPSK	99.7%	50.3	25	50.2	2	0	0	1189.68	87	96
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	13	14	32	0.03%	13.5%	LGAVFNQVAFPLQYTPR	99.7%	77.8	25	77.8	4	0	0	1921.03	770	786
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	13	14	32	0.03%	13.5%	MFLYNLTLQR	99.7%	54.6	25	50.3	2	0	0	1298.69	1	10
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	13	14	32	0.03%	13.5%	NENQLIIFADDTYPR	99.7%	91.7	25	91.7	2	0	0	1808.88	1017	1031
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	13	14	32	0.03%	13.5%	NFGDQPDIR	99.7%	47.5	25	40.8	2	0	0	1061.50	260	268
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	13	14	32	0.03%	13.5%	SVAGGFVYTYK	99.7%	61.9	25	57.6	3	0	0	1191.60	919	929
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	13	14	32	0.03%	13.5%	TPVEEVPAAIAPFQGR	99.7%	66.3	25	59.9	2	0	0	1681.89	943	958
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	13	14	32	0.03%	13.5%	TVLDPVTGDLSDTR	99.7%	94.3	25	94.3	4	0	0	1488.75	677	690
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	13	14	32	0.03%	13.5%	YFDTVPVAAAMCVLK	99.7%	48.2	25	48.2	3	0	0	1684.84	329	343
Splicing factor 3B subunit 4	SF3B4	SF3B4_HUMAN	44.4	100.0%	2	2	2	0.00%	5.0%	LYGKPIR	94.8%	28.4	25	11.2	1	0	0	846.52	79	85
Splicing factor 3B subunit 4	SF3B4	SF3B4_HUMAN	44.4	100.0%	2	2	2	0.00%	5.0%	NQDATVYVGGLDEK	99.7%	83.2	25	77.1	1	0	0	1508.72	10	23
Splicing factor 3B subunit 5	SF3B5	SF3B5_HUMAN	10.1	100.0%	2	3	5	0.00%	30.2%	MLQPCGPPADKPEEN	99.7%	48.7	25	48.7	4	0	0	1682.75	72	86
Splicing factor 3B subunit 5	SF3B5	SF3B5_HUMAN	10.1	100.0%	2	3	5	0.00%	30.2%	YIGTGHADTTK	99.5%	38.7	25	38.7	1	0	0	1163.57	18	28
Splicing factor 45	RBM17	SPF45_HUMAN	45.0	99.9%	2	2	3	0.00%	5.5%	IIVGDATEKDASK	99.7%	53.9	25	41.4	2	0	0	1346.72	277	289
Splicing factor 45	RBM17	SPF45_HUMAN	45.0	99.9%	2	2	3	0.00%	5.5%	LLQSQLQVK	97.6%	31.7	25	26	1	0	0	1056.64	25	33
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	7	10	20	0.02%	39.2%	AVIDLNNR	99.7%	60.1	25	45.3	2	0	0	914.51	126	133
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	7	10	20	0.02%	39.2%	GGFCNFMHLKPISR	99.7%	41.3	25	38.5	0	4	0	1663.82	166	179
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	7	10	20	0.02%	39.2%	NPQNSSQSADGLR	99.7%	97.2	25	93.4	3	0	0	1373.64	54	66
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	7	10	20	0.02%	39.2%	QYEMGECTR	99.7%	55.3	25	49	4	0	0	1173.47	157	165
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	7	10	20	0.02%	39.2%	VNCSFYFK	99.7%	50.8	25	50.8	2	0	0	1064.49	16	23
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	7	10	20	0.02%	39.2%	WFNGQPIHAELSPVTDFR	99.7%	54.3	25	54.3	1	2	0	2114.05	134	151
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	7	10	20	0.02%	39.2%	YGEVEEMNVCDNLGDHLVGNVYVK	99.7%	52.2	25	52.2	0	2	0	2769.25	93	116
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	15	29	0.03%	26.9%	ELLTSFGPLK	99.3%	37.3	25	28.5	2	0	0	1104.63	277	286
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	15	29	0.03%	26.9%	GAKEEHGGLIR	99.7%	51.9	25	42.3	2	0	0	1166.63	68	78
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	15	29	0.03%	26.9%	IFVEFTSVFDCQK	99.7%	67.8	25	67.8	2	0	0	1619.78	432	444
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	15	29	0.03%	26.9%	LFIGGLPNYLNDDQVK	99.7%	57.8	25	45.6	2	0	0	1805.94	261	276
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	15	29	0.03%	26.9%	LGGLTQAPGNPVLAVQINQDK	99.7%	62.6	25	62.6	2	1	0	2133.17	175	195
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	15	29	0.03%	26.9%	NFAFLEFR	99.7%	59.6	25	49.5	2	0	0	1043.53	196	203
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	15	29	0.03%	26.9%	SIEIPRPVDGVEVPGCGK	99.7%	65.5	25	61.6	2	2	0	1908.99	414	431
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	15	29	0.03%	26.9%	SVDETTQAMAFDGIIFQGQSLK	99.7%	102	25	102	4	4	0	2402.15	204	225
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	15	29	0.03%	26.9%	YCDPDSYHR	99.7%	66	25	66	2	2	0	1212.47	463	471
Splicing factor, arginine/serine-rich 15	SCAF4	SFR15_HUMAN	125.9	100.0%	3	3	5	0.00%	3.3%	DLSIGNPIPTVVSGAR	99.7%	58.9	25	58.9	2	0	0	1595.88	778	793
Splicing factor, arginine/serine-rich 15	SCAF4	SFR15_HUMAN	125.9	100.0%	3	3	5	0.00%	3.3%	TTPTQPSEQK	96.6%	30.2	25	18.3	1	0	0	1116.55	236	245
Splicing factor, arginine/serine-rich 15	SCAF4	SFR15_HUMAN	125.9	100.0%	3	3	5	0.00%	3.3%	VPGLYVIDSIVR	99.7%	60.1	25	60.1	2	0	0	1330.77	60	71
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	5	5	8	0.01%	10.5%	AELDDTPMR	99.5%	38.7	25	38.7	1	0	0	1063.47	350	358
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	5	5	8	0.01%	10.5%	AVVIVDDR	99.7%	42	25	32.3	4	0	0	886.50	400	407
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	5	5	8	0.01%	10.5%	FAQHGTFEYEYSQR	99.7%	34.3	25	34.3	0	1	0	1762.78	480	493
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	5	5	8	0.01%	10.5%	FATHAAALSVR	99.7%	50.7	25	43.2	2	0	0	1143.63	366	376
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	5	5	8	0.01%	10.5%	FGQGGAGPVGGQGPR	99.7%	50.6	25	50.6	2	0	0	1341.67	667	681
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	5	5	8	0.01%	10.5%	LFVGNLPADITEDEFKR	99.7%	39.6	25	36.5	0	2	0	1964.01	299	315
SRA stem-loop-interacting RNA-binding protein, mitochondrial	SLIRP	SLIRP_HUMAN	12.3	99.8%	2	2	4	0.00%	25.7%	GLGWVQFSSEEGLR	99.7%	42.7	25	42.7	2	0	0	1564.78	61	74
SRA stem-loop-interacting RNA-binding protein, mitochondrial	SLIRP	SLIRP_HUMAN	12.3	99.8%	2	2	4	0.00%	25.7%	NALQQENHIIDGVK	99.7%	70.7	25	70.6	2	0	0	1578.82	75	88
SRSF protein kinase 1	SRPK1	SRPK1_HUMAN	74.3	100.0%	4	4	9	0.01%	7.3%	EMVVQLLDDFK	99.7%	52.1	25	52.1	1	0	0	1336.68	142	152

SRSF protein kinase 1	SRPK1	SRPK1_HUMAN	74.3	100.0%	4	4	9	0.01%	7.3%	HFTEDIQTR	99.7%	47.9	25	41.1	4	0	0	1146.55	507	515
SRSF protein kinase 1	SRPK1	SRPK1_HUMAN	74.3	100.0%	4	4	9	0.01%	7.3%	SAEHYTETALDEIR	99.7%	66.9	25	59.5	2	0	0	1634.77	113	126
SRSF protein kinase 1	SRPK1	SRPK1_HUMAN	74.3	100.0%	4	4	9	0.01%	7.3%	STAGNFLVNPLEPK	99.6%	39.9	25	36	2	0	0	1486.79	473	486
SRSF protein kinase 2	SRPK2	SRPK2_HUMAN	77.5	99.8%	2	2	3	0.00%	4.8%	AADLLVNPLDPR	99.7%	50	25	46.1	2	0	0	1293.72	508	519
SRSF protein kinase 2	SRPK2	SRPK2_HUMAN	77.5	99.8%	2	2	3	0.00%	4.8%	HFTEDIQTR	99.7%	47.9	25	41.1	4	0	0	1146.55	540	548
SRSF protein kinase 2	SRPK2	SRPK2_HUMAN	77.5	99.8%	2	2	3	0.00%	4.8%	TVSASSTGDLPK	98.4%	33.3	25	28.5	1	0	0	1162.60	492	503
Stathmin	STMN1	STMN1_HUMAN	17.3	99.8%	2	2	3	0.00%	15.4%	AIEENNNFSK	99.7%	50.6	25	0	1	0	0	1165.55	86	95
Stathmin	STMN1	STMN1_HUMAN	17.3	99.8%	2	2	3	0.00%	15.4%	ASGQAFELILSPR	99.7%	44.6	25	23.4	2	0	0	1388.75	15	27
Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	NSDHL	NSDHL_HUMAN	41.9	99.9%	2	2	4	0.00%	5.9%	DPQLVPILIEAAR	99.7%	43.7	25	39	2	0	0	1434.83	208	220
Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	NSDHL	NSDHL_HUMAN	41.9	99.9%	2	2	4	0.00%	5.9%	FFLGDLCSR	99.7%	54.1	25	52.6	2	0	0	1114.54	80	88
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	9	17	0.02%	35.1%	AEQINQAAGEASAVLAK	99.7%	124	25	121	2	0	0	1670.87	234	250
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	9	17	0.02%	35.1%	APVPGTPDSLSSGSSR	99.7%	51.2	25	48.8	2	0	0	1514.74	322	337
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	9	17	0.02%	35.1%	ASYGVEDPEYAVTQLAQTTMR	99.7%	99.6	25	89.1	1	1	0	2330.10	115	135
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	9	17	0.02%	35.1%	DVQGTDASLDEELDRVK	99.7%	96	25	96	2	0	0	1889.91	338	354
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	9	17	0.02%	35.1%	ESAINVAEGKK	99.7%	42.4	25	33.5	2	0	0	1145.62	212	222
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	9	17	0.02%	35.1%	ILEPGLNILIPVLDR	99.7%	88.3	25	88.3	3	0	0	1675.02	58	72
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	9	17	0.02%	35.1%	NTVVLFVPQQEAWVVER	99.7%	45.8	25	39.7	2	0	0	2014.08	35	51
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	9	17	0.02%	35.1%	QAQILASEAEK	99.4%	38.3	25	33.3	2	0	0	1187.63	223	233
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	18	41	0.04%	33.0%	AQFEGIVTDLIR	99.7%	86.8	25	78.8	4	0	0	1361.74	349	360
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	18	41	0.04%	33.0%	ASNGDAWVEAHGK	99.7%	55.5	25	55.5	2	0	0	1341.62	147	159
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	18	41	0.04%	33.0%	DAGQISGLNVLR	99.7%	77	25	65.7	4	0	0	1242.68	207	218
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	18	41	0.04%	33.0%	ETGVDLTK	96.6%	30.2	25	13.4	1	0	0	862.45	293	300
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	18	41	0.04%	33.0%	LLGQFTLIGIPPAPR	99.7%	53.5	25	53.5	4	0	0	1592.95	499	513
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	18	41	0.04%	33.0%	LYSPSQIGAFVLMK	99.7%	68.8	25	67.3	2	0	0	1569.83	160	173
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	18	41	0.04%	33.0%	NAVITVPAYFNDSQR	99.7%	82	25	73.9	2	0	0	1694.85	188	202
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	18	41	0.04%	33.0%	QAASSLQQASLK	99.7%	90.5	25	83.7	1	0	0	1231.66	635	646
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	18	41	0.04%	33.0%	QAVTNPNNTFYATK	99.7%	81.5	25	81.5	2	0	0	1568.77	108	121
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	18	41	0.04%	33.0%	RYDDPEVQK	99.7%	45	25	38.7	2	0	0	1149.55	127	135
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	18	41	0.04%	33.0%	SDIGEVILVGGMTR	99.7%	94.4	25	86.7	3	0	0	1446.76	378	391
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	18	41	0.04%	33.0%	SQVFSTAADGQTQVEIK	99.7%	106	25	98.3	1	0	0	1808.90	469	485
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	18	41	0.04%	33.0%	STNGDTFLGGEDFDQALLR	99.7%	101	25	92.3	2	0	0	2055.96	266	284
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	18	41	0.04%	33.0%	TTPSVVAFTADGER	99.7%	107	25	104	4	0	0	1450.72	86	99
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	18	41	0.04%	33.0%	VINEPTAAALAYGLDK	99.7%	142	25	139	3	0	0	1645.88	219	234
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	18	41	0.04%	33.0%	VLENAEGAR	99.7%	60.8	25	55	2	0	0	958.50	77	85
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	17	18	41	0.04%	33.0%	VQQTVQDLFGR	99.7%	54.3	25	49	2	0	0	1290.68	395	405
Striatin-interacting protein 1	STRIP1	STRP1_HUMAN	95.6	100.0%	2	2	3	0.00%	2.4%	ILLAAAPTSK	99.7%	41	25	31	2	0	0	984.61	527	536
Striatin-interacting protein 1	STRIP1	STRP1_HUMAN	95.6	100.0%	2	2	3	0.00%	2.4%	NLFSCINLLR	95.3%	28.8	25	17.2	1	0	0	1249.67	664	673
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	ADQDRLDLEER	97.4%	31.2	25	20.6	1	0	0	1359.65	402	412
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	AEEDTQFNYHR	99.7%	55.4	25	43.6	2	0	0	1409.61	178	188
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	AFVSMVYSEEGAEDR	99.7%	96.6	25	94.7	2	0	0	1689.74	78	92
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	DKFQETSDEFEAAR	99.7%	61	25	61	1	1	0	1672.75	1036	1049
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	DLIHGAPVGKPAANR	99.7%	39	25	39	0	2	0	1515.84	63	77
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	DLTLEENQVK	99.7%	70.9	25	48.6	2	0	0	1188.61	364	373
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	DLTLEENQVKK	99.4%	38	25	38	1	0	0	1316.71	364	374
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	ELNQVMEQLGDAR	99.7%	76.9	25	76.9	3	0	0	1502.73	476	488
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	GEPETFLPLDYLEVKPTDEK	96.4%	30	25	30	1	0	0	2320.16	565	584
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	HLALNLQEK	98.8%	35	25	29.4	2	0	0	1065.61	726	734
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	IIDETMAQLQDLK	99.7%	84.6	25	74.9	2	0	0	1533.78	862	874
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	KYQIAVTK	97.6%	31.6	25	0	1	0	0	950.57	529	536
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	LGIQLDFEK	99.7%	46	25	34.1	2	0	0	1062.58	817	825
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	LNEQQSVLQR	99.7%	61.2	25	34.3	2	0	0	1214.65	1010	1019

Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	LREIEENQK	98.1%	32.6	25	16.9	2	0	0	1158.61	425	433
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	LTEELKEQMK	99.7%	46.4	25	34.9	4	0	0	1248.65	681	690
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	LYHNEVEIEK	99.7%	41	25	30.1	2	2	0	1273.64	228	237
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	NFLVFQGAVESIAMK	99.7%	79.8	25	73.6	4	0	0	1669.86	132	146
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	NMDAIIVDSEK	99.7%	50.1	25	37.2	2	0	0	1250.59	541	551
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	QIIGPFQR	95.9%	29.4	25	17	1	0	0	958.55	19	26
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	QVQSQAHGLQMR	99.7%	54.5	25	43.7	1	0	0	1382.70	700	711
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	SGELAQEYDKR	99.7%	51.7	25	43.4	2	0	0	1295.62	161	171
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	SGVISGGASDLK	99.7%	57.5	25	36.6	2	0	0	1090.57	649	660
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	SKLESELANFGPR	99.7%	50.1	25	39.5	1	0	0	1447.75	735	747
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	SNLMDAISFVLGEK	99.7%	80.6	25	69.7	3	0	0	1523.78	39	52
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	TALFEEISR	99.7%	66.8	25	61.3	2	0	0	1065.56	152	160
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	TVALDGTLFQK	99.7%	48.6	25	31.3	2	0	0	1192.66	638	648
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	VIVGGSSEYK	98.6%	33.9	25	32.9	1	0	0	1038.55	97	106
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	VLTFDLTKYPDANPNPNEQ	99.7%	56.5	25	56.4	1	0	0	2176.06	1215	1233
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	VVQLHEYSEELEK	99.7%	77.7	25	77.7	2	0	0	1602.80	111	123
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	37	61	0.06%	28.9%	YSQSDLEQTK	99.7%	69.9	25	56.2	2	0	0	1198.56	714	723
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	ALNHEIEELEK	98.3%	26.7	25	17.2	0	2	0	1324.67	276	286
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	AMNVLTEAEER	99.7%	59.2	25	52.2	2	0	0	1278.60	987	997
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	ASNLQDLVYK	99.6%	40.4	25	31.1	1	0	0	1150.61	59	68
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	ASVSITFDNSDKK	99.7%	47.7	25	41.9	2	0	0	1411.71	77	89
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	DQEALEAVKR	99.7%	43.4	25	35	2	0	0	1158.61	447	456
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	DTSATTALELVAGER	99.7%	94.2	25	81.3	2	0	0	1533.78	534	548
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	EGMFNNANVLFK	97.3%	31.1	25	20	1	0	0	1383.67	1147	1158
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	EIEHLSR	99.7%	41	25	22.7	2	0	0	883.46	226	232
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	ENLTELSGGQR	99.7%	95.2	25	80.5	2	0	0	1203.60	1080	1090
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	EVITAQDTVIK	99.7%	54.1	25	46.8	1	0	0	1216.68	880	890
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	FQELKDVQDELR	99.7%	59	25	52.7	1	0	0	1519.78	678	689
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	FVDGVSTVAR	99.7%	79.6	25	67.4	2	0	0	1050.56	1161	1170
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	GLVASLISVK	99.7%	56.4	25	53.6	2	0	0	986.62	524	533
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	HLFGQPNSAYDFK	98.7%	34.3	25	29.2	1	0	0	1523.73	946	958
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	IKELDHNISK	99.7%	46.7	25	41.1	2	0	0	1196.66	910	919
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	ILTTIEDLDQKK	99.7%	77	25	55.7	2	0	0	1416.79	1015	1026
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	ITDGLHALQEASNK	99.7%	66.6	25	63.3	1	0	0	1496.77	355	368
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	LKETYEALLAR	99.7%	69.3	25	68	2	0	0	1306.74	492	502
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	LQEELSENDKK	99.7%	53.1	25	45.9	2	0	0	1332.66	263	273
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	LYNVVVDTEVTGK	99.7%	101	25	97.4	2	0	0	1436.76	549	561
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	QQLEAVNEAIK	99.7%	41.8	25	36.1	2	0	0	1242.67	838	848
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	SAEELKEMQDK	99.7%	48	25	37	3	0	0	1307.61	249	259
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	SIILEGFK	97.1%	30.9	25	25	1	0	0	906.53	5	12
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	SLEDALAEAQR	99.7%	87.3	25	75.2	2	0	0	1202.60	298	308
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	SQAASILTK	98.9%	35	25	21.4	2	0	0	918.53	669	677
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	SYESQIEVMAAEVAK	99.7%	54.4	25	5.53	1	0	0	1654.80	849	863
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	TIEESEETLK	99.7%	52.3	25	43.3	2	0	0	1178.58	751	760
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	TILEEEITPTIQK	99.7%	74.7	25	60.8	2	0	0	1514.83	197	209
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	29	30	51	0.05%	28.0%	TVTLGGDVFDPHGTLSGGAR	99.7%	36.6	25	36.6	0	2	0	1956.98	649	668
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	AELGTDLLSQLSLEDQK	99.7%	97.8	25	95.4	2	0	0	1859.96	779	795
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	AILNGIDSINK	99.7%	42	25	42	2	0	0	1157.65	504	514
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	AKLDELSAK	99.0%	35.7	25	16.2	2	0	0	974.55	237	245
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	ALDQFVNFSEQK	99.7%	75.1	25	68.1	2	0	0	1425.70	986	997
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	ALEYTIYNQELNETR	99.7%	88.5	25	71.3	2	0	0	1856.90	222	236

Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	DKMEDIER	98.2%	33	25	26.5	1	0	0	1035.48	265	272
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	DLEDTEANKEK	99.7%	47.6	25	47.4	2	0	0	1291.60	419	429
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	DLQDELAGNSEQR	99.7%	64.1	25	59.3	1	0	0	1474.68	311	323
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	DQTIVDPFSSK	99.7%	43.2	25	12	2	0	0	1236.61	16	26
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	DTAYPETNDAIPMISK	99.7%	42.4	25	42.4	1	0	0	1765.83	597	612
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	EENAEQQALAAK	99.7%	79.5	25	65.9	2	0	0	1301.63	475	486
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	ELGSLPQEAFEK	99.7%	56.9	25	41.8	2	0	0	1347.68	945	956
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	GALTGGYYDTR	99.7%	58.8	25	50.5	2	0	0	1173.55	662	672
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	GSQFTSKEER	99.0%	35.5	25	30.4	1	0	0	1168.56	382	391
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	IKLEGIITR	98.9%	35.2	25	11.1	1	0	0	1042.66	819	827
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	INQMATAPDSQR	99.7%	64.1	25	57.1	4	0	0	1331.64	144	155
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	KAEEELGELEAK	99.7%	90	25	74.4	2	0	0	1345.68	684	695
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	KEESISLMK	99.5%	38.8	25	32.6	2	0	0	1080.56	172	180
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	KYEAIQLTFK	99.0%	35.4	25	35.4	1	0	0	1240.69	1025	1034
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	LALLHEGTGPR	99.7%	55.4	25	49.2	2	0	0	1163.65	62	72
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	LFYHIVDSDEVSTK	99.7%	57.6	25	50.9	1	0	0	1652.82	558	571
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	MNLPGEVTFLPLNK	99.7%	71.5	25	61.8	4	0	0	1588.84	579	592
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	NDVMNLLESAGFSR	99.7%	100	25	99.8	4	0	0	1552.74	119	132
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	NFSEVFQK	98.9%	35.3	25	19.6	2	0	0	998.49	1039	1046
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	QVIIQGFR	99.7%	44.4	25	28	2	0	0	960.56	5	12
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	SEDLDNSIDKTEAGIK	99.7%	71.7	25	68.2	1	0	0	1734.84	880	895
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	SLDQAINDK	99.7%	41.5	25	30	2	0	0	1003.51	401	409
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	SMEVSTQLAR	99.7%	53.3	25	45.3	4	0	0	1121.56	635	644
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	VDALNDEIR	99.7%	57.6	25	33.8	1	0	0	1044.53	797	805
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	VETYLNENLR	99.7%	66.8	25	44.8	2	0	0	1250.64	828	837
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	31	36	60	0.06%	29.3%	VSHIDVITAEMAK	99.7%	67.2	25	61.9	1	0	0	1413.74	1195	1207
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	26	27	51	0.05%	21.8%	DNTSVYHISGK	99.7%	42.6	25	41.2	2	0	0	1220.59	192	202
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	26	27	51	0.05%	21.8%	DTLVADNLDQATR	99.7%	107	25	102	2	0	0	1431.71	714	726
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	26	27	51	0.05%	21.8%	ELEANVLATAPDK	99.7%	64.4	25	64.4	2	0	0	1370.72	841	853
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	26	27	51	0.05%	21.8%	FTASIQR	97.4%	31.4	25	19.4	2	0	0	822.45	821	827
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	26	27	51	0.05%	21.8%	FTQLDLEDVQVR	99.7%	84.8	25	80.3	2	0	0	1462.75	390	401
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	26	27	51	0.05%	21.8%	HNTAVSQLTK	99.7%	64	25	58	2	0	0	1098.59	513	522
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	26	27	51	0.05%	21.8%	IAEMETQKEK	98.5%	33.6	25	25.7	2	0	0	1206.60	334	343
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	26	27	51	0.05%	21.8%	IFNLSGGEK	98.3%	33.2	25	18.2	2	0	0	964.51	1188	1196
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	26	27	51	0.05%	21.8%	IHEDTKEINEK	99.7%	45.9	25	41.2	2	0	0	1355.68	344	354
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	26	27	51	0.05%	21.8%	LGDLGAIDEK	99.6%	40.5	25	32.4	2	0	0	1030.54	619	628
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	26	27	51	0.05%	21.8%	LHNTIVEINNHK	99.3%	30.3	25	30.3	0	2	0	1431.77	887	898
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	26	27	51	0.05%	21.8%	LLEENVSAFK	99.7%	56.6	25	48	2	0	0	1149.62	858	867
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	26	27	51	0.05%	21.8%	LTQEETNFK	99.7%	55.8	25	47.8	2	0	0	1109.55	565	573
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	26	27	51	0.05%	21.8%	NAQFIIISLR	99.7%	81.5	25	74.5	2	0	0	1174.69	1243	1252
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	26	27	51	0.05%	21.8%	NLLQELK	98.0%	32.4	25	12	1	0	0	857.51	992	998
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	26	27	51	0.05%	21.8%	NNMFEISDR	99.7%	46.7	25	41.4	1	0	0	1141.49	1253	1261
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	26	27	51	0.05%	21.8%	NTNAAEESLPEIQK	99.7%	95.3	25	92.8	2	0	0	1543.76	975	988
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	26	27	51	0.05%	21.8%	QAFYFALR	99.5%	39.1	25	22.9	2	0	0	1015.54	706	713
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	26	27	51	0.05%	21.8%	QLDECASAITK	99.7%	68.1	25	65.5	2	0	0	1235.59	912	922
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	26	27	51	0.05%	21.8%	QNIGVATFIGLDK	99.7%	61.5	25	55.3	2	0	0	1375.76	661	673
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	26	27	51	0.05%	21.8%	SNNIINETTTR	99.7%	62.6	25	55.3	3	0	0	1262.63	435	445
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	26	27	51	0.05%	21.8%	TEYDAVAEK	98.5%	33.6	25	31.8	1	0	0	1025.48	868	876
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	26	27	51	0.05%	21.8%	VAELDKITYER	99.7%	60.4	25	59.9	2	0	0	1336.71	1107	1117
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	26	27	51	0.05%	21.8%	VIQENEHALQK	99.7%	73.1	25	69.2	2	0	0	1308.69	999	1009
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	26	27	51	0.05%	21.8%	VLDAIIQEK	99.7%	53.1	25	47	2	0	0	1028.60	599	607

Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	26	27	51	0.05%	21.8%	VVTLQGQIIEQSGTMTGGGSK	99.7%	100	25	100	3	0	0	2107.07	737	757
Structural maintenance of chromosomes protein 6	SMC6	SMC6_HUMAN	126.3	100.0%	2	2	2	0.00%	1.9%	IEAENKYDAIK	96.0%	29.5	25	18.5	1	0	0	1293.67	774	784
Structural maintenance of chromosomes protein 6	SMC6	SMC6_HUMAN	126.3	100.0%	2	2	2	0.00%	1.9%	SATGSVVSTR	98.7%	34.5	25	26.5	1	0	0	964.51	158	167
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	SDHB	SDHB_HUMAN	31.6	100.0%	2	2	2	0.00%	9.3%	DLVPDLSNFYAQYK	99.7%	47.5	25	47.5	1	0	0	1672.82	138	151
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	SDHB	SDHB_HUMAN	31.6	100.0%	2	2	2	0.00%	9.3%	IKNEVDSTLTFR	99.7%	50.4	25	50.4	1	0	0	1422.76	79	90
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	8	12	22	0.02%	31.8%	GGQTHLGLPVFNTVK	99.7%	57.3	25	57.3	1	2	0	1567.86	91	105
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	8	12	22	0.02%	31.8%	IGIMPGHIHK	98.2%	32.9	25	30	1	0	0	1102.62	183	192
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	8	12	22	0.02%	31.8%	IICQGFTGK	99.0%	35.6	25	25.8	2	0	0	1023.53	58	66
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	8	12	22	0.02%	31.8%	ISALQSAGVVVSMSPAQLGTTIYK	99.7%	74.9	25	74.9	1	2	0	2437.30	315	338
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	8	12	22	0.02%	31.8%	LIGPNCPGVINPGECK	99.7%	71.9	25	68.4	3	0	0	1724.85	167	182
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	8	12	22	0.02%	31.8%	LVGGTTPGK	99.7%	48.7	25	39.6	2	0	0	829.48	82	90
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	8	12	22	0.02%	31.8%	MGHAGAIIAGGK	99.7%	70.6	25	67.5	4	0	0	1082.58	297	308
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	8	12	22	0.02%	31.8%	QGTFHSQQALEYGTK	99.7%	49.1	25	45.4	2	2	0	1694.81	67	81
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	12	12	23	0.02%	27.6%	CDVIAQGIVMAVK	99.7%	93.6	25	78.1	2	0	0	1403.74	384	396
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	12	12	23	0.02%	27.6%	DLEIKIPVVVR	98.7%	34.3	25	34.3	2	0	0	1280.79	397	407
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	12	12	23	0.02%	27.6%	EPIDIEEGIKK	99.0%	35.6	25	27.3	2	0	0	1270.69	206	216
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	12	12	23	0.02%	27.6%	EQALQLAQK	99.7%	44.9	25	37.4	2	0	0	1028.57	217	225
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	12	12	23	0.02%	27.6%	ICNQVLVCER	99.7%	63.3	25	56.9	2	0	0	1290.63	151	160
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	12	12	23	0.02%	27.6%	ILACDDLDEAAR	99.7%	83.3	25	73.5	2	0	0	1361.64	427	438
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	12	12	23	0.02%	27.6%	INFDSNSAYR	99.7%	77.4	25	73	2	0	0	1186.55	275	284
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	12	12	23	0.02%	27.6%	IVFSPEEAK	97.2%	31	25	27.7	1	0	0	1019.54	121	129
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	12	12	23	0.02%	27.6%	LSEIVTLAK	99.7%	56.2	25	35.8	2	0	0	973.59	443	451
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	12	12	23	0.02%	27.6%	LYSLFLK	99.3%	37	25	26.9	2	0	0	883.53	243	249
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	12	12	23	0.02%	27.6%	MGFPPNIVESAAENMVK	99.7%	66.1	25	63.9	2	0	0	1833.89	226	242
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	12	12	23	0.02%	27.6%	SPDEAYAIAK	99.7%	66.2	25	65	2	0	0	1064.53	79	88
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	13	24	0.02%	26.9%	EAQVYQAFK	99.7%	52.6	25	49.7	2	0	0	1083.55	339	347
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	13	24	0.02%	26.9%	ETYLAILMDR	99.7%	53.8	25	47.6	4	0	0	1240.62	151	160
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	13	24	0.02%	26.9%	FFVADTANEALEAAK	99.7%	105	25	105	2	0	0	1596.79	59	73
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	13	24	0.02%	26.9%	ILNNSGLPITSAIDLEDAAK	99.7%	82.9	25	82.9	2	0	0	2055.10	404	423
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	13	24	0.02%	26.9%	ILNNSGLPITSAIDLEDAAKK	97.6%	25.4	25	25.4	0	1	0	2183.19	404	424
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	13	24	0.02%	26.9%	INFDDNAEFR	99.7%	71.9	25	63.6	2	0	0	1240.56	260	269
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	13	24	0.02%	26.9%	LEGTNVQEAQK	99.7%	72.7	25	54.8	2	0	0	1216.62	393	403
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	13	24	0.02%	26.9%	LYNLFLK	99.7%	48.2	25	35.5	2	0	0	910.54	228	234
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	13	24	0.02%	26.9%	MAENLGFVGPLK	99.7%	87.9	25	79.1	4	0	0	1275.68	207	218
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	13	24	0.02%	26.9%	QMIGYNLATK	99.5%	38.8	25	27.5	1	0	0	1154.59	119	128
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	13	24	0.02%	26.9%	VMVAEALDISR	99.7%	88.2	25	78.1	2	0	0	1203.64	140	150
SUMO-conjugating enzyme UBC9	UBE2I	UBC9_HUMAN	18.0	99.8%	2	2	2	0.00%	13.9%	DHPFGFVAVPTK	97.0%	30.7	25	24.7	1	0	0	1314.68	19	30
SUMO-conjugating enzyme UBC9	UBE2I	UBC9_HUMAN	18.0	99.8%	2	2	2	0.00%	13.9%	GTPWEGGLFK	96.0%	29.5	25	29.5	1	0	0	1091.55	50	59
SUN domain-containing protein 2	SUN2	SUN2_HUMAN	80.3	100.0%	3	3	4	0.00%	6.3%	DSSPHFQAEQR	99.7%	45.9	25	37.6	2	0	0	1301.59	265	275
SUN domain-containing protein 2	SUN2	SUN2_HUMAN	80.3	100.0%	3	3	4	0.00%	6.3%	IGLADYALESGGASVISTR	99.7%	104	25	101	1	0	0	1879.98	544	562
SUN domain-containing protein 2	SUN2	SUN2_HUMAN	80.3	100.0%	3	3	4	0.00%	6.3%	LTTAASLLDVFVLTR	99.7%	49	25	49	1	0	0	1619.94	191	205
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	15	16	30	0.03%	15.5%	AIGNTELENK	99.7%	48.2	25	39.8	2	0	0	1088.56	1013	1022
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	15	16	30	0.03%	15.5%	DVDFEGTDEPIFGK	99.7%	69.8	25	69.8	2	0	0	1568.71	65	78
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	15	16	30	0.03%	15.5%	EYPFILDAFQR	99.7%	62.1	25	50.3	4	0	0	1398.71	135	145
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	15	16	30	0.03%	15.5%	GIVILMVDEK	99.7%	46	25	45.9	1	0	0	1132.63	533	542
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	15	16	30	0.03%	15.5%	IVIPNEESVVIYYK	99.7%	56.3	25	55.5	2	0	0	1665.91	615	628
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	15	16	30	0.03%	15.5%	LDFNTDEEKK	99.6%	39.8	25	29	1	0	0	1238.59	409	418
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	15	16	30	0.03%	15.5%	LGFATSSDVIEMK	99.7%	58.6	25	45.1	1	0	0	1397.70	861	873
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	15	16	30	0.03%	15.5%	LTEQLAGPLR	99.7%	80.5	25	67.2	2	0	0	1097.63	924	933
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	15	16	30	0.03%	15.5%	MTDVFEGSIIR	99.7%	65.6	25	58.4	4	0	0	1267.64	985	995
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	15	16	30	0.03%	15.5%	NFQPVIIFSFSK	99.7%	49.6	25	44.6	3	0	0	1426.77	385	396

Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	15	16	30	0.03%	15.5%	RLEELLR	99.7%	45	25	11.1	2	0	0	928.56	999	1005
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	15	16	30	0.03%	15.5%	SFYQFQHYR	99.7%	50.7	25	42.1	2	0	0	1275.59	588	596
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	15	16	30	0.03%	15.5%	TVLQMDELK	97.3%	31.2	25	25.2	2	0	0	1076.57	844	852
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	15	16	30	0.03%	15.5%	VEEINPEYMLEK	99.3%	37.3	25	26.9	1	0	0	1493.72	576	587
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	15	16	30	0.03%	15.5%	YCLPFLQPGR	99.4%	38.2	25	36.7	1	0	0	1250.64	649	658
Suppressor of SWI4 1 homolog	PPAN	SSF1_HUMAN	53.2	100.0%	4	4	6	0.01%	9.9%	LPGGPTLTFQVK	99.7%	54.1	25	49.6	2	0	0	1257.72	102	113
Suppressor of SWI4 1 homolog	PPAN	SSF1_HUMAN	53.2	100.0%	4	4	6	0.01%	9.9%	TEEELQAILEAK	99.7%	63.3	25	50.6	1	0	0	1373.72	304	315
Suppressor of SWI4 1 homolog	PPAN	SSF1_HUMAN	53.2	100.0%	4	4	6	0.01%	9.9%	VGGSDEEASGIPSR	99.7%	74.8	25	70.6	2	0	0	1360.63	356	369
Suppressor of SWI4 1 homolog	PPAN	SSF1_HUMAN	53.2	100.0%	4	4	6	0.01%	9.9%	VMEPLTASR	96.6%	30.2	25	24.4	1	0	0	1019.52	53	61
Surfeit locus protein 4	SURF4	SURF4_HUMAN	30.4	100.0%	4	4	8	0.01%	18.2%	GQNDLMGTAEDFADQFLR	99.7%	72.4	25	72.4	2	0	0	2043.91	2	19
Surfeit locus protein 4	SURF4	SURF4_HUMAN	30.4	100.0%	4	4	8	0.01%	18.2%	LCLISTFLEDGIR	99.7%	75.1	25	65.4	2	0	0	1536.81	31	43
Surfeit locus protein 4	SURF4	SURF4_HUMAN	30.4	100.0%	4	4	8	0.01%	18.2%	QYLPHVAR	98.8%	34.6	25	26	1	0	0	983.54	23	30
Surfeit locus protein 4	SURF4	SURF4_HUMAN	30.4	100.0%	4	4	8	0.01%	18.2%	SMFAGVPTMR	99.6%	40.9	25	33.1	3	0	0	1128.52	140	149
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	5	5	7	0.01%	5.6%	ALNIVDQEGSLLGK	99.7%	63.1	25	62.3	1	0	0	1456.80	215	228
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	5	5	7	0.01%	5.6%	ATTGTQTLLSSGTR	99.7%	60.3	25	50.7	2	0	0	1393.73	696	709
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	5	5	7	0.01%	5.6%	GADQKPTSADCAVR	98.9%	35	25	35	1	0	0	1475.69	646	659
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	5	5	7	0.01%	5.6%	IPLGLDLK	97.0%	30.6	25	23	1	0	0	868.55	298	305
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	5	5	7	0.01%	5.6%	YSLSGSVAHSR	99.7%	76.2	25	73	2	0	0	1163.58	63	73
Survival motor neuron protein	SMN1	SMN_HUMAN	31.8	99.9%	2	2	3	0.00%	7.8%	ETCVVVYTGYGNR	99.7%	73.7	25	71	2	0	0	1517.71	121	133
Survival motor neuron protein	SMN1	SMN_HUMAN	31.8	99.9%	2	2	3	0.00%	7.8%	NTAASLQQWK	99.7%	47.4	25	39	1	0	0	1146.59	84	93
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	20	35	0.03%	18.3%	ANYAVDAYFR	99.7%	43.2	25	36.2	1	0	0	1189.56	740	749
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	20	35	0.03%	18.3%	CNELQDIEK	99.7%	42.7	25	23.4	2	0	0	1148.53	891	899
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	20	35	0.03%	18.3%	CNTLITLIER	99.7%	53.3	25	42	2	0	0	1232.67	1001	1010
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	20	35	0.03%	18.3%	DFNQFIK	97.9%	32.2	25	10.8	2	0	0	911.46	849	855
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	20	35	0.03%	18.3%	DIDILNSAGK	99.7%	65.4	25	41.7	2	0	0	1045.55	431	440
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	20	35	0.03%	18.3%	EIQEPDPTYEEK	99.7%	50.8	25	41.8	1	0	0	1477.67	72	83
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	20	35	0.03%	18.3%	ESEITDEDIDGILER	99.7%	90.9	25	90.9	2	0	0	1733.81	666	680
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	20	35	0.03%	18.3%	FITDNTVEER	99.7%	54.8	25	44.7	2	0	0	1223.59	607	616
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	20	35	0.03%	18.3%	LDGQTPHDER	99.7%	54.7	25	44.1	2	0	0	1167.54	529	538
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	20	35	0.03%	18.3%	LDSIVIQQGR	99.7%	73.4	25	62.5	2	0	0	1128.64	627	636
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	20	35	0.03%	18.3%	LLNILMQLR	99.7%	75.7	25	60.4	4	0	0	1113.68	446	454
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	20	35	0.03%	18.3%	NPELPNAAQAQK	99.7%	66.2	25	60.3	2	0	0	1280.66	803	814
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	20	35	0.03%	18.3%	QDSINAYNEPNSTK	99.2%	36.4	25	31.1	1	0	0	1580.72	539	552
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	20	35	0.03%	18.3%	QNLLSVGDYR	99.7%	74.4	25	51.9	2	0	0	1164.60	133	142
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	20	35	0.03%	18.3%	SVCLIGDKEQR	99.7%	63.3	25	42.6	1	0	0	1304.66	257	267
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	20	35	0.03%	18.3%	TEQEEDEELLTESSK	99.7%	95.6	25	95.6	1	0	0	1766.78	146	160
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	20	35	0.03%	18.3%	VLIFSQMTR	99.7%	60.2	25	54.8	4	0	0	1094.60	502	510
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	20	35	0.03%	18.3%	YLVIDEAHR	99.7%	49	25	45.3	2	0	0	1115.58	304	312
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	SMARCD2	SMRD2_HUMAN	58.9	99.9%	2	2	3	0.00%	3.8%	IYISNTFSPSK	98.8%	34.9	25	29.7	1	0	0	1256.65	196	206
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	SMARCD2	SMRD2_HUMAN	58.9	99.9%	2	2	3	0.00%	3.8%	LLGVHTQTR	99.3%	37.3	25	16.4	2	0	0	1024.59	320	328
Symplekin	SYMPK	SYMPK_HUMAN	141.2	99.8%	2	2	5	0.00%	2.0%	ATNLCFAER	99.7%	46.2	25	27.6	1	0	0	1081.51	965	973
Symplekin	SYMPK	SYMPK_HUMAN	141.2	99.8%	2	2	5	0.00%	2.0%	VVLEAPLITESALEVVR	99.7%	73.6	25	73.6	4	0	0	1838.06	667	683
Syntaxin-18	STX18	STX18_HUMAN	38.7	100.0%	2	2	2	0.00%	6.9%	LIGEMNSLFDEVR	99.7%	70.5	25	70.5	1	0	0	1538.75	242	254
Syntaxin-18	STX18	STX18_HUMAN	38.7	100.0%	2	2	2	0.00%	6.9%	TCSEAIQQLR	99.7%	50.1	25	22.9	1	0	0	1205.59	106	115
Syntaxin-binding protein 2	STXBP2	STXB2_HUMAN	66.5	100.0%	3	3	5	0.00%	6.4%	ADTPSLGEGPEK	94.7%	28.3	25	24.3	1	0	0	1200.57	214	225
Syntaxin-binding protein 2	STXBP2	STXB2_HUMAN	66.5	100.0%	3	3	5	0.00%	6.4%	LIVPVLLDAAVPAYDK	99.7%	75.1	25	74.9	2	0	0	1696.99	388	403
Syntaxin-binding protein 2	STXBP2	STXB2_HUMAN	66.5	100.0%	3	3	5	0.00%	6.4%	YETTGLSEAR	99.7%	52.5	25	41	2	0	0	1126.54	266	275
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	6	8	17	0.02%	15.2%	FGGNPGGFGNQGGFGNSR	99.7%	116	25	110	2	0	0	1726.77	276	293
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	6	8	17	0.02%	15.2%	FTEYETQVK	99.7%	50.4	25	37.5	5	0	0	1144.55	152	160
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	6	8	17	0.02%	15.2%	GISVHISNAEPK	99.7%	54.7	25	52.1	2	0	0	1251.67	252	263
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	6	8	17	0.02%	15.2%	KMDETDASSAVK	99.7%	82.3	25	64.7	3	0	0	1281.60	84	95

TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	6	8	17	0.02%	15.2%	MDETDASSAVK	99.7%	56.3	25	55.8	3	0	0	1153.50	85	95
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	6	8	17	0.02%	15.2%	TSDLIVLGLPWK	99.7%	75	25	60.1	2	0	0	1341.78	103	114
Target of EGR1 protein 1	TOE1	TOE1_HUMAN	56.5	100.0%	3	3	5	0.00%	6.7%	ALLNLPGTQTSGEAK	99.0%	35.8	25	29.5	1	0	0	1499.81	348	362
Target of EGR1 protein 1	TOE1	TOE1_HUMAN	56.5	100.0%	3	3	5	0.00%	6.7%	SILSLGLACFK	99.7%	54.6	25	46.8	2	0	0	1208.67	96	106
Target of EGR1 protein 1	TOE1	TOE1_HUMAN	56.5	100.0%	3	3	5	0.00%	6.7%	YAAEFHAR	99.7%	49.4	25	41.8	2	0	0	964.46	231	238
TATA-binding protein-associated factor 172	BTAF1	BTAF1_HUMAN	206.9	100.0%	2	2	3	0.00%	1.1%	AVTLAVQPR	99.7%	47.3	25	27.8	1	0	0	954.57	745	753
TATA-binding protein-associated factor 172	BTAF1	BTAF1_HUMAN	206.9	100.0%	2	2	3	0.00%	1.1%	IAAGQAVEAIVK	99.7%	70.6	25	66.3	2	0	0	1169.69	60	71
TBC1 domain family member 15	TBC1D15	TBC15_HUMAN	79.5	99.8%	2	2	3	0.00%	2.9%	EFSFLDILR	99.5%	38.9	25	31.6	1	0	0	1139.61	539	547
TBC1 domain family member 15	TBC1D15	TBC15_HUMAN	79.5	99.8%	2	2	3	0.00%	2.9%	TQLIQLSTLLR	99.7%	56.4	25	51.7	2	0	0	1285.78	497	507
TBC1 domain family member 4	TBC1D4	TBCD4_HUMAN	146.6	100.0%	4	4	7	0.01%	4.1%	FEINLISPDTK	99.7%	60.8	25	58.3	1	0	0	1276.68	364	374
TBC1 domain family member 4	TBC1D4	TBCD4_HUMAN	146.6	100.0%	4	4	7	0.01%	4.1%	IQALESNLENLLTR	99.7%	92.2	25	87.6	3	0	0	1613.89	1227	1240
TBC1 domain family member 4	TBC1D4	TBCD4_HUMAN	146.6	100.0%	4	4	7	0.01%	4.1%	LLPADALVNCDLLLR	99.7%	45	25	43	2	0	0	1695.95	1268	1282
TBC1 domain family member 4	TBC1D4	TBCD4_HUMAN	146.6	100.0%	4	4	7	0.01%	4.1%	QAFSTAAALQSAK	99.7%	55.1	25	54.8	1	0	0	1293.68	435	447
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	AFHNEAQVNPER	99.7%	71.6	25	71.6	4	4	0	1411.67	469	480
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	AFHNEAQVNPERK	99.7%	48.6	25	38.2	2	3	0	1539.77	469	481
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	DCLINAAK	99.7%	45	25	29	4	0	0	904.46	146	153
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	DDKHGSYEDAVHSGALND	99.7%	68.5	25	68.5	2	3	0	1929.82	539	556
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	EQLAIAEFAR	99.7%	77.5	25	66.2	13	0	0	1147.61	434	443
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	EVGDGTTSVVIIAAELLK	99.7%	86.9	25	82.4	3	0	0	1815.01	85	102
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	FATEAAITILR	99.7%	94.2	25	74.1	10	0	0	1205.69	516	526
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	GANDFMCDEMER	99.7%	78.2	25	78.2	11	0	0	1474.54	379	390
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	HGSYEDAVHSGALND	99.7%	92.2	25	91.2	2	0	0	1571.67	542	556
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	IACLDFSLQK	99.7%	80.5	25	75.1	4	0	0	1194.62	234	243
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	ICDDELILIK	99.7%	59.4	25	46.2	5	0	0	1231.66	356	365
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	IHPTSVISGYR	98.8%	34.8	25	34.8	2	1	0	1229.66	112	122
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	ILATGANVILTTGGIDDMCLK	99.7%	80.9	25	80.7	3	0	0	2192.13	278	298
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	LGVQVVITDPEK	99.7%	81.9	25	81.7	2	0	0	1297.74	248	259
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	LGVQVVITDPEKLDQIR	99.7%	55.7	25	55.7	2	2	0	1923.09	248	264
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	LLEVEHPAAK	99.7%	64	25	56	9	0	0	1106.62	64	73
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	MLVDDIGDVTITNDGATILK	99.7%	147	25	145	4	0	0	2120.08	44	63
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	QAGVFEPTIVK	99.7%	56.3	25	44.7	4	0	0	1188.66	500	510
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	SLHDALCVVK	99.7%	57.6	25	53.5	4	0	0	1141.60	391	400
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	SLLVIPNTLAVNAAQDSTDLVAK	99.7%	104	25	104	12	2	0	2353.30	444	466
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	SQNVMAAASIANIVK	99.7%	128	25	124	7	0	0	1532.81	19	33
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	SSLGPVGLDK	99.7%	60.1	25	36.4	4	0	0	972.54	34	43
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	TSASIILR	99.7%	79	25	64.6	2	0	0	860.52	371	378
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	VLCELADLQDK	99.7%	85.2	25	76.4	2	0	0	1303.66	74	84
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	WIGLDLSNGKPR	99.7%	61.5	25	57.9	2	2	0	1355.74	485	496
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	YFVEAGAMAVR	99.7%	79.7	25	70.8	5	0	0	1213.60	299	309
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	27	39	144	0.14%	55.8%	YPVNSVNILK	99.7%	49.3	25	33.5	3	0	0	1146.65	190	199
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	16	21	37	0.04%	37.2%	AAHSEGNTTAGLDMR	99.7%	87.4	25	87.4	2	4	0	1530.70	467	481
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	16	21	37	0.04%	37.2%	AGADEERAETAR	97.5%	31.5	25	28.7	1	0	0	1275.59	14	25
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	16	21	37	0.04%	37.2%	DASLMVTNDGATILK	99.7%	69	25	59.3	1	0	0	1548.79	58	72
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	16	21	37	0.04%	37.2%	EALLSSAVDHGSDEVK	99.7%	97.7	25	92.7	2	2	0	1656.81	139	154
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	16	21	37	0.04%	37.2%	EAVAMESYAK	99.7%	44.7	25	44.7	2	0	0	1098.51	432	441
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	16	21	37	0.04%	37.2%	EGTIGDMAILGITESFQVK	99.7%	78.7	25	78.7	1	0	0	2009.03	482	500
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	16	21	37	0.04%	37.2%	GATQQILDEAER	99.7%	78.4	25	74	2	0	0	1330.66	377	388
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	16	21	37	0.04%	37.2%	HGINCFINR	99.7%	58.9	25	52.8	2	0	0	1130.55	285	293
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	16	21	37	0.04%	37.2%	ILIANTGMDTDKIK	99.7%	80.5	25	65.6	4	0	0	1532.84	237	250
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	16	21	37	0.04%	37.2%	LAVEAVLR	99.7%	57.5	25	16.6	2	0	0	870.54	182	189
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	16	21	37	0.04%	37.2%	LKGSGNLEAIHIIK	99.2%	29.7	25	13.6	0	2	0	1492.88	190	203

T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	16	21	37	0.04%	37.2%	LTSFIGAIAIGDLVK	99.7%	104	25	97.6	2	0	0	1517.89	26	40
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	16	21	37	0.04%	37.2%	VAEIEHAEK	99.7%	53.3	25	51.1	2	0	0	1025.53	264	272
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	16	21	37	0.04%	37.2%	VAEIEHAEKEK	99.7%	52.2	25	44	2	1	0	1282.66	264	274
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	16	21	37	0.04%	37.2%	VLVDMSR	97.6%	31.6	25	17.5	1	0	0	819.44	83	89
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	16	21	37	0.04%	37.2%	VQDDEVGDGTTSVTVLAAELLR	99.7%	126	25	126	2	0	0	2288.16	90	111
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	34	135	0.13%	53.4%	ALIAGGGAPEIELALR	99.7%	110	25	110	14	0	0	1550.89	420	435
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	34	135	0.13%	53.4%	AQDIEAGDGTTSVVIIAGSLLDSCTK	99.7%	122	25	122	2	2	0	2621.30	97	122
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	34	135	0.13%	53.4%	AYILNLVK	99.5%	39.5	25	36.5	4	0	0	933.58	281	288
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	34	135	0.13%	53.4%	DALSDLALHFLNK	99.7%	97.5	25	88	11	2	0	1456.78	307	319
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	34	135	0.13%	53.4%	DIEREDIEFICK	99.7%	55.5	25	55.5	5	1	0	1566.75	327	338
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	34	135	0.13%	53.4%	ETLLNSATTSLNSK	99.7%	95.9	25	90.9	2	0	0	1478.77	161	174
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	34	135	0.13%	53.4%	FSNISAAK	99.7%	43.2	25	35.5	2	0	0	837.45	35	42
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	34	135	0.13%	53.4%	GAYQDRDKPAQIR	99.7%	41	25	36.5	0	2	0	1517.78	22	34
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	34	135	0.13%	53.4%	GDVTITNDGATILK	99.7%	102	25	93	4	0	0	1417.75	66	79
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	34	135	0.13%	53.4%	GIHPTIISESFQK	99.7%	52.2	25	47.9	5	2	0	1456.78	127	139
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	34	135	0.13%	53.4%	IDDVVNTR	99.7%	59.4	25	53.6	4	0	0	931.48	532	539
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	34	135	0.13%	53.4%	IGLIQFCLSAPK	99.7%	67.8	25	60.8	11	0	0	1346.75	246	257
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	34	135	0.13%	53.4%	KTGCNVLLIQK	99.7%	55.8	25	34.7	1	0	0	1273.73	292	302
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	34	135	0.13%	53.4%	LGGTIDDCELVEGLVLTQK	99.7%	83.8	25	83.8	3	0	0	2060.06	214	232
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	34	135	0.13%	53.4%	LVIEEAER	99.7%	59.4	25	54.7	8	0	0	958.52	396	403
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	34	135	0.13%	53.4%	MIQDGKGDVTITNDGATILK	99.7%	92.9	25	86.9	2	6	0	2106.08	60	79
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	34	135	0.13%	53.4%	MLVELSK	99.1%	36.3	25	6.03	3	0	0	835.46	90	96
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	34	135	0.13%	53.4%	QMQVLHPAAR	99.7%	72.3	25	67.9	4	0	0	1150.62	80	89
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	34	135	0.13%	53.4%	SIHDALCVIR	99.7%	57.2	25	0	6	0	0	1183.63	404	413
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	34	135	0.13%	53.4%	TDMDNQIVVSDYAQMDR	99.7%	120	25	120	4	0	0	2032.86	258	274
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	34	135	0.13%	53.4%	TGCNVLLIQK	99.7%	54.5	25	41.2	6	0	0	1145.63	293	302
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	34	135	0.13%	53.4%	TLSGMESYCVR	99.7%	64.1	25	60	9	0	0	1302.58	442	452
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	34	135	0.13%	53.4%	VIDPATATSVDLR	99.7%	108	25	103	10	0	0	1357.73	194	206
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	23	34	135	0.13%	53.4%	VVSQYSSLLSPMSVNAVMK	99.7%	105	25	105	6	0	0	2072.04	175	193
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	AVTIFIR	99.7%	46.7	25	27.8	3	0	0	819.51	382	388
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	CPTLEQYAMR	99.7%	41.1	25	33.5	2	0	0	1284.57	440	449
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	DKMLVIEQCK	99.7%	45.1	25	42.3	1	0	0	1279.64	369	378
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	DTEPLIQTAK	99.6%	40.8	25	40.1	2	0	0	1115.59	161	170
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	DVDFELIK	99.0%	35.6	25	16.1	2	0	0	978.51	203	210
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	DVDFELIKVEGK	99.7%	72.8	25	64.6	2	0	0	1391.74	203	214
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	EKFEEMIQQIK	99.7%	56.8	25	47	2	1	0	1438.72	283	293
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	EMNPALGIDCLHK	99.7%	77.2	25	70.6	4	0	0	1513.71	484	496
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	FEEMIQQIK	99.7%	42.3	25	30.9	3	0	0	1181.59	285	293
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	FSELTAEK	99.7%	55.8	25	44.3	1	0	0	924.47	345	352
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	GVIVDKDFSHPQMPK	99.7%	66.9	25	66.9	3	4	0	1697.87	227	241
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	HKLDVTSVEDYK	98.0%	26.1	25	24.8	0	2	0	1433.73	264	275
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	IADGYEQAAR	99.7%	87.8	25	80.5	6	0	0	1093.53	133	142
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	IAILTCPFEPPKPK	99.7%	48.5	25	48.5	2	0	0	1610.90	248	261
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	IDDIRKPGESEE	99.7%	47.7	25	35.2	2	0	0	1387.67	530	541
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	ISDSVLVDIKDTEPLIQTAK	99.7%	45.7	25	44.9	0	2	0	2185.20	151	170
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	KQQISLATQMVR	99.7%	57.6	25	52.3	3	2	0	1402.78	514	525
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	LDVTSVEDYK	99.7%	74.4	25	69.1	2	0	0	1168.57	266	275
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	LGFAGLVQEISFGTTK	99.7%	98.6	25	98.6	6	0	0	1667.90	353	368
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	LMGLEALK	98.7%	34.2	25	19.3	3	0	0	890.50	28	35
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	LMVELSK	99.7%	42.9	25	12	3	0	0	835.46	90	96
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	MIIEEAKR	99.7%	57.2	25	43.7	4	0	0	989.54	393	400

T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	MLVIEQCK	99.7%	44.3	25	31.8	2	0	0	1036.52	371	378
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	QQISLATQMVR	99.7%	54.5	25	46.8	4	0	0	1290.68	515	525
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	RDVDFELIK	99.6%	40.6	25	7.44	1	0	0	1134.62	202	210
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	SLHDALCVIR	99.7%	57.2	25	0	6	0	0	1183.63	401	410
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	TSLGPNGLDK	99.7%	56.2	25	50.2	2	0	0	1001.53	50	59
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	VAIEHLDK	99.7%	52.5	25	33.6	2	0	0	924.52	143	150
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	29	41	90	0.09%	46.4%	WVGGPEIELIAIATGGR	99.7%	77.3	25	69.4	6	0	0	1738.95	324	340
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	19	22	56	0.05%	41.3%	ALEIIPR	99.5%	39.3	25	36	4	0	0	811.50	441	447
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	19	22	56	0.05%	41.3%	ATISNDGATILK	99.7%	59.1	25	43.7	2	0	0	1203.66	56	67
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	19	22	56	0.05%	41.3%	CAMTALSSK	96.8%	30.4	25	22.6	1	0	0	968.45	158	166
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	19	22	56	0.05%	41.3%	CQVFEETQIGGER	99.7%	78.7	25	72.9	3	0	0	1552.71	345	357
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	19	22	56	0.05%	41.3%	GGAEQFMEETER	99.7%	76.8	25	76.8	2	0	0	1383.58	376	387
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	19	22	56	0.05%	41.3%	IKEIAVTVK	98.3%	33.2	25	28.9	2	0	0	1000.64	136	144
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	19	22	56	0.05%	41.3%	LLDVVHPAAK	99.7%	51	25	42.5	4	0	0	1062.63	68	77
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	19	22	56	0.05%	41.3%	LPIGDVATQYFADR	99.7%	96.2	25	94.6	3	0	0	1565.80	293	306
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	19	22	56	0.05%	41.3%	NDSVVAGGGAIEMELSK	99.7%	91.5	25	91.5	2	0	0	1692.81	402	418
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	19	22	56	0.05%	41.3%	QLCDNAGFDATNILNK	99.7%	102	25	88.1	2	0	0	1793.85	448	463
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	19	22	56	0.05%	41.3%	QQLLIGAYAK	97.1%	30.8	25	23	1	0	0	1104.64	431	440
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	19	22	56	0.05%	41.3%	SLHDAIMIVR	99.7%	52.6	25	47.6	4	0	0	1154.64	388	397
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	19	22	56	0.05%	41.3%	SQDAEVGDGTTSVTLLAAEFLK	99.7%	136	25	136	4	2	0	2252.13	85	106
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	19	22	56	0.05%	41.3%	TATQLAVNK	99.7%	60.2	25	51.2	4	0	0	945.54	127	135
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	19	22	56	0.05%	41.3%	TCTFILR	99.5%	39.4	25	14.2	2	0	0	910.48	369	375
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	19	22	56	0.05%	41.3%	TFSYAGFEMQPK	99.7%	70.5	25	70.5	4	0	0	1421.64	219	230
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	19	22	56	0.05%	41.3%	VPEEDLKR	99.7%	53.2	25	45.1	4	0	0	985.53	314	321
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	19	22	56	0.05%	41.3%	VQGGALEDSQLVAGVAFK	99.7%	115	25	115	2	0	0	1788.95	200	217
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	19	22	56	0.05%	41.3%	YNFFTGCPK	99.7%	61.2	25	44.3	4	0	0	1133.51	358	366
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	ACTILLR	99.7%	53.3	25	34.8	3	0	0	846.49	371	377
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	ALDDMISTLK	99.7%	74.4	25	65.6	6	0	0	1106.58	129	138
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	ALDDMISTLKK	99.7%	49.5	25	38.3	4	0	0	1234.67	129	139
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	AMTGVEQWPYR	99.7%	83.7	25	81.5	4	0	0	1337.63	428	438
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	AVAQALEVIPR	99.7%	88.7	25	79.3	16	0	0	1166.69	439	449
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	EILSEVER	99.7%	41.4	25	15.3	5	0	0	974.52	382	389
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	EIQVQHPAAK	99.7%	64.5	25	52.6	10	0	0	1120.61	69	78
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	ELGIWEPLAVK	99.7%	69.8	25	64.8	8	0	0	1254.71	492	502
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	GISDLAQHYLMR	99.7%	79.4	25	75.5	13	3	0	1403.71	295	306
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	IDDIVSGHK	99.7%	61.8	25	45.9	7	0	0	983.52	519	527
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	IDDIVSGHKK	98.0%	32.4	25	24.3	2	0	0	1111.61	519	528
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	IGDEYFTFITDCK	99.7%	75.4	25	69.2	2	0	0	1608.73	355	367
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	IGDEYFTFITDCKDPK	99.6%	39.6	25	38.2	2	1	0	1948.90	355	370
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	IPGGIIEDSCVLR	99.7%	87.7	25	76.7	6	0	0	1428.75	204	216
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	IVLLDSSLEYK	99.7%	76.1	25	70.3	6	0	0	1279.71	238	248
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	IVLLDSSLEYKK	99.7%	50.3	25	47.6	2	0	0	1407.81	238	249
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	IVSRPEELR	99.4%	37.8	25	15.9	2	0	0	1098.63	331	339
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	IVSRPEELREDDVGTGAGLLEIK	99.7%	52.9	25	52.9	0	2	0	2496.33	331	353
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	KGESQTDIEITR	99.7%	86.3	25	54.5	2	2	0	1376.70	249	260
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	KVQSGNINAAK	97.6%	31.6	25	31.6	1	0	0	1129.63	21	31
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	MLLDPMGGIVMTNDGNAILR	99.7%	92.8	25	92.8	14	3	0	2131.07	49	68
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	MVQFEENGR	99.7%	47.8	25	43.8	2	0	0	1109.50	182	190
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	MVQFEENGRK	99.7%	43.7	25	34.6	3	0	0	1237.60	182	191
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	NLQDAMQVCR	99.7%	69.4	25	63.5	9	0	0	1250.56	390	399
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	NVLLDPQLVPGGGASEMAVAHALTEK	98.9%	28.6	25	21.2	0	2	0	2617.37	400	425

T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	SMIEISR	99.6%	40.3	25	24.9	2	0	0	835.43	79	85
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	TAVETAVLLLR	99.7%	99.8	25	90.1	4	0	0	1185.72	508	518
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	TLIQNCGASTIR	99.7%	86.5	25	72.7	6	0	0	1333.69	450	461
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	VQSGNINAAK	98.1%	32.7	25	21.2	1	0	0	1001.54	22	31
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	30	44	161	0.15%	52.7%	WSSLACNIALDAVK	99.7%	99.5	25	93.1	6	0	0	1547.79	168	181
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	14	0.01%	19.5%	AIADTGANVVVTGGK	99.7%	72.3	25	66.4	2	0	0	1372.74	282	296
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	14	0.01%	19.5%	AVDDGVNTFK	99.7%	65.9	25	56.9	2	0	0	1065.52	391	400
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	14	0.01%	19.5%	DIDEVSSLLR	99.7%	66.8	25	48.5	2	0	0	1146.60	156	165
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	14	0.01%	19.5%	DMLEAGILDTYLGK	98.8%	34.7	25	34.7	1	0	0	1554.77	491	504
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	14	0.01%	19.5%	ETEGDVTSVK	99.5%	39.4	25	33	1	0	0	1064.51	226	235
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	14	0.01%	19.5%	FAEAFEAIPR	99.7%	73.6	25	66	2	0	0	1150.59	441	450
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	14	0.01%	19.5%	IAVYSCPFDGMITETK	99.7%	46.9	25	46.9	1	0	0	1847.86	239	254
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	14	0.01%	19.5%	LFVTNDAATILR	99.7%	90.3	25	82.2	2	0	0	1333.75	63	74
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	14	0.01%	19.5%	LYAVHQEGNK	99.3%	37	25	32	1	0	0	1158.59	467	476
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	32	105	0.10%	46.7%	ALQFLEEVK	99.7%	61.7	25	54.8	2	0	0	1076.60	130	138
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	32	105	0.10%	46.7%	AQAALAVNISAAR	99.7%	89.9	25	79.4	3	0	0	1255.71	16	28
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	32	105	0.10%	46.7%	AQLGVQAFADALLIIPK	99.7%	73.3	25	72.3	3	0	0	1768.04	433	449
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	32	105	0.10%	46.7%	DGNVLLHEMQIQHPTASLIAK	99.7%	46.3	25	46.3	0	4	0	2315.22	59	79
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	32	105	0.10%	46.7%	EGIVALRR	98.5%	33.9	25	17	2	0	0	913.56	308	315
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	32	105	0.10%	46.7%	EMDRETLIDVAR	99.7%	49.5	25	39.6	3	3	0	1447.72	142	153
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	32	105	0.10%	46.7%	ETLIDVAR	99.7%	51.1	25	44.2	2	0	0	916.51	146	153
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	32	105	0.10%	46.7%	GFVVINQK	99.7%	41.2	25	18.3	2	0	0	904.53	288	295
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	32	105	0.10%	46.7%	GIDPFSLDALSK	99.7%	90.5	25	36.7	12	0	0	1262.66	296	307
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	32	105	0.10%	46.7%	GLQDVLR	99.6%	40.8	25	15.2	2	0	0	800.46	29	35
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	32	105	0.10%	46.7%	GLVLDHGAR	99.7%	58.6	25	41.6	11	0	0	937.52	209	217
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	32	105	0.10%	46.7%	HKSETDTSLIR	99.7%	46.2	25	45.2	2	2	0	1286.67	198	208
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	32	105	0.10%	46.7%	HTLTQIK	98.5%	33.8	25	13.3	2	0	0	840.49	382	388
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	32	105	0.10%	46.7%	IITEGFEAAK	99.7%	68.9	25	37.4	6	0	0	1078.58	118	127
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	32	105	0.10%	46.7%	KFIEDR	99.5%	39.5	25	13.4	1	0	0	807.44	265	270
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	32	105	0.10%	46.7%	KQDEPIDLFMIEIMEMK	99.7%	35.8	25	35.8	0	3	0	2158.01	181	197
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	32	105	0.10%	46.7%	MLVSGAGDIK	99.7%	52.2	25	34.3	5	0	0	1006.52	46	55
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	32	105	0.10%	46.7%	QADLYISEGLHPR	99.7%	64.7	25	64.4	6	3	0	1498.77	105	117
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	32	105	0.10%	46.7%	SETDTSLIR	99.7%	65.1	25	53.5	6	0	0	1021.52	200	208
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	32	105	0.10%	46.7%	TEVNSGFFYK	99.7%	63	25	56.1	4	0	0	1191.57	242	251
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	32	105	0.10%	46.7%	VATAQDDITGDGTTSNVLIIGELLK	99.7%	103	25	96.2	2	2	0	2544.34	80	104
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	32	105	0.10%	46.7%	VCGDSDKGFVVINQK	99.7%	69	25	69	2	2	0	1665.83	281	295
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	23	32	105	0.10%	46.7%	VLAQNSGFDLQETLVK	99.7%	106	25	106	8	0	0	1761.94	450	465
Telomere length regulation protein TEL2 homolog	TELO2	TELO2_HUMAN	91.7	100.0%	3	3	4	0.00%	4.7%	AVLICLAQLGEPELR	97.4%	31.3	25	31.3	1	0	0	1681.93	363	377
Telomere length regulation protein TEL2 homolog	TELO2	TELO2_HUMAN	91.7	100.0%	3	3	4	0.00%	4.7%	LQQENLAEFFPQNYFR	99.3%	37.5	25	36.3	1	0	0	2043.99	171	186
Telomere length regulation protein TEL2 homolog	TELO2	TELO2_HUMAN	91.7	100.0%	3	3	4	0.00%	4.7%	LVEQVPDR	99.6%	39.9	25	32.4	2	0	0	955.52	255	262
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	4	4	9	0.01%	2.4%	IGISDISSLSEK	99.7%	68.8	25	60.7	2	0	0	1248.67	1700	1711
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	4	4	9	0.01%	2.4%	ITSELSEANALELLSK	99.7%	71.3	25	71.3	2	0	0	1717.92	88	103
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	4	4	9	0.01%	2.4%	LIAEQTLQENLIEK	99.7%	89.1	25	85.8	2	0	0	1641.91	1468	1481
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	4	4	9	0.01%	2.4%	LVSDIIDPVALEIPLSK	99.7%	71.8	25	71.6	3	0	0	1822.06	2399	2415
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	7	7	12	0.01%	9.0%	AVYTLYQQR	99.7%	63.9	25	54.2	2	0	0	1141.60	505	513
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	7	7	12	0.01%	9.0%	LAAVQLLQFLAPK	99.7%	57.4	25	57.4	2	0	0	1411.87	116	128
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	7	7	12	0.01%	9.0%	LLLQHAPLR	99.7%	42.5	25	35.8	2	0	0	1060.66	866	874
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	7	7	12	0.01%	9.0%	LQNATPTNFK	97.0%	30.6	25	30.6	1	0	0	1133.60	25	34
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	7	7	12	0.01%	9.0%	SQNFDILQSAISK	99.7%	96.5	25	90.8	2	0	0	1450.75	747	759
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	7	7	12	0.01%	9.0%	VGPEELPVVGQLLR	99.7%	51.4	25	51.4	2	0	0	1505.87	852	865
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	7	7	12	0.01%	9.0%	VLDILLEQYPALITGR	99.7%	58.3	25	58.3	1	0	0	1814.04	163	178

Testis-expressed sequence 264 protein	TEX264	TX264_HUMAN	34.2	99.8%	2	2	3	0.00%	8.0%	ETSAATLSPGASSR	99.7%	87.1	25	83.9	2	0	0	1334.65	237	250
Testis-expressed sequence 264 protein	TEX264	TX264_HUMAN	34.2	99.8%	2	2	3	0.00%	8.0%	LFTESCSISPK	99.7%	41	25	32.4	1	0	0	1268.62	63	73
Tetratricopeptide repeat protein 19, mitochondrial	TTC19	TTC19_HUMAN	42.5	99.8%	2	2	4	0.00%	5.8%	ALQISEEIQGER	99.7%	43.2	25	37.9	2	0	0	1372.71	263	274
Tetratricopeptide repeat protein 19, mitochondrial	TTC19	TTC19_HUMAN	42.5	99.8%	2	2	4	0.00%	5.8%	LASIYAAQNR	99.7%	49.1	25	37.1	2	0	0	1106.60	185	194
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	6	6	10	0.01%	4.7%	AALVDYLDGK	99.7%	41	25	41	1	0	0	1064.56	682	691
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	6	6	10	0.01%	4.7%	ASELNPESIYSVFK	99.7%	54.4	25	54	2	0	0	1583.80	624	637
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	6	6	10	0.01%	4.7%	LSDYDSSEEAIR	99.7%	70.9	25	62.1	1	0	0	1384.62	363	374
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	6	6	10	0.01%	4.7%	SGPGLIGLGIK	99.7%	62.8	25	41.8	2	0	0	1011.62	271	281
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	6	6	10	0.01%	4.7%	TLDQISDADNIPGLLVLK	99.7%	52.6	25	50.8	2	0	0	1925.06	375	392
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	6	6	10	0.01%	4.7%	VVAQYAQR	99.7%	41.4	25	35.7	2	0	0	934.51	1202	1209
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	4	4	10	0.01%	9.7%	IHSDTFASGGER	99.7%	49.1	25	43	2	0	0	1276.59	337	348
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	4	4	10	0.01%	9.7%	SFLESIDDALAEK	99.7%	80.8	25	73.9	2	0	0	1437.71	116	128
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	4	4	10	0.01%	9.7%	VLLQAFDVVER	99.7%	68	25	60.9	4	0	0	1288.73	105	115
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	4	4	10	0.01%	9.7%	YGYTDIDLLSAAK	99.7%	77.8	25	77.4	2	0	0	1429.72	250	262
Thioredoxin	TXN	THIO_HUMAN	11.7	100.0%	3	3	9	0.01%	19.0%	EKLEATINELV	99.7%	46.1	25	42.9	3	0	0	1258.69	95	105
Thioredoxin	TXN	THIO_HUMAN	11.7	100.0%	3	3	9	0.01%	19.0%	VGEFSGANK	99.7%	50.9	25	41.7	4	0	0	908.45	86	94
Thioredoxin	TXN	THIO_HUMAN	11.7	100.0%	3	3	9	0.01%	19.0%	VGEFSGANKEK	99.5%	38.8	25	27	2	0	0	1165.58	86	96
Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3	PRDX3_HUMAN	27.7	99.8%	2	2	4	0.00%	10.2%	DYGVLLEGSGLALR	99.7%	108	25	102	2	0	0	1462.79	171	184
Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3	PRDX3_HUMAN	27.7	99.8%	2	2	4	0.00%	10.2%	GLFIIDPNGVIK	99.7%	47	25	44.7	2	0	0	1285.75	185	196
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	13	13	25	0.02%	8.7%	ADQLDYENFR	99.7%	42.5	25	42.5	1	0	0	1270.57	1085	1094
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	13	13	25	0.02%	8.7%	AEGGYFGQIR	99.7%	53.7	25	45.5	2	0	0	1097.54	711	720
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	13	13	25	0.02%	8.7%	FLCCMLETVTR	99.7%	52.8	25	45.8	1	0	0	1429.66	1042	1052
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	13	13	25	0.02%	8.7%	FVELVHQQK	99.7%	45.5	25	40.7	2	0	0	1127.62	999	1007
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	13	13	25	0.02%	8.7%	GEFLHLCR	99.7%	49.5	25	39.9	1	0	0	1031.51	22	29
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	13	13	25	0.02%	8.7%	GSPVNALQNKR	99.7%	49	25	36.3	1	0	0	1183.65	406	416
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	13	13	25	0.02%	8.7%	LDPETLESLGLIK	99.7%	86.4	25	73.9	2	0	0	1427.80	127	139
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	13	13	25	0.02%	8.7%	LGLLEALLK	99.7%	48.7	25	41.3	3	0	0	969.63	346	354
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	13	13	25	0.02%	8.7%	LIALAICK	99.2%	36.5	25	21.1	2	0	0	901.55	378	385
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	13	13	25	0.02%	8.7%	TPATTPEAR	99.7%	48.1	25	38.4	2	0	0	943.48	1285	1293
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	13	13	25	0.02%	8.7%	TPNFSTLLCYDR	99.7%	64.5	25	63.8	2	0	0	1486.70	1008	1019
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	13	13	25	0.02%	8.7%	VFSDIIYTVASCTENEASR	99.7%	82.1	25	82.1	2	0	0	2162.01	1020	1038
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	13	13	25	0.02%	8.7%	VLNLGQALER	99.7%	52.9	25	42	4	0	0	1112.64	1137	1146
THO complex subunit 3	THOC3	THOC3_HUMAN	38.8	100.0%	3	4	6	0.01%	6.0%	TASVFLLEK	97.2%	31	25	20.9	1	0	0	1007.58	78	86
THO complex subunit 3	THOC3	THOC3_HUMAN	38.8	100.0%	3	4	6	0.01%	6.0%	TASVFLLEKDR	99.7%	50.7	25	50.7	2	0	0	1278.71	78	88
THO complex subunit 3	THOC3	THOC3_HUMAN	38.8	100.0%	3	4	6	0.01%	6.0%	YVLGMQELFR	99.7%	53.2	25	47.1	3	0	0	1255.65	34	43
THO complex subunit 4	ALYREF	THOC4_HUMAN	26.9	100.0%	6	8	18	0.02%	35.0%	MDMSLDDIIK	99.7%	64.8	25	53.1	2	0	0	1180.56	5	14
THO complex subunit 4	ALYREF	THOC4_HUMAN	26.9	100.0%	6	8	18	0.02%	35.0%	QLPDKWQHDLFDSGFGGGAGVETGGK	99.7%	62.5	25	62.5	0	2	0	2703.28	82	107
THO complex subunit 4	ALYREF	THOC4_HUMAN	26.9	100.0%	6	8	18	0.02%	35.0%	QQLSAEELDAQLDAYNAR	99.7%	108	25	107	2	2	0	2034.97	236	253
THO complex subunit 4	ALYREF	THOC4_HUMAN	26.9	100.0%	6	8	18	0.02%	35.0%	QYNGVPLDGRPMNIQLVTSQIDAQR	99.7%	45.6	25	45.6	0	2	0	2829.43	165	189
THO complex subunit 4	ALYREF	THOC4_HUMAN	26.9	100.0%	6	8	18	0.02%	35.0%	SLGTADVHFER	99.7%	69	25	54	6	1	0	1231.61	145	155
THO complex subunit 4	ALYREF	THOC4_HUMAN	26.9	100.0%	6	8	18	0.02%	35.0%	WQHDLFDSGFGGGAGVETGGK	99.7%	52.5	25	52.5	0	1	0	2121.96	87	107
THO complex subunit 6 homolog	THOC6	THOC6_HUMAN	37.5	100.0%	3	3	6	0.01%	10.6%	TSLEVPEINALLLVPK	99.7%	69.1	25	69.1	2	0	0	1736.02	122	137
THO complex subunit 6 homolog	THOC6	THOC6_HUMAN	37.5	100.0%	3	3	6	0.01%	10.6%	VDVFTNLGYR	99.7%	64.2	25	54.2	2	0	0	1183.61	326	335
THO complex subunit 6 homolog	THOC6	THOC6_HUMAN	37.5	100.0%	3	3	6	0.01%	10.6%	VLTAAGNSCR	99.7%	51.4	25	44.4	2	0	0	1048.52	316	325
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	4	4	7	0.01%	6.2%	GFQEVVTPNIFNSR	99.2%	36.6	25	34.9	1	0	0	1607.82	368	381
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	4	4	7	0.01%	6.2%	IYGISFPDPK	99.7%	51.2	25	37.7	2	0	0	1136.60	297	306
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	4	4	7	0.01%	6.2%	LADFGVLHR	99.7%	56	25	46.6	2	0	0	1027.57	434	442
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	4	4	7	0.01%	6.2%	NELSGALTGLTR	99.7%	80.9	25	52.8	2	0	0	1231.66	443	454
Threonine--tRNA ligase, mitochondrial	TARS2	SYTM_HUMAN	81.0	100.0%	4	4	6	0.01%	5.4%	AEASGGLGGLTR	99.7%	63.5	25	52.3	1	0	0	1088.57	439	450
Threonine--tRNA ligase, mitochondrial	TARS2	SYTM_HUMAN	81.0	100.0%	4	4	6	0.01%	5.4%	LADFGALHR	99.7%	64	25	50.7	2	0	0	999.54	430	438
Threonine--tRNA ligase, mitochondrial	TARS2	SYTM_HUMAN	81.0	100.0%	4	4	6	0.01%	5.4%	LVELQNTR	99.2%	36.5	25	27	1	0	0	972.55	703	710

Threonine--tRNA ligase, mitochondrial	TARS2	SYTM_HUMAN	81.0	100.0%	4	4	6	0.01%	5.4%	VYNALVAFIR	99.7%	81.9	25	76.6	2	0	0	1165.67	331	340
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	3	3	5	0.00%	6.9%	AANNIASLLTK	99.7%	50.4	25	39.6	2	0	0	1115.64	359	369
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	3	3	5	0.00%	6.9%	AVLLTQDTK	98.6%	34.1	25	14.1	1	0	0	988.57	441	449
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	3	3	5	0.00%	6.9%	TGSVDIIVTDLPFGK	99.7%	80.1	25	76.7	2	0	0	1561.85	397	411
Thymidine kinase, cytosolic	TK1	KITH_HUMAN	25.5	100.0%	4	4	6	0.01%	20.1%	GQIQVILGPMFSGK	98.5%	33.8	25	33.8	1	0	0	1474.81	19	32
Thymidine kinase, cytosolic	TK1	KITH_HUMAN	25.5	100.0%	4	4	6	0.01%	20.1%	LTAVCMECFR	99.2%	37	25	37	1	0	0	1286.57	149	158
Thymidine kinase, cytosolic	TK1	KITH_HUMAN	25.5	100.0%	4	4	6	0.01%	20.1%	TVIVAALDGTFQR	99.7%	72.8	25	66.3	2	0	0	1390.77	118	130
Thymidine kinase, cytosolic	TK1	KITH_HUMAN	25.5	100.0%	4	4	6	0.01%	20.1%	YSSSFCTHDR	99.7%	58.9	25	55.5	2	0	0	1259.51	61	70
Thymidylate kinase	DTYMK	KTHY_HUMAN	23.8	99.8%	2	2	3	0.00%	10.8%	GALIVLEGVDR	99.7%	42.5	25	29.3	1	0	0	1141.66	6	16
Thymidylate kinase	DTYMK	KTHY_HUMAN	23.8	99.8%	2	2	3	0.00%	10.8%	KLVEALCAAGHR	99.7%	44	25	44	0	2	0	1324.72	25	36
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	12	14	45	0.04%	14.9%	ASAVSELSPR	99.7%	72.6	25	65.8	6	0	0	1016.54	236	245
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	12	14	45	0.04%	14.9%	DSRPSQAAGDNQGDEAK	99.7%	53.1	25	40.4	1	2	0	1745.77	186	202
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	12	14	45	0.04%	14.9%	EESAASGGAAYTK	99.7%	72.5	25	70.2	4	0	0	1241.56	334	346
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	12	14	45	0.04%	14.9%	EQTFSGGTSQDTK	99.7%	79.4	25	78	3	0	0	1385.62	203	215
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	12	14	45	0.04%	14.9%	GSFSDTGLGDGK	99.7%	67	25	66.7	6	0	0	1140.52	376	387
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	12	14	45	0.04%	14.9%	SIFQHIQSAQSQR	99.7%	47.2	25	43.1	3	4	0	1529.78	609	621
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	12	14	45	0.04%	14.9%	SPLQSVVVR	99.7%	51.4	25	36.2	5	0	0	984.58	253	261
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	12	14	45	0.04%	14.9%	SPPSTGSTYGSSQK	99.7%	68	25	68	2	0	0	1383.64	320	333
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	12	14	45	0.04%	14.9%	TDSEKPFR	99.7%	42.6	25	29.1	2	0	0	979.48	397	404
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	12	14	45	0.04%	14.9%	TEELEEESFPER	99.7%	71.3	25	60.5	2	0	0	1494.66	487	498
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	12	14	45	0.04%	14.9%	VIGANKNQEEEK	97.9%	32.1	25	24.2	1	0	0	1358.69	456	467
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	12	14	45	0.04%	14.9%	YKDDPVDLR	99.6%	40.5	25	23.6	4	0	0	1120.56	710	718
Tight junction protein ZO-2	TJP2	ZO2_HUMAN	134.0	100.0%	3	3	4	0.00%	2.9%	AEQMASVQNAQR	99.7%	51.7	25	44.5	1	0	0	1348.63	665	676
Tight junction protein ZO-2	TJP2	ZO2_HUMAN	134.0	100.0%	3	3	4	0.00%	2.9%	EDAVLYLLEIPK	99.7%	99.3	25	97.3	2	0	0	1402.78	569	580
Tight junction protein ZO-2	TJP2	ZO2_HUMAN	134.0	100.0%	3	3	4	0.00%	2.9%	ETPQSLAFTR	99.7%	43.2	25	30.9	1	0	0	1149.59	618	627
Torsin-1A-interacting protein 1	TOR1AIP1	TOIP1_HUMAN	66.2	100.0%	3	3	6	0.01%	6.7%	FESFPAGSTLIFYK	95.0%	28.6	25	28.6	1	0	0	1606.82	481	494
Torsin-1A-interacting protein 1	TOR1AIP1	TOIP1_HUMAN	66.2	100.0%	3	3	6	0.01%	6.7%	SELGNQSPSTSSR	99.7%	46.6	25	46.2	1	0	0	1349.63	309	321
Torsin-1A-interacting protein 1	TOR1AIP1	TOIP1_HUMAN	66.2	100.0%	3	3	6	0.01%	6.7%	SQPAILLLTAAR	99.7%	64	25	58.8	4	0	0	1253.76	405	416
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	6	7	13	0.01%	26.9%	ATTPADGEEPAPEAEALAAAR	99.7%	109	25	109	2	2	0	2037.97	6	26
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	6	7	13	0.01%	26.9%	DYIQSTMETEK	99.5%	39.2	25	38.7	2	0	0	1360.59	124	134
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	6	7	13	0.01%	26.9%	FLSGLELVK	99.7%	47.2	25	38.1	2	0	0	1005.60	32	40
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	6	7	13	0.01%	26.9%	GVDLYVLEK	99.7%	62.8	25	46.1	2	0	0	1035.57	197	205
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	6	7	13	0.01%	26.9%	TIGQVLAR	96.8%	30.4	25	8.5	1	0	0	857.52	145	152
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	6	7	13	0.01%	26.9%	TPQGLSNLAK	99.7%	66.1	25	59.3	2	0	0	1028.57	135	144
Trafficking protein particle complex subunit 1	TRAPPC1	TPPC1_HUMAN	16.8	100.0%	4	5	10	0.01%	26.9%	DGFLAFQTSR	99.7%	60.5	25	48.4	2	0	0	1141.56	59	68
Trafficking protein particle complex subunit 1	TRAPPC1	TPPC1_HUMAN	16.8	100.0%	4	5	10	0.01%	26.9%	LHYYETPTGIK	99.7%	55.2	25	45.1	2	0	0	1321.68	71	81
Trafficking protein particle complex subunit 1	TRAPPC1	TPPC1_HUMAN	16.8	100.0%	4	5	10	0.01%	26.9%	SRLDSYVR	99.7%	50.6	25	36.1	2	0	0	995.53	128	135
Trafficking protein particle complex subunit 1	TRAPPC1	TPPC1_HUMAN	16.8	100.0%	4	5	10	0.01%	26.9%	TVHNLYLFDR	99.7%	44.8	25	38.9	2	2	0	1277.66	2	11
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	11	11	19	0.02%	7.8%	AVATYHANTER	99.7%	55.7	25	46.6	2	0	0	1232.60	503	513
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	11	11	19	0.02%	7.8%	DSDAGSSTPTTSTR	99.7%	64.3	25	50.4	2	0	0	1382.60	1416	1429
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	11	11	19	0.02%	7.8%	DTALETALNAK	99.7%	65.4	25	47.5	2	0	0	1146.60	427	437
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	11	11	19	0.02%	7.8%	ELPEYYELIR	99.7%	57.5	25	55.4	2	0	0	1324.68	1493	1502
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	11	11	19	0.02%	7.8%	GLDPVEILQER	99.7%	69.7	25	62.8	2	0	0	1268.68	360	370
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	11	11	19	0.02%	7.8%	IQELENLPGSLAGDLR	99.7%	83.7	25	76.3	2	0	0	1724.92	382	397
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	11	11	19	0.02%	7.8%	LCTVNSVEEK	99.7%	42.8	25	30	1	0	0	1178.57	1204	1213
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	11	11	19	0.02%	7.8%	LLLTGTPLQNK	99.7%	61.2	25	0	2	0	0	1197.72	907	917
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	11	11	19	0.02%	7.8%	LTQVLNTHYVAPR	98.4%	26.8	25	18.4	0	1	0	1511.83	893	905
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	11	11	19	0.02%	7.8%	QLSEVFIQLPSR	99.5%	39.2	25	23.5	1	0	0	1416.78	1480	1491
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	11	11	19	0.02%	7.8%	VIQAGMFDQK	99.5%	39.2	25	31.2	2	0	0	1136.58	1228	1237
Transcription and mRNA export factor ENY2	ENY2	ENY2_HUMAN	11.5	99.8%	2	2	3	0.00%	17.8%	ALVPDSVKK	95.8%	29.3	25	22	1	0	0	956.58	77	85
Transcription and mRNA export factor ENY2	ENY2	ENY2_HUMAN	11.5	99.8%	2	2	3	0.00%	17.8%	TFLAQHASL	99.2%	36.7	25	36.7	2	0	0	987.53	93	101

Transcription elongation factor B polypeptide 1	TCEB1	ELOC_HUMAN	12.5	100.0%	3	3	5	0.00%	41.1%	AMLSGPGQFAENETNEVNFR	99.7%	54.7	25	54.7	1	0	0	2227.01	44	63
Transcription elongation factor B polypeptide 1	TCEB1	ELOC_HUMAN	12.5	100.0%	3	3	5	0.00%	41.1%	LISSDGHEFIVK	99.7%	41	25	41	2	0	0	1344.72	21	32
Transcription elongation factor B polypeptide 1	TCEB1	ELOC_HUMAN	12.5	100.0%	3	3	5	0.00%	41.1%	TYGGCEGPDAMYVK	99.5%	39.5	25	39.5	2	0	0	1563.65	7	20
Transcription elongation factor, mitochondrial	TEFM	TEFM_HUMAN	41.7	99.9%	2	2	3	0.00%	4.7%	QFLFDSILK	99.5%	39.2	25	30.2	2	0	0	1110.62	302	310
Transcription elongation factor, mitochondrial	TEFM	TEFM_HUMAN	41.7	99.9%	2	2	3	0.00%	4.7%	SINIVEHR	97.2%	31	25	28.8	1	0	0	967.53	96	103
Transcription elongation regulator 1	TCERG1	TCRG1_HUMAN	123.9	99.8%	2	2	3	0.00%	1.9%	EALFNEFVAAAR	99.7%	63	25	59.5	2	0	0	1337.68	770	781
Transcription elongation regulator 1	TCERG1	TCRG1_HUMAN	123.9	99.8%	2	2	3	0.00%	1.9%	VFFYNPTTR	99.3%	37.1	25	29.5	1	0	0	1144.58	544	552
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	12	13	21	0.02%	37.4%	AEWQVYKEEISR	99.7%	77	25	77	2	2	0	1537.76	105	116
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	12	13	21	0.02%	37.4%	ELTLLGKPK	99.7%	41.6	25	34.9	1	0	0	998.62	148	156
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	12	13	21	0.02%	37.4%	EQLPIFK	98.8%	34.9	25	16.8	1	0	0	874.50	63	69
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	12	13	21	0.02%	37.4%	FSKEQLPIFK	98.9%	35	25	24.7	2	0	0	1236.70	60	69
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	12	13	21	0.02%	37.4%	IYQDAYR	99.7%	41.5	25	36.9	2	0	0	928.45	98	104
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	12	13	21	0.02%	37.4%	KIYQDAYR	98.9%	35.3	25	23.5	1	0	0	1056.55	97	104
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	12	13	21	0.02%	37.4%	KPVSSYLR	97.1%	30.9	25	20.6	1	0	0	949.55	52	59
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	12	13	21	0.02%	37.4%	NLSDSEKELYIQHAK	99.7%	47.2	25	40.9	0	2	0	1774.90	191	205
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	12	13	21	0.02%	37.4%	SAYNVYVAER	99.7%	85.1	25	67.5	3	0	0	1171.57	160	169
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	12	13	21	0.02%	37.4%	SWEEQMIEVGR	99.7%	63	25	52.8	2	0	0	1363.63	217	227
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	12	13	21	0.02%	37.4%	SWEEQMIEVGRK	99.7%	53	25	53	1	0	0	1491.73	217	228
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	12	13	21	0.02%	37.4%	WRELPDSK	97.1%	30.8	25	26.2	1	0	0	1030.53	88	95
Transcriptional activator protein Pur-alpha	PURA	PURA_HUMAN	34.9	100.0%	3	4	6	0.01%	18.0%	FFFDVGSNK	95.9%	29.3	25	27.8	1	0	0	1060.51	231	239
Transcriptional activator protein Pur-alpha	PURA	PURA_HUMAN	34.9	100.0%	3	4	6	0.01%	18.0%	GPGLGSTQGQTIALPAQGLIEFR	99.7%	75.2	25	75.2	1	1	0	2311.24	177	199
Transcriptional activator protein Pur-alpha	PURA	PURA_HUMAN	34.9	100.0%	3	4	6	0.01%	18.0%	LIDDYGVEEEPAELPEGTSLTVDNKR	99.7%	85.2	25	79.1	0	3	0	2889.40	205	230
Transcriptional activator protein Pur-beta	PURB	PURB_HUMAN	33.2	100.0%	3	3	4	0.00%	11.5%	GGGEQETQELASK	99.7%	74.5	25	69	2	0	0	1333.62	25	37
Transcriptional activator protein Pur-beta	PURB	PURB_HUMAN	33.2	100.0%	3	3	4	0.00%	11.5%	GGGGGPCGFQPASR	99.7%	45.6	25	45.6	1	0	0	1304.58	11	24
Transcriptional activator protein Pur-beta	PURB	PURB_HUMAN	33.2	100.0%	3	3	4	0.00%	11.5%	VSEVKPSYR	99.7%	52	25	43.1	1	0	0	1064.57	247	255
Transducin beta-like protein 2	TBL2	TBL2_HUMAN	49.8	99.8%	2	2	2	0.00%	5.8%	AFIVWLANGDTLR	99.6%	39.6	25	39.6	1	0	0	1475.80	150	162
Transducin beta-like protein 2	TBL2	TBL2_HUMAN	49.8	99.8%	2	2	2	0.00%	5.8%	LQQQLTQAQETLK	99.7%	73.2	25	72.6	1	0	0	1528.83	428	440
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	18	20	37	0.04%	27.9%	AFTYINLDK	99.3%	37.1	25	32.6	1	0	0	1084.57	478	486
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	18	20	37	0.04%	27.9%	AVLGTSNFK	99.7%	45.5	25	42	1	0	0	936.51	487	495
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	18	20	37	0.04%	27.9%	DSAQNSVIIVDK	99.7%	84.6	25	71.2	2	0	0	1288.67	194	205
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	18	20	37	0.04%	27.9%	GFVEPDHYVVVGAQR	99.7%	77.1	25	69.6	1	2	0	1672.84	395	409
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	18	20	37	0.04%	27.9%	ILNIFGVIK	99.7%	54.8	25	39.6	3	0	0	1016.65	386	394
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	18	20	37	0.04%	27.9%	LAQMFSDMVLK	99.5%	39.5	25	33.6	2	0	0	1282.65	429	439
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	18	20	37	0.04%	27.9%	LAVDEEENADNNTK	99.7%	78.3	25	61.8	2	0	0	1561.70	40	53
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	18	20	37	0.04%	27.9%	LDSTDFTGTIK	99.1%	36.2	25	30.2	1	0	0	1197.60	135	145
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	18	20	37	0.04%	27.9%	LLNENSYVPR	99.7%	73.6	25	59.2	2	0	0	1204.63	146	155
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	18	20	37	0.04%	27.9%	LTVSNVLK	99.2%	36.6	25	7.27	2	0	0	873.54	375	382
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	18	20	37	0.04%	27.9%	LVYLVENPGGYVAYSK	99.7%	101	25	98.7	2	0	0	1771.93	209	224
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	18	20	37	0.04%	27.9%	QVDGDNSHVEMK	98.4%	33.4	25	31.4	1	0	0	1358.60	28	39
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	18	20	37	0.04%	27.9%	SAFSNLFGGEPLSYTR	99.7%	92.2	25	91.9	2	0	0	1745.85	7	22
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	18	20	37	0.04%	27.9%	SGVGTALLLK	99.7%	56.7	25	41.6	2	0	0	958.59	419	428
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	18	20	37	0.04%	27.9%	SSGLPNIPVQTISR	99.7%	48.4	25	41.8	2	0	0	1468.81	326	339
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	18	20	37	0.04%	27.9%	VEYHFLSPYVSPK	99.7%	51.9	25	51.2	2	2	0	1565.80	681	693
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	18	20	37	0.04%	27.9%	VSASPLLYTLIEK	99.7%	102	25	98.2	3	0	0	1433.83	496	508
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	18	20	37	0.04%	27.9%	YNSQLLSFVR	99.7%	55.6	25	50.1	2	0	0	1226.65	614	623
Transformation/transcription domain-associated protein	TRRAP	TRRAP_HUMAN	437.6	100.0%	2	2	2	0.00%	0.6%	LGFTPSVTIEQR	99.7%	45.6	25	42.8	1	0	0	1347.73	1992	2003
Transformation/transcription domain-associated protein	TRRAP	TRRAP_HUMAN	437.6	100.0%	2	2	2	0.00%	0.6%	VYPQAVYFPIR	97.3%	31.1	25	29.4	1	0	0	1352.74	3260	3270
Transformer-2 protein homolog alpha	TRA2A	TRA2A_HUMAN	32.7	100.0%	5	6	22	0.02%	25.5%	ANPDPNTCLGVFGLSLYTTER	99.7%	74.3	25	74.3	2	0	0	2325.12	113	133
Transformer-2 protein homolog alpha	TRA2A	TRA2A_HUMAN	32.7	100.0%	5	6	22	0.02%	25.5%	GFAFVYFER	99.7%	63.4	25	45.7	6	0	0	1135.56	161	169
Transformer-2 protein homolog alpha	TRA2A	TRA2A_HUMAN	32.7	100.0%	5	6	22	0.02%	25.5%	IDDSKEAMER	99.7%	71.9	25	58.7	4	0	0	1193.55	170	179
Transformer-2 protein homolog alpha	TRA2A	TRA2A_HUMAN	32.7	100.0%	5	6	22	0.02%	25.5%	IRVDYSITK	99.6%	40.5	25	21.8	4	0	0	1094.62	190	198

Transformer-2 protein homolog alpha	TRA2A	TRA2A_HUMAN	32.7	100.0%	5	6	22	0.02%	25.5%	RSPSPYYSR	99.4%	38.2	25	23.5	3	0	0	1112.55	259	267
Transformer-2 protein homolog alpha	TRA2A	TRA2A_HUMAN	32.7	100.0%	5	6	22	0.02%	25.5%	SPSPYYSR	99.7%	46.3	25	26.5	1	0	0	956.45	260	267
Transformer-2 protein homolog alpha	TRA2A	TRA2A_HUMAN	32.7	100.0%	5	6	22	0.02%	25.5%	YGPLSGVNVVYDQR	99.7%	69.9	25	62.1	6	0	0	1566.79	142	155
Transformer-2 protein homolog beta	TRA2B	TRA2B_HUMAN	33.7	100.0%	8	9	21	0.02%	30.9%	AAQDRDQIYR	97.8%	25.7	25	25	1	3	0	1235.61	252	261
Transformer-2 protein homolog beta	TRA2B	TRA2B_HUMAN	33.7	100.0%	8	9	21	0.02%	30.9%	ANPDPNCCLGVFGLSLYTTER	99.7%	41.7	25	41.7	1	0	0	2384.10	112	132
Transformer-2 protein homolog beta	TRA2B	TRA2B_HUMAN	33.7	100.0%	8	9	21	0.02%	30.9%	GFAFVYFENVDDAK	99.7%	92.9	25	80.2	4	0	0	1621.75	160	173
Transformer-2 protein homolog beta	TRA2B	TRA2B_HUMAN	33.7	100.0%	8	9	21	0.02%	30.9%	GYDDRDYYSR	95.1%	28.7	25	28.7	1	0	0	1309.54	229	238
Transformer-2 protein homolog beta	TRA2B	TRA2B_HUMAN	33.7	100.0%	8	9	21	0.02%	30.9%	IRVDFSITK	99.7%	41.9	25	21.6	3	0	0	1078.63	189	197
Transformer-2 protein homolog beta	TRA2B	TRA2B_HUMAN	33.7	100.0%	8	9	21	0.02%	30.9%	RSPSPYYSR	99.4%	38.2	25	23.5	3	0	0	1112.55	263	271
Transformer-2 protein homolog beta	TRA2B	TRA2B_HUMAN	33.7	100.0%	8	9	21	0.02%	30.9%	SPSPYYSR	99.7%	46.3	25	26.5	1	0	0	956.45	264	271
Transformer-2 protein homolog beta	TRA2B	TRA2B_HUMAN	33.7	100.0%	8	9	21	0.02%	30.9%	YGPIADVSIVYDQQSR	99.7%	99	25	96.3	4	0	0	1810.90	141	156
Transgelin-2	TAGLN2	TAGL2_HUMAN	22.4	100.0%	3	3	4	0.00%	16.6%	GASQAGMTGYGMPR	99.7%	46.6	25	46.5	2	0	0	1415.60	183	196
Transgelin-2	TAGLN2	TAGL2_HUMAN	22.4	100.0%	3	3	4	0.00%	16.6%	GPAYGLSR	98.3%	33.2	25	25.1	1	0	0	820.43	5	12
Transgelin-2	TAGLN2	TAGL2_HUMAN	22.4	100.0%	3	3	4	0.00%	16.6%	NFSDNQLQEGK	98.8%	34.8	25	34.8	1	0	0	1279.59	161	171
Transitional endoplasmic reticulum ATPase	VCP	TERA_HUMAN	89.3	100.0%	3	3	3	0.00%	5.2%	GILLYGPPGTGK	99.7%	47.5	25	0	1	0	0	1172.67	240	251
Transitional endoplasmic reticulum ATPase	VCP	TERA_HUMAN	89.3	100.0%	3	3	3	0.00%	5.2%	LDQLIYIPLPDEK	99.2%	36.7	25	36.7	1	0	0	1556.86	639	651
Transitional endoplasmic reticulum ATPase	VCP	TERA_HUMAN	89.3	100.0%	3	3	3	0.00%	5.2%	NAPAIIFIDELDAIAPK	99.7%	64.9	25	58.9	1	0	0	1811.00	296	312
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	5	5	10	0.01%	19.3%	AQNKPFYVVAESFK	99.4%	30.9	25	30.9	0	2	0	1627.85	221	234
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	5	5	10	0.01%	19.3%	DGATILTHAYSR	99.7%	56.5	25	51.5	2	0	0	1304.66	121	132
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	5	5	10	0.01%	19.3%	DKGETIQGLR	99.7%	41.9	25	28	2	0	0	1116.60	37	46
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	5	5	10	0.01%	19.3%	FISLASLEYSDYSK	99.7%	110	25	102	2	0	0	1622.79	75	88
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	5	5	10	0.01%	19.3%	VLEAAVAAK	99.7%	61.5	25	38.8	2	0	0	871.52	137	145
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	6	6	10	0.01%	20.2%	AVTGTHTLALAAK	99.7%	81.2	25	80.5	2	0	0	1253.72	247	259
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	6	6	10	0.01%	20.2%	IESFVETLK	96.7%	30.2	25	26.3	1	0	0	1065.58	15	23
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	6	6	10	0.01%	20.2%	LSPQFPNEEDSFHK	99.0%	35.8	25	35.8	1	0	0	1674.78	274	287
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	6	6	10	0.01%	20.2%	MTAAQPSETTVGNMVR	99.7%	87.2	25	81.4	3	0	0	1724.79	68	83
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	6	6	10	0.01%	20.2%	QIITDHR	99.0%	35.7	25	25.5	1	0	0	882.48	44	50
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	6	6	10	0.01%	20.2%	SDESDQQESLHK	99.7%	54.2	25	46.6	2	0	0	1402.61	100	111
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	7	7	13	0.01%	17.0%	ASPSTAGETPSGVK	99.7%	57.2	25	57.2	3	0	0	1288.64	129	142
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	7	7	13	0.01%	17.0%	ILQEAWTEGR	99.7%	77.2	25	61.2	2	0	0	1202.62	345	354
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	7	7	13	0.01%	17.0%	LGLQYSQGLVSGSNAR	99.7%	79.7	25	73	2	0	0	1649.86	210	225
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	7	7	13	0.01%	17.0%	LPEYPQVDDLLLR	99.7%	55.2	25	53.6	2	0	0	1570.85	144	156
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	7	7	13	0.01%	17.0%	VGTAQLALVAR	99.7%	98	25	77.9	2	0	0	1098.66	418	428
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	7	7	13	0.01%	17.0%	VSLFSHLPQYSR	95.3%	22.9	25	14.2	0	1	0	1433.75	177	188
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	7	7	13	0.01%	17.0%	VVVVDSRPWLEGR	99.0%	35.4	25	13.6	1	0	0	1511.83	358	370
Translation initiation factor eIF-2B subunit epsilon	EIF2B5	EI2BE_HUMAN	80.4	100.0%	4	4	5	0.00%	5.8%	GYNPAEVGAAGK	99.5%	39	25	31.2	1	0	0	1133.56	482	493
Translation initiation factor eIF-2B subunit epsilon	EIF2B5	EI2BE_HUMAN	80.4	100.0%	4	4	5	0.00%	5.8%	IITSELYR	99.7%	52.2	25	41	1	0	0	994.56	122	129
Translation initiation factor eIF-2B subunit epsilon	EIF2B5	EI2BE_HUMAN	80.4	100.0%	4	4	5	0.00%	5.8%	VFQNEVLGTLQR	99.7%	83.1	25	76.4	2	0	0	1403.76	552	563
Translation initiation factor eIF-2B subunit epsilon	EIF2B5	EI2BE_HUMAN	80.4	100.0%	4	4	5	0.00%	5.8%	YCALLLPLLK	99.7%	44.9	25	44.9	1	0	0	1203.72	617	626
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	4	4	5	0.00%	13.9%	DFIGVDSTGKR	99.6%	40.7	25	31.4	1	0	0	1194.61	156	166
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	4	4	5	0.00%	13.9%	HLVGVDSLIGPETQIGEK	99.4%	31	25	31	0	1	0	1892.01	350	367
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	4	4	5	0.00%	13.9%	KGQDSIEPVPGQK	99.7%	82.9	25	81.7	2	0	0	1382.73	134	146
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	4	4	5	0.00%	13.9%	LLSALCPEEPPVHSSAQIVSK	96.0%	23.4	25	23.4	0	1	0	2262.18	329	349
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	AALLETLSLLLAK	99.7%	73.4	25	73.4	3	0	0	1355.85	2324	2336
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	ADYTSHLR	99.7%	57.8	25	43.4	2	0	0	962.47	2184	2191
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	AGSVELLGAMAYCAPK	99.7%	74.5	25	69.7	2	0	0	1637.80	1515	1530
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	AIITALGVER	99.7%	74.2	25	49.7	2	0	0	1042.63	1872	1881
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	ALADENEFVR	99.7%	58.2	25	44.5	2	0	0	1163.57	1785	1794
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	ALGTLVSHVTLR	99.7%	58.5	25	47.8	2	0	0	1266.75	915	926
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	ALQAAIQQLAEAQPEATAK	99.7%	86.5	25	86.5	1	0	0	1952.04	69	87
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	ALVAVLLSR	99.7%	55	25	40.4	3	0	0	941.61	568	576

Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	ASLLDPVPEVR	98.1%	32.7	25	24.7	2	0	0	1195.67	1664	1674
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	AVMSNLSAHGVK	99.7%	57.3	25	48.2	4	0	0	1213.64	1485	1496
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	AYSDQAIVNLLK	99.7%	79.3	25	57.2	2	0	0	1334.73	2610	2621
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	CLQTLLDTK	98.7%	34.6	25	25.9	1	0	0	1091.58	1595	1603
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	DLAPYLPSVTPGLK	98.5%	33.9	25	25.5	2	0	0	1470.82	1650	1663
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	EDAGGMIQR	99.7%	43.1	25	32.2	1	0	0	976.45	1372	1380
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	EEFAIMQTPAGELYDK	99.7%	45.4	25	45.4	2	0	0	1841.86	761	776
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	EGVLTGSPEQKEEAAK	99.7%	56.5	25	53.5	1	0	0	1672.84	2270	2285
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	GAAYGLAGLVK	99.7%	64.4	25	52.5	2	0	0	1019.59	1396	1406
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	GIKEEVQLTSK	99.7%	42.2	25	30.1	2	0	0	1231.69	819	829
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	GLGILSLK	99.7%	41.9	25	12.1	2	0	0	800.52	1407	1414
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	GVTSILPVLR	99.4%	38	25	35.8	2	0	0	1054.66	2260	2269
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	HHIETGGGQLPAK	99.7%	39.7	25	39.7	1	1	0	1344.70	2538	2550
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	HLDQIIPR	99.7%	41.5	25	34.6	2	0	0	991.57	705	712
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	IDPEAFITR	99.7%	46.9	25	37	2	0	0	1061.56	696	704
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	ILPEIIPILEEGLR	99.7%	50	25	50	2	0	0	1604.96	1960	1973
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	IVVSNTPR	99.7%	41.5	25	35.5	2	0	0	885.52	1910	1917
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	LFCLTLHR	96.1%	29.6	25	21.9	1	0	0	1059.58	53	60
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	LMDEAVLALR	99.7%	62.2	25	51.2	4	0	0	1130.62	314	323
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	LMPEIVATASK	97.7%	31.8	25	25.6	1	0	0	1159.64	1735	1745
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	LMQQLLESDKYAER	96.2%	23.7	25	17	0	1	0	1723.87	1381	1394
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	LTEVLTDSHVK	99.7%	56.5	25	46.7	1	0	0	1241.67	1543	1553
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	LYRPPPVLDALGR	99.7%	46.5	25	46.5	1	2	0	1466.85	1209	1221
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	NAPNDASYDAVR	99.7%	77.5	25	73.9	2	0	0	1292.59	1305	1316
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	NLLHSLQSSGIGSK	99.7%	66.7	25	60.5	2	2	0	1440.78	88	101
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	QAGAEALSQAVAR	99.7%	83.4	25	59.5	2	0	0	1271.67	1177	1189
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	QGEEVFQSLSK	99.7%	42.6	25	36.5	2	0	0	1251.62	2624	2634
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	QLSSCLPNIVPK	95.6%	29.1	25	22.8	1	0	0	1355.74	1531	1542
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	SALLDFYMK	99.7%	42.4	25	33.8	4	0	0	1087.55	221	229
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	SDTQLVVR	99.0%	35.6	25	4.87	2	0	0	917.51	1894	1901
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	SGAAQGLAEVMAGLGVEK	99.7%	75.6	25	70.1	2	0	0	1687.87	1714	1731
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	SIIQSAQQDSIK	99.7%	59.5	25	53.2	3	0	0	1317.70	777	788
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	SIIQSAQQDSIKK	99.7%	49.6	25	39.4	2	0	0	1445.80	777	789
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	SLVSGLIR	99.3%	37.3	25	9.49	2	0	0	844.53	2192	2199
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	SWCQEELSVAVK	99.7%	43.8	25	40	1	0	0	1435.69	937	948
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	VDENGPELLPR	99.7%	79.4	25	68.1	2	0	0	1238.64	1027	1037
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	VISESPPDQWEAR	99.7%	49.2	25	48.3	2	0	0	1513.73	1222	1234
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	VLAFLSSVAGDALTR	99.7%	69.6	25	69.6	4	0	0	1519.85	2093	2107
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	VLAGLYMGR	99.7%	54.3	25	47.8	1	0	0	979.54	1885	1893
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	VLPLEALVTDAGEVTEAGK	99.7%	101	25	99.7	3	2	0	1912.03	617	635
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	49	56	104	0.10%	21.1%	YLLDSCAPLLR	99.7%	60.6	25	55.5	2	0	0	1320.70	241	251
Translin-associated protein X	TSNAX	TSNAX_HUMAN	33.1	100.0%	3	3	4	0.00%	12.4%	DITVESKR	95.4%	28.9	25	16.5	1	0	0	947.52	62	69
Translin-associated protein X	TSNAX	TSNAX_HUMAN	33.1	100.0%	3	3	4	0.00%	12.4%	QVYDGFSFIGNTGPYEVSK	99.1%	36.3	25	36.3	1	0	0	2108.00	223	241
Translin-associated protein X	TSNAX	TSNAX_HUMAN	33.1	100.0%	3	3	4	0.00%	12.4%	SFQQELDAR	99.7%	46.6	25	40.3	2	0	0	1093.53	41	49
Translocation protein SEC63 homolog	SEC63	SEC63_HUMAN	88.0	100.0%	3	3	5	0.00%	3.8%	AYAALTDEESR	99.7%	62.4	25	45.8	2	0	0	1225.57	148	158
Translocation protein SEC63 homolog	SEC63	SEC63_HUMAN	88.0	100.0%	3	3	5	0.00%	3.8%	VLLLSHLAR	99.7%	54.5	25	54.5	2	0	0	1021.65	303	311
Translocation protein SEC63 homolog	SEC63	SEC63_HUMAN	88.0	100.0%	3	3	5	0.00%	3.8%	YSGDQILIR	99.7%	41.5	25	35.5	1	0	0	1064.57	218	226
Translocator protein	TSPO	TSPOA_HUMAN	18.8	99.8%	2	2	6	0.01%	9.5%	ELGGFTEK	99.7%	52.7	25	20.2	4	0	0	880.44	70	77
Translocator protein	TSPO	TSPOA_HUMAN	18.8	99.8%	2	2	6	0.01%	9.5%	FVHGEGLR	96.6%	30.1	25	21.3	2	0	0	914.48	25	32
Translocon-associated protein subunit alpha	SSR1	SSRA_HUMAN	32.2	99.8%	2	2	4	0.00%	9.1%	GEDFPANNIVK	99.7%	57.1	25	50.7	2	0	0	1203.60	92	102
Translocon-associated protein subunit alpha	SSR1	SSRA_HUMAN	32.2	99.8%	2	2	4	0.00%	9.1%	GTEDFIVESLDASFR	99.7%	77.4	25	77	2	0	0	1685.80	111	125

Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	6	7	21	0.02%	37.0%	FFDEESYSLLR	99.7%	77	25	74	6	0	0	1405.66	106	116
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	6	7	21	0.02%	37.0%	FFDEESYSLLRK	99.7%	55.5	25	55.5	2	0	0	1533.76	106	117
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	6	7	21	0.02%	37.0%	NNEDISIIPPLFTVSVDHR	99.7%	53.1	25	52.8	0	2	0	2166.12	121	139
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	6	7	21	0.02%	37.0%	SAHAGTYEVR	99.7%	45.9	25	37	4	0	0	1090.53	96	105
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	6	7	21	0.02%	37.0%	VQNMALYADVGGK	99.7%	86	25	78.8	5	0	0	1365.68	61	73
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	6	7	21	0.02%	37.0%	YQVSWSLDHK	99.7%	48.7	25	36.4	2	0	0	1262.62	86	95
Translocon-associated protein subunit gamma	SSR3	SSRG_HUMAN	21.1	99.8%	2	3	4	0.00%	13.0%	EDAVSKEVTR	98.9%	35.3	25	23	1	0	0	1133.58	93	102
Translocon-associated protein subunit gamma	SSR3	SSRG_HUMAN	21.1	99.8%	2	3	4	0.00%	13.0%	QQSEEDLLLQDFSR	99.7%	81.9	25	70	2	1	0	1707.82	9	22
Transmembrane 9 superfamily member 3	TM9SF3	TM9S3_HUMAN	67.9	100.0%	3	3	7	0.01%	5.4%	NLSGQPNFPCR	99.7%	47.4	25	47.4	2	0	0	1289.61	419	429
Transmembrane 9 superfamily member 3	TM9SF3	TM9S3_HUMAN	67.9	100.0%	3	3	7	0.01%	5.4%	YFSLPFCVGSK	99.7%	48.8	25	41.8	3	0	0	1304.63	60	70
Transmembrane 9 superfamily member 3	TM9SF3	TM9S3_HUMAN	67.9	100.0%	3	3	7	0.01%	5.4%	YLDPSFFQHR	99.7%	46.9	25	36.4	2	0	0	1309.63	211	220
Transmembrane and coiled-coil domain-containing protein 1	TMCO1	TMCO1_HUMAN	21.2	100.0%	3	3	5	0.00%	16.5%	ETITESAGR	99.7%	44.4	25	32.2	2	0	0	963.47	55	63
Transmembrane and coiled-coil domain-containing protein 1	TMCO1	TMCO1_HUMAN	21.2	100.0%	3	3	5	0.00%	16.5%	ILGLAPSR	98.3%	33.2	25	29.6	2	0	0	826.51	161	168
Transmembrane and coiled-coil domain-containing protein 1	TMCO1	TMCO1_HUMAN	21.2	100.0%	3	3	5	0.00%	16.5%	QAGGFLGPPPPSGK	99.7%	49.5	25	41.2	1	0	0	1309.69	173	186
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	8	11	24	0.02%	38.4%	DLLVTGAYEISDQSGGAGGLR	99.7%	93	25	93	2	0	0	2079.04	51	71
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	8	11	24	0.02%	38.4%	IPDQLVILDMK	99.7%	65.5	25	51.7	6	0	0	1284.72	117	127
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	8	11	24	0.02%	38.4%	ITDSAGHILYSK	99.7%	70.6	25	61.3	2	2	0	1304.68	76	87
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	8	11	24	0.02%	38.4%	ITDSAGHILYSKEDATK	99.7%	64.4	25	64.4	2	4	0	1848.93	76	92
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	8	11	24	0.02%	38.4%	LEDLSESIVNDFAYMK	99.7%	48.5	25	42.7	1	0	0	1889.88	154	169
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	8	11	24	0.02%	38.4%	LKPLEVELR	99.5%	39	25	35.2	1	0	0	1096.67	144	152
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	8	11	24	0.02%	38.4%	NYEEIAK	99.3%	37.4	25	30.3	2	0	0	866.43	134	140
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	8	11	24	0.02%	38.4%	NYEEIAKVEK	99.7%	41.3	25	31.7	2	0	0	1222.63	134	143
Transmembrane protein 109	TMEM109	TM109_HUMAN	26.2	99.8%	2	2	3	0.00%	9.1%	EAPVDVLTQIGR	99.7%	71.2	25	65.3	2	0	0	1297.71	48	59
Transmembrane protein 109	TMEM109	TM109_HUMAN	26.2	99.8%	2	2	3	0.00%	9.1%	RDFAPPGQQK	98.6%	33.9	25	33.9	1	0	0	1143.59	37	46
Transmembrane protein 11, mitochondrial	TMEM11	TMM11_HUMAN	21.5	100.0%	4	5	14	0.01%	21.4%	KIYELYAV	96.3%	29.9	25	25.8	1	0	0	998.56	185	192
Transmembrane protein 11, mitochondrial	TMEM11	TMM11_HUMAN	21.5	100.0%	4	5	14	0.01%	21.4%	LPLHTLTSSTPVVLVR	99.7%	59.8	25	59.8	4	3	0	1733.03	146	161
Transmembrane protein 11, mitochondrial	TMEM11	TMM11_HUMAN	21.5	100.0%	4	5	14	0.01%	21.4%	YIVIEPTR	99.7%	47.7	25	40.7	3	0	0	990.56	59	66
Transmembrane protein 11, mitochondrial	TMEM11	TMM11_HUMAN	21.5	100.0%	4	5	14	0.01%	21.4%	YQVEYDAYK	99.7%	45.7	25	42	3	0	0	1178.54	134	142
Transmembrane protein 126A	TMEM126A	T126A_HUMAN	21.5	100.0%	5	5	11	0.01%	27.7%	ALQLSEPGKEIH	99.5%	38.7	25	38.7	2	0	0	1321.71	184	195
Transmembrane protein 126A	TMEM126A	T126A_HUMAN	21.5	100.0%	5	5	11	0.01%	27.7%	GNILSYWIR	99.7%	45.8	25	36.2	4	0	0	1121.61	142	150
Transmembrane protein 126A	TMEM126A	T126A_HUMAN	21.5	100.0%	5	5	11	0.01%	27.7%	KINQLPEAER	99.7%	49.7	25	28.8	2	0	0	1197.66	20	29
Transmembrane protein 126A	TMEM126A	T126A_HUMAN	21.5	100.0%	5	5	11	0.01%	27.7%	SNNKENITIVDISR	99.0%	35.5	25	35.5	1	0	0	1602.84	6	19
Transmembrane protein 126A	TMEM126A	T126A_HUMAN	21.5	100.0%	5	5	11	0.01%	27.7%	YQSALLPHK	99.6%	40.7	25	38.3	2	0	0	1056.58	133	141
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	4	4	8	0.01%	15.0%	ALLANALTSALR	99.7%	119	25	109	4	0	0	1213.73	58	69
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	4	4	8	0.01%	15.0%	GSNSLPLLR	99.7%	45.8	25	33.3	1	0	0	956.55	135	143
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	4	4	8	0.01%	15.0%	LDTAMWLSR	99.7%	71.1	25	56.2	2	0	0	1092.55	23	31
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	4	4	8	0.01%	15.0%	TLFNELR	96.1%	29.6	25	13	1	0	0	892.49	206	212
Transmembrane protein 97	TMEM97	TMM97_HUMAN	20.8	100.0%	2	2	3	0.00%	13.1%	EFKDPLLQEPPAWFK	99.0%	28.9	25	26.9	0	1	0	1844.96	53	67
Transmembrane protein 97	TMEM97	TMM97_HUMAN	20.8	100.0%	2	2	3	0.00%	13.1%	ELYPVEFR	99.7%	41.4	25	29.7	2	0	0	1052.54	37	44
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	24	0.02%	16.3%	ALVMLLEVR	99.7%	69.3	25	63.3	3	0	0	1059.62	246	254
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	24	0.02%	16.3%	ATVGILITTIASK	99.7%	95.3	25	95.3	2	0	0	1287.79	116	128
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	24	0.02%	16.3%	ESQSPDTTIQR	99.7%	51.8	25	40	2	0	0	1261.60	29	39
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	24	0.02%	16.3%	FSDQFPLPLK	99.7%	63	25	59	2	0	0	1191.64	880	889
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	24	0.02%	16.3%	GDVEEDETIPDSEQDIRPR	99.7%	39.2	25	39.2	0	2	0	2200.00	328	346
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	24	0.02%	16.3%	GELQNWPDLLPK	99.7%	53.4	25	44	2	0	0	1409.74	129	140
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	24	0.02%	16.3%	QSSFALLGDLTK	99.7%	89	25	75.1	2	0	0	1279.69	693	704
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	24	0.02%	16.3%	SECLNNIGDSSPLIR	99.7%	65.5	25	65.5	2	0	0	1674.81	101	115
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	24	0.02%	16.3%	SITCWTLSR	98.8%	34.6	25	17.8	1	0	0	1123.56	464	472
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	24	0.02%	16.3%	SNILTLMYQCMQDK	99.7%	97.9	25	96.2	2	0	0	1744.81	674	687
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	24	0.02%	16.3%	TLLENTAITIGR	99.7%	73.5	25	62.8	2	0	0	1301.74	774	785
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	24	0.02%	16.3%	YSDIDIILLK	99.7%	50.9	25	47	2	0	0	1192.68	318	327

Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	19	0.02%	13.4%	ASFWLGELQR	99.7%	43.7	25	35.7	2	0	0	1206.63	30	39
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	19	0.02%	13.4%	ETTVGAVTVTHK	99.7%	51.4	25	31.1	2	0	0	1242.67	882	893
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	19	0.02%	13.4%	GTALVLAR	99.7%	60	25	40	2	0	0	800.50	564	571
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	19	0.02%	13.4%	IFTELCETFLEK	99.7%	85	25	70.1	2	0	0	1529.76	298	309
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	19	0.02%	13.4%	IVCTPGQGLGDLR	99.7%	51.4	25	51.4	2	0	0	1385.72	310	322
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	19	0.02%	13.4%	LGEHLYK	98.2%	32.8	25	17.1	1	0	0	859.47	349	355
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	19	0.02%	13.4%	SLDSFLLSPEAAVGLLK	99.7%	97.6	25	97.6	2	0	0	1759.98	547	563
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	19	0.02%	13.4%	SVDPENNPTLVEVLEGVVR	99.7%	90.7	25	90.7	2	0	0	2066.08	450	468
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	19	0.02%	13.4%	TNDEVIHGIFK	98.3%	33.3	25	10.1	2	0	0	1272.66	356	366
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	19	0.02%	13.4%	VIQEIWPVLSETLNK	99.7%	56.6	25	51.3	2	0	0	1768.98	637	651
Treacle protein	TCOF1	TCOF_HUMAN	152.1	100.0%	5	5	7	0.01%	3.7%	AGPVAVQVK	99.7%	41.4	25	32.8	1	0	0	868.53	592	600
Treacle protein	TCOF1	TCOF_HUMAN	152.1	100.0%	5	5	7	0.01%	3.7%	ASEAQPPVAR	99.0%	35.5	25	32	1	0	0	1025.54	1084	1093
Treacle protein	TCOF1	TCOF_HUMAN	152.1	100.0%	5	5	7	0.01%	3.7%	GSLGQGTAPVLPGK	99.7%	61.4	25	55.4	2	0	0	1281.72	733	746
Treacle protein	TCOF1	TCOF_HUMAN	152.1	100.0%	5	5	7	0.01%	3.7%	TSQVGAASAPAK	99.5%	39.2	25	39.2	1	0	0	1087.57	368	379
Treacle protein	TCOF1	TCOF_HUMAN	152.1	100.0%	5	5	7	0.01%	3.7%	VLTELLEQER	99.7%	51.3	25	39.3	2	0	0	1229.67	1318	1327
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	8	10	30	0.03%	25.4%	FFVMTSLR	99.7%	53.2	25	30.4	8	0	0	1000.53	199	206
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	8	10	30	0.03%	25.4%	FIHDQTSPNPK	99.7%	54.8	25	44	4	2	0	1283.64	150	160
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	8	10	30	0.03%	25.4%	GLSSLLYGSIPK	99.7%	74.6	25	53.5	2	0	0	1234.70	86	97
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	8	10	30	0.03%	25.4%	GTYQGLTATVLK	99.7%	64.7	25	56.7	4	0	0	1251.69	179	190
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	8	10	30	0.03%	25.4%	MQGLEAHK	96.4%	30	25	14.5	1	0	0	913.46	248	255
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	8	10	30	0.03%	25.4%	NTWDCGLQILK	99.7%	50.6	25	40.1	4	0	0	1347.67	258	268
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	8	10	30	0.03%	25.4%	SHGVLGLYR	97.9%	32.2	25	28.9	1	0	0	1001.55	77	85
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	8	10	30	0.03%	25.4%	TQLQLDER	99.7%	57.3	25	40.4	4	0	0	1002.52	51	58
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	30	61	0.06%	39.3%	ADMVIEAVFEDLSLK	99.7%	94.3	25	94.3	2	0	0	1695.85	441	455
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	30	61	0.06%	39.3%	ALMGLYHGQVLCK	99.7%	41.4	25	41.4	2	0	0	1489.77	338	350
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	30	61	0.06%	39.3%	ALTSFER	99.3%	37.3	25	21.8	2	0	0	823.43	416	422
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	30	61	0.06%	39.3%	CLAPMMSEVIR	99.6%	40.3	25	33	1	0	0	1306.63	550	560
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	30	61	0.06%	39.3%	DATLTALDR	99.7%	72.3	25	33.8	2	0	0	975.51	391	399
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	30	61	0.06%	39.3%	DGPGFYTTR	99.7%	46.9	25	30.2	2	0	0	1013.47	541	549
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	30	61	0.06%	39.3%	DLNSDMDSILASLK	99.7%	89.4	25	87	2	0	0	1521.75	647	660
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	30	61	0.06%	39.3%	DSIFSNLTGQLDYQGFEK	99.7%	86.4	25	86.4	2	0	0	2061.98	423	440
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	30	61	0.06%	39.3%	DTSASAVAVGLK	99.7%	78.8	25	59.2	3	0	0	1118.61	520	531
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	30	61	0.06%	39.3%	FGELVMTK	99.7%	43.3	25	27.3	1	0	0	940.48	327	334
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	30	61	0.06%	39.3%	FGGGNPELLTQMVSK	99.7%	83	25	76.8	4	0	0	1577.80	611	625
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	30	61	0.06%	39.3%	GFYIYQEGVK	99.7%	71	25	65.7	2	0	0	1203.60	635	644
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	30	61	0.06%	39.3%	ILQEGVDPK	99.7%	48.8	25	38	2	0	0	998.55	561	569
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	30	61	0.06%	39.3%	KALTSFER	96.8%	30.5	25	20.4	2	0	0	951.53	415	422
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	30	61	0.06%	39.3%	LTAYAMTIPFVR	99.7%	75.8	25	65.4	5	0	0	1382.75	268	279
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	30	61	0.06%	39.3%	MGLVDQLVEPLGPGLKPPEER	99.7%	53	25	53	0	2	0	2290.21	215	235
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	30	61	0.06%	39.3%	MQLLEIITTEK	99.7%	89.2	25	79.9	6	0	0	1318.73	506	516
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	30	61	0.06%	39.3%	MVGVPAALDMMLTGR	99.7%	53.7	25	52.1	5	0	0	1561.79	191	205
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	30	61	0.06%	39.3%	SEVSSDEDIQFR	99.7%	86.4	25	83.3	2	0	0	1411.63	665	676
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	30	61	0.06%	39.3%	TGIEQGSDAGYLCESQK	99.7%	119	25	116	2	0	0	1842.82	310	326
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	30	61	0.06%	39.3%	TIEYLEEVAITFAK	99.7%	65.1	25	63	1	0	0	1626.86	236	249
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	30	61	0.06%	39.3%	TLQEVTQLSQEAQR	99.7%	97.3	25	82.2	2	1	0	1630.84	112	125
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	30	61	0.06%	39.3%	TVLGTPEVLLGALPGAGGTQR	99.7%	101	25	101	2	2	0	2007.12	167	187
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	30	61	0.06%	39.3%	VIGMHYFSPVDK	98.8%	34.9	25	26.8	2	0	0	1392.70	494	505
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	18	18	33	0.03%	40.7%	AALTGLLHR	99.7%	64.2	25	51.8	1	0	0	951.57	82	90
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	18	18	33	0.03%	40.7%	AMDSDWFAENYMGR	99.7%	47	25	47	1	0	0	1724.67	392	405
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	18	18	33	0.03%	40.7%	AQDEGLLSDVVPFK	99.7%	43.4	25	42.4	1	0	0	1517.78	255	268
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	18	18	33	0.03%	40.7%	DFMYVSQDPKDQLLLGPTYATPK	98.7%	27.8	25	27.8	0	1	0	2627.31	339	361

Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	18	18	33	0.03%	40.7%	DLMPHDLAR	99.3%	37.2	25	30.8	2	0	0	1083.53	73	81
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	18	18	33	0.03%	40.7%	DNGIRPSSLEQMAK	99.7%	45.7	25	35.3	2	0	0	1545.77	278	291
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	18	18	33	0.03%	40.7%	DQLLLGPTYATPK	99.7%	56.8	25	48.4	2	0	0	1416.77	349	361
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	18	18	33	0.03%	40.7%	EAALGAGFSDK	99.7%	65.2	25	57	2	0	0	1065.52	118	128
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	18	18	33	0.03%	40.7%	EVVDYIIFGTVIQEVK	99.7%	87.9	25	87.3	3	0	0	1852.01	96	111
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	18	18	33	0.03%	40.7%	FNNWGGSLSLGHPFGATGCR	99.7%	61.3	25	60.6	0	2	0	2134.99	417	436
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	18	18	33	0.03%	40.7%	KAQDEGLLSDVVPFK	99.7%	67.1	25	67.1	2	0	0	1645.88	254	268
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	18	18	33	0.03%	40.7%	KLMLDLNK	99.6%	40.1	25	12.4	2	0	0	990.57	181	188
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	18	18	33	0.03%	40.7%	LAAAFAVSR	99.7%	75.8	25	61.4	2	0	0	905.52	230	238
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	18	18	33	0.03%	40.7%	LVMAAANR	99.7%	60	25.3	49.5	2	0	0	845.47	437	444
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	18	18	33	0.03%	40.7%	NVVVVDGVR	99.7%	56	25	47.9	2	0	0	956.55	53	61
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	18	18	33	0.03%	40.7%	TPFLLSGTSYK	99.7%	57.2	25	48	2	0	0	1213.65	62	72
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	18	18	33	0.03%	40.7%	VGLPPLEK	98.6%	34.2	25	34.2	2	0	0	852.52	409	416
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	18	18	33	0.03%	40.7%	VPGKDTVTK	99.2%	36.5	25	25.3	2	0	0	944.54	269	277
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	62	0.06%	26.2%	AAGFKDPLLASGTDGVGTK	99.7%	43.1	25	43.1	0	2	0	1804.94	481	499
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	62	0.06%	26.2%	AFAHITGGGLLENIPR	99.7%	35.2	25	33	0	2	0	1665.91	677	692
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	62	0.06%	26.2%	AIAFLQQPR	99.7%	57	25	41.5	3	0	0	1043.60	425	433
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	62	0.06%	26.2%	AVQEIMQEK	99.6%	39.8	25	33.9	3	0	0	1091.54	170	178
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	62	0.06%	26.2%	ENLISALEEAKK	99.7%	56.2	25	40.3	2	0	0	1344.74	394	405
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	62	0.06%	26.2%	EQTEQILR	98.0%	32.5	25	22.5	2	0	0	1016.54	744	751
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	62	0.06%	26.2%	ESGVDIAAGNMLVK	99.7%	68.3	25	67.7	4	0	0	1403.72	439	452
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	62	0.06%	26.2%	FGDPECQVILPLLK	99.7%	72.6	25	65.1	4	0	0	1628.87	293	306
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	62	0.06%	26.2%	GDTVATLSER	99.7%	46.3	25	18.3	2	0	0	1048.53	966	975
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	62	0.06%	26.2%	IKDTVLQR	99.7%	51.2	25	28.6	2	0	0	972.58	250	257
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	62	0.06%	26.2%	ILSGPFVQK	98.0%	32.4	25	11	1	0	0	988.58	898	906
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	62	0.06%	26.2%	ISNTAISISDHTALAQFCK	99.7%	53	25	53	0	4	0	2077.04	45	63
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	62	0.06%	26.2%	IYSHSLLPVLR	99.7%	49.5	25	41.7	2	2	0	1297.76	661	671
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	62	0.06%	26.2%	LDLSVTEAVVAGIAK	99.7%	85.1	25	77.3	2	0	0	1485.85	543	557
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	62	0.06%	26.2%	MLNIHPSLLPSFK	99.7%	50.9	25	41.1	2	1	0	1496.83	911	923
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	62	0.06%	26.2%	QVLVAPGNAGTACSEK	99.7%	83.1	25	82.8	3	0	0	1601.80	29	44
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	62	0.06%	26.2%	SAGVQCFGPTAEAAQLESSKR	99.3%	30.3	25	30	0	4	0	2194.06	88	108
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	62	0.06%	26.2%	TFNCGVGAVLVVSK	99.7%	90.7	25	89	2	0	0	1450.77	730	743
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	62	0.06%	26.2%	VDLGGFAGLFDLK	99.7%	102	25	102	5	0	0	1351.73	468	480
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	62	0.06%	26.2%	VLAVTAIR	99.7%	64.5	25	32.5	4	0	0	842.55	386	393
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	21	25	62	0.06%	26.2%	VLEFNCR	99.7%	41.7	25	37.8	4	0	0	937.46	286	292
Triosephosphate isomerase	TPI1	TPIS_HUMAN	30.8	99.8%	2	2	5	0.00%	9.8%	TATPQQAQEVHEK	99.7%	54.6	25	52.3	4	0	0	1466.72	213	225
Triosephosphate isomerase	TPI1	TPIS_HUMAN	30.8	99.8%	2	2	5	0.00%	9.8%	VVLAYEPVWAIGTGK	99.7%	64.8	25	56.1	1	0	0	1602.89	198	212
TRMT1-like protein	TRMT1L	TRM1L_HUMAN	81.7	100.0%	3	3	5	0.00%	6.1%	NLGIVSVTSTDISSLYAK	99.7%	89	25	89	2	0	0	1868.00	391	408
TRMT1-like protein	TRMT1L	TRM1L_HUMAN	81.7	100.0%	3	3	5	0.00%	6.1%	QLIFCTLAALAEER	99.7%	84.8	25	82.1	1	0	0	1634.86	261	274
TRMT1-like protein	TRMT1L	TRM1L_HUMAN	81.7	100.0%	3	3	5	0.00%	6.1%	SSYIAASTAKPPK	99.7%	55.4	25	52.1	2	0	0	1320.72	214	226
tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6	TRMT6	TRM6_HUMAN	55.8	99.8%	2	2	4	0.00%	3.8%	ILSIMYYAR	95.9%	29.4	25	29.2	1	0	0	1129.61	167	175
tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6	TRMT6	TRM6_HUMAN	55.8	99.8%	2	2	4	0.00%	3.8%	NADGLIVASR	99.7%	46.2	25	39.8	3	0	0	1015.55	368	377
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	20	42	0.04%	28.9%	EDPFVFIPEDDPLFPPIEK	99.7%	44.3	25	44.3	2	0	0	2244.11	517	535
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	20	42	0.04%	28.9%	EGVILTNESAASTGQPDNDVTEGQR	99.3%	30.3	25	30.3	0	1	0	2588.21	713	737
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	20	42	0.04%	28.9%	FYALDPSFPR	99.0%	35.5	25	33.8	2	0	0	1212.60	536	545
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	20	42	0.04%	28.9%	GAEQLAEGGR	99.7%	88.2	25	75.9	3	0	0	987.49	306	315
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	20	42	0.04%	28.9%	IITVSMEDVK	99.7%	51.5	25	43.6	4	0	0	1134.61	619	628
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	20	42	0.04%	28.9%	ILCDVPCSGDGTMR	99.4%	37.9	25	37.9	1	0	0	1580.69	265	278
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	20	42	0.04%	28.9%	ILDMCAAPGSK	99.7%	71.6	25	71.6	1	0	0	1162.56	180	190
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	20	42	0.04%	28.9%	ILLTQENPFFR	99.7%	79.6	25	70.2	6	0	0	1377.75	629	639
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	20	42	0.04%	28.9%	KLSSETYSQAK	99.7%	62.5	25	58.9	3	0	0	1241.64	640	650

tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	20	42	0.04%	28.9%	LAQEGIYTLYPFINSR	99.7%	74.2	25	74.2	2	0	0	1884.99	603	618
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	20	42	0.04%	28.9%	LFEHYYQELK	97.5%	31.5	25	21.3	2	0	0	1369.68	47	56
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	20	42	0.04%	28.9%	LQAMHLER	99.7%	48.3	25	34.8	1	0	0	997.52	401	408
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	20	42	0.04%	28.9%	LQIDVDGR	99.5%	38.8	25	28.8	1	0	0	915.49	249	256
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	20	42	0.04%	28.9%	LQQQQRPEDAEDGAEGGGK	99.7%	37	25	37	0	2	0	2012.93	10	28
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	20	42	0.04%	28.9%	LSSETYSQAK	99.7%	66.4	25	60.1	2	0	0	1113.54	641	650
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	20	42	0.04%	28.9%	MMGLEVLGEK	99.7%	41.5	25	39.9	3	0	0	1106.56	701	710
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	20	42	0.04%	28.9%	NNSGEEFDCAFR	99.7%	69.4	25	69.4	2	0	0	1445.58	591	602
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	20	42	0.04%	28.9%	SEGALELADVSNELPGLK	99.7%	119	25	114	4	0	0	1841.95	339	356
tRNA-splicing endonuclease subunit Sen34	TSEN34	SEN34_HUMAN	33.7	99.8%	2	2	2	0.00%	8.7%	FGGDFLVYPGDPLR	99.6%	40.6	25	39.5	1	0	0	1552.78	240	253
tRNA-splicing endonuclease subunit Sen34	TSEN34	SEN34_HUMAN	33.7	99.8%	2	2	2	0.00%	8.7%	LGLPLLLMPEEAR	99.3%	37	25	37	1	0	0	1451.83	46	58
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	9	11	20	0.02%	21.4%	GGGVGGFLPAMK	99.7%	48.8	25	39.9	2	0	0	1090.57	56	67
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	9	11	20	0.02%	21.4%	GMAAAGNYAWVNR	99.7%	70	25	57.3	1	0	0	1380.65	309	321
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	9	11	20	0.02%	21.4%	GQVCVMIHSGSR	99.7%	78.9	25	78.9	2	0	0	1330.64	252	263
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	9	11	20	0.02%	21.4%	LVMEEAPESYK	99.7%	68.2	25	68.2	2	0	0	1311.61	466	476
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	9	11	20	0.02%	21.4%	NVTDVVNTCHDAGISK	99.7%	77.5	25	77.5	1	0	0	1729.82	477	492
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	9	11	20	0.02%	21.4%	QIGNVAALPGIVHR	99.7%	37.5	25	37.5	2	2	0	1444.84	68	81
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	9	11	20	0.02%	21.4%	SSMTFLTR	99.7%	53.8	25	39.7	2	0	0	942.47	322	329
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	9	11	20	0.02%	21.4%	SYNDELQFLEK	99.7%	66.8	25	33.6	2	0	0	1385.66	4	14
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	9	11	20	0.02%	21.4%	VEQHVVDGKER	99.7%	42.6	25	36	2	2	0	1295.67	358	368
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	55.2%	AVCMLSNTTAIAEAWAR	99.7%	133	25	120	22	10	0	1880.90	374	390
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	55.2%	AVFVDLEPTVIDEVR	99.7%	103	25	103	50	8	0	1701.91	65	79
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	55.2%	AYHEQLSVAEITNACFEPANQMVK	99.7%	69.2	25	67.8	0	13	0	2766.29	281	304
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	55.2%	DVNAAIATIK	99.7%	81.7	25	62.9	17	0	0	1015.58	327	336
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	55.2%	EDAANNYAR	99.7%	47.2	25	45.7	2	0	0	1023.45	97	105
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	55.2%	EDMAALEK	99.7%	59.4	25	39.2	4	0	0	906.42	423	430
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	55.2%	EIIDLVLDR	99.7%	94.1	25	86.5	46	0	0	1085.62	113	121
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	55.2%	FDGALNVDLTEFQTNLVPYPR	99.7%	111	25	111	9	0	0	2409.21	244	264
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	55.2%	FDLMYAK	99.7%	46.7	25	32.2	6	0	0	887.43	395	401
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	55.2%	IHFPLATYAPVISAEK	99.7%	94.4	25	88.2	18	17	0	1756.96	265	280
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	55.2%	LDHKFDLMYAK	99.7%	54.8	25	40.4	11	10	0	1380.70	391	401
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	55.2%	LIGQIVSSITASLR	99.7%	77.3	25	75.5	2	0	0	1457.87	230	243
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	55.2%	LSVDYGKK	99.7%	47	25	37.6	13	0	0	909.50	157	164
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	55.2%	NLDIERPTYTNLNR	99.7%	63.9	25	61.7	12	12	0	1718.88	216	229
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	55.2%	QLFHPEQLITGK	99.7%	58.2	25	0	8	4	0	1410.77	85	96
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	55.2%	QLFHPEQLITGKEDAANNYAR	99.7%	71.5	25	71.5	2	14	0	2415.21	85	105
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	55.2%	RNLDIERPTYTNLNR	99.7%	41.5	25	39.3	2	2	0	1874.98	215	229
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	55.2%	TIGGGDDSFNTFFSETGAGK	99.7%	128	25	128	31	0	0	2007.89	41	60
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	55.2%	TIQFVDWCPTGFK	99.7%	88.3	25	83.8	19	0	0	1598.77	340	352
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	55.2%	VGINYQPPTVVPGGDLAK	99.7%	78	25	78	25	0	0	1824.99	353	370
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	55.2%	YMACCLLYR	99.7%	47.1	25	42.6	26	0	0	1249.55	312	320
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	39	449	0.43%	55.4%	AVCMLSNTTAIAEAWAR	99.7%	133	25	120	22	10	0	1880.90	374	390
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	39	449	0.43%	55.4%	AVFVDLEPTVIDEVR	99.7%	103	25	103	50	8	0	1701.91	65	79
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	39	449	0.43%	55.4%	AYHEQLSVAEITNACFEPANQMVK	99.7%	69.2	25	67.8	0	13	0	2766.29	281	304
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	39	449	0.43%	55.4%	DVNAAIATIK	99.7%	81.7	25	62.9	17	0	0	1015.58	327	336
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	39	449	0.43%	55.4%	EDAANNYAR	99.7%	47.2	25	45.7	2	0	0	1023.45	97	105
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	39	449	0.43%	55.4%	EDMAALEK	99.7%	59.4	25	39.2	4	0	0	906.42	423	430
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	39	449	0.43%	55.4%	EIIDLVLDR	99.7%	94.1	25	86.5	46	0	0	1085.62	113	121
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	39	449	0.43%	55.4%	FDGALNVDLTEFQTNLVPYPR	99.7%	111	25	111	9	0	0	2409.21	244	264
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	39	449	0.43%	55.4%	FDLMYAK	99.7%	46.7	25	32.2	6	0	0	887.43	395	401
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	39	449	0.43%	55.4%	IHFPLATYAPVISAEK	99.7%	94.4	25	88.2	18	17	0	1756.96	265	280

Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	39	449	0.43%	55.4%	LDHKFDLMYAK	99.7%	54.8	25	40.4	11	10	0	1380.70	391	401
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	39	449	0.43%	55.4%	LISQIVSSITASLR	99.7%	101	25	101	17	6	0	1487.88	230	243
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	39	449	0.43%	55.4%	LSVDYGKK	99.7%	47	25	37.6	13	0	0	909.50	157	164
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	39	449	0.43%	55.4%	NLDIERPTYTNLNR	99.7%	63.9	25	61.7	12	12	0	1718.88	216	229
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	39	449	0.43%	55.4%	QLFHPEQLITGK	99.7%	58.2	25	0	8	4	0	1410.77	85	96
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	39	449	0.43%	55.4%	QLFHPEQLITGKEDAANNYAR	99.7%	71.5	25	71.5	2	14	0	2415.21	85	105
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	39	449	0.43%	55.4%	RNLDIERPTYTNLNR	99.7%	41.5	25	39.3	2	2	0	1874.98	215	229
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	39	449	0.43%	55.4%	RSIQFVDWCPTGFK	99.4%	31.3	25	30.6	1	1	0	1740.85	339	352
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	39	449	0.43%	55.4%	SIQFVDWCPTGFK	99.7%	92.8	25	91.5	30	0	0	1584.75	340	352
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	39	449	0.43%	55.4%	TIGGGDDSFNTFFSETGAGK	99.7%	128	25	128	31	0	0	2007.89	41	60
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	39	449	0.43%	55.4%	VGINYQPPTVVPGGDLAK	99.7%	78	25	78	25	0	0	1824.99	353	370
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	39	449	0.43%	55.4%	YMACCLLYR	99.7%	47.1	25	42.6	26	0	0	1249.55	312	320
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	55.5%	AVCMLSNTTAVAEAWAR	99.7%	95.6	25	95.6	2	3	0	1866.88	374	390
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	55.5%	AVFVDLEPTVIDEVR	99.7%	103	25	103	50	8	0	1701.91	65	79
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	55.5%	AYHEQLTVAEITNACFEPANQMVK	99.1%	29.2	25	29.2	0	2	0	2764.31	281	304
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	55.5%	DVNAAIATIK	99.7%	81.7	25	62.9	17	0	0	1015.58	327	336
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	55.5%	EDAANNYAR	99.7%	47.2	25	45.7	2	0	0	1023.45	97	105
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	55.5%	EDMAALEK	99.7%	59.4	25	39.2	4	0	0	906.42	423	430
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	55.5%	EIIDLVLDR	99.7%	94.1	25	86.5	46	0	0	1085.62	113	121
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	55.5%	FDGALNVDLTEFQTNLVPYPR	99.7%	111	25	111	9	0	0	2409.21	244	264
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	55.5%	FDLMYAK	99.7%	46.7	25	32.2	6	0	0	887.43	395	401
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	55.5%	IHFPLATYAPVISAEK	99.7%	94.4	25	88.2	18	17	0	1756.96	265	280
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	55.5%	LDHKFDLMYAK	99.7%	54.8	25	40.4	11	10	0	1380.70	391	401
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	55.5%	LISQIVSSITASLR	99.7%	101	25	101	17	6	0	1487.88	230	243
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	55.5%	LSVDYGKK	99.7%	47	25	37.6	13	0	0	909.50	157	164
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	55.5%	NLDIERPTYTNLNR	99.7%	63.9	25	61.7	12	12	0	1718.88	216	229
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	55.5%	QLFHPEQLITGK	99.7%	58.2	25	0	8	4	0	1410.77	85	96
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	55.5%	QLFHPEQLITGKEDAANNYAR	99.7%	71.5	25	71.5	2	14	0	2415.21	85	105
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	55.5%	RNLDIERPTYTNLNR	99.7%	41.5	25	39.3	2	2	0	1874.98	215	229
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	55.5%	TIGGGDDSFNTFFSETGAGK	99.7%	128	25	128	31	0	0	2007.89	41	60
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	55.5%	TIQFVDWCPTGFK	99.7%	88.3	25	83.8	19	0	0	1598.77	340	352
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	55.5%	VGINYQPPTVVPGGDLAK	99.7%	78	25	78	25	0	0	1824.99	353	370
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	55.5%	YMACCLLYR	99.7%	47.1	25	42.6	26	0	0	1249.55	312	320
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	AILVDLEPGTMDSVR	99.7%	93.5	25	87.6	44	0	0	1615.84	63	77
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	ALTVPELTQQVFDAK	99.7%	72	25	72	28	5	0	1659.90	283	297
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	89.7	25	0	0	7	0	3327.53	123	154
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	EIVHIQAGQCGNQIGAK	99.7%	92.1	25	0	4	4	0	1822.92	3	19
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	EVDEQMLNVQNK	99.7%	84.4	25	81.2	22	0	0	1462.68	325	336
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	FPGQLNADLR	99.7%	64.2	25	50.4	18	0	0	1130.60	242	251
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	FPGQLNADLRK	99.7%	36.8	25	34.4	8	5	0	1258.69	242	252
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	FWEVISDEHGIDPTGTYHGDSDLQLDR	99.7%	70.8	25	35.5	0	4	0	3102.41	20	46
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	GHYTEGAELVDSVLDVVR	99.7%	146	25	140	4	9	0	1958.98	104	121
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	GHYTEGAELVDSVLDVVRK	99.7%	58.9	25	56.6	0	3	0	2087.08	104	122
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	IMNTFSVVPSPK	99.7%	94.3	25	87.3	32	0	0	1319.70	163	174
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	IREEYPDR	99.5%	39.1	25	26.3	9	0	0	1077.53	155	162
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	ISEQFTAMFR	99.7%	84.2	25	76.2	30	0	0	1229.60	381	390
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	ISVYYNEATGGK	99.7%	85.8	25	85.8	30	0	0	1301.64	47	58
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	KLAVNMVPFPR	99.7%	72.3	25	72	4	2	0	1271.73	252	262
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	LAVNMVPFPR	99.7%	80.1	25	69.2	39	0	0	1143.63	253	262
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	LHFFMPGFAPLTSR	99.7%	55	25	43.5	26	26	0	1620.84	263	276
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	LTTPTYGDLNHLVSATMSGVTTCLR	99.7%	104	25	101	3	15	0	2708.34	217	241

Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	MAVTFIGNSTAIQELFK	99.7%	138	25	137	22	1	0	1869.98	363	379
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	MAVTFIGNSTAIQELFKR	99.7%	44.1	25	44.1	0	6	0	2026.08	363	380
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	MREIVHIQAGQCGNQIGAK	99.7%	68.2	25	0	0	8	0	2110.06	1	19
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	MSMKEVDEQMLNVQNK	99.7%	62.5	25	60.2	8	20	0	1971.88	321	336
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	NMMAACDPR	99.7%	54.8	25	8.22	18	0	0	1081.42	298	306
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	NSSYFVEWIPNNVK	99.7%	79.9	25	69.6	17	0	0	1696.83	337	350
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	RISEQFTAMFR	99.7%	51.2	25	46	2	2	0	1385.70	380	390
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	SGPFGQIFRPDNFVFGQSGAGNNWAK	99.7%	89.2	25	89.2	0	6	0	2798.34	78	103
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	TAVCDIPPR	99.7%	63.1	25	55.5	33	0	0	1028.52	351	359
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	54	538	0.51%	74.3%	YLTVAAVFR	99.7%	88.6	25	82.4	14	0	0	1039.59	310	318
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	32	0.03%	60.9%	AILVDLEPGTMDSVR	99.7%	93.5	25	87.6	44	0	0	1615.84	63	77
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	32	0.03%	60.9%	ALTVPELTQQMFDSK	99.7%	92.4	25	41.3	12	0	0	1707.86	283	297
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	32	0.03%	60.9%	EIVHIQAGQCGNQIGAK	99.7%	92.1	25	0	4	4	0	1822.92	3	19
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	32	0.03%	60.9%	EVDEQMLNVQNK	99.7%	84.4	25	81.2	22	0	0	1462.68	325	336
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	32	0.03%	60.9%	FPGQLNADLR	99.7%	64.2	25	50.4	18	0	0	1130.60	242	251
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	32	0.03%	60.9%	FPGQLNADLRK	99.7%	36.8	25	34.4	8	5	0	1258.69	242	252
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	32	0.03%	60.9%	GHYTEGAELVDSVLDVVR	99.7%	146	25	140	4	9	0	1958.98	104	121
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	32	0.03%	60.9%	GHYTEGAELVDSVLDVVRK	99.7%	58.9	25	56.6	0	3	0	2087.08	104	122
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	32	0.03%	60.9%	IMNTFSVMPSPK	99.7%	90.8	25	81.4	10	0	0	1351.67	163	174
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	32	0.03%	60.9%	INVYYNEATGNK	99.7%	71.1	25	70.5	4	0	0	1385.67	47	58
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	32	0.03%	60.9%	IREEYPDR	99.5%	39.1	25	26.3	9	0	0	1077.53	155	162
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	32	0.03%	60.9%	ISEQFTAMFR	99.7%	84.2	25	76.2	30	0	0	1229.60	381	390
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	32	0.03%	60.9%	KLAVNMVPFPR	99.7%	72.3	25	72	4	2	0	1271.73	252	262
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	32	0.03%	60.9%	LAVNMVPFPR	99.7%	80.1	25	69.2	39	0	0	1143.63	253	262
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	32	0.03%	60.9%	LHFFMPGFAPLTSR	99.7%	55	25	43.5	26	26	0	1620.84	263	276
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	32	0.03%	60.9%	LTTPTYGDLNHLVSATMSGVTTCLR	99.7%	104	25	101	3	15	0	2708.34	217	241
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	32	0.03%	60.9%	MREIVHIQAGQCGNQIGAK	99.7%	68.2	25	0	0	8	0	2110.06	1	19
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	32	0.03%	60.9%	MSATFIGNSTAIQELFK	99.7%	119	25	0	11	0	0	1873.94	363	379
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	32	0.03%	60.9%	MSATFIGNSTAIQELFKR	99.7%	43.5	25	3.06	0	4	0	2014.04	363	380
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	32	0.03%	60.9%	MSMKEVDEQMLNVQNK	99.7%	62.5	25	60.2	8	20	0	1971.88	321	336
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	32	0.03%	60.9%	NMMAACDPR	99.7%	54.8	25	8.22	18	0	0	1081.42	298	306
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	32	0.03%	60.9%	NSSYFVEWIPNNVK	99.7%	79.9	25	69.6	17	0	0	1696.83	337	350
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	32	0.03%	60.9%	RISEQFTAMFR	99.7%	51.2	25	46	2	2	0	1385.70	380	390
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	32	0.03%	60.9%	SGPFGQIFRPDNFVFGQSGAGNNWAK	99.7%	89.2	25	89.2	0	6	0	2798.34	78	103
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	32	0.03%	60.9%	TAVCDIPPR	99.7%	63.1	25	55.5	33	0	0	1028.52	351	359
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	32	0.03%	60.9%	YLTVAAIFR	99.7%	78.6	25	64.1	6	0	0	1053.61	310	318
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	14	0.01%	64.0%	ALTVPELTQQMFDAK	99.7%	98.3	25	98.3	20	0	0	1691.87	283	297
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	14	0.01%	64.0%	AVLVDLEPGTMDSVR	99.7%	109	25	88.4	20	0	0	1617.82	63	77
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	14	0.01%	64.0%	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	89.7	25	0	0	7	0	3327.53	123	154
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	14	0.01%	64.0%	EIVHLQAGQCGNQIGAK	99.7%	92.1	25	0	4	4	0	1822.92	3	19
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	14	0.01%	64.0%	EVDEQMLSVQSK	99.7%	74.8	25	67.4	2	0	0	1392.67	325	336
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	14	0.01%	64.0%	FPGQLNADLR	99.7%	64.2	25	50.4	18	0	0	1130.60	242	251
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	14	0.01%	64.0%	FPGQLNADLRK	99.7%	36.8	25	34.4	8	5	0	1258.69	242	252
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	14	0.01%	64.0%	IMNTFSVVPSPK	99.7%	94.3	25	87.3	32	0	0	1319.70	163	174
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	14	0.01%	64.0%	INVYYNEATGGNYVPR	99.7%	106	25	106	2	0	0	1829.88	47	62
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	14	0.01%	64.0%	IREEFPDR	98.4%	33.4	25	18.8	2	0	0	1061.54	155	162
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	14	0.01%	64.0%	ISEQFTAMFR	99.7%	84.2	25	76.2	30	0	0	1229.60	381	390
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	14	0.01%	64.0%	KLAVNMVPFPR	99.7%	72.3	25	72	4	2	0	1271.73	252	262
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	14	0.01%	64.0%	LAVNMVPFPR	99.7%	80.1	25	69.2	39	0	0	1143.63	253	262
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	14	0.01%	64.0%	LHFFMPGFAPLTSR	99.7%	55	25	43.5	26	26	0	1620.84	263	276
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	14	0.01%	64.0%	LTTPTYGDLNHLVSATMSGVTTCLR	99.7%	104	25	101	3	15	0	2708.34	217	241

Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	14	0.01%	64.0%	MAATFIGNSTAIQELFK	99.7%	98.8	25	2.1	8	0	0	1857.94	363	379
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	14	0.01%	64.0%	MREIVHLQAGQCGNQIGAK	99.7%	68.2	25	0	0	8	0	2110.06	1	19
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	14	0.01%	64.0%	NMMAACDPR	99.7%	54.8	25	8.22	18	0	0	1081.42	298	306
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	14	0.01%	64.0%	NSSYFVEWIPNNVK	99.7%	79.9	25	69.6	17	0	0	1696.83	337	350
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	14	0.01%	64.0%	RISEQFTAMFR	99.7%	51.2	25	46	2	2	0	1385.70	380	390
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	14	0.01%	64.0%	SGPFGQIFRPDNFVFGQSGAGNNWAK	99.7%	89.2	25	89.2	0	6	0	2798.34	78	103
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	14	0.01%	64.0%	TAVCDIPPR	99.7%	63.1	25	55.5	33	0	0	1028.52	351	359
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	4	4	14	0.01%	64.0%	YLTVAAVFR	99.7%	88.6	25	82.4	14	0	0	1039.59	310	318
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	ALTVPELTQQMFDAK	99.7%	98.3	25	98.3	20	0	0	1691.87	283	297
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	AVLVDLEPGTMDSVR	99.7%	109	25	88.4	20	0	0	1617.82	63	77
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	89.7	25	0	0	7	0	3327.53	123	154
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	EIVHLQAGQCGNQIGAK	99.7%	92.1	25	0	4	4	0	1822.92	3	19
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	EVDEQMLNVQNK	99.7%	84.4	25	81.2	22	0	0	1462.68	325	336
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	FPGQLNADLR	99.7%	64.2	25	50.4	18	0	0	1130.60	242	251
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	FPGQLNADLRK	99.7%	36.8	25	34.4	8	5	0	1258.69	242	252
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	GHYTEGAELVDSVLDVVR	99.7%	146	25	140	4	9	0	1958.98	104	121
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	GHYTEGAELVDSVLDVVRK	99.7%	58.9	25	56.6	0	3	0	2087.08	104	122
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	IMNTFSVVPSPK	99.7%	94.3	25	87.3	32	0	0	1319.70	163	174
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	INVYYNEATGGK	99.7%	81.4	25	68.7	10	0	0	1328.65	47	58
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	IREEYPDR	99.5%	39.1	25	26.3	9	0	0	1077.53	155	162
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	ISEQFTAMFR	99.7%	84.2	25	76.2	30	0	0	1229.60	381	390
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	KLAVNMVPFPR	99.7%	72.3	25	72	4	2	0	1271.73	252	262
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	LAVNMVPFPR	99.7%	80.1	25	69.2	39	0	0	1143.63	253	262
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	LHFFMPGFAPLTSR	99.7%	55	25	43.5	26	26	0	1620.84	263	276
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	LTTPTYGDLNHLVSATMSGVTTCLR	99.7%	104	25	101	3	15	0	2708.34	217	241
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	MREIVHLQAGQCGNQIGAK	99.7%	68.2	25	0	0	8	0	2110.06	1	19
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	MSATFIGNSTAIQELFK	99.7%	119	25	0	11	0	0	1873.94	363	379
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	MSATFIGNSTAIQELFKR	99.7%	43.5	25	3.06	0	4	0	2014.04	363	380
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	MSMKEVDEQMLNVQNK	99.7%	62.5	25	60.2	8	20	0	1971.88	321	336
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	NMMAACDPR	99.7%	54.8	25	8.22	18	0	0	1081.42	298	306
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	NSSYFVEWIPNNVK	99.7%	79.9	25	69.6	17	0	0	1696.83	337	350
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	RISEQFTAMFR	99.7%	51.2	25	46	2	2	0	1385.70	380	390
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	SGPFGQIFRPDNFVFGQSGAGNNWAK	99.7%	89.2	25	89.2	0	6	0	2798.34	78	103
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	TAVCDIPPR	99.7%	63.1	25	55.5	33	0	0	1028.52	351	359
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	5	8	65	0.06%	68.1%	YLTVAAVFR	99.7%	88.6	25	82.4	14	0	0	1039.59	310	318
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	9	0.01%	30.5%	AALVDLEPGTMDSVR	99.7%	74	25	74	3	0	0	1573.79	63	77
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	9	0.01%	30.5%	ALTVPELTQQMFDAR	99.7%	67	25	66.7	4	0	0	1719.87	283	297
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	9	0.01%	30.5%	FPGQLNADLR	99.7%	64.2	25	50.4	18	0	0	1130.60	242	251
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	9	0.01%	30.5%	FPGQLNADLRK	99.7%	36.8	25	34.4	8	5	0	1258.69	242	252
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	9	0.01%	30.5%	IMNTFSVMPSPK	99.7%	90.8	25	81.4	10	0	0	1351.67	163	174
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	9	0.01%	30.5%	IREEFPDR	98.4%	33.4	25	18.8	2	0	0	1061.54	155	162
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	9	0.01%	30.5%	ISEQFSAMFR	99.7%	73.9	25	69.4	1	0	0	1231.58	381	390
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	9	0.01%	30.5%	KLAVNMVPFPR	99.7%	72.3	25	72	4	2	0	1271.73	252	262
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	9	0.01%	30.5%	LAVNMVPFPR	99.7%	80.1	25	69.2	39	0	0	1143.63	253	262
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	9	0.01%	30.5%	LHFFMPGFAPLTSR	99.7%	55	25	43.5	26	26	0	1620.84	263	276
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	9	0.01%	30.5%	MASTFIGNSTAIQELFK	99.7%	106	25	15.2	10	0	0	1857.94	363	379
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	9	0.01%	30.5%	MASTFIGNSTAIQELFKR	99.7%	35.7	25	1.01	0	1	0	2030.04	363	380
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	9	0.01%	30.5%	NMMAACDPR	99.7%	54.8	25	8.22	18	0	0	1081.42	298	306
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	5	9	0.01%	30.5%	NSSYFVEWIPNNVK	99.7%	79.9	25	69.6	17	0	0	1696.83	337	350
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	6	7	11	0.01%	15.7%	AVLLDLEPR	99.7%	52	25	45.9	2	0	0	1025.60	64	72
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	6	7	11	0.01%	15.7%	DVFFYQADDEHYIPR	99.7%	74.6	25	74.6	1	0	0	1914.87	49	63

Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	6	7	11	0.01%	15.7%	EAFLEQFR	99.7%	53.6	25	38.1	2	0	0	1039.52	402	409
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	6	7	11	0.01%	15.7%	KTTVLDVMR	99.7%	42	25	32.9	1	0	0	1062.60	287	295
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	6	7	11	0.01%	15.7%	LTQNADCVVVLDNTALNR	99.7%	93	25	93	2	0	0	2016.02	195	212
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	6	7	11	0.01%	15.7%	VIHSILNSPYAK	99.7%	49.3	25	44.1	2	1	0	1341.75	73	84
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	8	8	16	0.02%	7.7%	AVTHTSPEDVSFAESR	99.7%	40.7	25	37.7	0	2	0	1732.81	800	815
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	8	8	16	0.02%	7.7%	DAAAVLVSR	99.7%	57	25	36.2	2	0	0	901.51	205	213
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	8	8	16	0.02%	7.7%	GACSVGTNVR	99.7%	41.2	25	24.9	2	0	0	1020.49	455	464
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	8	8	16	0.02%	7.7%	ILQIAESYLIVSDK	99.7%	69.2	25	69.2	2	0	0	1591.89	189	202
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	8	8	16	0.02%	7.7%	ITQLLGLPTYR	98.9%	35.2	25	35.2	2	0	0	1274.75	969	979
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	8	8	16	0.02%	7.7%	LDGNLLTQPGQAR	99.7%	60.2	25	53.1	2	0	0	1382.74	170	182
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	8	8	16	0.02%	7.7%	LQQVLTGLR	99.7%	63.1	25	40.8	2	0	0	1027.63	791	799
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	8	8	16	0.02%	7.7%	VIEQLLVGLK	99.7%	60.3	25	42	2	0	0	1111.71	361	370
Tyrosine-protein kinase CSK	CSK	CSK_HUMAN	50.7	100.0%	3	3	4	0.00%	7.8%	GDVLTIVAVTK	99.7%	63.6	25	50.5	1	0	0	1115.67	33	43
Tyrosine-protein kinase CSK	CSK	CSK_HUMAN	50.7	100.0%	3	3	4	0.00%	7.8%	LLYPPETGLFLVR	95.5%	29	25	26.6	2	0	0	1517.87	95	107
Tyrosine-protein kinase CSK	CSK	CSK_HUMAN	50.7	100.0%	3	3	4	0.00%	7.8%	NVLVSEDNVAK	99.6%	39.8	25	35.9	1	0	0	1187.63	319	329
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	AFCEPGNVENNGVLSFIK	99.7%	78.8	25	72	2	0	0	1994.96	248	265
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	AMLESIGVPLEK	99.7%	88	25	76.5	6	0	0	1302.70	103	114
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	APWELLELR	99.7%	54.1	25	37.7	6	0	0	1126.63	85	93
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	DFAAEVVHPGDLK	99.7%	65.9	25	49	2	0	0	1397.71	298	310
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	EYTLDVYR	99.4%	38.4	25	32.4	2	0	0	1058.52	128	135
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	GQPDEELKPK	99.3%	37.3	25	27.4	2	0	0	1140.59	475	484
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	GTDYQLSK	99.3%	37.5	25	15.7	2	0	0	911.45	120	127
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	GVESQGMLLCASIEGINR	99.7%	85.7	25	71.7	2	0	0	1949.94	433	450
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	HPDADSLYVEK	99.7%	51.9	25	37.6	2	0	0	1273.61	381	391
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	HVLFPLK	99.0%	35.8	25	28.6	1	0	0	853.53	266	272
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	IDVGEAEPR	99.7%	65.3	25	53.1	4	0	0	985.50	392	400
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	IITVEKHPDADSLYVEK	99.7%	72.8	25	72.8	2	2	0	1957.03	375	391
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	ISEECIAQWK	99.7%	63.9	25	59.8	2	0	0	1263.60	497	506
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	IYWGTATTGKPHVAYFVPMSK	99.4%	31.1	25	31.1	0	1	0	2354.20	38	58
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	KIFTFAEK	99.4%	38	25	28.3	2	0	0	983.56	190	197
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	KLASAAYPDPSK	99.7%	59	25	53	2	0	0	1247.66	335	346
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	LASAAYPDPSK	99.7%	69.7	25	56.5	2	0	0	1119.57	336	346
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	LLDPIREK	99.2%	36.9	25	26.1	2	0	0	983.59	320	327
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	LSSVVTQHDSK	99.7%	73.8	25	69.2	3	1	0	1200.62	136	146
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	LSSVVTQHDSKK	99.7%	64.5	25	57	3	1	0	1328.72	136	147
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	LVVVLCNLKPQK	99.7%	61	25	57.7	2	0	0	1410.85	419	430
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	MSSSEEESKIDLLDR	99.7%	71.5	25	62.3	2	2	0	1754.81	223	237
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	NLQEVLGEEK	99.7%	49.7	25	40.2	2	0	0	1158.60	17	26
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	NSEPEEVIPSR	99.7%	48.6	25	43.3	2	0	0	1256.61	357	367
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	NSVEVALNK	99.7%	64.9	25	51	2	0	0	973.53	311	319
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	QVEPLDPPAGSAPGEHVFVK	99.7%	38.3	25	38.3	1	2	0	2074.06	451	470
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	RVHLMNPMVPGLTGSK	97.8%	25.6	25	22.7	0	1	0	1768.92	207	222
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	SEFVILR	99.0%	35.8	25	25.6	2	0	0	863.50	273	279
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	SEFVILRDEK	99.7%	51.9	25	37.9	2	0	0	1235.66	273	282
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	TVVSGLVQFVPK	99.7%	75.2	25	63.8	2	0	0	1273.75	401	412
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	TYTAYVDLEK	99.7%	45.3	25	38.5	2	0	0	1202.59	288	297
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	VDAQFGGIDQR	99.7%	66.7	25	53.8	2	0	0	1205.59	179	189
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	VHLMNPMVPGLTGSK	99.7%	51.9	25	21.9	4	0	0	1596.82	208	222
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	VSYYENVIK	99.5%	39.5	25	37.8	2	0	0	1114.58	94	102
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	41	88	0.08%	67.0%	YLPALGYSK	99.7%	41.2	25	26.9	2	0	0	1011.55	198	206
U1 small nuclear ribonucleoprotein 70 kDa	SNRNP70	RU17_HUMAN	51.6	100.0%	5	5	8	0.01%	10.8%	DPIPYLPPLEK	98.2%	33	25	24.6	2	0	0	1281.71	17	27

U1 small nuclear ribonucleoprotein 70 kDa	SNRNP70	RU17_HUMAN	51.6	100.0%	5	5	8	0.01%	10.8%	EFEVYGPIKR	99.6%	40.1	25	31.5	2	0	0	1237.66	122	131
U1 small nuclear ribonucleoprotein 70 kDa	SNRNP70	RU17_HUMAN	51.6	100.0%	5	5	8	0.01%	10.8%	RQQEVETELK	98.0%	32.5	25	17.8	1	0	0	1259.66	78	87
U1 small nuclear ribonucleoprotein 70 kDa	SNRNP70	RU17_HUMAN	51.6	100.0%	5	5	8	0.01%	10.8%	VLVDVER	96.8%	30.4	25	14.4	1	0	0	829.48	174	180
U1 small nuclear ribonucleoprotein 70 kDa	SNRNP70	RU17_HUMAN	51.6	100.0%	5	5	8	0.01%	10.8%	VNYDTTESK	98.3%	33.1	25	23.8	2	0	0	1056.48	110	118
U1 small nuclear ribonucleoprotein A	SNRPA	SNRPA_HUMAN	31.3	100.0%	6	6	10	0.01%	24.5%	AVQGGGATPVVGAVQGPVPGMPPMTQAPR	99.7%	36.9	25	36.9	0	2	0	2759.40	124	152
U1 small nuclear ribonucleoprotein A	SNRPA	SNRPA_HUMAN	31.3	100.0%	6	6	10	0.01%	24.5%	EVSSATNALR	99.7%	72.8	25	43.2	2	0	0	1047.54	61	70
U1 small nuclear ribonucleoprotein A	SNRPA	SNRPA_HUMAN	31.3	100.0%	6	6	10	0.01%	24.5%	GQAFVIFK	99.7%	52.5	25	43.1	3	0	0	909.52	53	60
U1 small nuclear ribonucleoprotein A	SNRPA	SNRPA_HUMAN	31.3	100.0%	6	6	10	0.01%	24.5%	KAVQGGGATPVVGAVQGPVPGMPPMTQAPR	99.7%	42	25	42	0	1	0	2887.49	123	152
U1 small nuclear ribonucleoprotein A	SNRPA	SNRPA_HUMAN	31.3	100.0%	6	6	10	0.01%	24.5%	SMQGFPFYDKPMR	99.7%	51.2	25	45.1	1	0	0	1603.74	71	83
U1 small nuclear ribonucleoprotein A	SNRPA	SNRPA_HUMAN	31.3	100.0%	6	6	10	0.01%	24.5%	TDSDIIAK	97.4%	31.3	25	21	1	0	0	862.45	89	96
U1 small nuclear ribonucleoprotein C	SNRPC	RU1C_HUMAN	17.4	100.0%	3	3	5	0.00%	24.5%	FYCDYCDTYLTHDSPSVR	99.7%	46	25	46	0	2	0	2298.94	4	21
U1 small nuclear ribonucleoprotein C	SNRPC	RU1C_HUMAN	17.4	100.0%	3	3	5	0.00%	24.5%	TTAAFQQGK	95.8%	29.3	25	19	1	0	0	951.49	53	61
U1 small nuclear ribonucleoprotein C	SNRPC	RU1C_HUMAN	17.4	100.0%	3	3	5	0.00%	24.5%	WMEEQAQSLIDK	99.7%	79.9	25	72.3	2	0	0	1477.70	41	52
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	8	8	13	0.01%	31.4%	GLLQSGQIPGR	99.7%	70.7	25	26.1	2	0	0	1125.64	222	232
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	8	8	13	0.01%	31.4%	KLDGFPLLR	99.7%	41.8	25	31.8	1	0	0	1058.64	56	64
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	8	8	13	0.01%	31.4%	LDGFPLLR	95.8%	29.3	25	22.8	1	0	0	930.54	57	64
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	8	8	13	0.01%	31.4%	LTAELIEQAAQYTNAVR	99.7%	78.1	25	74	2	0	0	1890.99	4	20
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	8	8	13	0.01%	31.4%	NAIANASTLAEVER	99.7%	98.8	25	93	2	0	0	1458.75	206	219
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	8	8	13	0.01%	31.4%	SLTYLSILR	99.7%	48.8	25	43.1	2	0	0	1065.63	114	122
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	8	8	13	0.01%	31.4%	TFNPGAGLPTDK	99.7%	51.7	25	47	2	0	0	1217.62	180	191
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	8	8	13	0.01%	31.4%	TLLVNNNR	98.8%	34.6	25	14.2	1	0	0	943.53	68	75
U2 small nuclear ribonucleoprotein B"	SNRPB2	RU2B_HUMAN	25.5	99.9%	2	2	4	0.00%	12.9%	ELGSSTNALR	99.7%	56.4	25	34.8	2	0	0	1047.54	58	67
U2 small nuclear ribonucleoprotein B"	SNRPB2	RU2B_HUMAN	25.5	99.9%	2	2	4	0.00%	12.9%	GQAFVIFK	99.7%	52.5	25	43.1	3	0	0	909.52	50	57
U2 small nuclear ribonucleoprotein B"	SNRPB2	RU2B_HUMAN	25.5	99.9%	2	2	4	0.00%	12.9%	TVEQTATTTNK	99.7%	83.9	25	75	2	0	0	1193.60	112	122
U2 snRNP-associated SURP motif-containing protein	U2SURP	SR140_HUMAN	118.3	99.8%	2	2	3	0.00%	2.5%	LYLVSDVLYNSSAK	99.7%	76.7	25	76.7	2	0	0	1571.83	595	608
U2 snRNP-associated SURP motif-containing protein	U2SURP	SR140_HUMAN	118.3	99.8%	2	2	3	0.00%	2.5%	LYSILQGDSPTK	99.7%	70.1	25	58.7	1	0	0	1321.70	477	488
U3 small nucleolar RNA-interacting protein 2	RRP9	U3IP2_HUMAN	51.8	99.7%	2	2	3	0.00%	3.4%	LKEDVLEQR	99.7%	46.2	25	34.8	2	0	0	1129.62	112	120
U3 small nucleolar RNA-interacting protein 2	RRP9	U3IP2_HUMAN	51.8	99.7%	2	2	3	0.00%	3.4%	LYLEQLR	94.6%	28.3	25	20.4	1	0	0	934.54	85	91
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	15	23	57	0.05%	35.5%	ASEVMGPVEAAPEYR	99.7%	93.1	25	93.1	6	0	0	1605.76	77	91
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	15	23	57	0.05%	35.5%	IEEYISK	99.7%	42.1	25	33.1	2	0	0	881.46	67	73
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	15	23	57	0.05%	35.5%	IMGVAGGLTNLSK	99.7%	85.8	25	67.3	4	0	0	1260.70	231	243
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	15	23	57	0.05%	35.5%	IYEYVESR	99.7%	59.5	25	51.1	4	0	0	1058.52	204	211
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	15	23	57	0.05%	35.5%	LEEACDMALELNASK	99.7%	79	25	79	3	0	0	1709.77	187	201
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	15	23	57	0.05%	35.5%	LGLTEIR	99.7%	57	25	19.2	2	0	0	801.48	366	372
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	15	23	57	0.05%	35.5%	LGLTEIRK	99.7%	47.7	25	35.7	2	0	0	929.58	366	373
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	15	23	57	0.05%	35.5%	MFAEIMMK	98.1%	32.6	25	25.3	3	0	0	1032.46	59	66
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	15	23	57	0.05%	35.5%	MPACNIMLLGAQR	99.7%	83.6	25	66.6	6	0	0	1490.73	244	256
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	15	23	57	0.05%	35.5%	MSFIAPNLSIIIGASTAAK	99.7%	88.4	25	88.4	4	0	0	1921.05	212	230
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	15	23	57	0.05%	35.5%	QVKPLPAPLDGQR	99.5%	31.5	25	31	0	1	0	1418.81	339	351
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	15	23	57	0.05%	35.5%	SSGTASSVAFTPLQGLEIVNPQAAEK	99.7%	81.8	25	81.8	2	2	0	2602.34	445	470
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	15	23	57	0.05%	35.5%	VDSFHESTEGK	99.7%	61.5	25	60.3	6	1	0	1235.55	305	315
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	15	23	57	0.05%	35.5%	VGYELKDEIER	99.7%	73.2	25	53.9	4	2	0	1350.69	316	326
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	15	23	57	0.05%	35.5%	YFSSMAEFLK	99.7%	62.2	25	57.1	3	0	0	1238.58	479	488
U4/U6.U5 tri-snRNP-associated protein 1	SART1	SNUT1_HUMAN	90.3	100.0%	3	3	4	0.00%	5.4%	EAAGTTAAAGTGGATEQPPR	99.7%	122	25	122	1	0	0	1813.87	12	31
U4/U6.U5 tri-snRNP-associated protein 1	SART1	SNUT1_HUMAN	90.3	100.0%	3	3	4	0.00%	5.4%	LEQGGTADGLR	99.7%	55.9	25	49.8	1	0	0	1116.56	351	361
U4/U6.U5 tri-snRNP-associated protein 1	SART1	SNUT1_HUMAN	90.3	100.0%	3	3	4	0.00%	5.4%	LQAQSLSTVGPR	99.7%	74	25	73.2	2	0	0	1256.70	374	385
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	AALETDENLLLCAPTGAGK	99.7%	96.6	25	84.6	2	0	0	1943.97	491	509
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	ANSNLVLQADR	99.7%	68.4	25	56.5	2	0	0	1200.63	15	25
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	DEPTGEVLSLVGK	99.7%	84.4	25	74.5	2	0	0	1343.71	34	46
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	DIDAFWLQR	99.7%	64.3	25	50.6	2	0	0	1163.58	262	270
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	DILCGAADEVLAVLK	99.7%	71	25	58.7	2	0	0	1586.85	130	144

U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	DTLGLFLR	99.7%	57	25	32.3	1	0	0	934.54	746	753
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	EEEKLELQK	99.1%	36	25	27.5	1	0	0	1145.61	1031	1039
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	EEEVTGPVIAPLFPQK	99.7%	71.8	25	71.8	2	0	0	1753.94	2044	2059
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	EEGWWVVIGDAK	99.7%	47.3	25	32.1	2	0	0	1388.68	2061	2072
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	EGSASTEVLR	99.7%	54.4	25	43.5	2	0	0	1048.53	754	763
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	ESIEEPSAK	99.7%	43.3	25	31.8	1	0	0	989.48	1050	1058
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	FQIMNEIVYEK	99.7%	64.7	25	52.3	4	0	0	1413.71	701	711
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	FYDDAIVSQK	99.7%	76.8	25	66.6	2	0	0	1185.58	275	284
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	GTQVYSPEK	98.7%	34.4	25	21	2	0	0	1008.50	830	838
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	HLILPEK	99.6%	40	25	28.2	2	0	0	849.52	1288	1294
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	IIYIAPMR	99.1%	36	25	24.8	3	0	0	992.56	538	545
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	IVALSSSLSNAK	99.7%	99.9	25	92.4	2	0	0	1189.68	1487	1498
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	KADEVLEILK	99.7%	56.1	25	42.6	2	0	0	1157.68	285	294
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	KPVIVFVPSR	99.7%	62.4	25	57.1	2	0	0	1141.71	1557	1566
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	LIGLSATLPNYEDVATFLR	99.7%	55.8	25	55.8	2	0	0	2093.13	648	666
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	LPDMLNAEIVLGNVQNAK	99.7%	89.2	25	89.2	1	0	0	1955.03	897	914
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	LTAIDILTTCAADIQR	99.7%	108	25	98.9	2	0	0	1774.94	1571	1586
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	LYDLNHNEIGELIR	99.4%	31.4	25	26.2	0	2	0	1698.88	1153	1166
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	MEADPELSK	96.1%	29.6	25	22.3	1	0	0	1019.47	350	358
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	MLLQSSEGR	99.6%	40.5	25	28.2	1	0	0	1036.51	1367	1375
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	MQLSAELQSDTEEILSK	99.7%	98.7	25	88.6	2	0	0	1937.94	1902	1918
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	MTQNPNYYNLQGISHR	99.7%	41.4	25	41.4	0	3	0	1951.91	1764	1779
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	NALLQLTDSQIADVAR	99.7%	114	25	107	2	0	0	1727.93	1994	2009
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	NIEMTQEDVR	99.7%	63	25	43.6	4	0	0	1234.57	638	647
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	NQVLVFVHSR	99.7%	63.8	25	60.6	2	1	0	1198.67	719	728
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	SGGPVVVLVQLER	99.7%	57.2	25	57.2	2	0	0	1352.79	2031	2043
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	SLVQEMVGSFGK	99.7%	98.5	25	98.5	5	0	0	1281.65	546	557
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	SNSLISIKR	97.9%	32.2	25	23.6	1	0	0	1017.61	2073	2081
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	SPTLYGISHDDLK	99.7%	70.1	25	65.3	2	0	0	1445.73	932	944
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	TGNFQVTELGR	99.7%	69.7	25	61.9	2	0	0	1221.62	976	986
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	TNLLLQAHLSR	99.7%	71.3	25	63.9	2	0	0	1265.73	1891	1901
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	TYTQLVR	98.7%	34.3	25	26.2	1	0	0	880.49	604	610
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	VELTITPDFQWDEK	99.7%	62.4	25	55.5	2	0	0	1720.84	1200	1213
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	VFSLSSEFK	99.2%	36.7	25	23.7	2	0	0	1043.54	1017	1025
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	VPIPVKESIEEPSAK	99.2%	29.8	25	29.3	0	1	0	1622.90	1044	1058
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	VVLLTGETSTDLK	99.7%	106	25	99.7	2	0	0	1375.77	1405	1417
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	WLSCETQLPVSFR	99.7%	77.5	25	68.8	2	0	0	1622.80	1275	1287
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	YAQAGFEGFK	99.7%	61.7	25	59.2	2	0	0	1117.53	470	479
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	44	50	88	0.08%	24.4%	YPPPTELLDLQPLPVSALR	99.7%	50.8	25	50.8	1	0	0	2119.18	1295	1313
U5 small nuclear ribonucleoprotein 40 kDa protein	SNRNP40	SNR40_HUMAN	39.3	100.0%	6	6	11	0.01%	19.0%	CSWSPDGSK	99.1%	36	25	34.8	2	0	0	1023.42	291	299
U5 small nuclear ribonucleoprotein 40 kDa protein	SNRNP40	SNR40_HUMAN	39.3	100.0%	6	6	11	0.01%	19.0%	FVYVWDTTSR	99.3%	37.3	25	37.2	2	0	0	1273.62	308	317
U5 small nuclear ribonucleoprotein 40 kDa protein	SNRNP40	SNR40_HUMAN	39.3	100.0%	6	6	11	0.01%	19.0%	IFQGNVHNFEK	99.7%	54.7	25	46.5	2	0	0	1332.67	276	286
U5 small nuclear ribonucleoprotein 40 kDa protein	SNRNP40	SNR40_HUMAN	39.3	100.0%	6	6	11	0.01%	19.0%	RGPQLVCTGSDDGTVK	98.0%	32.5	25	29.1	1	0	0	1689.82	162	177
U5 small nuclear ribonucleoprotein 40 kDa protein	SNRNP40	SNR40_HUMAN	39.3	100.0%	6	6	11	0.01%	19.0%	TVAVWDSETGER	99.7%	46.5	25	39.4	2	0	0	1349.63	132	143
U5 small nuclear ribonucleoprotein 40 kDa protein	SNRNP40	SNR40_HUMAN	39.3	100.0%	6	6	11	0.01%	19.0%	VWDVRPFAPK	97.6%	31.6	25	31.6	2	0	0	1214.67	261	270
UAP56-interacting factor	FYTTD1	UIF_HUMAN	35.8	100.0%	4	4	6	0.01%	16.7%	GVPLQFDINSVGK	99.7%	41.4	25	38.8	1	0	0	1373.74	273	285
UAP56-interacting factor	FYTTD1	UIF_HUMAN	35.8	100.0%	4	4	6	0.01%	16.7%	LVGATATSSPPPK	99.7%	47.5	25	41.9	2	0	0	1225.68	8	20
UAP56-interacting factor	FYTTD1	UIF_HUMAN	35.8	100.0%	4	4	6	0.01%	16.7%	NIEQYFPVLK	98.5%	33.7	25	22.8	1	0	0	1250.68	129	138
UAP56-interacting factor	FYTTD1	UIF_HUMAN	35.8	100.0%	4	4	6	0.01%	16.7%	VQAQLNTEQLLDDVVAK	99.7%	97.2	25	97.2	2	0	0	1884.01	199	215
Ubiquinol-cytochrome-c reductase complex assembly factor 1	UQCC1	UQCC1_HUMAN	34.6	99.8%	2	2	2	0.00%	7.0%	IIEAMGFTGPLK	99.4%	37.9	25	35.2	1	0	0	1276.70	96	107
Ubiquinol-cytochrome-c reductase complex assembly factor 1	UQCC1	UQCC1_HUMAN	34.6	99.8%	2	2	2	0.00%	7.0%	TDFEEFFLR	99.7%	55.2	25	50.9	1	0	0	1203.57	128	136

Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	7	7	10	0.01%	3.4%	IFLLECNVR	99.7%	43.6	25	38.8	1	0	0	1163.62	2224	2232
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	7	7	10	0.01%	3.4%	LAAAVAGPGGLSGSTLVDGR	99.7%	68.1	25	68.1	1	0	0	1768.96	682	701
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	7	7	10	0.01%	3.4%	LEAASSALGGPTLTHAVTR	99.7%	35.6	25	30.8	0	2	0	1851.99	877	895
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	7	7	10	0.01%	3.4%	LVSIPELLSAVK	99.5%	39	25	39	1	0	0	1268.78	358	369
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	7	7	10	0.01%	3.4%	TLLSLCGAEK	98.6%	34	25	7.3	1	0	0	1091.58	1575	1584
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	7	7	10	0.01%	3.4%	VAVATILEK	98.5%	33.6	25	30.7	2	0	0	943.58	2236	2244
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	7	7	10	0.01%	3.4%	VLYNLEVLSSK	99.7%	60.2	25	60.2	2	0	0	1264.71	1174	1184
Ubiquitin conjugation factor E4 B	UBE4B	UBE4B_HUMAN	146.2	99.8%	2	2	2	0.00%	2.5%	ILDPAYPDITLPLNSDVPK	99.7%	50.7	25	50.7	1	0	0	2081.12	857	875
Ubiquitin conjugation factor E4 B	UBE4B	UBE4B_HUMAN	146.2	99.8%	2	2	2	0.00%	2.5%	YFSGPAITLENTR	95.6%	29.1	25	28.6	1	0	0	1468.74	611	623
Ubiquitin thioesterase OTUB1	OTUB1	OTUB1_HUMAN	31.3	100.0%	4	4	8	0.01%	17.0%	EYAEDDNIYQQK	99.7%	49.1	25	49.1	2	0	0	1515.66	60	71
Ubiquitin thioesterase OTUB1	OTUB1	OTUB1_HUMAN	31.3	100.0%	4	4	8	0.01%	17.0%	FFEHFIEGGR	99.7%	58.3	25	47.1	2	0	0	1238.60	189	198
Ubiquitin thioesterase OTUB1	OTUB1	OTUB1_HUMAN	31.3	100.0%	4	4	8	0.01%	17.0%	IQQEIAVQNPLVSER	99.7%	116	25	104	2	0	0	1723.93	37	51
Ubiquitin thioesterase OTUB1	OTUB1	OTUB1_HUMAN	31.3	100.0%	4	4	8	0.01%	17.0%	LLTSGYLQR	99.7%	60.7	25	47.3	2	0	0	1050.59	177	185
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	9	76	0.07%	56.4%	CCLTYCFNKPEDK	99.7%	69.7	25	69.6	4	1	0	1734.73	144	156
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	9	76	0.07%	56.4%	ECPSDECGAGVFMASHFDR	99.7%	64.8	25	64.8	3	3	0	2187.85	120	138
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	9	76	0.07%	56.4%	ESTLHLVLR	99.7%	62.9	25	49.3	11	0	0	1067.62	64	72
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	9	76	0.07%	56.4%	IQDKEGIPPDQQR	99.7%	57.9	25	57.9	6	0	0	1523.78	30	42
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	9	76	0.07%	56.4%	TITLEVEPSDTIENVK	99.7%	94.3	25	89.8	28	0	0	1787.93	12	27
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	9	76	0.07%	56.4%	TLSDYNIQK	99.7%	55.9	25	42.7	16	0	0	1081.55	55	63
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	9	76	0.07%	56.4%	YYKVDENGK	98.7%	34.5	25	20.9	4	0	0	1115.54	105	113
Ubiquitin-conjugating enzyme E2 N	UBE2N	UBE2N_HUMAN	17.1	99.9%	2	2	3	0.00%	12.5%	IYHPNVDK	95.3%	28.8	25	19.6	1	0	0	985.51	75	82
Ubiquitin-conjugating enzyme E2 N	UBE2N	UBE2N_HUMAN	17.1	99.9%	2	2	3	0.00%	12.5%	TNEAQAIETAR	99.7%	79.3	25	67.8	2	0	0	1203.60	131	141
Ubiquitin-like modifier-activating enzyme 1	UBA1	UBA1_HUMAN	117.9	100.0%	4	4	5	0.00%	6.5%	AAVATFLQSVQVPEFTPK	95.6%	29.1	25	29.1	1	0	0	1933.04	785	802
Ubiquitin-like modifier-activating enzyme 1	UBA1	UBA1_HUMAN	117.9	100.0%	4	4	5	0.00%	6.5%	LAGTQPLEVLEAVQR	99.7%	74.2	25	74.2	1	0	0	1623.91	679	693
Ubiquitin-like modifier-activating enzyme 1	UBA1	UBA1_HUMAN	117.9	100.0%	4	4	5	0.00%	6.5%	NEEDAAELVALAQAVNAR	99.7%	74.3	25	70.8	1	0	0	1883.95	351	368
Ubiquitin-like modifier-activating enzyme 1	UBA1	UBA1_HUMAN	117.9	100.0%	4	4	5	0.00%	6.5%	SLVASLAEPDFVVTDFAK	99.7%	57.1	25	57.1	2	0	0	1909.00	305	322
Ubiquitin-protein ligase E3A	UBE3A	UBE3A_HUMAN	100.7	100.0%	3	3	4	0.00%	4.5%	EFVNLYSDYILNK	99.7%	44.5	25	38.4	1	0	0	1617.82	712	724
Ubiquitin-protein ligase E3A	UBE3A	UBE3A_HUMAN	100.7	100.0%	3	3	4	0.00%	4.5%	IGDSSQGDNNLQK	99.7%	59.6	25	53.8	1	0	0	1375.65	214	226
Ubiquitin-protein ligase E3A	UBE3A	UBE3A_HUMAN	100.7	100.0%	3	3	4	0.00%	4.5%	VFSSAEALVQSFR	99.7%	80.2	25	71.7	2	0	0	1440.75	156	168
Ubiquitin-protein ligase E3C	UBE3C	UBE3C_HUMAN	123.9	100.0%	3	3	5	0.00%	2.9%	LPEFYDETLLR	99.7%	54.8	25	50.3	2	0	0	1395.72	1057	1067
Ubiquitin-protein ligase E3C	UBE3C	UBE3C_HUMAN	123.9	100.0%	3	3	5	0.00%	2.9%	NAIIIQSFIR	99.7%	47.2	25	39.8	2	0	0	1174.69	48	57
Ubiquitin-protein ligase E3C	UBE3C	UBE3C_HUMAN	123.9	100.0%	3	3	5	0.00%	2.9%	VTQLYVPASR	99.7%	46.6	25	39	1	0	0	1133.63	639	648
UDP-glucose 6-dehydrogenase	UGDH	UGDH_HUMAN	55.0	100.0%	3	3	4	0.00%	6.1%	VLIGGDETPEGQR	99.7%	43.5	25	43.1	1	0	0	1370.69	178	190
UDP-glucose 6-dehydrogenase	UGDH	UGDH_HUMAN	55.0	100.0%	3	3	4	0.00%	6.1%	VTVVDVNESR	99.7%	48.3	25	40.3	2	0	0	1117.58	32	41
UDP-glucose 6-dehydrogenase	UGDH	UGDH_HUMAN	55.0	100.0%	3	3	4	0.00%	6.1%	YIEACAR	97.8%	32	25	26.4	1	0	0	882.41	108	114
UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	OGT	OGT1_HUMAN	116.9	99.9%	2	2	3	0.00%	1.9%	AATGEEVPR	99.7%	57.7	25	41.7	2	0	0	929.47	817	825
UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	OGT	OGT1_HUMAN	116.9	99.9%	2	2	3	0.00%	1.9%	LVSIVADQLEK	99.7%	45.5	25	38.7	1	0	0	1214.70	489	499
Uncharacterized protein C11orf84	C11orf84	CK084_HUMAN	41.0	100.0%	3	3	4	0.00%	8.7%	AESPSPAPPPGLR	99.7%	48.2	25	33.8	1	0	0	1275.67	306	318
Uncharacterized protein C11orf84	C11orf84	CK084_HUMAN	41.0	100.0%	3	3	4	0.00%	8.7%	DREVAEGGLPR	99.7%	42.2	25	27.4	1	0	0	1198.62	295	305
Uncharacterized protein C11orf84	C11orf84	CK084_HUMAN	41.0	100.0%	3	3	4	0.00%	8.7%	GTLDLQVIR	98.9%	35.1	25	26.2	2	0	0	1014.59	319	327
Uncharacterized protein C19orf52	C19orf52	CS052_HUMAN	29.2	99.8%	2	2	3	0.00%	8.5%	ESEAFVQR	99.7%	47.4	25	36.3	2	0	0	965.47	105	112
Uncharacterized protein C19orf52	C19orf52	CS052_HUMAN	29.2	99.8%	2	2	3	0.00%	8.5%	VVGPQQLHSETNER	99.7%	61.8	25	57.8	1	0	0	1593.80	198	211
Uncharacterized protein C2orf47, mitochondrial	C2orf47	CB047_HUMAN	32.5	100.0%	4	5	8	0.01%	16.8%	EFTQGVKPDWTIAR	99.7%	55	25	41.5	1	3	0	1647.85	270	283
Uncharacterized protein C2orf47, mitochondrial	C2orf47	CB047_HUMAN	32.5	100.0%	4	5	8	0.01%	16.8%	FDLLEELVAK	99.7%	53.3	25	43.3	1	0	0	1176.65	164	173
Uncharacterized protein C2orf47, mitochondrial	C2orf47	CB047_HUMAN	32.5	100.0%	4	5	8	0.01%	16.8%	MIVLGFSNPINWVR	99.7%	63.3	25	63.3	1	0	0	1661.88	110	123
Uncharacterized protein C2orf47, mitochondrial	C2orf47	CB047_HUMAN	32.5	100.0%	4	5	8	0.01%	16.8%	QLLSASYEFQR	99.7%	45.9	25	43.3	2	0	0	1341.68	259	269
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	5	5	9	0.01%	6.2%	EICELTGIDQSVLER	99.7%	59.6	25	50.9	1	0	0	1761.87	308	322
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	5	5	9	0.01%	6.2%	EQLLQSNPVLEAFGNAK	99.7%	112	25	112	2	0	0	1857.97	140	156
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	5	5	9	0.01%	6.2%	IFLLTNNNLLLADQK	99.7%	92.7	25	92.7	2	0	0	1729.98	1007	1021
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	5	5	9	0.01%	6.2%	IIIAEVVNK	99.7%	49.4	25	39.5	2	0	0	998.62	987	995
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	5	5	9	0.01%	6.2%	VSTTLNVAQAYYAR	99.7%	62.3	25	55	2	0	0	1556.81	336	349

Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	10	10	19	0.02%	12.7%	DGTIDFTPGSELLITK	99.7%	75.5	25	70.4	2	0	0	1706.89	1032	1047
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	10	10	19	0.02%	12.7%	GEELLSPLNLEQAAYAR	99.7%	94.6	25	84.3	2	0	0	1873.97	362	378
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	10	10	19	0.02%	12.7%	LGTDEISPR	99.7%	87.4	25	68.8	2	0	0	987.51	901	909
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	10	10	19	0.02%	12.7%	LLQFYAETCPAPER	99.7%	65.4	25	44.7	2	0	0	1694.82	153	166
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	10	10	19	0.02%	12.7%	LLQSNPVLEAFGNAK	99.7%	76.1	25	76.1	2	0	0	1600.87	174	188
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	10	10	19	0.02%	12.7%	NPQSYLYLVK	98.2%	33	25	33	2	0	0	1224.66	260	269
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	10	10	19	0.02%	12.7%	TSFLLNLR	99.7%	63.7	25	59.8	2	0	0	963.56	814	821
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	10	10	19	0.02%	12.7%	VLQALGSEPIQYAVPVVK	99.7%	58.7	25	58.7	2	0	0	1911.10	910	927
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	10	10	19	0.02%	12.7%	VNSININQGSITFAGGPGR	99.7%	65.1	25	65.1	1	0	0	1901.98	1013	1031
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	10	10	19	0.02%	12.7%	YLGLLENLR	99.7%	45	25	44.2	2	0	0	1090.63	648	656
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	6	6	9	0.01%	6.1%	IGELVGVLVNHFK	99.3%	37.6	25	34	1	0	0	1424.83	942	954
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	6	6	9	0.01%	6.1%	NYDTTIHGK	99.3%	37.6	25	37.6	1	0	0	1048.51	367	375
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	6	6	9	0.01%	6.1%	SYIHEVAR	99.5%	39.4	25	32.5	2	0	0	974.51	738	745
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	6	6	9	0.01%	6.1%	TLFTLEELR	99.7%	43.2	25	28.1	2	0	0	1121.62	686	694
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	6	6	9	0.01%	6.1%	VIVQQPGER	99.2%	36.7	25	30.1	2	0	0	1025.57	191	199
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	6	6	9	0.01%	6.1%	VTDEMFLEALNSK	99.0%	35.7	25	22.6	1	0	0	1496.73	466	478
Unhealthy ribosome biogenesis protein 2 homolog	URB2	URB2_HUMAN	170.5	100.0%	3	3	4	0.00%	2.5%	ADVQAVVSAVTLLR	99.7%	43.4	25	6.59	2	0	0	1441.84	1262	1275
Unhealthy ribosome biogenesis protein 2 homolog	URB2	URB2_HUMAN	170.5	100.0%	3	3	4	0.00%	2.5%	GGIFQPELLSSYK	99.7%	48.3	25	36.2	1	0	0	1438.76	243	255
Unhealthy ribosome biogenesis protein 2 homolog	URB2	URB2_HUMAN	170.5	100.0%	3	3	4	0.00%	2.5%	VAEFSLSGSQR	99.7%	54.8	25	44.7	1	0	0	1180.60	107	117
UPF0420 protein C16orf58	C16orf58	CP058_HUMAN	51.0	99.9%	2	2	4	0.00%	4.1%	GEVLDPTAANR	99.7%	55.7	25	52	2	0	0	1142.58	303	313
UPF0420 protein C16orf58	C16orf58	CP058_HUMAN	51.0	99.9%	2	2	4	0.00%	4.1%	KESWVVVK	97.2%	30.9	25	21	2	0	0	974.57	414	421
UPF0444 transmembrane protein C12orf23	C12orf23	CL023_HUMAN	11.7	99.8%	2	2	3	0.00%	30.2%	GGVSAVAGGVTAVGSAVVNK	99.7%	95.4	25	91.4	2	0	0	1699.93	85	104
UPF0444 transmembrane protein C12orf23	C12orf23	CL023_HUMAN	11.7	99.8%	2	2	3	0.00%	30.2%	TAVTTVPSMGIGLVK	98.0%	32.5	25	18.9	1	0	0	1489.83	70	84
UPF0488 protein C8orf33	C8orf33	CH033_HUMAN	25.0	100.0%	4	5	9	0.01%	21.0%	AAAYSAQVQPVDGATR	99.7%	88.5	25	80.5	3	0	0	1604.80	183	198
UPF0488 protein C8orf33	C8orf33	CH033_HUMAN	25.0	100.0%	4	5	9	0.01%	21.0%	AHPLGDEGGTASK	99.1%	29.4	25	14.5	1	2	0	1239.60	57	69
UPF0488 protein C8orf33	C8orf33	CH033_HUMAN	25.0	100.0%	4	5	9	0.01%	21.0%	LPGPVSSAR	99.7%	47.6	25	24.5	2	0	0	883.50	28	36
UPF0488 protein C8orf33	C8orf33	CH033_HUMAN	25.0	100.0%	4	5	9	0.01%	21.0%	QKEQAIGAIR	99.7%	49.7	25	26.5	1	0	0	1113.64	134	143
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	11	12	19	0.02%	23.3%	AALGPLVTGLYDVQAFK	99.7%	78.5	25	78.5	2	0	0	1762.97	6	22
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	11	12	19	0.02%	23.3%	AAWEAYLSR	99.7%	65.5	25	38.6	1	0	0	1066.53	469	477
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	11	12	19	0.02%	23.3%	FADIGNTVK	99.7%	44.2	25	32.1	1	0	0	964.51	315	323
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	11	12	19	0.02%	23.3%	FGDFVLK	98.5%	33.8	25	23.6	2	0	0	825.45	23	29
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	11	12	19	0.02%	23.3%	IASWADLVNAHVVPGSGVVK	99.7%	34.7	25	34.7	0	1	0	2019.10	333	352
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	11	12	19	0.02%	23.3%	KFADIGNTVK	99.7%	56	25	44.1	1	0	0	1092.60	314	323
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	11	12	19	0.02%	23.3%	KVDAETVGR	99.7%	59.7	25	44.7	2	0	0	974.53	188	196
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	11	12	19	0.02%	23.3%	LHSVCTLSK	98.5%	33.6	25	25.8	2	0	0	1044.55	170	178
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	11	12	19	0.02%	23.3%	MLEILEQQK	99.7%	44.8	25	33.5	3	0	0	1131.61	179	187
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	11	12	19	0.02%	23.3%	SGLSSPIYIDLR	99.7%	59	25	45.7	2	0	0	1320.72	30	41
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	11	12	19	0.02%	23.3%	VTDAIVLLDR	99.7%	93.7	25	67.1	2	0	0	1114.65	146	155
Uridine-cytidine kinase 2	UCK2	UCK2_HUMAN	29.3	99.8%	2	2	3	0.00%	8.1%	IVQLLGQNEVDYR	99.1%	36.1	25	36.1	1	0	0	1546.82	40	52
Uridine-cytidine kinase 2	UCK2	UCK2_HUMAN	29.3	99.8%	2	2	3	0.00%	8.1%	YADVIIPR	99.7%	42.2	25	42.2	2	0	0	946.54	203	210
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	7	8	14	0.01%	29.4%	EITGIGPSTTTETETIAK	99.7%	95.7	25	95.6	2	0	0	1848.94	215	232
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	7	8	14	0.01%	29.4%	ELALPGELTQSR	99.7%	77.5	25	70.1	2	0	0	1313.71	94	105
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	7	8	14	0.01%	29.4%	FESPESQASAEQPEM	99.7%	59.2	25	59.2	2	0	0	1682.69	313	327
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	7	8	14	0.01%	29.4%	HYLFYDGESVSGK	99.7%	49.8	25	46.5	2	0	0	1501.70	39	51
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	7	8	14	0.01%	29.4%	LFLAGYDPTPTMR	99.7%	77.7	25	77.7	4	0	0	1497.74	250	262
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	7	8	14	0.01%	29.4%	QQEIILWR	98.6%	34	25	30.6	1	0	0	1085.61	289	296
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	7	8	14	0.01%	29.4%	YEIMDGAPVKGESIPIR	99.7%	42.7	25	41.6	0	1	0	1890.96	233	249
Vacuolar protein sorting-associated protein 29	VPS29	VPS29_HUMAN	20.5	100.0%	2	2	4	0.00%	12.6%	GDFDENLNYPEQK	99.6%	40.4	25	40.4	2	0	0	1568.69	61	73
Vacuolar protein sorting-associated protein 29	VPS29	VPS29_HUMAN	20.5	100.0%	2	2	4	0.00%	12.6%	TLAGDVHIVR	99.7%	82.1	25	75.5	2	0	0	1080.62	51	60
Vacuolar protein sorting-associated protein 33B	VPS33B	VP33B_HUMAN	70.6	99.8%	2	2	4	0.00%	3.4%	FIFLTTAVTNSAR	99.7%	53.8	25	42.4	2	0	0	1440.78	595	607
Vacuolar protein sorting-associated protein 33B	VPS33B	VP33B_HUMAN	70.6	99.8%	2	2	4	0.00%	3.4%	IIEQVLER	97.7%	31.9	25	6.57	2	0	0	999.58	524	531

Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	10	17	0.02%	16.5%	EDGPGIPADIK	99.1%	36	25	26	1	0	0	1111.56	313	323
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	10	17	0.02%	16.5%	ENDAVTIQVLNQLIQK	99.7%	71	25	58.6	1	0	0	1826.00	734	749
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	10	17	0.02%	16.5%	ESPESEGPIYEGLIL	99.7%	42.3	25	42.3	1	0	0	1632.80	782	796
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	10	17	0.02%	16.5%	ILVGTNLVR	99.7%	58.4	25	42.6	2	0	0	984.62	218	226
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	10	17	0.02%	16.5%	IPVDTYNNILTVLK	99.7%	75.8	25	75.8	3	0	0	1602.91	404	417
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	10	17	0.02%	16.5%	LFDIFSQQVATVIQSR	99.7%	63.2	25	54.8	2	0	0	1852.00	324	339
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	10	17	0.02%	16.5%	LLDEAIQAVK	99.7%	58.5	25	38.9	2	0	0	1099.64	15	24
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	10	17	0.02%	16.5%	LNLEHIATSSAVSK	99.7%	43.7	25	43.7	1	0	0	1469.80	383	396
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	10	17	0.02%	16.5%	LSQLEGVNVER	99.7%	63	25	56.4	2	0	0	1243.66	227	237
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	10	17	0.02%	16.5%	SEDPDQQYLILNTAR	99.7%	90.8	25	85.5	2	0	0	1762.86	500	514
Vacuolar protein-sorting-associated protein 25	VPS25	VPS25_HUMAN	20.7	100.0%	2	2	3	0.00%	9.1%	LIYQWVSR	99.0%	35.7	25	28.3	1	0	0	1064.59	110	117
Vacuolar protein-sorting-associated protein 25	VPS25	VPS25_HUMAN	20.7	100.0%	2	2	3	0.00%	9.1%	SSFLIMWR	99.7%	43.9	25	28.1	2	0	0	1055.53	95	102
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	10	10	15	0.01%	9.8%	DPGVITYDLPTPPGEK	99.7%	67.6	25	67.2	2	0	0	1698.86	274	289
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	10	10	15	0.01%	9.8%	GALINVPPPFLGLPR	95.8%	29.3	25	29.3	1	0	0	1560.93	619	633
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	10	10	15	0.01%	9.8%	IQQQQPPPGEK	96.1%	29.6	25	25.4	1	0	0	1249.65	253	263
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	10	10	15	0.01%	9.8%	ITPAHDQNDYEVGQR	99.5%	31.7	25	29.6	0	1	0	1742.81	592	606
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	10	10	15	0.01%	9.8%	KVDEAIALFQK	99.4%	38	25	33.3	1	0	0	1261.72	1252	1262
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	10	10	15	0.01%	9.8%	LHEEGIIYR	97.9%	32.3	25	23.5	1	0	0	1129.60	462	470
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	10	10	15	0.01%	9.8%	LQQTEAELR	99.7%	52.6	25	39.1	2	0	0	1087.57	1243	1251
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	10	10	15	0.01%	9.8%	LSAAVTEAFVR	99.7%	91.6	25	83.9	2	0	0	1163.64	451	461
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	10	10	15	0.01%	9.8%	SSAQDPQAVLGALGR	99.7%	74.5	25	74.5	2	0	0	1469.77	123	137
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	10	10	15	0.01%	9.8%	VPLEVQEADEAK	99.7%	68.7	25	68.7	2	0	0	1327.67	1231	1242
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	6	7	14	0.01%	11.6%	FSFTLPYPVK	98.1%	32.8	25	32.3	2	0	0	1198.65	310	319
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	6	7	14	0.01%	11.6%	LESEGSPETLTNLR	99.7%	102	25	94.3	2	0	0	1545.78	133	146
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	6	7	14	0.01%	11.6%	LESEGSPETLTNLRK	99.7%	74	25	65.3	2	0	0	1673.87	133	147
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	6	7	14	0.01%	11.6%	LRLESEGSPETLTNLR	99.7%	78.3	25	72.8	2	2	0	1814.96	131	146
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	6	7	14	0.01%	11.6%	QVNITVQK	99.7%	43.8	25	31.5	2	0	0	929.54	77	84
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	6	7	14	0.01%	11.6%	VSQWWER	99.7%	45	25	29.7	2	0	0	990.48	86	92
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	4	4	16	0.02%	12.3%	LLETLFVHR	99.7%	69.2	25	44.4	4	0	0	1127.66	142	150
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	4	4	16	0.02%	12.3%	LPVGTTATLYFR	99.7%	78.2	25	78.2	4	0	0	1338.74	68	79
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	4	4	16	0.02%	12.3%	SLKDEDVLQK	99.7%	60.5	25	46.6	4	0	0	1174.63	58	67
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	4	4	16	0.02%	12.3%	YDFTSSR	99.5%	39.1	25	18.3	4	0	0	875.39	117	123
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	34	0.03%	23.0%	AENSSLNLIGK	99.7%	69.2	25	50.4	2	0	0	1145.62	188	198
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	34	0.03%	23.0%	DFQSGQHVIVR	99.7%	58.8	25	48.8	2	0	0	1285.66	28	38
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	34	0.03%	23.0%	DIEAMDPSILK	99.7%	50.6	25	40.8	3	0	0	1231.62	151	161
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	34	0.03%	23.0%	GILLYGPPGCGK	99.7%	42	25	30.2	2	0	0	1231.65	255	266
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	34	0.03%	23.0%	IAEESNFPFIK	99.7%	42.4	25	32.9	2	0	0	1294.67	556	566
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	34	0.03%	23.0%	KLLIIGTTSR	99.7%	48.3	25	37.4	2	0	0	1101.70	639	648
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	34	0.03%	23.0%	LLDYVPIGPR	99.7%	58.5	25	52.5	2	0	0	1142.66	608	617
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	34	0.03%	23.0%	LLIIGTTSR	99.7%	52.4	25	46.4	2	0	0	973.60	640	648
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	34	0.03%	23.0%	MEIGLPDEK	99.7%	48	25	39.4	1	0	0	1031.51	393	401
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	34	0.03%	23.0%	NFSGAELEGLVR	99.7%	88.7	25	73.9	2	0	0	1291.66	435	446
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	34	0.03%	23.0%	SIDSNPYDTDK	99.7%	42.2	25	42.2	2	0	0	1254.55	106	116
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	34	0.03%	23.0%	SQLSCVVVDDIER	99.7%	105	25	101	2	0	0	1519.74	595	607
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	34	0.03%	23.0%	TPLVSVLLEGPPHSGK	99.7%	59.3	25	56.1	2	1	0	1630.92	534	549
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	34	0.03%	23.0%	VLDDGELLVQQTK	99.7%	88.7	25	88.7	2	0	0	1457.78	517	529
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	34	0.03%	23.0%	VVNGPEILNK	99.7%	42	25	23	2	0	0	1082.62	284	293
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	34	0.03%	23.0%	YVGESEANIR	99.7%	54.8	25	49	2	0	0	1137.55	294	303
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	19	34	0.03%	23.0%	YVGESEANIRK	99.7%	42.2	25	34.2	1	0	0	1265.65	294	304
Vesicle-trafficking protein SEC22b	SEC22B	SC22B_HUMAN	24.6	99.8%	2	2	4	0.00%	10.2%	NLGSINTELQDVQR	99.7%	81.9	25	75.4	2	0	0	1586.81	134	147
Vesicle-trafficking protein SEC22b	SEC22B	SC22B_HUMAN	24.6	99.8%	2	2	4	0.00%	10.2%	VLLTMIAR	99.7%	61	25	56.2	2	0	0	916.56	2	9

Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	DGQVINETSQHHDDLE	99.7%	61	25	57.2	5	1	0	1836.80	451	466
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	DNLAEDIMR	99.7%	56.5	25	54.4	5	0	0	1076.50	176	184
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	EEAENTLQSFR	99.7%	71.3	25	60.4	3	0	0	1323.62	197	207
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	EKLQEEMLQR	99.7%	49.2	25	35.1	4	0	0	1303.67	187	196
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	EMEENFAVEAANYQDTIGR	99.7%	118	25	118	7	3	0	2186.97	346	364
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	ETNLDSLPLVDTHSK	99.7%	72.2	25	60.2	4	1	0	1668.84	425	439
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	ETNLDSLPLVDTHSKR	99.7%	65.2	25	63.1	2	3	0	1824.95	425	440
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	EYQDLLNVK	99.7%	58.5	25	57	6	0	0	1121.58	382	390
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	FADLSEAANR	99.7%	60.6	25	51.4	2	0	0	1093.53	295	304
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	FANYIDK	99.3%	37.6	25	30.5	2	0	0	870.44	114	120
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	FANYIDKVR	99.7%	76.2	25	64.7	4	0	0	1125.61	114	122
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	ILLAELEQLK	99.7%	70.5	25	56.1	4	0	0	1169.71	130	139
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	ILLAELEQLKGQGK	99.7%	74.7	25	74.7	4	4	0	1539.91	130	143
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	ISLPLPNFSSLNLR	99.7%	89.4	25	67.8	7	0	0	1570.90	411	424
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	KLLEGEESR	99.7%	57.8	25	41	2	0	0	1060.56	402	410
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	KVESLQEEIAFLK	99.7%	111	25	110	4	2	0	1533.85	223	235
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	LGDLYEEEMR	99.7%	62.9	25	60	5	0	0	1270.56	146	155
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	LLEGEESR	99.7%	51.1	25	40.2	5	0	0	932.47	403	410
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	LLQDSVDFSLADAINTEFK	99.7%	109	25	102	8	2	0	2126.07	79	97
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	LQDEIQNMK	99.7%	57.1	25	55.2	4	0	0	1118.55	365	373
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	LQDEIQNMKEEMAR	99.7%	88.4	25	79	7	8	0	1734.82	365	378
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	LQEEMLQR	99.7%	47.5	25	33.5	4	0	0	1062.53	189	196
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	LQEEMLQREEAENTLQSFR	99.7%	53.3	25	53.3	0	4	0	2351.13	189	207
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	MALDIEIATYR	99.7%	79.4	25	60.5	2	0	0	1311.66	391	401
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	MFGGPGTASRPSSSR	99.7%	37.7	25	34.7	2	2	0	1510.71	14	28
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	NLQEAEEWYK	99.7%	56.3	25	56.3	4	0	0	1309.61	283	292
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	QDVDNASLAR	99.7%	77.8	25	62	9	0	0	1088.53	208	217
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	QQYESVAAK	99.7%	66.5	25	52.5	2	0	0	1023.51	274	282
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	QVDQLTNDK	99.7%	65.6	25	52.4	2	0	0	1060.53	160	168
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	QVDQLTNDKAR	99.7%	57.7	25	38.5	2	1	0	1287.67	160	170
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	QVQSLTCEVDALK	99.7%	85.2	25	76.3	3	0	0	1490.75	322	334
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	QVQSLTCEVDALKGTNESLER	99.7%	72.1	25	69.9	0	2	0	2377.17	322	342
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	RQVDQLTNDK	99.7%	50	25	41.9	2	2	0	1216.63	159	168
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	SLYASSPGGVYATR	99.7%	92.7	25	92.7	7	0	0	1428.71	51	64
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	SYVTTSTR	99.7%	48.8	25	38.3	2	0	0	914.46	29	36
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	TNEKVELQELNDR	99.7%	70.4	25	59.2	4	3	0	1587.80	101	113
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	TYSLGSALRPSTSR	99.7%	41.4	25	41.4	1	2	0	1495.79	37	50
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	VELQELNDR	99.7%	60.6	25	54.8	3	0	0	1115.57	105	113
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	VESLQEEIAFLK	99.7%	89.2	25	56.2	2	0	0	1405.76	224	235
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	40	66	194	0.18%	73.8%	VEVERDNLAEDIMR	99.7%	50.1	25	50.1	5	4	0	1704.82	171	184
Vitamin K epoxide reductase complex subunit 1	VKORC1	VKOR1_HUMAN	18.2	99.8%	2	2	6	0.01%	14.7%	ALCDVGTAISCSR	99.7%	86.4	25	85.8	4	0	0	1409.65	41	53
Vitamin K epoxide reductase complex subunit 1	VKORC1	VKOR1_HUMAN	18.2	99.8%	2	2	6	0.01%	14.7%	GSTWGSPGWVR	99.7%	41	25	19.5	2	0	0	1189.57	2	12
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	10	10	17	0.02%	50.2%	GYGFGLIK	97.6%	31.6	25	24.1	2	0	0	854.48	21	28
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	10	10	17	0.02%	50.2%	KLETAVNLAWTAGNSNTR	99.7%	59.7	25	59.7	0	2	0	1946.01	201	218
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	10	10	17	0.02%	50.2%	LTFDSSFSPNTGK	99.7%	62.4	25	57.1	2	0	0	1400.67	97	109
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	10	10	17	0.02%	50.2%	LTFDSSFSPNTGKK	99.7%	63	25	61.2	2	0	0	1528.76	97	110
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	10	10	17	0.02%	50.2%	LTLSALLDGK	99.7%	88.2	25	0	13	0	0	1030.61	257	266
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	10	10	17	0.02%	50.2%	SENGLEFTSSGSANTETTK	99.7%	110	25	110	1	0	0	1959.88	35	53
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	10	10	17	0.02%	50.2%	VNNSSLIGLGYTQTLKPGIK	99.4%	31.1	25	31.1	0	1	0	2103.18	237	256
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	10	10	17	0.02%	50.2%	VTQSNFAVGYK	99.7%	75.6	25	66.9	2	0	0	1213.62	164	174
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	10	10	17	0.02%	50.2%	WNTDNTLGTEITVEDQLAR	99.7%	111	25	111	1	0	0	2176.05	75	93

Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	10	10	17	0.02%	50.2%	WTEYGLTFTEK	99.7%	71.5	25	68.2	2	0	0	1374.66	64	74
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	10	10	17	0.02%	50.2%	YQIDPDACFSAK	99.7%	62.2	25	60.3	2	0	0	1414.63	225	236
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	12	33	0.03%	50.0%	GFGFGLVK	98.7%	34.5	25	25.8	1	0	0	824.47	32	39
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	12	33	0.03%	50.0%	LTFDTTFSPNTGK	99.7%	87.1	25	77.7	2	0	0	1428.70	108	120
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	12	33	0.03%	50.0%	LTFDTTFSPNTGKK	99.7%	61.2	25	61.2	2	0	0	1556.80	108	121
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	12	33	0.03%	50.0%	LTLSALVDGK	99.7%	88.5	25	75.7	4	0	0	1016.60	268	277
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	12	33	0.03%	50.0%	NNFAVGYR	99.7%	49.8	25	44.1	4	0	0	940.46	178	185
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	12	33	0.03%	50.0%	SCSGVEFSTSGSSNTDTGK	99.7%	133	25	133	3	0	0	1907.79	46	64
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	12	33	0.03%	50.0%	TGDFQLHTNVNDGTEFGGSIYQK	99.7%	55.4	25	55.4	0	2	0	2528.17	186	208
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	12	33	0.03%	50.0%	VNNSSLIGVGYTQTLRPGVK	99.7%	70.9	25	70.9	2	2	0	2103.16	248	267
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	12	33	0.03%	50.0%	WCEYGLTFTEK	99.7%	57.6	25	57.6	2	0	0	1433.64	75	85
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	12	33	0.03%	50.0%	WNTDNTLGTEIAIEDQICQGLK	99.7%	72	25	72	2	0	0	2519.21	86	107
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	12	33	0.03%	50.0%	YQLDPTASISAK	99.7%	62.7	25	53.8	7	0	0	1293.67	236	247
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	12	14	50	0.05%	47.3%	GYGFGMVK	99.5%	38.8	25	24.1	4	0	0	874.41	21	28
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	12	14	50	0.05%	47.3%	IETSINLAWTAGSNNTR	99.7%	102	25	98.9	2	0	0	1847.92	202	218
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	12	14	50	0.05%	47.3%	LSQNNFALGYK	99.7%	71.4	25	58.9	6	0	0	1254.65	164	174
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	12	14	50	0.05%	47.3%	LTLDTIFVPNTGK	99.7%	95.1	25	95	4	0	0	1418.79	97	109
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	12	14	50	0.05%	47.3%	LTLDTIFVPNTGKK	99.7%	43.8	25	35.9	4	3	0	1546.88	97	110
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	12	14	50	0.05%	47.3%	LTLSALIDGK	99.7%	88.2	25	0	13	0	0	1030.61	257	266
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	12	14	50	0.05%	47.3%	SCSGVEFSTSGHAYTDTGK	98.5%	33.7	25	33.7	1	0	0	1990.84	35	53
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	12	14	50	0.05%	47.3%	VCNYGLTFTQK	99.7%	68.6	25	60.9	4	0	0	1330.65	64	74
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	12	14	50	0.05%	47.3%	VNNASLIGLGYTQTLRPGVK	99.7%	88	25	88	3	2	0	2101.18	237	256
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	12	14	50	0.05%	47.3%	WNTDNTLGTEISWENK	99.7%	76.3	25	76.3	2	0	0	1907.88	75	90
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	12	14	50	0.05%	47.3%	YKVCNYGLTFTQK	99.7%	42.7	25	42.7	1	0	0	1621.80	62	74
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	12	14	50	0.05%	47.3%	YMLDCR	97.8%	32	25	32	1	0	0	873.36	225	230
V-set and immunoglobulin domain-containing protein 8	VSIG8	VSIG8_HUMAN	43.9	100.0%	3	3	5	0.00%	8.2%	CYASGGSQPLSYK	99.7%	59.7	25	59.7	2	0	0	1417.64	167	179
V-set and immunoglobulin domain-containing protein 8	VSIG8	VSIG8_HUMAN	43.9	100.0%	3	3	5	0.00%	8.2%	INHGSLPHLQQR	95.7%	23.2	25	23.2	0	1	0	1399.76	85	96
V-set and immunoglobulin domain-containing protein 8	VSIG8	VSIG8_HUMAN	43.9	100.0%	3	3	5	0.00%	8.2%	ISGHHYPYR	98.5%	33.8	25	28.9	2	0	0	1129.55	183	191
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	5	5	6	0.01%	9.2%	GVNVSALSR	99.7%	57.4	25	44.4	1	0	0	902.51	121	129
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	5	5	6	0.01%	9.2%	LPANHPLLTGQR	97.3%	25	25	24.1	0	1	0	1316.74	221	232
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	5	5	6	0.01%	9.2%	TALVANTSNMPVAAR	99.7%	65	25	51.7	2	0	0	1515.79	309	323
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	5	5	6	0.01%	9.2%	TVISQSLSK	99.1%	36	25	20.4	1	0	0	962.55	257	265
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	5	5	6	0.01%	9.2%	VGHSELVGEIIR	99.7%	52.5	25	44.9	1	0	0	1308.73	45	56
V-type proton ATPase subunit d 1	ATP6V0D1	VA0D1_HUMAN	40.3	100.0%	3	3	6	0.01%	9.4%	LYPEGLAQLAR	99.7%	48.5	25	45.7	2	0	0	1230.68	247	257
V-type proton ATPase subunit d 1	ATP6V0D1	VA0D1_HUMAN	40.3	100.0%	3	3	6	0.01%	9.4%	NIVWIAECIAQR	99.7%	62.5	25	59.8	2	0	0	1472.77	328	339
V-type proton ATPase subunit d 1	ATP6V0D1	VA0D1_HUMAN	40.3	100.0%	3	3	6	0.01%	9.4%	NVADYYPEYK	99.7%	46.5	25	46.5	2	0	0	1261.57	266	275
WASH complex subunit 7	KIAA1033	WASH7_HUMAN	136.4	99.8%	2	2	3	0.00%	1.6%	HLNTINIR	97.0%	30.7	25	24.8	1	0	0	980.56	814	821
WASH complex subunit 7	KIAA1033	WASH7_HUMAN	136.4	99.8%	2	2	3	0.00%	1.6%	MLVDVFAPEFR	99.7%	54.3	25	45.1	2	0	0	1323.68	993	1003
WASH complex subunit strumpellin	KIAA0196	STRUM_HUMAN	134.3	99.8%	2	2	3	0.00%	2.1%	LASALDLPLLR	99.5%	39.3	25	39.3	1	0	0	1181.73	589	599
WASH complex subunit strumpellin	KIAA0196	STRUM_HUMAN	134.3	99.8%	2	2	3	0.00%	2.1%	TALNNTLDLSNVR	99.7%	77.3	25	77.3	2	0	0	1430.76	312	324
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	8	8	16	0.02%	17.7%	DYSGQGVVK	96.1%	29.6	25	19	2	0	0	952.47	397	405
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	8	8	16	0.02%	17.7%	GPVTDVAYSHDGAFLAVCDASK	99.2%	30	25	30	0	2	0	2280.06	490	511
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	8	8	16	0.02%	17.7%	IAVVGEGR	99.7%	47.7	25	27.3	2	0	0	800.46	117	124
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	8	8	16	0.02%	17.7%	LATGSDDNCAAFFEGPPFK	99.7%	53.7	25	52.5	2	0	0	2043.91	162	180
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	8	8	16	0.02%	17.7%	LYSILGTTLKDEGK	99.7%	85.1	25	71.2	2	0	0	1537.85	471	484
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	8	8	16	0.02%	17.7%	VFASLPQVER	99.7%	41.9	25	39.5	2	0	0	1145.63	8	17
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	8	8	16	0.02%	17.7%	YAPSGFYIASGDVSGK	99.7%	102	25	97.9	2	0	0	1618.77	66	81
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	8	8	16	0.02%	17.7%	YEYQPFAGK	96.1%	29.6	25	24.1	2	0	0	1102.52	96	104
WD repeat-containing protein 5	WDR5	WDR5_HUMAN	36.6	100.0%	4	4	7	0.01%	14.7%	FTLAGHTK	98.7%	34.5	25	19.5	2	0	0	874.48	39	46
WD repeat-containing protein 5	WDR5	WDR5_HUMAN	36.6	100.0%	4	4	7	0.01%	14.7%	IWDTASGQCLK	97.6%	31.6	25	28.9	1	0	0	1278.61	197	207
WD repeat-containing protein 5	WDR5	WDR5_HUMAN	36.6	100.0%	4	4	7	0.01%	14.7%	TLIDDDNPPVSFVK	99.7%	50.4	25	48.5	2	0	0	1559.80	208	221

WD repeat-containing protein 5	WDR5	WDR5_HUMAN	36.6	100.0%	4	4	7	0.01%	14.7%	TLPAHSDPVSAVHFNR	99.7%	36.8	25	30.6	0	2	0	1747.89	166	181
WD repeat-containing protein 6	WDR6	WDR6_HUMAN	121.7	100.0%	3	3	5	0.00%	4.3%	ATSELILLPVTGLECVGDR	99.7%	60	25	60	2	0	0	2043.08	12	30
WD repeat-containing protein 6	WDR6	WDR6_HUMAN	121.7	100.0%	3	3	5	0.00%	4.3%	GLGVSALCFK	98.1%	32.6	25	26.2	1	0	0	1051.56	334	343
WD repeat-containing protein 6	WDR6	WDR6_HUMAN	121.7	100.0%	3	3	5	0.00%	4.3%	VVPINTPTAAVDQTLFPGK	99.7%	52	25	52	2	0	0	1968.08	419	437
WD repeat-containing protein 82	WDR82	WDR82_HUMAN	35.1	100.0%	6	7	15	0.01%	26.8%	GVVMHTFGGYANSK	98.8%	28	25	27.5	0	1	0	1467.70	226	239
WD repeat-containing protein 82	WDR82	WDR82_HUMAN	35.1	100.0%	6	7	15	0.01%	26.8%	HTGPITCLQFNPK	95.9%	29.4	25	27.3	1	0	0	1512.76	281	293
WD repeat-containing protein 82	WDR82	WDR82_HUMAN	35.1	100.0%	6	7	15	0.01%	26.8%	IHVWNGESGIK	97.2%	31	25	25.7	1	0	0	1239.65	263	273
WD repeat-containing protein 82	WDR82	WDR82_HUMAN	35.1	100.0%	6	7	15	0.01%	26.8%	LILISTNGSFIR	99.7%	78.3	25	70.2	2	0	0	1333.78	208	219
WD repeat-containing protein 82	WDR82	WDR82_HUMAN	35.1	100.0%	6	7	15	0.01%	26.8%	VVALSMSPVDDTFISGSLDK	99.7%	111	25	108	7	0	0	2097.04	110	129
WD repeat-containing protein 82	WDR82	WDR82_HUMAN	35.1	100.0%	6	7	15	0.01%	26.8%	YTHAANTVVYSSNK	99.7%	82.4	25	82.2	3	0	0	1554.75	71	84
WD40 repeat-containing protein SMU1	SMU1	SMU1_HUMAN	57.5	99.8%	2	2	3	0.00%	3.5%	IQSGQCLR	97.5%	31.5	25	15.7	1	0	0	961.49	293	300
WD40 repeat-containing protein SMU1	SMU1	SMU1_HUMAN	57.5	99.8%	2	2	3	0.00%	3.5%	NPEHFVVCNR	99.2%	36.7	25	36.7	2	0	0	1271.59	409	418
WW domain-binding protein 11	WBP11	WBP11_HUMAN	70.0	99.8%	2	2	3	0.00%	3.1%	AQLSQYFDAVK	99.7%	73.7	25	70	2	0	0	1269.65	119	129
WW domain-binding protein 11	WBP11	WBP11_HUMAN	70.0	99.8%	2	2	3	0.00%	3.1%	TSAYGPPTR	97.2%	30.9	25	26	1	0	0	949.47	170	178
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	20	45	0.04%	22.5%	AFREEAIK	99.7%	41.8	25	12.9	2	0	0	963.53	641	648
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	20	45	0.04%	22.5%	ANPQVGVAFPHIK	96.8%	30.4	25	27.8	1	0	0	1377.76	401	413
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	20	45	0.04%	22.5%	CFSVLGFCK	99.7%	57.2	25	53.1	2	0	0	1117.52	339	347
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	20	45	0.04%	22.5%	EDGSGDRGDGPFR	99.4%	30.9	25	30.9	1	2	0	1364.58	172	184
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	20	45	0.04%	22.5%	EEASGSSVTAEEAK	99.7%	121	25	121	4	0	0	1394.63	689	702
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	20	45	0.04%	22.5%	EEASGSSVTAEEAKK	99.7%	87	25	73.6	4	0	0	1522.72	689	703
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	20	45	0.04%	22.5%	FFMGNQVLK	98.7%	34.4	25	23.8	3	0	0	1099.56	355	363
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	20	45	0.04%	22.5%	HIEIFTDLSSR	99.7%	55.3	25	46.1	2	0	0	1317.68	131	141
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	20	45	0.04%	22.5%	LFQCLLHR	99.7%	44.6	25	31.4	3	0	0	1086.59	490	497
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	20	45	0.04%	22.5%	LGGHGPSFPLK	99.3%	37.2	25	19.6	2	0	0	1109.61	185	195
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	20	45	0.04%	22.5%	LTIGSNLSIR	99.7%	61.2	25	48.5	2	0	0	1073.63	251	260
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	20	45	0.04%	22.5%	QYMFSSLK	99.7%	42.8	25	33.2	2	0	0	1003.49	432	439
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	20	45	0.04%	22.5%	SQLDIIIHSLK	99.7%	63	25	54.5	2	0	0	1266.74	145	155
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	20	45	0.04%	22.5%	TDTLEDLFPTTK	99.7%	88.5	25	79.9	2	0	0	1380.69	470	481
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	20	45	0.04%	22.5%	TLFPLIEAK	99.4%	38.4	25	27.8	2	0	0	1031.61	535	543
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	20	45	0.04%	22.5%	VITMFVQR	99.7%	62.8	25	45.7	4	0	0	993.56	37	44
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	20	45	0.04%	22.5%	YGSDIVPFSK	99.7%	63.2	25	53.7	5	0	0	1112.56	316	325
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	19	38	0.04%	28.4%	DIISIAEDEDLR	99.7%	54.2	25	48.5	1	0	0	1388.69	219	230
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	19	38	0.04%	28.4%	DSLIFLVDASK	99.7%	87.8	25	80.6	8	0	0	1207.66	36	46
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	19	38	0.04%	28.4%	DTGIFLDLMHLK	99.7%	51.8	25	49.6	4	0	0	1402.74	195	206
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	19	38	0.04%	28.4%	ELVYPPDYNPEGK	95.2%	28.8	25	28.2	1	0	0	1520.73	527	539
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	19	38	0.04%	28.4%	EVAALCR	98.2%	32.9	25	17.6	1	0	0	818.42	393	399
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	19	38	0.04%	28.4%	ILELDQFK	99.7%	44.1	25	13.1	2	0	0	1005.56	116	123
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	19	38	0.04%	28.4%	IMATPEQVGK	99.7%	58.2	25	42.6	4	0	0	1089.56	452	461
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	19	38	0.04%	28.4%	IMLFTNEDNPHGNDSAK	99.7%	97.2	25	97.2	2	3	0	1902.87	166	182
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	19	38	0.04%	28.4%	LGSLVDEFK	99.7%	52.9	25	37.2	2	0	0	1007.54	518	526
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	19	38	0.04%	28.4%	NIPPYFVALVPQEEELDDQK	95.8%	29.2	25	29.2	1	0	0	2344.17	405	424
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	19	38	0.04%	28.4%	NIYVLQELDNPGAK	99.7%	111	25	102	2	0	0	1573.82	101	114
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	19	38	0.04%	28.4%	SDSFENPVLQQHFR	99.7%	64.2	25	64.2	2	2	0	1703.81	475	488
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	19	38	0.04%	28.4%	TFNTSTGGLLLPSDTKR	99.7%	81.3	25	81.3	2	0	0	1807.96	302	318
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	14	19	38	0.04%	28.4%	VEYSEEELK	95.1%	28.7	25	22.1	1	0	0	1125.53	557	565
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	5	5	11	0.01%	27.7%	AGEAPTENPAPPTQQSSAE	99.6%	40.2	25	40.2	1	0	0	1881.85	354	372
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	5	5	11	0.01%	27.7%	DGVPEGAQLQGPVHR	99.7%	65.3	25	60.1	3	0	0	1559.79	269	283
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	5	5	11	0.01%	27.7%	EDVFVHQTAIK	99.7%	54.7	25	43.1	3	0	0	1286.67	114	124
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	5	5	11	0.01%	27.7%	GAEAANVTGPDGVPVEGSR	99.7%	84.7	25	83.6	2	0	0	1782.86	151	169
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	5	5	11	0.01%	27.7%	IQAGEIGEMK	99.7%	49.9	25	40.1	3	0	0	1091.54	259	268
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	5	5	11	0.01%	27.7%	IQAGEIGEMKDGVPEGAQLQGPVHR	99.7%	53.4	25	53.4	0	2	0	2632.32	259	283

Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	5	5	11	0.01%	27.7%	NDTKEDVFVHQTAIK	99.7%	92.1	25	88	4	5	0	1744.89	110	124
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	5	5	11	0.01%	27.7%	NGYGFINR	99.7%	57.6	25	52.4	5	0	0	940.46	102	109
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	5	5	11	0.01%	27.7%	SVGDGETVEFDVVEGEK	99.7%	114	25	108	7	0	0	1795.82	134	150
YTH domain-containing family protein 2	YTHDF2	YTHD2_HUMAN	62.3	100.0%	4	4	9	0.01%	7.4%	DTQEVPLEK	97.3%	31.1	25	23.2	1	0	0	1058.54	528	536
YTH domain-containing family protein 2	YTHDF2	YTHD2_HUMAN	62.3	100.0%	4	4	9	0.01%	7.4%	LENNENKPVTNSR	99.7%	35.9	25	33.2	0	2	0	1514.76	515	527
YTH domain-containing family protein 2	YTHDF2	YTHD2_HUMAN	62.3	100.0%	4	4	9	0.01%	7.4%	LGSTEVASNVPK	99.7%	81.2	25	71.5	4	0	0	1201.64	194	205
YTH domain-containing family protein 2	YTHDF2	YTHD2_HUMAN	62.3	100.0%	4	4	9	0.01%	7.4%	SYSEDDIHR	99.7%	51.6	25	51.6	2	0	0	1121.49	417	425
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	12	14	26	0.02%	19.3%	DQKEEGNDYDTR	99.7%	42.8	25	42.8	2	0	0	1469.61	256	267
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	12	14	26	0.02%	19.3%	DVFLNGSYNDYVR	99.7%	54.7	25	54.7	1	0	0	1561.73	582	594
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	12	14	26	0.02%	19.3%	GISPIVFDR	99.5%	39.4	25	29.7	2	0	0	1003.56	306	314
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	12	14	26	0.02%	19.3%	GVWSTLPVNEK	99.7%	70.2	25	66.9	2	0	0	1229.65	375	385
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	12	14	26	0.02%	19.3%	IGLEVDR	99.7%	48.8	25	24.4	1	0	0	801.45	155	161
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	12	14	26	0.02%	19.3%	QLVSKPLSSSVSNNKR	99.7%	44.4	25	44.4	0	2	0	1743.97	68	83
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	12	14	26	0.02%	19.3%	SATEYKNEEYQR	99.7%	62.9	25	54.1	2	1	0	1517.69	91	102
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	12	14	26	0.02%	19.3%	SEASDSGSESVSFTDGSVR	99.7%	144	25	142	1	0	0	1903.82	268	286
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	12	14	26	0.02%	19.3%	SGSSASESYAGSEK	99.7%	87.8	25	84.3	3	0	0	1346.57	315	328
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	12	14	26	0.02%	19.3%	SNNHENVSLAK	99.7%	59.1	25	54.7	3	2	0	1212.60	362	372
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	12	14	26	0.02%	19.3%	SVILIFSVR	99.7%	63.6	25	58.3	1	0	0	1033.64	396	404
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	12	14	26	0.02%	19.3%	YVLQDAR	99.7%	44.3	25	28.5	3	0	0	864.46	350	356
Zinc finger CCCH domain-containing protein 11A	ZC3H11A	ZC11A_HUMAN	89.1	100.0%	4	4	5	0.00%	6.1%	AAVAVVPLVSEDK	96.7%	30.3	25	15.6	2	0	0	1297.74	700	712
Zinc finger CCCH domain-containing protein 11A	ZC3H11A	ZC11A_HUMAN	89.1	100.0%	4	4	5	0.00%	6.1%	ASQLSVQQNK	99.6%	40.4	25	30.9	1	0	0	1102.59	115	124
Zinc finger CCCH domain-containing protein 11A	ZC3H11A	ZC11A_HUMAN	89.1	100.0%	4	4	5	0.00%	6.1%	KVEAPETNIDK	99.3%	37.6	25	16.9	1	0	0	1243.65	310	320
Zinc finger CCCH domain-containing protein 11A	ZC3H11A	ZC11A_HUMAN	89.1	100.0%	4	4	5	0.00%	6.1%	NLQEGNEVDSQSSIR	99.7%	99	25	99	1	0	0	1675.79	522	536
Zinc finger CCCH domain-containing protein 18	ZC3H18	ZCH18_HUMAN	106.4	100.0%	4	4	4	0.00%	5.3%	GGQYENFR	96.0%	29.4	25	22.9	1	0	0	970.44	382	389
Zinc finger CCCH domain-containing protein 18	ZC3H18	ZCH18_HUMAN	106.4	100.0%	4	4	4	0.00%	5.3%	KPAPPPAPPQATK	96.0%	29.5	25	29.4	1	0	0	1299.74	639	651
Zinc finger CCCH domain-containing protein 18	ZC3H18	ZCH18_HUMAN	106.4	100.0%	4	4	4	0.00%	5.3%	SSSYSSYSSR	99.7%	56.6	25	45.4	1	0	0	1110.47	576	585
Zinc finger CCCH domain-containing protein 18	ZC3H18	ZCH18_HUMAN	106.4	100.0%	4	4	4	0.00%	5.3%	TLSGSGSGSGSSYSGSSSR	99.7%	98	25	98	1	0	0	1707.74	683	701
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	100.0%	9	11	20	0.02%	26.0%	AVHNSVAAQLTGVAGH	99.7%	87.9	25	87.9	1	2	0	1531.80	389	404
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	100.0%	9	11	20	0.02%	26.0%	DFVVGALILR	99.7%	70.5	25	65.7	2	0	0	1102.66	183	192
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	100.0%	9	11	20	0.02%	26.0%	DPAGEAVDPR	99.7%	41.7	25	37.5	2	0	0	1026.49	103	112
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	100.0%	9	11	20	0.02%	26.0%	EFDVSFR	98.8%	34.8	25	24.8	1	0	0	899.43	212	218
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	100.0%	9	11	20	0.02%	26.0%	FGIWTGEYK	99.7%	42.7	25	42.7	2	0	0	1100.54	291	299
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	100.0%	9	11	20	0.02%	26.0%	ICFQGDEGACPTR	99.7%	81.3	25	74.9	2	0	0	1510.64	170	182
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	100.0%	9	11	20	0.02%	26.0%	NETVDVEDIVTWLK	99.7%	82.6	25	70.6	2	0	0	1660.84	262	275
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	100.0%	9	11	20	0.02%	26.0%	SIGMDPSDIYAVIQIPGSR	99.7%	96.6	25	92.1	4	0	0	2035.02	193	211
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	100.0%	9	11	20	0.02%	26.0%	TLFILFR	98.9%	35.3	25	35.3	2	0	0	909.56	255	261
Zinc finger CCHC domain-containing protein 9	ZCCHC9	ZCHC9_HUMAN	30.5	99.8%	2	2	3	0.00%	8.9%	GSFEGTSQNLPK	99.7%	61.7	25	45.9	2	0	0	1264.62	27	38
Zinc finger CCHC domain-containing protein 9	ZCCHC9	ZCHC9_HUMAN	30.5	99.8%	2	2	3	0.00%	8.9%	VDPALGEFPFAK	99.2%	36.7	25	28.8	1	0	0	1290.67	174	185
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	9	14	27	0.03%	35.0%	EEVEHMIQK	99.7%	51.2	25	42.3	3	0	0	1142.55	57	65
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	9	14	27	0.03%	35.0%	IVLNSIEQYQAHVSGFK	99.7%	78.6	25	78.6	2	2	0	1933.02	246	262
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	9	14	27	0.03%	35.0%	LADPAVTDFPAGK	99.7%	81.3	25	71.7	2	0	0	1301.67	225	237
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	9	14	27	0.03%	35.0%	LWEAVSGAQPVGR	99.7%	70.1	25	58.7	2	0	0	1369.72	44	56
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	9	14	27	0.03%	35.0%	NQCLFTNTQCK	99.7%	65.1	25	61.2	2	0	0	1413.63	66	76
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	9	14	27	0.03%	35.0%	TVASSLGQIPMQR	99.7%	86.5	25	64.8	5	0	0	1387.74	270	282
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	9	14	27	0.03%	35.0%	VCCALLISESQK	99.7%	87.6	25	79.4	2	0	0	1407.70	77	88
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	9	14	27	0.03%	35.0%	YLAIHGMETLK	99.7%	48.2	25	40.5	3	2	0	1291.67	104	114
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	9	14	27	0.03%	35.0%	YLAIHGMETLKGETK	98.3%	26.8	25	26.2	0	2	0	1690.88	104	118
Zinc finger protein 622	ZNF622	ZN622_HUMAN	54.3	99.8%	2	2	3	0.00%	4.4%	GSATYCTVCSK	95.7%	29.2	25	29.2	1	0	0	1233.52	64	74
Zinc finger protein 622	ZNF622	ZN622_HUMAN	54.3	99.8%	2	2	3	0.00%	4.4%	NVVAVGTGGR	99.7%	60.8	25	50.6	2	0	0	929.52	157	166
Zinc finger protein 768	ZNF768	ZN768_HUMAN	60.2	100.0%	4	4	7	0.01%	8.2%	AFADSSYLLR	99.7%	65	25	49.5	2	0	0	1142.58	325	334
Zinc finger protein 768	ZNF768	ZN768_HUMAN	60.2	100.0%	4	4	7	0.01%	8.2%	AFSQSSDLIR	99.4%	38.3	25	20.8	2	0	0	1123.57	521	530

Zinc finger protein 768	ZNF768	ZN768_HUMAN	60.2	100.0%	4	4	7	0.01%	8.2%	FGQSSVLAIHAR	99.7%	67.9	25	64.9	2	0	0	1285.70	438	449
Zinc finger protein 768	ZNF768	ZN768_HUMAN	60.2	100.0%	4	4	7	0.01%	8.2%	TQSPEFEAQSSK	97.4%	31.3	25	24.1	1	0	0	1338.62	158	169
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	16	16	38	0.04%	18.2%	AGYSQGATQYTQAQQTR	99.7%	110	25	110	1	0	0	1858.87	192	208
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	16	16	38	0.04%	18.2%	AISSASSPQSPGDALR	99.7%	78.6	25	68.9	4	0	0	1543.77	954	969
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	16	16	38	0.04%	18.2%	AISSASSPQSPGDALRR	97.9%	25.9	25	25.8	0	1	0	1699.87	954	970
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	16	16	38	0.04%	18.2%	ANGLQSCVIIIR	99.7%	48.1	25	40.5	2	0	0	1343.75	916	927
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	16	16	38	0.04%	18.2%	EDITSSAQFALR	99.7%	90.2	25	85.4	5	0	0	1337.67	1008	1019
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	16	16	38	0.04%	18.2%	GLTTTGNSSLNSTSNTK	99.7%	130	25	130	4	0	0	1682.82	468	484
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	16	16	38	0.04%	18.2%	HATIYPTEEELQAVQK	95.1%	22.7	25	15.3	0	1	0	1856.94	731	746
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	16	16	38	0.04%	18.2%	INFVGGNK	96.4%	30	25	18.1	2	0	0	848.46	502	509
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	16	16	38	0.04%	18.2%	IVSITER	95.7%	29.2	25	16.6	1	0	0	817.48	747	753
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	16	16	38	0.04%	18.2%	KVNPDLQVEVKPSIR	99.7%	57.2	25	57.2	0	2	0	1721.99	613	627
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	16	16	38	0.04%	18.2%	LCECSFNDPNAK	97.0%	30.7	25	27.3	1	0	0	1454.60	586	597
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	16	16	38	0.04%	18.2%	LVSDSLSEHEK	99.7%	62.8	25	55.3	6	0	0	1243.62	757	767
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	16	16	38	0.04%	18.2%	MQVTITLTSPIIR	99.7%	51.8	25	44.9	1	0	0	1488.85	861	873
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	16	16	38	0.04%	18.2%	NVNLVLLCSEKPSK	99.7%	56.1	25	46.8	1	0	0	1600.87	805	818
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	16	16	38	0.04%	18.2%	STAPAVAYDSK	99.7%	73.3	25	60.8	2	0	0	1109.55	148	158
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	16	16	38	0.04%	18.2%	STPVTSAVQIPEVK	99.7%	84.9	25	77.8	4	0	0	1455.81	528	541

Table S-1-5. List of proteins identified in immunoprecipitation product of H7N9 NS1 (Replicate 2)

Protein name	Gene name	Accession number	M.W. (kDa)	Protein probability	No. of unique peptide	No. of unique spectra	No. of total spectra	Percentage of total spectra	Sequence coverage	Peptide sequence	Best peptide probability	Mascot			No. of spectra			Calculated +1H peptide mass (AMU)	Peptide index	
												ion score	identity score	delta ion score	+2H	+3H	+4H		start	stop
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	PDK1	PDK1_HUMAN	49.2	100.0%	4	4	5	0.00%	11.0%	AIYDFTDTVIR	99.7%	53.2	25	51	1	0	0	1313.67	134	144
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	PDK1	PDK1_HUMAN	49.2	100.0%	4	4	5	0.00%	11.0%	AVPLAGFGYGLPISR	99.7%	54.3	25	54.3	2	0	0	1517.85	349	363
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	PDK1	PDK1_HUMAN	49.2	100.0%	4	4	5	0.00%	11.0%	EISLLPDNLLR	97.5%	31	25	29.8	1	0	0	1282.74	93	103
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	PDK1	PDK1_HUMAN	49.2	100.0%	4	4	5	0.00%	11.0%	LYAQYFQGDLK	99.7%	42.5	25	36.3	1	0	0	1345.68	364	374
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 3, mitochondrial	PDK3	PDK3_HUMAN	46.9	99.8%	2	2	3	0.00%	7.9%	AAPLAGFGYGLPISR	99.4%	37.4	25	29.5	2	0	0	1489.82	318	332
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 3, mitochondrial	PDK3	PDK3_HUMAN	46.9	99.8%	2	2	3	0.00%	7.9%	SPEDPQVLDNFLQVLIK	99.1%	35.4	25	35.4	1	0	0	1955.05	98	114
10 kDa heat shock protein, mitochondrial	HSPE1	CH10_HUMAN	10.9	100.0%	3	3	6	0.01%	25.5%	GGEIQPVSVK	99.7%	52.6	25	40.2	2	0	0	1013.56	57	66
10 kDa heat shock protein, mitochondrial	HSPE1	CH10_HUMAN	10.9	100.0%	3	3	6	0.01%	25.5%	GKGGEIQPVSVK	98.3%	32.7	25	23.8	2	0	0	1198.68	55	66
10 kDa heat shock protein, mitochondrial	HSPE1	CH10_HUMAN	10.9	100.0%	3	3	6	0.01%	25.5%	VLQATVVAVGSGSK	99.7%	126	25	120	2	0	0	1315.76	41	54
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	AFIPAIDSFGFETDLR	99.7%	94.5	25	93.9	4	0	0	1798.90	873	888
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	DSIVQGFQWGTR	99.7%	86.1	25	79.7	2	0	0	1393.69	764	775
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	EGPLCDELIR	99.7%	45.9	25	42.1	2	0	0	1201.59	776	785
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	FFDDPMLLELAK	99.7%	74.1	25	68.5	6	0	0	1438.73	952	963
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	GGGQIIPTAR	99.5%	38.6	25	28.7	6	0	0	969.55	804	813
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	GHVTQDAPIPGSPLYTIK	99.7%	103	25	103	2	2	0	1894.01	855	872
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	GLSEDVSISK	99.7%	64.6	25	53.8	3	0	0	1034.54	942	951
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	GNEEAQIFRPLK	99.7%	66.7	25	56	4	0	0	1401.75	570	581
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	IAVEPVNPSELPK	99.7%	62.6	25	57.9	3	0	0	1392.77	590	602
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	ILAQVVGDVDTSLPR	99.7%	85.8	25	75.1	2	0	0	1582.88	380	394
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	ILDAVVAQEPLHR	99.7%	58.9	25	55.9	3	4	0	1460.82	791	803
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	ITMIAEPLEK	99.7%	55.4	25	39.2	4	0	0	1160.62	685	694
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	IYADTFGDINYQEFAK	99.7%	125	25	124	5	0	0	1894.89	326	341
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	KGLSEDVSISK	99.7%	65.1	25	56.9	2	0	0	1162.63	941	951
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	LGEFFQTK	99.7%	49.6	25	43.9	4	0	0	969.50	714	721
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	MYSTDDGVQFHAFGR	97.9%	26.1	25	26.1	0	2	0	1746.75	481	495
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	SFVEFILEPLYK	99.7%	78.6	25	74.7	4	0	0	1484.80	368	379
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	SIVIRPLEPQPAPHLAR	95.7%	23.5	25	23.5	0	1	0	1894.10	915	931
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	STPVTVVLPDTK	99.7%	70.6	25	63.7	6	0	0	1256.71	183	194
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	TLDELGIHLTK	99.7%	65.8	25	65.8	3	0	0	1239.69	395	405
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	VADPVVTFCETVVETSSLK	99.7%	97.7	25	89.4	4	0	0	2081.05	655	673
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	VLGENYTLEDEEDSQICTVGR	99.7%	116	25	116	2	0	0	2427.10	509	529
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	VLSGTIHAGQPVK	99.7%	99.9	25	94.7	5	0	0	1306.75	496	508
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	VPAGNWVLIEGVDQPIVK	99.7%	79.2	25	79.2	2	2	0	1934.07	544	561
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	VVYSAFLMATPR	98.0%	32	25	22.4	1	0	0	1354.72	815	826
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	YDQDLCYTDILFTEQER	99.6%	39	25	39	1	0	0	2208.98	161	177
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	27	32	95	0.09%	36.2%	YDWDLLAAR	99.7%	66.8	25	59.4	4	0	0	1122.56	722	730
14-3-3 protein beta/alpha	YWHAB	1433B_HUMAN	28.1	99.8%	2	3	5	0.00%	21.1%	AVTEQGHELSNEER	99.7%	65.4	25	61.2	2	1	0	1598.74	30	43
14-3-3 protein beta/alpha	YWHAB	1433B_HUMAN	28.1	99.8%	2	3	5	0.00%	21.1%	DSTLIMQLLR	99.2%	36	25	20	1	0	0	1205.66	215	224
14-3-3 protein beta/alpha	YWHAB	1433B_HUMAN	28.1	99.8%	2	3	5	0.00%	21.1%	EMQPTHPIR	99.7%	57.6	25	47.4	2	0	0	1108.56	161	169
14-3-3 protein beta/alpha	YWHAB	1433B_HUMAN	28.1	99.8%	2	3	5	0.00%	21.1%	NLLSVAYK	98.2%	32.4	25	13.8	2	0	0	907.52	44	51
14-3-3 protein beta/alpha	YWHAB	1433B_HUMAN	28.1	99.8%	2	3	5	0.00%	21.1%	YLSEVASGDNK	99.7%	59	25	49.3	2	0	0	1182.56	130	140
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	7	7	10	0.01%	35.3%	DSTLIMQLLR	99.2%	36	25	20	1	0	0	1205.66	216	225
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	7	7	10	0.01%	35.3%	EAAENSLVAYK	99.7%	52.3	25	49.4	2	0	0	1194.60	143	153
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	7	7	10	0.01%	35.3%	HLIPAANTGESK	97.7%	31.4	25	24.4	1	0	0	1237.65	107	118
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	7	7	10	0.01%	35.3%	IISSIEQKEENK	99.2%	36.2	25	28.4	1	0	0	1417.75	62	73

14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	7	7	10	0.01%	35.3%	LICCDILDVLDK	99.7%	77.9	25	71.7	2	0	0	1476.74	95	106
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	7	7	10	0.01%	35.3%	NLLSVAYK	98.2%	32.4	25	13.8	2	0	0	907.52	43	50
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	7	7	10	0.01%	35.3%	VAGMDVELTVEER	99.7%	80.8	25	66.9	2	0	0	1463.70	30	42
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	7	7	10	0.01%	35.3%	YLAEFATGNDR	99.7%	42.9	25	42.9	1	0	0	1256.59	131	141
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	7	7	10	0.01%	35.3%	YLAEFATGNDRK	99.6%	39.7	25	29.5	1	0	0	1384.69	131	142
14-3-3 protein gamma	YWHAG	1433G_HUMAN	28.3	100.0%	3	3	5	0.00%	21.1%	AYSEAHEISK	99.7%	49.4	25	44.5	2	0	0	1134.54	153	162
14-3-3 protein gamma	YWHAG	1433G_HUMAN	28.3	100.0%	3	3	5	0.00%	21.1%	DSTLIMQLLR	99.2%	36	25	20	1	0	0	1205.66	218	227
14-3-3 protein gamma	YWHAG	1433G_HUMAN	28.3	100.0%	3	3	5	0.00%	21.1%	NLLSVAYK	98.2%	32.4	25	13.8	2	0	0	907.52	43	50
14-3-3 protein gamma	YWHAG	1433G_HUMAN	28.3	100.0%	3	3	5	0.00%	21.1%	NVTELNEPLSNEER	99.7%	89.3	25	89.3	2	0	0	1643.79	29	42
14-3-3 protein gamma	YWHAG	1433G_HUMAN	28.3	100.0%	3	3	5	0.00%	21.1%	YLAEVATGEK	99.2%	36.2	25	31.1	1	0	0	1080.56	133	142
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	99.9%	2	2	4	0.00%	21.6%	AVTEQGAELSNEER	99.7%	99.1	25	91	2	0	0	1532.72	28	41
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	99.9%	2	2	4	0.00%	21.6%	DSTLIMQLLR	99.2%	36	25	20	1	0	0	1205.66	213	222
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	99.9%	2	2	4	0.00%	21.6%	EMQPTHPIR	99.7%	57.6	25	47.4	2	0	0	1108.56	159	167
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	99.9%	2	2	4	0.00%	21.6%	NLLSVAYK	98.2%	32.4	25	13.8	2	0	0	907.52	42	49
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	99.9%	2	2	4	0.00%	21.6%	YLAEVACGDDRK	99.7%	59	25	54.7	2	0	0	1396.65	128	139
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	7	7	13	0.01%	33.9%	DICNDVLSLLEK	99.7%	66	25	56.7	2	0	0	1418.72	92	103
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	7	7	13	0.01%	33.9%	DSTLIMQLLR	99.2%	36	25	20	1	0	0	1205.66	213	222
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	7	7	13	0.01%	33.9%	EMQPTHPIR	99.7%	57.6	25	47.4	2	0	0	1108.56	159	167
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	7	7	13	0.01%	33.9%	GIVDQSQQAYQEAFEISK	99.7%	108	25	108	2	0	0	2040.99	140	157
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	7	7	13	0.01%	33.9%	NLLSVAYK	98.2%	32.4	25	13.8	2	0	0	907.52	42	49
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	7	7	13	0.01%	33.9%	SVTEQGAELSNEER	99.7%	98.9	25	94.9	2	0	0	1548.71	28	41
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	7	7	13	0.01%	33.9%	YLAEVAAGDDKK	99.7%	58.5	25	45.8	2	0	0	1279.65	128	139
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	6	6	7	0.01%	15.7%	AGQVFLEELGNHK	99.7%	91.8	25	88.7	1	0	0	1441.74	205	217
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	6	6	7	0.01%	15.7%	GEEVGELSR	99.7%	40.5	25	14.8	1	0	0	975.47	361	369
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	6	6	7	0.01%	15.7%	ILVLDDTNHER	99.1%	35.6	25	31.3	1	0	0	1324.69	118	128
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	6	6	7	0.01%	15.7%	LDEDLAAYCR	99.7%	67.7	25	55.3	1	0	0	1225.55	103	112
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	6	6	7	0.01%	15.7%	NQWQLSADDLKK	99.6%	39	25	31.6	1	0	0	1445.74	165	176
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	100.0%	6	6	7	0.01%	15.7%	RPPGVLHCTTK	99.7%	41.5	25	26.7	0	2	0	1265.68	245	255
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	13	15	29	0.03%	38.6%	ADHDFVVQEDFMK	99.7%	49.7	25	49.7	1	0	0	1596.70	357	369
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	13	15	29	0.03%	38.6%	ALQSVGQIVGEVLK	99.7%	90.2	25	90.2	4	0	0	1440.84	49	62
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	13	15	29	0.03%	38.6%	AVASQLDCNFLK	99.7%	78.7	25	68.7	2	0	0	1365.68	186	197
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	13	15	29	0.03%	38.6%	EVIELPLTNPELFQR	99.7%	61.3	25	58.5	2	0	0	1797.97	147	161
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	13	15	29	0.03%	38.6%	FSEGTSADREIQR	96.3%	29.5	25	24.2	1	0	0	1495.71	243	255
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	13	15	29	0.03%	38.6%	GCLLYGPPGTGK	99.7%	51.8	25	51.8	1	0	0	1219.61	169	180
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	13	15	29	0.03%	38.6%	HGEIDYEAIVK	99.7%	68.6	25	60.5	2	0	0	1273.64	323	333
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	13	15	29	0.03%	38.6%	IHAGPITK	97.1%	30.4	25	27.4	2	0	0	836.50	315	322
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	13	15	29	0.03%	38.6%	IHIDLPNEQAR	97.3%	30.7	25	30.7	1	0	0	1305.69	299	309
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	13	15	29	0.03%	38.6%	KIHIDLPNEQAR	99.7%	43.9	25	43.1	0	2	0	1433.79	298	309
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	13	15	29	0.03%	38.6%	NVCTEAGMFAIR	99.7%	81.2	25	73.3	4	0	0	1384.63	345	356
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	13	15	29	0.03%	38.6%	VALDMTTLTIMR	99.7%	93	25	88.2	5	0	0	1364.73	98	109
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	13	15	29	0.03%	38.6%	VVSSSIVDKYIGESAR	99.7%	48.8	25	48	0	2	0	1709.91	198	213
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	19	39	0.04%	45.7%	AICTEAGLMALR	99.7%	57.8	25	48.3	5	0	0	1305.67	397	408
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	19	39	0.04%	45.7%	APQETYADIGGLDNQIQEIK	99.7%	88.2	25	80.9	2	1	0	2203.09	179	198
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	19	39	0.04%	45.7%	AVANQTSATFLR	99.7%	79.7	25	68.6	5	0	0	1278.68	238	249
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	19	39	0.04%	45.7%	DDLSGADIK	99.7%	40.8	25	26.4	1	0	0	933.45	388	396
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	19	39	0.04%	45.7%	GVILYGPPGTGK	99.7%	58.9	25	0	5	0	0	1158.65	221	232
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	19	39	0.04%	45.7%	IETLDPALIRPGR	98.6%	27.9	25	17.5	0	3	0	1450.84	334	346
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	19	39	0.04%	45.7%	IFQIHTSR	99.7%	42	25	26.1	2	0	0	1001.55	364	371
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	19	39	0.04%	45.7%	KQEGTPEGLYL	99.7%	62.5	25	47.6	2	0	0	1234.63	430	440
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	19	39	0.04%	45.7%	KYEPPVPTR	98.0%	32	25	16	3	0	0	1086.59	24	32
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	19	39	0.04%	45.7%	LPLVTPHTQCR	99.7%	58	25	49.9	2	0	0	1321.70	49	59

26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	19	39	0.04%	45.7%	MTLADDVTLDDLIMAK	99.7%	67.1	25	36.6	3	0	0	1780.87	372	387
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	19	39	0.04%	45.7%	NQEQMKPLEEKQEEER	99.7%	34.1	25	29.5	0	2	0	2044.96	81	96
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	19	39	0.04%	45.7%	TMLELLNQLDGFDSR	99.7%	88.6	25	88.1	4	0	0	1751.86	308	322
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	19	39	0.04%	45.7%	VAEEHAPSIVFIDEIDAIGTK	99.7%	79.6	25	79.6	0	2	0	2254.16	273	293
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	19	39	0.04%	45.7%	VIMATNR	95.0%	28.3	25	21.4	2	0	0	804.44	327	333
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	14	19	39	0.04%	45.7%	VVGSELIQK	99.7%	84.7	25	70.7	2	0	0	972.57	250	258
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	18	24	49	0.05%	50.1%	AMEVDERPTEQYSDIGGLDK	99.7%	63.2	25	63.2	0	3	0	2269.03	174	193
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	18	24	49	0.05%	50.1%	APSIIFIDELDAIGTK	99.7%	57.1	25	52.5	2	0	0	1702.93	279	294
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	18	24	49	0.05%	50.1%	AVCVEAGMIALR	99.7%	88.1	25	79.3	3	0	0	1305.67	398	409
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	18	24	49	0.05%	50.1%	CTDDFNGAQCK	98.9%	34.6	25	34.6	1	0	0	1315.50	387	397
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	18	24	49	0.05%	50.1%	DSYLILETLPTEYDSR	99.7%	90.4	25	84.7	2	0	0	1914.93	156	171
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	18	24	49	0.05%	50.1%	EKFENLGIQPPK	98.9%	34.7	25	28.1	1	0	0	1399.76	210	221
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	18	24	49	0.05%	50.1%	FENLGIQPPK	99.7%	48.2	25	28.5	1	0	0	1142.62	212	221
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	18	24	49	0.05%	50.1%	GVLMYGPPGTGK	99.7%	69.9	25	63.5	4	0	0	1192.60	222	233
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	18	24	49	0.05%	50.1%	IMQIHSR	99.3%	36.8	25	21.4	2	0	0	884.48	365	371
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	18	24	49	0.05%	50.1%	KMNVSPDVNYEELAR	99.7%	81.1	25	74	0	4	0	1780.85	372	386
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	18	24	49	0.05%	50.1%	LAGPQLVQMFIGDGAK	99.7%	77.1	25	77.1	5	0	0	1644.88	251	266
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	18	24	49	0.05%	50.1%	LLDSEIK	96.9%	30.2	25	9.14	1	0	0	817.47	47	53
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	18	24	49	0.05%	50.1%	MSTEEIIQR	99.7%	63	25	33.3	4	0	0	1106.55	36	44
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	18	24	49	0.05%	50.1%	QIQELVEAIVLPMNHK	99.7%	41.9	25	41.9	0	1	0	1862.02	194	209
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	18	24	49	0.05%	50.1%	QTYFLPVIGLVDAEK	99.7%	84.2	25	73.6	6	0	0	1692.92	130	144
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	18	24	49	0.05%	50.1%	TMLELLNQLDGFQPNTQVK	99.7%	99.1	25	99.1	3	0	0	2189.13	309	327
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	18	24	49	0.05%	50.1%	VDILDPALLR	99.7%	62.9	25	49.8	4	0	0	1124.67	335	344
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	18	24	49	0.05%	50.1%	VIAATNRVDILDPALLR	99.7%	66	25	66	0	2	0	1850.09	328	344
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	19	33	0.03%	36.4%	ADTLDPALLRPGR	99.3%	36.8	25	36.8	1	0	0	1394.78	314	326
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	19	33	0.03%	36.4%	AVAHHTTAAFIR	99.7%	54.6	25	51.3	2	2	0	1294.70	218	229
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	19	33	0.03%	36.4%	EAVELPLTHFELYK	99.7%	68.9	25	62.2	2	0	0	1688.89	179	192
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	19	33	0.03%	36.4%	EFLHAQEEVKR	99.7%	48.3	25	28.5	2	1	0	1385.72	71	81
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	19	33	0.03%	36.4%	ELLKPNASVALHK	99.7%	59.5	25	58	0	2	0	1419.83	122	134
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	19	33	0.03%	36.4%	ENAPAIIFIDEIDAIATK	99.7%	66.7	25	66.7	2	2	0	1944.03	256	273
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	19	33	0.03%	36.4%	FDAQTGADREVQR	97.0%	30.3	25	27.6	1	0	0	1492.71	275	287
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	19	33	0.03%	36.4%	GVLMYGPPGCGK	99.7%	61.7	25	61.7	4	0	0	1251.59	201	212
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	19	33	0.03%	36.4%	ILLELLNQMDGFDQNVNVK	99.7%	87.9	25	87.9	4	1	0	2219.14	288	306
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	19	33	0.03%	36.4%	LIFSTITSK	98.9%	34.4	25	31.9	1	0	0	1009.59	343	351
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	19	33	0.03%	36.4%	RFDAQTGADR	99.3%	36.7	25	25.3	2	0	0	1136.54	274	283
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	19	33	0.03%	36.4%	RLIFSTITSK	97.5%	31.1	25	31.1	2	0	0	1165.69	342	351
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	19	33	0.03%	36.4%	VIMATNR	95.0%	28.3	25	21.4	2	0	0	804.44	307	313
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	13	19	33	0.03%	36.4%	VVGSEFVQK	99.7%	73.3	25	60.2	2	0	0	992.54	230	238
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	24	30	58	0.06%	57.7%	ALDEGDIALLK	99.7%	84	25	71.9	2	0	0	1157.64	24	34
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	24	30	58	0.06%	57.7%	ELFEMAR	98.2%	32.5	25	26.6	1	0	0	895.43	259	265
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	24	30	58	0.06%	57.7%	ESDTGLAPPALWDLAADK	99.0%	35.2	25	33.8	2	0	0	1869.92	67	84
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	24	30	58	0.06%	57.7%	FDDGAGGDNEVQR	99.7%	89	25	89	3	0	0	1379.58	285	297
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	24	30	58	0.06%	57.7%	FVNLGIEPPK	99.7%	53.5	25	34.1	4	0	0	1113.63	201	210
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	24	30	58	0.06%	57.7%	FVNLGIEPPKGVLLFGPPGTGK	98.9%	28.6	25	28.6	0	1	0	2237.27	201	222
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	24	30	58	0.06%	57.7%	FVVDLSDQVAPTDIEEGMR	99.7%	98.3	25	80	4	0	0	2121.02	121	139
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	24	30	58	0.06%	57.7%	GVLLFGPPGTGK	99.7%	48.7	25	40.7	2	0	0	1142.66	211	222
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	24	30	58	0.06%	57.7%	IATEKDFLEAVNK	99.7%	62.8	25	54.8	2	2	0	1477.79	403	415
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	24	30	58	0.06%	57.7%	IEFSLPDLEGR	99.7%	46	25	37.9	2	0	0	1275.66	341	351
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	24	30	58	0.06%	57.7%	IINADSEDPK	99.7%	63.4	25	48.3	2	0	0	1101.54	101	110
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	24	30	58	0.06%	57.7%	IINADSEDPKYIINVK	99.7%	86.6	25	86.6	2	1	0	1831.98	101	116
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	24	30	58	0.06%	57.7%	INELTGIK	99.7%	43.5	25	33.3	1	0	0	887.52	59	66

26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	24	30	58	0.06%	57.7%	KINELTGIK	99.7%	42.2	25	27.7	2	0	0	1015.61	58	66
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	24	30	58	0.06%	57.7%	LCPNSTGAEIR	99.7%	47.4	25	36.7	2	0	0	1217.59	376	386
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	24	30	58	0.06%	57.7%	LREVVETPLLHPER	99.7%	49.2	25	44.3	1	2	0	1687.95	187	200
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	24	30	58	0.06%	57.7%	PDYLGADQRK	99.7%	45.8	25	33.3	2	0	0	1162.59	2	11
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	24	30	58	0.06%	57.7%	QTLQSEQPLQVAR	99.7%	64.1	25	57.4	1	0	0	1497.80	85	97
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	24	30	58	0.06%	57.7%	QVEDDIQQLLK	99.7%	93.5	25	80.3	2	0	0	1328.71	47	57
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	24	30	58	0.06%	57.7%	SVCTEAGMFAIR	99.7%	67.9	25	67.1	5	0	0	1357.62	387	398
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	24	30	58	0.06%	57.7%	TDACFIR	99.7%	53.1	25	42.1	2	0	0	882.41	233	239
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	24	30	58	0.06%	57.7%	TMLELINQLDGFDPR	99.7%	80.1	25	71.2	4	0	0	1777.88	298	312
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	24	30	58	0.06%	57.7%	TYGQSTYSR	99.4%	37.1	25	33	2	0	0	1062.49	35	43
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	24	30	58	0.06%	57.7%	VIGSELVQK	99.6%	39.8	25	23	2	0	0	972.57	240	248
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	55	0.05%	57.9%	AVAHHTDCTFIR	99.7%	53	25	35.7	2	2	0	1427.68	202	213
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	55	0.05%	57.9%	EELQLLQEQGSYVGEVVR	99.7%	104	25	104	2	0	0	2076.06	61	78
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	55	0.05%	57.9%	EHAPSIIFMDEIDSIGSSR	99.5%	32.5	25	32.5	0	3	0	2120.00	240	258
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	55	0.05%	57.9%	ELFVMAR	99.7%	53.5	25	44.6	4	0	0	881.46	233	239
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	55	0.05%	57.9%	FVVDVDKNIDINDVTPNCR	99.7%	48.5	25	47.5	0	2	0	2233.09	95	113
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	55	0.05%	57.9%	GVCTEAGMYALR	99.7%	68.9	25	64.5	4	0	0	1327.61	361	372
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	55	0.05%	57.9%	GVLLYGPPGTGK	99.7%	58.9	25	0	5	0	0	1158.65	185	196
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	55	0.05%	57.9%	IAELMPGASGAEVK	99.7%	71.6	25	55.1	4	0	0	1372.71	347	360
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	55	0.05%	57.9%	IDILDSALLRPGR	99.7%	45.6	25	37	2	1	0	1438.84	298	310
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	55	0.05%	57.9%	IEELQLIVNDK	99.7%	95.8	25	84.1	2	0	0	1313.73	28	38
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	55	0.05%	57.9%	LEGGSGGDSEVQR	99.7%	83	25	83	4	0	0	1290.59	259	271
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	55	0.05%	57.9%	RVHVTQEDFEMAVAK	99.7%	49.5	25	49.5	0	1	0	1775.87	375	389
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	55	0.05%	57.9%	TMLELLNQLDGFEATK	99.7%	105	25	105	4	0	0	1838.92	272	287
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	55	0.05%	57.9%	VALRNDSYTLHK	99.7%	51.6	25	44.2	0	2	0	1416.76	114	125
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	55	0.05%	57.9%	VDPLVSLMMVEK	99.7%	54.1	25	49.3	1	0	0	1360.72	131	142
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	55	0.05%	57.9%	VIMATNR	95.0%	28.3	25	21.4	2	0	0	804.44	291	297
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	55	0.05%	57.9%	VPDSTYEMIGGLDK	99.7%	103	25	100	4	0	0	1540.72	143	156
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	26	55	0.05%	57.9%	VSGSELVQK	99.7%	71.2	25	35.3	4	0	0	946.52	214	222
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	30	50	0.05%	34.8%	AAVESLGFILFR	99.7%	90.5	25	88.4	4	0	0	1322.75	617	628
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	30	50	0.05%	34.8%	DNLEWLAR	99.7%	40.3	25	33.2	1	0	0	1016.52	388	395
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	30	50	0.05%	34.8%	DTSEDIEELVEPVAAHGPK	99.7%	82.9	25	82.3	2	1	0	2035.98	916	934
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	30	50	0.05%	34.8%	EAINLLEPMTNDPVNYVR	99.7%	93.2	25	93.2	4	0	0	2104.04	667	684
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	30	50	0.05%	34.8%	EALQLMATYLPK	99.7%	50.6	25	44.2	4	0	0	1377.74	418	429
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	30	50	0.05%	34.8%	FTATASLGVIHK	99.7%	37.1	25	35.5	0	2	0	1244.70	402	413
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	30	50	0.05%	34.8%	GLAVGIALVMYGR	99.7%	78.2	25	76.8	2	0	0	1335.75	547	559
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	30	50	0.05%	34.8%	HGGSLGLGLAAMGTAR	99.6%	33.3	25	33.3	0	1	0	1468.77	475	490
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	30	50	0.05%	34.8%	LLHVAVSDVNDDVRR	99.7%	52.5	25	52.5	0	2	0	1707.91	602	616
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	30	50	0.05%	34.8%	MEEADALIESLCR	99.7%	94.7	25	89.4	4	0	0	1536.70	560	572
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	30	50	0.05%	34.8%	NAQAIEDMVGYAQETQHEK	99.4%	31	25	31	0	1	0	2161.98	525	543
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	30	50	0.05%	34.8%	NNNTDLMILK	99.5%	37.8	25	29.4	2	0	0	1175.61	345	354
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	30	50	0.05%	34.8%	QAIGIALETR	99.7%	41.1	25	37	1	0	0	1071.62	149	158
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	30	50	0.05%	34.8%	QDVYDLLK	99.7%	56.5	25	24.2	2	0	0	993.53	491	498
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	30	50	0.05%	34.8%	SNCKPSTFAYPAPLEVPK	99.4%	31.2	25	26.9	0	2	0	2006.01	804	821
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	30	50	0.05%	34.8%	TILESNDVPGMLAYSLK	99.7%	78.4	25	77.7	3	0	0	1866.95	166	182
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	30	50	0.05%	34.8%	TNLYQDDAVTGEAAGLALGLVMLGSK	99.7%	56.3	25	56.3	0	1	0	2607.33	499	524
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	30	50	0.05%	34.8%	TPEQCPSVVSLLSESYNPHVR	99.7%	61.1	25	61.1	0	2	0	2399.17	629	649
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	30	50	0.05%	34.8%	TVGTPIASVPGSTNTGTVPGSEK	99.7%	61.7	25	61.7	1	0	0	2157.10	270	292
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	30	50	0.05%	34.8%	TVGTPIASVPGSTNTGTVPGSEKDSDSMETEEK	99.7%	54.7	25	54.7	0	3	0	3324.53	270	302
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	30	50	0.05%	34.8%	VINDKHDDVMAK	99.7%	64.4	25	59.6	2	0	0	1384.69	716	727
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	30	50	0.05%	34.8%	VLTMPETCR	95.4%	28.6	25	26.6	1	0	0	1106.53	891	899

26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	30	50	0.05%	34.8%	VSTAVLSITAK	99.7%	93.8	25	90.1	2	0	0	1089.65	828	838
26S proteasome non-ATPase regulatory subunit 10	PSMD10	PSD10_HUMAN	24.4	100.0%	4	4	6	0.01%	28.8%	ASTNIQDTEGNTPLHLACDEERVEEAK	99.7%	75.9	25	74.1	0	2	0	3027.40	163	189
26S proteasome non-ATPase regulatory subunit 10	PSMD10	PSD10_HUMAN	24.4	100.0%	4	4	6	0.01%	28.8%	LEELKESILADK	99.7%	64.4	25	52.5	2	0	0	1387.77	19	30
26S proteasome non-ATPase regulatory subunit 10	PSMD10	PSD10_HUMAN	24.4	100.0%	4	4	6	0.01%	28.8%	LLVSQGASIYIENKEEK	95.9%	23.6	25	15.9	0	1	0	1921.03	190	206
26S proteasome non-ATPase regulatory subunit 10	PSMD10	PSD10_HUMAN	24.4	100.0%	4	4	6	0.01%	28.8%	MIHILLYYK	98.5%	33.3	25	29	1	0	0	1193.68	154	162
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	6	6	8	0.01%	17.3%	IMLNTPEDVQALVSGK	99.7%	68.2	25	62.6	1	0	0	1714.90	259	274
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	6	6	8	0.01%	17.3%	LYDNLLEQNLIR	99.7%	51.9	25	51.9	2	0	0	1503.82	326	337
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	6	6	8	0.01%	17.3%	TGQAAELGGLLK	99.7%	52.7	25	44.6	1	0	0	1157.65	60	71
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	6	6	8	0.01%	17.3%	TTANAIYCPPK	99.7%	61.6	25	55.4	1	0	0	1235.61	195	205
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	6	6	8	0.01%	17.3%	VQIEHISSLIK	99.7%	58.4	25	58.4	2	0	0	1266.74	345	355
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	6	6	8	0.01%	17.3%	YVRPFLNSISK	95.7%	23.4	25	23.4	0	1	0	1323.74	72	82
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	8	9	17	0.02%	24.5%	DLPVSEQQER	99.7%	61.3	25	61.3	2	0	0	1200.59	187	196
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	8	9	17	0.02%	24.5%	GSIDEVDKR	98.6%	33.7	25	24.1	1	0	0	1018.52	322	330
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	8	9	17	0.02%	24.5%	LNIGDLQVTK	99.7%	52.7	25	41.5	2	0	0	1100.63	123	132
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	8	9	17	0.02%	24.5%	QMTDPNVALTFLEK	99.7%	55.1	25	54.1	4	0	0	1622.81	86	99
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	8	9	17	0.02%	24.5%	SSDEAVILCK	99.7%	57.1	25	34.9	2	0	0	1121.55	106	115
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	8	9	17	0.02%	24.5%	TAWGQQPDLAANEAQLLR	99.7%	59.5	25	58.7	2	0	0	1982.01	253	270
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	8	9	17	0.02%	24.5%	VLDLQQIK	99.7%	57	25	43.5	2	0	0	956.58	340	347
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	8	9	17	0.02%	24.5%	YYQTIGNHASYYK	99.7%	70.2	25	70.2	2	0	0	1607.75	162	174
26S proteasome non-ATPase regulatory subunit 14	PSMD14	PSDE_HUMAN	34.6	100.0%	6	9	16	0.02%	27.7%	AVAVVVDPIQSVK	99.7%	81	25	81	2	0	0	1324.78	140	152
26S proteasome non-ATPase regulatory subunit 14	PSMD14	PSDE_HUMAN	34.6	100.0%	6	9	16	0.02%	27.7%	AVEEEDKMTPEQLAIK	99.7%	57.3	25	57.3	4	0	0	1830.92	258	273
26S proteasome non-ATPase regulatory subunit 14	PSMD14	PSDE_HUMAN	34.6	100.0%	6	9	16	0.02%	27.7%	HYYSITINYR	99.0%	35.2	25	30.5	1	0	0	1329.66	199	208
26S proteasome non-ATPase regulatory subunit 14	PSMD14	PSDE_HUMAN	34.6	100.0%	6	9	16	0.02%	27.7%	LINANMMVLGHEPR	99.7%	37.2	25	31.9	2	2	0	1594.82	162	175
26S proteasome non-ATPase regulatory subunit 14	PSMD14	PSDE_HUMAN	34.6	100.0%	6	9	16	0.02%	27.7%	VIDVFAMPQSGTGVSVEAVDPVFQAK	99.7%	35.8	25	35.8	0	3	0	2707.37	69	94
26S proteasome non-ATPase regulatory subunit 14	PSMD14	PSDE_HUMAN	34.6	100.0%	6	9	16	0.02%	27.7%	VVIDAFR	99.5%	38	25	32.8	2	0	0	819.47	155	161
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	APVQPQQSPAAAPGGTDEKPSGK	99.7%	53.6	25	53.6	0	2	0	2218.11	9	31
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	AVPLALALISVSNPR	99.7%	58.3	25	58.3	2	2	0	1520.92	689	703
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	CALGVFR	97.7%	31.4	25	24.4	2	0	0	822.43	251	257
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	DIDENAYAK	99.7%	40.8	25	40.8	2	0	0	1038.47	220	228
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	DKAPVQPQQSPAAAPGGTDEKPSGK	99.7%	62	25	62	0	2	0	2461.23	7	31
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	DPNNLFMVR	99.7%	46.8	25	33.6	6	0	0	1121.54	755	763
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	DTSLYRPALEELRR	99.7%	36.1	25	31.6	0	2	0	1718.92	67	80
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	EDVLTLLLPVMGDSK	99.7%	91.6	25	82.5	5	0	0	1629.88	495	509
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	ELDIMEPK	99.7%	44.5	25	26.6	3	0	0	990.48	336	343
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	EPLLTLVK	99.7%	44	25	44	1	0	0	912.58	182	189
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	EWQELDDAEK	99.7%	51.2	25	43.3	2	0	0	1262.55	169	178
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	FAADIISVLAMTMSGER	99.7%	90.3	25	24.6	6	0	0	1827.90	121	137
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	FGGSGSQVDSAR	99.7%	119	25	101	5	0	0	1167.54	358	369
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	FSHDADPEVSYNSIFAMGMVGSGTNNAR	99.7%	85.7	25	81.6	0	1	0	3006.30	713	740
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	GTLTLCPYHSDR	99.7%	53.3	25	53.3	2	0	0	1419.67	774	785
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	LAQGLTHLGK	99.7%	50.8	25	49.2	2	0	0	1037.61	764	773
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	LGSIFGLGLAYAGSNR	99.7%	91.6	25	91.6	2	2	0	1595.85	479	494
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	LNILDTLSK	99.7%	56.6	25	32.6	3	0	0	1016.60	704	712
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	LVGSQEELASWGHEYVR	99.7%	48.9	25	46.6	0	2	0	1959.96	144	160
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	MLVTFDEELRPLPVSVR	99.7%	42.3	25	42.3	1	2	0	2001.08	829	845
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	MNLASSFVNGFVNAAFGQDK	99.7%	94.6	25	94.6	1	0	0	2133.01	370	389
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	NECDPALALLSDYVLHNSNTMR	99.7%	37.8	25	37.8	0	2	0	2533.18	457	478
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	QMAFMLGR	97.5%	31	25	24.5	1	0	0	953.47	293	300
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	SETELKDTYAR	99.7%	59.8	25	59.8	2	1	0	1312.64	546	556
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	SFANTLVDVCAYAGSGNVLK	99.7%	111	25	105	2	0	0	2086.03	589	608
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	SGALLACGIVNSGVR	99.7%	95.2	25	93.7	2	0	0	1473.78	442	456

26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	SHYVLYGLVAAMQPR	99.7%	34.9	25	34.9	0	2	0	1720.88	814	828
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	SSTTSMTSVPKPLK	99.7%	72	25	69.4	4	0	0	1463.78	84	97
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	TITGFQTHTTPVLLAHGER	99.7%	51	25	51	0	2	0	2079.10	861	879
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	VGQAVDVVGQAGKPK	99.7%	86.4	25	77.9	6	2	0	1452.82	846	860
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	VQQLLHICSEHFDSK	97.9%	26.1	25	26.1	0	1	0	1840.90	609	623
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	WLPLGLGLNHLGK	97.8%	31.5	25	31.5	1	0	0	1417.83	557	569
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	YGEPTLR	98.6%	33.5	25	25.4	2	0	0	835.43	681	687
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	46	92	0.09%	50.9%	YLYSSEDYIK	99.7%	48.8	25	37.9	2	0	0	1280.60	432	441
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	64	0.06%	45.3%	AIQLEYSEAR	99.7%	80.1	25	73.3	2	0	0	1179.60	297	306
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	64	0.06%	45.3%	AIQLEYSEARR	99.4%	37	25	32.7	1	0	0	1335.70	297	307
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	64	0.06%	45.3%	ALDLVAAK	99.7%	53.5	25	29.4	2	0	0	800.49	202	209
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	64	0.06%	45.3%	APQHTAVGFK	99.7%	47.6	25	42	2	0	0	1055.56	316	325
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	64	0.06%	45.3%	AVQGFFTSNNATR	99.7%	78.8	25	78.8	2	0	0	1412.69	116	128
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	64	0.06%	45.3%	DGVIEASINHEK	99.7%	52.2	25	34.2	2	0	0	1311.65	444	455
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	64	0.06%	45.3%	DLESAEERR	97.0%	30.3	25	24	2	0	0	1104.53	504	512
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	64	0.06%	45.3%	ELDTVTLEDIKEHVK	99.7%	71.8	25	69.6	2	2	0	1768.93	66	80
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	64	0.06%	45.3%	EMIDIYSTR	99.7%	52.2	25	39.5	4	0	0	1127.54	462	470
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	64	0.06%	45.3%	EPQLAFHQR	99.7%	66.7	25	51.1	2	0	0	1125.58	471	479
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	64	0.06%	45.3%	EQQDLEFAK	99.7%	45.2	25	44.5	2	0	0	1107.53	515	523
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	64	0.06%	45.3%	EREQQDLEFAK	99.7%	54	25	46.5	2	0	0	1392.68	513	523
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	64	0.06%	45.3%	FNQVLDQFGEK	99.7%	72.8	25	47.6	2	0	0	1324.65	375	385
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	64	0.06%	45.3%	HDADGQATLLNLLLR	99.7%	90.5	25	90.5	2	0	0	1649.90	242	256
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	64	0.06%	45.3%	ISDDLMQK	99.7%	50.9	25	34.7	4	0	0	949.47	187	194
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	64	0.06%	45.3%	ISLADIAQK	99.7%	70.9	25	31	2	0	0	958.56	417	425
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	64	0.06%	45.3%	KAPQHTAVGFK	99.7%	46.6	25	44.3	2	0	0	1183.66	315	325
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	64	0.06%	45.3%	LQLDSPEDAEFIVAK	99.7%	96.7	25	82.5	2	0	0	1674.86	426	440
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	64	0.06%	45.3%	MISLSYSR	99.7%	45.3	25	41.9	4	0	0	956.49	409	416
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	64	0.06%	45.3%	NYLHYSLYDQAEK	99.7%	75.2	25	67.3	2	2	0	1643.77	257	269
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	64	0.06%	45.3%	RLNHYVLYK	96.1%	23.8	25	15.6	0	1	0	1205.68	107	115
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	64	0.06%	45.3%	SLMPYFLLTQAVR	99.7%	91.6	25	78	6	0	0	1538.84	356	368
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	64	0.06%	45.3%	SVFPEQANNNEWAR	99.7%	65.8	25	63.8	2	0	0	1661.77	274	287
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	64	0.06%	45.3%	VYEFLDKLDVVR	99.7%	70.2	25	66.5	2	2	0	1495.82	217	228
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	25	32	64	0.06%	45.3%	YLYYTGR	99.6%	39.4	25	30	2	0	0	935.46	288	294
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	3	3	5	0.00%	12.7%	AAAASAAEAGIATTGTEDSDDALLK	99.1%	29.7	25	29.7	0	1	0	2320.12	238	262
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	3	3	5	0.00%	12.7%	ITFCTGIR	99.7%	50.6	25	41.7	2	0	0	967.50	84	91
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	3	3	5	0.00%	12.7%	LQAQQDAVNIVCHSK	99.3%	30.8	25	19.9	0	2	0	1710.86	26	40
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	42	0.04%	45.8%	DNNMAPYYEALCK	99.7%	49.2	25	49.2	2	0	0	1604.67	47	59
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	42	0.04%	45.8%	DWLFAPHYR	96.8%	30	25	21	2	0	0	1204.59	285	293
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	42	0.04%	45.8%	FLLSLPEHR	99.7%	55.3	25	48.5	2	0	0	1111.63	24	32
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	42	0.04%	45.8%	GAEILEVLHSLPAVR	99.7%	73.7	25	73.7	5	0	0	1603.92	243	257
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	42	0.04%	45.8%	GDAAVRDELMAAVR	99.7%	59	25	55.8	3	4	0	1473.75	33	46
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	42	0.04%	45.8%	IDKVNEIVETNRPDSK	99.7%	41.2	25	41.2	0	2	0	1856.97	347	362
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	42	0.04%	45.8%	IGLFYMDNDLITR	99.7%	95.4	25	94.8	4	0	0	1570.79	147	159
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	42	0.04%	45.8%	IHAYSQLLESYR	99.7%	48.8	25	43.3	2	1	0	1479.76	301	312
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	42	0.04%	45.8%	KGDLLLNR	99.7%	49	25	33.2	2	0	0	928.56	372	379
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	42	0.04%	45.8%	LDEELEDAEK	99.7%	61.5	25	55.1	1	0	0	1190.54	84	93
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	42	0.04%	45.8%	NWQYQETIKK	99.4%	37.2	25	37.2	1	0	0	1337.68	363	372
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	42	0.04%	45.8%	PLENLEEEGLPK	99.7%	64.8	25	64.8	2	0	0	1367.71	2	13
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	42	0.04%	45.8%	PLENLEEEGLPKNPDLR	97.3%	25.2	25	25.2	0	1	0	1963.01	2	18
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	42	0.04%	45.8%	QYLFSLYECR	99.7%	56.2	25	53.5	2	0	0	1378.65	258	267
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	42	0.04%	45.8%	SLIEEGGDWDRR	98.2%	32.3	25	32.3	1	0	0	1432.68	166	177

26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	42	0.04%	45.8%	VNEIVETNRPDSK	99.7%	63.3	25	52.7	2	1	0	1500.77	350	362
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	17	23	42	0.04%	45.8%	VYQGLYCVAIR	99.7%	82.6	25	81.4	2	0	0	1341.70	182	192
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	5	5	9	0.01%	13.4%	DIQTNVYIK	99.5%	37.8	25	26.5	2	0	0	1093.59	219	227
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	5	5	9	0.01%	13.4%	ILFFNTPK	99.1%	35.7	25	16.9	2	0	0	979.56	290	297
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	5	5	9	0.01%	13.4%	ILFTEATR	99.7%	43.1	25	27	2	0	0	950.53	282	289
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	5	5	9	0.01%	13.4%	LVLLELNFLPTTGTK	99.7%	68.8	25	68.8	2	0	0	1658.97	121	135
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	5	5	9	0.01%	13.4%	QVIEYAR	97.8%	31.6	25	15.3	1	0	0	878.47	338	344
26S proteasome non-ATPase regulatory subunit 9	PSMD9	PSMD9_HUMAN	24.7	99.8%	2	2	4	0.00%	9.9%	ANYDVLESQK	99.3%	36.4	25	34.4	2	0	0	1166.57	39	48
26S proteasome non-ATPase regulatory subunit 9	PSMD9	PSMD9_HUMAN	24.7	99.8%	2	2	4	0.00%	9.9%	KLGQSESQGPPR	99.7%	70.1	25	70.1	2	0	0	1283.67	123	134
28S ribosomal protein S10, mitochondrial	MRPS10	RT10_HUMAN	23.0	100.0%	4	5	9	0.01%	28.4%	AVLDSYEYFAVLAAK	99.7%	91.8	25	91.8	2	0	0	1659.86	86	100
28S ribosomal protein S10, mitochondrial	MRPS10	RT10_HUMAN	23.0	100.0%	4	5	9	0.01%	28.4%	DLTKPVVTISDEPDILYKR	99.4%	31.3	25	31.3	0	1	0	2202.20	57	75
28S ribosomal protein S10, mitochondrial	MRPS10	RT10_HUMAN	23.0	100.0%	4	5	9	0.01%	28.4%	FTLLQSVHIYK	99.7%	55.9	25	43.3	2	0	0	1348.76	118	128
28S ribosomal protein S10, mitochondrial	MRPS10	RT10_HUMAN	23.0	100.0%	4	5	9	0.01%	28.4%	NLPEGVAMEVTK	99.7%	49.6	25	45.7	4	0	0	1287.66	163	174
28S ribosomal protein S11, mitochondrial	MRPS11	RT11_HUMAN	20.6	100.0%	4	6	10	0.01%	22.2%	FSIYPPIPGEESSLR	94.6%	28	25	28	1	0	0	1691.86	60	74
28S ribosomal protein S11, mitochondrial	MRPS11	RT11_HUMAN	20.6	100.0%	4	6	10	0.01%	22.2%	GTGIAAQTAGIAAAAR	99.7%	102	25	95.4	2	0	0	1399.77	123	138
28S ribosomal protein S11, mitochondrial	MRPS11	RT11_HUMAN	20.6	100.0%	4	6	10	0.01%	22.2%	KFEEIPIAHIK	99.6%	32.8	25	32.8	2	1	0	1324.76	79	89
28S ribosomal protein S11, mitochondrial	MRPS11	RT11_HUMAN	20.6	100.0%	4	6	10	0.01%	22.2%	KGTGIAAQTAGIAAAAR	99.7%	128	25	121	2	2	0	1527.86	122	138
28S ribosomal protein S12, mitochondrial	MRPS12	RT12_HUMAN	15.2	99.8%	2	2	6	0.01%	14.5%	GVVLCTFTR	99.7%	44.8	25	28.6	4	0	0	1052.56	60	68
28S ribosomal protein S12, mitochondrial	MRPS12	RT12_HUMAN	15.2	99.8%	2	2	6	0.01%	14.5%	LGPTEGRPQLK	99.2%	36.3	25	21.6	2	0	0	1195.68	49	59
28S ribosomal protein S14, mitochondrial	MRPS14	RT14_HUMAN	15.1	99.8%	2	3	8	0.01%	18.8%	ILQDVADEEIAALPR	99.7%	71.6	25	68	4	0	0	1652.89	66	80
28S ribosomal protein S14, mitochondrial	MRPS14	RT14_HUMAN	15.1	99.8%	2	3	8	0.01%	18.8%	MAYEYADER	99.7%	80.3	25	77.6	4	0	0	1147.47	43	51
28S ribosomal protein S15, mitochondrial	MRPS15	RT15_HUMAN	29.8	100.0%	4	4	8	0.01%	13.6%	IVANPEDTR	99.7%	46	25	36.9	2	0	0	1014.52	115	123
28S ribosomal protein S15, mitochondrial	MRPS15	RT15_HUMAN	29.8	100.0%	4	4	8	0.01%	13.6%	NTNYDVFEK	99.7%	50.8	25	36.8	2	0	0	1129.52	172	180
28S ribosomal protein S15, mitochondrial	MRPS15	RT15_HUMAN	29.8	100.0%	4	4	8	0.01%	13.6%	SYEEHLEK	99.5%	37.8	25	26.5	2	0	0	1034.48	138	145
28S ribosomal protein S15, mitochondrial	MRPS15	RT15_HUMAN	29.8	100.0%	4	4	8	0.01%	13.6%	YLLMSIDQR	99.7%	63.5	25	50.3	2	0	0	1138.59	155	163
28S ribosomal protein S16, mitochondrial	MRPS16	RT16_HUMAN	15.3	100.0%	3	4	8	0.01%	26.3%	AREVLLASQK	99.7%	47.9	25	35.1	2	0	0	1114.66	115	124
28S ribosomal protein S16, mitochondrial	MRPS16	RT16_HUMAN	15.3	100.0%	3	4	8	0.01%	26.3%	FVEQLGSYDPLPNSHGEK	99.7%	57.5	25	53	2	2	0	2016.97	47	64
28S ribosomal protein S16, mitochondrial	MRPS16	RT16_HUMAN	15.3	100.0%	3	4	8	0.01%	26.3%	LVALNLDR	99.7%	64.1	25	48.6	2	0	0	913.55	65	72
28S ribosomal protein S17, mitochondrial	MRPS17	RT17_HUMAN	14.5	99.8%	2	2	5	0.00%	15.4%	HELAEIVFK	99.7%	49.9	25	49.9	3	0	0	1085.60	79	87
28S ribosomal protein S17, mitochondrial	MRPS17	RT17_HUMAN	14.5	99.8%	2	2	5	0.00%	15.4%	NLEELNISSAQ	99.7%	85.8	25	67.8	2	0	0	1217.60	120	130
28S ribosomal protein S18a, mitochondrial	MRPS18A	RT18A_HUMAN	22.2	100.0%	6	7	13	0.01%	28.1%	ESPNPPNPSGQCPICR	99.7%	72.8	25	72.8	3	0	0	1809.80	59	74
28S ribosomal protein S18a, mitochondrial	MRPS18A	RT18A_HUMAN	22.2	100.0%	6	7	13	0.01%	28.1%	ITGLCQEEHR	99.1%	35.6	25	33.8	1	0	0	1242.59	104	113
28S ribosomal protein S18a, mitochondrial	MRPS18A	RT18A_HUMAN	22.2	100.0%	6	7	13	0.01%	28.1%	KITGLCQEEHR	99.4%	31.1	25	31.1	0	2	0	1370.68	103	113
28S ribosomal protein S18a, mitochondrial	MRPS18A	RT18A_HUMAN	22.2	100.0%	6	7	13	0.01%	28.1%	LPEGVVPK	98.9%	34.5	25	26.4	1	0	0	838.50	135	142
28S ribosomal protein S18a, mitochondrial	MRPS18A	RT18A_HUMAN	22.2	100.0%	6	7	13	0.01%	28.1%	MPVGSPLLR	99.5%	38.2	25	20.8	4	0	0	969.56	174	182
28S ribosomal protein S18a, mitochondrial	MRPS18A	RT18A_HUMAN	22.2	100.0%	6	7	13	0.01%	28.1%	WAPGSVKPIYK	96.7%	29.9	25	25.6	2	0	0	1245.70	154	164
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	4	5	12	0.01%	21.7%	LYQGHLQEESGPPPESMPK	99.7%	43.1	25	35.9	0	3	0	2140.00	219	237
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	4	5	12	0.01%	21.7%	TPAEASSTGQTGPQSAL	99.7%	62.9	25	61.8	2	0	0	1602.76	242	258
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	4	5	12	0.01%	21.7%	VVGNPCPICR	99.7%	53.3	25	46.6	3	0	0	1171.57	100	109
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	4	5	12	0.01%	21.7%	YLESEEYQER	99.7%	66.3	25	66.3	4	0	0	1345.59	58	67
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	4	5	7	0.01%	11.8%	FMEPYIFGSR	99.7%	50.1	25	41.9	3	0	0	1246.59	101	110
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	4	5	7	0.01%	11.8%	GIILFISR	99.7%	59.5	25	47.3	2	0	0	918.58	140	147
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	4	5	7	0.01%	11.8%	HSDFFNVK	99.5%	38.1	25	25.7	1	0	0	993.48	69	76
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	4	5	7	0.01%	11.8%	RQQVEALYR	98.5%	33.1	25	22.3	1	0	0	1162.63	264	272
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	13	18	34	0.03%	35.6%	DQAAEGINLIK	99.7%	71.6	25	60	2	0	0	1171.63	319	329
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	13	18	34	0.03%	35.6%	IDGLLIDQIQR	99.7%	71.8	25	51.1	2	0	0	1283.73	281	291
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	13	18	34	0.03%	35.6%	ILTPIIFKEENLR	99.7%	63.5	25	63.5	2	2	0	1585.93	204	216
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	13	18	34	0.03%	35.6%	KIDGLLIDQIQR	99.7%	76.7	25	69.7	2	2	0	1411.83	280	291
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	13	18	34	0.03%	35.6%	LMTQAQLEEATR	99.7%	96	25	79.3	4	0	0	1390.70	105	116
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	13	18	34	0.03%	35.6%	MIQVYFPK	99.7%	48.3	25	43.4	4	0	0	1041.54	192	199
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	13	18	34	0.03%	35.6%	MPPVLEER	99.5%	38.4	25	22.6	2	0	0	986.50	128	135

28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	13	18	34	0.03%	35.6%	MTGLNLQK	99.7%	47.1	25	27.5	2	0	0	904.49	82	89
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	13	18	34	0.03%	35.6%	TFKPAIQELKPPTYK	94.7%	22.6	25	22.6	0	1	0	1760.99	90	104
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	13	18	34	0.03%	35.6%	TYEDIDKR	99.4%	37.7	25	21.5	1	0	0	1039.51	249	256
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	13	18	34	0.03%	35.6%	VPINDVLAEDK	99.7%	75.8	25	70.8	2	0	0	1212.65	136	146
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	13	18	34	0.03%	35.6%	VPINDVLAEDKILEGTETTK	99.7%	47.7	25	47.7	0	2	0	2185.16	136	155
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	13	18	34	0.03%	35.6%	YVFTDISYSIPHR	99.7%	62.9	25	62.9	2	2	0	1597.80	156	168
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	7	8	15	0.01%	35.8%	AFDLFNPNFK	99.7%	73.9	25	73.7	2	0	0	1212.60	84	93
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	7	8	15	0.01%	35.8%	AKFYSVYGSGQR	99.7%	64.9	25	64.9	2	0	0	1362.68	72	83
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	7	8	15	0.01%	35.8%	ALLAEGVILR	99.7%	68.4	25	44.2	2	0	0	1054.66	124	133
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	7	8	15	0.01%	35.8%	ALLAEGVILRR	98.7%	33.8	25	26.1	2	0	0	1210.76	124	134
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	7	8	15	0.01%	35.8%	FVEKYTELQK	98.5%	33.1	25	28.8	1	0	0	1284.68	99	108
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	7	8	15	0.01%	35.8%	LETVGSIFSR	99.7%	76.2	25	63.1	2	0	0	1108.60	6	15
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	7	8	15	0.01%	35.8%	LGETDEEKLFVETGK	99.7%	71.5	25	69.5	2	2	0	1694.85	109	123
28S ribosomal protein S24, mitochondrial	MRPS24	RT24_HUMAN	19.0	100.0%	3	3	6	0.01%	10.8%	LHLQTVPSK	99.7%	49.7	25	45.4	2	0	0	1022.60	153	161
28S ribosomal protein S24, mitochondrial	MRPS24	RT24_HUMAN	19.0	100.0%	3	3	6	0.01%	10.8%	TVEDVFLR	99.7%	41.3	25	32.1	2	0	0	978.53	86	93
28S ribosomal protein S24, mitochondrial	MRPS24	RT24_HUMAN	19.0	100.0%	3	3	6	0.01%	10.8%	TVEDVFLRK	99.7%	40.6	25	31.1	2	0	0	1106.62	86	94
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	8	11	17	0.02%	54.3%	ECICEVEGQVPCPSLVPLPK	98.8%	34	25	34	1	0	0	2311.11	138	157
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	8	11	17	0.02%	54.3%	NMTPSPFLR	97.6%	31.3	25	14.3	1	0	0	1078.54	69	77
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	8	11	17	0.02%	54.3%	NPWVQIMMFK	99.5%	38.2	25	31.4	2	0	0	1325.64	59	68
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	8	11	17	0.02%	54.3%	QLSHPANFGPR	98.5%	27.5	25	24.5	0	2	0	1223.63	122	132
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	8	11	17	0.02%	54.3%	SNKEIMEHIR	96.4%	29.6	25	23.9	1	0	0	1272.64	94	103
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	8	11	17	0.02%	54.3%	TLQYLSQGNVVFK	99.7%	83.8	25	69.9	2	0	0	1496.81	12	24
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	8	11	17	0.02%	54.3%	TLQYLSQGNVVFKDSVK	99.5%	38.3	25	38.3	1	0	0	1926.03	12	28
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	8	11	17	0.02%	54.3%	VMTVNYNTHGELGEGAR	99.7%	75.8	25	75.8	3	4	0	1847.87	29	45
28S ribosomal protein S26, mitochondrial	MRPS26	RT26_HUMAN	24.2	99.8%	2	3	4	0.00%	14.1%	KAEEVQAWAQR	99.7%	65.9	25	57.2	2	1	0	1315.68	142	152
28S ribosomal protein S26, mitochondrial	MRPS26	RT26_HUMAN	24.2	99.8%	2	3	4	0.00%	14.1%	VNMPPAVDPAEFFVLMER	99.7%	56.4	25	55.4	1	0	0	2062.01	42	59
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	9	10	17	0.02%	23.9%	EALDVLGAVLK	99.7%	91.3	25	82.2	2	0	0	1127.67	278	288
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	9	10	17	0.02%	23.9%	EEIDHAEYYLYK	99.7%	47.2	25	41.7	2	0	0	1572.72	83	94
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	9	10	17	0.02%	23.9%	IESEGLLSLTTQLVK	99.7%	95.3	25	90.7	2	0	0	1630.93	347	361
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	9	10	17	0.02%	23.9%	KLPVSSLTISR	99.7%	50.7	25	47.5	2	1	0	1200.73	64	74
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	9	10	17	0.02%	23.9%	LIDNISSR	98.9%	34.5	25	10.4	1	0	0	917.51	75	82
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	9	10	17	0.02%	23.9%	LPQYLER	99.7%	43	25	20.6	2	0	0	918.50	327	333
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	9	10	17	0.02%	23.9%	LVEQLDIEETEQSK	99.7%	106	25	98.4	2	0	0	1660.83	313	326
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	9	10	17	0.02%	23.9%	NFGASLLLPGLK	99.7%	73.3	25	70	2	0	0	1229.73	203	214
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	9	10	17	0.02%	23.9%	VAASPEDIK	99.7%	45.5	25	37.1	1	0	0	929.49	266	274
28S ribosomal protein S28, mitochondrial	MRPS28	RT28_HUMAN	20.8	100.0%	3	4	13	0.01%	15.5%	AGGFASALER	99.7%	61	25	42.1	4	0	0	978.50	49	58
28S ribosomal protein S28, mitochondrial	MRPS28	RT28_HUMAN	20.8	100.0%	3	4	13	0.01%	15.5%	LLDLELTSR	99.7%	72.6	25	62.1	4	0	0	1059.60	144	152
28S ribosomal protein S28, mitochondrial	MRPS28	RT28_HUMAN	20.8	100.0%	3	4	13	0.01%	15.5%	NVESFASMLR	99.7%	72.5	25	72.4	5	0	0	1169.56	76	85
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	10	10	19	0.02%	27.6%	AYLPQELLGK	99.5%	37.9	25	27.6	2	0	0	1131.64	322	331
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	10	10	19	0.02%	27.6%	EGFDALDPFIPILVSNYNPK	99.7%	47.7	25	47.7	1	0	0	2249.15	332	351
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	10	10	19	0.02%	27.6%	ELLFLSNANPSLLER	99.7%	91.3	25	90.5	2	0	0	1715.93	379	393
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	10	10	19	0.02%	27.6%	FDQPLEASTWLK	99.7%	66.9	25	52.2	2	0	0	1434.73	178	189
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	10	10	19	0.02%	27.6%	GSPLGEVVEQGITR	99.7%	79.4	25	75.5	3	0	0	1441.76	219	232
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	10	10	19	0.02%	27.6%	KAYLPQELLGK	99.7%	51.4	25	51.4	1	0	0	1259.74	321	331
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	10	10	19	0.02%	27.6%	NATDAVGIVLK	99.7%	68.9	25	62.5	2	0	0	1100.63	235	245
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	10	10	19	0.02%	27.6%	NTSFAYPAIR	99.7%	53.6	25	46.8	2	0	0	1139.58	114	123
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	10	10	19	0.02%	27.6%	TFSEACLMVR	99.7%	51.8	25	46.5	2	0	0	1229.57	93	102
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	10	10	19	0.02%	27.6%	YLLYGEK	99.5%	38.4	25	28.8	2	0	0	885.47	124	130
28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	4	5	9	0.01%	14.9%	EAPETDTSPSLWDVEFAK	99.7%	64.1	25	64.1	2	0	0	2021.93	267	284
28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	4	5	9	0.01%	14.9%	IQFDEGYDNYPGQEK	99.7%	93.5	25	93.5	2	0	0	1802.79	226	240
28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	4	5	9	0.01%	14.9%	ISFSNIISDMK	99.7%	84.3	25	75.9	4	0	0	1254.64	199	209

28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	4	5	9	0.01%	14.9%	SELLSQLQQHEEESR	99.6%	32.9	25	32.9	0	1	0	1812.87	175	189
28S ribosomal protein S33, mitochondrial	MRPS33	RT33_HUMAN	12.6	99.8%	2	2	3	0.00%	19.8%	LFGEVTRPTNSK	98.3%	32.8	25	24.6	1	0	0	1348.72	18	29
28S ribosomal protein S33, mitochondrial	MRPS33	RT33_HUMAN	12.6	99.8%	2	2	3	0.00%	19.8%	LFSELPLAK	99.7%	40.5	25	25.9	2	0	0	1017.60	36	44
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	4	5	17	0.02%	17.0%	AWGILTFK	98.9%	34.4	25	31.5	4	0	0	935.54	114	121
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	4	5	17	0.02%	17.0%	LLQLLGR	99.7%	59.9	25	20	4	0	0	812.54	64	70
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	4	5	17	0.02%	17.0%	LPLFGLGR	99.7%	50.2	25	43.2	6	0	0	872.54	71	78
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	4	5	17	0.02%	17.0%	VRPDYTAQNLDHGK	99.7%	42.2	25	39.7	1	2	0	1613.80	100	113
28S ribosomal protein S35, mitochondrial	MRPS35	RT35_HUMAN	36.8	100.0%	6	6	10	0.01%	24.8%	EGNLELLK	99.3%	36.9	25	20.6	2	0	0	915.51	100	107
28S ribosomal protein S35, mitochondrial	MRPS35	RT35_HUMAN	36.8	100.0%	6	6	10	0.01%	24.8%	HFPIEIDSTDYVSSGPSVR	99.7%	76.1	25	71.6	1	0	0	2106.01	146	164
28S ribosomal protein S35, mitochondrial	MRPS35	RT35_HUMAN	36.8	100.0%	6	6	10	0.01%	24.8%	LSSLNLDDHAK	99.7%	70.4	25	56.9	2	0	0	1212.62	177	187
28S ribosomal protein S35, mitochondrial	MRPS35	RT35_HUMAN	36.8	100.0%	6	6	10	0.01%	24.8%	NILETLLQMK	99.7%	53.6	25	44.8	2	0	0	1202.68	261	270
28S ribosomal protein S35, mitochondrial	MRPS35	RT35_HUMAN	36.8	100.0%	6	6	10	0.01%	24.8%	NMEINKEELLGTK	99.7%	44.4	25	35.8	2	0	0	1518.78	275	287
28S ribosomal protein S35, mitochondrial	MRPS35	RT35_HUMAN	36.8	100.0%	6	6	10	0.01%	24.8%	SVVSLKNEEENENSISQYK	99.7%	73	25	72.7	1	0	0	2197.06	295	313
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	7	8	15	0.01%	19.5%	EECGPLPIVVASPR	99.7%	59.3	25	55.9	2	0	0	1523.79	375	388
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	7	8	15	0.01%	19.5%	GAAGFSIGK	99.5%	38.1	25	19.7	2	0	0	807.44	252	260
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	7	8	15	0.01%	19.5%	LTADELWK	99.7%	46.8	25	40.3	2	0	0	975.51	93	100
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	7	8	15	0.01%	19.5%	NGAVQTIAQR	99.7%	41.4	25	35	1	0	0	1057.57	151	160
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	7	8	15	0.01%	19.5%	VSGSINMLSLTQGLFR	99.7%	72.4	25	72.3	4	0	0	1722.92	336	351
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	7	8	15	0.01%	19.5%	YEDHTIFHDISLR	99.7%	43.9	25	43.9	0	2	0	1645.80	285	297
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	7	8	15	0.01%	19.5%	YGFLWPGLNVPLMK	99.7%	44.5	25	44.5	2	0	0	1650.87	137	150
28S ribosomal protein S6, mitochondrial	MRPS6	RT06_HUMAN	14.2	99.8%	2	2	4	0.00%	12.8%	DLENLGER	99.5%	38.5	25	22.6	2	0	0	945.46	38	45
28S ribosomal protein S6, mitochondrial	MRPS6	RT06_HUMAN	14.2	99.8%	2	2	4	0.00%	12.8%	TIEALMDR	99.7%	42.4	25	35.8	2	0	0	964.48	25	32
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	8	8	13	0.01%	31.4%	FYQVPVPLPDR	99.1%	35.5	25	28.4	2	0	0	1330.72	167	177
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	8	8	13	0.01%	31.4%	FYQVPVPLPDRR	95.9%	23.6	25	23.4	0	1	0	1486.82	167	178
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	8	8	13	0.01%	31.4%	KPVEELTEEEKYVR	99.7%	49.2	25	49.2	0	1	0	1748.91	53	66
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	8	8	13	0.01%	31.4%	LLEAFHNQGPVIK	99.7%	64	25	59.1	2	0	0	1465.82	209	221
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	8	8	13	0.01%	31.4%	LLEAFHNQGPVIKR	99.7%	36.8	25	34.6	0	1	0	1621.92	209	222
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	8	8	13	0.01%	31.4%	NCEPMIGLVPILK	99.1%	35.8	25	28.8	1	0	0	1499.80	151	163
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	8	8	13	0.01%	31.4%	SLMIQTLEAVK	98.1%	32.2	25	27.2	1	0	0	1232.69	109	119
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	8	8	13	0.01%	31.4%	TSSVFEDPVISK	99.7%	63.7	25	59.2	4	0	0	1308.67	82	93
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	10	10	16	0.02%	29.0%	AIAYLFPSGLFEK	99.6%	39.1	25	36.7	2	0	0	1455.79	107	119
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	10	10	16	0.02%	29.0%	ALCSFVTEDEVEWMR	99.7%	67.1	25	67.1	1	0	0	1887.83	351	365
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	10	10	16	0.02%	29.0%	ETYTEDFIKK	97.5%	31.1	25	20.4	2	0	0	1273.63	67	76
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	10	10	16	0.02%	29.0%	HDVTCTVSGGGR	99.7%	61.1	25	61.1	2	0	0	1245.56	326	337
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	10	10	16	0.02%	29.0%	HLANMMGEDPETFTQEDIDR	99.7%	43.8	25	35.4	0	1	0	2381.00	87	106
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	10	10	16	0.02%	29.0%	HPEQIFPR	97.6%	31.3	25	26.5	1	0	0	1023.54	127	134
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	10	10	16	0.02%	29.0%	LLTSQCGAAEEEFVQR	99.7%	104	25	104	2	0	0	1837.88	228	243
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	10	10	16	0.02%	29.0%	LSDLDYMQFIR	99.7%	59.5	25	50.3	2	0	0	1416.68	213	223
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	10	10	16	0.02%	29.0%	QIEEFNIGK	98.8%	34.3	25	27.3	2	0	0	1077.56	77	85
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	100.0%	10	10	16	0.02%	29.0%	QIEEFNIGKR	96.7%	29.9	25	14	1	0	0	1233.66	77	86
2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	GCAT	KBL_HUMAN	45.3	100.0%	2	2	3	0.00%	8.4%	ALGGASGGYTTGPGPLVSLLR	99.7%	66.3	25	66.3	1	0	0	1944.06	266	286
2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	GCAT	KBL_HUMAN	45.3	100.0%	2	2	3	0.00%	8.4%	GIFVIGFSYPVVPK	99.7%	47.3	25	47.3	2	0	0	1522.87	370	383
2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	BCKDHA	ODBA_HUMAN	50.5	99.8%	2	2	2	0.00%	6.7%	AVAENQPFLIEAMTYR	99.2%	36	25	32.9	1	0	0	1852.93	317	332
2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	BCKDHA	ODBA_HUMAN	50.5	99.8%	2	2	2	0.00%	6.7%	VDGNDVFAVYNATK	99.7%	108	25	108	1	0	0	1512.73	298	311
2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	BCKDHB	ODBB_HUMAN	43.1	100.0%	4	4	8	0.01%	13.5%	LGVSCEVIDLR	99.7%	75.2	25	58.6	2	0	0	1260.66	295	305
2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	BCKDHB	ODBB_HUMAN	43.1	100.0%	4	4	8	0.01%	13.5%	MNLFQSVTSALDNSLAK	99.7%	98.2	25	95.6	2	0	0	1854.93	71	87
2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	BCKDHB	ODBB_HUMAN	43.1	100.0%	4	4	8	0.01%	13.5%	SGDLFNCGSLTIR	99.7%	63	25	60.4	2	0	0	1439.69	171	183
2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	BCKDHB	ODBB_HUMAN	43.1	100.0%	4	4	8	0.01%	13.5%	TIIPWDVDTICK	99.2%	35.9	25	27.3	2	0	0	1460.75	306	317
39S ribosomal protein L1, mitochondrial	MRPL1	RM01_HUMAN	36.9	100.0%	3	3	5	0.00%	13.2%	FQILDFTSPK	99.7%	46.4	25	35.9	2	0	0	1195.64	109	118
39S ribosomal protein L1, mitochondrial	MRPL1	RM01_HUMAN	36.9	100.0%	3	3	5	0.00%	13.2%	NVEPFTSVLSLPYPFASEINK	99.7%	43	25	43	1	0	0	2352.21	136	156
39S ribosomal protein L1, mitochondrial	MRPL1	RM01_HUMAN	36.9	100.0%	3	3	5	0.00%	13.2%	VAVFTENASEVK	99.7%	66	25	58.9	2	0	0	1293.67	157	168

39S ribosomal protein L10, mitochondrial	MRPL10	RM10_HUMAN	29.3	100.0%	2	2	4	0.00%	11.1%	EIAAVFQDNR	99.7%	54	25	53.3	2	0	0	1162.59	85	94
39S ribosomal protein L10, mitochondrial	MRPL10	RM10_HUMAN	29.3	100.0%	2	2	4	0.00%	11.1%	TVPFLPLLGGCIDDTILSR	99.7%	48.1	25	48.1	2	0	0	2087.12	170	188
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	9	10	19	0.02%	54.2%	AGLAMPGPPLGPVLGQR	99.7%	51.9	25	47.5	4	0	0	1646.91	26	42
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	9	10	19	0.02%	54.2%	AQDEAFALQDVPLSSVVR	99.7%	62.7	25	62.7	2	0	0	1945.00	125	142
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	9	10	19	0.02%	54.2%	DLSSEELAAFQK	99.7%	81.9	25	67.1	2	0	0	1337.66	158	169
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	9	10	19	0.02%	54.2%	DLSSEELAAFQKER	99.7%	69.4	25	66.6	2	0	0	1622.80	158	171
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	9	10	19	0.02%	54.2%	EADLAAQEEAAKK	99.7%	58.7	25	56.4	2	0	0	1373.69	180	192
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	9	10	19	0.02%	54.2%	GVSINQFCK	99.7%	47.3	25	36.8	2	0	0	1052.52	43	51
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	9	10	19	0.02%	54.2%	IGQPTVSYFLK	99.7%	58.6	25	53.4	2	0	0	1252.69	82	92
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	9	10	19	0.02%	54.2%	KPEVGGVIR	99.7%	50.2	25	41.7	2	0	0	954.57	13	21
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	9	10	19	0.02%	54.2%	QTGKEVAGLVTLK	97.5%	31.1	25	27.7	1	0	0	1343.79	103	115
39S ribosomal protein L12, mitochondrial	MRPL12	RM12_HUMAN	21.3	99.9%	2	2	4	0.00%	11.6%	KLVESLPQEIK	99.7%	69.6	25	58.7	2	0	0	1283.76	163	173
39S ribosomal protein L12, mitochondrial	MRPL12	RM12_HUMAN	21.3	99.9%	2	2	4	0.00%	11.6%	NYIQGINLVQAK	99.7%	62.4	25	52.6	2	0	0	1360.76	151	162
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	7	9	15	0.01%	41.0%	APQQWATFAR	99.7%	53	25	45.1	2	0	0	1175.60	7	16
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	7	9	15	0.01%	41.0%	IWYLLDGK	94.8%	28.1	25	13.6	1	0	0	1007.56	17	24
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	7	9	15	0.01%	41.0%	LAAMASIR	99.7%	55.2	25	42.9	2	0	0	848.47	31	38
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	7	9	15	0.01%	41.0%	LAIYGMLPK	99.3%	36.9	25	27	3	0	0	1021.58	106	114
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	7	9	15	0.01%	41.0%	NLVEELPQPR	98.4%	33	25	33	1	0	0	1194.65	140	149
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	7	9	15	0.01%	41.0%	RLDEYTQEEIDAFPR	99.7%	45	25	39.6	0	2	0	1881.90	154	168
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	7	9	15	0.01%	41.0%	VYSSHTGYPGGFR	99.7%	65.3	25	63.6	2	2	0	1427.67	76	88
39S ribosomal protein L14, mitochondrial	MRPL14	RM14_HUMAN	15.9	100.0%	3	4	8	0.01%	29.0%	FDSNNVVLIEDNGNPVGTR	99.7%	86.9	25	86.9	2	0	0	2060.00	100	118
39S ribosomal protein L14, mitochondrial	MRPL14	RM14_HUMAN	15.9	100.0%	3	4	8	0.01%	29.0%	VLAIAQNFV	99.6%	39.8	25	39.8	2	0	0	974.57	137	145
39S ribosomal protein L14, mitochondrial	MRPL14	RM14_HUMAN	15.9	100.0%	3	4	8	0.01%	29.0%	VVDNSALGNSPYHR	99.7%	50.7	25	44.7	2	2	0	1528.75	40	53
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	6	6	12	0.01%	24.0%	GVTIQPLKR	99.6%	39	25	28	2	0	0	1011.63	126	134
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	6	6	12	0.01%	24.0%	ILKPTDENLLK	99.7%	45.9	25	39.1	2	0	0	1283.76	282	292
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	6	6	12	0.01%	24.0%	LGFEGGQTPFYIR	99.7%	66.7	25	60.8	2	0	0	1484.75	65	77
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	6	6	12	0.01%	24.0%	LQYLIDLGR	99.7%	59.8	25	54.2	2	0	0	1090.63	101	109
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	6	6	12	0.01%	24.0%	VDPSQPIDLTQLVNGR	99.7%	67.1	25	67.1	2	0	0	1751.93	110	125
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	6	6	12	0.01%	24.0%	VSLANLKPNPGSK	99.7%	49.3	25	42.8	2	0	0	1324.76	22	34
39S ribosomal protein L16, mitochondrial	MRPL16	RM16_HUMAN	28.5	100.0%	6	6	10	0.01%	27.5%	GAIDHYVTPVK	99.7%	45.6	25	30.9	2	0	0	1199.64	145	155
39S ribosomal protein L16, mitochondrial	MRPL16	RM16_HUMAN	28.5	100.0%	6	6	10	0.01%	27.5%	IATANMLGIR	99.7%	49.7	25	38.5	1	0	0	1059.60	218	227
39S ribosomal protein L16, mitochondrial	MRPL16	RM16_HUMAN	28.5	100.0%	6	6	10	0.01%	27.5%	NNQNPWTFER	99.7%	45.2	25	42.9	2	0	0	1305.60	208	217
39S ribosomal protein L16, mitochondrial	MRPL16	RM16_HUMAN	28.5	100.0%	6	6	10	0.01%	27.5%	TLLPVPSFEDVSIPEKPK	99.4%	37.7	25	37.4	2	0	0	1996.10	32	49
39S ribosomal protein L16, mitochondrial	MRPL16	RM16_HUMAN	28.5	100.0%	6	6	10	0.01%	27.5%	VLSPYDLTHK	99.4%	37.3	25	27.5	1	0	0	1172.63	229	238
39S ribosomal protein L16, mitochondrial	MRPL16	RM16_HUMAN	28.5	100.0%	6	6	10	0.01%	27.5%	VPAPFKPITR	99.7%	50.6	25	35.7	2	0	0	1125.68	124	133
39S ribosomal protein L17, mitochondrial	MRPL17	RM17_HUMAN	20.1	99.8%	2	2	6	0.01%	9.1%	LFQVLAPR	99.7%	58.3	25	46.1	4	0	0	943.57	89	96
39S ribosomal protein L17, mitochondrial	MRPL17	RM17_HUMAN	20.1	99.8%	2	2	6	0.01%	9.1%	MGLGPESR	99.7%	41.3	25	34.4	2	0	0	846.41	18	25
39S ribosomal protein L18, mitochondrial	MRPL18	RM18_HUMAN	20.6	100.0%	5	5	10	0.01%	24.4%	LQSAMTEGGVVLR	99.7%	68.6	25	57.9	2	0	0	1360.73	161	173
39S ribosomal protein L18, mitochondrial	MRPL18	RM18_HUMAN	20.6	100.0%	5	5	10	0.01%	24.4%	LQSAMTEGGVVLREPQR	99.7%	34.4	25	32.3	0	2	0	1886.98	161	177
39S ribosomal protein L18, mitochondrial	MRPL18	RM18_HUMAN	20.6	100.0%	5	5	10	0.01%	24.4%	NLELLSVAR	99.7%	57.2	25	27.2	2	0	0	1014.59	55	63
39S ribosomal protein L18, mitochondrial	MRPL18	RM18_HUMAN	20.6	100.0%	5	5	10	0.01%	24.4%	NVVACESIGR	99.7%	58.3	25	50.1	2	0	0	1104.55	121	130
39S ribosomal protein L18, mitochondrial	MRPL18	RM18_HUMAN	20.6	100.0%	5	5	10	0.01%	24.4%	VVVSASTR	99.5%	38.3	25	30.7	2	0	0	818.47	101	108
39S ribosomal protein L19, mitochondrial	MRPL19	RM19_HUMAN	33.5	100.0%	5	5	9	0.01%	17.5%	FDLCLTEQQMK	99.7%	49.7	25	49.7	1	0	0	1428.65	245	255
39S ribosomal protein L19, mitochondrial	MRPL19	RM19_HUMAN	33.5	100.0%	5	5	9	0.01%	17.5%	FLSPEFIPR	99.7%	49.4	25	44.2	2	0	0	1105.60	75	83
39S ribosomal protein L19, mitochondrial	MRPL19	RM19_HUMAN	33.5	100.0%	5	5	9	0.01%	17.5%	GLGATFILR	99.7%	69.9	25	58.7	2	0	0	947.57	144	152
39S ribosomal protein L19, mitochondrial	MRPL19	RM19_HUMAN	33.5	100.0%	5	5	9	0.01%	17.5%	ISQFLGICIQR	99.7%	69.8	25	67.8	2	0	0	1334.73	130	140
39S ribosomal protein L19, mitochondrial	MRPL19	RM19_HUMAN	33.5	100.0%	5	5	9	0.01%	17.5%	VTTADPYASGK	99.4%	37.2	25	34.7	2	0	0	1109.55	119	129
39S ribosomal protein L2, mitochondrial	MRPL2	RM02_HUMAN	33.3	99.9%	2	2	3	0.00%	12.1%	EGDAHPLGALPVGTLINNVESEPGR	98.9%	28.8	25	28.8	0	1	0	2542.29	178	202
39S ribosomal protein L2, mitochondrial	MRPL2	RM02_HUMAN	33.3	99.9%	2	2	3	0.00%	12.1%	SADIALVAGGSR	99.7%	54.1	25	45	2	0	0	1116.60	136	147
39S ribosomal protein L20, mitochondrial	MRPL20	RM20_HUMAN	17.4	100.0%	4	4	8	0.01%	22.1%	ITAASQEHGLK	99.7%	54.5	25	54.5	2	0	0	1154.62	72	82
39S ribosomal protein L20, mitochondrial	MRPL20	RM20_HUMAN	17.4	100.0%	4	4	8	0.01%	22.1%	KVLADLAIYEPK	99.7%	40.2	25	34.4	2	0	0	1359.79	100	111

39S ribosomal protein L20, mitochondrial	MRPL20	RM20_HUMAN	17.4	100.0%	4	4	8	0.01%	22.1%	VLADLAIYEPK	99.7%	89.3	25	78.3	2	0	0	1231.69	101	111
39S ribosomal protein L20, mitochondrial	MRPL20	RM20_HUMAN	17.4	100.0%	4	4	8	0.01%	22.1%	YPALIGNLVK	97.7%	31.4	25	23.8	2	0	0	1087.65	83	92
39S ribosomal protein L21, mitochondrial	MRPL21	RM21_HUMAN	22.8	100.0%	4	4	6	0.01%	16.1%	IVTTPQTVLR	99.7%	42.9	25	30.5	1	0	0	1127.68	185	194
39S ribosomal protein L21, mitochondrial	MRPL21	RM21_HUMAN	22.8	100.0%	4	4	6	0.01%	16.1%	KVNEMIVTGQYGR	99.7%	48	25	48	1	0	0	1510.77	82	94
39S ribosomal protein L21, mitochondrial	MRPL21	RM21_HUMAN	22.8	100.0%	4	4	6	0.01%	16.1%	LFAVVHFASR	99.7%	65	25	55.3	2	0	0	1146.64	95	104
39S ribosomal protein L21, mitochondrial	MRPL21	RM21_HUMAN	22.8	100.0%	4	4	6	0.01%	16.1%	VNEMIVTGQYGR	99.7%	70.2	25	46.2	2	0	0	1382.67	83	94
39S ribosomal protein L22, mitochondrial	MRPL22	RM22_HUMAN	23.6	100.0%	5	6	12	0.01%	25.7%	EVLLEAQDMAVR	99.7%	87.9	25	82	4	0	0	1389.70	113	124
39S ribosomal protein L22, mitochondrial	MRPL22	RM22_HUMAN	23.6	100.0%	5	6	12	0.01%	25.7%	EYIQQLR	99.7%	47.3	25	0	2	0	0	949.51	192	198
39S ribosomal protein L22, mitochondrial	MRPL22	RM22_HUMAN	23.6	100.0%	5	6	12	0.01%	25.7%	LVEGPPPPPEPPK	99.7%	64.2	25	64.2	2	0	0	1353.74	172	184
39S ribosomal protein L22, mitochondrial	MRPL22	RM22_HUMAN	23.6	100.0%	5	6	12	0.01%	25.7%	RPAEIYHCR	99.7%	38.8	25	35.8	0	2	0	1201.59	63	71
39S ribosomal protein L22, mitochondrial	MRPL22	RM22_HUMAN	23.6	100.0%	5	6	12	0.01%	25.7%	SNLYIAESTSGR	99.7%	103	25	99.8	2	0	0	1297.64	132	143
39S ribosomal protein L24, mitochondrial	MRPL24	RM24_HUMAN	24.9	100.0%	4	4	7	0.01%	19.9%	GTMIPSEAPLLHR	99.7%	38.5	25	38.2	0	2	0	1437.75	106	118
39S ribosomal protein L24, mitochondrial	MRPL24	RM24_HUMAN	24.9	100.0%	4	4	7	0.01%	19.9%	IIPKPEFPR	99.3%	36.7	25	30	1	0	0	1096.65	153	161
39S ribosomal protein L24, mitochondrial	MRPL24	RM24_HUMAN	24.9	100.0%	4	4	7	0.01%	19.9%	KPTEIEWR	99.1%	35.4	25.2	27.3	2	0	0	1058.56	129	136
39S ribosomal protein L24, mitochondrial	MRPL24	RM24_HUMAN	24.9	100.0%	4	4	7	0.01%	19.9%	TLQEEVMEAMGIK	99.7%	58.3	25	53.8	2	0	0	1478.72	193	205
39S ribosomal protein L27, mitochondrial	MRPL27	RM27_HUMAN	16.1	100.0%	2	2	3	0.00%	14.2%	CLYALEEGIVR	99.7%	41.2	25	35.3	1	0	0	1322.68	88	98
39S ribosomal protein L27, mitochondrial	MRPL27	RM27_HUMAN	16.1	100.0%	2	2	3	0.00%	14.2%	NTEAVDLITR	99.7%	68.2	25	57	2	0	0	1131.60	110	119
39S ribosomal protein L28, mitochondrial	MRPL28	RM28_HUMAN	30.2	100.0%	2	2	2	0.00%	5.9%	AAIYDKYK	99.2%	36.1	25	24.3	1	0	0	971.52	185	192
39S ribosomal protein L28, mitochondrial	MRPL28	RM28_HUMAN	30.2	100.0%	2	2	2	0.00%	5.9%	LPGHYLR	98.4%	33	25	21.4	1	0	0	855.48	24	30
39S ribosomal protein L32, mitochondrial	MRPL32	RM32_HUMAN	21.4	99.8%	2	2	3	0.00%	12.2%	HVLCAYCYEK	99.4%	37.4	25	37.3	2	0	0	1342.59	120	129
39S ribosomal protein L32, mitochondrial	MRPL32	RM32_HUMAN	21.4	99.8%	2	2	3	0.00%	12.2%	NNIDVCPECGHLK	99.7%	40.4	25	40.4	1	0	0	1555.70	105	117
39S ribosomal protein L33, mitochondrial	MRPL33	RM33_HUMAN	7.6	99.8%	2	3	4	0.00%	38.5%	LTLLHYDPVVK	98.0%	32	25	32	2	0	0	1297.75	41	51
39S ribosomal protein L33, mitochondrial	MRPL33	RM33_HUMAN	7.6	99.8%	2	3	4	0.00%	38.5%	MVSEAGTGFCFNTK	99.7%	55	25	54.7	2	0	0	1564.68	20	33
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	5	5	9	0.01%	16.3%	ESLLLQVR	99.7%	49.8	25	34.8	2	0	0	957.57	216	223
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	5	5	9	0.01%	16.3%	ETYCPVIVDNLIQLCK	99.7%	54.9	25	54.9	2	0	0	1964.98	174	189
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	5	5	9	0.01%	16.3%	MILFAFGSALAQAR	99.7%	48	25	46.2	1	0	0	1495.81	313	326
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	5	5	9	0.01%	16.3%	VLEQPVVVQSVGTDGR	99.7%	78.7	25	78	2	0	0	1682.91	335	350
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	5	5	9	0.01%	16.3%	VYEIPGLEPITFAGK	99.7%	82.1	25	77.2	2	0	0	1633.88	49	63
39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	6	6	10	0.01%	20.0%	DLFHGATFVPR	99.7%	50.4	25	42.2	2	0	0	1259.65	160	170
39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	6	6	10	0.01%	20.0%	LAEYYGLYR	99.7%	69.2	25	60.1	2	0	0	1147.58	151	159
39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	6	6	10	0.01%	20.0%	LAFLLFK	99.7%	40.1	25	36.6	2	0	0	851.54	268	274
39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	6	6	10	0.01%	20.0%	QDQPIDFSEDARPSPCYQLAQR	99.7%	34.9	25	32.8	0	1	0	2621.21	275	296
39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	6	6	10	0.01%	20.0%	TASVPLDAVR	98.2%	32.5	25	23.2	1	0	0	1028.57	127	136
39S ribosomal protein L38, mitochondrial	MRPL38	RM38_HUMAN	44.6	100.0%	6	6	10	0.01%	20.0%	VAEGQVTCPYLPPFPAR	99.7%	57	25	53.2	2	0	0	1901.96	245	261
39S ribosomal protein L39, mitochondrial	MRPL39	RM39_HUMAN	38.7	100.0%	4	4	6	0.01%	13.6%	DAHALIYK	99.5%	38.4	25	32.4	1	0	0	930.50	205	212
39S ribosomal protein L39, mitochondrial	MRPL39	RM39_HUMAN	38.7	100.0%	4	4	6	0.01%	13.6%	DLPFETLEVEAK	99.7%	77.9	25	66.4	2	0	0	1390.71	213	224
39S ribosomal protein L39, mitochondrial	MRPL39	RM39_HUMAN	38.7	100.0%	4	4	6	0.01%	13.6%	IGDFIDVSEGPLIPR	99.7%	55.2	25	53.9	2	0	0	1627.87	257	271
39S ribosomal protein L39, mitochondrial	MRPL39	RM39_HUMAN	38.7	100.0%	4	4	6	0.01%	13.6%	TDPGTVFVMNK	99.7%	40.3	25	39.4	1	0	0	1208.60	73	83
39S ribosomal protein L4, mitochondrial	MRPL4	RM04_HUMAN	34.9	100.0%	4	5	10	0.01%	18.3%	ATENPEQVASEGLPEPVLR	99.7%	94.4	25	91.9	2	0	0	2036.03	31	49
39S ribosomal protein L4, mitochondrial	MRPL4	RM04_HUMAN	34.9	100.0%	4	5	10	0.01%	18.3%	GPTSYYYMLPMK	99.7%	55	25	51.5	3	0	0	1482.66	157	168
39S ribosomal protein L4, mitochondrial	MRPL4	RM04_HUMAN	34.9	100.0%	4	5	10	0.01%	18.3%	KVELPVPTHR	98.9%	34.5	25	26.8	2	0	0	1175.69	50	59
39S ribosomal protein L4, mitochondrial	MRPL4	RM04_HUMAN	34.9	100.0%	4	5	10	0.01%	18.3%	VGLADLHPDVFATAPR	99.7%	40.4	25	40.4	1	2	0	1678.89	77	92
39S ribosomal protein L41, mitochondrial	MRPL41	RM41_HUMAN	15.4	100.0%	3	3	6	0.01%	22.6%	DFKDGTFDPDNLEK	98.3%	32.8	25	32.8	2	0	0	1640.74	103	116
39S ribosomal protein L41, mitochondrial	MRPL41	RM41_HUMAN	15.4	100.0%	3	3	6	0.01%	22.6%	LFQLYPR	99.7%	43	25	38.9	2	0	0	936.53	127	133
39S ribosomal protein L41, mitochondrial	MRPL41	RM41_HUMAN	15.4	100.0%	3	3	6	0.01%	22.6%	YGFEPTQEGK	99.7%	43.2	25	31.1	2	0	0	1155.53	117	126
39S ribosomal protein L43, mitochondrial	MRPL43	RM43_HUMAN	23.4	100.0%	4	4	8	0.01%	19.1%	EVIDFAR	97.1%	30.5	25	10.7	1	0	0	849.45	50	56
39S ribosomal protein L43, mitochondrial	MRPL43	RM43_HUMAN	23.4	100.0%	4	4	8	0.01%	19.1%	FLASVLHNGLGR	99.7%	55.3	25	48.1	2	0	0	1283.72	10	21
39S ribosomal protein L43, mitochondrial	MRPL43	RM43_HUMAN	23.4	100.0%	4	4	8	0.01%	19.1%	LADQSGLDVIR	99.7%	70	25	58.8	3	0	0	1186.64	104	114
39S ribosomal protein L43, mitochondrial	MRPL43	RM43_HUMAN	23.4	100.0%	4	4	8	0.01%	19.1%	SVEEISTLVQK	99.7%	62.7	25	37.4	2	0	0	1232.67	93	103
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	8	9	14	0.01%	31.6%	EAVLLNLK	98.8%	34.4	25	25.5	1	0	0	899.56	113	120
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	8	9	14	0.01%	31.6%	IINPMGLLVEELK	99.7%	53.7	25	53.5	3	0	0	1468.84	234	246

39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	8	9	14	0.01%	31.6%	LIAEGPGETVLVAEEEAAR	99.7%	131	25	131	2	0	0	1954.01	280	298
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	8	9	14	0.01%	31.6%	LQENFSLDLLK	99.7%	58.3	25	45.5	2	0	0	1319.72	79	89
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	8	9	14	0.01%	31.6%	LYGFTENR	99.7%	47.3	25	41.3	2	0	0	999.49	304	311
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	8	9	14	0.01%	31.6%	NLVDFLTGEEVVCHVAR	97.1%	30.5	25	30.5	1	0	0	1957.98	155	171
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	8	9	14	0.01%	31.6%	QSGGTTALPLYFVGLYCDK	99.7%	70	25	70	2	0	0	2090.03	260	278
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	8	9	14	0.01%	31.6%	TAFVNSCYIK	99.7%	46.3	25	44.3	1	0	0	1202.59	90	99
39S ribosomal protein L45, mitochondrial	MRPL45	RM45_HUMAN	35.4	100.0%	3	3	4	0.00%	7.8%	IKDFPEK	96.3%	29.5	25	2.22	1	0	0	876.48	134	140
39S ribosomal protein L45, mitochondrial	MRPL45	RM45_HUMAN	35.4	100.0%	3	3	4	0.00%	7.8%	IKDYDANFK	94.7%	28.1	25	20.5	1	0	0	1113.56	125	133
39S ribosomal protein L45, mitochondrial	MRPL45	RM45_HUMAN	35.4	100.0%	3	3	4	0.00%	7.8%	QTLAIYDR	99.7%	53.9	25	42	2	0	0	979.52	220	227
39S ribosomal protein L46, mitochondrial	MRPL46	RM46_HUMAN	31.7	100.0%	4	5	9	0.01%	15.4%	ALLLTGDFSQAGNK	99.7%	98.5	25	91.2	2	0	0	1434.76	236	249
39S ribosomal protein L46, mitochondrial	MRPL46	RM46_HUMAN	31.7	100.0%	4	5	9	0.01%	15.4%	NLVLLVR	99.4%	37	25	12.9	1	0	0	826.55	156	162
39S ribosomal protein L46, mitochondrial	MRPL46	RM46_HUMAN	31.7	100.0%	4	5	9	0.01%	15.4%	SLYSDHELR	98.1%	32.3	25	17	2	0	0	1119.54	82	90
39S ribosomal protein L46, mitochondrial	MRPL46	RM46_HUMAN	31.7	100.0%	4	5	9	0.01%	15.4%	TLATLSENNMEAK	99.7%	70.5	25	68.6	4	0	0	1421.69	191	203
39S ribosomal protein L47, mitochondrial	MRPL47	RM47_HUMAN	29.5	100.0%	6	7	11	0.01%	20.4%	KFPHLAEAQK	99.7%	42.9	25	27.7	2	0	0	1168.65	237	246
39S ribosomal protein L47, mitochondrial	MRPL47	RM47_HUMAN	29.5	100.0%	6	7	11	0.01%	20.4%	LLQTGQER	96.9%	30.2	25	20.5	1	0	0	944.52	155	162
39S ribosomal protein L47, mitochondrial	MRPL47	RM47_HUMAN	29.5	100.0%	6	7	11	0.01%	20.4%	NMLLTLEQEAK	99.4%	37.2	25	24	2	0	0	1289.68	110	120
39S ribosomal protein L47, mitochondrial	MRPL47	RM47_HUMAN	29.5	100.0%	6	7	11	0.01%	20.4%	NMLLTLEQEAKR	99.7%	54	25	40.2	3	0	0	1461.77	110	121
39S ribosomal protein L47, mitochondrial	MRPL47	RM47_HUMAN	29.5	100.0%	6	7	11	0.01%	20.4%	SGAAWTCQQLR	99.7%	46.4	25	41.7	2	0	0	1277.61	81	91
39S ribosomal protein L47, mitochondrial	MRPL47	RM47_HUMAN	29.5	100.0%	6	7	11	0.01%	20.4%	VVQEREDALR	96.5%	29.7	25	10.4	1	0	0	1214.65	145	154
39S ribosomal protein L48, mitochondrial	MRPL48	RM48_HUMAN	23.9	100.0%	3	4	8	0.01%	17.0%	ARPELEELLAK	99.7%	58.4	25	45.4	2	0	0	1268.72	200	210
39S ribosomal protein L48, mitochondrial	MRPL48	RM48_HUMAN	23.9	100.0%	3	4	8	0.01%	17.0%	MLLDSVLTTHER	99.7%	75.9	25	75.8	4	0	0	1414.74	144	155
39S ribosomal protein L48, mitochondrial	MRPL48	RM48_HUMAN	23.9	100.0%	3	4	8	0.01%	17.0%	TIEVLQLQDQGSK	99.7%	107	25	98.8	2	0	0	1458.78	131	143
39S ribosomal protein L49, mitochondrial	MRPL49	RM49_HUMAN	19.2	100.0%	4	4	7	0.01%	27.7%	FVESVDEYQFVER	99.7%	91.2	25	90.3	2	0	0	1646.77	38	50
39S ribosomal protein L49, mitochondrial	MRPL49	RM49_HUMAN	19.2	100.0%	4	4	7	0.01%	27.7%	GYFDQELK	97.9%	31.7	25	24.2	1	0	0	999.48	151	158
39S ribosomal protein L49, mitochondrial	MRPL49	RM49_HUMAN	19.2	100.0%	4	4	7	0.01%	27.7%	KVEGDIWALQK	99.7%	64	25	60	2	0	0	1286.71	112	122
39S ribosomal protein L49, mitochondrial	MRPL49	RM49_HUMAN	19.2	100.0%	4	4	7	0.01%	27.7%	TPVTQVNEVTGTLR	99.7%	86.5	25	86.5	2	0	0	1514.82	135	148
39S ribosomal protein L53, mitochondrial	MRPL53	RM53_HUMAN	12.1	99.8%	2	2	4	0.00%	20.5%	STNLNCSVIADVR	99.7%	56.6	25	56.6	2	0	0	1448.72	44	56
39S ribosomal protein L53, mitochondrial	MRPL53	RM53_HUMAN	12.1	99.8%	2	2	4	0.00%	20.5%	TFLQTVSSEK	99.7%	43.6	25	39.7	2	0	0	1139.59	32	41
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	6	7	12	0.01%	24.3%	ENLELILTQSVENVGVR	99.7%	55.4	25	55.4	3	0	0	1913.03	92	108
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	6	7	12	0.01%	24.3%	LLPQGLAVYASPENK	99.7%	63.7	25	51.6	2	0	0	1599.87	123	137
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	6	7	12	0.01%	24.3%	LLPQGLAVYASPENKK	99.7%	43.7	25	43.7	1	0	0	1727.97	123	138
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	6	7	12	0.01%	24.3%	LPEEPITR	99.7%	45	25	36	1	0	0	954.53	208	215
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	6	7	12	0.01%	24.3%	NLGVVVAPHTLK	99.4%	37.5	25	34.3	2	0	0	1247.75	196	207
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	6	7	12	0.01%	24.3%	VPMSVVNFEKPK	99.7%	46.2	25	36.8	3	0	0	1374.75	233	244
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	8	12	18	0.02%	46.7%	DLAPIGIR	95.2%	28.5	25	25.4	1	0	0	854.51	185	192
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	8	12	18	0.02%	46.7%	GGIVGMTLPIAR	99.7%	75.7	25	65	3	0	0	1200.68	173	184
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	8	12	18	0.02%	46.7%	GLVAVITGGASGLGLATAER	99.7%	132	25	132	1	1	0	1813.02	10	29
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	8	12	18	0.02%	46.7%	GQTHTLEDFQR	99.7%	45.7	25	44.2	2	1	0	1331.63	106	116
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	8	12	18	0.02%	46.7%	GVIINTASVAAFEGQVGQAAYSASK	99.7%	115	25	115	2	2	0	2439.25	148	172
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	8	12	18	0.02%	46.7%	LVAGEMGQNEPDQGGQR	99.7%	91.7	25	91.7	2	0	0	1785.82	131	147
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	8	12	18	0.02%	46.7%	VDVAVNCAGIAVASK	99.7%	110	25	109	2	0	0	1473.77	85	99
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	8	12	18	0.02%	46.7%	VLDVNLMGTFNVIR	99.5%	38.5	25	38.5	1	0	0	1606.86	117	130
3-ketoacyl-CoA thiolase, mitochondrial	ACAA2	THIM_HUMAN	41.9	99.8%	2	2	4	0.00%	5.5%	DFTATDLSEFAAK	99.7%	94.7	25	94.3	2	0	0	1415.67	26	38
3-ketoacyl-CoA thiolase, mitochondrial	ACAA2	THIM_HUMAN	41.9	99.8%	2	2	4	0.00%	5.5%	ETPALTINR	99.7%	47.7	25	41.3	2	0	0	1014.56	82	90
3-keto-steroid reductase	HSD17B7	DHB7_HUMAN	38.2	99.8%	2	2	4	0.00%	6.2%	ALFFGLFSR	99.7%	54.7	25	44.3	2	0	0	1057.58	103	111
3-keto-steroid reductase	HSD17B7	DHB7_HUMAN	38.2	99.8%	2	2	4	0.00%	6.2%	YATDLLSVALNR	99.7%	54	25	53.6	2	0	0	1335.73	198	209
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	5	6	21	0.02%	20.6%	AEAGAGSATEFQFR	99.7%	93.6	25	86	4	0	0	1441.67	140	153
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	5	6	21	0.02%	20.6%	EQFAWR	95.1%	28.4	25	11.4	1	0	0	836.40	60	65
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	5	6	21	0.02%	20.6%	GYVKEQFAWR	99.7%	53.5	25	43.7	4	0	0	1283.65	56	65
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	5	6	21	0.02%	20.6%	IAIYELLFK	99.7%	64.9	25	64.9	4	0	0	1109.66	9	17
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	5	6	21	0.02%	20.6%	KAEAGAGSATEFQFR	99.7%	116	25	110	4	4	0	1569.77	139	153

40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	17	46	0.05%	53.8%	CPFTGNVSIR	99.7%	64.8	25	47	10	0	0	1150.57	60	69
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	17	46	0.05%	53.8%	DVQIGDIVTVGECRPLSK	99.7%	96.2	25	91.1	4	2	0	1986.03	119	136
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	17	46	0.05%	53.8%	DYLHYIR	99.2%	36	25	23.7	3	0	0	979.50	91	97
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	17	46	0.05%	53.8%	EAIEGTYIDK	99.7%	64.1	25	51.6	2	0	0	1138.56	49	58
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	17	46	0.05%	53.8%	EAIEGTYIDKK	99.7%	57.9	25	45.6	8	2	0	1266.66	49	59
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	17	46	0.05%	53.8%	ILSGVVTK	99.7%	47.4	25	24.6	1	0	0	816.52	72	79
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	17	46	0.05%	53.8%	KCPFTGNVSIR	99.7%	43.8	25	33.8	2	0	0	1278.66	59	69
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	17	46	0.05%	53.8%	NMSVHLSPCFR	99.7%	60.7	25	50.4	4	1	0	1363.62	108	118
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	17	46	0.05%	53.8%	QPTIFQNK	96.9%	30.2	25	18.5	2	0	0	975.53	13	20
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	17	46	0.05%	53.8%	RDYLHYIR	99.3%	36.9	25	15.8	1	0	0	1135.60	90	97
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	17	46	0.05%	53.8%	RVLLGETGK	99.4%	37.4	25	23.3	1	0	0	972.58	22	30
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	17	46	0.05%	53.8%	VLLGETGK	98.8%	34.2	25	28.7	1	0	0	816.48	23	30
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	17	46	0.05%	53.8%	VLLGETGKEK	99.7%	53.5	25	31.4	2	0	0	1073.62	23	32
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	10	33	0.03%	57.6%	DVIEEYFK	99.2%	35.8	25	35.8	1	0	0	1042.51	122	129
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	10	33	0.03%	57.6%	ESQAKDVIEEYFK	99.7%	56	25	46.6	2	0	0	1585.77	117	129
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	10	33	0.03%	57.6%	KVVGCSCVVVK	99.7%	58.5	25	49.3	5	0	0	1234.66	102	112
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	10	33	0.03%	57.6%	LGEWVGLCK	99.7%	59.6	25	56.1	8	0	0	1061.55	85	93
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	10	33	0.03%	57.6%	LVEALCAEHQINLIK	99.7%	66.3	25	66.3	2	2	0	1750.95	64	78
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	10	33	0.03%	57.6%	QAHLCVLASNCDEPMYVK	99.7%	57	25	46.8	0	4	0	2150.97	46	63
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	10	33	0.03%	57.6%	TALIHDGLAR	99.7%	57.5	25	39	5	0	0	1066.60	24	33
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	10	33	0.03%	57.6%	VVGCSCVVVK	99.7%	52.9	25	42.4	4	0	0	1106.57	103	112
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	7	9	33	0.03%	43.7%	GLAPDLPEDLYHLIK	99.7%	69.7	25	61.1	4	0	0	1693.92	79	93
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	7	9	33	0.03%	43.7%	GLTPSQIGVILR	99.7%	79.6	25	65.4	4	0	0	1253.76	44	55
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	7	9	33	0.03%	43.7%	KGLTPSQIGVILR	99.7%	85.1	25	85.1	4	2	0	1381.85	43	55
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	7	9	33	0.03%	43.7%	LILIESR	99.7%	45.2	25	25.4	4	0	0	843.53	115	121
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	7	9	33	0.03%	43.7%	LTSDDVKEQIYK	99.7%	83.5	25	82.9	10	2	0	1438.74	28	39
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	7	9	33	0.03%	43.7%	RSVPTWLK	97.1%	30.4	25	3.13	1	0	0	986.58	20	27
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	7	9	33	0.03%	43.7%	YESSTASALVA	99.7%	41.2	25	41.2	2	0	0	1098.53	141	151
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	16	70	0.07%	41.7%	ADRDESSPYAAMLAAQDVAQR	99.7%	55.4	25	55.4	2	6	0	2281.05	64	84
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	16	70	0.07%	41.7%	CKELGITALHIK	99.7%	70.3	25	58.5	4	2	0	1382.78	85	96
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	16	70	0.07%	41.7%	DESSPYAAMLAAQDVAQR	99.7%	92.3	25	76.4	8	0	0	1922.89	67	84
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	16	70	0.07%	41.7%	ELGITALHIK	99.7%	55.7	25	46.4	4	0	0	1094.66	87	96
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	16	70	0.07%	41.7%	IEDVTPIPSDSTR	99.7%	64.6	25	57.8	6	0	0	1429.72	129	141
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	16	70	0.07%	41.7%	IEDVTPIPSDSTRR	99.7%	51.1	25	48.2	2	3	0	1585.82	129	142
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	16	70	0.07%	41.7%	IGRIEDVTPIPSDSTR	99.7%	68	25	67.6	4	4	0	1755.92	126	141
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	16	70	0.07%	41.7%	TKTPGPGAQSALR	99.7%	49.9	25	39.6	4	4	0	1283.71	105	117
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	16	70	0.07%	41.7%	TPGPGAQSALR	99.7%	77.9	25	77.9	17	0	0	1054.56	107	117
40S ribosomal protein S15	RPS15	RS15_HUMAN	17.0	100.0%	3	7	21	0.02%	22.1%	DMIILPEMVGSMVGVYNGK	99.7%	87.5	25	53.8	10	0	0	2085.01	82	100
40S ribosomal protein S15	RPS15	RS15_HUMAN	17.0	100.0%	3	7	21	0.02%	22.1%	EAPPMEKPEVVK	99.7%	56.1	25	43	4	0	0	1353.71	66	77
40S ribosomal protein S15	RPS15	RS15_HUMAN	17.0	100.0%	3	7	21	0.02%	22.1%	KEAPPMEKPEVVK	99.7%	58.5	25	51.4	2	5	0	1497.80	65	77
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	10	14	50	0.05%	60.0%	DLEKWQNNLLPSR	98.6%	33.6	25	28.8	1	0	0	1612.84	85	97
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	10	14	50	0.05%	60.0%	FDVQLKDLEK	99.7%	58.1	25	17.1	8	2	0	1234.67	79	88
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	10	14	50	0.05%	60.0%	FLTVMMK	99.7%	42.6	25	22.5	8	0	0	869.46	37	43
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	10	14	50	0.05%	60.0%	HGYIGEFEIIDDHR	99.7%	78.2	25	69.6	2	4	0	1700.80	44	57
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	10	14	50	0.05%	60.0%	IVVNLTGR	99.7%	51.6	25	41.9	4	0	0	871.54	61	68
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	10	14	50	0.05%	60.0%	LNKCGVISPR	99.5%	37.9	25	27.7	1	0	0	1143.63	69	78
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	10	14	50	0.05%	60.0%	MNVLADALK	99.7%	57.9	25	34.5	12	0	0	990.53	4	12
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	10	14	50	0.05%	60.0%	QVLIRPCSK	98.9%	34.6	25	18.8	2	0	0	1100.62	24	32
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	10	14	50	0.05%	60.0%	VRMNVLADALK	99.7%	38.5	25	30.6	0	2	0	1245.70	2	12
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	10	14	50	0.05%	60.0%	WQNNLLPSR	99.7%	42.8	25	41.2	4	0	0	1127.60	89	97
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	19	89	0.09%	54.8%	ALVAYYQK	99.7%	48.4	25	46.9	7	0	0	955.52	91	98

40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	19	89	0.09%	54.8%	DILIQYDR	99.7%	46	25	27.4	2	0	0	1035.55	110	117
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	19	89	0.09%	54.8%	EIKDILIQYDR	99.7%	76.3	25	67.5	11	6	0	1405.77	107	117
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	19	89	0.09%	54.8%	GGGHVAQIYAIR	99.7%	60.8	25	58.3	8	2	0	1241.68	74	85
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	19	89	0.09%	54.8%	GPLQSVQVFGR	99.7%	82.6	25	68.3	5	0	0	1187.65	5	15
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	19	89	0.09%	54.8%	LLEPVLLLGK	99.7%	56.3	25	56.3	9	0	0	1094.72	51	60
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	19	89	0.09%	54.8%	LLEPVLLLGKER	99.7%	74.4	25	74.4	4	0	0	1379.86	51	62
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	19	89	0.09%	54.8%	PSKGPLQSVQVFGR	99.7%	67.4	25	67.4	4	4	0	1499.83	2	15
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	19	89	0.09%	54.8%	TLLVADPR	99.7%	48.9	25	19.9	7	0	0	884.52	118	125
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	19	89	0.09%	54.8%	TLLVADPRR	99.7%	46.5	25	36.2	4	0	0	1040.62	118	126
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	19	89	0.09%	54.8%	VKGGGHVAQIYAIR	99.7%	71.4	25	70.7	2	2	0	1468.84	72	85
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	19	89	0.09%	54.8%	VNGRPLEMIEPR	99.7%	35.1	25	34.2	5	7	0	1426.75	34	45
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	9	14	42	0.04%	47.4%	IAGYVTHLMK	99.7%	54	25	43.8	11	0	0	1132.62	50	59
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	9	14	42	0.04%	47.4%	IAGYVTHLMKR	99.2%	29.9	25	27.5	1	1	0	1304.71	50	60
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	9	14	42	0.04%	47.4%	LGNDFHTNK	99.7%	60.4	25	46.5	3	0	0	1045.51	24	32
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	9	14	42	0.04%	47.4%	LGNDFHTNKR	99.7%	43	25	30.3	4	5	0	1201.61	24	33
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	9	14	42	0.04%	47.4%	LLDFGSLSNLQVTQPTVGMNFK	99.7%	44.2	25	42.6	4	2	0	2425.24	108	129
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	9	14	42	0.04%	47.4%	RVCEEIAIIPSK	99.2%	36.2	25	28.1	2	0	0	1414.77	33	44
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	9	14	42	0.04%	47.4%	VCEEIAIIPSK	99.7%	72.7	25	45.3	4	0	0	1258.67	34	44
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	9	14	42	0.04%	47.4%	VCEEIAIIPSKK	99.7%	62.4	25	49.6	4	0	0	1386.77	34	45
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN	15.6	100.0%	9	14	42	0.04%	47.4%	VIIEKYYTR	99.7%	62.5	25	54.7	1	0	0	1184.67	15	23
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	18	22	77	0.08%	65.1%	ADIDLTKR	99.7%	61.8	25	40.7	2	0	0	931.52	48	55
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	18	22	77	0.08%	65.1%	AGELTEDEVER	99.7%	58.4	25	55.6	7	0	0	1247.58	56	66
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	18	22	77	0.08%	65.1%	DGKYSQVLANGLDNK	99.7%	59.2	25	59.2	2	1	0	1621.82	92	106
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	18	22	77	0.08%	65.1%	FQHILR	97.3%	30.7	25	17	2	0	0	813.47	9	14
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	18	22	77	0.08%	65.1%	HFWGLR	99.0%	35.2	25	26.4	2	0	0	815.43	125	130
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	18	22	77	0.08%	65.1%	IAFAITAIK	99.7%	72.8	25	62	2	0	0	947.59	26	34
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	18	22	77	0.08%	65.1%	IPDWFLNR	99.7%	50.8	25	38.4	14	0	0	1060.56	79	86
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	18	22	77	0.08%	65.1%	KADIDLTK	99.7%	41.6	25	31.1	4	0	0	903.51	47	54
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	18	22	77	0.08%	65.1%	KIAFAITAIK	99.7%	55.6	25	55.6	2	0	0	1075.69	25	34
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	18	22	77	0.08%	65.1%	LREDLER	97.9%	31.8	25	8.8	1	0	0	930.50	107	113
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	18	22	77	0.08%	65.1%	RAGELTEDEVER	99.7%	67.3	25	54.2	5	2	0	1403.68	55	66
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	18	22	77	0.08%	65.1%	RYAHVVLR	96.1%	29.3	25	13.5	1	0	0	1013.60	39	46
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	18	22	77	0.08%	65.1%	VITIMQNPR	99.7%	63.3	25	50.4	12	0	0	1071.60	67	75
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	18	22	77	0.08%	65.1%	VLNTNIDGR	99.7%	59.5	25	55.1	9	0	0	1001.54	15	23
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	18	22	77	0.08%	65.1%	VLNTNIDGRR	95.3%	28.5	25	16.8	1	0	0	1157.64	15	24
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	18	22	77	0.08%	65.1%	YAHVVLRK	98.4%	32.9	25	26.7	2	0	0	985.59	40	47
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	18	22	77	0.08%	65.1%	YSQVLANGLDNK	99.7%	97.2	25	88.9	2	0	0	1321.67	95	106
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	18	22	77	0.08%	65.1%	YSQVLANGLDNKLR	99.7%	85.6	25	77.1	2	2	0	1590.86	95	108
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	22	0.02%	55.9%	ALAAFLKK	97.0%	30.3	25	26.6	2	0	0	861.56	17	24
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	22	0.02%	55.9%	DLDRIAGQVAAANK	97.8%	25.9	25	25.9	0	1	0	1441.78	130	143
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	22	0.02%	55.9%	DVNQQEFVR	99.7%	64.1	25	51.3	7	0	0	1134.55	8	16
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	22	0.02%	55.9%	ELAPYDENWFYTR	99.7%	68.2	25	61.3	2	0	0	1703.77	44	56
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	22	0.02%	55.9%	IAGQVAAANK	99.7%	59.8	25	52.2	2	0	0	942.54	134	143
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	22	0.02%	55.9%	LKVPEWVDTVK	99.7%	62.9	25	46.7	1	1	0	1313.75	28	38
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	22	0.02%	55.9%	NGVMPSHFSR	95.0%	28.3	25	20.5	1	0	0	1147.53	85	94
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	22	0.02%	55.9%	PGVTVKDVNQQEFVR	95.8%	29	25	28.9	1	0	0	1715.91	2	16
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	22	0.02%	55.9%	RVLQALEGLK	98.1%	32.1	25	14.5	2	0	0	1126.69	102	111
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	11	22	0.02%	55.9%	VLQALEGLK	99.7%	67.1	25	51.6	2	0	0	970.59	103	111
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	12	20	85	0.08%	43.7%	AEDKEWMPVTK	99.7%	66.4	25	44.3	6	2	0	1349.64	55	65
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	12	20	85	0.08%	43.7%	AFVAIGDYNGHVGLGVK	99.7%	90.9	25	90.1	7	2	0	1716.91	126	142
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	12	20	85	0.08%	43.7%	ATFDAISK	99.7%	44.6	25	26.5	2	0	0	852.45	239	246

40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	12	20	85	0.08%	43.7%	GCTATLGNFAK	99.7%	62.9	25	55.1	8	0	0	1139.55	228	238
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	12	20	85	0.08%	43.7%	GTGIVSAPVPK	99.7%	51.3	25	51.3	6	0	0	1025.60	201	211
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	12	20	85	0.08%	43.7%	IGKPHTVPCK	99.7%	41.2	25	30.5	2	0	0	1136.62	174	183
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	12	20	85	0.08%	43.7%	KLLMMAGIDDCYTSAR	99.7%	99.3	25	96.3	5	8	0	1844.87	212	227
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	12	20	85	0.08%	43.7%	LLMMAGIDDCYTSAR	99.7%	82.5	25	15.1	8	0	0	1732.77	213	227
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	12	20	85	0.08%	43.7%	LSIVPVRR	99.7%	42.8	25	24.5	6	0	0	939.61	160	167
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	12	20	85	0.08%	43.7%	SLEEIYLFSLPIK	99.7%	104	25	101	7	0	0	1551.87	77	89
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	12	20	85	0.08%	43.7%	SPYQEFTDHLVK	99.7%	62	25	55.1	5	4	0	1463.72	264	275
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	12	20	85	0.08%	43.7%	TYSYLTPDLWK	99.7%	68.4	25	66.7	7	0	0	1386.69	247	257
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	5	8	20	0.02%	29.4%	DTGKTPVEPEVAIHR	99.7%	71.5	25	71.5	2	2	0	1648.87	5	19
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	5	8	20	0.02%	29.4%	LIDLHSPSEIVK	99.7%	53.5	25	40.6	5	2	0	1350.76	88	99
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	5	8	20	0.02%	29.4%	RLIDLHSPSEIVK	99.7%	52.7	25	42.7	2	0	0	1506.86	87	99
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	5	8	20	0.02%	29.4%	TPVEPEVAIHR	99.7%	59.7	25	59.7	2	3	0	1247.67	9	19
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	5	8	20	0.02%	29.4%	VCADLIR	99.7%	40.7	25	28.4	2	0	0	846.45	35	41
40S ribosomal protein S21	RPS21	RS21_HUMAN	9.1	99.8%	2	2	6	0.01%	22.9%	MGESDDSILR	99.7%	60.1	25	53.3	2	0	0	1138.50	62	71
40S ribosomal protein S21	RPS21	RS21_HUMAN	9.1	99.8%	2	2	6	0.01%	22.9%	TYAICGAIR	99.3%	36.9	25	32.7	4	0	0	1024.52	52	60
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	5	6	21	0.02%	29.4%	AHLGTALK	99.0%	35	25	21	2	0	0	810.48	30	37
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	5	6	21	0.02%	29.4%	ANPFGGASHAK	99.7%	52.9	25	49.5	11	0	0	1056.52	38	48
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	5	6	21	0.02%	29.4%	GHAVGDIPGVR	99.7%	41.4	25	34.3	2	0	0	1077.58	109	119
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	5	6	21	0.02%	29.4%	KGHAVGDIPGVR	99.7%	57.2	25	38.5	2	2	0	1205.68	108	119
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	5	6	21	0.02%	29.4%	VANVSLLALYK	99.7%	88.3	25	88.3	2	0	0	1190.71	125	135
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	10	49	0.05%	30.1%	KQMVIDVLHPGK	99.7%	57.9	25	57.9	2	4	0	1380.77	21	32
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	10	49	0.05%	30.1%	QMVIDVLHPGK	99.7%	62.2	25	59.5	4	1	0	1236.68	22	32
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	10	49	0.05%	30.1%	TTGFGMIYDSLDYAK	99.7%	77.8	25	77.8	21	0	0	1681.78	69	83
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	10	49	0.05%	30.1%	TTGFGMIYDSLDYAKK	99.7%	56.1	25	56.1	2	0	0	1809.87	69	84
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	10	49	0.05%	30.1%	TTPDVIFVFGFR	99.7%	56.8	25	56.8	15	0	0	1398.74	50	61
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	7	8	40	0.04%	36.0%	AALQELLSK	99.7%	64.9	25	51.4	12	0	0	972.57	86	94
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	7	8	40	0.04%	36.0%	AQVIYTR	99.2%	36.1	25	28.6	3	0	0	850.48	105	111
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	7	8	40	0.04%	36.0%	ATYDKLCK	98.8%	34.1	25	27.4	2	0	0	998.50	53	60
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	7	8	40	0.04%	36.0%	DKLNNLVLFDK	99.7%	60.9	25	56.6	5	2	0	1318.74	42	52
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	7	8	40	0.04%	36.0%	LITPAVVSER	99.7%	66.7	25	54.7	13	0	0	1084.64	67	76
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	7	8	40	0.04%	36.0%	LNNLVLFDK	99.7%	52.9	25	46.5	2	0	0	1075.61	44	52
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	7	8	40	0.04%	36.0%	LNNLVLFDKATYDK	99.7%	46.6	25	46.6	1	0	0	1653.88	44	57
40S ribosomal protein S26	RPS26	RS26_HUMAN	13.0	100.0%	4	5	30	0.03%	44.3%	DISEASVFDAYVLPK	99.7%	83.7	25	71.6	15	0	0	1653.84	52	66
40S ribosomal protein S26	RPS26	RS26_HUMAN	13.0	100.0%	4	5	30	0.03%	44.3%	FRPAGAAPRPPPKPM	99.7%	46.8	25	45.3	1	0	0	1589.87	101	115
40S ribosomal protein S26	RPS26	RS26_HUMAN	13.0	100.0%	4	5	30	0.03%	44.3%	LHYCVSCAIHSK	99.7%	71.8	25	70.6	2	2	0	1474.69	71	82
40S ribosomal protein S26	RPS26	RS26_HUMAN	13.0	100.0%	4	5	30	0.03%	44.3%	NIVEAAAVR	99.7%	67.7	25	57.7	10	0	0	942.54	43	51
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	5	10	33	0.03%	40.5%	DLLHPSPEEEK	99.7%	45.2	25	39.4	2	2	0	1293.63	6	16
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	5	10	33	0.03%	40.5%	DLLHPSPEEEKR	99.5%	32.3	25	32.3	2	1	0	1449.73	6	17
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	5	10	33	0.03%	40.5%	LTEGCSFR	99.7%	50.9	25	48.8	6	0	0	969.45	73	80
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	5	10	33	0.03%	40.5%	LVQSPNSYFMDVK	99.7%	73.6	25	71.7	17	0	0	1527.75	24	36
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	5	10	33	0.03%	40.5%	RLVQSPNSYFMDVK	99.7%	42.3	25	42.3	2	1	0	1699.85	23	36
40S ribosomal protein S28	RPS28	RS28_HUMAN	7.8	99.8%	2	2	4	0.00%	30.4%	EGDVLTLLESER	99.7%	73	25	61.7	2	0	0	1360.70	52	63
40S ribosomal protein S28	RPS28	RS28_HUMAN	7.8	99.8%	2	2	4	0.00%	30.4%	VEFMDDTSR	99.1%	35.6	25	35.6	2	0	0	1115.47	32	40
40S ribosomal protein S29	RPS29	RS29_HUMAN	6.7	99.8%	2	2	2	0.00%	14.3%	KYGLNMCR	98.3%	32.8	25	29.8	1	0	0	1057.49	33	40
40S ribosomal protein S29	RPS29	RS29_HUMAN	6.7	99.8%	2	2	2	0.00%	14.3%	YGLNMCR	98.3%	32.8	25	32.8	1	0	0	913.40	34	40
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	28	119	0.12%	76.5%	ACYGVLR	99.7%	43.5	25	29.8	2	0	0	838.42	118	124
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	28	119	0.12%	76.5%	AELNEFLTR	99.7%	70.5	25	54.5	11	0	0	1092.57	19	27
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	28	119	0.12%	76.5%	DEILPTTPISEQK	99.7%	79.8	25	64.7	5	0	0	1470.77	215	227
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	28	119	0.12%	76.5%	ELAEDGYSGVEVR	99.7%	90.7	25	82.5	14	0	0	1423.67	28	40
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	28	119	0.12%	76.5%	ELTAVVQK	99.7%	49.7	25	32.8	2	0	0	887.52	68	75

40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	28	119	0.12%	76.5%	FGFPEGSVELYAEK	99.7%	86.8	25	78.5	12	0	0	1572.76	77	90
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	28	119	0.12%	76.5%	FIMESGAK	99.7%	47.9	25	25.2	4	0	0	898.43	125	132
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	28	119	0.12%	76.5%	FVADGIFK	99.7%	44.6	25	38.8	2	0	0	896.49	11	18
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	28	119	0.12%	76.5%	FVDGLMIHSGDPVNYYVDTAVR	99.7%	81.2	25	81.2	4	5	0	2468.19	152	173
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	28	119	0.12%	76.5%	GCEVVVSGK	99.7%	56.6	25	51.3	2	0	0	934.47	133	141
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	28	119	0.12%	76.5%	GCEVVVSGKLR	99.7%	45.2	25	36.5	1	0	0	1203.65	133	143
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	28	119	0.12%	76.5%	GGKPEPPAMPQPVPTA	99.7%	53	25	47.9	8	0	0	1589.80	228	243
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	28	119	0.12%	76.5%	GLCAIAQAESLR	99.7%	78.6	25	62.9	10	0	0	1288.67	95	106
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	28	119	0.12%	76.5%	IMLPWDPTGK	99.7%	45.9	25	40.1	6	0	0	1173.60	188	197
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	28	119	0.12%	76.5%	IRELTAVVQK	99.7%	49.4	25	39.1	3	0	0	1156.70	66	75
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	28	119	0.12%	76.5%	KFVADGIFK	99.7%	42.2	25	28.2	3	0	0	1024.58	10	18
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	28	119	0.12%	76.5%	KPLPDHVSIVEPK	99.7%	47.4	25	42.4	2	2	0	1458.83	202	214
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	28	119	0.12%	76.5%	RACYGVLR	96.2%	29.4	25	15.6	1	0	0	994.53	117	124
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	28	119	0.12%	76.5%	RFGFPEGSVELYAEK	99.7%	49.5	25	42	1	0	0	1728.86	76	90
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	28	119	0.12%	76.5%	TEIIILATR	99.7%	64.8	25	63.6	17	0	0	1029.63	46	54
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	21	28	119	0.12%	76.5%	TQNVLGEK	99.7%	41	25	23.4	2	0	0	888.48	55	62
40S ribosomal protein S30	FAU	RS30_HUMAN	6.6	100.0%	3	3	10	0.01%	20.3%	FVNVVPTFGK	99.7%	47.8	25	47.8	8	0	0	1107.62	42	51
40S ribosomal protein S30	FAU	RS30_HUMAN	6.6	100.0%	3	3	10	0.01%	20.3%	FVNVVPTFGKK	97.1%	30.5	25	30.5	1	0	0	1235.71	42	52
40S ribosomal protein S30	FAU	RS30_HUMAN	6.6	100.0%	3	3	10	0.01%	20.3%	RFVNVVPTFGK	96.3%	29.4	25	29.4	1	0	0	1263.72	41	51
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	18	28	118	0.12%	62.5%	ACQSIYPLHDVFVR	99.7%	79.4	25	71.7	4	5	0	1704.85	200	213
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	18	28	118	0.12%	62.5%	ADGYEPPVQESV	99.7%	61	25	61	4	0	0	1290.58	253	264
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	18	28	118	0.12%	62.5%	APAMFNIR	99.7%	59.9	25	52.9	10	0	0	919.48	35	42
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	18	28	118	0.12%	62.5%	ATGDETGAKVER	99.7%	44.5	25	34.2	1	0	0	1233.61	241	252
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	18	28	118	0.12%	62.5%	DWYDVK	99.1%	35.6	25	25.4	2	0	0	825.38	29	34
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	18	28	118	0.12%	62.5%	EVQTNDLKEVVNK	99.7%	84.2	25	76.4	6	0	0	1515.80	175	187
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	18	28	118	0.12%	62.5%	KDWYDVK	95.0%	28.3	25	14	1	0	0	953.47	28	34
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	18	28	118	0.12%	62.5%	KMMEIMTR	98.8%	34.1	25	25	2	0	0	1039.51	167	174
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	18	28	118	0.12%	62.5%	LFCVGFTK	99.7%	49.6	25	36.1	6	0	0	971.50	137	144
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	18	28	118	0.12%	62.5%	LIPDSIGKDIEK	99.7%	57.2	25	50.4	6	0	0	1327.75	188	199
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	18	28	118	0.12%	62.5%	LITEDVQGK	99.7%	61.5	25	42.2	7	0	0	1002.55	86	94
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	18	28	118	0.12%	62.5%	LMELHGEGSSSGK	99.7%	77.2	25	73.5	12	6	0	1347.62	228	240
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	18	28	118	0.12%	62.5%	MMEIMTR	99.7%	45.3	25	13.3	8	0	0	927.41	168	174
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	18	28	118	0.12%	62.5%	NCLTNFHGMDLTR	99.7%	76.8	25	67.6	8	6	0	1578.72	95	107
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	18	28	118	0.12%	62.5%	TSYAQHQQVR	99.7%	79.2	25	60.4	4	1	0	1217.60	153	162
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	18	28	118	0.12%	62.5%	TTDGYLLR	99.7%	65.6	25	39.9	7	0	0	938.49	129	136
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	18	28	118	0.12%	62.5%	VFEVSLADLQNDEVAFR	99.7%	91.1	25	90.3	6	0	0	1951.98	66	82
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	18	28	118	0.12%	62.5%	VFEVSLADLQNDEVAFRK	99.7%	98.8	25	98.8	2	4	0	2080.07	66	83
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	20	29	126	0.12%	65.0%	DANGNSFATR	99.7%	73.5	25	67.2	4	0	0	1052.48	212	221
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	20	29	126	0.12%	65.0%	ECLPLIIFLR	99.7%	58.2	25	51.6	6	0	0	1273.73	40	49
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	20	29	126	0.12%	65.0%	ERHPGSFDVVHVK	99.7%	61.1	25	56	2	4	0	1506.78	199	211
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	20	29	126	0.12%	65.0%	FDTGNLCMVTGGANLGR	99.7%	109	25	108	11	2	0	1782.83	175	191
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	20	29	126	0.12%	65.0%	GIPHLVTHDAR	99.7%	57.9	25	50.3	4	3	0	1215.66	135	145
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	20	29	126	0.12%	65.0%	GNKPWISLPR	99.7%	43.7	25	37.8	5	0	0	1167.66	231	240
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	20	29	126	0.12%	65.0%	HPGSFDVVHVK	99.7%	55.9	25	55.5	3	3	0	1221.64	201	211
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	20	29	126	0.12%	65.0%	ITPEEAKYK	99.0%	34.9	25	21.1	1	0	0	1078.58	114	122
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	20	29	126	0.12%	65.0%	LRECLPLIIFLR	99.7%	46.9	25	46.9	2	4	0	1542.92	38	49
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	20	29	126	0.12%	65.0%	LSNIFVIGK	99.7%	63.4	25	57.8	15	0	0	990.60	222	230
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	20	29	126	0.12%	65.0%	LTGVFAPRPSTGPHK	99.7%	57.8	25	50.4	4	0	0	1564.86	23	37
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	20	29	126	0.12%	65.0%	LTIAEER	99.5%	38.2	25	12.6	7	0	0	831.46	246	252
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	20	29	126	0.12%	65.0%	TDITYPAGFMDVISIDK	99.7%	79.6	25	79.6	13	0	0	1885.93	78	94
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	20	29	126	0.12%	65.0%	TIRYPDPLIK	99.7%	38.1	25	27.9	1	4	0	1215.71	146	155

40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	20	29	126	0.12%	65.0%	VNDTIQIDLETGK	99.7%	107	25	107	10	0	0	1445.75	156	168
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	20	29	126	0.12%	65.0%	VNDTIQIDLETGKITDFIK	97.3%	25.1	25	25.1	0	1	0	2163.15	156	174
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	20	29	126	0.12%	65.0%	VRTDITYPAGFMDVISIDK	99.7%	43.3	25	36.8	0	2	0	2157.09	76	94
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	20	29	126	0.12%	65.0%	YALTGDEVK	99.7%	53	25	44.7	5	0	0	995.50	54	62
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	20	29	126	0.12%	65.0%	YALTGDEVKK	99.7%	62.3	25	51.1	6	0	0	1123.60	54	63
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	20	29	126	0.12%	65.0%	YPDPLIK	99.6%	39.1	25	17.4	4	0	0	845.48	149	155
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	5	5	12	0.01%	27.5%	KAQCPIVER	99.7%	41.8	25	37.1	2	0	0	1100.59	63	71
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	5	5	12	0.01%	27.5%	LTNSMMMHGR	99.7%	40.4	25	40.4	1	0	0	1177.53	72	81
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	5	5	12	0.01%	27.5%	QAVDVSPLR	99.7%	72.9	25	61.7	3	0	0	984.55	137	145
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	5	5	12	0.01%	27.5%	TIAECLADELINAAK	99.7%	113	25	108	2	0	0	1631.83	168	182
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	5	5	12	0.01%	27.5%	VNQAIWLLCTGAR	99.7%	87.7	25	81.2	4	0	0	1501.79	147	159
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	14	19	56	0.06%	45.4%	DIPGLTDTTVPR	99.7%	80.4	25	68.2	12	0	0	1284.68	120	131
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	14	19	56	0.06%	45.4%	GCIVDANLSVLNLVIVK	99.7%	109	25	88.3	5	0	0	1827.04	99	115
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	14	19	56	0.06%	45.4%	ISGGNDKQGFPMK	99.3%	36.5	25	36.5	1	0	0	1394.67	52	64
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	14	19	56	0.06%	45.4%	KLFNLSK	99.7%	43.7	25	26	2	0	0	849.52	143	149
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	14	19	56	0.06%	45.4%	LFNLSKEDDVR	99.7%	57.7	25	43.9	3	2	0	1335.69	144	154
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	14	19	56	0.06%	45.4%	LIEVDDER	99.7%	53.8	25	46.9	6	0	0	988.49	15	22
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	14	19	56	0.06%	45.4%	LIEVDDERK	99.7%	47.8	25	37.4	2	0	0	1116.59	15	23
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	14	19	56	0.06%	45.4%	LNISFPATGCQK	99.7%	72.8	25	71.5	2	0	0	1335.67	3	14
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	14	19	56	0.06%	45.4%	MATEVAADALGEEWK	99.7%	117	25	116	8	0	0	1620.76	32	46
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	14	19	56	0.06%	45.4%	MATEVAADALGEEWKGYVVR	99.7%	80	25	80	3	4	0	2195.08	32	51
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	14	19	56	0.06%	45.4%	MKLNISFPATGCQK	99.7%	75.6	25	62.3	2	0	0	1610.80	1	14
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	14	19	56	0.06%	45.4%	NKEEAAEYAK	99.6%	40	25	31	2	0	0	1152.55	202	211
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	14	19	56	0.06%	45.4%	RMATEVAADALGEEWK	99.7%	38.1	25	34.2	0	1	0	1792.85	31	46
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	14	19	56	0.06%	45.4%	TFYEKR	94.8%	28.1	25	21.2	1	0	0	843.44	26	31
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	14	15	33	0.03%	54.6%	AIIIFVPVPQLK	99.7%	65.2	25	65.2	6	0	0	1337.86	59	70
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	14	15	33	0.03%	54.6%	AQQNNVEHKVETFSGVYK	99.7%	87.4	25	87.4	2	2	0	2078.03	161	178
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	14	15	33	0.03%	54.6%	DVNFEFPEFQL	99.7%	71.2	25	69.4	3	0	0	1384.64	184	194
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	14	15	33	0.03%	54.6%	EIEVGGGR	98.5%	33.2	25	27.7	2	0	0	816.42	50	57
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	14	15	33	0.03%	54.6%	ELNITAAK	99.7%	46	25	34.2	2	0	0	859.49	42	49
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	14	15	33	0.03%	54.6%	HVVFIAQR	97.8%	31.5	25	29	3	0	0	969.56	91	98
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	14	15	33	0.03%	54.6%	ILPKPTR	98.0%	32	25	9.96	2	0	0	824.54	100	106
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	14	15	33	0.03%	54.6%	KAIIIFVPVPQLK	99.3%	36.8	25	36.8	3	0	0	1465.95	58	70
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	14	15	33	0.03%	54.6%	LTGKDVNFEFPEFQL	99.7%	58.3	25	58.3	2	0	0	1783.89	180	194
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	14	15	33	0.03%	54.6%	RILPKPTR	95.0%	28.3	25	26.4	1	0	0	980.64	99	106
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	14	15	33	0.03%	54.6%	TLTAVHDAILEDLVFPSEIVGK	99.7%	34.1	25	28.5	0	1	0	2367.28	121	142
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	14	15	33	0.03%	54.6%	TLTAVHDAILEDLVFPSEIVGKR	99.7%	64.2	25	64.2	0	1	0	2523.38	121	143
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	14	15	33	0.03%	54.6%	VETFSGVYK	99.5%	38.7	25	15.4	2	0	0	1029.53	170	178
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	14	15	33	0.03%	54.6%	VHLDKAQQNNVEHK	96.1%	29.3	25	28.7	1	0	0	1659.86	156	169
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	19	70	0.07%	59.1%	ADGYVLEGK	99.7%	75.9	25	60.4	2	0	0	951.48	185	193
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	19	70	0.07%	59.1%	ADGYVLEGKELEFYLR	99.7%	45.4	25	45.4	2	2	0	1901.96	185	200
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	19	70	0.07%	59.1%	ELEFYLR	98.6%	33.6	25	26.5	2	0	0	969.50	194	200
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	19	70	0.07%	59.1%	ELEFYLRK	96.5%	29.6	25	16.9	1	0	0	1097.60	194	201
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	19	70	0.07%	59.1%	IIDVVYNASNNELVR	99.7%	118	25	112	14	2	0	1718.91	78	92
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	19	70	0.07%	59.1%	ISSLLEEQFQQGK	99.7%	71.1	25	51.1	9	0	0	1506.78	158	170
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	19	70	0.07%	59.1%	KYELGRPAANTK	99.7%	58.8	25	52.4	3	2	0	1347.74	26	37
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	19	70	0.07%	59.1%	LDVGNFSWGSECCTR	99.7%	93.8	25	93.8	2	0	0	1787.75	60	74
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	19	70	0.07%	59.1%	LDVGNFSWGSECCTRK	99.3%	30.7	25	30.3	0	2	0	1915.84	60	75
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	19	70	0.07%	59.1%	LLACIASRPGQCGR	99.7%	44.7	25	41.3	2	2	0	1558.79	171	184
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	19	70	0.07%	59.1%	LTPEEEEILNK	99.7%	73.7	25	64.7	6	0	0	1314.68	129	139
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	19	70	0.07%	59.1%	NCIVLIDSTPYR	99.7%	89.3	25	72.6	11	0	0	1450.74	99	110

40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	19	70	0.07%	59.1%	QWYESHYALPLGR	99.7%	45	25	45	2	2	0	1619.80	111	123
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	19	70	0.07%	59.1%	YELGRPAANTK	99.7%	44.9	25	30.5	2	0	0	1219.64	27	37
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	71	0.07%	55.2%	ELLTLDEKDPR	99.4%	37.2	25	32.6	1	0	0	1328.71	59	69
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	71	0.07%	55.2%	HIDFSLR	99.4%	37.4	25	13.9	1	0	0	887.47	156	162
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	71	0.07%	55.2%	IEDFLER	99.7%	50.8	25	38.3	2	0	0	921.47	102	108
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	71	0.07%	55.2%	IEDFLERR	98.3%	32.8	25	18.5	2	0	0	1077.57	102	109
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	71	0.07%	55.2%	IGVLDEGK	99.7%	52.4	25	23.5	6	0	0	830.46	84	91
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	71	0.07%	55.2%	IGVLDEGKMK	99.7%	51.7	25	44.3	4	0	0	1089.60	84	93
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	71	0.07%	55.2%	KQVVNIPSFIVR	99.7%	66.2	25	66.2	3	1	0	1399.84	139	150
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	71	0.07%	55.2%	LDQELKLIGEYGLR	97.5%	31.1	25	26.8	1	0	0	1646.91	25	38
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	71	0.07%	55.2%	LFEGNALLR	99.7%	70.1	25	53	14	0	0	1032.58	71	79
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	71	0.07%	55.2%	LFEGNALLRR	95.1%	28.3	25	20.4	2	0	0	1188.68	71	80
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	71	0.07%	55.2%	LIGEYGLR	99.7%	51.7	25	33	2	0	0	920.52	31	38
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	71	0.07%	55.2%	LQTQVFK	99.4%	37.6	25	17.1	2	0	0	863.50	110	116
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	71	0.07%	55.2%	MKLDYILGLK	99.7%	52.8	25	35	4	0	0	1193.70	92	101
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	71	0.07%	55.2%	QVVNIPSFIVR	99.7%	51.4	25	42.6	9	0	0	1271.75	140	150
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	71	0.07%	55.2%	RLFEGNALLR	99.7%	55.5	25	35.4	2	0	0	1188.68	70	79
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	71	0.07%	55.2%	RLQTQVFK	98.3%	32.6	25	23.5	1	0	0	1019.60	109	116
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	71	0.07%	55.2%	SPYGGGRPGR	99.7%	47.5	25	31.9	7	0	0	1003.51	163	172
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	71	0.07%	55.2%	SRLDQELK	99.7%	42.4	25	15.9	6	0	0	988.54	23	30
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	19	22	71	0.07%	55.2%	VKFTLAK	98.1%	32.2	25	25.3	1	0	0	806.51	46	52
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	6	6	17	0.02%	25.4%	AIVAIENPADVSVISSR	99.7%	81.9	25	81.9	3	0	0	1740.95	64	80
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	6	6	17	0.02%	25.4%	FAAATGATPIAGR	99.7%	103	25	89.4	5	0	0	1203.65	90	102
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	6	6	17	0.02%	25.4%	FTPGTFTNQIQAAFR	99.7%	58.3	25	54.6	2	0	0	1698.86	103	117
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	6	6	17	0.02%	25.4%	KSDGIYIINLK	99.7%	56	25	28.2	2	0	0	1263.73	42	52
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	6	6	17	0.02%	25.4%	LLVVTDPR	99.7%	51.8	25	44.5	3	0	0	912.55	121	128
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	6	6	17	0.02%	25.4%	YVDIAIPCNNK	99.7%	45	25	39.8	2	0	0	1306.65	156	166
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	15	0.01%	16.2%	ADLLLSTQPGREEGSPLELER	99.7%	56.2	25	53.4	0	1	0	2310.19	593	613
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	15	0.01%	16.2%	FTGLSKEELLK	99.7%	43.8	25	38.7	2	0	0	1264.71	161	171
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	15	0.01%	16.2%	GLVLGPIHK	99.7%	43.2	25	36.8	2	0	0	933.59	258	266
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	15	0.01%	16.2%	GQSEDPGSLLSLFR	99.7%	55.9	25	48.5	2	0	0	1505.76	511	524
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	15	0.01%	16.2%	LKLEPHEGLLLR	99.7%	43.9	25	43.9	0	1	0	1417.85	614	625
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	15	0.01%	16.2%	LLTSFLPAQLLR	99.7%	59.8	25	55.1	2	0	0	1371.84	440	451
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	15	0.01%	16.2%	VAEDEAEAAAAAK	99.7%	100	25	91.2	2	0	0	1245.60	148	160
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	15	0.01%	16.2%	VILDLTPNYR	99.7%	55.3	25	50.7	3	0	0	1203.67	304	313
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	8	9	16	0.02%	11.3%	DQPAFTPSGILTPHALGSR	95.6%	23.3	25	20.2	0	1	0	1965.02	428	446
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	8	9	16	0.02%	11.3%	ELTMASLPFTFDVER	99.7%	65.9	25	65.9	4	0	0	1755.86	316	330
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	8	9	16	0.02%	11.3%	LFSIVRPR	99.2%	35.9	25	21.3	1	0	0	987.61	88	95
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	8	9	16	0.02%	11.3%	NLTVILSDASAPGEGEHK	98.8%	28.4	25	28.4	0	1	0	1837.93	190	207
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	8	9	16	0.02%	11.3%	NSLGGDVLFVGK	99.7%	59.2	25	54.6	2	0	0	1205.65	677	688
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	8	9	16	0.02%	11.3%	NSPGSQVASNPR	99.7%	81.2	25	75.7	5	0	0	1213.59	447	458
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	8	9	16	0.02%	11.3%	VREEILAK	95.9%	29.1	25	11.7	1	0	0	957.57	135	142
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	8	9	16	0.02%	11.3%	YAWQGVALLPFVDER	99.7%	54.2	25	51.1	1	0	0	1763.91	642	656
5'-AMP-activated protein kinase catalytic subunit alpha-2	PRKAA2	AAPK2_HUMAN	62.3	100.0%	2	2	2	0.00%	4.9%	IADFGLSNMMSDGEFLR	99.7%	69.8	25	69.8	1	0	0	1934.86	155	171
5'-AMP-activated protein kinase catalytic subunit alpha-2	PRKAA2	AAPK2_HUMAN	62.3	100.0%	2	2	2	0.00%	4.9%	MPPLIADSPK	99.7%	42.1	25	35.4	1	0	0	1084.57	370	379
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	6	6	10	0.01%	20.5%	AFFALVTNGVR	99.7%	47.3	25	47.3	1	0	0	1194.66	60	70
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	6	6	10	0.01%	20.5%	FDVINLAAEK	99.7%	60.5	25	50	2	0	0	1119.60	244	253
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	6	6	10	0.01%	20.5%	LPVIDPESGNTLYILTHK	99.7%	47.7	25	47.7	0	2	0	2010.09	153	170
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	6	6	10	0.01%	20.5%	LVEAEVHR	99.7%	53	25	50.7	2	0	0	952.52	292	299
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	6	6	10	0.01%	20.5%	LVVFDTSLQVK	99.7%	41.8	25	41.8	1	0	0	1248.72	48	58
5'-AMP-activated protein kinase subunit gamma-1	PRKAG1	AAKG1_HUMAN	37.6	100.0%	6	6	10	0.01%	20.5%	VSALPVVDEK	99.7%	50.4	25	39.8	2	0	0	1056.59	225	234

5-methylcytosine rRNA methyltransferase NSUN4	NSUN4	NSUN4_HUMAN	43.1	99.9%	2	2	2	0.00%	5.7%	NLAANDLSPSR	99.7%	47	25	34.4	1	0	0	1157.59	199	209
5-methylcytosine rRNA methyltransferase NSUN4	NSUN4	NSUN4_HUMAN	43.1	99.9%	2	2	2	0.00%	5.7%	VLVDVPCTTDR	99.7%	48.4	25	46.3	1	0	0	1274.64	252	262
5'-nucleotidase domain-containing protein 2	NT5DC2	NT5D2_HUMAN	60.7	100.0%	3	3	4	0.00%	6.5%	MQTYQDAESR	99.7%	43.5	25	43.5	1	0	0	1228.53	411	420
5'-nucleotidase domain-containing protein 2	NT5DC2	NT5D2_HUMAN	60.7	100.0%	3	3	4	0.00%	6.5%	QGNLFDFLR	99.5%	38.1	25	24.5	2	0	0	1109.57	336	344
5'-nucleotidase domain-containing protein 2	NT5DC2	NT5D2_HUMAN	60.7	100.0%	3	3	4	0.00%	6.5%	QLFLITNSPFSFVDK	99.7%	74.3	25	74.3	1	0	0	1755.93	263	277
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	19	25	46	0.05%	38.7%	AAVEEGIVLGGGCALLR	99.7%	101	25	94.7	2	0	0	1684.91	430	446
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	19	25	46	0.05%	38.7%	ALMLQGVDLLADAVAVTMGPK	98.9%	28.7	25	28.7	0	1	0	2145.13	38	58
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	19	25	46	0.05%	38.7%	CEFQDAYVLLSEK	99.7%	72.7	25	46.5	2	0	0	1601.75	237	249
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	19	25	46	0.05%	38.7%	CIPALDSLTPANEDQK	99.7%	101	25	99.8	2	0	0	1771.85	447	462
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	19	25	46	0.05%	38.7%	GANPVEIR	99.7%	43.7	25	17	2	0	0	855.47	134	141
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	19	25	46	0.05%	38.7%	GANPVEIRR	95.6%	28.7	25	18.8	1	0	0	1011.57	134	142
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	19	25	46	0.05%	38.7%	GYISPYFINTSK	99.7%	62.8	25	56.3	2	0	0	1389.70	222	233
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	19	25	46	0.05%	38.7%	IGIEIIKR	99.7%	55	25	29	2	0	0	941.61	463	470
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	19	25	46	0.05%	38.7%	ISSIQSIVPALEIANAHR	99.7%	46.3	25	46.3	2	2	0	1919.07	251	268
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	19	25	46	0.05%	38.7%	LVQDVANNTNEEAGDGTTTATVLAR	99.7%	161	25	161	2	2	0	2560.25	97	121
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	19	25	46	0.05%	38.7%	NAGVEGSLIVEK	99.7%	76.7	25	60.8	2	0	0	1215.66	482	493
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	19	25	46	0.05%	38.7%	TLNDELEIIEGMK	99.7%	80.8	25	75.2	2	0	0	1504.76	206	218
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	19	25	46	0.05%	38.7%	TVIIEQSWGSPK	99.7%	69.8	25	60.7	2	0	0	1344.72	61	72
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	19	25	46	0.05%	38.7%	VGEVIVTK	99.7%	61.4	25	45.7	2	0	0	844.51	345	352
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	19	25	46	0.05%	38.7%	VGEVIVTKDDAMLLK	99.7%	67.2	25	66.8	3	3	0	1630.91	345	359
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	19	25	46	0.05%	38.7%	VGGTSDVEVNEK	99.7%	98.4	25	92.1	3	0	0	1233.60	406	417
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	19	25	46	0.05%	38.7%	VGGTSDVEVNEKK	99.7%	72.3	25	64.2	2	1	0	1361.69	406	418
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	19	25	46	0.05%	38.7%	VGLQVVAVK	99.7%	77.5	25	74.8	2	0	0	912.59	293	301
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	19	25	46	0.05%	38.7%	VTDALNATR	99.7%	86.4	25	69.6	2	0	0	960.51	421	429
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	10	21	0.02%	20.6%	AIADWYNEK	99.5%	37.8	25	35	2	0	0	1109.53	151	159
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	10	21	0.02%	20.6%	ALDAAFYK	98.2%	32.4	25	29.2	2	0	0	898.47	352	359
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	10	21	0.02%	20.6%	ALLQEMPLTALLR	99.7%	77.3	25	73.8	5	0	0	1468.86	271	283
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	10	21	0.02%	20.6%	FLCFGSEGGTYYIK	99.7%	71.3	25	71	2	0	0	1641.76	36	49
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	10	21	0.02%	20.6%	GGMALALAVTK	99.7%	64	25	49.8	2	0	0	1047.59	160	170
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	10	21	0.02%	20.6%	LGLENAEALIR	99.7%	73.5	25	65.4	2	0	0	1198.68	53	63
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	10	21	0.02%	20.6%	LSHLKPSSEGLAIVTK	99.7%	48.8	25	48.8	0	2	0	1679.97	185	200
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	10	21	0.02%	20.6%	MTANSVLEPGNSEVSLVCEK	99.7%	77.3	25	77.3	2	0	0	2180.02	288	307
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	9	10	21	0.02%	20.6%	WRPDEEILK	99.7%	51.8	25	39.1	2	0	0	1185.63	343	351
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	21	67	0.07%	55.8%	AFLADPSAFVAAAPVAAATTAAPAAAAAPAK	99.7%	102	25	102	2	6	0	2752.47	267	297
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	21	67	0.07%	55.8%	AGAIAPCEVTVPAQNTGLGPEK	99.7%	82.2	25	82.2	2	2	0	2180.10	113	134
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	21	67	0.07%	55.8%	CFIVGADNVGSK	99.5%	38	25	32.9	1	0	0	1266.61	27	38
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	21	67	0.07%	55.8%	DMLLANK	99.2%	36.1	25	29.2	1	0	0	804.43	100	106
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	21	67	0.07%	55.8%	DMLLANKVPAAAR	99.7%	52.3	25	43.4	2	0	0	1369.76	100	112
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	21	67	0.07%	55.8%	EDLTEIR	99.7%	46.1	25	25.3	2	0	0	875.45	93	99
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	21	67	0.07%	55.8%	EDLTEIRDMLLANK	99.7%	72.4	25	70.7	4	2	0	1660.86	93	106
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	21	67	0.07%	55.8%	GHLENNPALEK	99.7%	64.9	25	48.4	4	2	0	1221.62	67	77
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	21	67	0.07%	55.8%	GNVGFVFTK	99.7%	55.9	25	45.2	7	0	0	968.52	84	92
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	21	67	0.07%	55.8%	GNVGFVFTKEDLTEIR	99.7%	58.6	25	58.6	2	0	0	1824.95	84	99
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	21	67	0.07%	55.8%	GTIEILSDVQLIK	99.7%	78	25	68.5	5	0	0	1428.83	150	162
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	21	67	0.07%	55.8%	IIQLLDDYPK	99.7%	76.2	25	62.9	2	0	0	1217.68	17	26
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	21	67	0.07%	55.8%	TSFFQALGITTK	99.7%	93.6	25	93.6	14	0	0	1313.71	135	146
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	21	67	0.07%	55.8%	VEAKEESEESDEDMGFGLFD	99.7%	105	25	105	4	0	0	2278.92	298	317
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	15	21	67	0.07%	55.8%	VLALSVETDYTFPLAEK	99.7%	93.9	25	93.3	3	0	0	1896.00	248	264
60S acidic ribosomal protein P2	RPLP2	RLA2_HUMAN	11.7	100.0%	4	6	12	0.01%	69.6%	ILDSVGIEADDDRLNK	99.7%	79.2	25	76.1	3	2	0	1772.90	26	41
60S acidic ribosomal protein P2	RPLP2	RLA2_HUMAN	11.7	100.0%	4	6	12	0.01%	69.6%	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	99.7%	80.4	25	80.4	1	2	0	2774.43	62	94
60S acidic ribosomal protein P2	RPLP2	RLA2_HUMAN	11.7	100.0%	4	6	12	0.01%	69.6%	NIEDVIAQGIGK	99.7%	102	25	90.2	2	0	0	1256.68	50	61

60S acidic ribosomal protein P2	RPLP2	RLA2_HUMAN	11.7	100.0%	4	6	12	0.01%	69.6%	YVASYLLAALGGNSSPSAK	99.7%	67.1	25	58.3	2	0	0	1868.98	3	21
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	16	25	54	0.05%	64.0%	AKVDEFPLCGHMVSDEYEQLSSEALEAAR	99.7%	140	25	139	0	2	0	3281.51	41	69
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	16	25	54	0.05%	64.0%	EHVIEALR	95.2%	28.5	25	21.4	1	0	0	966.54	146	153
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	16	25	54	0.05%	64.0%	FNADEFEDMVAEK	99.7%	88.4	25	88.4	2	0	0	1560.65	176	188
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	16	25	54	0.05%	64.0%	FNADEFEDMVAEKR	99.7%	100	25	92.1	2	3	0	1700.76	176	189
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	16	25	54	0.05%	64.0%	GAFGKPQGTVAR	99.7%	65.5	25	54	4	0	0	1188.65	117	128
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	16	25	54	0.05%	64.0%	GPLDKWR	99.2%	36.2	25	29.1	2	0	0	871.48	204	210
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	16	25	54	0.05%	64.0%	ICANKYMVK	99.6%	39.9	25	38.2	2	0	0	1142.57	70	78
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	16	25	54	0.05%	64.0%	IFDLGRK	98.5%	33.1	25	0	2	0	0	848.50	33	39
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	16	25	54	0.05%	64.0%	IRIFDLGR	99.7%	46.5	25	32.1	2	0	0	989.59	31	38
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	16	25	54	0.05%	64.0%	LQNKEHVIEALR	99.7%	63.7	25	63.7	2	2	0	1449.82	142	153
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	16	25	54	0.05%	64.0%	MLSCAGADR	99.7%	62.1	25	51.2	4	0	0	980.43	102	110
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	16	25	54	0.05%	64.0%	MLSCAGADRLQTGMR	99.7%	45.8	25	41.6	2	5	0	1666.78	102	116
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	16	25	54	0.05%	64.0%	RLIPDGCGVK	99.7%	42.1	25	29.5	2	0	0	1114.60	189	198
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	16	25	54	0.05%	64.0%	VDEFPLCGHMVSDEYEQLSSEALEAAR	99.7%	69.9	25	69.9	0	4	0	3082.38	43	69
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	16	25	54	0.05%	64.0%	VHIGQVIMSIR	99.7%	53.1	25	53.1	6	4	0	1252.72	129	139
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	16	25	54	0.05%	64.0%	VRLHPFHVIR	99.7%	44.3	25	44.3	0	1	0	1273.76	89	98
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	11	22	48	0.05%	43.8%	AGKFPSLLTHNENMVAK	97.9%	26	25	25.8	0	1	0	1872.96	131	147
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	11	22	48	0.05%	43.8%	AVDIPHMDIEALK	99.7%	54.3	25	52.5	4	2	0	1467.75	79	91
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	11	22	48	0.05%	43.8%	AVDIPHMDIEALKK	99.7%	72.9	25	68	4	5	0	1579.85	79	92
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	11	22	48	0.05%	43.8%	DTLYEAVR	99.7%	55.4	25	31.6	5	0	0	966.49	8	15
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	11	22	48	0.05%	43.8%	FPSLLTHNENMVAK	99.7%	65.3	25	57.5	5	4	0	1600.82	134	147
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	11	22	48	0.05%	43.8%	FSVCVLGDQQHCDEAK	99.7%	76	25	76	2	2	0	1892.83	63	78
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	11	22	48	0.05%	43.8%	ILGPGLNK	99.7%	43.9	25	29.5	2	0	0	811.50	123	130
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	11	22	48	0.05%	43.8%	KNWQNVR	95.6%	28.8	25	21.6	1	0	0	944.51	196	202
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	11	22	48	0.05%	43.8%	KYDAFLASESLIK	99.7%	71.6	25	71.6	2	2	0	1484.80	106	118
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	11	22	48	0.05%	43.8%	VLCLAVAVGHVK	99.7%	78.7	25	78.7	4	2	0	1265.74	162	173
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	11	22	48	0.05%	43.8%	YDAFLASESLIK	98.8%	34.3	25	34.3	1	0	0	1356.70	107	118
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	7	9	40	0.04%	30.3%	AEEILEK	98.2%	32.3	25	15.8	2	0	0	831.45	79	85
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	7	9	40	0.04%	30.3%	AEEILEKGLK	98.8%	34.1	25	25.5	1	0	0	1129.65	79	88
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	7	9	40	0.04%	30.3%	IAVHCTVR	99.7%	48.3	25	40.2	3	0	0	955.51	68	75
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	7	9	40	0.04%	30.3%	ISKEEAMR	99.7%	56.9	25	39.1	3	0	0	963.49	157	164
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	7	9	40	0.04%	30.3%	VLEQLTGQTPVFSK	99.7%	106	25	101	17	0	0	1546.85	39	52
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	7	9	40	0.04%	30.3%	WFQQKYDGIILPGK	99.5%	32.5	25	27.7	1	2	0	1692.91	165	178
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	7	9	40	0.04%	30.3%	YDGIILPGK	99.7%	72.8	25	70.4	11	0	0	975.55	170	178
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	6	8	31	0.03%	54.5%	CTGGEVGATSALAPK	99.7%	113	25	95.6	4	0	0	1418.69	17	31
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	6	8	31	0.03%	54.5%	EILGTAQSVGCNVDGR	99.7%	101	25	101	4	0	0	1675.81	131	146
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	6	8	31	0.03%	54.5%	HPHDIIDDINSGAVECPAS	99.7%	66.7	25	66.7	2	0	0	2046.92	147	165
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	6	8	31	0.03%	54.5%	HSGNITFDEIVNIAR	99.7%	93.3	25	93.3	3	4	0	1685.86	100	114
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	6	8	31	0.03%	54.5%	IGPLGLSPK	99.7%	57.4	25	40.8	8	0	0	881.55	32	40
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	6	8	31	0.03%	54.5%	QAQIEVVPSASALIIK	99.7%	85.8	25	85.8	4	2	0	1666.97	68	83
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	67	0.07%	33.6%	GFSLEELR	99.7%	54.1	25	43.4	13	0	0	950.49	75	82
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	67	0.07%	33.6%	LATQLTGPVMPVR	99.7%	61.4	25	60.4	11	0	0	1382.78	146	158
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	67	0.07%	33.6%	RVATWFNQPAR	99.7%	52.8	25	43.8	2	2	0	1345.71	21	31
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	67	0.07%	33.6%	SKLILFPR	98.9%	34.4	25	34.4	2	0	0	973.62	122	129
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	67	0.07%	33.6%	STESLQANVQR	99.7%	86.8	25	79.9	15	0	0	1232.62	106	116
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	67	0.07%	33.6%	TIGISVDPR	99.7%	67.6	25	50.8	9	0	0	957.54	93	101
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	67	0.07%	33.6%	VATWFNQPAR	99.7%	67.1	25	55.6	6	0	0	1189.61	22	31
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	67	0.07%	33.6%	VATWFNQPARK	98.7%	33.8	25	33.3	1	0	0	1317.71	22	32
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	9	11	67	0.07%	33.6%	VITEEEKNFK	99.7%	54	25	42.4	6	0	0	1236.65	168	177
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	9	9	21	0.02%	37.9%	CEGINISGNFYR	99.7%	68	25	58.1	1	0	0	1429.65	38	49

60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	9	9	21	0.02%	37.9%	IDKYTEVLK	99.7%	57.1	25	29.8	2	0	0	1108.63	189	197
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	9	9	21	0.02%	37.9%	KFAYLGR	99.7%	49.1	25	37.6	2	0	0	854.49	134	140
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	9	9	21	0.02%	37.9%	LAHEVGWK	99.4%	37.4	25	28.3	1	0	0	939.50	141	148
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	9	9	21	0.02%	37.9%	LKYLAFLR	99.7%	49.1	25	42.8	2	0	0	1023.64	52	59
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	9	9	21	0.02%	37.9%	RMVVPAALK	99.3%	36.4	25	19.5	2	0	0	984.60	117	125
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	9	9	21	0.02%	37.9%	VFDGIPPPYDKK	99.6%	39.4	25	37.7	4	0	0	1375.73	104	115
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	9	9	21	0.02%	37.9%	YQAVTATLEEK	99.7%	67.6	25	61.2	6	0	0	1252.64	149	159
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	9	9	21	0.02%	37.9%	YQAVTATLEEKR	99.7%	44.3	25	41.3	1	0	0	1408.74	149	160
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	8	79	0.08%	27.9%	ALVDGPCTQVR	99.7%	72	25	66.3	6	0	0	1215.62	36	46
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	8	79	0.08%	27.9%	CMQLTDFILK	99.7%	53.8	25	40	11	0	0	1268.64	54	63
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	8	79	0.08%	27.9%	LVAIVDVIDQNR	99.7%	95.1	25	89.4	34	0	0	1354.77	24	35
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	8	79	0.08%	27.9%	MTDFDRFK	99.6%	38.9	25	35	8	0	0	1059.49	104	111
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	8	79	0.08%	27.9%	RFVEVGR	99.7%	45.4	25	37	4	0	0	862.49	5	11
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	8	79	0.08%	27.9%	VAYVSFGPHAGK	99.7%	63.3	25	54.1	16	0	0	1232.64	12	23
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	6	9	21	0.02%	26.0%	GATYGKPVHHGVNQLK	99.7%	67.3	25	58.9	2	2	0	1705.91	78	93
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	6	9	21	0.02%	26.0%	NPDTQWITKPVHK	99.7%	46.1	25	42.8	1	2	0	1563.83	145	157
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	6	9	21	0.02%	26.0%	NTLQLHR	99.7%	49.4	25	36.9	3	0	0	881.50	196	202
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	6	9	21	0.02%	26.0%	QLSALHR	97.1%	30.5	25	8.09	2	0	0	824.47	32	38
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	6	9	21	0.02%	26.0%	RNPDTQWITKPVHK	99.6%	32.7	25	32.7	1	2	0	1719.93	144	157
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	6	9	21	0.02%	26.0%	SLQSVAEER	99.7%	52.9	25	40	6	0	0	1018.52	97	105
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	15	43	0.04%	46.7%	EQIVPKPEEEVAQK	99.7%	70.1	25	60.6	2	0	0	1623.86	154	167
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	15	43	0.04%	46.7%	EQIVPKPEEEVAQKK	99.7%	44.2	25	34.8	2	1	0	1751.95	154	168
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	15	43	0.04%	46.7%	ETAQAIKGMHIR	98.4%	27.1	25	26.3	0	2	0	1370.72	31	42
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	15	43	0.04%	46.7%	GLDVDSLVIEHIQVNK	99.7%	65.2	25	58.9	2	0	0	1778.96	106	121
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	15	43	0.04%	46.7%	KSAEFLLHMLK	99.7%	46.1	25	36	4	0	0	1316.74	86	96
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	15	43	0.04%	46.7%	QWGWTQGR	99.7%	42.1	25	30.1	2	0	0	1018.49	75	82
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	15	43	0.04%	46.7%	QWGWTQGRWPK	99.4%	37.2	25	20	2	0	0	1429.71	75	85
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	15	43	0.04%	46.7%	SAEFLLHMLK	99.7%	60.8	25	52	9	1	0	1188.64	87	96
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	15	43	0.04%	46.7%	VRYSLDPENPTK	99.7%	49.7	25	49.2	2	0	0	1418.73	2	13
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	15	43	0.04%	46.7%	YLKDVTLQK	99.7%	49.4	25	41	6	0	0	1107.64	47	55
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	15	43	0.04%	46.7%	YSLDPENPTK	99.7%	62.3	25	58.4	8	0	0	1163.56	4	13
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	12	72	0.07%	46.3%	APGTPHSHTKPYVR	99.7%	46.8	25	46.7	3	3	0	1547.81	155	168
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	12	72	0.07%	46.3%	GCGTVLLSGPR	99.7%	77	25	65.6	8	0	0	1116.58	133	143
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	12	72	0.07%	46.3%	ILTFDQLALDSPK	99.7%	115	25	107	25	0	0	1460.80	120	132
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	12	72	0.07%	46.3%	LKVCALR	99.4%	37.1	25	27.7	2	0	0	859.52	98	104
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	12	72	0.07%	46.3%	RTNSTFNQVVLK	99.7%	49.3	25	17.1	2	0	0	1406.78	38	49
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	12	72	0.07%	46.3%	TAVVVGTITDDVR	99.7%	120	25	110	11	0	0	1345.73	79	91
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	12	72	0.07%	46.3%	TAVVVGTITDDVRVQEVPK	99.7%	82.1	25	81.2	2	2	0	2026.12	79	97
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	12	72	0.07%	46.3%	TNRPPLSLSR	99.7%	42.2	25	33.3	4	0	0	1140.65	56	65
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	12	72	0.07%	46.3%	TNSTFNQVVLK	99.7%	65.6	25	50.3	5	0	0	1250.67	39	49
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	10	12	72	0.07%	46.3%	TNSTFNQVVLKR	99.7%	55.1	25	48.3	5	0	0	1406.78	39	50
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	60	0.06%	59.1%	AHSIQIMK	99.7%	49.8	25	36.2	4	0	0	927.51	121	128
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	60	0.06%	59.1%	AHSIQIMKVEEIAASK	95.7%	23.4	25	23.4	0	1	0	1770.94	121	136
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	60	0.06%	59.1%	ASGTLREYK	97.8%	31.6	25	20.6	1	0	0	1024.54	3	11
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	60	0.06%	59.1%	DLTTAGAVTQCYR	99.7%	72	25	72	8	0	0	1455.69	99	111
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	60	0.06%	59.1%	DLTTAGAVTQCYRDMGAR	99.7%	51.6	25	51.6	0	2	0	2001.91	99	116
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	60	0.06%	59.1%	EYKVVGR	96.4%	29.6	25	23.1	2	0	0	850.48	9	15
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	60	0.06%	59.1%	EYRDLTTAGAVTQCYR	99.7%	59.3	25	52.4	3	4	0	1903.90	96	111
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	60	0.06%	59.1%	FWYFVSQLKK	99.2%	35.8	25	29.2	1	0	0	1345.73	44	53
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	60	0.06%	59.1%	IFAPNHVVAK	99.7%	49.4	25	39.7	7	0	0	1095.63	32	41
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	60	0.06%	59.1%	IKFPLPHR	99.7%	43.6	25	33.2	2	0	0	1007.62	150	157

60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	60	0.06%	59.1%	KSSGEIVYCGQVFEK	99.7%	74.5	25	69.9	2	2	0	1730.84	56	70
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	60	0.06%	59.1%	NFGIWLR	99.7%	40.8	25	24.6	5	0	0	905.50	77	83
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	60	0.06%	59.1%	SSGEIVYCGQVFEK	99.7%	96.7	25	94	12	0	0	1602.75	57	70
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	60	0.06%	59.1%	VEEIAASKCR	99.7%	40.9	25	33.9	2	0	0	1162.59	129	138
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	15	18	60	0.06%	59.1%	VKNFGIWLR	99.7%	49.1	25	41.7	2	0	0	1132.66	75	83
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	8	9	26	0.03%	27.6%	HMYHSLYLK	98.7%	33.9	25	25.5	2	0	0	1191.60	118	126
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	8	9	26	0.03%	27.6%	ILMEHIHK	98.8%	34.1	25	22.6	6	0	0	1036.56	137	144
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	8	9	26	0.03%	27.6%	KLLADQAEAR	99.7%	64.1	25	60.5	3	0	0	1114.62	153	162
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	8	9	26	0.03%	27.6%	KVWLDPNETNEIANANSR	99.7%	49.1	25	44.5	0	2	0	2071.02	21	38
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	8	9	26	0.03%	27.6%	LLADQAEAR	99.7%	71	25	59.7	7	0	0	986.53	154	162
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	8	9	26	0.03%	27.6%	LLADQAEARR	96.4%	29.6	25	12.8	2	0	0	1142.63	154	163
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	8	9	26	0.03%	27.6%	RLASSVLR	98.1%	32.3	25	19.3	1	0	0	901.56	9	16
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	8	9	26	0.03%	27.6%	VWLDPNETNEIANANSR	99.7%	127	25	127	3	0	0	1942.93	22	38
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	10	15	46	0.05%	53.1%	EKGTWVQLK	95.1%	28.4	25	13.3	1	0	0	1088.61	121	129
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	10	15	46	0.05%	53.1%	GDIVDIKGMGTVQK	99.7%	53.9	25	44.4	4	0	0	1460.78	37	50
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	10	15	46	0.05%	53.1%	GTWVQLK	96.3%	29.5	25	14.6	2	0	0	831.47	123	129
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	10	15	46	0.05%	53.1%	GTWVQLKR	99.7%	49.2	25	33.2	4	0	0	987.57	123	130
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	10	15	46	0.05%	53.1%	HGVVPLATYMR	99.7%	61.8	25	61.8	9	1	0	1243.66	22	32
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	10	15	46	0.05%	53.1%	INVRIEHIK	97.2%	30.5	25	21	1	0	0	1121.68	89	97
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	10	15	46	0.05%	53.1%	KGDIVDIK	99.7%	48.2	25	12.7	1	0	0	887.52	36	43
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	10	15	46	0.05%	53.1%	SRDSFLK	96.7%	29.9	25	14.1	1	0	0	852.46	101	107
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	10	15	46	0.05%	53.1%	TNGKEPELLEPIPYEFMA	99.7%	50.3	25	50.3	5	0	0	2094.01	143	160
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	10	15	46	0.05%	53.1%	VYNVTQHAVGIVVNK	99.7%	113	25	107	10	7	0	1640.91	64	78
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	32	0.03%	36.7%	AGNLGGGVVTIER	99.7%	94.5	25	85.9	8	0	0	1242.68	53	65
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	32	0.03%	36.7%	ITVTSEVPFSK	99.7%	76.2	25	73.9	10	0	0	1207.66	70	80
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	32	0.03%	36.7%	ITVTSEVPFSKR	99.7%	71	25	70.2	2	2	0	1363.76	70	81
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	32	0.03%	36.7%	NNLRDWLR	98.3%	32.7	25	9.31	2	0	0	1086.58	94	101
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	32	0.03%	36.7%	SKITVTSEVPFSK	99.7%	87.9	25	85.9	4	2	0	1422.78	68	80
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	32	0.03%	36.7%	VVANSKESYELR	99.7%	55.1	25	46.6	2	0	0	1394.73	102	113
60S ribosomal protein L22-like 1	RPL22L1	RL22L_HUMAN	14.6	99.8%	2	3	6	0.01%	26.2%	NNLRDWLR	98.3%	32.7	25	9.31	2	0	0	1086.58	88	95
60S ribosomal protein L22-like 1	RPL22L1	RL22L_HUMAN	14.6	99.8%	2	3	6	0.01%	26.2%	TGNLGNVVHIER	99.7%	50.7	25	36.8	2	0	0	1308.70	48	59
60S ribosomal protein L22-like 1	RPL22L1	RL22L_HUMAN	14.6	99.8%	2	3	6	0.01%	26.2%	VVASDKETYELR	99.7%	83.9	25	83.9	2	2	0	1409.73	96	107
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	9	17	61	0.06%	52.9%	ECADLWPR	99.7%	54.5	25	36.7	6	0	0	1046.47	124	131
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	9	17	61	0.06%	52.9%	GSAITGPVAK	99.7%	52.4	25	43.1	7	0	0	900.52	114	123
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	9	17	61	0.06%	52.9%	ISLGLPVGAVINCADNTGAK	99.7%	72.2	25	68.4	6	1	0	1970.04	16	35
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	9	17	61	0.06%	52.9%	KVHPAVVIR	99.7%	42.1	25	42.1	1	0	0	1018.65	75	83
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	9	17	61	0.06%	52.9%	LNRLPAAGVGDMVMATVK	99.7%	66.5	25	19.7	3	5	0	1858.99	49	66
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	9	17	61	0.06%	52.9%	LPAAGVGDMVMATVK	99.7%	96.7	25	29.8	22	0	0	1475.76	52	66
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	9	17	61	0.06%	52.9%	LPAAGVGDMVMATVKK	99.7%	70.4	25	70.4	4	3	0	1587.86	52	67
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	9	17	61	0.06%	52.9%	NLYIISVK	99.7%	47.1	25	47.1	2	0	0	949.57	36	43
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	9	17	61	0.06%	52.9%	VHPAVVIR	99.0%	34.9	25	34.9	1	0	0	890.56	76	83
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	10	14	70	0.07%	42.3%	EAPAPPKAEAK	99.7%	51.4	25	51.1	4	0	0	1108.60	8	18
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	10	14	70	0.07%	42.3%	FPLTTESAMK	99.7%	53	25	44.2	9	0	0	1140.56	79	88
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	10	14	70	0.07%	42.3%	FPLTTESAMKK	99.6%	39.8	25	22.8	4	0	0	1268.66	79	89
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	10	14	70	0.07%	42.3%	KLYDIDVAK	99.7%	59.4	25	56	4	0	0	1064.60	115	123
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	10	14	70	0.07%	42.3%	LAPDYDALDVANK	99.7%	94.7	25	91.9	19	0	0	1404.70	140	152
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	10	14	70	0.07%	42.3%	LDHYAIIK	99.7%	52.9	25	17.7	3	0	0	972.55	71	78
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	10	14	70	0.07%	42.3%	LYDIDVAK	99.7%	47.3	25	38.1	4	0	0	936.50	116	123
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	10	14	70	0.07%	42.3%	NKLDHYAIIK	99.7%	51.6	25	20.4	2	2	0	1214.69	69	78
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	10	14	70	0.07%	42.3%	VNTLIRPDGEK	99.7%	58	25	51	13	1	0	1241.69	124	134
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	10	14	70	0.07%	42.3%	VNTLIRPDGEKK	99.7%	49.9	25	49.3	2	3	0	1369.78	124	135

60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	14	93	0.09%	35.7%	AITGASLADIMAK	99.7%	105	25	92.4	41	0	0	1261.68	81	93
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	14	93	0.09%	35.7%	AITGASLADIMAKR	99.7%	49.2	25	49.2	3	0	0	1433.78	81	94
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	14	93	0.09%	35.7%	CESAFLSK	99.7%	49.5	25	42.4	6	0	0	941.44	36	43
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	14	93	0.09%	35.7%	CESAFLSKR	99.7%	49.9	25	30	2	0	0	1097.54	36	44
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	14	93	0.09%	35.7%	MKVELCSFSGYK	99.7%	76.8	25	66.3	8	4	0	1448.69	1	12
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	14	93	0.09%	35.7%	QINWTVLYR	99.7%	46	25	26.7	9	0	0	1192.65	48	56
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	14	93	0.09%	35.7%	TDGKVFQFLNAK	99.4%	31	25	31	0	2	0	1367.73	24	35
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	14	93	0.09%	35.7%	VELCSFSGYK	99.7%	64.6	25	55	2	0	0	1189.56	3	12
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	14	93	0.09%	35.7%	VFQFLNAK	99.7%	51.2	25	26	16	0	0	966.54	28	35
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	14	45	0.04%	46.9%	ANGTTVHVGIHPSK	99.7%	73.4	25	65.1	2	2	0	1417.75	90	103
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	14	45	0.04%	46.9%	DDEVQVVR	99.7%	70.5	25	50.3	4	0	0	959.48	52	59
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	14	45	0.04%	46.9%	FNPFVTSDR	99.7%	44.2	25	34.4	7	0	0	1082.53	3	11
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	14	45	0.04%	46.9%	HFNAPSHIR	99.0%	35	25	30.8	2	0	0	1078.55	18	26
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	14	45	0.04%	46.9%	IMSSPLSK	99.1%	35.4	25	23.6	2	0	0	878.47	29	36
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	14	45	0.04%	46.9%	KDDEVQVVR	99.7%	67.6	25	50.5	7	0	0	1087.57	51	59
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	14	45	0.04%	46.9%	KIMSSPLSK	96.6%	29.8	25	18.6	1	0	0	990.57	28	36
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	14	45	0.04%	46.9%	KYVIYIER	99.7%	54.5	25	50.2	4	0	0	1083.62	77	84
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	14	45	0.04%	46.9%	MKFNPFVTSDR	99.7%	66.9	25	61.9	7	1	0	1357.66	1	11
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	14	45	0.04%	46.9%	YKEETIEK	99.7%	47.5	25	39	2	0	0	1039.53	135	142
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	11	14	45	0.04%	46.9%	YVIYIER	99.7%	44.7	25	42.9	4	0	0	955.52	78	84
60S ribosomal protein L26-like 1	RPL26L1	RL26L_HUMAN	17.3	99.8%	2	2	6	0.01%	46.9%	ANGTTVHVGIHPSK	99.7%	73.4	25	65.1	2	2	0	1417.75	90	103
60S ribosomal protein L26-like 1	RPL26L1	RL26L_HUMAN	17.3	99.8%	2	2	6	0.01%	46.9%	DDEVQVVR	99.7%	70.5	25	50.3	4	0	0	959.48	52	59
60S ribosomal protein L26-like 1	RPL26L1	RL26L_HUMAN	17.3	99.8%	2	2	6	0.01%	46.9%	FNPFVTSDR	99.7%	44.2	25	34.4	7	0	0	1082.53	3	11
60S ribosomal protein L26-like 1	RPL26L1	RL26L_HUMAN	17.3	99.8%	2	2	6	0.01%	46.9%	HFNAPSHVR	99.3%	36.9	25	29.7	2	0	0	1064.54	18	26
60S ribosomal protein L26-like 1	RPL26L1	RL26L_HUMAN	17.3	99.8%	2	2	6	0.01%	46.9%	IMSSPLSK	99.1%	35.4	25	23.6	2	0	0	878.47	29	36
60S ribosomal protein L26-like 1	RPL26L1	RL26L_HUMAN	17.3	99.8%	2	2	6	0.01%	46.9%	KDDEVQVVR	99.7%	67.6	25	50.5	7	0	0	1087.57	51	59
60S ribosomal protein L26-like 1	RPL26L1	RL26L_HUMAN	17.3	99.8%	2	2	6	0.01%	46.9%	KIMSSPLSK	96.6%	29.8	25	18.6	1	0	0	990.57	28	36
60S ribosomal protein L26-like 1	RPL26L1	RL26L_HUMAN	17.3	99.8%	2	2	6	0.01%	46.9%	KYVIYIER	99.7%	54.5	25	50.2	4	0	0	1083.62	77	84
60S ribosomal protein L26-like 1	RPL26L1	RL26L_HUMAN	17.3	99.8%	2	2	6	0.01%	46.9%	MKFNPFVTSDR	99.7%	66.9	25	61.9	7	1	0	1357.66	1	11
60S ribosomal protein L26-like 1	RPL26L1	RL26L_HUMAN	17.3	99.8%	2	2	6	0.01%	46.9%	YKEELIEK	99.4%	37.3	25	17.5	4	0	0	1051.57	135	142
60S ribosomal protein L26-like 1	RPL26L1	RL26L_HUMAN	17.3	99.8%	2	2	6	0.01%	46.9%	YVIYIER	99.7%	44.7	25	42.9	4	0	0	955.52	78	84
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	7	12	43	0.04%	47.8%	NIDDGTSDRPYSHALVAGIDR	99.7%	45.5	25	45.5	2	2	0	2272.10	28	48
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	7	12	43	0.04%	47.8%	NKWFFQK	98.6%	33.4	25	12.5	2	0	0	997.53	127	133
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	7	12	43	0.04%	47.8%	TVVNKDVFR	99.5%	38.8	25	32.7	2	0	0	1077.61	94	102
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	7	12	43	0.04%	47.8%	VVLVLAGR	99.7%	48.4	25	40.7	6	0	0	826.55	10	17
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	7	12	43	0.04%	47.8%	VYNYNHLMPTR	99.7%	52.6	25	48.5	9	6	0	1407.68	74	84
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	7	12	43	0.04%	47.8%	YSVDIPLDK	99.7%	44	25	37	11	0	0	1049.55	85	93
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	7	12	43	0.04%	47.8%	YSVDIPLDKTVVNK	99.7%	68.4	25	58.9	2	1	0	1590.87	85	98
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	6	7	32	0.03%	38.5%	INFDKYHPGYFGK	99.7%	72.8	25	68.4	2	2	0	1585.78	43	55
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	6	7	32	0.03%	38.5%	LWTLVSEQTR	99.7%	62.8	25	53.1	4	0	0	1232.66	78	87
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	6	7	32	0.03%	38.5%	NKTGAAPIIDVVR	99.7%	35.8	25	28.3	0	2	0	1353.79	93	105
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	6	7	32	0.03%	38.5%	NQSFCPTVNLDK	99.7%	58.4	25	53.7	5	0	0	1422.67	66	77
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	6	7	32	0.03%	38.5%	SGYYKVLGK	99.6%	39.9	25	35.6	2	0	0	1014.56	106	114
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	6	7	32	0.03%	38.5%	TGAAPIIDVVR	99.7%	73	25	73	15	0	0	1111.65	95	105
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	42	0.04%	41.6%	GVVVVIKR	99.7%	45.1	25	36.5	3	0	0	869.59	59	66
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	42	0.04%	41.6%	KPATSYVR	99.7%	42.9	25	25.5	2	0	0	921.52	72	79
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	42	0.04%	41.6%	KTVGVEPAADGK	99.7%	78.5	25	68.9	4	0	0	1171.63	47	58
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	42	0.04%	41.6%	NCSSFLIK	99.2%	35.9	25	16.2	4	0	0	968.49	12	19
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	42	0.04%	41.6%	NCSSFLIKR	99.7%	53.6	25	44.6	2	0	0	1124.59	12	20
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	42	0.04%	41.6%	NKQTYSTEPNNLK	99.7%	58.7	25	54.8	5	2	0	1536.77	21	33
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	42	0.04%	41.6%	QTYSTEPNNLK	99.7%	52.7	25	42.8	7	0	0	1294.63	23	33

60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	42	0.04%	41.6%	TVGVEPAADGK	99.7%	56.1	25	46	4	0	0	1043.54	48	58
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	42	0.04%	41.6%	TVGVEPAADGKGVVVVIK	99.7%	77.9	25	72.1	4	1	0	1738.01	48	65
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	42	0.04%	41.6%	YNGLIHR	99.7%	44.7	25	27.9	2	0	0	872.47	40	46
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	11	13	42	0.04%	41.6%	YNGLIHRK	99.6%	39.9	25	28.5	2	0	0	1000.57	40	47
60S ribosomal protein L29	RPL29	RL29_HUMAN	17.8	100.0%	4	5	31	0.03%	21.4%	AQAAAPASVPAQAPK	99.7%	86.1	25	81.6	20	0	0	1377.75	135	149
60S ribosomal protein L29	RPL29	RL29_HUMAN	17.8	100.0%	4	5	31	0.03%	21.4%	AQAAAPASVPAQAPKR	99.7%	61.3	25	61.3	2	2	0	1533.85	135	150
60S ribosomal protein L29	RPL29	RL29_HUMAN	17.8	100.0%	4	5	31	0.03%	21.4%	LAYIAHPK	99.2%	35.8	25	32	6	0	0	912.53	96	103
60S ribosomal protein L29	RPL29	RL29_HUMAN	17.8	100.0%	4	5	31	0.03%	21.4%	YESLKGVDPK	94.9%	28.2	25	17.4	1	0	0	1135.60	29	38
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	33	95	0.09%	46.2%	AFMGPLKK	96.0%	29.2	25	19.1	2	0	0	891.51	387	394
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	33	95	0.09%	46.2%	AGMTHIVR	99.7%	54.3	25	45.3	4	0	0	884.48	51	58
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	33	95	0.09%	46.2%	AHLMEIQVNGGTVAEK	99.7%	130	25	127	1	4	0	1696.87	178	193
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	33	95	0.09%	46.2%	DDPSKPVHLTAFLGYK	99.7%	49.2	25	48	2	1	0	1787.93	35	50
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	33	95	0.09%	46.2%	ERLEQQVPVNQVFGQDEMIDVIGVTK	99.7%	61	25	61	0	4	0	2987.51	199	224
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	33	95	0.09%	46.2%	FQTMEEK	99.0%	35	25	25.5	1	0	0	912.41	379	385
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	33	95	0.09%	46.2%	HGSLGFLPR	99.7%	60.1	25	55.3	10	0	0	983.54	11	19
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	33	95	0.09%	46.2%	IGQGYLIK	99.7%	58.7	25	30.9	7	0	0	891.53	287	294
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	33	95	0.09%	46.2%	IGQGYLIKDGK	99.7%	58	25	51.3	2	0	0	1191.67	287	297
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	33	95	0.09%	46.2%	KSLLVQTK	99.2%	35.8	25	25.3	1	0	0	916.58	349	356
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	33	95	0.09%	46.2%	KVACIGAWHPAR	99.7%	70.6	25	70.6	2	2	0	1365.72	250	261
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	33	95	0.09%	46.2%	LEQQVPVNQVFGQDEMIDVIGVTK	99.7%	63.3	25	63.3	2	4	0	2686.38	201	224
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	33	95	0.09%	46.2%	NNASTDYDLSDK	99.7%	77.2	25	77.2	15	0	0	1342.58	301	312
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	33	95	0.09%	46.2%	SFPKDDPSKPVHLTAFLGYK	98.8%	28.5	25	28.5	0	2	0	2247.18	31	50
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	33	95	0.09%	46.2%	SINPLGGFVHYGEVTNDFVMLK	99.7%	61	25	61	0	3	0	2437.22	313	334
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	33	95	0.09%	46.2%	TVFAEHISDECK	99.7%	74.1	25	74.1	5	1	0	1435.65	104	115
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	33	95	0.09%	46.2%	TVFAEHISDECKR	99.7%	65.3	25	59.9	3	4	0	1591.75	104	116
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	33	95	0.09%	46.2%	VACIGAWHPAR	99.7%	88.7	25	82.5	4	3	0	1237.63	251	261
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	33	95	0.09%	46.2%	VIAHTQMR	99.7%	47.7	25	37.2	4	0	0	955.51	162	169
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	20	33	95	0.09%	46.2%	YCQVIR	98.1%	32.2	25	23.7	2	0	0	838.42	156	161
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	13	49	0.05%	59.1%	KSEIEYYAMLAK	99.7%	81.9	25	80.4	7	4	0	1461.73	57	68
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	13	49	0.05%	59.1%	KSLESINSR	99.7%	54	25	40.9	2	0	0	1033.56	9	17
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	13	49	0.05%	59.1%	LVILANNCPALR	99.7%	79.2	25	61.5	6	0	0	1353.77	45	56
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	13	49	0.05%	59.1%	LVILANNCPALRK	99.7%	44.1	25	34.5	2	0	0	1481.86	45	57
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	13	49	0.05%	59.1%	SEIEYYAMLAK	99.7%	91	25	85.1	10	0	0	1317.64	58	68
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	13	49	0.05%	59.1%	SLESINSR	99.7%	41.3	25	32.9	2	0	0	905.47	10	17
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	13	49	0.05%	59.1%	TGVHHYSGNNIELGTACGK	99.7%	89.1	25	89.1	3	6	0	2014.94	69	87
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	13	49	0.05%	59.1%	VCTLAIIDPGDSDIIR	99.7%	96.9	25	89.2	7	0	0	1757.91	91	106
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	9	10	50	0.05%	56.8%	EMGTPDVR	99.7%	47.3	25	35.3	6	0	0	920.41	56	63
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	9	10	50	0.05%	56.8%	EYTINIHK	99.6%	38.9	25	22.9	2	0	0	1017.54	24	31
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	9	10	50	0.05%	56.8%	EYTINIHKR	99.7%	55.4	25	39.8	4	0	0	1173.64	24	32
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	9	10	50	0.05%	56.8%	FAMKEMGTPDVR	99.7%	49.5	25	39.6	4	0	0	1413.65	52	63
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	9	10	50	0.05%	56.8%	IHGVGFKK	97.9%	31.8	25	29	4	0	0	885.53	33	40
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	9	10	50	0.05%	56.8%	LYTLVTYVPVTTFK	99.7%	74.6	25	74.6	8	0	0	1644.92	102	115
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	9	10	50	0.05%	56.8%	NEDEDSPNKLYTLVTYVPVTTFK	99.7%	34.1	25	34.1	0	2	0	2673.33	93	115
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	9	10	50	0.05%	56.8%	NLQTVNVDEN	99.7%	66.3	25	64.4	4	0	0	1145.54	116	125
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	9	10	50	0.05%	56.8%	SAINEVVTR	99.7%	75.8	25	61.7	16	0	0	988.54	15	23
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	6	14	39	0.04%	37.0%	AALRPLVKPK	97.4%	30.8	25	22.1	1	0	0	1092.73	2	11
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	6	14	39	0.04%	37.0%	ELEVLLMCNK	99.7%	54.1	25	49.3	8	0	0	1248.63	84	93
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	6	14	39	0.04%	37.0%	FKGQILMPNIGYGSNK	99.7%	65.2	25	65.2	4	4	0	1782.92	49	64
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	6	14	39	0.04%	37.0%	GQILMPNIGYGSNK	99.7%	63.5	25	55.2	5	0	0	1507.76	51	64
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	6	14	39	0.04%	37.0%	GQILMPNIGYGSNKK	99.7%	54.8	25	52.6	3	1	0	1619.86	51	65
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	6	14	39	0.04%	37.0%	SYCAEIAHNVSSK	99.7%	84.3	25	76.6	12	1	0	1465.67	94	106

60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	9	32	0.03%	40.2%	AFLIEEQK	99.7%	49.2	25	28.7	9	0	0	977.53	94	101
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	9	32	0.03%	40.2%	AYGGSMCAK	99.7%	46.6	25	46.6	2	0	0	944.40	77	85
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	9	32	0.03%	40.2%	IVYLYTK	99.7%	45	25	29.4	2	0	0	899.52	30	36
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	9	32	0.03%	40.2%	IVYLYTKK	99.7%	41.2	25	27.9	3	0	0	1027.62	30	37
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	9	32	0.03%	40.2%	LSYNTASNK	99.7%	58.3	25	40.7	6	0	0	997.49	11	19
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	9	32	0.03%	40.2%	LSYNTASNKTR	99.6%	39.5	25	24.3	2	0	0	1254.64	11	21
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	9	32	0.03%	40.2%	RAFLIEEQK	98.9%	34.8	25	23	2	0	0	1133.63	93	101
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	9	32	0.03%	40.2%	RLSYNTASNK	99.7%	43.1	25	35.8	4	0	0	1153.60	10	19
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	9	9	32	0.03%	40.2%	SACGVCPGR	99.7%	43.2	25	42	2	0	0	963.41	44	52
60S ribosomal protein L35	RPL35	RL35_HUMAN	14.6	100.0%	4	6	23	0.02%	29.3%	QLDDLKVELSQLR	99.7%	84.4	25	62.3	2	2	0	1556.86	20	32
60S ribosomal protein L35	RPL35	RL35_HUMAN	14.6	100.0%	4	6	23	0.02%	29.3%	VLTVINQTQK	99.7%	64.6	25	60.5	12	0	0	1143.67	57	66
60S ribosomal protein L35	RPL35	RL35_HUMAN	14.6	100.0%	4	6	23	0.02%	29.3%	VLTVINQTQKENLR	99.7%	79.9	25	79.9	2	2	0	1655.94	57	70
60S ribosomal protein L35	RPL35	RL35_HUMAN	14.6	100.0%	4	6	23	0.02%	29.3%	YKPLDLRPK	99.6%	39	25	39	3	0	0	1129.67	78	86
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	7	8	27	0.03%	40.9%	AIFAGYKR	98.6%	33.6	25	25.8	2	0	0	925.53	9	16
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	7	8	27	0.03%	40.9%	DETEFYLGK	99.7%	51.5	25	45.6	4	0	0	1101.51	37	45
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	7	8	27	0.03%	40.9%	DETEFYLGKR	99.7%	46.9	25	40.7	4	0	0	1257.61	37	46
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	7	8	27	0.03%	40.9%	IEGVYAR	99.0%	34.9	25	15.6	3	0	0	807.44	30	36
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	7	8	27	0.03%	40.9%	NNTVTPGGKPNK	99.7%	52.9	25	47.3	2	0	0	1226.65	55	66
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	7	8	27	0.03%	40.9%	VMLYPSR	98.5%	33.3	25	26.6	4	0	0	881.46	103	109
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	7	8	27	0.03%	40.9%	VMLYPSRI	99.6%	39.5	25	38.4	8	0	0	994.54	103	110
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	7	12	27	0.03%	40.0%	ALRYPMAVGLNK	99.7%	40.3	25	30.9	1	2	0	1348.74	2	13
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	7	12	27	0.03%	40.0%	EELSNVLAAMR	99.7%	87.7	25	80.5	5	0	0	1232.63	88	98
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	7	12	27	0.03%	40.0%	EELSNVLAAMRK	97.6%	31.2	25	23.5	1	0	0	1376.72	88	99
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	7	12	27	0.03%	40.0%	EVCGFAPYER	99.5%	38	25	38	7	0	0	1227.55	46	55
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	7	12	27	0.03%	40.0%	RAMELLK	99.0%	34.8	25	14.8	1	0	0	860.50	56	62
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	7	12	27	0.03%	40.0%	REELSNVLAAMR	99.7%	68.4	25	64.5	3	2	0	1388.73	87	98
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	7	12	27	0.03%	40.0%	YPMAVGLNK	99.7%	46.1	25	38	5	0	0	1008.52	5	13
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	5	6	17	0.02%	36.8%	DSLYAQGR	99.5%	37.9	25	34	2	0	0	909.44	31	38
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	5	6	17	0.02%	36.8%	GKDSLYAQGR	99.7%	58.5	25	51.1	4	0	0	1094.56	29	38
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	5	6	17	0.02%	36.8%	KGQVIQF	96.0%	29.2	25	22.4	1	0	0	819.47	100	106
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	5	6	17	0.02%	36.8%	LECVEPNCR	99.7%	46.4	25	46.4	6	0	0	1176.51	70	78
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	5	6	17	0.02%	36.8%	QSGYGGQTKPIFR	99.7%	53.1	25	51.1	2	2	0	1438.74	45	57
60S ribosomal protein L37a	RPL37A	RL37A_HUMAN	10.3	100.0%	4	5	24	0.02%	51.1%	AVGIWHCGSCMK	99.7%	47	25	47	5	0	0	1421.61	51	62
60S ribosomal protein L37a	RPL37A	RL37A_HUMAN	10.3	100.0%	4	5	24	0.02%	51.1%	KIEISQHAK	99.7%	46.5	25	41.3	7	0	0	1053.61	28	36
60S ribosomal protein L37a	RPL37A	RL37A_HUMAN	10.3	100.0%	4	5	24	0.02%	51.1%	TVAGGAWTYNTTSAVTVK	99.7%	96.9	25	95.1	11	0	0	1826.93	63	80
60S ribosomal protein L37a	RPL37A	RL37A_HUMAN	10.3	100.0%	4	5	24	0.02%	51.1%	YTCSFCGK	95.1%	28.4	25	28.4	1	0	0	1022.41	37	44
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	5	7	29	0.03%	51.4%	IEEIKDFLLTAR	99.7%	49.8	25	49.8	4	2	0	1447.82	5	16
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	5	7	29	0.03%	51.4%	LKQSLPPGLAVK	99.7%	54.5	25	54.5	5	0	0	1250.78	56	67
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	5	7	29	0.03%	51.4%	QSLPPGLAVK	99.7%	78.6	25	72.9	8	0	0	1009.60	58	67
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	5	7	29	0.03%	51.4%	YLYTLVITDK	99.7%	59	25	50.1	2	0	0	1228.68	41	50
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	5	7	29	0.03%	51.4%	YLYTLVITDKEK	99.7%	66.4	25	63.7	6	2	0	1485.82	41	52
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	30	121	0.12%	46.8%	AAAAAAALQAK	99.7%	97.8	25	88.7	15	0	0	956.55	354	364
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	30	121	0.12%	46.8%	APIRPDIVNFVHTNLR	99.7%	55.8	25	55.8	0	6	0	1862.04	30	45
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	30	121	0.12%	46.8%	AWNDIKK	98.3%	32.7	25	21.4	2	0	0	874.48	176	182
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	30	121	0.12%	46.8%	EAVLLLKK	96.8%	30.1	25	18.8	2	0	0	913.61	166	173
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	30	121	0.12%	46.8%	FCIWTESAFR	99.7%	56.2	25	47	10	0	0	1316.61	249	258
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	30	121	0.12%	46.8%	GPCIIYNEDNGIIK	99.7%	67.3	25	63.8	2	0	0	1605.79	206	219
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	30	121	0.12%	46.8%	IEEVPELPLVVEDK	99.7%	66.9	25	66.9	2	0	0	1608.87	144	157
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	30	121	0.12%	46.8%	IEEVPELPLVVEDKVEGYK	99.7%	63.9	25	63.9	1	0	0	2185.16	144	162
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	30	121	0.12%	46.8%	KLDELYGTWR	99.7%	59.1	25	48.4	4	2	0	1280.66	259	268
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	30	121	0.12%	46.8%	LAPGGHVGR	99.7%	57.4	25	46.7	2	0	0	863.48	240	248

60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	30	121	0.12%	46.8%	LDELYGTWR	99.7%	44.7	25	44.7	1	0	0	1152.57	260	268
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	30	121	0.12%	46.8%	MINTDLSR	99.7%	61.4	25	50.1	8	0	0	949.48	284	291
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	30	121	0.12%	46.8%	NIPGITLLNVSK	99.7%	93.8	25	93.8	14	0	0	1268.76	223	234
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	30	121	0.12%	46.8%	NVTLPAVFK	99.7%	41	25	27.2	5	0	0	988.58	21	29
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	30	121	0.12%	46.8%	QPYAVSELAGHQTSAESWGTGR	99.7%	107	25	107	2	3	0	2332.10	50	71
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	30	121	0.12%	46.8%	RGPCIIYNEDNGIIK	99.7%	68.9	25	53.9	2	4	0	1761.90	205	219
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	30	121	0.12%	46.8%	SGQGAFGNMCR	99.7%	57	25	57	7	0	0	1184.49	87	97
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	30	121	0.12%	46.8%	SNYNLPMHK	99.6%	39.4	25	39.4	11	0	0	1119.53	275	283
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	30	121	0.12%	46.8%	TKEAVLLLK	99.7%	52.5	25	45.9	3	0	0	1014.66	164	172
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	30	121	0.12%	46.8%	VDKAAAAAAALQAK	99.7%	77.2	25	56.3	1	0	0	1298.74	351	364
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	30	121	0.12%	46.8%	YAICSALAASALPALVMSK	99.7%	79.7	25	79.7	7	5	0	1937.02	122	140
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	32	74	0.07%	40.4%	DIICQIAYAR	99.7%	60.2	25	43.3	2	0	0	1222.63	59	68
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	32	74	0.07%	40.4%	EFNAEVHR	99.7%	47.1	25	36.9	2	0	0	1001.48	189	196
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	32	74	0.07%	40.4%	EFNAEVHRK	99.4%	37.7	25	28.3	2	0	0	1129.57	189	197
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	32	74	0.07%	40.4%	FPGYDSESK	99.7%	47.5	25	44.7	2	0	0	1029.45	180	188
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	32	74	0.07%	40.4%	GAVDGGLSIPHSTK	99.7%	93.6	25	85.2	2	2	0	1338.70	165	178
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	32	74	0.07%	40.4%	GAVDGGLSIPHSTKR	99.7%	61.6	25	61.4	2	2	0	1494.80	165	179
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	32	74	0.07%	40.4%	HIMGQNVADYMR	99.7%	63.9	25	51.2	8	4	0	1434.66	198	209
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	32	74	0.07%	40.4%	IEGDMIVCAAYAHELPK	99.7%	82.8	25	82.8	4	5	0	1916.92	69	85
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	32	74	0.07%	40.4%	KHIMGQNVADYMR	99.5%	32.5	25	31.6	1	3	0	1578.75	197	209
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	32	74	0.07%	40.4%	NSVTPDMMEEMYK	99.7%	85.4	25	85.4	3	0	0	1574.65	229	241
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	32	74	0.07%	40.4%	NSVTPDMMEEMYKK	99.7%	81.2	25	81.2	9	1	0	1702.75	229	242
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	32	74	0.07%	40.4%	RFPGYDSESK	99.7%	40.5	25	28.5	3	0	0	1185.55	179	188
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	32	74	0.07%	40.4%	VGLTNYAAAYCTGLLLAR	99.7%	96.8	25	90.3	5	2	0	1927.01	90	107
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	32	74	0.07%	40.4%	VTNRDIICQIAYAR	99.7%	39.7	25	30	0	2	0	1692.89	55	68
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	15	32	74	0.07%	40.4%	YLMEEDEDAYKK	99.7%	63.8	25	55	4	4	0	1533.68	210	221
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	21	73	0.07%	43.4%	AIPQLQGYLR	99.7%	59.1	25	48.6	4	0	0	1158.66	263	272
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	21	73	0.07%	43.4%	ASITPGTILIILTGR	99.7%	116	25	116	12	2	0	1525.93	142	156
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	21	73	0.07%	43.4%	AVDSQILPK	99.7%	57.8	25	30.2	3	0	0	970.56	252	260
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	21	73	0.07%	43.4%	EKYEITEQR	99.7%	42.8	25	36.7	3	0	0	1195.60	238	246
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	21	73	0.07%	43.4%	FVIATSTK	99.7%	46.3	25	46.3	2	0	0	866.50	193	200
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	21	73	0.07%	43.4%	HLTDAYFKK	99.7%	42.4	25	34.5	2	0	0	1122.59	211	219
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	21	73	0.07%	43.4%	HQEGEIFDTEK	99.7%	67.2	25	67.2	3	0	0	1332.61	227	237
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	21	73	0.07%	43.4%	HQEGEIFDTEKEK	99.7%	73.4	25	73.4	2	2	0	1589.74	227	239
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	21	73	0.07%	43.4%	QLASGLLLVTGPLVLNR	99.7%	118	25	118	8	3	0	1764.07	167	183
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	21	73	0.07%	43.4%	SVFALTNGIYPHK	99.7%	70.8	25	70.4	6	2	0	1446.77	273	285
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	21	73	0.07%	43.4%	VLATVTKPVGGDK	99.7%	73.3	25	66.4	8	2	0	1284.75	88	100
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	21	73	0.07%	43.4%	YEITEQR	99.7%	46.8	25	39.2	2	0	0	938.46	240	246
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	21	73	0.07%	43.4%	YEITEQRK	99.5%	38.1	25	31.5	2	0	0	1066.55	240	247
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	21	73	0.07%	43.4%	YYPTEDVPR	99.7%	68.8	25	65	2	0	0	1139.54	115	123
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	21	73	0.07%	43.4%	YYPTEDVPRK	99.1%	35.7	25	33	2	1	0	1267.63	115	124
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	19	55	0.05%	49.6%	AGNFYVPAEPK	99.7%	51.1	25	47.2	3	0	0	1192.60	78	88
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	19	55	0.05%	49.6%	ASINMLR	99.7%	67.8	25	50.1	6	0	0	804.44	128	134
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	19	55	0.05%	49.6%	EANNFLWPFK	99.7%	45.2	25	39.2	6	0	0	1265.63	203	212
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	19	55	0.05%	49.6%	EVPAVPETLKK	99.0%	29.2	25	26.5	1	1	0	1210.70	10	20
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	19	55	0.05%	49.6%	FKEANNFLWPFK	99.7%	56.8	25	49.5	2	0	0	1540.79	201	212
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	19	55	0.05%	49.6%	IALTDNALIAR	99.7%	95.7	25	82.6	7	0	0	1170.68	167	177
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	19	55	0.05%	49.6%	IVEPYIAWGYPNLK	99.7%	71.9	25	40.7	7	0	0	1662.89	135	148
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	19	55	0.05%	49.6%	KAGNFYVPAEPK	99.7%	51.7	25	48.5	4	2	0	1320.69	77	88
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	19	55	0.05%	49.6%	QIFNGTFVK	99.2%	36.2	25	31.8	2	0	0	1053.57	116	124
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	19	55	0.05%	49.6%	RIALTDNALIAR	99.7%	75.4	25	64.3	2	2	0	1326.79	166	177

60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	19	55	0.05%	49.6%	SVNELIYK	99.7%	55.7	25	42.2	2	0	0	965.53	149	156
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	19	55	0.05%	49.6%	SVNELIYKR	99.7%	49.6	25	41.1	4	0	0	1121.63	149	157
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	19	55	0.05%	49.6%	TTHFVEGGDAGNREDQINR	99.7%	61.6	25	61.6	2	1	0	2115.98	224	242
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	14	19	55	0.05%	49.6%	YGIICMEDLIHEIYTVGK	99.5%	38.5	25	38.2	1	0	0	2170.06	182	199
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	56	0.06%	45.5%	AGVNTVTTLVENK	99.7%	99.1	25	95.6	9	0	0	1345.73	138	150
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	56	0.06%	45.5%	AGVNTVTTLVENKK	99.7%	83.2	25	83.2	2	2	0	1473.83	138	151
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	56	0.06%	45.5%	HWGGNVLGPK	99.7%	43.6	25	43.6	2	0	0	1064.56	236	245
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	56	0.06%	45.5%	KMGVPYCIIK	99.7%	45.4	25	35.8	3	3	0	1208.65	176	185
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	56	0.06%	45.5%	KVAPAPAVVK	99.7%	46.9	25	45.8	2	0	0	979.63	11	20
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	56	0.06%	45.5%	KVVNPLFEK	99.7%	41.8	25	25	2	0	0	1073.64	26	34
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	56	0.06%	45.5%	LKVPPAINQFTQALDR	99.7%	50.3	25	50.3	2	2	0	1811.02	74	89
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	56	0.06%	45.5%	MGVPYCIIK	99.2%	36.3	25	29.7	3	0	0	1080.56	177	185
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	56	0.06%	45.5%	NFGIGQDIQPK	99.7%	79.9	25	63.2	3	0	0	1216.63	38	48
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	56	0.06%	45.5%	QTATQLLK	99.7%	48.5	25	29	2	0	0	902.53	90	97
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	56	0.06%	45.5%	RHWGGNVLGPK	99.7%	38.8	25	38.8	0	2	0	1220.66	235	245
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	56	0.06%	45.5%	TCTTVAFTQVNSEDK	99.7%	117	25	105	2	0	0	1700.78	198	212
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	56	0.06%	45.5%	TCTTVAFTQVNSEDKGALAK	99.7%	90.1	25	90.1	3	2	0	2141.05	198	217
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	56	0.06%	45.5%	TNYNDRYDEIR	99.7%	46.1	25	41.7	1	2	0	1458.66	224	234
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	56	0.06%	45.5%	VAPAPAVVKK	95.8%	28.9	25	28.9	1	0	0	979.63	12	21
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	25	56	0.06%	45.5%	VPPAINQFTQALDR	99.7%	102	25	93.2	4	2	0	1569.84	76	89
60S ribosomal protein L7-like 1	RPL7L1	RL7L_HUMAN	28.7	100.0%	3	3	5	0.00%	16.3%	IDGVSLLVQR	99.7%	76.4	25	55.5	2	0	0	1099.65	96	105
60S ribosomal protein L7-like 1	RPL7L1	RL7L_HUMAN	28.7	100.0%	3	3	5	0.00%	16.3%	IVEPYVTWGFPNLK	97.2%	30.5	25	28.2	1	0	0	1662.89	133	146
60S ribosomal protein L7-like 1	RPL7L1	RL7L_HUMAN	28.7	100.0%	3	3	5	0.00%	16.3%	TIPLTDNTVIEEHLGK	99.7%	57.1	25	56.9	2	0	0	1779.95	164	179
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	9	13	37	0.04%	35.8%	AQLNIGNVLPVGTMPEGTIVCCLEEKPGDR	99.7%	56.9	25	56.9	0	3	0	3283.61	94	123
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	9	13	37	0.04%	35.8%	ASGNYATVISHNPETK	99.7%	86.8	25	86.8	6	3	0	1688.82	129	144
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	9	13	37	0.04%	35.8%	ASGNYATVISHNPETKK	99.7%	58.1	25	57.2	2	3	0	1816.92	129	145
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	9	13	37	0.04%	35.8%	AVDFAER	99.7%	49.6	25	41.9	2	0	0	807.40	31	37
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	9	13	37	0.04%	35.8%	AVVGVVAGGGR	99.7%	89.3	25	74.6	8	0	0	941.55	164	174
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	9	13	37	0.04%	35.8%	DIIHDPGR	99.4%	37.5	25	27.7	2	0	0	922.47	47	54
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	9	13	37	0.04%	35.8%	GIVKDIIHDPGR	99.6%	33.5	25	32.7	2	2	0	1319.74	43	54
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	9	13	37	0.04%	35.8%	IDKPILK	97.7%	31.5	25	14	2	0	0	826.54	175	181
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	9	13	37	0.04%	35.8%	KVGLIAAR	98.0%	32.1	25	20.8	2	0	0	827.55	234	241
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	16	36	0.04%	39.6%	DFNHINVELSLLGK	99.7%	53.1	25	45.2	2	2	0	1598.85	37	50
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	16	36	0.04%	39.6%	DFNHINVELSLLGKK	99.7%	44.4	25	44.4	0	2	0	1726.95	37	51
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	16	36	0.04%	39.6%	FLDGIYVSEK	99.7%	66.2	25	54.5	10	0	0	1170.60	175	184
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	16	36	0.04%	39.6%	KFLDGIYVSEK	99.7%	69.5	25	60.4	2	1	0	1298.70	174	184
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	16	36	0.04%	39.6%	MRPGVACSVSQAQK	99.7%	51.7	25	48.9	2	4	0	1534.75	128	141
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	16	36	0.04%	39.6%	NFLGEKYIR	96.9%	30.2	25	11.5	1	0	0	1139.62	116	124
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	16	36	0.04%	39.6%	TICSHVQNMIK	99.7%	64.7	25	59.8	4	4	0	1330.66	72	82
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	16	36	0.04%	39.6%	TVIVKGPR	96.3%	29.5	25	29.5	1	0	0	869.56	24	31
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	9	16	36	0.04%	39.6%	VDKWWGNR	98.0%	32	25	24.9	1	0	0	1060.53	57	64
60S ribosome subunit biogenesis protein NIP7 homolog	NIP7	NIP7_HUMAN	20.5	99.8%	2	3	3	0.00%	13.3%	LHVTALDYLAPYAK	99.7%	41.3	25	35	1	0	0	1574.86	81	94
60S ribosome subunit biogenesis protein NIP7 homolog	NIP7	NIP7_HUMAN	20.5	99.8%	2	3	3	0.00%	13.3%	MRPLTEEETR	97.6%	31.1	25	23.3	2	0	0	1261.62	1	10
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	PFKFB3	F263_HUMAN	59.6	99.9%	2	2	3	0.00%	4.4%	IGGDSGLSSR	99.7%	42.7	25	37.4	2	0	0	948.47	265	274
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	PFKFB3	F263_HUMAN	59.6	99.9%	2	2	3	0.00%	4.4%	YPTGESYQDLVQR	99.7%	55	25	48.9	1	0	0	1555.74	357	369
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	8	8	13	0.01%	15.1%	AIGVLTSGGDAQGMNAAVR	99.7%	137	25	137	4	0	0	1787.91	26	44
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	8	8	13	0.01%	15.1%	EWSGLLEELAR	99.7%	57	25	29.5	2	0	0	1302.67	140	150
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	8	8	13	0.01%	15.1%	FTTDDSICVLGISK	99.7%	54.6	25	50.1	1	0	0	1555.77	711	724
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	8	8	13	0.01%	15.1%	GGTPSAFDR	99.7%	44.6	25	29.5	1	0	0	907.43	311	319
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	8	8	13	0.01%	15.1%	MLAIYDGFDGFAK	99.7%	43.7	25	43.7	2	0	0	1447.69	443	455
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	8	8	13	0.01%	15.1%	NGQIDKEAVQK	99.7%	45.8	25	34.7	2	0	0	1229.65	151	161

6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	8	8	13	0.01%	15.1%	NVIFQPVAELK	99.7%	46	25	39.7	1	0	0	1257.72	726	736
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	8	8	13	0.01%	15.1%	NVIFQPVAELKK	98.9%	34.4	25	32.3	1	0	0	1385.82	726	737
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	8	8	13	0.01%	15.1%	SFAGNLNTYK	99.7%	49.3	25	44.4	2	0	0	1114.55	386	395
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	8	8	13	0.01%	15.1%	TFVLEVMGR	99.7%	63	25	47.4	2	0	0	1051.56	211	219
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	8	8	13	0.01%	15.1%	YLEEIATQMR	99.7%	68	25	55.4	2	0	0	1253.62	487	496
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	12	15	27	0.03%	20.6%	AIGVLTSGGDAQGMNAAVR	99.7%	137	25	137	4	0	0	1787.91	17	35
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	12	15	27	0.03%	20.6%	AVAFSPVTELKK	99.5%	38.2	25	38.2	1	0	0	1289.75	716	727
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	12	15	27	0.03%	20.6%	GGTPSAFDR	99.7%	44.6	25	29.5	1	0	0	907.43	302	310
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	12	15	27	0.03%	20.6%	GQLESIVENIR	99.7%	68.4	25	56.9	2	0	0	1257.68	475	485
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	12	15	27	0.03%	20.6%	IMEVIDAITTTAQSHQR	99.7%	50.2	25	10.5	0	4	0	1929.97	185	201
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	12	15	27	0.03%	20.6%	LPLMECVQMTK	99.7%	43.2	25	43.2	1	0	0	1349.66	346	356
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	12	15	27	0.03%	20.6%	SNFSLAILNVGAPAAGMNAAVR	99.7%	55.1	25	55.1	1	0	0	2144.13	398	419
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	12	15	27	0.03%	20.6%	TFVLEVMGR	99.7%	63	25	47.4	2	0	0	1051.56	202	210
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	12	15	27	0.03%	20.6%	TNVLGHLQQGGAPTPFDR	99.7%	63.4	25	62.1	1	3	0	1907.97	655	672
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	12	15	27	0.03%	20.6%	VFANAPDSACVIGLK	99.7%	64.5	25	58.7	3	0	0	1561.80	699	713
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	12	15	27	0.03%	20.6%	VNVEHMTEK	99.7%	47.5	25	40.7	2	0	0	1086.52	606	614
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	12	15	27	0.03%	20.6%	VTVLGHVQR	99.7%	65.7	25	58.8	2	0	0	1008.59	293	301
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	7	7	10	0.01%	15.3%	ALVFQPVAELK	99.7%	81.3	25	76.1	2	0	0	1214.71	717	727
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	7	7	10	0.01%	15.3%	DLQANVEHLVQK	99.7%	59.2	25	52.9	2	0	0	1393.74	604	615
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	7	7	10	0.01%	15.3%	GGTPSAFDR	99.7%	44.6	25	29.5	1	0	0	907.43	302	310
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	7	7	10	0.01%	15.3%	GITNLCVIGGDGSLTGADTFR	99.7%	128	25	128	2	0	0	2124.04	109	129
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	7	7	10	0.01%	15.3%	IFANTPDSGCVLGMR	99.7%	53.7	25	53.7	1	0	0	1637.78	700	714
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	7	7	10	0.01%	15.3%	SEWSDLLSDLQK	99.7%	44.7	25	38.4	1	0	0	1420.70	130	141
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	7	7	10	0.01%	15.3%	TFVLEVMGR	99.7%	63	25	47.4	2	0	0	1051.56	202	210
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	7	7	10	0.01%	15.3%	VGIFTGAR	99.7%	44	25	30.4	1	0	0	820.47	40	47
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	7	7	10	0.01%	15.3%	VLVVHDGFEGLAK	99.7%	53.5	25	49.9	1	0	0	1383.76	433	445
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	7	7	10	0.01%	15.3%	VTVLGHVQR	99.7%	65.7	25	58.8	2	0	0	1008.59	293	301
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	6	8	13	0.01%	16.4%	AGQAVDDFIEK	99.7%	48.1	25	34	2	0	0	1192.58	77	87
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	6	8	13	0.01%	16.4%	FQFDGDKK	95.3%	28.5	25	22.6	1	0	0	984.48	310	317
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	6	8	13	0.01%	16.4%	GILFVGSGVSGGEEGAR	99.7%	97.7	25	97.6	2	0	0	1591.81	120	136
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	6	8	13	0.01%	16.4%	IISYAQGFMLLR	99.7%	78.8	25	73.9	4	0	0	1427.77	332	343
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	6	8	13	0.01%	16.4%	LVPLLDTGDIIIDGGNSEYR	99.7%	96.3	25	96.3	2	0	0	2160.12	88	107
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	6	8	13	0.01%	16.4%	YGPSLMPGGNK	99.7%	51.5	25	46.2	2	0	0	1120.55	137	147
6-pyruvoyl tetrahydrobiopterin synthase	PTS	PTPS_HUMAN	16.4	100.0%	3	3	4	0.00%	24.8%	VLPVGVLYK	98.3%	32.8	25	29.8	1	0	0	987.62	121	129
6-pyruvoyl tetrahydrobiopterin synthase	PTS	PTPS_HUMAN	16.4	100.0%	3	3	4	0.00%	24.8%	VYETDNNIVVYKGE	99.7%	53.6	25	50.8	2	0	0	1642.80	132	145
6-pyruvoyl tetrahydrobiopterin synthase	PTS	PTPS_HUMAN	16.4	100.0%	3	3	4	0.00%	24.8%	YMEEAIMQPLDHK	99.4%	37.2	25	31.5	1	0	0	1620.74	79	91
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	19	33	0.03%	35.2%	DAGTIAGLNVMR	99.7%	87.7	25	77.6	4	0	0	1217.63	186	197
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	19	33	0.03%	35.2%	ELEEIVQPIISK	99.7%	61.5	25	48.7	2	0	0	1397.79	622	633
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	19	33	0.03%	35.2%	IINEPTAAAIAYGLDK	99.7%	112	25	111	2	0	0	1659.90	198	213
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	19	33	0.03%	35.2%	IINEPTAAAIAYGLDKR	99.7%	105	25	105	1	2	0	1816.00	198	214
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	19	33	0.03%	35.2%	ITITNDQNR	98.9%	34.7	25	24.2	2	0	0	1074.55	524	532
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	19	33	0.03%	35.2%	ITPSYVAFTPEGER	99.7%	54.5	25	54.5	2	0	0	1566.78	61	74
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	19	33	0.03%	35.2%	LYGSAGPPPTGEEDTAEKDEL	99.7%	115	25	115	1	0	0	2175.99	634	654
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	19	33	0.03%	35.2%	MKETAEAYLGK	99.7%	40.5	25	38	1	0	0	1240.62	153	163
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	19	33	0.03%	35.2%	NQLTSNPENTVFDAK	99.7%	94.6	25	86	2	0	0	1677.81	82	96
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	19	33	0.03%	35.2%	SDIDEIVLVGGSTR	99.7%	56.9	25	56.9	2	0	0	1460.76	354	367
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	19	33	0.03%	35.2%	SQIFSTASDNQPTVTIK	99.7%	105	25	91.4	2	0	0	1836.93	448	464
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	19	33	0.03%	35.2%	TFAPEEISAMVLTK	99.7%	85	25	83.9	3	0	0	1552.79	139	152
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	19	33	0.03%	35.2%	TKPYIQVDIGGGQTK	99.7%	57.7	25	55.3	1	0	0	1604.86	124	138
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	19	33	0.03%	35.2%	TWNDPSVQQDIK	99.7%	57.6	25	53.9	2	0	0	1430.69	102	113
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	19	33	0.03%	35.2%	VEIIANDQGNR	99.7%	72.3	25	0	2	0	0	1228.63	50	60

78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	19	33	0.03%	35.2%	VLEDSDLKK	99.3%	36.6	25	19.7	2	0	0	1046.57	345	353
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	19	33	0.03%	35.2%	VTHAVVTVPAYFNDAQR	99.7%	57.5	25	56.7	0	2	0	1887.97	165	181
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	16	19	33	0.03%	35.2%	VYEGERPLTK	99.7%	56.3	25	52.5	2	0	0	1191.64	465	474
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	4	5	18	0.02%	11.6%	FLPGYVGGIQEGAVTPAGVVNK	99.7%	109	25	109	4	4	0	2173.17	121	142
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	4	5	18	0.02%	11.6%	LLVSGFWGVAR	99.7%	95.9	25	90.4	4	0	0	1204.68	394	404
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	4	5	18	0.02%	11.6%	SLDGVTNDR	98.9%	34.6	25	25.6	2	0	0	976.47	14	22
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	4	5	18	0.02%	11.6%	VIECSYTSADGQR	99.7%	97.4	25	90.7	4	0	0	1485.66	377	389
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	18	47	0.05%	45.2%	DGLTDVYNK	99.7%	48.1	25	41.7	2	0	0	1024.49	182	190
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	18	47	0.05%	45.2%	EAYMGNVLQGGEGQAPTR	99.7%	101	25	101	8	0	0	1893.88	88	105
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	18	47	0.05%	45.2%	EEVKEAYMGNVLQGGEGQAPTR	98.8%	28.5	25	28.5	0	1	0	2379.12	84	105
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	18	47	0.05%	45.2%	ENGTVTAANASTLNDGAAALVLMTADAAK	99.7%	47	25	47	0	2	0	2761.37	274	302
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	18	47	0.05%	45.2%	EVVIVSATR	99.7%	69.2	25	66.5	4	0	0	973.57	41	49
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	18	47	0.05%	45.2%	GSTPYGGVKLEDLIVK	99.7%	62.7	25	53.8	1	0	0	1675.93	166	181
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	18	47	0.05%	45.2%	IHMGSCAENTAK	99.7%	59.3	25	59.3	2	1	0	1318.59	191	202
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	18	47	0.05%	45.2%	IVGHLTHALK	99.7%	47.7	25	41.3	3	0	0	1088.66	394	403
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	18	47	0.05%	45.2%	LEDLIVK	99.4%	37.5	25	25.3	3	0	0	829.50	175	181
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	18	47	0.05%	45.2%	LNVTPLAR	99.3%	36.5	25	28.8	4	0	0	883.54	304	311
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	18	47	0.05%	45.2%	MLEIDPQK	99.2%	35.9	25	23.4	1	0	0	989.50	366	373
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	18	47	0.05%	45.2%	NEQDAYAINSYTR	99.7%	112	25	112	4	0	0	1544.70	209	221
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	18	47	0.05%	45.2%	QAVLGAGLPISTPCTTINK	99.7%	104	25	104	3	0	0	1941.05	106	124
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	18	47	0.05%	45.2%	RLNVTPLAR	99.1%	35.6	25	33.7	3	0	0	1039.64	303	311
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	18	47	0.05%	45.2%	TPIGSFLGSLSLLPATK	99.7%	97.7	25	96.2	4	0	0	1701.98	50	66
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	16	18	47	0.05%	45.2%	VNINGGAVSLGHPIGMSGAR	99.7%	49.3	25	47.5	0	1	0	1922.99	374	393
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	13	13	20	0.02%	7.2%	DEPIHILNVAIK	99.7%	49.9	25	42.3	1	0	0	1361.78	1283	1294
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	13	13	20	0.02%	7.2%	DFTVASPAEFVTR	99.7%	49.6	25	47	1	0	0	1439.72	99	111
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	13	13	20	0.02%	7.2%	DIIVIGNDITYR	99.7%	50.7	25	39.5	2	0	0	1391.75	1676	1687
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	13	13	20	0.02%	7.2%	FVVMVTPEDLK	99.7%	45.5	25	42.2	1	0	0	1277.68	153	163
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	13	13	20	0.02%	7.2%	IGLAEEIR	99.7%	56.3	25	41.2	2	0	0	900.52	1724	1731
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	13	13	20	0.02%	7.2%	IGSFGPQEDLLFLR	99.7%	56.2	25	53.2	2	0	0	1591.85	1688	1701
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	13	13	20	0.02%	7.2%	IIQQAGQVWFPDSAFK	97.3%	30.8	25	30.2	1	0	0	1834.95	2010	2025
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	13	13	20	0.02%	7.2%	ILNVPQELYEK	99.7%	51.6	25	47.7	2	0	0	1345.74	278	288
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	13	13	20	0.02%	7.2%	ITDIIGKEEGIGPENLR	99.7%	36.9	25	36.9	0	1	0	1854.00	1782	1798
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	13	13	20	0.02%	7.2%	ITSENPDEGFKPSSGTVQELNFR	99.7%	49.2	25	49.2	0	2	0	2552.23	510	532
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	13	13	20	0.02%	7.2%	LPELLLK	97.7%	31.3	25	10.4	2	0	0	825.54	218	224
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	13	13	20	0.02%	7.2%	VEVGTEVTDYR	99.7%	61.4	25	59.9	2	0	0	1267.62	1410	1420
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	13	13	20	0.02%	7.2%	VQQAELHTGSLPR	99.7%	67.4	25	61.3	1	0	0	1435.77	826	838
Acidic fibroblast growth factor intracellular-binding protein	FIBP	FIBP_HUMAN	41.9	99.8%	2	2	3	0.00%	6.0%	DYAAIVFFANNR	99.0%	35.2	25	35.2	1	0	0	1400.70	172	183
Acidic fibroblast growth factor intracellular-binding protein	FIBP	FIBP_HUMAN	41.9	99.8%	2	2	3	0.00%	6.0%	YYAFDEAFVR	99.7%	50.5	25	50.5	2	0	0	1280.59	96	105
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.8%	2	5	11	0.01%	36.6%	AGFAGDDAPR	99.7%	78.5	25	67.2	23	0	0	976.45	21	30
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.8%	2	5	11	0.01%	36.6%	AVFPSIVGRPR	99.7%	73.3	25	73.3	5	0	0	1198.71	31	41
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.8%	2	5	11	0.01%	36.6%	DLTDYLMK	99.7%	59	25	45.9	11	0	0	998.49	186	193
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.8%	2	5	11	0.01%	36.6%	DSYVGDEAQSK	99.7%	83.8	25	79.1	13	0	0	1198.52	53	63
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.8%	2	5	11	0.01%	36.6%	DSYVGDEAQSKR	99.7%	72.4	25	69.7	12	1	0	1354.62	53	64
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.8%	2	5	11	0.01%	36.6%	EITALAPSTMK	99.7%	68.5	25	63.9	37	0	0	1177.61	318	328
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.8%	2	5	11	0.01%	36.6%	GYSFVTTAER	99.7%	45.8	25	37.1	1	0	0	1130.55	199	208
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.8%	2	5	11	0.01%	36.6%	HQGVMVGMGQK	99.7%	60.7	25	29.6	12	4	0	1187.57	42	52
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.8%	2	5	11	0.01%	36.6%	IIAPPERK	99.7%	45.1	25	28.5	2	0	0	923.57	331	338
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.8%	2	5	11	0.01%	36.6%	IKIIAPPER	98.3%	32.7	25	32.7	1	0	0	1036.65	329	337
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.8%	2	5	11	0.01%	36.6%	IWHHTFYNELR	99.7%	47.3	25	46.9	2	5	0	1515.75	87	97
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.8%	2	5	11	0.01%	36.6%	LDLAGRDLTDYLMK	99.7%	50.6	25	46.4	4	2	0	1623.84	180	193
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.8%	2	5	11	0.01%	36.6%	RGILTLK	98.5%	33.2	25	17.2	1	0	0	800.54	64	70

Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.8%	2	5	11	0.01%	36.6%	SYELPDGQVITIGNER	99.7%	118	25	105	18	0	0	1790.89	241	256
Actin, alpha cardiac muscle 1	ACTC1	ACTC_HUMAN	42.0	99.8%	2	5	11	0.01%	36.6%	YPIEHGIITNWDDMEK	99.7%	46.8	25	24.7	4	6	0	1960.91	71	86
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	43	286	0.28%	70.1%	AGFAGDDAPR	99.7%	78.5	25	67.2	23	0	0	976.45	19	28
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	43	286	0.28%	70.1%	AVFPSIVGRPR	99.7%	73.3	25	73.3	5	0	0	1198.71	29	39
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	43	286	0.28%	70.1%	CDVDIRK	99.5%	38.3	25	14.4	2	0	0	905.45	285	291
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	43	286	0.28%	70.1%	CPEALFQPSFLGMESCGIHETTFNSIMK	99.7%	35.7	25	35.7	0	3	0	3231.46	257	284
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	43	286	0.28%	70.1%	DLTDYLMK	99.7%	59	25	45.9	11	0	0	998.49	184	191
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	43	286	0.28%	70.1%	DLYANTVLSGGTTMYPGIADR	99.7%	119	25	119	21	4	0	2231.07	292	312
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	43	286	0.28%	70.1%	DSYVGDEAQSK	99.7%	83.8	25	79.1	13	0	0	1198.52	51	61
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	43	286	0.28%	70.1%	DSYVGDEAQSKR	99.7%	72.4	25	69.7	12	1	0	1354.62	51	62
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	43	286	0.28%	70.1%	EITALAPSTMK	99.7%	68.5	25	63.9	37	0	0	1177.61	316	326
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	43	286	0.28%	70.1%	GYSFTTTAER	99.7%	87.4	25	79.8	26	0	0	1132.53	197	206
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	43	286	0.28%	70.1%	HQGVMVGMGQK	99.7%	60.7	25	29.6	12	4	0	1187.57	40	50
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	43	286	0.28%	70.1%	IIAPPERK	99.7%	45.1	25	28.5	2	0	0	923.57	329	336
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	43	286	0.28%	70.1%	IKIIAPPER	98.3%	32.7	25	32.7	1	0	0	1036.65	327	335
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	43	286	0.28%	70.1%	IWHHTFYNELR	99.7%	47.3	25	46.9	2	5	0	1515.75	85	95
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	43	286	0.28%	70.1%	KDLYANTVLSGGTTMYPGIADR	99.7%	77.7	25	77.7	1	4	0	2343.17	291	312
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	43	286	0.28%	70.1%	LCYVALDFEQEMATAASSSSLEK	99.7%	150	25	150	13	12	0	2566.17	216	238
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	43	286	0.28%	70.1%	LDLAGRDLTDYLMK	99.7%	50.6	25	46.4	4	2	0	1623.84	178	191
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	43	286	0.28%	70.1%	QEYDESGPSIVHR	99.7%	59.5	25	55.3	5	6	0	1516.70	360	372
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	43	286	0.28%	70.1%	QEYDESGPSIVHRK	98.1%	26.5	25	24	0	2	0	1644.80	360	373
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	43	286	0.28%	70.1%	RGILTLK	98.5%	33.2	25	17.2	1	0	0	800.54	62	68
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	43	286	0.28%	70.1%	SYELPDGQVITIGNER	99.7%	118	25	105	18	0	0	1790.89	239	254
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	43	286	0.28%	70.1%	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	99.7%	75.4	25	75.4	0	11	0	3199.61	148	177
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN	41.7	100.0%	23	43	286	0.28%	70.1%	VAPEEHPVLLTEAPLNPK	99.7%	81.7	25	45.8	14	9	0	1954.06	96	113
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	5	7	12	0.01%	16.2%	DLMVGDEASELR	99.7%	69.9	25	59.4	3	0	0	1350.62	54	65
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	5	7	12	0.01%	16.2%	GYAFNHSADFETVR	99.7%	68.6	25	59.5	2	0	0	1613.73	201	214
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	5	7	12	0.01%	16.2%	ILLTEPPMNPTK	99.7%	56.2	25	47.8	4	0	0	1353.74	107	118
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	5	7	12	0.01%	16.2%	KVVVCDNGTGFVK	96.3%	29.5	25	29.5	1	0	0	1422.74	7	19
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	5	7	12	0.01%	16.2%	LCYVGYNIEQEQK	99.7%	78.8	25	75.2	2	0	0	1643.77	220	232
Actin-related protein 2/3 complex subunit 2	ARPC2	ARPC2_HUMAN	34.3	100.0%	2	2	2	0.00%	6.7%	DNTINLIHTFR	99.7%	44.2	25	39.5	1	0	0	1343.71	238	248
Actin-related protein 2/3 complex subunit 2	ARPC2	ARPC2_HUMAN	34.3	100.0%	2	2	2	0.00%	6.7%	MILLEVNNR	99.7%	57.2	25	51	1	0	0	1101.61	1	9
Actin-related protein 2/3 complex subunit 3	ARPC3	ARPC3_HUMAN	20.5	99.8%	2	2	3	0.00%	12.4%	LIGNMALLPIR	98.8%	34.2	25	34.2	2	0	0	1226.73	15	25
Actin-related protein 2/3 complex subunit 3	ARPC3	ARPC3_HUMAN	20.5	99.8%	2	2	3	0.00%	12.4%	VFDPQNDKPSK	97.9%	31.9	25	24.5	1	0	0	1274.64	148	158
Actin-related protein 2/3 complex subunit 4	ARPC4	ARPC4_HUMAN	19.7	100.0%	3	3	7	0.01%	17.3%	AENFFILR	99.5%	37.9	25	27.5	2	0	0	1009.55	98	105
Actin-related protein 2/3 complex subunit 4	ARPC4	ARPC4_HUMAN	19.7	100.0%	3	3	7	0.01%	17.3%	ELLLQPVTISR	99.7%	56.9	25	52.2	4	0	0	1268.76	45	55
Actin-related protein 2/3 complex subunit 4	ARPC4	ARPC4_HUMAN	19.7	100.0%	3	3	7	0.01%	17.3%	IVAEEFLKNF	96.8%	30	25	30	1	0	0	1209.65	159	168
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	5	5	8	0.01%	13.9%	DITYFIQQLLR	99.7%	64.1	25	48.5	2	0	0	1409.78	199	209
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	5	5	8	0.01%	13.9%	FMEQVIFK	98.8%	34.1	25	32.3	2	0	0	1041.54	92	99
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	5	5	8	0.01%	13.9%	LGYAGNTEPQFIIPSCIAIK	99.7%	49.8	25	47.2	1	0	0	2192.14	19	38
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	5	5	8	0.01%	13.9%	LSEELSGGR	99.7%	62.6	25	44.7	2	0	0	947.48	349	357
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	5	5	8	0.01%	13.9%	YSYVCPDLVK	96.0%	29.2	25	29.2	1	0	0	1243.60	231	240
Activated RNA polymerase II transcriptional coactivator p15	SUB1	TCP4_HUMAN	14.4	100.0%	4	4	6	0.01%	40.9%	DDNMFQIGK	99.7%	41.4	25	41.4	2	0	0	1083.48	60	68
Activated RNA polymerase II transcriptional coactivator p15	SUB1	TCP4_HUMAN	14.4	100.0%	4	4	6	0.01%	40.9%	ELVSSSSSGSDSDSEVDKK	99.7%	77.3	25	77.3	2	0	0	1942.87	6	24
Activated RNA polymerase II transcriptional coactivator p15	SUB1	TCP4_HUMAN	14.4	100.0%	4	4	6	0.01%	40.9%	EQISDIDDAVR	99.7%	61.6	25	54.6	1	0	0	1260.61	115	125
Activated RNA polymerase II transcriptional coactivator p15	SUB1	TCP4_HUMAN	14.4	100.0%	4	4	6	0.01%	40.9%	GISLNPEQWSQLK	97.5%	31.1	25	25.5	1	0	0	1499.79	102	114
Activating signal cointegrator 1 complex subunit 1	ASCC1	ASCC1_HUMAN	45.5	100.0%	2	2	2	0.00%	4.3%	FQEEVLAK	99.6%	39.5	25	18.4	1	0	0	963.51	181	188
Activating signal cointegrator 1 complex subunit 1	ASCC1	ASCC1_HUMAN	45.5	100.0%	2	2	2	0.00%	4.3%	YNLYTAEGK	99.7%	45.9	25	41	1	0	0	1058.52	323	331
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	8	8	10	0.01%	3.9%	AGRPQFDDQGK	97.7%	25.8	25	25.8	0	1	0	1218.59	1690	1700
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	8	8	10	0.01%	3.9%	DLADWLNIK	99.7%	44.8	25	35.3	2	0	0	1087.58	1498	1506
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	8	8	10	0.01%	3.9%	RLEPLGIIVK	99.7%	42.8	25	38	1	0	0	1137.74	553	562

Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	8	8	10	0.01%	3.9%	SVGDVALSQIVR	99.7%	45.9	25	37.2	1	0	0	1243.70	595	606
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	8	8	10	0.01%	3.9%	TGYFSSTDLGR	99.7%	74.4	25	67.6	2	0	0	1203.56	973	983
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	8	8	10	0.01%	3.9%	TVAAELAIFR	99.7%	59.4	25	54.2	1	0	0	1090.63	1356	1365
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	8	8	10	0.01%	3.9%	VFNKYPTSK	98.9%	34.7	25	23.1	1	0	0	1083.58	1366	1374
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	8	8	10	0.01%	3.9%	VIELTGDVTPDMK	99.7%	45.1	25	45.1	1	0	0	1417.72	1404	1416
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	6	7	11	0.01%	20.4%	ADATNVNNWHWTER	99.7%	45.6	25	45.6	1	0	0	1713.77	17	30
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	6	7	11	0.01%	20.4%	DASNWSTDKLK	99.5%	38.3	25	19.8	1	0	0	1264.62	31	41
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	6	7	11	0.01%	20.4%	EAMGIYISTLK	99.7%	53.3	25	45.6	4	0	0	1241.64	146	156
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	6	7	11	0.01%	20.4%	ETFLTSPEELYR	99.4%	37.2	25	32	2	0	0	1484.73	213	224
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	6	7	11	0.01%	20.4%	GIPAPEEERTR	99.7%	44.5	25	38.5	1	0	0	1254.64	306	316
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	100.0%	6	7	11	0.01%	20.4%	LDGEASINNR	99.7%	66.5	25	49.7	2	0	0	1088.53	64	73
Active regulator of SIRT1	RPS19BP1	AROS_HUMAN	15.4	99.8%	2	2	3	0.00%	25.0%	GLELLAASEAPRDPPGQAKPR	99.7%	60.3	25	53.2	0	1	0	2173.17	9	29
Active regulator of SIRT1	RPS19BP1	AROS_HUMAN	15.4	99.8%	2	2	3	0.00%	25.0%	STVAESVSQQILR	99.7%	61.8	25	48.8	2	0	0	1417.76	84	96
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	22	39	0.04%	32.0%	FFTEEVDSR	99.7%	63	25	56	2	0	0	1129.52	77	85
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	22	39	0.04%	32.0%	FSMGSVVAGLLK	99.7%	68.3	25	63.8	4	0	0	1224.67	305	316
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	22	39	0.04%	32.0%	GIILAGTEEQK	99.7%	52.5	25	39.2	2	0	0	1158.64	152	162
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	22	39	0.04%	32.0%	GSNTCEVHFENTK	99.7%	40.8	25	40.8	1	0	0	1522.66	267	279
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	22	39	0.04%	32.0%	ILLIFEGTNEILR	99.7%	74.1	25	74.1	2	0	0	1530.89	421	433
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	22	39	0.04%	32.0%	IPVENILGEVGDGFK	99.7%	91.2	25	90.4	2	0	0	1586.84	280	294
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	22	39	0.04%	32.0%	ITAFIVER	99.7%	53	25	45.5	2	0	0	948.55	242	249
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	22	39	0.04%	32.0%	LASGEHIAAFCLTEPASGSDAASIR	99.7%	39.3	25	28.2	0	1	0	2531.22	169	193
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	22	39	0.04%	32.0%	LIEMTAEYACTR	99.7%	74.7	25	74.7	3	0	0	1473.67	318	329
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	22	39	0.04%	32.0%	LSEFGLIQEK	99.7%	70.9	25	50.4	2	0	0	1163.63	336	345
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	22	39	0.04%	32.0%	TEVVDSDGSVK	98.1%	32.1	25	31.2	1	0	0	1135.55	229	239
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	22	39	0.04%	32.0%	TEVVDSDGSVKDK	99.7%	44.7	25	39	1	0	0	1378.67	229	241
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	22	39	0.04%	32.0%	TIMEEQLVLK	99.7%	53.4	25	33.2	2	0	0	1203.67	522	531
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	22	39	0.04%	32.0%	TVETLLLR	99.7%	52.5	25	30.8	2	0	0	944.58	511	518
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	22	39	0.04%	32.0%	VAMNILNSGR	99.7%	78.7	25	66.6	2	0	0	1090.57	295	304
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	22	39	0.04%	32.0%	VSQQILEK	99.7%	44.2	25	29.5	2	0	0	944.54	601	608
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	22	39	0.04%	32.0%	VSTVMDTVGR	99.7%	79.2	25	69.6	4	0	0	1064.54	460	469
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	22	39	0.04%	32.0%	YAPENLDEQIK	98.9%	34.6	25	22.6	2	0	0	1319.65	589	599
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	19	22	39	0.04%	32.0%	YAPENLDEQIKK	99.7%	41.5	25	38.6	2	0	0	1447.74	589	600
Acyl-coenzyme A thioesterase 13	ACOT13	ACO13_HUMAN	15.0	100.0%	3	3	7	0.01%	28.6%	GAPGVSVDMNITYMSPAK	99.7%	65	25	64.7	1	0	0	1869.87	78	95
Acyl-coenzyme A thioesterase 13	ACOT13	ACO13_HUMAN	15.0	100.0%	3	3	7	0.01%	28.6%	ITLVSAAPGK	99.7%	48.5	25	43.4	2	0	0	956.58	28	37
Acyl-coenzyme A thioesterase 13	ACOT13	ACO13_HUMAN	15.0	100.0%	3	3	7	0.01%	28.6%	TLAFTSVDLTNK	99.7%	83.1	25	77.2	4	0	0	1309.70	112	123
Acyl-coenzyme A thioesterase 8	ACOT8	ACOT8_HUMAN	35.9	99.8%	2	2	4	0.00%	7.8%	LFGGQIVGQALVAAAK	99.7%	80.4	25	80.4	2	0	0	1542.90	54	69
Acyl-coenzyme A thioesterase 8	ACOT8	ACOT8_HUMAN	35.9	99.8%	2	2	4	0.00%	7.8%	LPVLYQVER	99.7%	67.2	25	61.9	2	0	0	1116.64	92	100
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	ACOT9_HUMAN	49.9	100.0%	5	7	9	0.01%	11.8%	EIVGASTNWR	99.7%	43.7	25	38.3	1	0	0	1132.57	46	55
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	ACOT9_HUMAN	49.9	100.0%	5	7	9	0.01%	11.8%	IFGGFLMR	99.7%	64	25	56.7	3	0	0	940.51	310	317
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	ACOT9_HUMAN	49.9	100.0%	5	7	9	0.01%	11.8%	SLEICHPQER	99.7%	41.7	25	41.7	2	0	0	1268.61	295	304
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	ACOT9_HUMAN	49.9	100.0%	5	7	9	0.01%	11.8%	TYGESMLYLDGQR	99.7%	69.5	25	69.5	2	0	0	1532.71	408	420
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	ACOT9_HUMAN	49.9	100.0%	5	7	9	0.01%	11.8%	VHSEVASLQEK	99.6%	38.9	25	35.9	1	0	0	1226.64	373	383
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	6	7	12	0.01%	19.2%	ATVFLNPAACK	99.7%	56.2	25	55	2	0	0	1191.62	63	73
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	6	7	12	0.01%	19.2%	EQPVFAMTGLR	99.7%	47.4	25	39.2	3	0	0	1264.64	200	210
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	6	7	12	0.01%	19.2%	GDFITIGSR	99.7%	64.9	25	49.4	2	0	0	965.51	343	351
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	6	7	12	0.01%	19.2%	GETVPLDVLQIK	99.7%	49.5	25	40.9	2	0	0	1311.75	185	196
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	6	7	12	0.01%	19.2%	IPIGFIPLGETSSLSHTLFAESGNK	99.7%	48.6	25	48.6	0	1	0	2615.37	147	171
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	6	7	12	0.01%	19.2%	VQHITDATLAIVK	99.7%	57.5	25	57.5	2	0	0	1408.82	172	184
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	5	6	16	0.02%	35.6%	AELEIQKDALEPGQR	99.7%	71.3	25	66.4	2	2	0	1696.89	108	122
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	5	6	16	0.02%	35.6%	DISPVLKDPASFR	99.7%	45.8	25	45.8	3	0	0	1444.78	28	40
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	5	6	16	0.02%	35.6%	IDYIAGLDSR	99.7%	61	25	53.8	5	0	0	1122.58	58	67

Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	5	6	16	0.02%	35.6%	LAPVPFFSLLQYE	99.7%	47.4	25	47.4	2	0	0	1523.81	168	180
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	5	6	16	0.02%	35.6%	SFPDFPTPGVVFR	99.7%	57.1	25	54.5	2	0	0	1465.75	15	27
Adenosine 3'-phospho 5'-phosphosulfate transporter 1	SLC35B2	S35B2_HUMAN	47.5	100.0%	3	3	5	0.00%	7.6%	ASDEVPLAPR	99.7%	42.3	25	40.6	1	0	0	1054.55	88	97
Adenosine 3'-phospho 5'-phosphosulfate transporter 1	SLC35B2	S35B2_HUMAN	47.5	100.0%	3	3	5	0.00%	7.6%	FVSFPTQVLAK	98.1%	32.3	25	26.5	2	0	0	1236.70	206	216
Adenosine 3'-phospho 5'-phosphosulfate transporter 1	SLC35B2	S35B2_HUMAN	47.5	100.0%	3	3	5	0.00%	7.6%	SYGATATSPGER	99.6%	39.7	25	38.6	2	0	0	1196.55	137	148
Adenosylhomocysteinase	AHCY	SAHH_HUMAN	47.7	100.0%	3	3	4	0.00%	8.6%	GISEETTTGVHNLYK	99.7%	57.5	25	53	1	0	0	1648.82	152	166
Adenosylhomocysteinase	AHCY	SAHH_HUMAN	47.7	100.0%	3	3	4	0.00%	8.6%	SKFDNLYGCR	99.7%	45.3	25	44.6	1	0	0	1259.58	187	196
Adenosylhomocysteinase	AHCY	SAHH_HUMAN	47.7	100.0%	3	3	4	0.00%	8.6%	VPAINVNDSVTK	99.7%	56.9	25	56.9	2	0	0	1256.68	175	186
Adenylate kinase 2, mitochondrial	AK2	KAD2_HUMAN	26.5	99.8%	2	2	3	0.00%	8.8%	AVLLGPPGAGK	98.3%	32.8	25	32.8	2	0	0	979.59	18	28
Adenylate kinase 2, mitochondrial	AK2	KAD2_HUMAN	26.5	99.8%	2	2	3	0.00%	8.8%	NGFLLDGFPR	99.3%	36.8	25	26.3	1	0	0	1135.59	94	103
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	8	16	0.02%	33.6%	AVILGPPGSGK	99.2%	36.3	25	24.9	2	0	0	995.59	8	18
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	8	16	0.02%	33.6%	DVAKPVIELYK	99.5%	38	25	29	2	0	0	1274.74	176	186
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	8	16	0.02%	33.6%	GVLHQFSGTETNK	99.7%	63.4	25	59	2	0	0	1417.71	189	201
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	8	16	0.02%	33.6%	IWPYVYTLFSNK	99.7%	40.9	25	39.4	2	0	0	1530.80	202	213
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	8	16	0.02%	33.6%	LMMSELENR	99.7%	60.5	25	53.9	5	0	0	1122.53	72	80
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	8	16	0.02%	33.6%	SLLVPDHVITR	99.7%	43.1	25	34.9	2	0	0	1249.73	61	71
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	7	8	16	0.02%	33.6%	WIHPPSGR	95.9%	29.1	25	15.1	1	0	0	949.50	127	134
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	8	9	13	0.01%	20.5%	AFIITGQTYTR	99.7%	43.8	25	43.8	1	0	0	1270.68	235	245
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	8	9	13	0.01%	20.5%	FLEEEVYPLLKPYESVMK	99.7%	37.6	25	35.6	1	2	0	2214.14	460	477
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	8	9	13	0.01%	20.5%	NALDLLLPK	99.3%	36.6	25	26.2	1	0	0	996.61	126	134
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	8	9	13	0.01%	20.5%	QEGGDNDLIER	99.7%	48.1	25	32.1	2	0	0	1245.57	416	426
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	8	9	13	0.01%	20.5%	QELPFMATENIIMAMVK	99.7%	63.3	25	57.5	1	0	0	1965.98	375	391
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	8	9	13	0.01%	20.5%	SNLENIDFK	99.6%	38.9	25	33.8	1	0	0	1079.54	67	75
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	8	9	13	0.01%	20.5%	VLSQQAASVVK	99.7%	75.4	25	56.3	2	0	0	1129.66	405	415
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	8	9	13	0.01%	20.5%	YASPEMCFVFSDR	99.7%	61.8	25	61.8	2	0	0	1608.68	21	33
Adenylosuccinate synthetase isozyme 2	ADSS	PURA2_HUMAN	50.1	100.0%	6	7	10	0.01%	17.1%	ELPVNAQNYVR	99.7%	40.2	25	39.7	1	0	0	1302.68	420	430
Adenylosuccinate synthetase isozyme 2	ADSS	PURA2_HUMAN	50.1	100.0%	6	7	10	0.01%	17.1%	FIEDELQIPVK	99.4%	37.8	25	26.9	2	0	0	1330.73	431	441
Adenylosuccinate synthetase isozyme 2	ADSS	PURA2_HUMAN	50.1	100.0%	6	7	10	0.01%	17.1%	GREFGVTTGR	99.2%	36	25	29.4	2	0	0	1079.56	325	334
Adenylosuccinate synthetase isozyme 2	ADSS	PURA2_HUMAN	50.1	100.0%	6	7	10	0.01%	17.1%	LDILDMFTEIK	99.3%	36.5	25	29.3	2	0	0	1353.70	363	373
Adenylosuccinate synthetase isozyme 2	ADSS	PURA2_HUMAN	50.1	100.0%	6	7	10	0.01%	17.1%	VGIGAFPTEQDNEIGELLQTR	99.7%	72.2	25	72.2	1	0	0	2287.16	304	324
Adenylosuccinate synthetase isozyme 2	ADSS	PURA2_HUMAN	50.1	100.0%	6	7	10	0.01%	17.1%	VVDLLAQDADIVCR	99.7%	105	25	103	2	0	0	1586.82	46	59
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	11	0.01%	55.7%	AAYFGVYDTAK	99.7%	72.5	25	69.4	9	0	0	1205.58	189	199
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	11	0.01%	55.7%	DFLAGGVAAAVSK	99.7%	101	25	96.8	2	0	0	1205.65	11	23
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	11	0.01%	55.7%	EFHGLGDCIIK	99.7%	43.1	25	39.6	2	0	0	1288.64	153	163
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	11	0.01%	55.7%	EQGFLSFWR	99.7%	44.8	25	39.2	5	0	0	1169.57	64	72
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	11	0.01%	55.7%	GADIMYTGTVDCWR	99.7%	78.1	25	71.3	4	0	0	1644.71	246	259
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	11	0.01%	55.7%	GAWSNVLR	99.7%	62	25	41	6	0	0	902.48	273	280
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	11	0.01%	55.7%	GMGGAFVLVLYDEIK	99.7%	69.5	25	0	2	0	0	1627.84	281	295
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	11	0.01%	55.7%	GNLANVIR	99.4%	37.6	25	20	2	0	0	856.50	73	80
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	11	0.01%	55.7%	KGADIMYTGTVDCWR	99.7%	57.7	25	56.7	2	2	0	1772.81	245	259
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	11	0.01%	55.7%	LLLQVQHASK	99.7%	50.6	25	40.7	20	0	0	1136.68	34	43
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	11	0.01%	55.7%	MMMQSGR	97.8%	31.6	25	29.6	1	0	0	840.35	238	244
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	11	0.01%	55.7%	QLFLGGVDR	99.7%	63.3	25	35.3	2	0	0	1004.55	97	105
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	11	0.01%	55.7%	RMMMQSGR	99.7%	52.5	25	41.8	2	0	0	996.45	237	244
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	11	0.01%	55.7%	TAVAPIER	99.7%	42	25	30.4	6	0	0	856.49	24	31
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	11	0.01%	55.7%	YFAGNLASGGAAGATSLCFVYPLDFAR	99.4%	37.4	25	37.4	1	0	0	2796.35	112	138
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	11	0.01%	55.7%	YFPTQALNFAFK	99.7%	94.7	25	74.7	36	0	0	1446.74	81	92
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	4	11	0.01%	55.7%	YFPTQALNFAFKDK	99.7%	66.4	25	65	4	0	0	1689.86	81	94
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	19	23	144	0.14%	50.3%	AAYFGIYDTAK	99.7%	79.4	25	60.7	5	0	0	1219.60	189	199
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	19	23	144	0.14%	50.3%	DFLAGGVAAAISK	99.7%	95	25	84.5	9	0	0	1219.67	11	23
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	19	23	144	0.14%	50.3%	EQGVLSFWR	99.7%	70.1	25	64.8	20	0	0	1121.57	64	72

ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	19	23	144	0.14%	50.3%	GAWSNVLR	99.7%	62	25	41	6	0	0	902.48	273	280
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	19	23	144	0.14%	50.3%	GLGDCLVK	99.5%	37.9	25	20.5	3	0	0	861.45	156	163
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	19	23	144	0.14%	50.3%	GMGGAFVLVLYDEIK	99.7%	69.5	25	0	2	0	0	1627.84	281	295
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	19	23	144	0.14%	50.3%	GNLANVIR	99.4%	37.6	25	20	2	0	0	856.50	73	80
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	19	23	144	0.14%	50.3%	GTDIMYTGTLDCWR	99.7%	72.5	25	66.6	4	0	0	1688.74	246	259
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	19	23	144	0.14%	50.3%	GTDIMYTGTLDCWRK	99.7%	40.7	25	40.7	3	0	0	1832.83	246	260
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	19	23	144	0.14%	50.3%	KGTDIMYTGTLDCWR	99.7%	77.2	25	77.2	4	2	0	1816.84	245	259
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	19	23	144	0.14%	50.3%	LAADVGKAGAER	99.7%	49.2	25	38.2	1	0	0	1157.63	141	152
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	19	23	144	0.14%	50.3%	LLLQVQHASK	99.7%	50.6	25	40.7	20	0	0	1136.68	34	43
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	19	23	144	0.14%	50.3%	MMMQSGR	97.8%	31.6	25	29.6	1	0	0	840.35	238	244
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	19	23	144	0.14%	50.3%	QIFLGGVDK	99.7%	52	25	34.1	5	0	0	976.55	97	105
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	19	23	144	0.14%	50.3%	QIFLGGVDKR	99.7%	44.4	25	22.7	9	0	0	1132.65	97	106
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	19	23	144	0.14%	50.3%	RMMMQSGR	99.7%	52.5	25	41.8	2	0	0	996.45	237	244
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	19	23	144	0.14%	50.3%	TAVAPIER	99.7%	42	25	30.4	6	0	0	856.49	24	31
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	19	23	144	0.14%	50.3%	YFPTQALNFAFK	99.7%	94.7	25	74.7	36	0	0	1446.74	81	92
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	19	23	144	0.14%	50.3%	YFPTQALNFAFKDK	99.7%	66.4	25	65	4	0	0	1689.86	81	94
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	6	8	41	0.04%	58.7%	AAYFGVYDTAK	99.7%	72.5	25	69.4	9	0	0	1205.58	189	199
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	6	8	41	0.04%	58.7%	DFLAGGIAAAISK	99.7%	108	25	104	21	0	0	1233.68	11	23
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	6	8	41	0.04%	58.7%	EQGVLSFWR	99.7%	70.1	25	64.8	20	0	0	1121.57	64	72
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	6	8	41	0.04%	58.7%	GADIMYTGTVDCWR	99.7%	78.1	25	71.3	4	0	0	1644.71	246	259
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	6	8	41	0.04%	58.7%	GAWSNVLR	99.7%	62	25	41	6	0	0	902.48	273	280
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	6	8	41	0.04%	58.7%	GLGDCLVK	99.5%	37.9	25	20.5	3	0	0	861.45	156	163
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	6	8	41	0.04%	58.7%	GMGGAFVLVLYDELK	99.7%	69.5	25	0	2	0	0	1627.84	281	295
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	6	8	41	0.04%	58.7%	GNLANVIR	99.4%	37.6	25	20	2	0	0	856.50	73	80
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	6	8	41	0.04%	58.7%	KGADIMYTGTVDCWR	99.7%	57.7	25	56.7	2	2	0	1772.81	245	259
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	6	8	41	0.04%	58.7%	LAADVGKSGTER	99.0%	35	25	27.7	2	0	0	1203.63	141	152
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	6	8	41	0.04%	58.7%	LLLQVQHASK	99.7%	50.6	25	40.7	20	0	0	1136.68	34	43
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	6	8	41	0.04%	58.7%	MMMQSGR	97.8%	31.6	25	29.6	1	0	0	840.35	238	244
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	6	8	41	0.04%	58.7%	QIFLGGVDK	99.7%	52	25	34.1	5	0	0	976.55	97	105
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	6	8	41	0.04%	58.7%	RMMMQSGR	99.7%	52.5	25	41.8	2	0	0	996.45	237	244
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	6	8	41	0.04%	58.7%	TAVAPIER	99.7%	42	25	30.4	6	0	0	856.49	24	31
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	6	8	41	0.04%	58.7%	YFAGNLASGGAAGATSLCFVYPLDFAR	99.4%	37.4	25	37.4	1	0	0	2796.35	112	138
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	6	8	41	0.04%	58.7%	YFPTQALNFAFK	99.7%	94.7	25	74.7	36	0	0	1446.74	81	92
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	6	8	41	0.04%	58.7%	YFPTQALNFAFKDK	99.7%	66.4	25	65	4	0	0	1689.86	81	94
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN	20.7	100.0%	3	4	10	0.01%	44.8%	DAVLLVFANK	99.7%	72.8	25	60	4	0	0	1089.63	118	127
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN	20.7	100.0%	3	4	10	0.01%	44.8%	ILMVGLDAAGK	99.7%	82.1	25	66.9	10	0	0	1087.62	20	30
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN	20.7	100.0%	3	4	10	0.01%	44.8%	LGEIVTTIPTIGFNVETVEYK	99.7%	42.2	25	42.2	1	0	0	2323.24	39	59
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN	20.7	100.0%	3	4	10	0.01%	44.8%	NISFTVWDVGGQDK	99.7%	110	25	98.3	4	0	0	1565.76	60	73
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN	20.7	100.0%	3	4	10	0.01%	44.8%	QDLPNAMNAAEITDK	99.7%	71.2	25	69.3	2	0	0	1646.77	128	142
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN	20.7	100.0%	3	4	10	0.01%	44.8%	VNEAREELMR	99.7%	42.2	25	37.9	4	0	0	1262.62	100	109
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	6	8	20	0.02%	43.9%	ILMVGLDAAGK	99.7%	82.1	25	66.9	10	0	0	1087.62	20	30
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	6	8	20	0.02%	43.9%	IQEVADELQK	99.7%	56.5	25	39.5	3	0	0	1172.62	100	109
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	6	8	20	0.02%	43.9%	LGEIVTTIPTIGFNVETVEYK	99.7%	42.2	25	42.2	1	0	0	2323.24	39	59
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	6	8	20	0.02%	43.9%	MLLVDELR	99.3%	36.7	25	20.9	1	0	0	988.55	110	117
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	6	8	20	0.02%	43.9%	NICFTVWDVGGQDR	99.7%	83.7	25	77.7	2	0	0	1666.76	60	73
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	6	8	20	0.02%	43.9%	QDLPNAMAISEMTDK	99.7%	65.1	25	63.5	3	0	0	1663.77	128	142
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	100.0%	3	3	8	0.01%	36.7%	DAVLLVFANK	99.7%	72.8	25	60	4	0	0	1089.63	118	127
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	100.0%	3	3	8	0.01%	36.7%	ILMVGLDAAGK	99.7%	82.1	25	66.9	10	0	0	1087.62	20	30
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	100.0%	3	3	8	0.01%	36.7%	LGEIVTTIPTIGFNVETVEYK	99.7%	42.2	25	42.2	1	0	0	2323.24	39	59
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	100.0%	3	3	8	0.01%	36.7%	NICFTVWDVGGQDK	99.7%	89.3	25	86.4	2	0	0	1638.76	60	73
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	100.0%	3	3	8	0.01%	36.7%	VQESADELQK	99.7%	55.3	25	45.7	2	0	0	1146.56	100	109

ADP-ribosylation factor 6	ARF6	ARF6_HUMAN	20.1	100.0%	4	6	12	0.01%	30.3%	DAIILIFANK	99.7%	63.2	25	0	2	0	0	1117.66	114	123
ADP-ribosylation factor 6	ARF6	ARF6_HUMAN	20.1	100.0%	4	6	12	0.01%	30.3%	FNVWDVGGQDK	99.7%	71.3	25	58.2	2	0	0	1264.60	59	69
ADP-ribosylation factor 6	ARF6	ARF6_HUMAN	20.1	100.0%	4	6	12	0.01%	30.3%	ILMLGLDAAGK	99.7%	85.8	25	61.2	4	0	0	1117.63	16	26
ADP-ribosylation factor 6	ARF6	ARF6_HUMAN	20.1	100.0%	4	6	12	0.01%	30.3%	LGQSVTTIPTVGFNVETVTYK	99.7%	57.8	25	57.8	2	2	0	2254.20	35	55
ADP-ribosylation factor-like protein 1	ARL1	ARL1_HUMAN	20.4	100.0%	3	4	7	0.01%	16.0%	AILVVFANK	99.7%	65	25	62.9	2	0	0	974.60	119	127
ADP-ribosylation factor-like protein 1	ARL1	ARL1_HUMAN	20.4	100.0%	3	4	7	0.01%	16.0%	KWQIFK	97.5%	31	25	12.2	2	0	0	849.50	152	157
ADP-ribosylation factor-like protein 1	ARL1	ARL1_HUMAN	20.4	100.0%	3	4	7	0.01%	16.0%	SELVAMLEEEELRK	99.7%	42.6	25	41.2	3	0	0	1691.85	105	118
ADP-ribosylation factor-like protein 2	ARL2	ARL2_HUMAN	20.9	100.0%	5	6	12	0.01%	30.4%	ELQSLLVEER	99.7%	76.4	25	60.1	2	0	0	1215.66	105	114
ADP-ribosylation factor-like protein 2	ARL2	ARL2_HUMAN	20.9	100.0%	5	6	12	0.01%	30.4%	LAGATLLIFANK	99.7%	79.9	25	77.9	2	0	0	1231.74	115	126
ADP-ribosylation factor-like protein 2	ARL2	ARL2_HUMAN	20.9	100.0%	5	6	12	0.01%	30.4%	LLMLGLDNAGK	99.7%	73.7	25	58	4	0	0	1144.64	19	29
ADP-ribosylation factor-like protein 2	ARL2	ARL2_HUMAN	20.9	100.0%	5	6	12	0.01%	30.4%	LNIWDVGGQK	99.7%	56.2	25	48.2	2	0	0	1129.60	62	71
ADP-ribosylation factor-like protein 2	ARL2	ARL2_HUMAN	20.9	100.0%	5	6	12	0.01%	30.4%	QDLPGALSSNAIR	99.7%	73.1	25	60.5	2	0	0	1341.71	127	139
ADP-ribosylation factor-like protein 6	ARL6	ARL6_HUMAN	21.1	100.0%	3	3	3	0.00%	17.7%	IPILFFANK	99.7%	44.5	25	23.5	1	0	0	1062.63	123	131
ADP-ribosylation factor-like protein 6	ARL6	ARL6_HUMAN	21.1	100.0%	3	3	3	0.00%	17.7%	LSVLLGLK	97.3%	30.8	25	26.8	1	0	0	842.57	7	14
ADP-ribosylation factor-like protein 6	ARL6	ARL6_HUMAN	21.1	100.0%	3	3	3	0.00%	17.7%	SSSLSFTVFDMSGQGR	99.7%	68.6	25	68.6	1	0	0	1705.79	60	75
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	9	9	14	0.01%	12.3%	GAILTGPPGTGK	99.5%	38.3	25	38.3	1	0	0	1068.61	343	354
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	9	9	14	0.01%	12.3%	GLGYAQYLPK	94.9%	28.2	25	19.8	1	0	0	1109.60	602	611
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	9	9	14	0.01%	12.3%	GMGGLFSVGETTAK	99.2%	35.9	25	35.9	1	0	0	1370.66	284	297
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	9	9	14	0.01%	12.3%	ILINDAYKR	99.7%	46	25	31.2	1	0	0	1105.64	703	711
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	9	9	14	0.01%	12.3%	KTQVLQPEEK	99.7%	41.4	25	29.7	2	0	0	1199.66	559	568
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	9	9	14	0.01%	12.3%	NLETLQQELGIEGENR	99.7%	111	25	106	2	0	0	1842.92	225	240
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	9	9	14	0.01%	12.3%	VALLLLEK	99.7%	49.8	25	49.8	2	0	0	898.60	726	733
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	9	9	14	0.01%	12.3%	VGQISFDLPR	99.7%	90.7	25	67.1	2	0	0	1131.62	670	679
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	9	9	14	0.01%	12.3%	VSEEIFFGR	99.7%	64.1	25	45.2	2	0	0	1083.55	633	641
A-kinase anchor protein 8-like	AKAP8L	AKP8L_HUMAN	71.6	100.0%	3	3	3	0.00%	5.6%	IQFVCSLCK	99.7%	41.3	25	21.4	1	0	0	1154.57	387	395
A-kinase anchor protein 8-like	AKAP8L	AKP8L_HUMAN	71.6	100.0%	3	3	3	0.00%	5.6%	QTADFLQEYVTNK	99.7%	81.5	25	74.3	1	0	0	1556.76	427	439
A-kinase anchor protein 8-like	AKAP8L	AKP8L_HUMAN	71.6	100.0%	3	3	3	0.00%	5.6%	TFYEDEMASHLDSK	99.7%	67.3	25	67.3	1	0	0	1672.72	398	411
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	5	5	9	0.01%	11.0%	FAVALLDDSVR	99.7%	81.9	25	57.9	2	0	0	1205.65	166	176
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	5	5	9	0.01%	11.0%	GALLSVGWSTGR	99.7%	97.1	25	92.8	2	0	0	1203.65	467	478
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	5	5	9	0.01%	11.0%	GQWINLPVLQLTK	99.7%	55.6	25	44.9	1	0	0	1509.88	40	52
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	5	5	9	0.01%	11.0%	ILATTPSAVFR	99.7%	56	25	48.5	2	0	0	1175.68	302	312
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	5	5	9	0.01%	11.0%	VYNASSTIVPSLK	99.7%	62.2	25	55.4	2	0	0	1378.76	177	189
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	12	12	20	0.02%	14.6%	AAFLNFFR	99.7%	55	25	43.5	2	0	0	985.53	44	51
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	12	12	20	0.02%	14.6%	AGLDPDLETR	99.7%	43.9	25	30.7	2	0	0	1086.54	178	187
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	12	12	20	0.02%	14.6%	AGQEDVLFPVAR	99.7%	50.8	25	47.7	2	0	0	1301.68	581	592
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	12	12	20	0.02%	14.6%	EADGSLQPLPQR	97.7%	31.4	25	24.3	2	0	0	1310.67	251	262
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	12	12	20	0.02%	14.6%	ELGQSLAQEVK	99.7%	67	25	55.5	1	0	0	1201.64	791	801
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	12	12	20	0.02%	14.6%	GPLIVDTVSAESLSVLVK	99.7%	95.3	25	92.1	1	0	0	1827.05	881	898
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	12	12	20	0.02%	14.6%	GVQLDSAGLER	99.7%	61.3	25	49.8	2	0	0	1144.60	461	471
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	12	12	20	0.02%	14.6%	LDVTTQTPLTPEQLR	99.7%	94.6	25	85.5	2	0	0	1711.92	664	678
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	12	12	20	0.02%	14.6%	LLAVTGEQAQQAR	99.7%	83.9	25	71.5	2	0	0	1384.75	778	790
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	12	12	20	0.02%	14.6%	LVPSASVRPR	99.7%	44.6	25	44.6	1	0	0	1081.65	58	67
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	12	12	20	0.02%	14.6%	SLDEVYPDPVR	98.1%	32.3	25	29.1	1	0	0	1289.64	712	722
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	12	12	20	0.02%	14.6%	TGAVGDLVIIGDR	99.7%	70.6	25	61.8	2	0	0	1285.71	757	769
Alcohol dehydrogenase class-3	ADH5	ADHX_HUMAN	39.7	100.0%	5	5	8	0.01%	16.3%	AFELMHSGK	99.7%	49.5	25	39.6	2	0	0	1019.50	358	366
Alcohol dehydrogenase class-3	ADH5	ADHX_HUMAN	39.7	100.0%	5	5	8	0.01%	16.3%	AGDTVIPLYIPQCGECK	99.7%	50.5	25	50.5	2	0	0	1920.92	85	101
Alcohol dehydrogenase class-3	ADH5	ADHX_HUMAN	39.7	100.0%	5	5	8	0.01%	16.3%	IDPLAPLDK	95.6%	28.8	25	28.5	1	0	0	981.56	160	168
Alcohol dehydrogenase class-3	ADH5	ADHX_HUMAN	39.7	100.0%	5	5	8	0.01%	16.3%	IIGVDINKDK	99.7%	57.6	25	27.7	2	0	0	1114.65	219	228
Alcohol dehydrogenase class-3	ADH5	ADHX_HUMAN	39.7	100.0%	5	5	8	0.01%	16.3%	VDEFVTHNLSFDEINK	99.5%	31.9	25	31.9	0	1	0	1906.92	342	357
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	8	9	17	0.02%	20.5%	KIEEVVER	99.7%	57.6	25	42.4	2	0	0	1001.56	429	436
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	8	9	17	0.02%	20.5%	LAPALATGNTVVMK	99.7%	88.9	25	80.7	3	0	0	1385.78	196	209

Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	8	9	17	0.02%	20.5%	LLNLLADLVER	99.7%	69	25	61.5	2	0	0	1268.76	104	114
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	8	9	17	0.02%	20.5%	TFVEESIYNEFLER	99.7%	90.4	25	84	2	0	0	1775.85	325	338
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	8	9	17	0.02%	20.5%	VAEQTPLSALYLASLIK	99.7%	101	25	101	2	0	0	1817.04	210	226
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	8	9	17	0.02%	20.5%	VGNPFELDTQQGPQVDKEQFER	99.7%	55.5	25	55.5	0	2	0	2561.23	348	369
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	8	9	17	0.02%	20.5%	VLGYIQLGQK	99.7%	62.5	25	47.3	2	0	0	1118.66	370	379
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	8	9	17	0.02%	20.5%	YGLAAAVFTR	99.7%	110	25	105	2	0	0	1068.58	442	451
Aldehyde dehydrogenase, mitochondrial	ALDH2	ALDH2_HUMAN	56.4	100.0%	5	5	6	0.01%	12.2%	ELGEYGLQAYTEVK	99.7%	64.7	25	60.5	2	0	0	1599.79	493	506
Aldehyde dehydrogenase, mitochondrial	ALDH2	ALDH2_HUMAN	56.4	100.0%	5	5	6	0.01%	12.2%	LLCGGGIAADR	99.7%	51.1	25	38.7	1	0	0	1102.57	384	394
Aldehyde dehydrogenase, mitochondrial	ALDH2	ALDH2_HUMAN	56.4	100.0%	5	5	6	0.01%	12.2%	TIEEVVGR	99.6%	39.7	25	25.4	1	0	0	902.49	429	436
Aldehyde dehydrogenase, mitochondrial	ALDH2	ALDH2_HUMAN	56.4	100.0%	5	5	6	0.01%	12.2%	VAEQTPLTALYVANLIK	99.7%	40.5	25	40.5	1	0	0	1844.05	210	226
Aldehyde dehydrogenase, mitochondrial	ALDH2	ALDH2_HUMAN	56.4	100.0%	5	5	6	0.01%	12.2%	VIQVAAGSSNLKR	99.7%	45.2	25	45.2	1	0	0	1342.78	269	281
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	3	3	5	0.00%	6.8%	GISDPLTVFEQTEAAAR	99.7%	92.1	25	84.9	2	0	0	1804.91	587	603
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	3	3	5	0.00%	6.8%	GVQFAPFSTCR	99.4%	37.7	25	37.7	1	0	0	1269.60	556	566
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	3	3	5	0.00%	6.8%	YGSVAFPNFEQGVACLR	99.7%	51.2	25	51.2	2	0	0	1914.92	390	406
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	6	6	8	0.01%	14.5%	DLPLAQGIK	97.7%	31.5	25	25.6	1	0	0	954.56	529	537
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	6	6	8	0.01%	14.5%	GAPTTSLISVAVTK	99.7%	95.6	25	82.8	1	0	0	1344.77	219	232
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	6	6	8	0.01%	14.5%	MIGGPILPSER	99.7%	44	25	31.8	1	0	0	1169.63	163	173
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	6	6	8	0.01%	14.5%	QASVADYEETVKK	99.7%	48.9	25	36.1	1	0	0	1467.73	82	94
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	6	6	8	0.01%	14.5%	VGNPWDPNVLYGPLHTK	99.7%	35.5	25	35.5	0	2	0	1906.98	359	375
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	6	6	8	0.01%	14.5%	VNLLSFTGSTQVGK	99.7%	99.4	25	99.4	2	0	0	1450.79	267	280
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	15	18	32	0.03%	48.1%	ACYLSINPQK	99.7%	43.5	25	40.2	1	0	0	1193.60	221	230
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	15	18	32	0.03%	48.1%	ACYLSINPQKDETLETEK	99.7%	81.3	25	70.9	2	2	0	2139.03	221	238
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	15	18	32	0.03%	48.1%	AGFAGDQIPK	99.7%	61.8	25	41.1	2	0	0	1003.52	23	32
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	15	18	32	0.03%	48.1%	AQYYLPDGSTIEIGPSR	99.7%	114	25	113	2	0	0	1866.92	239	255
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	15	18	32	0.03%	48.1%	DQLQTFSEEHPVLLTEAPLNPR	99.7%	68.3	25	66.1	0	2	0	2534.29	97	118
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	15	18	32	0.03%	48.1%	DWNDMER	98.8%	34.2	25	26.7	1	0	0	965.38	82	88
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	15	18	32	0.03%	48.1%	EGYDFHSSSEFEIVK	99.7%	65	25	56.9	2	0	0	1773.80	201	215
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	15	18	32	0.03%	48.1%	ISAPQER	94.8%	28.1	25	12.4	1	0	0	800.43	330	336
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	15	18	32	0.03%	48.1%	IWQYVYSK	99.7%	44.2	25	32.8	2	0	0	1086.56	89	96
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	15	18	32	0.03%	48.1%	LLSEVKK	99.2%	36.2	25	17.2	2	0	0	816.52	314	320
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	15	18	32	0.03%	48.1%	LYSTWIGGSILASLDTFKK	99.7%	80.6	25	80.6	2	0	0	2100.14	337	355
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	15	18	32	0.03%	48.1%	TLFSNIVLSGGSTLFK	99.7%	122	25	120	3	1	0	1683.93	293	308
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	15	18	32	0.03%	48.1%	VMAGALEGDIFIGPK	99.7%	89.2	25	0	4	0	0	1533.80	47	61
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	15	18	32	0.03%	48.1%	YCFPNYVGRPK	99.7%	49.5	25	49.5	2	0	0	1400.68	33	43
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	15	18	32	0.03%	48.1%	YPMEHGIVK	98.6%	33.4	25	30.8	1	0	0	1089.54	73	81
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	13	35	0.03%	34.1%	AAVPSGASTGIYEALELR	99.7%	156	25	155	2	0	0	1804.94	33	50
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	13	35	0.03%	34.1%	DATNVGDEGGFAPNILENKEGLELLK	99.7%	67.3	25	67.3	0	2	0	2743.38	203	228
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	13	35	0.03%	34.1%	GNPTVEVDLFTSK	99.7%	42.7	25	4.82	1	0	0	1406.72	16	28
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	13	35	0.03%	34.1%	IGAEVYHNLK	99.7%	62.1	25	54.4	4	0	0	1143.62	184	193
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	13	35	0.03%	34.1%	KLNVTEQEK	99.7%	42.8	25	23.3	2	0	0	1088.59	81	89
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	13	35	0.03%	34.1%	LAMQEFMILPVGAANFR	99.7%	79.1	25	79.1	6	1	0	1907.99	163	179
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	13	35	0.03%	34.1%	SCNCLLLK	98.8%	34.3	25	24.6	2	0	0	1007.50	336	343
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	13	35	0.03%	34.1%	VNQIGSVTESLQACK	99.7%	117	25	0	4	0	0	1633.82	344	358
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	13	35	0.03%	34.1%	VVIGMDVAASEFFR	99.7%	69.7	25	68	2	0	0	1556.78	240	253
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	13	35	0.03%	34.1%	YISPDQLADLYK	99.7%	54	25	53.3	7	0	0	1425.73	270	281
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	11	13	35	0.03%	34.1%	YNQLLR	95.8%	29	25	22.4	2	0	0	806.45	407	412
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	11	11	17	0.02%	25.1%	ALEAELAALR	99.7%	61.6	25	52.2	2	0	0	1056.60	121	130
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	11	11	17	0.02%	25.1%	AQLEEASSAR	99.7%	49.4	25	49.4	2	0	0	1061.52	152	161
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	11	11	17	0.02%	25.1%	DVDGATLAR	99.6%	38.8	25	32.1	1	0	0	917.47	202	210
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	11	11	17	0.02%	25.1%	EYQDLLNVK	99.7%	58.9	25	47.5	6	0	0	1121.58	378	386
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	11	11	17	0.02%	25.1%	FANLNEQAAR	99.7%	69.3	25	46.8	2	0	0	1133.57	291	300

Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	11	11	17	0.02%	25.1%	LSGAGGAGGFR	99.7%	61.8	25	45.6	1	0	0	949.49	29	39
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	11	11	17	0.02%	25.1%	NLQSAEEWYK	99.7%	40.7	25	27.9	1	0	0	1267.60	279	288
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	11	11	17	0.02%	25.1%	RPPASDGLDLSQAAAR	99.7%	35.4	25	28.9	0	1	0	1624.84	68	83
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	11	11	17	0.02%	25.1%	SNIEETTISSQK	99.7%	51.2	25	50.7	1	0	0	1336.66	487	498
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	11	11	17	0.02%	25.1%	TIEIEGLR	99.6%	39.4	25	28.8	2	0	0	930.53	323	330
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	11	11	17	0.02%	25.1%	TNEKEQLQGLNDR	99.7%	64.1	25	57.5	2	0	0	1544.77	92	104
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	11	11	17	0.02%	25.1%	VGELFQR	99.7%	67.4	25	42.4	2	0	0	848.46	139	145
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	10	13	25	0.02%	41.0%	AILQATLR	99.7%	46.9	25	37.1	2	0	0	885.55	36	43
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	10	13	25	0.02%	41.0%	GAEADQIIEYLK	99.7%	82.6	25	70	3	0	0	1349.69	15	26
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	10	13	25	0.02%	41.0%	IEILAPPNGSVPGDR	98.9%	34.7	25	28.5	2	0	0	1534.82	236	250
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	10	13	25	0.02%	41.0%	IGCIITAR	99.7%	71.7	25	50.2	2	0	0	903.51	159	166
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	10	13	25	0.02%	41.0%	ITFDAFPGEPDKELNPK	99.7%	59.8	25	53	2	2	0	1917.96	251	267
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	10	13	25	0.02%	41.0%	IWEQIQPDLHTNDECVATYK	98.7%	27.9	25	27.9	0	1	0	2460.15	270	289
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	10	13	25	0.02%	41.0%	KQQSIAGSADSKPIDVSR	99.7%	38.9	25	38.9	0	1	0	1886.99	137	154
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	10	13	25	0.02%	41.0%	MVILLCNLKPAK	99.7%	53.8	25	53.8	2	0	0	1399.82	206	217
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	10	13	25	0.02%	41.0%	QQSIAGSADSKPIDVSR	99.7%	65.5	25	57	2	2	0	1758.90	138	154
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	10	13	25	0.02%	41.0%	TVVSGLVNHVPLEQMQNR	99.7%	60.7	25	59.7	0	4	0	2037.05	188	205
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	6	7	23	0.02%	25.9%	FLFSLFGQK	99.7%	43.7	25	33.7	6	0	0	1086.60	216	224
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	6	7	23	0.02%	25.9%	FSIQTMCPIEGEGNIAR	99.7%	103	25	101	6	0	0	1938.91	199	215
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	6	7	23	0.02%	25.9%	LLCEHFR	99.7%	41.3	25	29.1	3	0	0	974.49	141	147
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	6	7	23	0.02%	25.9%	SCENLAPFNTALK	99.7%	78.6	25	68.2	2	0	0	1464.72	305	317
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	6	7	23	0.02%	25.9%	SYGPAPGAGHVQEESNLSLQALESR	99.5%	31.9	25	31.9	0	1	0	2597.26	34	58
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	6	7	23	0.02%	25.9%	VLSTVHTHSSVK	99.7%	58	25	48.4	5	0	0	1294.71	148	159
Anaphase-promoting complex subunit 1	ANAPC1	APC1_HUMAN	216.5	100.0%	4	4	4	0.00%	2.6%	DLETLPFGIALPIR	95.8%	29	25	29	1	0	0	1554.89	943	956
Anaphase-promoting complex subunit 1	ANAPC1	APC1_HUMAN	216.5	100.0%	4	4	4	0.00%	2.6%	HSTSVSSLAER	99.6%	39.5	25	37.3	1	0	0	1173.59	919	929
Anaphase-promoting complex subunit 1	ANAPC1	APC1_HUMAN	216.5	100.0%	4	4	4	0.00%	2.6%	NFDFEGSLSPVIAPK	99.7%	61	25	61	1	0	0	1620.83	680	694
Anaphase-promoting complex subunit 1	ANAPC1	APC1_HUMAN	216.5	100.0%	4	4	4	0.00%	2.6%	VFITSDLCGQK	98.1%	32.2	25	19.3	1	0	0	1267.64	430	440
Anaphase-promoting complex subunit 10	ANAPC10	APC10_HUMAN	21.3	99.7%	2	2	2	0.00%	14.6%	IYTPVEESSIGKFPR	99.7%	48	25	48	1	0	0	1722.91	158	172
Anaphase-promoting complex subunit 10	ANAPC10	APC10_HUMAN	21.3	99.7%	2	2	2	0.00%	14.6%	VGNNFHNLQEIR	94.5%	22.5	25	17.5	0	1	0	1440.73	98	109
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	11	14	26	0.03%	21.4%	AGQERPSVTSYK	99.7%	59.8	25	57	2	1	0	1322.67	182	193
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	11	14	26	0.03%	21.4%	AIQLNSNSVQALLLK	99.7%	105	25	99.1	2	0	0	1611.94	365	379
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	11	14	26	0.03%	21.4%	ALTQRPDYIK	98.4%	32.9	25	18.5	1	0	0	1204.67	468	477
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	11	14	26	0.03%	21.4%	AYAFVHTGDNSR	99.7%	60.1	25	60.1	2	0	0	1337.62	242	253
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	11	14	26	0.03%	21.4%	DMAAAGLHSNVR	99.7%	67.8	25	60.6	4	0	0	1241.61	43	54
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	11	14	26	0.03%	21.4%	DNVDLLGSLADLYFR	99.7%	74.1	25	74.1	2	0	0	1710.87	269	283
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	11	14	26	0.03%	21.4%	FEQAQMLDPYLIK	99.7%	82.3	25	77.5	2	0	0	1595.81	294	306
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	11	14	26	0.03%	21.4%	GMDVYGYLLAR	99.7%	51.5	25	49.5	4	0	0	1257.63	307	317
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	11	14	26	0.03%	21.4%	LEDVENLGCR	99.7%	57	25	49.6	2	0	0	1204.56	321	330
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	11	14	26	0.03%	21.4%	VQEAIIHFR	99.7%	44.8	25	36.6	2	0	0	1112.62	389	397
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	11	14	26	0.03%	21.4%	YEDGIALLR	99.7%	64.1	25	52.9	2	0	0	1049.56	492	500
Ancient ubiquitous protein 1	AUP1	AUP1_HUMAN	53.0	99.8%	2	2	3	0.00%	6.3%	GTQSLPTASASK	99.7%	43.7	25	32.4	2	0	0	1147.60	414	425
Ancient ubiquitous protein 1	AUP1	AUP1_HUMAN	53.0	99.8%	2	2	3	0.00%	6.3%	LPPTPLLLFPEEEATNGR	99.7%	62.2	25	62.2	1	0	0	1994.06	217	234
Angio-associated migratory cell protein	AAMP	AAMP_HUMAN	46.7	99.8%	2	2	4	0.00%	5.5%	AVVGYEDGTIR	99.7%	60.7	25	56	2	0	0	1179.60	230	240
Angio-associated migratory cell protein	AAMP	AAMP_HUMAN	46.7	99.8%	2	2	4	0.00%	5.5%	DASLVVTTSGDHK	99.7%	61.2	25	53.6	2	0	0	1329.66	411	423
Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	ANFY1_HUMAN	128.4	99.8%	2	2	4	0.00%	1.5%	FQLQLLR	98.3%	32.7	25	8.32	2	0	0	917.56	145	151
Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	ANFY1_HUMAN	128.4	99.8%	2	2	4	0.00%	1.5%	GDLFAATFLIK	99.7%	54.7	25	35.8	2	0	0	1195.67	300	310
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.5%	AAMIWIVGEYAER	99.7%	84.3	25	78.3	2	0	0	1508.76	446	458
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.5%	CVSTLLDLIQTK	99.7%	79.5	25	64.3	2	0	0	1390.76	391	402
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.5%	DCPLNAEAASSK	99.7%	51.1	25	39.8	2	0	0	1262.57	865	876
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.5%	DLDYYGTLLK	99.7%	71.4	25	62.6	2	0	0	1200.61	273	282
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.5%	EYATEVDVDFVR	99.7%	90.8	25	90.8	2	0	0	1442.68	360	371

AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.5%	GLEISGTFTR	99.7%	72.2	25	69.2	2	0	0	1080.57	731	740
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.5%	ITEYLCEPLRK	99.4%	37.5	25	27.9	2	0	0	1421.75	118	128
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.5%	KGEIFELK	99.7%	44.4	25	25	2	0	0	963.55	12	19
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.5%	LASQANIAQVLAELK	99.7%	110	25	103	2	0	0	1568.90	345	359
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.5%	LLSTDPVAAK	99.2%	36.3	25	12.7	2	0	0	1014.58	529	538
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.5%	LQSSNIFTVAK	99.7%	60	25	57.7	2	0	0	1207.67	877	887
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.5%	LSHANSAVVLSAVK	99.7%	74.3	25	74.3	2	1	0	1395.80	248	261
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.5%	MEPLNNLQVAVK	98.7%	33.7	25	20.1	1	0	0	1371.73	806	817
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.5%	NINLIVQK	98.9%	34.6	25	31.2	2	0	0	941.58	305	312
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	15	16	30	0.03%	17.5%	YNDPIYVK	99.7%	41.7	25	28.2	2	0	0	1011.51	328	335
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	15	16	27	0.03%	20.0%	AALCAVHVIR	99.7%	75.9	25	74.6	2	0	0	1109.62	157	166
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	15	16	27	0.03%	20.0%	ADCASGIFLAAEK	99.7%	56	25	50.6	1	0	0	1352.65	398	410
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	15	16	27	0.03%	20.0%	AVEYNALFK	99.7%	49.1	25	37.8	1	0	0	1054.56	563	571
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	15	16	27	0.03%	20.0%	ELLYFLDSCEPEFK	99.7%	71.1	25	67.2	2	0	0	1789.84	384	397
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	15	16	27	0.03%	20.0%	FTCTVNR	99.7%	40.5	25	29.1	2	0	0	897.42	537	543
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	15	16	27	0.03%	20.0%	IEFTFER	99.7%	46.6	25	42	2	0	0	941.47	717	723
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	15	16	27	0.03%	20.0%	IGYLGAMLLLDER	99.7%	72.3	25	72.3	3	0	0	1463.79	84	96
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	15	16	27	0.03%	20.0%	NLIMSGYSPEHDVSGISDPFLQVR	99.7%	49.5	25	49.5	0	1	0	2677.29	225	248
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	15	16	27	0.03%	20.0%	SPDMLAHFR	98.3%	32.7	25	29.4	1	0	0	1089.51	205	213
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	15	16	27	0.03%	20.0%	SSFREEDNTYR	99.7%	35.3	25	23.1	0	2	0	1403.62	36	46
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	15	16	27	0.03%	20.0%	STIVDCLK	96.3%	29.5	25	14.6	1	0	0	935.49	348	355
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	15	16	27	0.03%	20.0%	TVQTDHNAVQR	99.7%	62.5	25	48.9	2	0	0	1268.63	335	345
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	15	16	27	0.03%	20.0%	VLAINILGR	99.7%	68.5	25	57	3	0	0	968.63	307	315
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	15	16	27	0.03%	20.0%	VLTTAGSYVR	99.7%	83.2	25	77.6	2	0	0	1066.59	425	434
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	15	16	27	0.03%	20.0%	YVALTSLLK	99.6%	38.9	25	38.9	2	0	0	1007.61	326	334
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	10	11	19	0.02%	30.3%	FEIPYFTTSGIQVR	99.7%	111	25	109	2	0	0	1657.86	380	393
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	10	11	19	0.02%	30.3%	HNNLYLVATSK	99.7%	50.5	25	33.1	2	0	0	1259.67	62	72
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	10	11	19	0.02%	30.3%	ILQEYITQEGHK	99.7%	67.2	25	42.7	2	0	0	1458.76	130	141
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	10	11	19	0.02%	30.3%	LETGAPRPPATVTNAVSWR	99.7%	48.5	25	48.5	0	2	0	2023.07	142	160
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	10	11	19	0.02%	30.3%	SGYQALPWVR	98.4%	32.8	25	25.2	1	0	0	1176.62	401	410
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	10	11	19	0.02%	30.3%	SVELEDVKFHQCVR	99.3%	30.5	25	21.8	0	2	0	1745.86	230	243
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	10	11	19	0.02%	30.3%	TISFIPPDGEFELMSYR	96.7%	29.9	25	26.9	1	0	0	2017.96	252	268
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	10	11	19	0.02%	30.3%	VFLSGMPELR	99.7%	54.1	25	50.5	4	0	0	1148.61	202	211
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	10	11	19	0.02%	30.3%	VVQVFSEYFK	99.7%	58	25	50.4	1	0	0	1245.65	87	96
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	10	11	19	0.02%	30.3%	YITQNGDYQLR	99.7%	53.5	25	51.7	2	0	0	1370.67	411	421
AP-1 complex subunit sigma-1A	AP1S1	AP1S1_HUMAN	18.7	100.0%	4	5	13	0.01%	25.3%	AIEQADLLQEEDESPR	99.7%	110	25	110	4	0	0	1842.87	134	149
AP-1 complex subunit sigma-1A	AP1S1	AP1S1_HUMAN	18.7	100.0%	4	5	13	0.01%	25.3%	ELMQVVLAR	99.7%	73.3	25	57.2	4	0	0	1058.60	34	42
AP-1 complex subunit sigma-1A	AP1S1	AP1S1_HUMAN	18.7	100.0%	4	5	13	0.01%	25.3%	FMLLFSR	99.6%	39.5	25	34.7	2	0	0	913.50	4	10
AP-1 complex subunit sigma-1A	AP1S1	AP1S1_HUMAN	18.7	100.0%	4	5	13	0.01%	25.3%	MCSFLEWR	99.7%	40.5	25	40.5	3	0	0	1128.50	46	53
AP-1 complex subunit sigma-2	AP1S2	AP1S2_HUMAN	18.6	99.8%	2	2	8	0.01%	21.0%	AIEQADLLQEEAETPR	99.7%	74.1	25	70.8	2	0	0	1812.90	133	148
AP-1 complex subunit sigma-2	AP1S2	AP1S2_HUMAN	18.6	99.8%	2	2	8	0.01%	21.0%	ELVQTVLAR	99.7%	67	25	46.1	6	0	0	1028.61	33	41
AP-1 complex subunit sigma-2	AP1S2	AP1S2_HUMAN	18.6	99.8%	2	2	8	0.01%	21.0%	MCSFLEWR	99.7%	40.5	25	40.5	3	0	0	1128.50	45	52
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	25	0.02%	19.9%	ACNQLGQFLQHR	99.7%	38	25	27.2	0	2	0	1471.72	330	341
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	25	0.02%	19.9%	ALLLSTYIK	99.7%	58.7	25	58.7	2	0	0	1021.63	539	547
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	25	0.02%	19.9%	EMGEAFAADIPR	99.7%	49	25	41.7	2	0	0	1306.61	142	153
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	25	0.02%	19.9%	FFQPTEMAAQDFFQR	99.7%	70.8	25	70.8	3	0	0	1862.85	864	878
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	25	0.02%	19.9%	FHLCSVATR	98.5%	33.3	25	27.8	1	0	0	1090.55	530	538
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	25	0.02%	19.9%	FINLFPETK	96.7%	29.9	25	22.7	1	0	0	1108.60	548	556
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	25	0.02%	19.9%	GLAVFISDIR	99.7%	80.8	25	62.4	2	0	0	1090.63	12	21
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	25	0.02%	19.9%	IAGDYVSEEVWYR	99.7%	73.7	25	72	1	0	0	1586.75	452	464
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	25	0.02%	19.9%	ILVAGDSMDSVK	99.7%	51.7	25	42.2	2	0	0	1234.63	154	165

AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	25	0.02%	19.9%	NNGVLFENQLLQIGVK	99.7%	73.3	25	71.7	2	0	0	1785.99	751	766
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	25	0.02%	19.9%	THIDTVINALK	99.7%	40.8	25	40.8	2	0	0	1224.69	368	378
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	25	0.02%	19.9%	TSVQFQNFSPTVVHPGDLQTQLAVQTK	99.7%	45.9	25	43.9	0	1	0	2970.53	784	810
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	25	0.02%	19.9%	VGGYILGEFGNLIAGDPR	99.7%	93.9	25	85	2	0	0	1847.97	499	516
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	25	0.02%	19.9%	YLALESMCTLASSEFSHEAVK	98.6%	27.8	25	27	0	2	0	2373.11	347	367
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	13	18	0.02%	24.7%	ACNQLGQFLQHR	99.7%	38	25	27.2	0	2	0	1471.72	329	340
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	13	18	0.02%	24.7%	ALLLSTYIK	99.7%	58.7	25	58.7	2	0	0	1021.63	538	546
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	13	18	0.02%	24.7%	AVDLLYAMCDR	99.7%	52.7	25	51.7	1	0	0	1326.62	388	398
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	13	18	0.02%	24.7%	EMAEAFAGEIPK	99.7%	79.1	25	71	1	0	0	1292.62	142	153
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	13	18	0.02%	24.7%	FFQPTEMASQDFFQR	99.7%	74.7	25	22.7	2	0	0	1878.85	826	840
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	13	18	0.02%	24.7%	FVNLFPEVKPTIQDVLR	98.9%	34.4	25	34.4	1	1	0	2015.13	547	563
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	13	18	0.02%	24.7%	GLAVFISDIR	99.7%	80.8	25	62.4	2	0	0	1090.63	12	21
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	13	18	0.02%	24.7%	IAGDYVSEEVWYR	99.7%	73.7	25	72	1	0	0	1586.75	451	463
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	13	18	0.02%	24.7%	LTECLETILNK	99.7%	47.8	25	47.6	1	0	0	1333.70	279	289
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	13	18	0.02%	24.7%	NNGVLFENQLLQIGLK	99.7%	51.9	25	51.9	2	0	0	1800.00	713	728
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	13	18	0.02%	24.7%	THIETVINALK	99.7%	41.7	25	39.3	2	0	0	1238.71	367	377
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	13	18	0.02%	24.7%	TTQIGCLLR	99.7%	43	25	29.1	2	0	0	1061.58	898	906
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	13	18	0.02%	24.7%	TVFEALQAPACHENLVK	98.0%	32.1	25	32.1	1	0	0	1926.97	481	497
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	13	18	0.02%	24.7%	VGGYILGEFGNLIAGDPR	99.7%	93.9	25	85	2	0	0	1847.97	498	515
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	13	18	0.02%	24.7%	VLVAGDTMDSVK	99.7%	55	25	37.8	3	0	0	1250.63	154	165
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	13	18	0.02%	24.7%	YGGTFQNVSVQLPITLNK	99.7%	88.6	25	88.6	1	0	0	1979.06	808	825
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	11	13	18	0.02%	24.7%	YLALESMCTLASSEFSHEAVK	98.6%	27.8	25	27	0	2	0	2373.11	346	366
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	9	9	15	0.01%	20.9%	ASENAIVWK	99.7%	42.7	25	32	2	0	0	1017.54	346	354
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	9	9	15	0.01%	20.9%	IPTPLNTSGVQVICMK	99.7%	43.6	25	43.6	1	0	0	1757.93	324	339
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	9	9	15	0.01%	20.9%	LNYSDHDVIK	99.7%	59.1	25	48.6	2	0	0	1203.60	411	420
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	9	9	15	0.01%	20.9%	MCDVMAAYFGK	99.7%	62.2	25	62.2	2	0	0	1292.55	85	95
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	9	9	15	0.01%	20.9%	SNFKPSLLAQK	99.7%	52.3	25	47.3	2	0	0	1232.70	309	319
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	9	9	15	0.01%	20.9%	SNIWLAAVTK	99.7%	53.1	25	46.1	1	0	0	1102.63	61	70
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	9	9	15	0.01%	20.9%	SPVTNIAR	96.4%	29.5	25	21.2	1	0	0	857.48	45	52
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	9	9	15	0.01%	20.9%	TFITQQGIK	99.4%	37.6	25	31.2	2	0	0	1035.58	131	139
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	9	9	15	0.01%	20.9%	VNVIHAR	99.7%	40.3	25	36.1	2	0	0	808.48	34	40
AP-2 complex subunit sigma	AP2S1	AP2S1_HUMAN	17.0	100.0%	3	3	5	0.00%	16.9%	FILIQNR	98.1%	32.1	25	10.6	2	0	0	903.54	4	10
AP-2 complex subunit sigma	AP2S1	AP2S1_HUMAN	17.0	100.0%	3	3	5	0.00%	16.9%	HTNFVEFR	99.0%	34.9	25	25	2	0	0	1049.52	46	53
AP-2 complex subunit sigma	AP2S1	AP2S1_HUMAN	17.0	100.0%	3	3	5	0.00%	16.9%	QLLMLQSLE	98.6%	33.6	25	26.4	1	0	0	1090.58	134	142
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	19	0.02%	11.7%	EGSTAQLIINTEK	99.7%	79	25	77.8	2	0	0	1403.74	1064	1076
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	19	0.02%	11.7%	ELKPVLSQG	96.4%	29.6	25	23.4	1	0	0	970.56	1086	1094
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	19	0.02%	11.7%	LLDSITVPVAR	99.7%	65	25	53.6	1	0	0	1183.70	486	496
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	19	0.02%	11.7%	LLTQYILNLGK	99.7%	83.6	25	82.7	4	0	0	1275.77	553	563
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	19	0.02%	11.7%	LQILNLGAK	99.7%	48.7	25	38	2	0	0	969.61	534	542
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	19	0.02%	11.7%	LVYVYLVR	98.9%	34.5	25	26.9	1	0	0	1024.62	97	104
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	19	0.02%	11.7%	LYSLDPEQK	99.2%	35.8	25	27.6	1	0	0	1092.56	177	185
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	19	0.02%	11.7%	NASELFPAVVK	99.7%	77.2	25	61.1	2	0	0	1174.65	75	85
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	19	0.02%	11.7%	QFAAATIQTIGR	99.7%	65.1	25	55.2	1	0	0	1276.70	419	430
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	19	0.02%	11.7%	TVIGSVLLR	99.7%	54.3	25	47.4	2	0	0	957.61	1077	1085
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	19	0.02%	11.7%	YAEEQQDLALLSISTFQR	99.7%	65.2	25	60.5	1	0	0	2112.06	105	122
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	12	12	19	0.02%	11.7%	YDQNYDIR	99.7%	59.7	25	47.5	1	0	0	1086.49	564	571
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	7	7	12	0.01%	6.2%	ALDLLYGMVSK	99.7%	76.4	25	70.5	2	0	0	1209.65	360	370
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	7	7	12	0.01%	6.2%	AVFHEEEQR	97.4%	30.8	25	21.5	1	0	0	1144.54	643	651
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	7	7	12	0.01%	6.2%	ILIEDSDQNLK	99.7%	52.4	25	46.2	2	0	0	1287.68	310	320
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	7	7	12	0.01%	6.2%	LFGALTPLEPR	99.3%	36.4	25	27	1	0	0	1213.69	244	254
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	7	7	12	0.01%	6.2%	MSFQNLLAK	99.7%	61.7	25	53.7	2	0	0	1051.56	1079	1087

AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	7	7	12	0.01%	6.2%	NYLSLAPLFFK	99.7%	47.9	25	47.9	3	0	0	1312.73	217	227
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	7	7	12	0.01%	6.2%	YLGLLAMSK	96.5%	29.7	25	25.4	1	0	0	995.56	321	329
AP-3 complex subunit sigma-1	AP3S1	AP3S1_HUMAN	21.7	100.0%	3	4	6	0.01%	18.1%	FYQPYSEDTQQQIIR	99.7%	77.1	25	73.3	2	0	0	1915.92	19	33
AP-3 complex subunit sigma-1	AP3S1	AP3S1_HUMAN	21.7	100.0%	3	4	6	0.01%	18.1%	NMNLPEIPR	99.3%	36.7	25	24.9	2	0	0	1099.56	167	175
AP-3 complex subunit sigma-1	AP3S1	AP3S1_HUMAN	21.7	100.0%	3	4	6	0.01%	18.1%	SEAGLAGAPAR	99.7%	61.6	25	50.3	2	0	0	999.52	150	160
AP-3 complex subunit sigma-2	AP3S2	AP3S2_HUMAN	22.0	100.0%	3	3	7	0.01%	16.1%	FPEEIQQQIVR	99.5%	38.3	25	33.8	1	0	0	1386.74	23	33
AP-3 complex subunit sigma-2	AP3S2	AP3S2_HUMAN	22.0	100.0%	3	3	7	0.01%	16.1%	NINLPEIPR	99.2%	36	25	32.3	2	0	0	1065.61	167	175
AP-3 complex subunit sigma-2	AP3S2	AP3S2_HUMAN	22.0	100.0%	3	3	7	0.01%	16.1%	SEGGLSAAPAR	99.7%	50.3	25	38.7	4	0	0	1015.52	150	160
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	23	49	0.05%	35.4%	AALSASEGEEVPQDK	99.7%	84.2	25	79.5	2	0	0	1530.73	113	127
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	23	49	0.05%	35.4%	ALGTEVIQLFPEK	99.7%	97.2	25	87.6	4	0	0	1444.80	325	337
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	23	49	0.05%	35.4%	CLIATGGTPR	99.7%	54.8	25	35.5	1	0	0	1045.55	256	265
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	23	49	0.05%	35.4%	DGEQHEDLNEVAK	99.7%	77.4	25	75.9	2	1	0	1483.67	594	606
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	23	49	0.05%	35.4%	ELWFSDDPNVTK	99.6%	39.7	25	32.7	2	0	0	1450.69	178	189
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	23	49	0.05%	35.4%	ILPEYLSNWTMEK	99.7%	64.9	25	59.8	3	0	0	1623.81	343	355
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	23	49	0.05%	35.4%	ISGLGLTPEQK	99.7%	53.1	25	44.7	4	0	0	1142.64	99	109
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	23	49	0.05%	35.4%	KVVQLDVR	97.8%	31.5	25	15.2	2	0	0	956.59	232	239
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	23	49	0.05%	35.4%	LFNIHED	98.5%	33.3	25	33.3	2	0	0	887.43	607	613
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	23	49	0.05%	35.4%	LNDGSQITYEK	99.7%	72.8	25	65.1	4	0	0	1267.62	245	255
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	23	49	0.05%	35.4%	SATEQSGTGIR	99.7%	67.2	25	51.2	2	0	0	1106.54	519	529
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	23	49	0.05%	35.4%	SNIWVAGDAACFYDIK	99.7%	102	25	102	3	0	0	1829.85	431	446
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	23	49	0.05%	35.4%	TGGLEIDSDFGGFR	99.7%	77.9	25	77.9	2	0	0	1470.69	409	422
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	23	49	0.05%	35.4%	VETDHIVAAVGLEPNVELAK	99.7%	45	25	45	0	2	0	2104.13	389	408
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	23	49	0.05%	35.4%	VLIVSEDPELPYMRPPLSK	99.7%	56.6	25	56.6	1	4	0	2183.18	159	177
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	23	49	0.05%	35.4%	VMPNAIVQSVGVSSGK	99.7%	100	25	98.9	4	0	0	1588.84	363	378
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	23	49	0.05%	35.4%	VNAELQAR	99.7%	55.7	25	43.6	2	0	0	900.49	423	430
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	18	23	49	0.05%	35.4%	VVQLDVR	99.7%	51	25	38.6	2	0	0	828.49	233	239
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	11	11	25	0.02%	9.7%	AAPCIYWLPLTDSQIVQK	99.7%	64.3	25	60.4	1	0	0	2103.09	1220	1237
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	11	11	25	0.02%	9.7%	GLLVDRPSETK	98.4%	32.9	25	19.7	4	0	0	1214.67	1097	1107
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	11	11	25	0.02%	9.7%	GVPAGNSDTEGGQPGR	99.7%	73.1	25	70.2	4	0	0	1498.69	832	847
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	11	11	25	0.02%	9.7%	KPSISITTESLK	99.7%	51.4	25	48.9	2	0	0	1303.75	861	872
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	11	11	25	0.02%	9.7%	RLSQPESAEK	99.4%	37.6	25	28.6	2	0	0	1144.60	708	717
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	11	11	25	0.02%	9.7%	SGVSITIDDPVR	99.7%	66.1	25	45.6	3	0	0	1258.66	987	998
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	11	11	25	0.02%	9.7%	SQEQEVLER	99.6%	38.8	25	25.2	1	0	0	1117.55	328	336
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	11	11	25	0.02%	9.7%	STLADYSAQK	98.0%	32.1	25	32.1	2	0	0	1083.53	507	516
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	11	11	25	0.02%	9.7%	TGTLVEEAFWIDK	99.7%	68.6	25	57.2	2	0	0	1508.76	1035	1047
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	11	11	25	0.02%	9.7%	VTLGDTLTR	99.7%	51.6	25	38.3	2	0	0	975.55	971	979
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	11	11	25	0.02%	9.7%	WGASTATTQK	99.7%	45.7	25	37.3	2	0	0	1050.52	851	860
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	36.4%	AAYPDLENPPLLVTPSQQAK	99.7%	107	25	107	3	0	0	2152.13	90	109
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	36.4%	AYQCVVLLQGK	99.7%	68.4	25	50.2	2	0	0	1278.69	290	300
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	36.4%	FGDYQCNSAMGISQMLK	99.7%	40.9	25	40.9	1	0	0	1949.86	110	126
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	36.4%	FPEILQK	99.7%	53.7	25	17.1	2	0	0	874.50	581	587
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	36.4%	GESFYQDR	99.1%	35.6	25	35.3	1	0	0	1001.43	334	341
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	36.4%	GFDILGIKPVQR	99.7%	47	25	41.7	4	2	0	1342.78	648	659
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	36.4%	GFVQVDDGRK	99.7%	47	25	34.7	4	0	0	1120.57	353	362
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	36.4%	GNTAAYLLYAFTR	99.7%	54.3	25	54.3	4	0	0	1460.75	528	540
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	36.4%	IVFVPGCSIPLTIVK	99.7%	84.5	25	68.3	2	0	0	1642.96	363	377
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	36.4%	LANIDEEMLQK	99.7%	68.7	25	55.9	4	0	0	1303.66	547	557
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	36.4%	LFEFAGYDVLR	99.7%	68.3	25	51.2	4	0	0	1329.68	224	234
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	36.4%	LLQQEEEIK	99.7%	51.5	25	33.7	2	0	0	1129.61	12	20
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	36.4%	LMDLLGEGLKR	99.7%	46.5	25	44.4	2	0	0	1244.70	462	472
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	36.4%	LNDYIFSFDK	99.7%	74.4	25	70.7	4	0	0	1261.61	513	522

Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	36.4%	MLLCEAVAAVMAK	99.7%	74.9	25	64.4	6	0	0	1422.72	635	647
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	36.4%	NMINIISR	99.7%	49.2	25	36.5	3	0	0	960.53	72	79
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	36.4%	SDGGYTYDTSDLAAIK	99.7%	97.1	25	89	4	0	0	1676.77	378	393
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	36.4%	SLTAEIDR	99.7%	44.1	25	29.2	2	0	0	904.47	21	28
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	36.4%	STIIGESISR	99.7%	97	25	80.8	4	0	0	1062.58	214	223
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	36.4%	VIVDFSSPNIAK	99.7%	61.5	25	48.2	1	0	0	1289.71	194	205
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	21	25	65	0.06%	36.4%	YADLSHNR	99.7%	57.7	25	50.1	4	0	0	975.46	505	512
Argininosuccinate synthase	ASS1	ASSY_HUMAN	46.5	100.0%	4	4	6	0.01%	8.7%	FELSCYSLAPQIK	99.7%	59.8	25	48.1	2	0	0	1555.78	128	140
Argininosuccinate synthase	ASS1	ASSY_HUMAN	46.5	100.0%	4	4	6	0.01%	8.7%	GQVYILGR	99.7%	42.5	25	33.2	2	0	0	905.52	356	363
Argininosuccinate synthase	ASS1	ASSY_HUMAN	46.5	100.0%	4	4	6	0.01%	8.7%	MPEFYNR	98.3%	32.7	25	30.9	1	0	0	956.43	147	153
Argininosuccinate synthase	ASS1	ASSY_HUMAN	46.5	100.0%	4	4	6	0.01%	8.7%	VFIEDVSR	99.7%	55.2	25	45.2	1	0	0	964.51	59	66
Armadillo repeat-containing protein 6	ARMC6	ARMC6_HUMAN	54.1	100.0%	5	5	8	0.01%	12.4%	AIAGNDDVKDAIVR	99.7%	72.8	25	72.8	1	0	0	1456.78	353	366
Armadillo repeat-containing protein 6	ARMC6	ARMC6_HUMAN	54.1	100.0%	5	5	8	0.01%	12.4%	DQSGVQELVK	99.0%	34.8	25	22.9	2	0	0	1102.57	336	345
Armadillo repeat-containing protein 6	ARMC6	ARMC6_HUMAN	54.1	100.0%	5	5	8	0.01%	12.4%	GAYPIIFTAWK	99.7%	61.2	25	55.3	2	0	0	1266.69	135	145
Armadillo repeat-containing protein 6	ARMC6	ARMC6_HUMAN	54.1	100.0%	5	5	8	0.01%	12.4%	IAQETFDAAVR	99.7%	58.9	25	51.9	1	0	0	1220.63	31	41
Armadillo repeat-containing protein 6	ARMC6	ARMC6_HUMAN	54.1	100.0%	5	5	8	0.01%	12.4%	IIVEGGGAVAALQAMK	99.7%	83.2	25	83.2	2	0	0	1527.86	407	422
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	15	17	29	0.03%	32.8%	ADWLSHYWMPK	99.1%	35.7	25	29.5	1	0	0	1449.66	530	540
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	15	17	29	0.03%	32.8%	AMTEDGFLAVCSEAK	99.7%	94.2	25	94.2	4	0	0	1644.72	148	162
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	15	17	29	0.03%	32.8%	APSPEKAEEESER	99.7%	59.5	25	59.5	2	0	0	1458.67	380	392
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	15	17	29	0.03%	32.8%	ASVGMYLISK	98.1%	32.2	25	27.1	2	0	0	1084.57	341	350
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	15	17	29	0.03%	32.8%	DVPLHALYDNVEK	99.7%	65.4	25	61.8	2	0	0	1512.77	209	221
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	15	17	29	0.03%	32.8%	EAFSDGITSVK	99.7%	71.4	25	66.2	2	0	0	1153.57	468	478
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	15	17	29	0.03%	32.8%	ELYLFDVLR	99.7%	58.1	25	46.2	2	0	0	1167.64	396	404
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	15	17	29	0.03%	32.8%	ETFEDSNLIPK	99.7%	42	25	31.1	2	0	0	1292.64	450	460
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	15	17	29	0.03%	32.8%	IGCLLSGGLDSSLVAATLLK	99.2%	36.2	25	36.2	1	0	0	1988.11	253	272
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	15	17	29	0.03%	32.8%	ILQEYVEHQVDDAMMANAAQK	99.7%	39.8	25	39.8	0	1	0	2436.12	484	504
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	15	17	29	0.03%	32.8%	LAVVDPLFGMQPIR	99.7%	70.1	25	65.6	4	0	0	1571.86	50	63
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	15	17	29	0.03%	32.8%	LFPGFEIETVK	99.7%	48.3	25	28.6	1	0	0	1279.69	222	232
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	15	17	29	0.03%	32.8%	TKEGYYYR	95.3%	28.5	25	21.5	1	0	0	1079.52	512	519
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	15	17	29	0.03%	32.8%	VPFLDHR	98.8%	34.1	25	25.8	2	0	0	883.48	418	424
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	15	17	29	0.03%	32.8%	WINATDPSAR	99.7%	40.1	25	33.3	2	0	0	1130.56	541	550
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	7	7	13	0.01%	17.7%	ASAELALGENSEVLK	99.7%	101	25	97.1	2	0	0	1530.80	108	122
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	7	7	13	0.01%	17.7%	DAGMQLQGYR	99.7%	50.4	25	30.4	2	0	0	1154.53	171	180
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	7	7	13	0.01%	17.7%	FVTVQTISGTGALR	99.7%	101	25	95.6	2	0	0	1449.81	126	139
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	7	7	13	0.01%	17.7%	IAAAILNTPDLR	99.7%	60.2	25	47	2	0	0	1267.74	326	337
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	7	7	13	0.01%	17.7%	IAAAILNTPDLRK	98.9%	34.5	25	34.5	1	0	0	1395.83	326	338
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	7	7	13	0.01%	17.7%	TCGFDFTGAVEDISK	99.7%	71.5	25	65.2	2	0	0	1646.74	186	200
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	100.0%	7	7	13	0.01%	17.7%	VGAFTMVCK	99.7%	44.2	25	36.4	2	0	0	1012.50	288	296
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	25	31	58	0.06%	59.3%	ADEVVWVR	99.7%	56	25	44.7	2	0	0	973.51	56	63
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	25	31	58	0.06%	59.3%	ALHHGIDLEK	97.2%	30.6	25	21.6	1	0	0	1132.61	442	451
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	25	31	58	0.06%	59.3%	EAGVEMGDEDDLSTPNEK	99.7%	100	25	100	2	0	0	1935.81	357	374
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	25	31	58	0.06%	59.3%	EIMDAAEDYAK	99.7%	66.7	25	64.5	3	0	0	1271.55	16	26
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	25	31	58	0.06%	59.3%	ESIVDVEGVVR	99.7%	86.2	25	77.1	2	0	0	1201.64	111	121
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	25	31	58	0.06%	59.3%	FGAPPHAGGGIGLER	99.7%	67.7	25	53.1	2	1	0	1435.74	461	475
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	25	31	58	0.06%	59.3%	FLEPTLR	98.6%	33.4	25	19.9	2	0	0	875.50	339	345
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	25	31	58	0.06%	59.3%	FQTEIQTVNK	99.7%	61.3	25	36.6	2	0	0	1207.63	321	330
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	25	31	58	0.06%	59.3%	GFVEIQTPK	99.7%	47.1	25	27.1	3	0	0	1018.56	214	222
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	25	31	58	0.06%	59.3%	IGSCTQQDVELHVQK	99.7%	75.8	25	75.7	2	1	0	1741.85	127	141
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	25	31	58	0.06%	59.3%	IHDPQLLTER	98.5%	27.6	25	19.5	0	2	0	1221.66	432	441
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	25	31	58	0.06%	59.3%	IISAASEGGANVFTVSYFK	99.7%	49.5	25	43.3	1	0	0	1961.00	223	241
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	25	31	58	0.06%	59.3%	IYVISLAEPR	99.7%	41.7	25	36.8	3	0	0	1160.67	142	151

Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	25	31	58	0.06%	59.3%	LEYCEALAMLR	99.7%	54.9	25	50.4	2	0	0	1368.67	346	356
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	25	31	58	0.06%	59.3%	LPLQLDDAVRPEAEGEEEGR	99.7%	58.8	25	57.8	2	2	0	2223.09	152	171
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	25	31	58	0.06%	59.3%	LQSGICHLFR	99.7%	67.6	25	58.7	2	1	0	1230.64	198	207
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	25	31	58	0.06%	59.3%	NNAYLAQSPQLYK	99.7%	91.2	25	83.3	2	0	0	1509.77	242	254
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	25	31	58	0.06%	59.3%	QCFLVLR	99.7%	41.2	25	20.6	2	0	0	935.51	75	81
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	25	31	58	0.06%	59.3%	QMCICADFEK	99.7%	48.1	25	45.3	3	0	0	1301.53	255	264
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	25	31	58	0.06%	59.3%	QQQFNVQALVAVGDHASK	99.7%	45.1	25	45.1	0	2	0	1940.00	82	99
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	25	31	58	0.06%	59.3%	QSNSYDMFMR	99.7%	59	25	57.5	2	0	0	1278.52	412	421
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	25	31	58	0.06%	59.3%	TSTSQAVFR	99.7%	59	25	51.5	2	0	0	996.51	189	197
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	25	31	58	0.06%	59.3%	VFSIGPVFR	99.7%	60.1	25	55.4	3	0	0	1021.58	265	273
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	25	31	58	0.06%	59.3%	VTMLFLGLHNVR	99.7%	69.1	25	61.9	2	0	0	1399.79	476	487
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	25	31	58	0.06%	59.3%	YGISSMIQSQEKPDR	99.7%	62	25	49.3	0	2	0	1754.84	29	43
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	13	14	25	0.02%	34.7%	AEGDISNVANGFK	99.7%	73.7	25	63.9	2	0	0	1321.64	359	371
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	13	14	25	0.02%	34.7%	CGLQFLGNIASR	99.7%	51.1	25	45.2	2	0	0	1335.68	134	145
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	13	14	25	0.02%	34.7%	ETTNIFSNCGCVR	99.7%	74.3	25	74.3	1	0	0	1557.68	346	358
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	13	14	25	0.02%	34.7%	ITSDEPLTKDDIPVFLR	99.7%	38.8	25	34.8	0	2	0	1959.04	254	270
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	13	14	25	0.02%	34.7%	LASEEPPDDEEALATIR	99.7%	93.6	25	90.2	2	0	0	1855.89	289	305
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	13	14	25	0.02%	34.7%	LIGNLCYK	99.7%	40.8	25	35.1	2	0	0	980.52	377	384
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	13	14	25	0.02%	34.7%	LSGVMVPAPIQDLEALR	99.7%	49.8	25	49.8	2	0	0	1824.99	11	27
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	13	14	25	0.02%	34.7%	NACIECSVNQNSIR	99.7%	78.9	25	69.3	2	0	0	1664.75	90	103
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	13	14	25	0.02%	34.7%	NLTEDNSQNQDLIAK	99.7%	77.8	25	77.8	1	0	0	1702.82	424	438
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	13	14	25	0.02%	34.7%	SPELVQAMFPK	99.7%	68.2	25	67	2	0	0	1262.65	227	237
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	13	14	25	0.02%	34.7%	VEQESLLTAFR	99.7%	82.6	25	72.3	2	0	0	1292.68	123	133
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	13	14	25	0.02%	34.7%	VLDILKK	96.4%	29.6	25	11.7	1	0	0	828.56	50	56
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	13	14	25	0.02%	34.7%	VTLLDLMIAK	99.7%	76.8	25	69	4	0	0	1116.67	244	253
Atlastin-3	ATL3	ATLA3_HUMAN	60.5	99.7%	2	2	2	0.00%	3.9%	DQHSFELDEK	99.6%	38.8	25	34	1	0	0	1247.55	35	44
Atlastin-3	ATL3	ATLA3_HUMAN	60.5	99.7%	2	2	2	0.00%	3.9%	EHQHEEIQNVR	94.6%	28	25	25	1	0	0	1418.68	240	250
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	11	15	24	0.02%	52.0%	HVVQSISTQQEK	99.7%	71.5	25	67.6	1	0	0	1383.72	222	233
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	11	15	24	0.02%	52.0%	HVVQSISTQQEKETIAK	99.7%	36.6	25	35.2	0	2	0	1926.03	222	238
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	11	15	24	0.02%	52.0%	HYLFDVQR	97.3%	30.7	25	24.4	2	0	0	1077.55	164	171
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	11	15	24	0.02%	52.0%	LAQLEEAK	99.2%	35.9	25	24.1	1	0	0	901.50	132	139
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	11	15	24	0.02%	52.0%	NNIAMALEVTYR	99.7%	57.6	25	57.1	1	0	0	1394.71	172	183
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	11	15	24	0.02%	52.0%	NRLDYHISVQNMMR	99.4%	31.1	25	26.6	0	2	0	1776.86	195	208
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	11	15	24	0.02%	52.0%	QASIQHIQNAIDTEK	99.7%	62.4	25	45.9	2	1	0	1695.87	140	154
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	11	15	24	0.02%	52.0%	QASIQHIQNAIDTEKSQQALVQK	98.6%	27.8	25	27.8	0	1	0	2578.36	140	162
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	11	15	24	0.02%	52.0%	TGVTGPYVLGTGLILYALSK	99.7%	85.4	25	85.4	2	1	0	2023.15	71	90
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	11	15	24	0.02%	52.0%	YGLIPEEFFQFLYPK	99.7%	54.3	25	54.3	5	0	0	1890.97	56	70
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	11	15	24	0.02%	52.0%	YGPFVADFADKLNEQK	99.7%	70	25	70	1	2	0	1841.91	116	131
ATP synthase mitochondrial F1 complex assembly factor 2	ATPAF2	ATPF2_HUMAN	32.8	99.8%	2	2	2	0.00%	6.9%	LEEEYQIQK	99.7%	41.1	25	32.5	1	0	0	1179.59	239	247
ATP synthase mitochondrial F1 complex assembly factor 2	ATPAF2	ATPF2_HUMAN	32.8	99.8%	2	2	2	0.00%	6.9%	LTVEQAVLLSR	99.7%	58.4	25	54.7	1	0	0	1228.73	228	238
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	AVDSLVPIGR	99.7%	71.3	25	65.5	10	0	0	1026.59	195	204
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	EAYPGDVFYLHSR	99.7%	88.8	25	86.8	10	3	0	1553.74	335	347
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	EIVTNFLAGFEA	99.7%	93.7	25	93.7	6	0	0	1310.66	542	553
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	ELIIGDR	98.7%	33.7	25	15.3	6	0	0	815.46	208	214
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	EPMQTGIK	99.7%	47.2	25	29.3	2	0	0	903.46	187	194
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	EVAAFAQFGSDLDAATQQLLSR	99.7%	127	25	127	5	4	0	2338.17	442	463
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	FENAFLSHVVSQHQALLGTIR	99.7%	81.6	25	81.6	0	2	0	2367.26	507	527
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	GIRPAINVGLSVSR	99.7%	66.2	25	66.2	3	2	0	1438.85	403	416
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	GMSLNLEPDNVGVVVFGNDK	99.7%	120	25	120	13	0	0	2104.04	104	123
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	GYLDKLEPSK	99.7%	41.4	25	30.2	4	0	0	1149.62	494	503
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	HALIIYDDLSK	99.7%	78.3	25	76.8	8	0	0	1287.69	306	316

ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	ILGADTSVDLEETGR	99.7%	140	25	136	12	0	0	1575.79	59	73
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	ISVREPMQTGIK	99.7%	57.8	25	50.4	2	1	0	1358.75	183	194
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	LELAQYR	99.7%	42.9	25	26.8	2	0	0	892.49	435	441
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	LKEIVTNFLAGFEA	99.7%	87.8	25	87.8	9	0	0	1551.84	540	553
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	LYCIYVAIGQK	99.7%	74.3	25	67.6	4	0	0	1327.71	242	252
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	NVQAEEMVEFSSGLK	99.7%	104	25	104	5	0	0	1667.79	89	103
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	QGQYSPMAIEEQVAVIYAGVR	99.7%	69.3	25	69.3	2	0	0	2325.15	473	493
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	QMSLLLR	99.7%	54	25	34.1	4	0	0	860.50	323	329
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	RLTDADAMK	96.6%	29.8	25	13.5	1	0	0	1020.51	262	270
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	RSTVAQLVK	98.1%	32.1	25	20.2	1	0	0	1001.61	253	261
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	RTGAIVDVPVGEELLGR	99.7%	47.2	25	41.3	0	2	0	1780.99	133	149
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	STVAQLVK	99.7%	64.9	25	41.2	5	0	0	845.51	254	261
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	TGAIVDVPVGEELLGR	99.7%	91.6	25	86.2	13	0	0	1624.89	134	149
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	TGTAEMSSILEER	99.7%	95.2	25	79.8	7	0	0	1423.67	46	58
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	TSIAIDTIINQK	99.7%	86.2	25	70.2	6	0	0	1316.74	219	230
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	VLSIGDGIAR	99.7%	66.4	25	53.5	16	0	0	1000.58	74	83
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	VVDALGNAIDGK	99.7%	75.6	25	68.8	8	0	0	1171.63	150	161
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	29	38	187	0.18%	57.5%	VVDALGNAIDGKGPIGSK	99.7%	84.4	25	84.4	6	3	0	1710.94	150	167
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	39	211	0.21%	49.1%	AHGGYSVFAGVGER	99.7%	108	25	103	7	6	0	1406.68	226	239
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	39	211	0.21%	49.1%	AIAELGIYPAVDPLDSTSR	99.7%	87.1	25	83.3	9	0	0	1988.03	388	406
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	39	211	0.21%	49.1%	DQEGQDVLLFIDNIFR	99.7%	103	25	103	1	0	0	1921.97	295	310
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	39	211	0.21%	49.1%	EGNDLYHEMIESGVINLK	99.7%	76.8	25	65.7	2	2	0	2061.00	242	259
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	39	211	0.21%	49.1%	FLSQPFQVAEVFTGHMGK	99.7%	72.5	25	72.5	4	7	0	2039.01	463	480
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	39	211	0.21%	49.1%	FTQAGSEVSALLGR	99.7%	108	25	93.9	9	0	0	1435.75	311	324
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	39	211	0.21%	49.1%	IGLFGGAGVGK	99.7%	54.2	25	44.8	8	0	0	975.56	202	212
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	39	211	0.21%	49.1%	IMDPNIVGSEHYDVAR	99.7%	83.2	25	80.1	8	9	0	1815.87	407	422
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	39	211	0.21%	49.1%	IMNVIGEPIDER	99.7%	66.9	25	55	15	0	0	1385.71	144	155
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	39	211	0.21%	49.1%	IMNVIGEPIDERGPIK	99.7%	71.9	25	70.4	5	2	0	1780.96	144	159
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	39	211	0.21%	49.1%	IPSAVGYQPTLATDMGTMQER	99.7%	119	25	119	13	3	0	2266.08	325	345
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	39	211	0.21%	49.1%	IPVGPETLGR	99.7%	57	25	50.5	8	0	0	1038.59	134	143
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	39	211	0.21%	49.1%	LVLEVAQHLGESTVR	99.7%	120	25	120	6	4	0	1650.92	95	109
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	39	211	0.21%	49.1%	TIAMDGTEGLVR	99.7%	77.3	25	67.3	13	0	0	1278.64	110	121
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	39	211	0.21%	49.1%	TVLIMELINNVAK	99.7%	102	25	88.5	20	0	0	1457.84	213	225
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	39	211	0.21%	49.1%	VALTGLTVAEYFR	99.7%	120	25	102	10	0	0	1439.79	282	294
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	39	211	0.21%	49.1%	VALVYGQMNEPPGAR	99.7%	94.5	25	84.8	15	0	0	1601.81	265	279
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	39	211	0.21%	49.1%	VLDSGAPIK	99.7%	78.6	25	58.2	6	0	0	899.52	125	133
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	39	211	0.21%	49.1%	VLDSGAPIKIPVGPETLGR	99.7%	83.1	25	82.4	6	6	0	1919.10	125	143
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	20	39	211	0.21%	49.1%	VVDLLAPYAK	99.7%	58.8	25	58.8	7	0	0	1088.64	189	198
ATP synthase subunit delta, mitochondrial	ATP5D	ATPD_HUMAN	17.5	99.8%	2	2	3	0.00%	13.7%	AQAELVGTADEATR	99.7%	104	25	99.3	2	0	0	1431.71	137	150
ATP synthase subunit delta, mitochondrial	ATP5D	ATPD_HUMAN	17.5	99.8%	2	2	3	0.00%	13.7%	IEANEALVK	99.7%	42.8	25	28.5	1	0	0	986.55	157	165
ATP synthase subunit e, mitochondrial	ATP5I	ATP5I_HUMAN	7.9	100.0%	3	3	5	0.00%	44.9%	ELAEDDSILK	97.4%	30.9	25	25.6	1	0	0	1132.57	60	69
ATP synthase subunit e, mitochondrial	ATP5I	ATP5I_HUMAN	7.9	100.0%	3	3	5	0.00%	44.9%	YNYLKPR	99.7%	48.3	25	42.1	2	0	0	953.52	30	36
ATP synthase subunit e, mitochondrial	ATP5I	ATP5I_HUMAN	7.9	100.0%	3	3	5	0.00%	44.9%	YSALFLGVAYGATR	99.7%	61.5	25	61.5	2	0	0	1488.78	16	29
ATP synthase subunit f, mitochondrial	ATP5J2	ATPK_HUMAN	10.9	99.8%	2	3	12	0.01%	25.5%	DFSPSGIFGAFQR	99.7%	67.6	25	62.8	8	0	0	1428.69	34	46
ATP synthase subunit f, mitochondrial	ATP5J2	ATPK_HUMAN	10.9	99.8%	2	3	12	0.01%	25.5%	LGELPSWILMR	99.7%	49.1	25	43	4	0	0	1330.72	23	33
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	37	0.04%	47.6%	IVNSAQTGSFK	99.7%	74.9	25	58.4	5	0	0	1151.61	56	66
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	37	0.04%	47.6%	KIVNSAQTGSFK	99.7%	73.6	25	70.9	4	0	0	1279.70	55	66
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	37	0.04%	47.6%	LATFWYYAK	99.7%	45.3	25	40.9	6	0	0	1162.59	27	35
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	37	0.04%	47.6%	TPALVNAAVTYSKPR	99.7%	86.6	25	83.9	8	8	0	1587.89	12	26
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	37	0.04%	47.6%	VELVPPTPAEIPR	99.7%	55.8	25	46.5	6	0	0	1417.81	36	48
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	33	0.03%	32.2%	ELIEIISGAAALD	99.7%	69.1	25	69.1	2	0	0	1314.72	286	298

ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	33	0.03%	32.2%	EVMLVGIGDK	99.7%	75.9	25	67.5	4	0	0	1076.57	127	136
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	33	0.03%	32.2%	EVMLVGIGDKIR	99.7%	87.7	25	60.5	4	0	0	1329.76	127	138
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	33	0.03%	32.2%	GLCGAIHSSIAK	99.7%	65.4	25	62.2	2	0	0	1213.64	101	112
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	33	0.03%	32.2%	HLLIGVSSDR	99.7%	64.7	25	56.9	4	0	0	1096.61	91	100
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	33	0.03%	32.2%	IYGLGSLALYEK	99.7%	88.9	25	83.7	3	0	0	1326.73	68	79
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	33	0.03%	32.2%	LTLTFNR	97.2%	30.6	25	22.9	1	0	0	864.49	271	277
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	33	0.03%	32.2%	NASEMIDKLTLTFNR	99.7%	96.9	25	96.5	4	4	0	1752.90	263	277
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	33	0.03%	32.2%	SEVATLTAAGK	99.7%	77.3	25	53.1	2	0	0	1047.57	116	126
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	10	16	33	0.03%	32.2%	THSDQFLVAFK	99.7%	73.4	25	64	2	1	0	1292.66	144	154
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	7	9	24	0.02%	40.4%	LSNTQGVVSAFSTMMSVHR	96.7%	24.5	25	24.5	0	1	0	2083.99	118	136
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	7	9	24	0.02%	40.4%	LVRPPVQVYGIEGR	99.7%	47	25	47	1	4	0	1582.91	27	40
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	7	9	24	0.02%	40.4%	SFLSQGQVLK	99.7%	46.4	25	39	2	0	0	1106.62	163	172
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	7	9	24	0.02%	40.4%	TDPSILGGMIVR	99.7%	61.8	25	51.1	6	0	0	1274.68	177	188
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	7	9	24	0.02%	40.4%	VAASVLNPYVK	99.7%	73.2	25	70.7	4	0	0	1160.67	74	84
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	7	9	24	0.02%	40.4%	VAQILKEPK	99.7%	40.1	25	27.4	2	0	0	1025.64	65	73
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	7	9	24	0.02%	40.4%	YATALYSAASK	99.7%	101	25	90.5	4	0	0	1145.58	41	51
ATPase family AAA domain-containing protein 1	ATAD1	ATAD1_HUMAN	40.7	99.8%	2	2	2	0.00%	6.4%	DAAFQNVLTHVCLD	99.7%	41.2	25	38.5	1	0	0	1602.76	348	361
ATPase family AAA domain-containing protein 1	ATAD1	ATAD1_HUMAN	40.7	99.8%	2	2	2	0.00%	6.4%	NEVVGLIFR	99.7%	46	25	37.4	1	0	0	1046.60	14	22
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	19	23	49	0.05%	33.9%	AEGPGRGDEPSPS	99.7%	48.9	25	46.3	2	0	0	1255.56	622	634
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	19	23	49	0.05%	33.9%	ATLNAFLYR	99.7%	63.2	25	52.3	2	0	0	1068.58	479	487
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	19	23	49	0.05%	33.9%	DALNLAQMQEQTLQLEQQSK	99.7%	118	25	112	3	1	0	2316.15	73	92
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	19	23	49	0.05%	33.9%	GEGAGPPPPLPPAQPGAEGGGDR	99.7%	86.1	25	82.2	2	0	0	2081.01	13	35
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	19	23	49	0.05%	33.9%	GLGDRPAPK	99.7%	48.9	25	39.7	2	0	0	910.51	36	44
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	19	23	49	0.05%	33.9%	INEMVHFDLPGQEERER	99.7%	41.6	25	41.6	0	2	0	2099.00	515	531
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	19	23	49	0.05%	33.9%	ITVLEALR	99.7%	58.2	25	38.2	4	0	0	914.57	339	346
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	19	23	49	0.05%	33.9%	LAQFDYGR	99.7%	51.4	25	21.2	4	0	0	969.48	554	561
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	19	23	49	0.05%	33.9%	LAQFDYGRK	99.7%	40.8	25	40.8	2	0	0	1097.57	554	562
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	19	23	49	0.05%	33.9%	LFDWANTSR	99.7%	56.3	25	44.4	3	0	0	1109.54	443	451
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	19	23	49	0.05%	33.9%	LGKPSLVR	99.7%	41.4	25	25.5	2	0	0	869.56	327	334
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	19	23	49	0.05%	33.9%	LLSRPQDALEGVVLSPSLEAR	99.7%	54.2	25	54.2	0	2	0	2250.25	355	375
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	19	23	49	0.05%	33.9%	LTEGMSGR	99.7%	52.2	25	42	2	0	0	850.41	569	576
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	19	23	49	0.05%	33.9%	NILMYGPPGTGK	99.7%	65.4	25	57.5	4	0	0	1263.64	395	406
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	19	23	49	0.05%	33.9%	QQQLLNEENLR	99.7%	62.1	25	53.2	2	0	0	1384.72	195	205
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	19	23	49	0.05%	33.9%	QTVLESIR	99.7%	47.5	25	28.6	2	0	0	945.54	268	275
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	19	23	49	0.05%	33.9%	TAGTLFGEGFR	99.7%	74	25	69.8	4	0	0	1155.58	276	286
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	19	23	49	0.05%	33.9%	VRDIAIATR	99.7%	40.6	25	36.9	2	0	0	1014.61	376	384
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	19	23	49	0.05%	33.9%	YVLKPATEGK	95.0%	28.3	25	17.8	2	0	0	1105.63	540	549
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	4	5	9	0.01%	24.2%	EALNLAQMQEQTLQLEQQSK	99.7%	100	25	100	1	0	0	2330.17	73	92
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	4	5	9	0.01%	24.2%	EYEAAVEQLK	99.2%	36.2	25	25.8	1	0	0	1179.59	95	104
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	4	5	9	0.01%	24.2%	GEGAGPPPPLPPAQPGAEGGGDR	99.7%	86.1	25	82.2	2	0	0	2081.01	13	35
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	4	5	9	0.01%	24.2%	GLGDRPAPK	99.7%	48.9	25	39.7	2	0	0	910.51	36	44
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	4	5	9	0.01%	24.2%	HILLYGPPGTGK	99.7%	46.1	25	32.5	2	0	0	1252.71	347	358
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	4	5	9	0.01%	24.2%	ITVLEALR	99.7%	58.2	25	38.2	4	0	0	914.57	291	298
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	4	5	9	0.01%	24.2%	LAQFDYGR	99.7%	51.4	25	21.2	4	0	0	969.48	506	513
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	4	5	9	0.01%	24.2%	LAQFDYGRK	99.7%	40.8	25	40.8	2	0	0	1097.57	506	514
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	4	5	9	0.01%	24.2%	LFDWANTSR	99.7%	56.3	25	44.4	3	0	0	1109.54	395	403
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	4	5	9	0.01%	24.2%	LGKPSLVR	99.7%	41.4	25	25.5	2	0	0	869.56	279	286
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	4	5	9	0.01%	24.2%	LKEYEAAVEQLK	99.7%	74.9	25	71.2	4	1	0	1420.77	93	104
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	4	5	9	0.01%	24.2%	LTEGMSGR	99.7%	52.2	25	42	2	0	0	850.41	521	528
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	4	5	9	0.01%	24.2%	QQQLLNEENLR	99.7%	62.1	25	53.2	2	0	0	1384.72	147	157
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	4	5	9	0.01%	24.2%	QTVLESIR	99.7%	47.5	25	28.6	2	0	0	945.54	220	227

ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	4	5	9	0.01%	24.2%	TAGTLFGEGFR	99.7%	74	25	69.8	4	0	0	1155.58	228	238
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	4	5	9	0.01%	24.2%	VRDIAIATR	99.7%	40.6	25	36.9	2	0	0	1014.61	328	336
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	5	5	8	0.01%	6.1%	LSSDTALLGR	98.6%	33.5	25	29.3	1	0	0	1032.57	275	284
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	5	5	8	0.01%	6.1%	SFQGALEFK	97.7%	31.4	25	21.3	1	0	0	1026.53	487	495
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	5	5	8	0.01%	6.1%	STVLSLLLR	99.7%	62.2	25	25.7	2	0	0	1001.64	534	542
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	5	5	8	0.01%	6.1%	TSLFSSILR	99.7%	46.3	25	31.8	2	0	0	1023.58	249	257
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	5	5	8	0.01%	6.1%	TVLVIAHR	98.2%	32.4	25	28.2	2	0	0	908.57	684	691
ATP-binding cassette sub-family B member 7, mitochondrial	ABCB7	ABCB7_HUMAN	82.6	100.0%	2	2	4	0.00%	2.9%	AGAAFFNEVR	99.7%	49.4	25	39.7	2	0	0	1081.54	201	210
ATP-binding cassette sub-family B member 7, mitochondrial	ABCB7	ABCB7_HUMAN	82.6	100.0%	2	2	4	0.00%	2.9%	VAISLGFLGGAK	99.7%	54.1	25	46.8	2	0	0	1132.67	140	151
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	4	4	7	0.01%	7.3%	DQVIYPDGREDQK	99.7%	51.4	25	38.2	1	0	0	1562.74	521	533
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	4	4	7	0.01%	7.3%	IANPDQLLTQDVEK	99.7%	95.7	25	95.7	3	0	0	1583.83	182	195
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	4	4	7	0.01%	7.3%	ITELMQVLK	99.7%	49.3	25	25.9	1	0	0	1090.62	391	399
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	4	4	7	0.01%	7.3%	VLGELWPLFGGR	99.6%	39.5	25	38.9	2	0	0	1343.75	485	496
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	7	14	0.01%	12.2%	ADIFMFDEPSSYLDVK	99.7%	95.4	25	95.4	4	0	0	1876.87	235	250
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	7	14	0.01%	12.2%	AIIKPQYVDQIPK	98.6%	27.8	25	23.9	0	1	0	1512.88	166	178
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	7	14	0.01%	12.2%	GSELQNYFTK	99.7%	55.7	25	46.8	2	0	0	1186.57	149	158
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	7	14	0.01%	12.2%	NVEDLSGGELQR	99.7%	44.6	25	37.1	1	0	0	1316.64	213	224
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	7	14	0.01%	12.2%	VAETANEEEVKK	99.7%	71.1	25	64.5	5	0	0	1346.68	333	344
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	7	14	0.01%	12.2%	VIVFDGVPSK	99.7%	41.2	25	31.8	1	0	0	1060.60	532	541
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	6	6	15	0.01%	7.8%	AVSEEQQPALK	99.7%	44.6	25	35.4	3	0	0	1199.63	164	174
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	6	6	15	0.01%	7.8%	GAVIVVSHDAR	99.7%	52	25	40.2	3	0	0	1123.62	790	800
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	6	6	15	0.01%	7.8%	GFNLPYQDAR	99.7%	51	25	34.3	3	0	0	1180.57	714	723
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	6	6	15	0.01%	7.8%	LQGQLEQGDDTAAER	99.7%	84.5	25	80.8	2	0	0	1630.77	397	411
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	6	6	15	0.01%	7.8%	STLLLLLTGK	99.7%	62.6	25	62.6	2	0	0	1058.68	665	674
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	6	6	15	0.01%	7.8%	VVFAELACR	99.5%	38	25	35.8	2	0	0	1064.56	751	759
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	13	24	0.02%	17.8%	ETTEVDLLTK	99.2%	36.2	25	27.3	2	0	0	1148.60	49	58
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	13	24	0.02%	17.8%	ILHGLGFTPAMQR	99.0%	29.2	25	26	0	2	0	1440.78	211	223
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	13	24	0.02%	17.8%	IPPPVIMVQNVSFK	99.7%	75.8	25	75.8	2	2	0	1568.89	391	404
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	13	24	0.02%	17.8%	LEELDADKAEMR	99.7%	66.5	25	57.2	2	0	0	1419.68	196	207
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	13	24	0.02%	17.8%	LLTGELLPTDGMIR	99.7%	98.7	25	90.5	4	0	0	1528.84	442	455
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	13	24	0.02%	17.8%	LVDEEPQLTK	99.5%	38.5	25	29	2	0	0	1171.62	609	618
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	13	24	0.02%	17.8%	MMASGLTER	99.4%	37.7	25	29.6	2	0	0	995.46	366	374
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	13	24	0.02%	17.8%	SMLLSAIGK	99.7%	43.2	25	34.6	2	0	0	935.52	125	133
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	13	24	0.02%	17.8%	WPGDILAYK	99.2%	36.3	25	28.4	2	0	0	1062.56	594	602
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	10	13	24	0.02%	17.8%	YYTGNYDQYVK	99.7%	66	25	61	2	0	0	1413.63	305	315
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	AFDSGIIPMEFVNK	99.7%	87.1	25	79.7	9	0	0	1583.78	949	962
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	AIVWGMQTR	99.7%	41.5	25	30.8	3	0	0	1061.56	499	507
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	AKPAMPQDSVPSPR	99.7%	46.8	25	46.8	3	0	0	1480.76	470	483
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	AVQGMLDFDYVCSR	99.7%	114	25	114	4	0	0	1660.75	508	521
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	DEPSVAAMVYPFTGDHK	99.7%	77.7	25	77.7	4	0	0	1879.85	522	538
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	DGVYVLDLAAK	99.7%	80.9	25	72.2	5	0	0	1163.63	210	220
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	DLVSSLTSGLLTIGDR	99.7%	111	25	110	8	0	0	1646.90	919	934
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	DYQGPLKEHEVTIFVR	97.0%	24.8	25	24.8	0	2	0	1931.00	363	378
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	EAGVFVPR	97.7%	31.4	25	19	1	0	0	874.48	781	788
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	EAYPEEAYIADLDAK	99.7%	104	25	104	4	0	0	1697.79	245	259
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	EGDYVLFHHEGGVDVGDVDAK	99.7%	52.6	25	52.6	0	2	0	2258.04	128	148
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	FGGALDAAAK	99.7%	78.3	25	53.7	2	0	0	920.48	935	944
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	FICTTSAIQNR	99.7%	74.5	25	69.7	5	0	0	1310.65	18	28
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	GQELIYAGMPITEVFK	99.7%	86	25	86	4	0	0	1811.93	849	864
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	GVTIIGPATVGGIKPGCFK	99.7%	83	25	83	2	0	0	1872.04	617	635
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	IGNTGGMLDNILASK	99.7%	99.1	25	93.5	7	0	0	1503.78	636	650

ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	KPASFMTSICDER	99.7%	79.3	25	68.5	2	2	0	1541.71	836	848
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	LGLVGVNLTLDGVK	99.7%	86.3	25	86.3	4	0	0	1397.84	69	82
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	LGQEATVGK	99.7%	66.8	25	49.2	4	0	0	902.49	89	97
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	LIMGIGHR	98.6%	33.5	25	19.9	1	0	0	912.51	969	976
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	LYRPGSVAYVSR	99.7%	43.7	25	37.5	3	4	0	1367.74	651	662
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	MIVVLGEIGGTEEYK	99.7%	121	25	121	4	0	0	1637.85	712	726
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	RGGPNYQEGLR	99.7%	46.3	25	38.2	2	0	0	1246.63	379	389
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	SAYDSTMETMNYAQIR	99.7%	98.3	25	98.3	7	0	0	1880.82	577	592
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	SGGMSNELNNIISR	99.7%	84.1	25	74.7	7	0	0	1507.72	663	676
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	SINNPDMR	98.4%	33	25	16.8	2	0	0	946.44	979	986
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	SMGFIGHYLDQK	99.7%	51	25	51	4	0	0	1395.67	1066	1077
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	STTLFSR	95.4%	28.6	25	14.7	1	0	0	811.43	489	495
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	TIAIIAEGIPEALTR	99.7%	111	25	105	10	0	0	1567.91	593	607
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	TILSLMTR	99.7%	45.1	25	31.1	6	0	0	934.54	322	329
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	TTDGVYEGVAIGGDR	99.7%	110	25	97.3	2	0	0	1509.72	677	691
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	VDATADYICK	99.7%	66.3	25	62.4	4	0	0	1155.54	221	230
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	VTPDTDWAR	99.4%	37.5	25	37.5	2	0	0	1060.51	34	42
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	WGDIEFPPPFGR	99.7%	45.8	25	45.7	5	0	0	1417.69	233	244
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	35	48	142	0.14%	40.1%	YQDTPGVK	95.2%	28.5	25	19	1	0	0	907.45	704	711
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	7	7	13	0.01%	13.7%	DLIEFGMIPEFVGR	99.7%	41	25	37.2	2	0	0	1638.82	486	499
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	7	7	13	0.01%	13.7%	DVGGEGVQQGLLK	99.7%	88.2	25	79.2	2	0	0	1299.69	374	386
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	7	7	13	0.01%	13.7%	LLQDANYNVEK	99.7%	53.7	25	44	2	0	0	1306.66	339	349
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	7	7	13	0.01%	13.7%	SGESNTHQDIEEKDR	99.7%	34.5	25	34.5	0	2	0	1744.77	463	477
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	7	7	13	0.01%	13.7%	SNILLLGPTGSGK	99.7%	76.6	25	72.8	2	0	0	1256.72	287	299
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	7	7	13	0.01%	13.7%	TLLAQTLAK	99.7%	40.5	25	36.5	1	0	0	958.59	300	308
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	7	7	13	0.01%	13.7%	YLGFGTPSNLGK	99.7%	49.6	25	43.6	2	0	0	1253.65	438	449
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	AAECNIVVTQPR	99.7%	80.1	25	69.4	7	0	0	1357.69	435	446
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	AAMEALVVEVTK	99.7%	86.9	25	75.8	14	0	0	1276.68	1105	1116
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	AENNSEVGASGYGVPGPTWDR	99.7%	88.2	25	88.2	4	0	0	2162.97	121	141
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	AIEPPPLDAVIEAEHTLR	99.7%	91.8	25	90.3	4	2	0	1971.05	820	837
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	DFVNYLVR	99.7%	58.3	25	46.5	9	0	0	1025.54	64	71
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	DINTDFLLVVLR	99.7%	86.7	25	74.1	8	0	0	1417.81	517	528
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	DVVQAYPEVR	99.7%	71.2	25	62.1	8	0	0	1175.61	529	538
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	EGETVEPYK	96.2%	29.3	25	23.3	1	0	0	1051.49	267	275
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	ELDALDANDELTPLGR	99.7%	109	25	95.4	10	0	0	1741.86	838	853
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	GANLKDYYSR	99.7%	57.7	25	51.5	4	0	0	1186.59	142	151
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	GISHVIVDEIHER	99.7%	65.5	25	65.5	2	5	0	1503.79	504	516
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	GMTLVTPLQLLLFASK	99.7%	108	25	105	11	0	0	1748.00	1058	1073
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	HLEMNPHFGSHR	99.5%	32	25	32	0	1	0	1477.68	669	680
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	ISAVSVAER	99.7%	74.5	25	59.8	7	0	0	931.52	448	456
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	KMTPSYEIR	99.7%	53.7	25	38.1	4	0	0	1124.58	16	24
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	KVFDPVPVGVTK	99.7%	65.7	25	61.5	6	0	0	1285.75	697	708
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	LAAQSCALSLVR	99.7%	84.2	25	77.4	9	0	0	1288.70	237	248
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	LAQFEPSQR	99.7%	57.1	25	52.6	7	0	0	1075.55	315	323
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	LETHMTPEMFR	99.7%	35	25	30.9	4	3	0	1391.64	785	795
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	LFTAHNNMTNYATVWASK	99.7%	40	25	40	0	4	0	2068.99	738	755
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	LGGIGQFLAK	99.7%	71.9	25	66.7	10	0	0	1003.59	810	819
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	LNMATLR	99.7%	59.9	25	42.9	5	0	0	818.46	945	951
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	LNQYFQK	99.7%	51.4	25	40.4	9	0	0	940.49	185	191
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	LQISHEAAACITGLR	99.7%	91.2	25	91.2	2	4	0	1639.86	1090	1104
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	LSMSQLNEK	99.7%	62.7	25	53.6	11	0	0	1049.53	622	630

ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	MGGEEAEIR	99.7%	82.2	25	68.8	13	0	0	991.45	930	938
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	MTPSYEIR	99.7%	48.3	25	42.8	1	0	0	996.48	17	24
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	NFLYAWCGK	99.7%	48.7	25	24.9	4	0	0	1158.54	6	14
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	QISRPSAAGINLMIGSTR	99.7%	34.3	25	34.3	0	1	0	1888.01	1137	1154
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	QLYHLGVVEAYSGLTK	99.7%	47.9	25	47.9	2	2	0	1777.95	249	264
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	QPAIISQLDPVNER	99.7%	87.4	25	86.7	4	0	0	1579.84	1117	1130
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	RISAVSVAER	99.7%	52.9	25	42.5	7	0	0	1087.62	447	456
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	RLNMATLR	99.2%	35.8	25	17.5	2	0	0	974.56	944	951
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	SFIAEMTIYIK	99.7%	72.8	25	65.6	2	0	0	1331.69	210	220
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	SSVNCPFSSQDMK	99.7%	72.7	25	72.7	4	0	0	1502.63	1025	1037
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	SSVNCPFSSQDMKYPSPFFVFGEK	97.3%	25.1	25	25.1	0	1	0	2801.26	1025	1048
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	TPLHEIALSIK	99.7%	50.9	25	45.4	2	6	0	1221.72	796	806
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	TTQVPQFILDDFIQNDR	99.7%	89.2	25	78.6	8	0	0	2050.02	418	434
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	VFDPVPVGVTK	99.7%	48.2	25	48.2	7	0	0	1157.66	698	708
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	VQSDGQIVLVDDWIK	99.7%	64.2	25	63.7	2	0	0	1714.90	1075	1089
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	VRPGFCFHLCSR	99.7%	37	25	37	0	2	0	1535.74	768	779
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	YGDGPRPPK	99.7%	49.9	25	47.1	11	0	0	986.51	1155	1163
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	YPSPFFVFGEK	99.7%	46.8	25	39	4	0	0	1317.65	1038	1048
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	YQILPLHSQIPR	99.7%	56.2	25	45.7	5	3	0	1464.83	681	692
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	45	62	278	0.27%	38.3%	YTQVGPDHNR	99.7%	51.8	25	41.4	10	0	0	1186.56	200	209
ATP-dependent RNA helicase DDX1	DDX1	DDX1_HUMAN	82.4	100.0%	4	4	7	0.01%	4.9%	ALIVEPSR	97.8%	31.6	25	30.8	1	0	0	884.52	289	296
ATP-dependent RNA helicase DDX1	DDX1	DDX1_HUMAN	82.4	100.0%	4	4	7	0.01%	4.9%	ELLIIGGVAAR	99.7%	88.2	25	83.3	2	0	0	1111.68	320	330
ATP-dependent RNA helicase DDX1	DDX1	DDX1_HUMAN	82.4	100.0%	4	4	7	0.01%	4.9%	FLICTDVAAR	99.7%	54.1	25	47.2	2	0	0	1165.60	568	577
ATP-dependent RNA helicase DDX1	DDX1	DDX1_HUMAN	82.4	100.0%	4	4	7	0.01%	4.9%	LNLSQVR	99.7%	48.6	25	23.1	2	0	0	829.49	359	365
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	6	7	10	0.01%	10.0%	ELAMQTFGVLK	99.7%	66.1	25	58.4	3	0	0	1236.67	262	272
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	6	7	10	0.01%	10.0%	ISDIQSQLEK	99.7%	51.4	25	9.31	1	0	0	1160.62	558	567
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	6	7	10	0.01%	10.0%	LGNGINIIVATPGR	99.7%	57.6	25	57.6	2	0	0	1394.81	298	311
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	6	7	10	0.01%	10.0%	NLQCLVIDEADR	99.7%	69.9	25	69.2	1	0	0	1445.71	326	337
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	6	7	10	0.01%	10.0%	QTMLFSATQTR	99.7%	74.9	25	59.3	2	0	0	1283.64	359	369
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	6	7	10	0.01%	10.0%	SIRPLLEGR	97.0%	30.4	25	22.6	1	0	0	1040.62	209	217
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	12	25	0.02%	23.4%	DPNSPLYSVK	99.7%	51.6	25	38.9	4	0	0	1119.57	82	91
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	12	25	0.02%	23.4%	GLAVNMVDSK	99.7%	60	25	54.5	2	0	0	1049.53	436	445
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	12	25	0.02%	23.4%	HSMNILNR	99.7%	43.8	25	35.4	2	0	0	984.50	446	453
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	12	25	0.02%	23.4%	IQEHFNK	99.1%	35.6	25	23.5	2	0	0	915.47	454	460
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	12	25	0.02%	23.4%	LDTDDLDEIEK	99.7%	68.3	25	62.5	2	0	0	1305.61	465	475
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	12	25	0.02%	23.4%	QYYVLCSSR	97.3%	30.8	25	27.3	1	0	0	1175.55	308	316
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	12	25	0.02%	23.4%	REEETLDTIK	98.3%	32.6	25	19.1	1	0	0	1233.63	298	307
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	12	25	0.02%	23.4%	SMTNLQIKEEK	99.7%	45.6	25	38	1	0	0	1320.68	19	29
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	12	25	0.02%	23.4%	SNLVDNTNQVEVLQR	99.7%	109	25	98.7	4	0	0	1728.89	67	81
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	12	25	0.02%	23.4%	TAAFVLAMLSR	99.7%	59.9	25	52.9	3	0	0	1179.66	144	154
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	11	12	25	0.02%	23.4%	VLVTTNVCAR	99.7%	56.8	25	56.5	3	0	0	1132.61	385	394
ATP-dependent RNA helicase DDX24	DDX24	DDX24_HUMAN	96.3	100.0%	2	2	2	0.00%	2.6%	DKLDILGAAETGSGK	99.7%	58.4	25	58.3	1	0	0	1474.78	229	243
ATP-dependent RNA helicase DDX24	DDX24	DDX24_HUMAN	96.3	100.0%	2	2	2	0.00%	2.6%	NLEQFAR	98.3%	32.7	25	15.2	1	0	0	877.45	629	635
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	10	11	23	0.02%	23.7%	DFLLKPELLR	98.8%	34.2	25	20.3	1	0	0	1243.74	48	57
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	10	11	23	0.02%	23.7%	DVQEIFR	99.1%	35.6	25	16	2	0	0	906.47	209	215
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	10	11	23	0.02%	23.7%	ELAFQISK	99.4%	37.6	25	29.8	2	0	0	935.52	123	130
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	10	11	23	0.02%	23.7%	GLAITFVSDENDAK	99.7%	83.3	25	79.2	2	0	0	1479.73	384	397
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	10	11	23	0.02%	23.7%	GSYVSIHSSGFR	99.7%	58.5	25	47.7	2	0	0	1296.63	36	47
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	10	11	23	0.02%	23.7%	ILNDVQDR	99.7%	44.5	25	31	2	0	0	972.51	398	405
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	10	11	23	0.02%	23.7%	ILVATNLFGR	99.7%	85	25	67.8	4	0	0	1103.66	339	348
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	10	11	23	0.02%	23.7%	NCPHVVVGTPGR	99.7%	57	25	43.4	2	2	0	1292.65	163	174

ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	10	11	23	0.02%	23.7%	VSVFFGGLSIK	99.7%	58.5	25	54.1	3	0	0	1153.66	144	154
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	10	11	23	0.02%	23.7%	YQQFKDFQR	97.8%	31.7	25	31.7	1	0	0	1259.62	329	337
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	19	32	0.03%	31.9%	DKDAYSSFGSR	99.7%	56.2	25	56.2	2	0	0	1232.55	65	75
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	19	32	0.03%	31.9%	DLLDLLVEAK	99.7%	70.8	25	58.2	2	0	0	1128.65	555	564
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	19	32	0.03%	31.9%	DLMACAQTGSGK	99.7%	66.6	25	60.7	3	0	0	1254.55	219	230
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	19	32	0.03%	31.9%	DREEALHQFR	99.2%	30.3	25	26.4	1	1	0	1300.64	479	488
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	19	32	0.03%	31.9%	ELAVQIYEEAR	99.7%	63.5	25	58.7	1	0	0	1320.68	277	287
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	19	32	0.03%	31.9%	GCHLLVATPGR	99.7%	52.2	25	52.2	1	0	0	1180.63	316	326
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	19	32	0.03%	31.9%	IGLDFCK	99.7%	48	25	42.7	2	0	0	852.43	336	342
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	19	32	0.03%	31.9%	IVEQDTMPPK	99.5%	37.9	25	32.2	2	0	0	1173.58	364	373
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	19	32	0.03%	31.9%	LEQELFSGGNTGINFEK	99.7%	110	25	107	2	0	0	1882.92	146	162
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	19	32	0.03%	31.9%	MLDMGFEPQIR	99.7%	71.9	25	41.9	8	0	0	1352.63	352	362
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	19	32	0.03%	31.9%	QSSGASSSSFSSSR	99.7%	90	25	86.5	2	0	0	1361.59	604	617
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	19	32	0.03%	31.9%	QYPISLVLAPTR	99.6%	40	25	29.9	2	0	0	1357.78	265	276
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	19	32	0.03%	31.9%	SFLLDLLNATGK	99.7%	92.2	25	85.3	2	0	0	1291.73	429	440
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	19	32	0.03%	31.9%	SPILVATAVAAR	99.7%	119	25	110	2	0	0	1168.70	492	503
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	19	32	0.03%	31.9%	VGNLGLATSFFNER	99.7%	62.5	25	62.5	2	0	0	1524.78	535	548
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	19	32	0.03%	31.9%	VGSTSENITQK	99.7%	67.9	25	55.1	2	0	0	1163.59	408	418
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	19	32	0.03%	31.9%	VRPCVVYGGADIGQQIR	99.7%	67.3	25	57	0	1	0	1887.99	295	311
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	19	32	0.03%	31.9%	YLVLDEADR	99.7%	58.4	25	39.9	2	0	0	1093.55	343	351
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	5	5	10	0.01%	11.0%	EGAFSNFPISEETIK	99.7%	59.7	25	59.7	5	0	0	1668.81	136	150
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	5	5	10	0.01%	11.0%	GVTYLFPIQVK	99.7%	66.6	25	49.9	2	0	0	1264.73	156	166
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	5	5	10	0.01%	11.0%	NGIDILVGTPGR	99.7%	75	25	65.7	4	0	0	1211.67	258	269
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	5	5	10	0.01%	11.0%	SRYEQVDLVGK	98.1%	32.2	25	2.01	2	0	0	1293.68	343	353
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	5	5	10	0.01%	11.0%	TFSFAIPLIER	99.7%	73.9	25	73.9	3	0	0	1293.72	188	198
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	5	5	10	0.01%	11.0%	VGVPSTMDLVK	99.7%	41.8	25	35	1	0	0	1145.62	514	524
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	5	5	10	0.01%	11.0%	VLVATNVAAR	99.7%	80.2	25	73.1	2	0	0	1013.61	441	450
ATP-dependent RNA helicase DDX54	DDX54	DDX54_HUMAN	98.6	100.0%	3	3	5	0.00%	3.5%	FEEEELQR	99.0%	35.1	25	24.5	1	0	0	1079.50	552	559
ATP-dependent RNA helicase DDX54	DDX54	DDX54_HUMAN	98.6	100.0%	3	3	5	0.00%	3.5%	SRPAPSPESIKR	99.3%	30.9	25	30.9	0	1	0	1324.73	522	533
ATP-dependent RNA helicase DDX54	DDX54	DDX54_HUMAN	98.6	100.0%	3	3	5	0.00%	3.5%	VADNAQQQYVR	99.7%	66.8	25	60.5	3	0	0	1291.64	511	521
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	12	12	17	0.02%	12.6%	AICSGFFR	97.0%	30.3	25	23.1	1	0	0	957.46	1106	1113
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	12	12	17	0.02%	12.6%	EEFPDFDEETGILPK	99.5%	38.4	25	38.4	1	0	0	1765.82	414	428
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	12	12	17	0.02%	12.6%	FEDCTSPETVIK	99.6%	39.3	25	35	1	0	0	1425.66	648	659
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	12	12	17	0.02%	12.6%	FSQYFYEAPIFTIPGR	99.7%	77.6	25	76.5	3	0	0	1935.96	725	740
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	12	12	17	0.02%	12.6%	IFDPAPPGSR	99.7%	47.7	25	45.6	2	0	0	1056.55	824	833
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	12	12	17	0.02%	12.6%	LIVTSATLDAVK	99.7%	87.7	25	87.7	2	0	0	1230.73	713	724
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	12	12	17	0.02%	12.6%	NGAEFTDSLISNLLR	99.7%	76.1	25	64.4	1	0	0	1649.85	73	87
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	12	12	17	0.02%	12.6%	NLVGETNEETSMR	99.7%	62.1	25	62.1	1	0	0	1479.67	353	365
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	12	12	17	0.02%	12.6%	NPDGSLSQAAMMQSALAK	99.7%	58.6	25	50	1	0	0	1851.86	467	484
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	12	12	17	0.02%	12.6%	TQMSILEQR	97.5%	31.1	25	21.4	1	0	0	1105.57	554	562
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	12	12	17	0.02%	12.6%	TTQITQYLAEAGYTSR	99.7%	94.4	25	94.4	1	0	0	1802.89	595	610
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	12	12	17	0.02%	12.6%	VANVADVVSK	99.7%	56.4	25	50.2	2	0	0	1001.56	306	315
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YMEL1_HUMAN	86.5	100.0%	5	5	7	0.01%	8.0%	LAETQNIAPSFVK	99.7%	49.6	25	48.5	1	0	0	1417.77	225	237
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YMEL1_HUMAN	86.5	100.0%	5	5	7	0.01%	8.0%	LGVMTYSDTGK	94.6%	28	25	28	1	0	0	1171.57	698	708
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YMEL1_HUMAN	86.5	100.0%	5	5	7	0.01%	8.0%	LSPETQSAIEQEIR	99.7%	67.9	25	66	2	0	0	1600.82	709	722
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YMEL1_HUMAN	86.5	100.0%	5	5	7	0.01%	8.0%	NLAEALLTYETLDAK	99.2%	35.9	25	32.6	1	0	0	1664.87	745	759
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YMEL1_HUMAN	86.5	100.0%	5	5	7	0.01%	8.0%	TGFAEGFLK	99.7%	53.3	25	49.5	2	0	0	969.50	270	278
Basic leucine zipper and W2 domain-containing protein 1	BZW1	BZW1_HUMAN	48.0	100.0%	3	3	6	0.01%	6.7%	AEVLSEEPILK	99.7%	65.9	25	56.2	2	0	0	1227.68	369	379
Basic leucine zipper and W2 domain-containing protein 1	BZW1	BZW1_HUMAN	48.0	100.0%	3	3	6	0.01%	6.7%	GFEDEVKK	99.1%	35.3	25	23.8	2	0	0	951.48	127	134
Basic leucine zipper and W2 domain-containing protein 1	BZW1	BZW1_HUMAN	48.0	100.0%	3	3	6	0.01%	6.7%	LMELFPANK	99.7%	52.1	25	39.3	2	0	0	1062.57	215	223
Basic leucine zipper and W2 domain-containing protein 2	BZW2	BZW2_HUMAN	48.2	99.8%	2	2	4	0.00%	4.5%	EGIAASFAVK	99.7%	60.5	25	49.9	2	0	0	992.54	180	189

Basic leucine zipper and W2 domain-containing protein 2	BZW2	BZW2_HUMAN	48.2	99.8%	2	2	4	0.00%	4.5%	LLELFPVNR	99.7%	45.2	25	37.9	2	0	0	1100.65	216	224
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	6	6	15	0.01%	8.0%	ETGYVVERPSTTK	99.7%	64.6	25	57.3	1	0	0	1466.75	463	475
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	6	6	15	0.01%	8.0%	LLASTLVHSVK	99.7%	61.6	25	61	4	0	0	1167.71	570	580
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	6	6	15	0.01%	8.0%	MAPVPLDDSNRPASLTK	99.1%	35.4	25	35.4	1	0	0	1827.93	551	567
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	6	6	15	0.01%	8.0%	NTEEEGLKYK	99.7%	44.8	25	30.9	3	0	0	1210.60	430	439
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	6	6	15	0.01%	8.0%	SSFYPDGGDQETAK	99.7%	48.5	25	38.2	3	0	0	1501.64	319	332
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	6	6	15	0.01%	8.0%	TIAPQNAPR	99.4%	37.4	25	25	3	0	0	967.53	304	312
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	8	8	14	0.01%	14.3%	AYVAVDGIPQGVLER	99.7%	75.1	25	71.3	2	0	0	1586.85	443	457
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	8	8	14	0.01%	14.3%	GQVWINGFNLGR	99.7%	44.8	25	44.2	1	0	0	1360.71	579	590
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	8	8	14	0.01%	14.3%	MFEIDYSR	99.7%	43.2	25	43.2	2	0	0	1060.48	31	38
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	8	8	14	0.01%	14.3%	SLYPLTFIQVK	99.7%	51.9	25	51.9	1	0	0	1308.76	400	410
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	8	8	14	0.01%	14.3%	TEAVASSLYDILAR	99.7%	77.1	25	65.7	2	0	0	1508.80	286	299
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	8	8	14	0.01%	14.3%	TVGAALDILCPSGPIK	99.7%	68.9	25	68.6	2	0	0	1611.88	384	399
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	8	8	14	0.01%	14.3%	VNYGAYINDFK	99.7%	54.9	25	46.9	2	0	0	1303.63	483	493
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	8	8	14	0.01%	14.3%	YISGSIHYSR	99.7%	63.7	25	61.2	2	0	0	1182.59	50	59
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	7	7	11	0.01%	19.1%	AVAQAGTVGTLLIVK	99.7%	101	25	100	2	0	0	1440.88	95	109
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	7	7	11	0.01%	19.1%	LEQPDPGAVAAAAILR	99.7%	46.4	25	44.9	2	0	0	1591.88	552	567
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	7	7	11	0.01%	19.1%	LSVLLLEK	99.7%	41.3	25	35.6	1	0	0	914.59	435	442
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	7	7	11	0.01%	19.1%	SPGADLLQVLTK	99.7%	82.9	25	73.1	2	0	0	1241.71	511	522
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	7	7	11	0.01%	19.1%	VAGALAEAGVGLEEIAK	99.7%	75.4	25	65.1	1	0	0	1597.88	163	179
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	7	7	11	0.01%	19.1%	VALLSGGGSGHEPAHAGFIGK	98.0%	26.3	25	21.5	0	1	0	1962.02	49	69
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	7	7	11	0.01%	19.1%	VAPAEPQEAPDSTAAGGSASK	99.7%	73.1	25	71.8	2	0	0	1940.92	352	372
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	AALLNQHYQVNFK	99.7%	47	25	46.9	2	0	0	1545.82	217	229
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	AYVDDTPAEQMK	99.7%	61.3	25	61.3	4	0	0	1383.61	289	300
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	DQDLEPGAPSMGAK	99.7%	62.7	25	42.2	4	0	0	1431.64	1464	1477
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	EYIPGQPPLSQSSDSSPTR	99.7%	50.8	25	45.9	2	0	0	2045.98	871	889
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	FVELPGAEMGK	99.7%	43.2	25	32.3	4	0	0	1177.59	187	197
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	GDIIQLQR	99.7%	51.1	25	25.2	2	0	0	942.54	667	674
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	GNAAWQEQLK	99.3%	36.6	25	24.2	2	0	0	1144.57	130	139
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	GSQFGQSCCLR	99.7%	46.3	25	46.3	3	0	0	1299.56	329	339
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	INEAVECLLSLK	99.7%	82.4	25	74.6	6	0	0	1388.75	850	861
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	KPYIWEYSR	98.4%	33	25	21.1	2	0	0	1241.63	417	425
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	KVIDPVAPR	99.5%	38.2	25	31.1	2	0	0	994.60	498	506
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	LGVENCYFPMFVSQSALEK	95.7%	28.9	25	28.9	1	0	0	2235.05	1071	1089
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	LLSVNIR	98.4%	33.1	25	17.1	1	0	0	814.51	1334	1340
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	LNLNNTVLSK	99.7%	60.5	25	47.8	4	0	0	1115.64	426	435
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	LNQWCNVVR	99.7%	62.2	25	51.5	2	0	0	1188.59	1144	1152
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	LTVAENEAETK	99.7%	70.3	25	69.7	8	0	0	1204.61	1390	1400
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	MFEIVFEDPK	99.7%	63.8	25	44.5	2	0	0	1254.61	1251	1260
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	NPEVGLKPVWYSPK	99.7%	59.5	25	59.5	2	0	0	1613.87	536	549
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	NQGGGLSSSGAGEGQGPK	99.7%	96.8	25	96.8	6	0	0	1587.74	992	1009
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	NSEPAGLETPEAK	99.7%	57.3	25	45.2	4	0	0	1342.65	890	902
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	SCQFVAVR	99.7%	48.6	25	34.1	4	0	0	966.48	1376	1383
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	SLIGVEYKPVSATGAEDKDK	97.7%	25.9	25	25.9	0	1	0	2107.09	944	963
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	SLYDEVAAQGEVVR	99.7%	100	25	94.3	5	0	0	1535.77	825	838
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	TGQEYKPGNPPAEIGQNISSNSSASILESK	99.7%	55.2	25	55.2	0	3	0	3103.52	795	824
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	VASQGEVVR	99.7%	59.9	25	45.3	4	0	0	944.52	908	916
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	VAVQGDVVR	99.7%	57.5	25	42.8	4	0	0	942.54	757	765
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	VIDPVAPR	99.7%	42.5	25	42.5	4	0	0	866.51	499	506
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	28	31	90	0.09%	22.9%	WFGFLEAQQAFQSVGTK	99.3%	36.5	25	30.4	2	0	0	1943.97	150	166
Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	MTHFD2	MTDC_HUMAN	37.9	100.0%	5	5	7	0.01%	21.4%	AGYITPVPGGVGPMTVAMLMK	99.7%	44.8	25	44.8	1	0	0	2090.09	302	322

Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	MTHFD2	MTDC_HUMAN	37.9	100.0%	5	5	7	0.01%	21.4%	EGAAVIDVGINR	99.7%	68.8	25	53.3	2	0	0	1213.65	267	278
Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	MTHFD2	MTDC_HUMAN	37.9	100.0%	5	5	7	0.01%	21.4%	ICNAVSPDKDVDGFHVINVGR	99.7%	34.1	25	34.1	0	1	0	2312.15	144	164
Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	MTHFD2	MTDC_HUMAN	37.9	100.0%	5	5	7	0.01%	21.4%	LVGDVDFEGVR	99.7%	55.6	25	39.2	2	0	0	1205.62	289	299
Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	MTHFD2	MTDC_HUMAN	37.9	100.0%	5	5	7	0.01%	21.4%	VHDPVTAKPK	95.3%	28.5	25	28.2	1	0	0	1091.62	279	288
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	8	8	14	0.01%	10.4%	ANSSVVSVNCK	99.7%	66.2	25	66.2	2	0	0	1164.57	587	597
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	8	8	14	0.01%	10.4%	EIPVESIEEVSK	99.7%	64.8	25	55.7	2	0	0	1358.71	258	269
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	8	8	14	0.01%	10.4%	ESQATLEER	99.1%	35.6	25	25	1	0	0	1062.51	5	13
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	8	8	14	0.01%	10.4%	GGLAGEFQR	97.7%	31.5	25	27.4	1	0	0	934.47	683	691
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	8	8	14	0.01%	10.4%	LGCFEIAK	99.7%	43.5	25	35	2	0	0	937.48	894	901
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	8	8	14	0.01%	10.4%	LLPGIEVLWTGPK	99.7%	41.2	25	38.5	2	0	0	1422.84	241	253
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	8	8	14	0.01%	10.4%	LLPIDGANDLFFQPPPLTPTSK	99.7%	51.9	25	51.9	2	0	0	2381.28	692	713
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	8	8	14	0.01%	10.4%	WELNTYLYAPK	99.7%	78.8	25	78.8	2	0	0	1397.71	88	98
Bifunctional purine biosynthesis protein PURH	ATIC	PUR9_HUMAN	64.6	100.0%	3	3	3	0.00%	7.3%	DVSELTGFPEMLGGR	96.2%	29.4	25	29.4	1	0	0	1623.77	50	64
Bifunctional purine biosynthesis protein PURH	ATIC	PUR9_HUMAN	64.6	100.0%	3	3	3	0.00%	7.3%	NLTALGLNLVASGGTAK	98.9%	34.7	25	32.5	1	0	0	1599.91	23	39
Bifunctional purine biosynthesis protein PURH	ATIC	PUR9_HUMAN	64.6	100.0%	3	3	3	0.00%	7.3%	YTQSNSVCYAK	99.7%	40.4	25	40.4	1	0	0	1320.59	427	437
Biliverdin reductase A	BLVRA	BIEA_HUMAN	33.4	99.8%	2	2	2	0.00%	8.1%	FGVVVVGVGR	99.7%	45.3	25	45.3	1	0	0	988.59	9	18
Biliverdin reductase A	BLVRA	BIEA_HUMAN	33.4	99.8%	2	2	2	0.00%	8.1%	SGSLENVPNVGVNK	99.7%	63.9	25	63.9	1	0	0	1413.73	235	248
BolA-like protein 2	BOLA2	BOLA2_HUMAN	10.1	99.9%	2	3	6	0.01%	29.1%	DLEAEHVEVEDTTLNR	99.7%	97	25	97	2	2	0	1869.88	15	30
BolA-like protein 2	BOLA2	BOLA2_HUMAN	10.1	99.9%	2	3	6	0.01%	29.1%	FEGKPLLQR	99.7%	49.4	25	49.1	2	0	0	1087.63	44	52
Bromodomain adjacent to zinc finger domain protein 1A	BAZ1A	BAZ1A_HUMAN	178.7	100.0%	3	3	5	0.00%	2.3%	DFIEDYVDILR	99.7%	47.9	25	47.7	2	0	0	1397.69	632	642
Bromodomain adjacent to zinc finger domain protein 1A	BAZ1A	BAZ1A_HUMAN	178.7	100.0%	3	3	5	0.00%	2.3%	IQSAIACTNIFPLGR	99.7%	82.7	25	77.3	2	0	0	1660.88	793	807
Bromodomain adjacent to zinc finger domain protein 1A	BAZ1A	BAZ1A_HUMAN	178.7	100.0%	3	3	5	0.00%	2.3%	IYQGTLGAIK	96.7%	29.9	25	25.4	1	0	0	1063.61	990	999
Bystin	BYSL	BYST_HUMAN	49.6	100.0%	4	4	5	0.00%	9.4%	EAIIVGSIITK	99.7%	58.1	25	51.8	1	0	0	1143.70	304	314
Bystin	BYSL	BYST_HUMAN	49.6	100.0%	4	4	5	0.00%	9.4%	EALLELLR	96.6%	29.8	25	22.5	1	0	0	956.58	399	406
Bystin	BYSL	BYST_HUMAN	49.6	100.0%	4	4	5	0.00%	9.4%	FYNLVLLPR	99.7%	52.4	25	41.1	2	0	0	1134.67	249	257
Bystin	BYSL	BYST_HUMAN	49.6	100.0%	4	4	5	0.00%	9.4%	GTGEAEEEYVGPR	99.7%	73.4	25	59	1	0	0	1393.62	41	53
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	AAEEIGIK	99.7%	52.4	25	33.9	2	0	0	830.46	59	66
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	AAQAPSSFQLLYDLK	99.7%	96.3	25	94.2	2	0	0	1651.87	805	819
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	APAEILNGK	99.7%	42.3	25	39.6	1	0	0	912.52	2	10
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	AYIQENLELVEK	99.7%	65.7	25	57.9	2	0	0	1448.76	722	733
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	DDSNLYINVK	99.7%	67.6	25	61.2	2	0	0	1180.58	47	56
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	EIGLLSEEVELYGETK	99.7%	101	25	101	3	0	0	1808.92	337	352
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	EQVPGFTPR	98.5%	33.1	25	24.4	3	0	0	1030.53	29	37
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	ETGVPIAGR	99.4%	37.2	25	30	2	0	0	899.49	158	166
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	FSDIQIR	99.7%	44.5	25	12.2	2	0	0	878.47	489	495
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	GALALAQAVQR	99.7%	87.5	25	80.9	4	0	0	1097.64	794	804
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	GDLNDCFIPCTPK	99.7%	46.4	25	46.4	2	0	0	1536.68	138	150
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	GEPVSAEDLGVSGALTVLMK	99.7%	51.1	25	51.1	1	0	0	1973.03	597	616
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	GVPTGFILPIR	99.7%	64.7	25	62.5	4	0	0	1169.70	879	889
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	IFHELTQTDK	99.7%	53.5	25	37.5	2	2	0	1231.63	464	473
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	ITIGQAPTEK	99.4%	37.2	25	34	1	0	0	1057.59	544	553
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	IYGADDIELLPEAQHK	99.7%	70.1	25	64.1	2	2	0	1811.92	833	848
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	KGEPVSAEDLGVSGALTVLMK	99.7%	40.8	25	40.4	0	2	0	2117.12	596	616
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	KITIGQAPTEK	99.7%	62.1	25	33.2	3	0	0	1185.68	543	553
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	KVVGDVAYDEAK	99.7%	67.7	25	62.5	2	0	0	1293.67	251	262
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	LAILQVGNR	99.7%	65.2	25	54.7	2	0	0	983.60	38	46
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	LDIDPETITWQR	99.7%	78.9	25	78.2	2	0	0	1486.75	521	532
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	LVGPEGFVVTEAGFGADIGMEK	99.7%	114	25	113	4	3	0	2239.10	658	679
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	MFGIPVVVAVNAFK	99.7%	74.1	25	74.1	5	0	0	1507.83	747	760
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	MHGGGPTVTAGLPLPK	99.7%	61.1	25	61.1	1	0	0	1532.83	706	721
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	QGFGNLPICMAK	95.1%	28.4	25	25.4	1	0	0	1335.66	855	866

C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	RFSDIQIR	97.1%	30.5	25	20.9	1	0	0	1034.57	488	495
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	TAHLDEEVNKGDILVVATGQPEMVK	99.7%	57.9	25	57.9	0	2	0	2709.38	199	223
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	TDPTTLTDEEINR	99.7%	73.9	25	68.2	2	0	0	1504.71	505	517
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	TDTESELDLISR	99.7%	90.8	25	83.3	2	0	0	1378.67	761	772
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	THLSLSHNPEQK	99.7%	68.8	25	68.3	2	2	0	1390.71	867	878
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	TPVPSDIDISR	99.7%	67	25	67	2	0	0	1199.63	314	324
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	VLLSALER	99.7%	64.2	25	46.2	5	0	0	900.55	355	362
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	VVGDVAYDEAK	99.7%	68.7	25	66.2	2	0	0	1165.57	252	262
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	VVGDVAYDEAKER	99.7%	59.6	25	55.8	1	0	0	1450.72	252	264
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	WMIQYNNLNLK	99.7%	55.5	25	35.9	4	0	0	1436.74	303	313
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	YSGLCPHVVVLVATVR	99.7%	60.8	25	60.8	0	2	0	1769.97	687	702
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	37	44	93	0.09%	44.1%	YVVVTGITPTPLGEGK	99.7%	103	25	103	2	0	0	1630.91	371	386
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	AAFALGGLGSGFASNR	99.7%	107	25	107	2	0	0	1495.77	556	571
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	AHWTPFEGQK	96.0%	29.1	25	27	1	0	0	1200.58	1769	1778
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	ASDPGLPAEEPK	99.7%	50.4	25	50.4	2	0	0	1210.60	1858	1869
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	ATGYPLAYVAAK	99.7%	50.5	25	50.5	2	0	0	1224.66	697	708
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	EATAGNPGGQTVR	99.7%	60.3	25	59.7	3	0	0	1257.62	359	371
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	ELSDLESAR	99.6%	39.2	25	33	2	0	0	1019.50	1067	1075
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	FLSSAAAVSK	99.7%	62.3	25	50.4	2	0	0	980.54	1110	1119
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	GEVAYIDGQVLVPPGYGQDVR	99.7%	49.7	25	47	2	0	0	2232.13	1790	1810
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	GEVRPELGSR	98.3%	32.8	25	21.4	1	0	0	1099.59	1658	1667
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	GHNQPCLLVGSGR	99.7%	44.2	25	44	2	0	0	1394.70	275	287
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	GQPLPPDLLQQAK	96.8%	30	25	30	1	0	0	1404.78	855	867
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	IIAHAQLLEQHR	99.7%	37.1	25	35.9	0	2	0	1428.81	843	854
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	ILALDCGLK	99.7%	49.5	25	33.4	2	0	0	1002.57	178	186
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	KEEILLIK	97.6%	31.2	25	16.2	2	0	0	985.63	1618	1625
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	LCPPGIPTPGSGLPPPR	99.6%	39.4	25	37.9	2	0	0	1712.92	378	394
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	LFVEALGQIGPAPPLK	99.7%	48.2	25	46.5	2	0	0	1649.96	1435	1450
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	LGGAVLSFSEATSSVQK	99.7%	101	25	101	2	0	0	1680.88	1987	2003
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	LGYPVLVR	99.7%	42.1	25	32.8	2	0	0	916.56	548	555
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	LLDTIGISQPQWR	99.7%	72.5	25	72.5	2	0	0	1526.83	1054	1066
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	LYLNETFSELR	99.7%	48.2	25	38.4	2	0	0	1384.71	1557	1567
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	MAEIGEHVAPSEAANSLEQAQAAAER	99.7%	49.8	25	49.8	0	2	0	2680.26	522	547
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	NILLTIGSYK	99.7%	41.4	25	33.4	2	0	0	1121.66	1314	1323
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	NKSELLPTVR	99.7%	42.7	25	36.1	2	0	0	1156.67	1324	1333
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	NSVTGGTAAFEPSVDYCVVK	99.7%	99.9	25	95.8	2	0	0	2100.99	720	739
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	QELGICPAVK	96.8%	30.1	25	5.37	1	0	0	1114.59	892	901
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	SFEEAFQK	99.1%	35.5	25	28.5	2	0	0	985.46	771	778
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	SILEQLAEK	99.7%	53.5	25	40	2	0	0	1030.58	1379	1387
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	SVGEVMGIGR	99.7%	53.5	25	45	4	0	0	1020.51	761	770
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	SVHICHVAR	98.6%	33.5	25	23.9	1	0	0	1078.56	1609	1617
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	TLGVDLVALATR	99.7%	77.3	25	65.1	2	0	0	1228.73	1229	1240
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	TPHVLVLGSGVYR	99.7%	46.9	25	46.9	1	2	0	1397.79	932	944
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	TSSSFAAAMAR	99.7%	78.4	25	78.3	4	0	0	1115.51	1976	1986
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	VFNTGGAPR	99.7%	47.3	25	36.4	2	0	0	918.48	169	177
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	VHVDCMTSQK	99.6%	39.4	25	31.4	1	0	0	1204.55	1451	1460
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	VIMGEEVEPVGLMTGSGVVGVK	99.7%	79.6	25	79.6	6	0	0	2187.14	1241	1262
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	VLGTPVETIELTEDR	99.7%	58.9	25	58.1	1	0	0	1671.88	501	515
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	VLGTSPEAIDSAENR	99.7%	110	25	109	2	0	0	1558.77	1034	1048
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	VNEISVEVDSDPR	99.7%	105	25	93.8	2	0	0	1458.71	2188	2200
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	39	43	81	0.08%	22.0%	VPQFSFSR	99.7%	41.7	25	35.5	2	0	0	967.50	1263	1270

Calcium uniporter protein, mitochondrial	MCU	MCU_HUMAN	39.9	100.0%	3	3	4	0.00%	9.1%	LEDLKEQLAPLEK	99.7%	69.8	25	63	1	0	0	1525.85	207	219
Calcium uniporter protein, mitochondrial	MCU	MCU_HUMAN	39.9	100.0%	3	3	4	0.00%	9.1%	QEYVYPEAR	97.8%	31.5	25	19.3	1	0	0	1154.55	287	295
Calcium uniporter protein, mitochondrial	MCU	MCU_HUMAN	39.9	100.0%	3	3	4	0.00%	9.1%	VAIYSPDGVR	98.9%	34.5	25	23.1	2	0	0	1076.57	125	134
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	AGQTTYSGVIDCFR	99.7%	83.1	25	83.1	2	0	0	1574.73	552	565
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	AGQTTYSGVIDCFRK	99.7%	73.6	25	73.6	2	0	0	1702.82	552	566
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	DLGIFGLYK	98.5%	33.3	25	31.6	1	0	0	1025.57	474	482
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	GLIPQLIGVAPEK	99.7%	66.6	25	0	4	0	0	1334.80	391	403
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	IVQLLAGVADQTK	99.7%	66.5	25	59.5	2	0	0	1355.79	56	68
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	KIYSTLAGTR	99.7%	52.8	25	40.1	2	0	0	1109.63	234	243
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	LATATFAGIENK	99.7%	79.8	25	64	2	0	0	1235.66	641	652
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	LQVAGEITTGPR	99.7%	62.8	25	51.2	2	0	0	1241.69	454	465
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	LTVNDFVR	99.7%	65.1	25	56.1	2	0	0	963.53	407	414
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	NIFLQYASTEVDGER	99.7%	90.2	25	83.2	2	0	0	1741.84	18	32
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	VSALNVLR	99.7%	73.4	25	51.4	2	0	0	871.54	466	473
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	5	5	9	0.01%	18.3%	YEGFFGLYR	99.7%	58.8	25	53.5	2	0	0	1151.55	382	390
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	41	0.04%	36.7%	AGQTTYSGVIDCFR	99.7%	83.1	25	83.1	2	0	0	1574.73	554	567
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	41	0.04%	36.7%	AGQTTYSGVIDCFRK	99.7%	73.6	25	73.6	2	0	0	1702.82	554	568
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	41	0.04%	36.7%	ASGDSARPVLLQVAESAYR	99.7%	56.8	25	55.9	1	2	0	1990.04	313	331
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	41	0.04%	36.7%	DIPFSAIYFPCYAHVK	99.4%	37.4	25	19.1	2	0	0	1927.94	493	508
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	41	0.04%	36.7%	DLGFFGIYK	99.7%	44.5	25	41.7	2	0	0	1059.55	476	484
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	41	0.04%	36.7%	FGLGSVAGAVGATAVYPIDLVK	99.7%	73.7	25	73.7	2	0	0	2105.16	332	353
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	41	0.04%	36.7%	GLLPQLLGVAPEK	99.7%	66.6	25	0	4	0	0	1334.80	393	405
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	41	0.04%	36.7%	IAPLEEGTLPFNLAEAQR	99.7%	86.2	25	86.2	2	1	0	1969.04	293	310
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	41	0.04%	36.7%	KIYSTLAGTR	99.7%	52.8	25	40.1	2	0	0	1109.63	235	244
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	41	0.04%	36.7%	LAVATFAGIENK	99.7%	91	25	84.6	2	0	0	1233.68	642	653
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	41	0.04%	36.7%	LQVAGEITTGPR	99.7%	62.8	25	51.2	2	0	0	1241.69	456	467
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	41	0.04%	36.7%	LTVNDFVR	99.7%	65.1	25	56.1	2	0	0	963.53	409	416
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	41	0.04%	36.7%	MTLADIER	99.7%	49.4	25	43	2	0	0	948.48	285	292
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	41	0.04%	36.7%	NGEFFMSPNDFVTR	99.7%	57.2	25	53.5	1	0	0	1676.74	30	43
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	41	0.04%	36.7%	SSPQFGVTLLTYELLQR	99.7%	73	25	73	1	0	0	1952.05	589	605
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	41	0.04%	36.7%	STGSFVGELMYK	99.7%	53.7	25	42.7	2	0	0	1318.63	361	372
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	41	0.04%	36.7%	TVELLSGVVDQTK	99.7%	98.8	25	89.6	2	0	0	1388.76	57	69
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	41	0.04%	36.7%	VSALSVVR	99.7%	52.1	25	44.4	2	0	0	830.51	468	475
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	41	0.04%	36.7%	YEGFFGLYR	99.7%	58.8	25	53.5	2	0	0	1151.55	384	392
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	20	22	41	0.04%	36.7%	YLNIFGESQPNPK	99.7%	65.6	25	65.6	1	0	0	1506.76	44	56
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	10	11	19	0.02%	23.9%	EGIPGLYR	96.5%	29.7	25	19.8	1	0	0	904.49	438	445
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	10	11	19	0.02%	23.9%	FWAYEQYKK	99.7%	42.6	25	35.1	2	0	0	1262.62	269	277
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	10	11	19	0.02%	23.9%	HEGLGAFYK	99.0%	34.9	25	34.9	2	0	0	1021.51	337	345
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	10	11	19	0.02%	23.9%	MNIFGGFR	99.7%	49	25	39.8	2	0	0	941.47	232	239
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	10	11	19	0.02%	23.9%	NGDGVVDIGELQEGLR	99.7%	95.1	25	95.1	2	0	0	1670.83	34	49
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	10	11	19	0.02%	23.9%	NLGIPLGQDAEEK	99.7%	49.3	25	48.4	2	0	0	1383.71	50	62
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	10	11	19	0.02%	23.9%	QLLAGGIAGAVSR	99.7%	105	25	97.9	2	0	0	1212.71	197	209
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	10	11	19	0.02%	23.9%	TGQYSGIYDCAK	99.7%	66.5	25	66.5	2	0	0	1362.60	321	332
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	10	11	19	0.02%	23.9%	VLPAVGISYVVYENMK	99.7%	81.2	25	74.6	3	0	0	1797.95	454	469
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	10	11	19	0.02%	23.9%	YETLFQALDR	99.0%	34.9	25	19.1	1	0	0	1255.63	24	33
Calmodulin-like protein 5	CALML5	CALL5_HUMAN	15.9	99.8%	2	2	4	0.00%	21.2%	AFSAVDTDGNGTINAQELGAALK	99.7%	123	25	123	2	0	0	2263.12	16	38
Calmodulin-like protein 5	CALML5	CALL5_HUMAN	15.9	99.8%	2	2	4	0.00%	21.2%	NLSEAQLR	99.7%	41.5	25	24.1	2	0	0	930.50	43	50
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	3	3	4	0.00%	3.3%	ASPAAPADGAAPAQPSIR	99.7%	78.3	25	78.3	1	0	0	1647.85	192	209
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	3	3	4	0.00%	3.3%	AVASSPAATNSEVK	99.7%	58.4	25	53.9	2	0	0	1331.68	550	563
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	3	3	4	0.00%	3.3%	SLDQYDFSR	96.5%	29.7	25	29.7	1	0	0	1130.51	23	31
Calpain-2 catalytic subunit	CAPN2	CAN2_HUMAN	80.0	99.8%	2	2	4	0.00%	2.6%	SDGFSIETCK	99.4%	37.5	25	37.5	2	0	0	1143.50	569	578

Calpain-2 catalytic subunit	CAPN2	CAN2_HUMAN	80.0	99.8%	2	2	4	0.00%	2.6%	SDTFINLR	99.7%	58.2	25	26.5	2	0	0	965.51	462	469
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	4	4	6	0.01%	11.1%	ILQAVNFPFLVR	99.7%	67.2	25	58.4	2	0	0	1416.84	95	106
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	4	4	6	0.01%	11.1%	KVEAPFIPK	98.5%	33.3	25	22.1	1	0	0	1028.61	310	318
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	4	4	6	0.01%	11.1%	NLLQVDLTK	98.4%	33	25	19.3	1	0	0	1043.61	272	280
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	KAPCB_HUMAN	40.6	100.0%	4	4	6	0.01%	11.1%	TLGTGSFGR	99.7%	43.2	25	43.2	2	0	0	895.46	49	57
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	6	8	16	0.02%	36.3%	GKPLALVEEIR	99.7%	55.2	25	54.7	2	2	0	1224.73	149	159
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	6	8	16	0.02%	36.3%	HVFLTGPPGVGK	99.7%	61.9	25	61.9	2	0	0	1208.68	4	15
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	6	8	16	0.02%	36.3%	IGFDVVTLSGTR	99.7%	84.6	25	79.7	2	0	0	1264.69	48	59
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	6	8	16	0.02%	36.3%	QTLSTPGTIILGTIPVPK	99.7%	80.1	25	80.1	2	0	0	1836.08	131	148
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	6	8	16	0.02%	36.3%	RIGFDVVTLSGTR	99.7%	49	25	49	2	2	0	1420.79	47	59
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	6	8	16	0.02%	36.3%	SSGVPVDGFYTEEVR	99.7%	97.1	25	91.9	2	0	0	1641.78	28	42
Carbamoyl-phosphate synthase [ammonia], mitochondrial	CPS1	CPSM_HUMAN	164.9	100.0%	3	3	5	0.00%	2.9%	IALGIPLPEIK	99.7%	42.9	25	28.3	2	0	0	1163.74	741	751
Carbamoyl-phosphate synthase [ammonia], mitochondrial	CPS1	CPSM_HUMAN	164.9	100.0%	3	3	5	0.00%	2.9%	IAPSFAVESIEDALK	99.7%	71.9	25	66.4	2	0	0	1589.84	561	575
Carbamoyl-phosphate synthase [ammonia], mitochondrial	CPS1	CPSM_HUMAN	164.9	100.0%	3	3	5	0.00%	2.9%	TAVDSGIPLLTNFQVTK	99.7%	57.9	25	49	1	0	0	1803.99	1455	1471
Carbonic anhydrase 2	CA2	CAH2_HUMAN	29.2	99.8%	2	2	3	0.00%	9.6%	AVQQPDGLAVLGIFLK	99.7%	53.7	25	53.7	2	0	0	1668.97	133	148
Carbonic anhydrase 2	CA2	CAH2_HUMAN	29.2	99.8%	2	2	3	0.00%	9.6%	GGPLDGTYR	99.7%	40.7	25	33.9	1	0	0	935.46	81	89
Carbonyl reductase [NADPH] 1	CBR1	CBR1_HUMAN	30.4	100.0%	3	3	5	0.00%	17.3%	EYGGLDVLVNNAGIAFK	99.7%	97.9	25	97.9	2	0	0	1779.93	80	96
Carbonyl reductase [NADPH] 1	CBR1	CBR1_HUMAN	30.4	100.0%	3	3	5	0.00%	17.3%	GQAAVQQLQAEGLSPR	99.7%	108	25	97.8	2	0	0	1652.87	43	58
Carbonyl reductase [NADPH] 1	CBR1	CBR1_HUMAN	30.4	100.0%	3	3	5	0.00%	17.3%	SETITEEELVGLMNK	99.7%	58.2	25	58.2	1	0	0	1692.84	160	174
Cartilage-associated protein	CRTAP	CRTAP_HUMAN	46.6	100.0%	3	4	6	0.01%	7.7%	FLQFAYFK	97.0%	30.3	25	10.3	1	0	0	1063.56	150	157
Cartilage-associated protein	CRTAP	CRTAP_HUMAN	46.6	100.0%	3	4	6	0.01%	7.7%	SYESLFIR	99.4%	37.2	25	32.7	1	0	0	1014.53	205	212
Cartilage-associated protein	CRTAP	CRTAP_HUMAN	46.6	100.0%	3	4	6	0.01%	7.7%	TSITDMELALPDFFK	99.7%	60.9	25	58	4	0	0	1727.86	224	238
Casein kinase II subunit alpha'	CSNK2A2	CSK22_HUMAN	41.2	99.8%	2	2	3	0.00%	6.0%	VLGTEELYGYLK	99.3%	36.7	25	29.8	1	0	0	1384.74	249	260
Casein kinase II subunit alpha'	CSNK2A2	CSK22_HUMAN	41.2	99.8%	2	2	3	0.00%	6.0%	VYAEVNSLR	99.7%	67.2	25	46.9	2	0	0	1050.56	12	20
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	11	22	0.02%	26.2%	ATHDGAPELGAGGTR	99.7%	67.4	25	66.2	2	2	0	1409.68	332	346
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	11	22	0.02%	26.2%	LFSEYHEK	99.7%	40.8	25	25.7	2	0	0	1052.50	125	132
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	11	22	0.02%	26.2%	LVNSQGQLR	99.7%	52.7	25	44.2	2	0	0	1014.57	74	82
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	11	22	0.02%	26.2%	MAFPLLDMVDLER	99.7%	49.7	25	39.1	6	0	0	1565.77	162	174
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	11	22	0.02%	26.2%	MLVSGQGPVMENAQGLGFR	99.7%	91.3	25	90.2	2	0	0	2022.97	134	152
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	11	22	0.02%	26.2%	NPQSTEPVLGGGEPPFHGHR	99.0%	29.2	25	29.2	0	1	0	2113.02	370	389
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	11	22	0.02%	26.2%	NVVTVDELR	99.7%	47.9	25	35.2	2	0	0	1044.57	153	161
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	11	22	0.02%	26.2%	RLVNSQGQLR	95.8%	29	25	15	1	0	0	1170.67	73	82
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	9	11	22	0.02%	26.2%	VPVVFVTNAGNILQHSK	99.7%	95.3	25	93.3	2	0	0	1823.02	83	99
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	10	16	0.02%	12.2%	AAALVLQTIWGYK	99.7%	66.9	25	66.9	2	0	0	1433.82	821	833
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	10	16	0.02%	12.2%	ALSAIADLLTNEHER	99.7%	88	25	83.7	2	1	0	1652.86	711	725
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	10	16	0.02%	12.2%	FVGDADLER	99.2%	36.3	25	23.1	1	0	0	1021.50	69	77
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	10	16	0.02%	12.2%	GIPVLVGLLDHPK	99.7%	57.8	25	57.8	2	0	0	1357.82	409	421
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	10	16	0.02%	12.2%	GYELLFQPEVVR	99.7%	61.1	25	49.9	4	0	0	1449.77	655	666
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	10	16	0.02%	12.2%	QDVYGPQPQVR	99.7%	42	25	26.8	1	0	0	1286.65	254	264
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	10	16	0.02%	12.2%	SLDNNYSTPNER	99.7%	41.5	25	41.5	1	0	0	1409.63	899	910
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	10	16	0.02%	12.2%	VGGSSVDLHR	99.7%	54.1	25	39.7	1	0	0	1026.53	265	274
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	10	16	0.02%	12.2%	YQEAAPNVANNTGPHAASCFGAK	99.2%	29.9	25	29.9	0	1	0	2375.08	600	622
CCAAT/enhancer-binding protein zeta	CEBPZ	CEBPZ_HUMAN	121.0	100.0%	6	6	8	0.01%	6.9%	ALLVQVVNK	99.7%	49.3	25	46.5	2	0	0	983.62	382	390
CCAAT/enhancer-binding protein zeta	CEBPZ	CEBPZ_HUMAN	121.0	100.0%	6	6	8	0.01%	6.9%	AYPYSQTGDDKVR	99.7%	48.3	25	38.4	1	0	0	1499.71	493	505
CCAAT/enhancer-binding protein zeta	CEBPZ	CEBPZ_HUMAN	121.0	100.0%	6	6	8	0.01%	6.9%	EESQIPVDEVFFHR	99.4%	37.5	25	37.4	1	0	0	1731.83	803	816
CCAAT/enhancer-binding protein zeta	CEBPZ	CEBPZ_HUMAN	121.0	100.0%	6	6	8	0.01%	6.9%	ELLITDLLPDNR	99.7%	41.4	25	39.1	1	0	0	1411.78	291	302
CCAAT/enhancer-binding protein zeta	CEBPZ	CEBPZ_HUMAN	121.0	100.0%	6	6	8	0.01%	6.9%	FTDADKETEIVK	99.7%	55.4	25	49.2	1	0	0	1395.70	647	658
CCAAT/enhancer-binding protein zeta	CEBPZ	CEBPZ_HUMAN	121.0	100.0%	6	6	8	0.01%	6.9%	GKENTDSVVMQPK	99.7%	66	25	63	2	0	0	1448.71	769	781
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	13	13	19	0.02%	6.1%	EPLLMSISTNLK	99.7%	44.3	25	44.3	1	0	0	1345.74	1459	1470
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	13	13	19	0.02%	6.1%	EVTAAQVAR	99.7%	43.3	25	30	2	0	0	944.52	284	292
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	13	13	19	0.02%	6.1%	GAFGVGQEQIDAFLK	99.7%	72.1	25	71.4	2	0	0	1579.81	194	208

CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	13	13	19	0.02%	6.1%	GNAPEGLPQLMEVVR	99.7%	44	25	40.5	1	0	0	1609.84	1800	1814
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	13	13	19	0.02%	6.1%	IVEPPENIQEK	99.7%	45.6	25	45.6	1	0	0	1295.68	1088	1098
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	13	13	19	0.02%	6.1%	LATEFELRK	95.7%	28.9	25	27.4	1	0	0	1106.62	1523	1531
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	13	13	19	0.02%	6.1%	NLDEQLSAPK	99.7%	45.4	25	36.5	2	0	0	1114.57	1311	1320
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	13	13	19	0.02%	6.1%	NLILSAFPR	99.7%	47.2	25	34.7	2	0	0	1030.60	2130	2138
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	13	13	19	0.02%	6.1%	SLLEVVVLSR	99.7%	69.8	25	22.3	2	0	0	1114.68	1641	1650
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	13	13	19	0.02%	6.1%	SNLQVSNEPGNR	97.5%	31	25	25.9	1	0	0	1314.64	2198	2209
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	13	13	19	0.02%	6.1%	SNYEAMIDR	99.2%	36.2	25	29.5	1	0	0	1114.48	1815	1823
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	13	13	19	0.02%	6.1%	SPVTFLSDLR	99.7%	73	25	63.3	2	0	0	1134.62	2188	2197
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	13	13	19	0.02%	6.1%	TVTVTRPTGVSFK	99.7%	64.8	25	52.6	1	0	0	1392.78	1051	1063
CCR4-NOT transcription complex subunit 2	CNOT2	CNOT2_HUMAN	59.7	99.8%	2	2	2	0.00%	5.6%	EGSGNPTPLINPLAGR	99.7%	70.6	25	70.6	1	0	0	1592.84	240	255
CCR4-NOT transcription complex subunit 2	CNOT2	CNOT2_HUMAN	59.7	99.8%	2	2	2	0.00%	5.6%	TNSMSSSGLGSPNR	99.7%	44	25	44	1	0	0	1410.63	155	168
CDGSH iron-sulfur domain-containing protein 3, mitochondrial	CISD3	CISD3_HUMAN	14.2	99.8%	2	2	3	0.00%	15.0%	MVALCTCK	97.9%	31.8	25	23.3	1	0	0	982.45	94	101
CDGSH iron-sulfur domain-containing protein 3, mitochondrial	CISD3	CISD3_HUMAN	14.2	99.8%	2	2	3	0.00%	15.0%	TPIKVELVAGK	98.8%	34.2	25	25	2	0	0	1154.71	45	55
CDP-diacylglycerol--inositol 3-phosphatidyltransferase	CDIPT	CDIPT_HUMAN	23.5	99.8%	2	3	12	0.01%	9.9%	MIDLSGNPVLR	99.7%	74.2	25	59.4	10	0	0	1214.66	122	132
CDP-diacylglycerol--inositol 3-phosphatidyltransferase	CDIPT	CDIPT_HUMAN	23.5	99.8%	2	3	12	0.01%	9.9%	NMAALDAADR	99.7%	49.9	25	47.1	2	0	0	1063.48	200	209
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	5	5	8	0.01%	6.0%	FAEFQYLQPGPPR	99.7%	59.3	25	57.9	1	0	0	1549.78	405	417
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	5	5	8	0.01%	6.0%	ILLTLGIR	99.7%	45.8	25	45.2	2	0	0	898.61	728	735
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	5	5	8	0.01%	6.0%	LAEAEETAR	99.7%	45.2	25	39	2	0	0	989.49	868	876
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	5	5	8	0.01%	6.0%	SPAPPLLHVAALGQK	99.5%	32.3	25	31.4	0	1	0	1498.87	124	138
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	5	5	8	0.01%	6.0%	VVTQNICQYR	99.6%	38.8	25	38	2	0	0	1280.64	748	757
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	5	5	8	0.01%	18.7%	IMESGSELSK	96.8%	30	25	24.4	1	0	0	1096.52	170	179
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	5	5	8	0.01%	18.7%	IYQWINELSSPETR	99.7%	87.3	25	73.5	1	0	0	1735.87	22	35
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	5	5	8	0.01%	18.7%	LTSLGVIGALVK	99.7%	83.1	25	76.8	2	0	0	1170.75	137	148
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	5	5	8	0.01%	18.7%	NLQEGQVTDPR	99.7%	56.6	25	43.5	2	0	0	1256.62	282	292
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	5	5	8	0.01%	18.7%	TVATFILQK	99.7%	63.7	25	47.7	2	0	0	1020.61	180	188
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	4	5	8	0.01%	7.8%	EFYEVVQSQR	99.7%	53.5	25	44.9	2	0	0	1284.62	9	18
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	4	5	8	0.01%	7.8%	LQEFLADMGLPLK	99.7%	50.5	25	43.4	3	0	0	1490.79	311	323
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	4	5	8	0.01%	7.8%	VQTFSIHFGFK	99.3%	36.9	25	28.1	1	0	0	1310.69	358	368
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	4	5	8	0.01%	7.8%	YVTDVGVLQR	99.7%	56.1	25	40.9	2	0	0	1149.63	238	247
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	15	17	39	0.04%	25.3%	AAGIEIQK	99.7%	46	25	35.5	2	0	0	829.48	193	200
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	15	17	39	0.04%	25.3%	ESDLPSAILQTSGVSEFTK	99.7%	122	25	122	5	0	0	2009.01	272	290
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	15	17	39	0.04%	25.3%	GGLNTPLHESDFSGVTPQR	99.6%	33.5	25	30.4	0	2	0	2011.98	381	399
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	15	17	39	0.04%	25.3%	GVDYNAEIPFEK	99.7%	58.3	25	58.3	2	0	0	1381.66	207	218
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	15	17	39	0.04%	25.3%	ILLGGYQSR	99.7%	61.1	25	39.3	4	0	0	1006.57	719	727
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	15	17	39	0.04%	25.3%	ILQEAQNLMALTNVDTPLK	99.7%	105	25	105	4	2	0	2112.14	362	380
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	15	17	39	0.04%	25.3%	LGLLGLPAPK	99.7%	73.9	25	73.9	4	0	0	978.63	478	487
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	15	17	39	0.04%	25.3%	LVLPAPQISDAELQEVVK	99.7%	93.2	25	92.6	3	0	0	1949.10	295	312
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	15	17	39	0.04%	25.3%	QVVQTPNTVLSTPFR	99.7%	72.2	25	62.8	2	0	0	1686.92	400	414
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	15	17	39	0.04%	25.3%	SGTTPKPVINSTPGR	99.6%	38.9	25	38.9	1	0	0	1511.82	427	441
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	15	17	39	0.04%	25.3%	TIAPIIGR	99.2%	36	25	36	1	0	0	840.53	84	91
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	15	17	39	0.04%	25.3%	TPSNGAEGLTPR	99.7%	91.1	25	81.1	1	0	0	1199.60	415	426
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	15	17	39	0.04%	25.3%	TVGFGTNNSEHITYLEHNPYEK	99.7%	46.6	25	46.6	0	2	0	2550.19	602	623
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	15	17	39	0.04%	25.3%	VGQASEIAR	99.7%	66.2	25	55.2	3	0	0	930.50	313	321
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	15	17	39	0.04%	25.3%	YADLLLEK	99.7%	45.9	25	40.6	1	0	0	964.54	788	795
Cell division cycle protein 16 homolog	CDC16	CDC16_HUMAN	71.7	99.8%	2	2	2	0.00%	2.9%	IYDALDNR	99.1%	35.4	25	26.8	1	0	0	979.48	139	146
Cell division cycle protein 16 homolog	CDC16	CDC16_HUMAN	71.7	99.8%	2	2	2	0.00%	2.9%	LCNEEQELLR	97.9%	31.9	25	27.1	1	0	0	1303.63	193	202
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	5	5	6	0.01%	9.9%	AWYGLGQTYEILK	99.7%	74.3	25	64.6	2	0	0	1541.80	401	413
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	5	5	6	0.01%	9.9%	IENMDTFSNLLYVR	99.2%	36	25	32.7	1	0	0	1714.85	297	310
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	5	5	6	0.01%	9.9%	MLVALGECYEK	94.6%	28	25	24.9	1	0	0	1328.62	435	445
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	5	5	6	0.01%	9.9%	MPFYCLYYYR	98.9%	34.5	25	31.6	1	0	0	1475.65	414	423

Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	5	5	6	0.01%	9.9%	YQNLIDVGFSK	99.7%	53.9	25	53.9	1	0	0	1283.66	251	261
Cell division cycle protein 27 homolog	CDC27	CDC27_HUMAN	91.9	99.8%	2	2	2	0.00%	3.0%	ESLVYFLIGK	98.8%	34.3	25	34.3	1	0	0	1168.66	736	745
Cell division cycle protein 27 homolog	CDC27	CDC27_HUMAN	91.9	99.8%	2	2	2	0.00%	3.0%	LAEGEQILSGGVFNK	99.7%	102	25	94.6	1	0	0	1561.82	85	99
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	6	6	10	0.01%	16.6%	DAVEQQGEVKK	96.6%	29.8	25	8.38	2	0	0	1230.63	176	186
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	6	6	10	0.01%	16.6%	EQDQRPLHPVANPHAEISTK	99.7%	59.8	25	59.8	0	1	0	2267.15	149	168
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	6	6	10	0.01%	16.6%	VFFTCNACGESVK	99.7%	55.6	25	54.3	1	0	0	1518.67	2	14
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	6	6	10	0.01%	16.6%	VFFTCNACGESVKK	99.7%	63.2	25	63.2	2	0	0	1646.77	2	15
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	6	6	10	0.01%	16.6%	VKDAVEQQGEVK	99.7%	88.1	25	53.4	2	0	0	1329.70	174	185
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	6	6	10	0.01%	16.6%	VRELLEQISAFDNVPR	99.7%	45.4	25	43.3	0	2	0	1886.01	94	109
Cellular nucleic acid-binding protein	CNBP	CNBP_HUMAN	19.5	99.8%	2	2	4	0.00%	11.9%	CGETGHVAINCSK	99.7%	63	25	51.7	2	0	0	1432.63	140	152
Cellular nucleic acid-binding protein	CNBP	CNBP_HUMAN	19.5	99.8%	2	2	4	0.00%	11.9%	TSEVNCYR	99.7%	44.6	25	37.3	2	0	0	1028.45	153	160
Cellular tumor antigen p53	TP53	P53_HUMAN	43.7	99.9%	2	2	6	0.01%	6.4%	ALPNNTSSSPQPK	99.7%	55	25	49	4	0	0	1340.68	307	319
Cellular tumor antigen p53	TP53	P53_HUMAN	43.7	99.9%	2	2	6	0.01%	6.4%	SVTCTYSPALNK	99.4%	37.7	25	37.6	2	0	0	1340.65	121	132
Centrin-2	CETN2	CETN2_HUMAN	19.7	99.8%	2	2	4	0.00%	14.5%	MISEIDKEGTGK	99.7%	51.2	25	51.2	2	0	0	1323.65	72	83
Centrin-2	CETN2	CETN2_HUMAN	19.7	99.8%	2	2	4	0.00%	14.5%	MNFGDFLTVMTQK	99.7%	65.5	25	47.3	2	0	0	1563.72	84	96
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	6	10	19	0.02%	35.3%	GAEHITTYTFNTHK	99.7%	72.9	25	72.9	2	2	0	1619.78	197	210
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	6	10	19	0.02%	35.3%	LLLDTFEYQGLVK	99.7%	102	25	87.2	2	0	0	1538.85	135	147
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	6	10	19	0.02%	35.3%	SGASGASAAPAASAAAALAPSATR	99.7%	89.6	25	89.6	2	0	0	1985.00	18	41
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	6	10	19	0.02%	35.3%	SMVTEEFNGSDWEK	99.7%	82.2	25	77.5	4	0	0	1658.70	248	261
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	6	10	19	0.02%	35.3%	SNPGGFGIAPHCLDEGTVR	99.7%	88.2	25	88.2	2	2	0	1983.93	229	247
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	6	10	19	0.02%	35.3%	SQAVEKPPSEKPR	98.9%	28.6	25	28.6	1	2	0	1452.78	53	65
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	6	6	7	0.01%	11.3%	AMGTLLNTAISEVIGK	99.7%	40.6	25	40.6	2	0	0	1633.88	652	667
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	6	6	7	0.01%	11.3%	DSVVLSLLK	99.7%	54.1	25	37.7	1	0	0	973.59	102	110
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	6	6	7	0.01%	11.3%	LAPILCDGTATFVDLVPGFR	99.7%	50.9	25	47	1	0	0	2162.13	563	582
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	6	6	7	0.01%	11.3%	NFSNMDDEENYSAASK	99.7%	86.1	25	86.1	1	0	0	1821.72	609	624
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	6	6	7	0.01%	11.3%	NLMTSEIHNTVK	99.7%	51.3	25	50.2	1	0	0	1402.70	413	424
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	6	6	7	0.01%	11.3%	QLLDLPLDTDLENEK	99.7%	47.2	25	47.2	1	0	0	1755.90	306	320
Chaperone activity of bc1 complex-like, mitochondrial	ADCK3	ADCK3_HUMAN	72.0	99.8%	2	2	2	0.00%	4.2%	AVLGSSPFLSEANAER	99.7%	105	25	92.1	1	0	0	1647.83	247	262
Chaperone activity of bc1 complex-like, mitochondrial	ADCK3	ADCK3_HUMAN	72.0	99.8%	2	2	2	0.00%	4.2%	TLNNDLGPNWR	99.6%	39.9	25	38.9	1	0	0	1299.64	315	325
Chitobiosyldiphosphodolichol beta-mannosyltransferase	ALG1	ALG1_HUMAN	52.5	99.8%	2	2	3	0.00%	5.6%	ETPLDLQHR	96.4%	29.6	25	21.7	1	0	0	1108.57	224	232
Chitobiosyldiphosphodolichol beta-mannosyltransferase	ALG1	ALG1_HUMAN	52.5	99.8%	2	2	3	0.00%	5.6%	IQIVGLTELQSLAVGPR	96.9%	30.2	25	30.2	2	0	0	1794.05	83	99
Chromatin target of PRMT1 protein	CHTOP	CHTOP_HUMAN	26.4	100.0%	5	9	25	0.02%	29.0%	ASMQQQQQLASAR	99.7%	105	25	91.4	13	0	0	1462.71	39	51
Chromatin target of PRMT1 protein	CHTOP	CHTOP_HUMAN	26.4	100.0%	5	9	25	0.02%	29.0%	EQLDNQLDAYMSK	99.7%	105	25	105	4	0	0	1570.71	214	226
Chromatin target of PRMT1 protein	CHTOP	CHTOP_HUMAN	26.4	100.0%	5	9	25	0.02%	29.0%	GHLDAELDAYMAQTDPETND	99.7%	86.5	25	86.5	1	0	0	2221.92	229	248
Chromatin target of PRMT1 protein	CHTOP	CHTOP_HUMAN	26.4	100.0%	5	9	25	0.02%	29.0%	LAQQMENRPSVQAALK	99.7%	56.4	25	33	4	2	0	1783.95	55	70
Chromatin target of PRMT1 protein	CHTOP	CHTOP_HUMAN	26.4	100.0%	5	9	25	0.02%	29.0%	NKQPTPVNIR	96.3%	29.4	25	18	1	0	0	1166.66	29	38
Chromobox protein homolog 3	CBX3	CBX3_HUMAN	20.8	99.8%	2	2	3	0.00%	14.8%	KVEEAEPEEFVVEK	99.7%	50.3	25	49.9	1	0	0	1661.83	21	34
Chromobox protein homolog 3	CBX3	CBX3_HUMAN	20.8	99.8%	2	2	3	0.00%	14.8%	WKDSDEADLVLAK	99.7%	52.2	25	35.4	2	0	0	1489.75	142	154
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	5	5	6	0.01%	6.5%	GGQAPGFLLR	99.7%	46.9	25	22.1	1	0	0	1015.57	10	19
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	5	5	6	0.01%	6.5%	GSVLIPGLVEGSTK	99.7%	48.6	25	34.7	2	0	0	1356.77	617	630
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	5	5	6	0.01%	6.5%	LLQPFLLR	95.6%	28.8	25	20.5	1	0	0	999.64	253	260
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	5	5	6	0.01%	6.5%	SFEQLVNLQK	99.7%	45.5	25	34.1	1	0	0	1205.65	591	600
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	5	5	6	0.01%	6.5%	YQDIEKESESASELHK	99.2%	30.3	25	30.3	0	1	0	1892.89	237	252
Chromodomain-helicase-DNA-binding protein 4	CHD4	CHD4_HUMAN	218.0	100.0%	9	10	16	0.02%	4.9%	APEPTPQQVAQQQ	99.7%	55.1	25	53.8	1	0	0	1421.70	1900	1912
Chromodomain-helicase-DNA-binding protein 4	CHD4	CHD4_HUMAN	218.0	100.0%	9	10	16	0.02%	4.9%	AYVSLFMR	99.4%	37.4	25	28.5	3	0	0	986.51	1458	1465
Chromodomain-helicase-DNA-binding protein 4	CHD4	CHD4_HUMAN	218.0	100.0%	9	10	16	0.02%	4.9%	GAADVEKVEEK	99.7%	45.9	25	23.9	2	0	0	1174.60	1637	1647
Chromodomain-helicase-DNA-binding protein 4	CHD4	CHD4_HUMAN	218.0	100.0%	9	10	16	0.02%	4.9%	IDGGITGNMR	98.7%	33.8	25	21.5	2	0	0	1049.50	1096	1105
Chromodomain-helicase-DNA-binding protein 4	CHD4	CHD4_HUMAN	218.0	100.0%	9	10	16	0.02%	4.9%	IGVMSLIR	99.6%	39.7	25	25.4	1	0	0	904.53	1496	1503
Chromodomain-helicase-DNA-binding protein 4	CHD4	CHD4_HUMAN	218.0	100.0%	9	10	16	0.02%	4.9%	NFEALNAR	98.7%	33.7	25	21.7	1	0	0	934.47	993	1000
Chromodomain-helicase-DNA-binding protein 4	CHD4	CHD4_HUMAN	218.0	100.0%	9	10	16	0.02%	4.9%	TVQTAVFLYSLYK	99.7%	44.8	25	44.8	2	0	0	1532.84	758	770
Chromodomain-helicase-DNA-binding protein 4	CHD4	CHD4_HUMAN	218.0	100.0%	9	10	16	0.02%	4.9%	VGGNIEVLGFNAR	99.7%	57.5	25	57.5	2	0	0	1345.72	1407	1419

Chromodomain-helicase-DNA-binding protein 4	CHD4	CHD4_HUMAN	218.0	100.0%	9	10	16	0.02%	4.9%	VLIFSQMTK	97.6%	31.2	25	27.6	2	0	0	1082.59	1069	1077
Chromosome transmission fidelity protein 18 homolog	CHTF18	CTF18_HUMAN	107.4	99.8%	2	2	3	0.00%	2.7%	NLIQTLVSGIAPATR	99.7%	62.4	25	62.4	1	0	0	1553.90	735	749
Chromosome transmission fidelity protein 18 homolog	CHTF18	CTF18_HUMAN	107.4	99.8%	2	2	3	0.00%	2.7%	VVQGLFDNFLR	99.7%	49	25	39	2	0	0	1307.71	648	658
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	23	25	64	0.06%	17.6%	ESNCYDPER	99.3%	36.5	25	36.5	1	0	0	1169.45	750	758
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	23	25	64	0.06%	17.6%	EVCFACVDGK	99.7%	48.3	25	48.3	3	0	0	1184.51	1255	1264
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	23	25	64	0.06%	17.6%	GQCDLELINVCNENSLFK	99.7%	82.2	25	82.2	3	0	0	2153.00	924	941
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	23	25	64	0.06%	17.6%	GQFSTDELVAEVEK	99.7%	68.3	25	64.8	1	0	0	1551.75	838	851
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	23	25	64	0.06%	17.6%	HELIEFR	98.9%	34.4	25	30.3	2	0	0	943.50	1502	1508
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	23	25	64	0.06%	17.6%	IHEGCEEPATHNALAK	99.7%	33.8	25	33.8	0	3	0	1776.83	866	881
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	23	25	64	0.06%	17.6%	ISGETIFVTAPHEATAGIIGVNR	99.7%	60.6	25	60.6	0	4	0	2353.25	298	320
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	23	25	64	0.06%	17.6%	IVLDNSVFSEHR	99.7%	68.2	25	68.2	4	1	0	1415.73	1011	1022
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	23	25	64	0.06%	17.6%	IYIDSNNNPER	99.7%	69.1	25	59.1	4	0	0	1334.63	882	892
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	23	25	64	0.06%	17.6%	LHIIEVGTPPTGNQPFPK	95.3%	23.1	25	17.9	0	1	0	1945.05	228	245
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	23	25	64	0.06%	17.6%	LLLPWLEAR	96.2%	29.3	25	22.4	1	0	0	1110.67	857	865
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	23	25	64	0.06%	17.6%	LLYNNVSNFGR	99.7%	60.4	25	58.3	4	0	0	1296.67	1216	1226
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	23	25	64	0.06%	17.6%	LPVVIGGLLDVDCSEDVIK	99.7%	80.4	25	80.4	3	0	0	2041.09	812	830
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	23	25	64	0.06%	17.6%	NLQNLLILTAIK	99.7%	78.9	25	76.2	3	0	0	1353.85	1023	1034
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	23	25	64	0.06%	17.6%	NNLAGAEELFAR	99.7%	82.1	25	81.4	4	0	0	1304.66	355	366
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	23	25	64	0.06%	17.6%	SVDPTLALSVYLR	99.7%	50.4	25	50.4	2	0	0	1433.80	469	481
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	23	25	64	0.06%	17.6%	TLQIFNIEMK	99.7%	50.6	25	38.7	5	0	0	1236.67	87	96
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	23	25	64	0.06%	17.6%	VANVELYYR	99.7%	75.2	25	72.8	4	0	0	1126.59	1398	1406
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	23	25	64	0.06%	17.6%	VDKLDASESLR	96.4%	29.6	25	24.1	1	0	0	1232.65	1610	1620
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	23	25	64	0.06%	17.6%	VGYTPDWIFLLR	99.4%	37.3	25	32.8	1	0	0	1479.80	508	519
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	23	25	64	0.06%	17.6%	VIQCFAETGQVQK	99.7%	89.7	25	72.4	5	0	0	1507.76	488	500
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	23	25	64	0.06%	17.6%	VVGAMQLYSVDR	99.7%	52.4	25	48.9	3	0	0	1337.69	177	188
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	23	25	64	0.06%	17.6%	WLLLTGISAQQNR	99.7%	66.9	25	61.5	1	0	0	1499.83	164	176
Clathrin light chain A	CLTA	CLCA_HUMAN	27.1	100.0%	3	3	4	0.00%	7.7%	LEALDANSR	99.1%	35.6	25	29.7	1	0	0	988.51	121	129
Clathrin light chain A	CLTA	CLCA_HUMAN	27.1	100.0%	3	3	4	0.00%	7.7%	LQSEPESIR	94.5%	27.9	25	8	1	0	0	1058.55	103	111
Clathrin light chain A	CLTA	CLCA_HUMAN	27.1	100.0%	3	3	4	0.00%	7.7%	LQSEPESIRK	97.3%	30.7	25	24.9	2	0	0	1186.64	103	112
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	19	19	30	0.03%	14.8%	DALLLSFK	95.1%	28.4	25	16.7	1	0	0	906.53	92	99
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	19	19	30	0.03%	14.8%	DGFVQNVHTPR	99.7%	41.8	25	37.3	2	0	0	1269.63	130	140
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	19	19	30	0.03%	14.8%	DLSGMFTTESR	99.7%	58.8	25	48.2	2	0	0	1243.56	703	713
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	19	19	30	0.03%	14.8%	ENGTMEIYQLPDWR	99.2%	35.9	25	34.4	1	0	0	1751.81	790	803
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	19	19	30	0.03%	14.8%	EVLLVALGSR	99.7%	85.1	25	68.3	2	0	0	1056.64	848	857
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	19	19	30	0.03%	14.8%	HGFLILSR	99.1%	35.7	25	27.2	1	0	0	942.55	572	579
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	19	19	30	0.03%	14.8%	IFLWSLR	99.7%	44.4	25	0	2	0	0	934.55	1190	1196
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	19	19	30	0.03%	14.8%	ISVLPAYLSYDAPWPVR	99.7%	66.8	25	66.8	1	0	0	1947.04	998	1014
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	19	19	30	0.03%	14.8%	LGNSLLLK	98.8%	34.3	25	24.3	2	0	0	857.55	388	395
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	19	19	30	0.03%	14.8%	LSVVEYDPGTHDLK	99.5%	38	25	32.5	1	0	0	1572.79	103	116
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	19	19	30	0.03%	14.8%	NLMVYMYLPEAK	99.7%	43.2	25	37.8	1	0	0	1471.73	1277	1288
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	19	19	30	0.03%	14.8%	NVLDGELLNR	99.7%	75.3	25	61.2	2	0	0	1142.62	1397	1406
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	19	19	30	0.03%	14.8%	QGELPLVK	99.2%	36.3	25	22.4	1	0	0	883.52	840	847
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	19	19	30	0.03%	14.8%	SSFLPSYIIDVR	99.7%	77.5	25	60.6	2	0	0	1396.75	183	194
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	19	19	30	0.03%	14.8%	TLSLHYFEEPELR	99.7%	33.8	25	33.8	0	1	0	1633.82	117	129
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	19	19	30	0.03%	14.8%	VLVDSSFGQPTTQGEAR	99.7%	97.5	25	96.2	2	0	0	1791.89	817	833
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	19	19	30	0.03%	14.8%	VYAVATSTNTPCAR	99.7%	86.9	25	82.5	2	0	0	1510.73	1033	1046
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	19	19	30	0.03%	14.8%	YIVQVSPLGIR	99.7%	55.1	25	35.1	2	0	0	1244.74	617	627
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	19	19	30	0.03%	14.8%	YLYLSTMER	99.6%	39.8	25	35.1	2	0	0	1175.58	1407	1415
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	8	8	13	0.01%	12.4%	DEQLLTNVLETLR	99.7%	65.9	25	57.8	1	0	0	1543.83	216	228
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	8	8	13	0.01%	12.4%	FLIDNPSEK	98.2%	32.5	25	6.42	1	0	0	1062.55	367	375
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	8	8	13	0.01%	12.4%	FSQIVNLK	99.0%	35	25	21.4	2	0	0	948.55	131	138

Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	8	8	13	0.01%	12.4%	IRDLLYEQYAIV	99.7%	53.4	25	53.4	2	0	0	1495.82	771	782
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	8	8	13	0.01%	12.4%	LGLNCAIYATIPVYK	99.7%	81.3	25	73.8	2	0	0	1695.91	78	92
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	8	8	13	0.01%	12.4%	LHETVDATSETHIYQVR	99.7%	51.1	25	51.1	0	2	0	1998.99	593	609
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	8	8	13	0.01%	12.4%	NSIILTYR	99.7%	61.3	25	42.4	1	0	0	979.56	351	358
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	8	8	13	0.01%	12.4%	VVLASQPDLECGFSR	99.7%	90.3	25	89	2	0	0	1677.83	325	339
Cleavage and polyadenylation specificity factor subunit 4	CPSF4	CPSF4_HUMAN	30.3	99.8%	2	2	3	0.00%	7.4%	MPECYFYSK	95.3%	28.5	25	22.1	1	0	0	1240.50	93	101
Cleavage and polyadenylation specificity factor subunit 4	CPSF4	CPSF4_HUMAN	30.3	99.8%	2	2	3	0.00%	7.4%	SGAAVCEFFLK	99.7%	55	25	55	2	0	0	1228.60	36	46
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	8	9	18	0.02%	33.9%	GVTQFGNK	99.6%	39.1	25	22.4	2	0	0	850.44	16	23
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	8	9	18	0.02%	33.9%	GVTQFGNKYIQQTKPLTLER	98.0%	26.4	25	26.4	0	1	0	2321.26	16	35
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	8	9	18	0.02%	33.9%	KLFLVQLQEK	99.7%	63.7	25	63.7	2	0	0	1245.76	173	182
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	8	9	18	0.02%	33.9%	LFLVQLQEK	99.7%	60.6	25	43.3	4	0	0	1117.66	174	182
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	8	9	18	0.02%	33.9%	LMTEILGR	99.7%	52.5	25	38.4	2	0	0	932.52	124	131
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	8	9	18	0.02%	33.9%	LPGGELNPGEDEVEGLKR	99.7%	83.6	25	83.6	2	2	0	1908.97	106	123
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	8	9	18	0.02%	33.9%	TINLYPLTNYTFGTKEPLYEK	98.7%	33.8	25	33.8	1	0	0	2505.29	36	56
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	8	9	18	0.02%	33.9%	YIQQTKPLTLER	99.7%	52.7	25	36.5	2	0	0	1489.84	24	35
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	7	8	14	0.01%	12.0%	AISSSAISR	99.7%	44.4	25	29.6	2	0	0	891.49	423	431
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	7	8	14	0.01%	12.0%	GAAPNVVYTYTGK	99.7%	83.9	25	81.9	2	0	0	1340.68	67	79
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	7	8	14	0.01%	12.0%	GDYGPPGR	99.1%	35.7	25	15.4	2	0	0	818.38	393	400
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	7	8	14	0.01%	12.0%	GFALVGVGSEASSK	99.7%	115	25	108	2	0	0	1308.68	125	138
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	7	8	14	0.01%	12.0%	KLMDLLPK	95.5%	28.7	25	8.52	1	0	0	957.58	139	146
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	7	8	14	0.01%	12.0%	LMDLLPK	97.3%	30.8	25	3.84	1	0	0	845.48	140	146
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	7	8	14	0.01%	12.0%	TPLSEAEFEEIMNR	99.7%	100	25	100	4	0	0	1681.77	407	420
Cleavage and polyadenylation specificity factor subunit 7	CPSF7	CPSF7_HUMAN	52.1	100.0%	5	5	9	0.01%	11.5%	LLELLPGK	99.5%	38.7	25	26.1	1	0	0	882.57	141	148
Cleavage and polyadenylation specificity factor subunit 7	CPSF7	CPSF7_HUMAN	52.1	100.0%	5	5	9	0.01%	11.5%	QNLSQFEAQAR	99.7%	83.7	25	73.5	2	0	0	1291.64	163	173
Cleavage and polyadenylation specificity factor subunit 7	CPSF7	CPSF7_HUMAN	52.1	100.0%	5	5	9	0.01%	11.5%	SSSTEPPPPVR	99.7%	40.8	25	30.9	2	0	0	1153.58	46	56
Cleavage and polyadenylation specificity factor subunit 7	CPSF7	CPSF7_HUMAN	52.1	100.0%	5	5	9	0.01%	11.5%	SYSVGASGSSSR	99.7%	75.1	25	69.4	2	0	0	1144.52	407	418
Cleavage and polyadenylation specificity factor subunit 7	CPSF7	CPSF7_HUMAN	52.1	100.0%	5	5	9	0.01%	11.5%	TPAILYTYSGLR	99.7%	67.9	25	64.2	2	0	0	1354.74	67	78
CLIP-associating protein 2	CLASP2	CLAP2_HUMAN	141.1	99.8%	2	2	2	0.00%	2.2%	MGADLLGSVQAK	99.7%	45.9	25	33.5	1	0	0	1189.62	745	756
CLIP-associating protein 2	CLASP2	CLAP2_HUMAN	141.1	99.8%	2	2	2	0.00%	2.2%	VLTTTALSTVSSGVQR	99.7%	70.9	25	62.3	1	0	0	1619.90	467	482
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	62	0.06%	23.7%	ASNLENSTYDLYTIPK	99.7%	98.2	25	90.9	4	0	0	1828.90	383	398
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	62	0.06%	23.7%	CPLSGACYSPEFK	98.0%	32.1	25	31.6	1	0	0	1515.66	1185	1197
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	62	0.06%	23.7%	DADSQNPDAPEGK	99.4%	37.7	25	36.8	1	0	0	1343.57	399	411
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	62	0.06%	23.7%	DADSQNPDAPEGKR	96.3%	29.5	25	29.5	1	0	0	1499.67	399	412
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	62	0.06%	23.7%	DVAVMQLR	99.7%	48.6	25	36	5	0	0	931.50	351	358
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	62	0.06%	23.7%	GFFEGTIASK	99.7%	59.6	25	56.5	4	0	0	1056.54	816	825
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	62	0.06%	23.7%	GHYNNVSCAVFHPR	99.7%	42.2	25	42.2	0	2	0	1657.77	247	260
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	62	0.06%	23.7%	GITGVDLFGTTDAVVK	99.7%	90.7	25	90.7	2	0	0	1592.85	183	198
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	62	0.06%	23.7%	KLDALCNIHENIR	99.7%	37.4	25	37.4	0	2	0	1595.83	517	529
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	62	0.06%	23.7%	KYDEVLHMVR	96.9%	24.7	25	23.6	0	1	0	1305.66	607	616
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	62	0.06%	23.7%	LLELGPKPEVAQQTR	99.7%	47.8	25	46.2	0	2	0	1678.95	1128	1142
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	62	0.06%	23.7%	LNDLIQR	99.7%	50.5	25	35.9	4	0	0	871.50	1003	1009
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	62	0.06%	23.7%	LSFLYLITGNLEK	99.7%	75.2	25	75.1	1	0	0	1510.85	703	715
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	62	0.06%	23.7%	LVGQSIIAYLQK	99.7%	99.2	25	99.2	4	0	0	1332.79	620	631
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	62	0.06%	23.7%	NLSPGAVESDVR	99.7%	60.7	25	48.6	4	0	0	1243.63	171	182
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	62	0.06%	23.7%	QELILSNSEDK	99.7%	48	25	40.6	1	0	0	1275.64	261	271
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	62	0.06%	23.7%	QLFLQTYAR	99.7%	50.6	25	37.9	3	0	0	1139.62	957	965
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	62	0.06%	23.7%	SILLSVPLLVVDNK	99.7%	81.7	25	81.7	5	0	0	1509.93	1031	1044
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	62	0.06%	23.7%	SSGLTAVWVAR	99.7%	76.1	25	56.4	2	0	0	1146.63	413	423
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	62	0.06%	23.7%	TALNLFFK	99.7%	50.6	25	45.7	2	0	0	953.55	1107	1114
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	62	0.06%	23.7%	TGVQTFR	97.2%	30.6	25	12	2	0	0	808.43	282	288
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	62	0.06%	23.7%	TLDLPIYVTR	99.7%	54	25	48.2	4	0	0	1190.68	563	572

Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	62	0.06%	23.7%	VQVPNCDEIFYAGTGNLLLR	99.7%	51.3	25	51.3	1	0	0	2279.15	448	467
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	62	0.06%	23.7%	VTTVTEIGKDVIGLR	99.7%	62.5	25	62.5	1	0	0	1600.93	1203	1217
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	25	26	62	0.06%	23.7%	YAVTTGDHGIIR	99.7%	47.9	25	41.1	3	0	0	1302.68	551	562
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	AAAQCYIDLIIK	99.7%	70.1	25	58.8	2	0	0	1378.74	280	291
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	CIYNLLQSSSPAVK	99.7%	82	25	77.9	2	0	0	1579.81	248	261
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	DLQHPNEFIR	99.4%	37.6	25	26.4	2	0	0	1268.64	108	117
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	EAADPLASK	95.0%	28.3	25	21.7	1	0	0	901.46	704	712
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	EAELLEPLMPAIR	99.7%	54.1	25	43.8	2	0	0	1481.80	129	141
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	EAGELKPEEEITVGPVQK	99.7%	74.8	25	69.4	2	0	0	1953.02	496	513
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	EDIQSVMTEIR	99.7%	63.1	25	63.1	1	0	0	1320.65	470	480
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	FVLPLQDHTIK	99.4%	31	25	26.8	1	1	0	1310.75	65	75
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	GALWILGEYCSTK	99.7%	75.2	25	73.2	4	0	0	1497.74	457	469
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	KPITDDDVDR	99.7%	57.9	25	34.1	2	0	0	1173.57	603	612
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	LKEAELLEPLMPAIR	99.4%	37.1	25	37.1	1	1	0	1722.98	127	141
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	LLLVFWEIVPK	99.7%	64.1	25	64.1	2	0	0	1356.83	77	87
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	LPGLLMTIIR	99.7%	69.2	25	58.8	4	0	0	1126.70	55	64
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	LVEKPSPLTLAPHDFANIK	99.7%	51.2	25	51.2	0	2	0	2090.16	768	786
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	LVTEMGTYATQSALSSSRPTK	99.3%	30.5	25	30.5	0	4	0	2228.12	514	534
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	MLEVFHAIK	99.7%	40.4	25	30.8	2	0	0	1087.60	442	450
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	NAVLAIYTIYR	99.7%	82	25	82	4	0	0	1296.73	154	164
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	NVEELVIVLK	99.7%	62.6	25	53.5	2	0	0	1155.70	352	361
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	NVTVQPDDPISFMQLTAK	99.7%	95.9	25	92	3	0	0	2004.01	662	679
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	SLGEIPIVESEIKK	99.7%	56.6	25	56.6	2	0	0	1541.88	482	495
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	SQGMALSLGDK	99.7%	56.3	25	38.9	2	0	0	1106.55	933	943
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	TLQLALDLVSSR	99.7%	106	25	106	2	0	0	1315.76	340	351
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	TNNVSEHEDTDKYR	99.7%	60.4	25	60.4	0	2	0	1707.76	367	380
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	VASTENGIIFGNIVYDVSGAASDR	99.7%	109	25	109	2	1	0	2455.21	791	814
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	VIIMILNGEK	99.7%	45.2	25	37.6	2	0	0	1129.67	45	54
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	VLQDLVMDILR	99.7%	82.2	25	73.2	5	0	0	1314.75	317	327
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	VLSECSPLMNDIFNK	99.7%	99.9	25	95.9	2	0	0	1766.85	619	633
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	VLSTPDLEVR	99.1%	35.3	25	21	2	0	0	1128.63	328	337
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	29	36	69	0.07%	37.9%	YVALVQEK	99.6%	38.9	25	27.8	2	0	0	949.54	568	575
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	6	6	12	0.01%	7.4%	AAESLADPTEYENLFPGLK	99.7%	59.3	25	55.9	3	0	0	2065.01	784	802
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	6	6	12	0.01%	7.4%	HSEVQQANLK	99.7%	56.4	25	48.8	3	0	0	1153.60	319	328
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	6	6	12	0.01%	7.4%	LPEAAFLAR	99.7%	61.7	25	48.8	3	0	0	987.56	751	759
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	6	6	12	0.01%	7.4%	TFEVCDLPVR	98.3%	32.7	25	29.4	1	0	0	1235.61	52	61
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	6	6	12	0.01%	7.4%	TMYLLGYIPK	97.6%	31.2	25	25.5	1	0	0	1198.65	560	569
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	6	6	12	0.01%	7.4%	VFNYNTLER	99.7%	40.1	25	30.2	1	0	0	1155.58	83	91
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	17	18	34	0.03%	33.1%	ENVNLAQIR	99.7%	76.8	25	54.9	2	0	0	1056.58	123	131
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	17	18	34	0.03%	33.1%	GKEVDNFVDK	99.7%	46	25	42.9	2	0	0	1150.57	232	241
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	17	18	34	0.03%	33.1%	GVQLQTHPNVDKK	99.7%	50.6	25	41.9	1	2	0	1463.80	324	336
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	17	18	34	0.03%	33.1%	IEGLLAAFPK	99.7%	53.6	25	35	2	0	0	1058.62	29	38
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	17	18	34	0.03%	33.1%	KNYCNIQVTK	99.7%	43.8	25	43.8	2	0	0	1267.65	476	485
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	17	18	34	0.03%	33.1%	LFTAESLIGLK	99.7%	76.6	25	64.2	2	0	0	1191.70	337	347
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	17	18	34	0.03%	33.1%	LYMVLITTK	99.7%	59.7	25	59.7	2	0	0	1081.63	64	72
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	17	18	34	0.03%	33.1%	NSNILEDLETLR	99.7%	76.3	25	69	4	0	0	1416.73	73	84
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	17	18	34	0.03%	33.1%	NTLEWCLPVIDAK	99.7%	65.1	25	55	2	0	0	1558.79	436	448
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	17	18	34	0.03%	33.1%	NYCNIQVTK	99.7%	40.7	25	36.9	1	0	0	1139.55	477	485
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	17	18	34	0.03%	33.1%	SEGETIMSSSMGK	99.7%	41.2	25	37.1	3	0	0	1359.58	244	256
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	17	18	34	0.03%	33.1%	SFPVNSDVGVLK	99.7%	53.5	25	53.5	1	0	0	1261.68	352	363
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	17	18	34	0.03%	33.1%	TFTEMDSHEEK	99.6%	39.2	25	34.2	2	0	0	1353.56	132	142

Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	17	18	34	0.03%	33.1%	TRIEGLLAAFPK	99.1%	35.5	25	29.6	2	0	0	1315.77	27	38
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	17	18	34	0.03%	33.1%	VAPAPARPSGPSK	98.2%	32.3	25	18.7	1	0	0	1234.69	212	224
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	17	18	34	0.03%	33.1%	VLLAAAVCTK	99.7%	63.8	25	56.8	2	0	0	1045.61	2	11
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	17	18	34	0.03%	33.1%	VTQVDGNSPVR	99.7%	49.9	25	36	1	0	0	1171.61	486	496
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	10	12	20	0.02%	43.5%	APPAPGPASGGSGEVDELFDVK	99.7%	102	25	102	2	0	0	2097.01	2	23
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	10	12	20	0.02%	43.5%	DSIVAELDR	94.6%	28	25	21.2	1	0	0	1017.52	98	106
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	10	12	20	0.02%	43.5%	DSIVAELDREMSR	98.0%	32	25	32	1	0	0	1536.73	98	110
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	10	12	20	0.02%	43.5%	ENDFDRLVLQYAPSA	98.9%	34.7	25	19.8	2	0	0	1737.84	294	308
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	10	12	20	0.02%	43.5%	FGVVLDEIKPSSAPELQAVR	99.7%	61.5	25	60.4	0	2	0	2155.18	66	85
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	10	12	20	0.02%	43.5%	LDRLDLAR	97.5%	31.1	25	27.7	1	0	0	971.56	159	166
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	10	12	20	0.02%	43.5%	LQDAYYIFQEMADK	99.7%	90.4	25	67.3	4	0	0	1734.80	198	211
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	10	12	20	0.02%	43.5%	MFADYLAHESR	99.7%	98.7	25	92.3	3	0	0	1339.61	86	96
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	10	12	20	0.02%	43.5%	NAFYIGSYQQCINEAQR	99.7%	97.7	25	97.7	2	0	0	2061.94	24	40
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	10	12	20	0.02%	43.5%	WEAAEGLLQEALDK	99.7%	77.4	25	75	2	0	0	1572.79	232	245
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	55	0.05%	34.1%	AIVDCIISIIEENSESK	99.7%	55.1	25	55.1	2	0	0	1919.96	416	432
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	55	0.05%	34.1%	ALCQITDSTMLQAIER	99.7%	83.7	25	83.7	2	0	0	1849.91	127	142
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	55	0.05%	34.1%	ALQQYTLEPSEKPFDLK	99.1%	29.8	25	20.9	0	2	0	2007.04	561	577
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	55	0.05%	34.1%	ATFYLNVLEQK	99.7%	63.1	25	51.9	2	0	0	1325.71	528	538
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	55	0.05%	34.1%	ELAPAVSVLQLFCSSPK	99.7%	124	25	124	7	0	0	1845.98	284	300
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	55	0.05%	34.1%	EMSCIAEDVIIVTSSLTK	99.7%	117	25	115	2	0	0	1996.00	94	111
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	55	0.05%	34.1%	FGAQNEEMLPSILVLLK	99.7%	56.1	25	50.8	4	0	0	1918.04	498	514
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	55	0.05%	34.1%	GGHDILVR	99.5%	38.1	25	11.4	1	0	0	866.48	836	843
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	55	0.05%	34.1%	ILHLLGQEGPK	99.7%	66.3	25	60.5	2	2	0	1204.71	455	465
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	55	0.05%	34.1%	LFQSNDPTLR	99.7%	67.9	25	51.5	2	0	0	1190.62	76	85
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	55	0.05%	34.1%	LLLLDTVTMQVTAR	99.7%	79.4	25	71.8	2	0	0	1589.89	846	859
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	55	0.05%	34.1%	QEIFQEQLAAVPEFR	99.7%	66.7	25	66.4	2	0	0	1804.92	610	624
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	55	0.05%	34.1%	SAVLQEAR	99.7%	40.5	25	14.3	2	0	0	873.48	25	32
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	55	0.05%	34.1%	SIATLAITTLLK	99.7%	99.1	25	99.1	6	0	0	1244.78	339	350
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	55	0.05%	34.1%	SLEELPVDIILASVG	98.2%	32.4	25	26.3	1	0	0	1554.86	860	874
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	55	0.05%	34.1%	SLPYNQPGTCYTLVALPK	99.7%	62.9	25	62.1	2	0	0	2022.04	697	714
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	55	0.05%	34.1%	SSPEPVALTESETEYVIR	99.7%	112	25	107	2	0	0	2006.99	632	649
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	55	0.05%	34.1%	SVPLATAPMAEQR	99.7%	53.6	25	49	2	0	0	1386.70	578	590
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	55	0.05%	34.1%	TLEEAVGNIVK	99.7%	41.9	25	38.5	1	0	0	1172.65	796	806
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	55	0.05%	34.1%	VFNETPINPR	99.7%	40.7	25	39.8	2	0	0	1186.62	33	42
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	55	0.05%	34.1%	VVLEHEEVR	99.7%	63.9	25	52.2	3	0	0	1109.59	480	488
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	55	0.05%	34.1%	VVVVQAISALCQK	99.7%	78.5	25	78.5	2	0	0	1414.81	377	389
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	6	6	16	0.02%	12.4%	AIVDCIISIVEENPESK	99.7%	94.2	25	94.1	2	0	0	1915.97	416	432
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	6	6	16	0.02%	12.4%	ATFYLNVLQQR	99.7%	57	25	54.6	3	0	0	1352.73	528	538
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	6	6	16	0.02%	12.4%	EMATISEDVIIVTSSLTK	99.7%	66.2	25	66.2	1	0	0	1937.01	94	111
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	6	6	16	0.02%	12.4%	IFNETPINPR	99.7%	51.7	25	38.1	4	0	0	1200.64	33	42
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	6	6	16	0.02%	12.4%	LFQSNDQTLR	99.7%	53.6	25	39.7	2	0	0	1221.62	76	85
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	6	6	16	0.02%	12.4%	SAVLQEAR	99.7%	40.5	25	14.3	2	0	0	873.48	25	32
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	6	6	16	0.02%	12.4%	SIATLAITTLLK	99.7%	99.1	25	99.1	6	0	0	1244.78	339	350
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	6	6	16	0.02%	12.4%	VVLENEAVR	99.7%	51.6	25	47.8	4	0	0	1028.57	480	488
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	6	6	16	0.02%	12.4%	VVVVQAISALCQK	99.7%	78.5	25	78.5	2	0	0	1414.81	377	389
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	4	4	11	0.01%	30.1%	AVLFCLSEDKK	99.7%	52.4	25	49.8	2	0	0	1309.68	35	45
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	4	4	11	0.01%	30.1%	HELQANCYEEVKDR	99.7%	50.5	25	50.5	0	1	0	1790.81	133	146
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	4	4	11	0.01%	30.1%	LGGSAVISLEGKPL	99.7%	91.5	25	88.9	2	0	0	1340.78	153	166
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	4	4	11	0.01%	30.1%	YALYDATYETK	99.7%	63.5	25	54.5	6	0	0	1337.63	82	92
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	4	4	7	0.01%	3.7%	FALTFGLDQLK	99.7%	45.2	25	0	2	0	0	1252.69	955	965
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	4	4	7	0.01%	3.7%	GVVTAEMFR	99.7%	55.6	25	46.8	1	0	0	1025.51	129	137

Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	4	4	7	0.01%	3.7%	ITELFAVALPQLLAK	99.7%	52.8	25	52.8	2	0	0	1626.98	563	577
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	4	4	7	0.01%	3.7%	YYNDYGDIIK	99.7%	49.7	25	48	2	0	0	1263.59	892	901
Coiled-coil domain-containing protein 137	CCDC137	CC137_HUMAN	33.2	100.0%	3	3	6	0.01%	13.5%	KGESDGAYIHR	99.7%	34.5	25	29.9	0	2	0	1232.60	118	128
Coiled-coil domain-containing protein 137	CCDC137	CC137_HUMAN	33.2	100.0%	3	3	6	0.01%	13.5%	MLLSPGGVSQPLTASLAR	99.7%	45.8	25	43.4	2	0	0	1797.99	230	247
Coiled-coil domain-containing protein 137	CCDC137	CC137_HUMAN	33.2	100.0%	3	3	6	0.01%	13.5%	NQDEQEIPFR	97.1%	30.5	25	19.7	2	0	0	1275.60	57	66
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	11	13	21	0.02%	27.7%	ARVEENFLK	99.7%	40	25	20	2	0	0	1105.60	411	419
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	11	13	21	0.02%	27.7%	ELLESNFTLVGDDGTNK	99.7%	119	25	119	2	0	0	1851.90	173	189
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	11	13	21	0.02%	27.7%	ELLESNFTLVGDDGTNKEATSTGK	99.3%	30.5	25	30.5	0	1	0	2526.22	173	196
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	11	13	21	0.02%	27.7%	EMQDLSEFCSDKPK	99.7%	54.3	25	53.9	1	1	0	1729.74	275	288
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	11	13	21	0.02%	27.7%	IMNEEDPEKQR	99.7%	59.1	25	58.7	4	0	0	1388.65	444	454
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	11	13	21	0.02%	27.7%	LAQAWFNTHR	98.4%	27.2	25	24.5	0	1	0	1243.63	163	172
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	11	13	21	0.02%	27.7%	LNQENEHIYNLWCSGR	99.7%	34.5	25	34.5	0	2	0	2032.93	197	212
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	11	13	21	0.02%	27.7%	MMRPVSDQVQIK	98.8%	28.3	25	22.6	0	1	0	1463.73	237	248
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	11	13	21	0.02%	27.7%	RQDLLNVLAR	99.7%	52	25	47.4	2	0	0	1197.71	227	236
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	11	13	21	0.02%	27.7%	TLLFTFNVPGSGNTYPK	99.7%	43.8	25	41.4	2	0	0	1855.96	358	374
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	11	13	21	0.02%	27.7%	VCCEGMLIQLR	99.7%	69.6	25	64	2	0	0	1378.66	213	223
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	6	6	12	0.01%	25.1%	AAANEQLTR	99.7%	63.9	25	51.3	2	0	0	973.51	96	104
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	6	6	12	0.01%	25.1%	LSENVIDR	99.7%	55.4	25	49	2	0	0	945.50	28	35
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	6	6	12	0.01%	25.1%	VAEELALEQAK	99.7%	85.1	25	73.3	2	0	0	1200.65	66	76
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	6	6	12	0.01%	25.1%	YESHPVCADLQAK	99.7%	44.4	25	39.5	2	0	0	1517.71	177	189
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	6	6	12	0.01%	25.1%	YSGAYGASVSDEELK	99.7%	115	25	115	2	0	0	1575.72	49	63
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	6	6	12	0.01%	25.1%	YSGAYGASVSDEELKR	99.7%	101	25	101	2	0	0	1731.82	49	64
Coiled-coil-helix-coiled-coil-helix domain-containing protein 6, mitochondrial	CHCHD6	CHCH6_HUMAN	26.5	99.8%	2	2	4	0.00%	6.8%	LSENVVNR	99.7%	51.2	25	43.4	2	0	0	930.50	30	37
Coiled-coil-helix-coiled-coil-helix domain-containing protein 6, mitochondrial	CHCHD6	CHCH6_HUMAN	26.5	99.8%	2	2	4	0.00%	6.8%	MESTIKPR	99.4%	37.2	25	28	2	0	0	961.51	184	191
Coilin	COIL	COIL_HUMAN	62.6	99.8%	2	2	3	0.00%	4.2%	NSSTIIQNPVETPK	99.7%	71.9	25	71.9	1	0	0	1527.80	445	458
Coilin	COIL	COIL_HUMAN	62.6	99.8%	2	2	3	0.00%	4.2%	VVTDLISLIR	99.7%	68.1	25	58.2	2	0	0	1128.70	37	46
Cold-inducible RNA-binding protein	CIRBP	CIRBP_HUMAN	18.6	99.8%	2	2	4	0.00%	14.0%	DSYDSYATHNE	99.7%	78.3	25	78.3	2	0	0	1301.49	162	172
Cold-inducible RNA-binding protein	CIRBP	CIRBP_HUMAN	18.6	99.8%	2	2	4	0.00%	14.0%	YGQISEVVVVKDR	99.7%	89.6	25	84.6	2	0	0	1491.82	29	41
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	C1QBP_HUMAN	31.4	100.0%	4	7	14	0.01%	22.0%	AFVDFLSDEIKEER	99.7%	81.4	25	79.5	2	2	0	1697.84	81	94
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	C1QBP_HUMAN	31.4	100.0%	4	7	14	0.01%	22.0%	EVSFQSTGESEWK	99.7%	74.4	25	66	2	0	0	1513.68	208	220
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	C1QBP_HUMAN	31.4	100.0%	4	7	14	0.01%	22.0%	MSGGWELELNGTEAK	99.7%	107	25	107	4	0	0	1637.75	105	119
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	C1QBP_HUMAN	31.4	100.0%	4	7	14	0.01%	22.0%	VEEQEPELTSTPNFVVEVIK	99.7%	67.9	25	67.9	2	2	0	2287.17	155	174
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	14	14	22	0.02%	11.0%	AIIDEFEQK	99.7%	45	25	42.9	2	0	0	1092.56	1280	1288
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	14	14	22	0.02%	11.0%	DLAYCVSQLPLTER	99.7%	61.5	25	61.4	2	0	0	1664.83	1225	1238
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	14	14	22	0.02%	11.0%	EAVLNAYR	99.7%	54.3	25	40.3	2	0	0	935.49	691	698
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	14	14	22	0.02%	11.0%	ELEIGQAGSQR	99.7%	77.7	25	71.9	2	0	0	1187.60	1302	1312
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	14	14	22	0.02%	11.0%	ESTGNMVTGQTVCK	99.1%	35.6	25	35.6	1	0	0	1527.68	584	597
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	14	14	22	0.02%	11.0%	GNAIYNLLPDIISR	99.7%	63.4	25	58.9	1	0	0	1558.86	1160	1173
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	14	14	22	0.02%	11.0%	IYQLLAK	97.8%	31.5	25	17.8	1	0	0	848.52	520	526
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	14	14	22	0.02%	11.0%	KITEAIGIISK	99.7%	56.8	25	56.8	2	0	0	1172.73	633	643
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	14	14	22	0.02%	11.0%	LLENPTINHQK	99.3%	36.4	25	24.6	1	0	0	1306.71	205	215
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	14	14	22	0.02%	11.0%	LSDADLAGPLQK	99.7%	57.5	25	41.1	2	0	0	1227.66	441	452
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	14	14	22	0.02%	11.0%	QTLAAFVPLLLK	99.7%	49.2	25	44.8	2	0	0	1313.82	1009	1020
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	14	14	22	0.02%	11.0%	SGGVNQYVVQEVLSIK	99.7%	60.7	25	60.7	2	0	0	1719.93	20	35
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	14	14	22	0.02%	11.0%	VACCPLER	95.1%	28.4	25	20.7	1	0	0	1004.47	764	771
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	14	14	22	0.02%	11.0%	VLQLFTR	99.2%	35.8	25	23	1	0	0	876.53	384	390
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	6	6	10	0.01%	8.4%	APLQQCAEDR	99.7%	70.1	25	65.3	2	0	0	1187.55	304	313
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	6	6	10	0.01%	8.4%	EAALAEVADEK	99.7%	42.7	25	32.4	2	0	0	1145.57	675	685
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	6	6	10	0.01%	8.4%	LLASPSSR	98.9%	34.5	25	25.6	1	0	0	830.47	84	91
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	6	6	10	0.01%	8.4%	VAAGTLDASTK	99.7%	58.4	25	58	2	0	0	1033.55	153	163
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	6	6	10	0.01%	8.4%	VDAVHADVYR	98.9%	34.6	25	22.2	1	0	0	1144.57	169	178

Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	6	6	10	0.01%	8.4%	VFDLQFSTDSPR	99.7%	99.2	25	99.1	2	0	0	1411.69	72	83
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	7	7	14	0.01%	8.8%	AIFDQLMTFGIEPFK	96.9%	30.2	25	30.2	1	0	0	1772.89	644	658
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	7	7	14	0.01%	8.8%	APIVTVGVNNDPADVR	99.7%	74.8	25	74.8	2	0	0	1636.87	471	486
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	7	7	14	0.01%	8.8%	IQAVLALSR	99.0%	34.9	25	29.9	1	0	0	970.60	160	168
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	7	7	14	0.01%	8.8%	LLSDFLDSEVSELR	99.7%	97.1	25	92.4	4	0	0	1622.83	695	708
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	7	7	14	0.01%	8.8%	LMFSGLLVSSR	99.7%	64.8	25	57.1	2	0	0	1209.67	718	728
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	7	7	14	0.01%	8.8%	LNLAQFLNEDLS	98.4%	32.9	25	32.9	1	0	0	1376.71	1004	1015
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	7	7	14	0.01%	8.8%	TQIVTEIISEIR	99.7%	92.4	25	88.3	3	0	0	1401.79	459	470
Condensin-2 complex subunit D3	NCAPD3	CNDD3_HUMAN	168.9	99.8%	2	2	4	0.00%	1.5%	FLVQEIMFDR	99.7%	53.6	25	50	2	0	0	1297.66	443	452
Condensin-2 complex subunit D3	NCAPD3	CNDD3_HUMAN	168.9	99.8%	2	2	4	0.00%	1.5%	TFAAQSLVQLLSK	99.7%	71.5	25	71.5	2	0	0	1405.81	372	384
Conserved oligomeric Golgi complex subunit 1	COG1	COG1_HUMAN	109.0	100.0%	3	3	3	0.00%	4.3%	ALQLLYDLR	99.7%	65.5	25	51.2	1	0	0	1104.64	806	814
Conserved oligomeric Golgi complex subunit 1	COG1	COG1_HUMAN	109.0	100.0%	3	3	3	0.00%	4.3%	ELLVSALQELESSTSNSPSNK	99.7%	62.8	25	62.8	1	0	0	2233.12	443	463
Conserved oligomeric Golgi complex subunit 1	COG1	COG1_HUMAN	109.0	100.0%	3	3	3	0.00%	4.3%	FGLLPLSMTSTR	99.0%	35.1	25	34.5	1	0	0	1322.71	911	922
Conserved oligomeric Golgi complex subunit 2	COG2	COG2_HUMAN	83.2	99.8%	2	2	2	0.00%	4.5%	ETSALEASSPLLTGQILER	99.7%	65.1	25	64.4	1	0	0	2015.07	154	172
Conserved oligomeric Golgi complex subunit 2	COG2	COG2_HUMAN	83.2	99.8%	2	2	2	0.00%	4.5%	IIQDLSDSCFGFLK	99.7%	61.8	25	61.8	1	0	0	1642.81	571	584
Conserved oligomeric Golgi complex subunit 4	COG4	COG4_HUMAN	89.1	100.0%	2	2	3	0.00%	3.4%	ELDPILTEVTLMNAR	99.7%	75.1	25	75.1	2	0	0	1714.90	351	365
Conserved oligomeric Golgi complex subunit 4	COG4	COG4_HUMAN	89.1	100.0%	2	2	3	0.00%	3.4%	LSQMATILNLER	99.7%	57.9	25	49.2	1	0	0	1388.76	730	741
Conserved oligomeric Golgi complex subunit 5	COG5	COG5_HUMAN	92.7	100.0%	3	3	3	0.00%	3.9%	IGALQGAVDR	99.7%	71.1	25	51.9	1	0	0	999.56	138	147
Conserved oligomeric Golgi complex subunit 5	COG5	COG5_HUMAN	92.7	100.0%	3	3	3	0.00%	3.9%	LEVENQAKR	94.7%	28.1	25	12.7	1	0	0	1086.59	237	245
Conserved oligomeric Golgi complex subunit 5	COG5	COG5_HUMAN	92.7	100.0%	3	3	3	0.00%	3.9%	LFDPINLVFPPGGR	99.7%	46.1	25	45	1	0	0	1541.85	493	506
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	11	11	16	0.02%	13.6%	AEGSSTASSGSQLAEGK	99.7%	88.2	25	88.2	2	0	0	1566.72	503	519
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	11	11	16	0.02%	13.6%	APSHSESALNNDSK	99.7%	51.6	25	44	1	0	0	1456.67	1073	1086
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	11	11	16	0.02%	13.6%	GVISTPVIR	99.7%	40.5	25	28.6	2	0	0	941.58	987	995
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	11	11	16	0.02%	13.6%	GVQGFQDYIEK	99.7%	61.1	25	48	1	0	0	1283.63	2	12
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	11	11	16	0.02%	13.6%	LLVDADNCLHR	99.2%	36.2	25	36.2	1	0	0	1325.66	46	56
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	11	11	16	0.02%	13.6%	LYEPDQLQELK	99.7%	40.9	25	31.9	2	0	0	1375.71	748	758
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	11	11	16	0.02%	13.6%	NIQDTSDLDAIAK	99.7%	88.1	25	77	2	0	0	1403.70	292	304
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	11	11	16	0.02%	13.6%	NQAAIQGRPPYAASAEEVAK	99.6%	32.6	25	32.6	0	1	0	2071.06	1010	1029
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	11	11	16	0.02%	13.6%	SPQTPELVEALAFR	99.7%	67.6	25	66.7	2	0	0	1557.83	652	665
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	11	11	16	0.02%	13.6%	SQGGVQPIPSQGGK	99.7%	54.2	25	51.2	1	0	0	1339.70	933	946
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	11	11	16	0.02%	13.6%	VAAASGHCGAFSGSDSSR	99.7%	50.6	25	50.6	0	1	0	1723.75	912	929
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	5	5	11	0.01%	11.2%	AESTPEIAEQR	99.7%	48.3	25	43.2	2	0	0	1230.60	225	235
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	5	5	11	0.01%	11.2%	DSQTQAILTK	99.7%	46.9	25	30.3	3	0	0	1104.59	239	248
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	5	5	11	0.01%	11.2%	EGSQGELTPANSQSR	99.7%	70.5	25	65.1	4	0	0	1560.72	472	486
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	5	5	11	0.01%	11.2%	LQFIADHCPTLR	98.2%	32.4	25	11.3	1	0	0	1470.75	60	71
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	5	5	11	0.01%	11.2%	TLYTQIR	99.2%	35.9	25	32.5	1	0	0	894.50	364	370
COP9 signalosome complex subunit 7a	COPS7A	CSN7A_HUMAN	30.3	100.0%	3	3	4	0.00%	12.7%	ELAESDFASTFR	99.7%	48.2	25	45.5	2	0	0	1372.64	54	65
COP9 signalosome complex subunit 7a	COPS7A	CSN7A_HUMAN	30.3	100.0%	3	3	4	0.00%	12.7%	LEVDYSIGR	99.7%	46	25	32.8	1	0	0	1051.54	152	160
COP9 signalosome complex subunit 7a	COPS7A	CSN7A_HUMAN	30.3	100.0%	3	3	4	0.00%	12.7%	VTGQNQEQFLLLAK	99.5%	38	25	29.8	1	0	0	1588.87	7	20
Coronin-1C	CORO1C	COR1C_HUMAN	53.3	99.8%	2	2	3	0.00%	2.7%	KTTDTASVQNEAK	99.7%	56.5	25	45.5	2	0	0	1392.70	428	440
Coronin-1C	CORO1C	COR1C_HUMAN	53.3	99.8%	2	2	3	0.00%	2.7%	TTDTASVQNEAK	99.7%	55.5	25	47	1	0	0	1264.60	429	440
COUP transcription factor 2	NR2F2	COT2_HUMAN	45.6	99.8%	2	2	3	0.00%	5.3%	IFQEQVEK	98.1%	32.2	25	14.7	1	0	0	1020.54	294	301
COUP transcription factor 2	NR2F2	COT2_HUMAN	45.6	99.8%	2	2	3	0.00%	5.3%	TVSSSVIEQLFFVR	99.7%	59.4	25	57.9	2	0	0	1611.87	372	385
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	5	5	8	0.01%	16.8%	FCTGLTQIETLFK	99.7%	72.3	25	68.4	2	0	0	1557.80	253	265
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	5	5	8	0.01%	16.8%	FSEVLKR	99.7%	41.6	25	16.8	2	0	0	878.51	308	314
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	5	5	8	0.01%	16.8%	LAVEALSSLDGDLAGR	99.7%	68.3	25	68.3	1	0	0	1586.84	157	172
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	5	5	8	0.01%	16.8%	LGFSEVELVQMVVDGVK	99.7%	41.1	25	39.2	1	0	0	1864.97	342	358
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	5	5	8	0.01%	16.8%	VLTPELYAELR	99.7%	50.7	25	37.4	2	0	0	1303.73	33	43
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	12	12	20	0.02%	15.7%	AIANVPPIQEK	99.7%	51	25	48.8	2	0	0	1179.67	517	527
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	12	12	20	0.02%	15.7%	AIYELAISQPR	99.6%	38.8	25	30.1	2	0	0	1260.69	661	671
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	12	12	20	0.02%	15.7%	ALDVDYR	96.6%	29.9	25	22.1	1	0	0	851.43	268	274

Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	12	12	20	0.02%	15.7%	APAEVQITAEQLLR	99.7%	69.3	25	59.9	1	0	0	1538.85	183	196
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	12	12	20	0.02%	15.7%	FAELETILGDIDR	99.7%	77.2	25	65.8	2	0	0	1491.77	646	658
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	12	12	20	0.02%	15.7%	FEENQKEFER	99.7%	44.4	25	33.5	2	0	0	1355.62	422	431
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	12	12	20	0.02%	15.7%	FVLVHPDVK	99.4%	37.7	25	25.1	2	0	0	1053.61	369	377
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	12	12	20	0.02%	15.7%	GIEDIIVSK	99.7%	57.5	25	43.2	2	0	0	973.56	467	475
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	12	12	20	0.02%	15.7%	LMLLESWR	99.7%	49.7	25	43.7	1	0	0	1047.57	752	759
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	12	12	20	0.02%	15.7%	LVESDAEAEAVR	99.7%	97.7	25	89	2	0	0	1288.64	500	511
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	12	12	20	0.02%	15.7%	SFEEEFGTASDKER	99.7%	88.3	25	88.3	1	0	0	1631.72	760	773
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	12	12	20	0.02%	15.7%	YTYMEEMLGNVAGAR	99.7%	81.2	25	81.2	2	0	0	1704.77	316	330
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	6	6	10	0.01%	20.2%	DVATVAFCDAQSTQEIHEK	95.4%	23.2	25	23.2	0	1	0	2148.99	47	65
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	6	6	10	0.01%	20.2%	GAALDVHESEPFSFSQGPLK	99.7%	39.2	25	38.3	0	1	0	2116.03	286	305
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	6	6	10	0.01%	20.2%	IGSGFDNIDIK	99.7%	60.7	25	45.6	2	0	0	1178.61	98	108
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	6	6	10	0.01%	20.2%	IRGETLGIIGLGR	99.7%	40	25	36.5	0	2	0	1354.82	172	184
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	6	6	10	0.01%	20.2%	QGAFLVNTAR	99.7%	57.6	25	47.9	2	0	0	1076.58	257	266
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	6	6	10	0.01%	20.2%	VGQAVALR	99.7%	62.3	25	50.2	2	0	0	813.49	185	192
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	6	6	10	0.01%	20.2%	VQSVEQIR	99.7%	42.8	25	20.6	2	0	0	958.53	156	163
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	4	4	6	0.01%	11.0%	GAALDVHESEPFSFAQGPLK	99.7%	38.6	25	38.6	0	1	0	2100.04	292	311
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	4	4	6	0.01%	11.0%	IGSGYDNVDIK	99.7%	48.7	25	42	2	0	0	1180.58	104	114
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	4	4	6	0.01%	11.0%	QGAFLVNAAR	99.7%	52.7	25	45.8	1	0	0	1046.57	263	272
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	4	4	6	0.01%	11.0%	VQSVEQIR	99.7%	42.8	25	20.6	2	0	0	958.53	162	169
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	19	22	43	0.04%	35.4%	ALEHSALAINHK	99.7%	54.8	25	53.6	2	2	0	1303.71	320	331
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	19	22	43	0.04%	35.4%	CSNPLDTSVK	97.7%	31.4	25	26.7	2	0	0	1120.53	218	227
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	19	22	43	0.04%	35.4%	ENFCNIHVSLVPQPSSTGEQK	99.7%	37.1	25	35.7	0	2	0	2371.13	173	193
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	19	22	43	0.04%	35.4%	FSDSYASVIK	99.7%	71	25	54.1	2	0	0	1116.56	310	319
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	19	22	43	0.04%	35.4%	FVGQDVEGER	99.7%	75.9	25	60.4	2	0	0	1135.54	499	508
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	19	22	43	0.04%	35.4%	GIIASSVGTILK	99.7%	65.2	25	63.2	2	0	0	1158.71	17	28
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	19	22	43	0.04%	35.4%	GLGLSPDLVVCR	99.7%	40.3	25	39.3	2	0	0	1285.69	206	217
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	19	22	43	0.04%	35.4%	IQAIAWAR	99.7%	62.2	25	45.3	2	0	0	928.54	382	389
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	19	22	43	0.04%	35.4%	IYQYVINK	99.7%	51.7	25	40.2	2	0	0	1040.58	93	100
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	19	22	43	0.04%	35.4%	KLYGDADYLEER	99.7%	76.2	25	73	2	2	0	1471.71	466	477
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	19	22	43	0.04%	35.4%	LCSAHGVLVPGGFGVR	99.7%	74.8	25	73.4	2	2	0	1625.86	361	376
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	19	22	43	0.04%	35.4%	LDLPIER	97.4%	30.8	25	11.5	1	0	0	855.49	270	276
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	19	22	43	0.04%	35.4%	LLETCSIALVGK	99.7%	85.7	25	75.6	2	0	0	1303.73	295	306
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	19	22	43	0.04%	35.4%	LYGDADYLEER	99.7%	85.1	25	72.6	2	0	0	1343.61	467	477
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	19	22	43	0.04%	35.4%	RLDLPIER	99.7%	42.4	25	27.9	2	0	0	1011.59	269	276
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	19	22	43	0.04%	35.4%	SCGLHVTSIK	99.7%	46.3	25	35.7	2	0	0	1101.57	29	38
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	19	22	43	0.04%	35.4%	VPLLLEEQGVVDYFLR	99.7%	56.3	25	56.1	2	0	0	1890.04	253	268
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	19	22	43	0.04%	35.4%	YIDSADLEPITSQEEPVR	99.7%	106	25	93.3	2	0	0	2062.00	336	353
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	19	22	43	0.04%	35.4%	YILVTGGVISGIGK	99.7%	117	25	117	2	0	0	1376.82	3	16
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	2	2	4	0.00%	8.5%	ALEHSALAINHK	99.7%	54.8	25	53.6	2	2	0	1303.71	320	331
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	2	2	4	0.00%	8.5%	GLGLSPDLIVCR	99.1%	35.2	25	33.5	2	0	0	1299.71	206	217
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	2	2	4	0.00%	8.5%	VPVLLEEQSIVK	99.7%	82.6	25	82.6	2	0	0	1353.80	253	264
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	2	2	4	0.00%	8.5%	YILVTGGVISGIGK	99.7%	117	25	117	2	0	0	1376.82	3	16
Cullin-4B	CUL4B	CUL4B_HUMAN	104.0	100.0%	2	2	3	0.00%	2.5%	ETVEEQASTTER	99.7%	82.7	25	82.7	1	0	0	1379.63	830	841
Cullin-4B	CUL4B	CUL4B_HUMAN	104.0	100.0%	2	2	3	0.00%	2.5%	TIDGILLLIER	99.7%	74.3	25	68.2	2	0	0	1255.76	346	356
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	AADIDQEVK	99.7%	46.1	25	27.7	2	0	0	988.49	578	586
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	AADIDQEVKER	99.7%	48.1	25	44.2	4	0	0	1273.64	578	588
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	ADVFHAYLSLLK	99.7%	53.4	25	47.3	1	1	0	1376.76	392	403
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	ALTLIAGSPLK	99.7%	90.2	25	88.7	5	0	0	1083.68	631	641
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	AVAALLTIPEAEK	99.7%	85.3	25	63.6	2	0	0	1325.77	1179	1191
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	DISSIGLK	95.2%	28.5	25	10	1	0	0	832.48	104	111

Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	DLLDTVLPHLYNETK	99.7%	76.6	25	69.3	4	0	0	1770.93	1043	1057
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	DSSSTNLESMDTS	99.7%	48.6	25	48.6	1	0	0	1389.53	1218	1230
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	EGPAVVGQFIQDVK	99.7%	61.7	25	57.2	6	0	0	1486.79	813	826
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	EVEMGPFK	97.2%	30.6	25	24.5	1	0	0	936.45	1065	1072
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	FMATNDLMTELQK	99.7%	91.5	25	91.5	6	0	0	1573.72	24	36
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	FTISDHPQPIDPLLK	99.7%	47.3	25	36.5	2	1	0	1720.93	991	1005
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	GYLISGSSYAR	99.7%	50.6	25	38.4	4	0	0	1173.59	972	982
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	HEMLPEFYK	97.3%	30.8	25	30.8	1	0	0	1193.57	365	373
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	HTVDDGLDIR	99.7%	56.2	25	48.1	2	0	0	1140.56	1073	1082
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	HTVDDGLDIRK	99.7%	42.2	25	37.2	1	0	0	1268.66	1073	1083
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	IGEYLEK	99.7%	50.2	25	40.2	2	0	0	851.45	249	255
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	ISGSILNELIGLVR	99.7%	60.4	25	46.1	1	0	0	1483.88	730	743
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	ITSEALLVTQQLVK	99.7%	85.3	25	76.5	4	1	0	1542.91	535	548
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	LGTLSALDILIK	99.7%	87.5	25	74.6	4	0	0	1256.78	668	679
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	LLEDKNGEVQNLAVK	99.7%	34.4	25	16.3	0	2	0	1669.91	56	70
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	LSTLCPSAVLQR	99.7%	48.7	25	44.6	2	0	0	1344.73	1130	1141
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	LTLIDPETLLPR	99.7%	70.2	25	70	8	0	0	1380.81	958	969
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	MLTFLMLVR	99.7%	44.8	25	19.9	6	0	0	1139.63	1121	1129
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	MLTGPVYSQSTALTHK	99.7%	103	25	98.3	4	4	0	1733.89	778	793
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	MTSSDKDFR	99.7%	44	25	37.3	2	0	0	1086.49	15	23
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	NCIGDFLK	98.9%	34.8	25	22.1	1	0	0	966.47	1006	1013
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	SVILEAFSSPSEEVK	99.7%	85.7	25	82.2	6	0	0	1621.83	859	873
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	TLEDPDLNVR	99.7%	70.8	25	57.4	2	0	0	1171.60	1014	1023
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	TVIGELPPASSGSALAANVCK	99.7%	117	25	117	2	0	0	2042.06	112	132
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	TVSPALISR	99.5%	38.8	25	25.3	2	0	0	943.56	374	382
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	TYIQCIAAISR	99.7%	97.8	25	89.5	3	0	0	1295.68	233	243
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	33	41	106	0.10%	30.6%	VIRPLDQPSSFDATPYIK	99.7%	66.8	25	66.8	2	3	0	2047.09	549	566
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	52	0.05%	49.2%	ALGTPNNEVWPEVESLQDYK	99.7%	66.1	25	66.1	2	0	0	2289.10	219	238
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	52	0.05%	49.2%	DLKPQNLLIDDK	98.4%	32.9	25	27.9	1	0	0	1411.78	128	139
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	52	0.05%	49.2%	DLKPQNLLIDDKGTIK	99.7%	47	25	47	2	4	0	1811.03	128	143
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	52	0.05%	49.2%	IGEGTYGVVYK	99.7%	91.7	25	43.6	4	0	0	1185.62	10	20
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	52	0.05%	49.2%	IRLESEEEGVPSTAIR	99.7%	83.1	25	83.1	3	0	0	1785.93	35	50
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	52	0.05%	49.2%	LADFGLAR	99.7%	44.4	25	0	8	0	0	862.48	144	151
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	52	0.05%	49.2%	LESEEEGVPSTAIR	99.7%	63.3	25	55.5	3	0	0	1516.75	37	50
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	52	0.05%	49.2%	MALNHPYFNDLDNQIK	99.7%	73.3	25	70.2	4	4	0	1948.92	280	295
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	52	0.05%	49.2%	MLIYDPAK	99.6%	39.8	25	35.3	2	0	0	950.50	267	274
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	52	0.05%	49.2%	MLIYDPAKR	99.7%	46.2	25	29.9	4	0	0	1106.60	267	275
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	52	0.05%	49.2%	NLDENGLDLLSK	99.7%	79.1	25	62.9	3	0	0	1330.69	255	266
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	52	0.05%	49.2%	SPEVLLGSAR	99.7%	75.3	25	63.4	2	0	0	1028.57	171	180
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	52	0.05%	49.2%	WKPGSLASHVK	99.7%	34.4	25	33.6	0	2	0	1209.67	244	254
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	21	52	0.05%	49.2%	YLDSIPPGQYMDSSLVK	99.7%	56.2	25	56.2	4	0	0	1912.94	90	106
Cyclin-dependent kinase 11B	CDK11B	CD11B_HUMAN	92.7	100.0%	3	3	4	0.00%	4.4%	APELLLGAK	99.7%	47.1	25	44.1	2	0	0	911.56	605	613
Cyclin-dependent kinase 11B	CDK11B	CD11B_HUMAN	92.7	100.0%	3	3	4	0.00%	4.4%	FGALLSDQGFDLMNK	99.4%	37.2	25	37.2	1	0	0	1671.81	688	702
Cyclin-dependent kinase 11B	CDK11B	CD11B_HUMAN	92.7	100.0%	3	3	4	0.00%	4.4%	IEEGTYGVVYR	99.7%	62.8	25	56.9	1	0	0	1285.64	444	454
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	10	18	0.02%	36.6%	ALFPGDSEIDQLFR	99.7%	77	25	73.5	2	0	0	1607.81	201	214
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	10	18	0.02%	36.6%	APEILLGCK	99.7%	63.8	25	61.6	2	0	0	1000.55	170	178
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	10	18	0.02%	36.6%	DLKPQNLLINTEGAIK	99.7%	59.6	25	59.6	2	2	0	1767.00	127	142
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	10	18	0.02%	36.6%	ELNHPNIVK	94.6%	28	25	15.1	1	0	0	1063.59	57	65
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	10	18	0.02%	36.6%	FMDASALTGIPLPLIK	99.7%	104	25	101	4	0	0	1686.95	90	105
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	10	18	0.02%	36.6%	IGEGTYGVVYK	99.7%	91.7	25	43.6	4	0	0	1185.62	10	20
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	10	18	0.02%	36.6%	IRLDTETEGVPSTAIR	99.7%	65.1	25	58.3	1	2	0	1757.94	35	50

Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	10	18	0.02%	36.6%	LADFGLAR	99.7%	44.4	25	0	8	0	0	862.48	143	150
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	10	18	0.02%	36.6%	LTGEVVALKK	99.7%	49	25	38.7	2	0	0	1057.66	25	34
Cyclin-dependent kinase 5	CDK5	CDK5_HUMAN	33.3	100.0%	2	2	2	0.00%	14.0%	DLKPQNLLINR	99.0%	35.2	25	35.1	1	0	0	1323.77	126	136
Cyclin-dependent kinase 5	CDK5	CDK5_HUMAN	33.3	100.0%	2	2	2	0.00%	14.0%	LADFGLAR	99.7%	44.4	25	0	8	0	0	862.48	142	149
Cyclin-dependent kinase 5	CDK5	CDK5_HUMAN	33.3	100.0%	2	2	2	0.00%	14.0%	LPDYKPYPMYPATTSLVNVVPK	99.6%	32.8	25	32.8	0	1	0	2509.31	233	254
Cyclin-dependent kinase 9	CDK9	CDK9_HUMAN	42.8	100.0%	3	3	6	0.01%	11.3%	GSQITQQSTNQSR	99.7%	89.7	25	81.2	2	0	0	1434.69	346	358
Cyclin-dependent kinase 9	CDK9	CDK9_HUMAN	42.8	100.0%	3	3	6	0.01%	11.3%	LADFGLAR	99.7%	44.4	25	0	8	0	0	862.48	165	172
Cyclin-dependent kinase 9	CDK9	CDK9_HUMAN	42.8	100.0%	3	3	6	0.01%	11.3%	LLVLDPAQR	99.7%	41.1	25	32.5	2	0	0	1024.62	295	303
Cyclin-dependent kinase 9	CDK9	CDK9_HUMAN	42.8	100.0%	3	3	6	0.01%	11.3%	NPATTNQTEFER	99.7%	69.6	25	63.2	2	0	0	1407.65	359	370
Cyclin-dependent kinase inhibitor 2A, isoforms 1/2/3	CDKN2A	CD2A1_HUMAN	16.5	99.8%	2	2	3	0.00%	18.6%	ALLEAGALPNAPNSYGR	98.8%	34.4	25	34.4	2	0	0	1713.89	30	46
Cyclin-dependent kinase inhibitor 2A, isoforms 1/2/3	CDKN2A	CD2A1_HUMAN	16.5	99.8%	2	2	3	0.00%	18.6%	EGFLDTLVVLHR	97.9%	31.7	25	31.7	1	0	0	1398.77	88	99
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	5	5	8	0.01%	10.7%	AAQELQEGQR	99.7%	79.6	25	56.3	2	0	0	1129.56	360	369
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	5	5	8	0.01%	10.7%	FDSPESHVGVAWR	99.6%	39.2	25	34.1	1	0	0	1486.71	197	209
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	5	5	8	0.01%	10.7%	IGDTPMVR	99.7%	46.6	25	38.7	2	0	0	904.46	84	91
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	5	5	8	0.01%	10.7%	PSETPQAEVGPTGCPHR	99.7%	52.6	25	52.5	0	1	0	1819.84	2	18
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	5	5	8	0.01%	10.7%	SNDEEAFTFAR	99.7%	72.5	25	72.5	2	0	0	1286.56	326	336
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	5	5	6	0.01%	13.3%	AIGTDEDLAHSSIR	99.7%	59.5	25	52.8	1	0	0	1484.73	394	407
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	5	5	6	0.01%	13.3%	GVGAIYIR	99.7%	50.8	25	31.8	1	0	0	848.50	264	271
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	5	5	6	0.01%	13.3%	IPLDVNDMK	99.7%	42.3	25	41.1	1	0	0	1044.54	240	248
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	5	5	6	0.01%	13.3%	KVYFHTDAAQAVGK	97.0%	24.7	25	24.7	0	1	0	1534.80	226	239
Cysteine desulfurase, mitochondrial	NFS1	NFS1_HUMAN	50.2	100.0%	5	5	6	0.01%	13.3%	SLEAEGFQVTYLPVQK	99.7%	82.8	25	80.1	2	0	0	1808.94	165	180
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	6	7	11	0.01%	14.8%	ADLTEYLSTHYK	99.7%	49.8	25	49.8	1	0	0	1440.70	214	225
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	6	7	11	0.01%	14.8%	FTGSEIR	98.7%	33.7	25	22.6	2	0	0	809.42	270	276
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	6	7	11	0.01%	14.8%	IAEVDASVVR	99.7%	75.6	25	44.9	2	0	0	1058.58	433	442
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	6	7	11	0.01%	14.8%	LCTSATESEVAR	99.7%	104	25	97.5	2	0	0	1323.62	379	390
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	6	7	11	0.01%	14.8%	MVLAAAGGVEHQQLLDLAQK	99.7%	49.3	25	49.3	0	3	0	2092.12	229	248
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	6	7	11	0.01%	14.8%	RIPLAEWESR	98.0%	32.1	25	32.1	1	0	0	1256.67	423	432
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	ATAAPAGAPPQPQDLEFTK	99.7%	72.5	25	66.9	2	0	0	1909.97	24	42
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	AVAFQNPQTHVIENLHAAAYR	99.7%	53.8	25	53.8	0	2	0	2350.21	163	183
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	ENMAYTVECLR	99.7%	61	25	54.2	4	0	0	1401.61	117	127
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	GSNTTSHLHQAVAK	99.7%	66.1	25	55.3	2	1	0	1450.74	302	315
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	LPNGLVIASLENYSPVSR	99.7%	110	25	110	2	2	0	1929.04	43	60
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	MALIGLGVSHPVLK	99.7%	69.6	25	69.6	2	4	0	1450.85	218	231
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	NALANPLYCPDYR	99.7%	64.6	25	54.6	2	0	0	1566.74	184	196
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	QVAEQFLNMR	99.7%	82.6	25	71.9	4	0	0	1235.62	232	241
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	RWEVADLQPQLK	99.7%	53.5	25	44.5	2	2	0	1482.81	148	159
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	SMAASGNLGHTPFVDEL	99.7%	79.1	25	79.1	4	0	0	1745.82	437	453
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	TIAQGNLSNTDVQAAK	99.7%	107	25	101	3	0	0	1630.84	360	375
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	VTSEELHYFVQNHFTSAR	99.7%	41.6	25	41.6	0	2	0	2165.04	200	217
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	WEVADLQPQLK	99.7%	73.3	25	60.6	2	0	0	1326.71	149	159
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	44	0.04%	43.5%	YEDFSNLGTTHLLR	99.7%	80.6	25	79.1	2	0	0	1665.82	71	84
Cytochrome b-c1 complex subunit 8	UQCRQ	QCR8_HUMAN	9.9	100.0%	3	4	7	0.01%	35.4%	HVISYSLSPFEQR	99.7%	70.6	25	70.6	2	2	0	1562.80	13	25
Cytochrome b-c1 complex subunit 8	UQCRQ	QCR8_HUMAN	9.9	100.0%	3	4	7	0.01%	35.4%	IRESFFR	97.3%	30.8	25	15.9	1	0	0	954.52	42	48
Cytochrome b-c1 complex subunit 8	UQCRQ	QCR8_HUMAN	9.9	100.0%	3	4	7	0.01%	35.4%	NPAAYENDK	99.5%	38.6	25	34.8	2	0	0	1021.46	74	82
Cytochrome b-c1 complex subunit Rieske, mitochondrial	UQCRFS1	UCRI_HUMAN	29.7	99.9%	2	3	6	0.01%	10.9%	NAVTQFVSSMSASADVLALAK	99.7%	91.7	25	91.7	2	0	0	2110.08	131	151
Cytochrome b-c1 complex subunit Rieske, mitochondrial	UQCRFS1	UCRI_HUMAN	29.7	99.9%	2	3	6	0.01%	10.9%	RLEVLDSTK	99.7%	45.1	25	38.9	4	0	0	1060.60	93	101
Cytochrome c oxidase assembly factor 3 homolog, mitochondrial	COA3	COA3_HUMAN	11.7	99.8%	2	2	3	0.00%	17.9%	FLDELEDEAK	99.0%	35	25	27.6	2	0	0	1208.57	84	93
Cytochrome c oxidase assembly factor 3 homolog, mitochondrial	COA3	COA3_HUMAN	11.7	99.8%	2	2	3	0.00%	17.9%	RGEAPFAQR	99.6%	38.8	25	25.2	1	0	0	1031.54	14	22
Cytochrome c oxidase assembly protein COX15 homolog	COX15	COX15_HUMAN	46.0	99.7%	2	2	3	0.00%	4.6%	LPETHQLLQLR	99.5%	32.1	25	30.8	0	2	0	1347.77	251	261
Cytochrome c oxidase assembly protein COX15 homolog	COX15	COX15_HUMAN	46.0	99.7%	2	2	3	0.00%	4.6%	YQQFPEFK	95.0%	28.3	25	27.5	1	0	0	1086.53	124	131
Cytochrome c oxidase protein 20 homolog	COX20	COX20_HUMAN	13.3	99.8%	2	2	2	0.00%	22.0%	ILYEGTHLDPER	98.3%	32.6	25	21.3	1	0	0	1442.73	99	110

Cytochrome c oxidase protein 20 homolog	COX20	COX20_HUMAN	13.3	99.8%	2	2	2	0.00%	22.0%	LLGFLDVENTPCAR	98.6%	33.6	25	30	1	0	0	1604.81	18	31
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	5	7	17	0.02%	18.9%	IFEMGPVFTL	99.7%	44.5	25	44.5	2	0	0	1169.59	218	227
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	5	7	17	0.02%	18.9%	ILYMTDEVNDPSLTIK	99.7%	95.8	25	94.5	7	0	0	1867.94	83	98
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	5	7	17	0.02%	18.9%	LLDVDNR	99.7%	50.2	25	27.5	2	0	0	844.45	135	141
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	5	7	17	0.02%	18.9%	LLDVDNRVVLPIEAPIR	99.7%	44.9	25	43.5	0	2	0	1932.13	135	151
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	5	7	17	0.02%	18.9%	VVLPIEAPIR	99.7%	50.2	25	50.2	4	0	0	1106.69	142	151
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	8	9	16	0.02%	12.4%	ANYLASPPLVIAYAIAGTIR	99.7%	59	25	59	2	0	0	2074.17	548	567
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	8	9	16	0.02%	12.4%	FVEFFGPGVAQLSIADR	99.7%	91.9	25	88.5	2	0	0	1852.96	277	293
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	8	9	16	0.02%	12.4%	GPFLLGIK	99.4%	37.3	25	28.8	2	0	0	844.53	786	793
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	8	9	16	0.02%	12.4%	NQDLEFER	99.7%	44.7	25	39	1	0	0	1050.49	142	149
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	8	9	16	0.02%	12.4%	SPPFFENLTLDLQPPK	99.7%	62.1	25	52.9	2	0	0	1842.96	645	660
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	8	9	16	0.02%	12.4%	VILQDFTGVPAVVDFAAMR	99.7%	66.9	25	66.9	2	1	0	2065.08	83	101
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	8	9	16	0.02%	12.4%	VLLEAAIR	99.7%	59.2	25	47.3	2	0	0	884.56	41	48
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	8	9	16	0.02%	12.4%	YQQAGLPLIVLAGK	99.7%	78.2	25	78.2	2	0	0	1470.87	759	772
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	AATSPALFNR	99.7%	60.2	25	43.4	2	0	0	1047.56	3079	3088
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	AERPDVDEKR	99.7%	37.9	25	36.2	0	2	0	1214.61	3719	3728
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	AISKDHLYGTLDPNTR	99.5%	32.2	25	32.2	0	1	0	1800.92	2258	2273
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	ALGEYLER	99.7%	52.1	25	47.3	2	0	0	950.49	1614	1621
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	ALGHQLGR	99.6%	39.2	25	28.6	2	0	0	851.48	1918	1925
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	ANEVEQMIR	99.7%	49.8	25	40.5	4	0	0	1089.54	3430	3438
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	ASVVTLPVYLNFTR	99.7%	59.8	25	58.1	3	0	0	1579.88	4602	4615
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	CYLTMTQALEAR	99.7%	91.6	25	85.4	2	0	0	1456.69	1888	1899
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	DAATIMQPYFTSNGLVTK	99.7%	71.9	25	69	2	0	0	1972.97	2418	2435
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	DLFQVAFNR	99.7%	73.5	25	64	6	0	0	1109.57	3862	3870
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	DLPPVSGSIIWAK	99.7%	53.4	25	53.4	2	0	0	1382.77	640	652
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	DSAIQQQVANLQMK	99.7%	97.1	25	89.6	4	0	0	1573.80	1229	1242
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	DYIPVDQEELRDYVK	99.7%	44.1	25	41.4	2	0	0	1881.92	2880	2894
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	EAIVNSCVFVHQTLHQANAR	98.9%	28.7	25	28.7	0	1	0	2294.15	3141	3160
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	EALELTDTGLLSGSEER	99.7%	104	25	97.9	2	0	0	1819.89	1302	1318
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	EFGPVVIDYGK	99.7%	40.7	25	40.7	2	0	0	1223.63	1101	1111
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	EGLMLDSHEELYK	99.7%	57.2	25	53	1	0	0	1563.74	3040	3052
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	EHINSVSAMK	99.7%	40.5	25	38.8	1	0	0	1131.55	1499	1508
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	EQPWVSVQPR	99.1%	35.3	25	29	1	0	0	1225.63	1348	1357
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	EVWNTYELDLVNYQNK	99.7%	61.8	25	61.8	2	0	0	2027.97	1468	1483
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	EYQTQLIQR	98.8%	34.4	25	21.5	2	0	0	1178.62	603	611
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	FNYGFEYLGVQDK	99.7%	105	25	105	2	0	0	1579.74	1866	1878
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	FQSISTEFLALMK	99.7%	81.1	25	76.1	2	0	0	1530.79	1568	1580
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	FTQDTQPHYIYSPR	99.7%	71.8	25	71.8	2	0	0	1752.83	2784	2797
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	GWENHVEGQK	98.8%	34.2	25	24	1	0	0	1183.55	672	681
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	HLLPVETQR	97.4%	30.8	25	23.8	1	0	0	1092.62	1559	1567
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	IAFIMDESNVLDSGFLER	99.7%	58.2	25	57.6	1	0	0	2072.00	2990	3007
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	IFTIESTR	99.7%	56.3	25	42.8	2	0	0	966.53	717	724
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	IFVFEPPPGVK	99.7%	47.7	25	36.9	2	0	0	1229.69	4144	4154
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	IMFEVQDLK	99.7%	47.2	25	37.8	2	0	0	1138.58	2341	2349
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	INEWLTLVEK	99.7%	64.8	25	53.5	2	0	0	1244.69	1698	1707
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	INMLVIELK	99.7%	71.4	25	52.5	2	0	0	1088.64	1396	1404
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	IQFVGACNPPTDPGR	99.7%	96.3	25	91.7	2	0	0	1628.79	2706	2720
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	IQGLTVEQAEAVVR	99.7%	97.3	25	88.4	3	0	0	1512.84	3924	3937
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	ITNQVIYLNPPIEECR	99.7%	60.2	25	60.2	2	0	0	1959.00	964	979
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	IWAHEALR	99.4%	37.6	25	19.9	2	0	0	995.54	2824	2831
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	KYEFGESDLR	99.7%	60.8	25	49.9	2	0	0	1243.60	4204	4213

Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	LAETVFNFQEK	99.7%	58.7	25	52.9	1	0	0	1325.67	836	846
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	LCDEQLSSQSHYDFGLR	99.5%	32.5	25	26	0	1	0	2054.92	2075	2091
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	LEGVEGVAHIIDPK	99.7%	53.2	25	52.5	1	0	0	1476.81	2244	2257
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	LFLTMEINPK	99.6%	39.9	25	32.3	2	0	0	1205.66	4124	4133
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	LGGSPFGPAGTGK	99.7%	68.2	25	64.7	2	0	0	1145.60	1900	1912
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	LKQDGDSFR	99.7%	49	25	35.7	2	0	0	1065.53	682	690
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	LLNTFLER	99.7%	51.5	25	44.1	2	0	0	1005.57	4264	4271
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	LQGEFQLR	99.7%	43.2	25	31	2	0	0	990.54	3734	3741
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	LRDQLGTAK	99.7%	48.5	25	38.7	2	0	0	1001.57	568	576
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	LSCLPAFK	99.6%	39.6	25	27.9	2	0	0	935.50	3938	3945
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	LSLSNAISTALPLTQLR	99.7%	52.4	25	51	1	0	0	1798.04	4575	4591
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	LVQTPLTDR	99.7%	52	25	42.4	2	0	0	1042.59	1879	1887
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	MVVLSLPR	99.7%	58	25	55.6	4	0	0	914.55	991	998
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	NVVHELR	99.5%	38.7	25	30.8	1	0	0	866.48	957	963
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	NYMSNPSYNYEIVNR	99.7%	93.8	25	90.6	2	0	0	1863.83	3370	3384
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	QLQNISLAAASGGAK	99.7%	42.8	25	34	1	0	0	1428.78	4488	4502
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	QNLDALLNQLK	99.7%	72.2	25	60.1	2	0	0	1269.72	1361	1371
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	QPQGHLLLIGVSGAGK	99.2%	29.9	25	29.9	0	2	0	1574.90	2928	2943
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	QTDVLQQLSIQMANAK	99.7%	84.6	25	79.5	1	0	0	1787.93	1850	1865
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	QYASYEFVQR	99.7%	59.8	25	52.3	2	0	0	1290.61	1379	1388
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	SFEWLSQMR	99.7%	57.5	25	47.6	3	0	0	1183.56	1835	1843
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	SIPLDEGEDEAQR	99.7%	73.5	25	70.3	2	0	0	1458.67	2384	2396
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	SIPLDEGEDEAQRR	97.8%	31.7	25	31.7	1	0	0	1614.77	2384	2397
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	SLETCMYDHK	99.7%	49.6	25	46.1	2	0	0	1283.54	863	872
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	SLLQALNEVK	99.7%	68.3	25	51.8	4	0	0	1114.65	3748	3757
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	SMANPPAAVK	96.8%	30	25	23.2	1	0	0	985.51	3309	3318
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	SNSLAFIK	99.4%	37.5	25	25	2	0	0	879.49	113	120
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	SPLVMDVLNIQGVQR	99.7%	85.9	25	83.7	4	0	0	1668.91	1585	1599
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	SSLQSQCLNEVLK	99.7%	84.1	25	69.5	2	0	0	1505.76	3706	3718
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	SVLVSAGNVK	98.8%	34.3	25	26.5	2	0	0	973.57	2095	2104
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	SVLVSAGNVKR	99.4%	37	25	30.4	2	0	0	1129.67	2095	2105
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	TEYLSNADER	99.7%	45.7	25	45.7	2	0	0	1197.54	3550	3559
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	TFSEILNR	99.7%	43.8	25	36.7	2	0	0	979.52	873	880
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	TFSSIPVSR	99.7%	51.5	25	45	2	0	0	993.54	4160	4168
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	TLINELVK	99.2%	35.9	25	7.62	2	0	0	929.57	4450	4457
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	TMTLFSALR	99.7%	64.8	25	59.7	2	0	0	1055.56	2602	2610
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	TPNGVVLAPVQLGK	99.7%	64.6	25	64.6	2	0	0	1392.82	2644	2657
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	TPVIDADKPVSSQLR	99.7%	79	25	76.6	2	2	0	1625.89	122	136
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	TPVSITEHPK	99.7%	54.2	25	50.3	2	0	0	1108.60	1688	1697
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	TSAPITCELLNK	99.7%	60	25	51.9	2	0	0	1346.70	1993	2004
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	TSFLDDAFRK	99.7%	63.6	25	60.1	2	0	0	1199.61	3612	3621
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	TVENIKDPLFR	99.7%	55.4	25	47.5	2	0	0	1331.73	4401	4411
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	VAAPDVVVPTLDTVR	99.7%	74.9	25	74.9	2	0	0	1551.87	2562	2576
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	VDNEFDQR	99.7%	55.8	25	49.1	2	0	0	1022.45	4256	4263
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	VEPLRNELQK	95.4%	28.6	25	14.5	1	0	0	1225.69	3409	3418
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	VLLTTQGVDMISK	99.7%	101	25	95.5	5	0	0	1404.78	4330	4342
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	VLRPQVTAVAQQNQGEVPEPQDMK	99.7%	53	25	50.4	0	3	0	2678.36	483	506
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	VMSQEIQEQLHK	99.7%	52.7	25	48.6	2	0	0	1469.74	3255	3266
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	VNFLPEIITLSK	99.7%	66.1	25	61	2	0	0	1373.80	737	748
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	VPLAIVNK	99.7%	43.4	25	42.7	1	0	0	853.55	760	767
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	VPQIEVETHK	99.7%	46.5	25	33.5	2	0	0	1179.64	2552	2561

Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	VPVNLLR	99.1%	35.5	25	23.2	3	0	0	810.52	4134	4140
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	VQYPQSQACK	98.6%	33.5	25	27.7	2	0	0	1208.57	625	634
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	VTDFGDKVEDPTFLNQLQSGVNR	96.6%	24.2	25	24.2	0	1	0	2579.27	229	251
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	VTFVNFTVTR	99.7%	91.7	25	87	2	0	0	1183.65	3696	3705
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	WQALLVQIR	97.3%	30.8	25	29.1	1	0	0	1126.67	1079	1087
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	WTDENIDTVALK	99.7%	66.3	25	63.8	2	0	0	1404.70	2845	2856
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	95	103	193	0.19%	23.4%	YATLATVSR	99.7%	55.4	25	45.5	2	0	0	981.54	2350	2358
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	6	7	11	0.01%	16.4%	IGILHENFQTLK	99.7%	45.2	25	37.2	2	2	0	1412.79	333	344
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	6	7	11	0.01%	16.4%	IPAVVVEK	99.7%	45.2	25	29.3	2	0	0	854.53	311	318
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	6	7	11	0.01%	16.4%	KPVTVSPTTPTSPTEGEAS	99.7%	67.3	25	67.3	1	0	0	1885.94	505	523
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	6	7	11	0.01%	16.4%	QPPTAAGRPVDASPR	96.7%	24.4	25	24.4	0	1	0	1519.80	386	400
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	6	7	11	0.01%	16.4%	SGQKPVLDVHAELDR	99.7%	45	25	40.6	0	1	0	1663.88	487	501
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	6	7	11	0.01%	16.4%	SVSSNVASVSPIPAGSK	99.7%	73.8	25	62	2	0	0	1586.84	412	428
Cytoplasmic dynein 2 heavy chain 1	DYNC2H1	DYHC2_HUMAN	492.6	100.0%	4	4	5	0.00%	1.2%	IAEALLSDLPGFR	98.8%	34.3	25	31.7	1	0	0	1401.77	502	514
Cytoplasmic dynein 2 heavy chain 1	DYNC2H1	DYHC2_HUMAN	492.6	100.0%	4	4	5	0.00%	1.2%	TVAGGGLETISNLK	99.7%	68.8	25	49.4	1	0	0	1359.75	999	1012
Cytoplasmic dynein 2 heavy chain 1	DYNC2H1	DYHC2_HUMAN	492.6	100.0%	4	4	5	0.00%	1.2%	VLSFPGGSLLLAGR	99.7%	75.3	25	75.3	2	0	0	1386.81	2643	2656
Cytoplasmic dynein 2 heavy chain 1	DYNC2H1	DYHC2_HUMAN	492.6	100.0%	4	4	5	0.00%	1.2%	VTTLTTHAGIR	99.7%	51.2	25	43.4	1	0	0	1169.66	1388	1398
Cytoplasmic dynein 2 light intermediate chain 1	DYNC2LI1	DC2L1_HUMAN	39.6	99.8%	2	2	3	0.00%	6.6%	GVINQLAFGIDK	99.7%	87.8	25	79.9	2	0	0	1274.71	232	243
Cytoplasmic dynein 2 light intermediate chain 1	DYNC2LI1	DC2L1_HUMAN	39.6	99.8%	2	2	3	0.00%	6.6%	YDVFQDFESEK	99.7%	46.1	25	46.1	1	0	0	1406.61	188	198
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	10	11	20	0.02%	9.7%	ALNLAYSSIYGSYR	99.7%	91.7	25	81.2	2	0	0	1577.80	893	906
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	10	11	20	0.02%	9.7%	AVGPSSTQLYMVR	99.7%	56	25	47.1	1	0	0	1424.72	551	563
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	10	11	20	0.02%	9.7%	DFVSEAYLITLGK	99.7%	97.9	25	0	3	0	0	1455.77	151	163
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	10	11	20	0.02%	9.7%	EANHNVSAPYGR	99.3%	36.6	25	33.4	1	2	0	1314.62	827	838
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	10	11	20	0.02%	9.7%	LGTPQQIAIAR	99.7%	61.3	25	54.5	2	0	0	1167.68	1066	1076
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	10	11	20	0.02%	9.7%	NVIQSVLQAIR	99.7%	53.4	25	37.2	1	0	0	1240.74	505	515
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	10	11	20	0.02%	9.7%	SLLQGTILQYVK	99.7%	69.4	25	69.4	2	0	0	1362.80	939	950
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	10	11	20	0.02%	9.7%	SSLEGPTILDIEK	99.7%	83.8	25	66.7	2	0	0	1401.75	582	594
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	10	11	20	0.02%	9.7%	TVEVLEPEVTK	99.7%	40.3	25	35.1	2	0	0	1243.68	111	121
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	10	11	20	0.02%	9.7%	YSNSEVVTGSGR	99.7%	98.6	25	94.8	2	0	0	1255.59	366	377
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	6	6	11	0.01%	3.7%	EGLDEVAGIINDAK	99.7%	59.8	25	55.4	2	0	0	1443.73	879	892
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	6	6	11	0.01%	3.7%	LDDIFEPVLIPEPK	99.7%	50.8	25	50.8	2	0	0	1624.88	1510	1523
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	6	6	11	0.01%	3.7%	LEAGDYADLVK	99.7%	41.5	25	35.1	1	0	0	1193.61	312	322
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	6	6	11	0.01%	3.7%	NLGIPIITVLGDSK	99.7%	45.2	25	43	3	0	0	1439.85	941	954
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	6	6	11	0.01%	3.7%	TALAATNPAVR	99.7%	45.2	25	34.2	1	0	0	1084.61	762	772
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	6	6	11	0.01%	3.7%	TTGEVVSGVVSK	99.7%	50.9	25	34.6	2	0	0	1162.63	85	96
Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	NUBP2_HUMAN	28.8	100.0%	2	2	4	0.00%	10.0%	STISTELALALR	99.7%	58	25	51.3	2	0	0	1274.73	29	40
Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	NUBP2_HUMAN	28.8	100.0%	2	2	4	0.00%	10.0%	VGILDVDLCGPSIPR	99.7%	66	25	62	2	0	0	1610.86	46	60
Cytosolic non-specific dipeptidase	CNDP2	CNDP2_HUMAN	52.9	99.8%	2	2	3	0.00%	3.8%	TGQEIPVNVR	99.7%	56.4	25	48.2	2	0	0	1112.61	150	159
Cytosolic non-specific dipeptidase	CNDP2	CNDP2_HUMAN	52.9	99.8%	2	2	3	0.00%	3.8%	YNYIEGTK	99.7%	49.2	25	41.9	1	0	0	987.48	454	461
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	115	0.11%	46.7%	AGTGVDNVDLEAATR	99.7%	119	25	99.2	10	0	0	1488.73	76	90
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	115	0.11%	46.7%	ALQSGQCAGAALDVFTEEPPRDR	99.7%	58.9	25	58.9	0	3	0	2488.19	248	270
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	115	0.11%	46.7%	ALVDHENVISCPHLGASTK	99.7%	87	25	87	1	2	0	2048.02	271	289
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	115	0.11%	46.7%	CGEEIAVQFVDMVK	99.7%	102	25	97.1	4	0	0	1624.77	295	308
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	115	0.11%	46.7%	DLPLLLFR	99.7%	53	25	46	14	0	0	986.60	462	469
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	115	0.11%	46.7%	EELIAELQDCEGLIVR	99.7%	88.9	25	88.9	3	0	0	1886.95	39	54
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	115	0.11%	46.7%	FMGTELNGK	99.7%	55.2	25	48.4	4	0	0	996.48	138	146
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	115	0.11%	46.7%	GGIVDEGALLR	99.7%	93.4	25	63.1	6	0	0	1099.61	237	247
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	115	0.11%	46.7%	GTIQVITQGTSLK	99.7%	91.6	25	87.6	8	0	0	1345.77	352	364
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	115	0.11%	46.7%	ILQDGGLQVVEK	99.7%	68	25	63.5	6	0	0	1298.73	22	33
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	115	0.11%	46.7%	MQSFGMK	99.6%	38.9	25	27	1	0	0	828.37	164	170
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	115	0.11%	46.7%	NAGNCLSPAVIVGLLK	99.7%	78.5	25	78.5	9	0	0	1625.90	365	380

D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	115	0.11%	46.7%	QADVNLVNAK	99.7%	68.5	25	52.3	2	0	0	1071.58	385	394
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	115	0.11%	46.7%	QHVTEAFQFHF	99.6%	39.3	25	29.8	1	0	0	1390.65	523	533
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	115	0.11%	46.7%	QIPQATASMK	99.7%	49.5	25	41.5	6	0	0	1090.56	120	129
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	115	0.11%	46.7%	TLGILGLGR	99.7%	66.5	25	53.8	11	0	0	899.57	147	155
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	115	0.11%	46.7%	TQTSDPAMLPTMIGLLAEAGVR	99.7%	116	25	111	7	5	0	2272.17	470	491
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	115	0.11%	46.7%	VLISDSLDPCCR	99.7%	80.2	25	80.2	2	0	0	1434.67	9	20
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	115	0.11%	46.7%	VLISDSLDPCCRK	99.7%	45.1	25	32.2	2	0	0	1562.77	9	21
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	20	27	115	0.11%	46.7%	VTADVINAAEK	99.7%	95	25	77.4	8	0	0	1130.61	59	69
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	7	8	16	0.02%	13.2%	ESVLTATSILNNPIVK	99.7%	90.7	25	89.2	2	0	0	1698.96	444	459
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	7	8	16	0.02%	13.2%	FGGSYGGR	99.7%	54.3	25	41.7	2	0	0	800.37	103	110
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	7	8	16	0.02%	13.2%	FGPYESYDSR	99.7%	50	25	50	2	0	0	1220.52	71	80
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	7	8	16	0.02%	13.2%	MAFTCSFCK	99.7%	44.8	25	38.8	4	0	0	1151.47	310	318
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	7	8	16	0.02%	13.2%	NQGGSSWEAPYSR	99.7%	48.5	25	48.5	2	0	0	1438.63	126	138
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	7	8	16	0.02%	13.2%	NSLDSFGGR	99.7%	48.1	25	35.6	2	0	0	952.45	117	125
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	7	8	16	0.02%	13.2%	SGYGFNEPEQSR	99.7%	48.3	25	48.2	2	0	0	1370.60	91	102
DDB1- and CUL4-associated factor 7	DCAF7	DCAF7_HUMAN	38.9	100.0%	4	4	7	0.01%	15.2%	DMFASVGADGSVR	99.7%	71.3	25	62.8	2	0	0	1311.60	190	202
DDB1- and CUL4-associated factor 7	DCAF7	DCAF7_HUMAN	38.9	100.0%	4	4	7	0.01%	15.2%	GVYPDLLATSGDYLR	99.7%	86.7	25	82.7	2	0	0	1639.83	82	96
DDB1- and CUL4-associated factor 7	DCAF7	DCAF7_HUMAN	38.9	100.0%	4	4	7	0.01%	15.2%	LALGSFVEEYNNK	99.7%	67.4	25	59.2	2	0	0	1483.74	34	46
DDB1- and CUL4-associated factor 7	DCAF7	DCAF7_HUMAN	38.9	100.0%	4	4	7	0.01%	15.2%	NTFDHPYPTTK	98.4%	33	25	30.5	1	0	0	1320.62	63	73
Decaprenyl-diphosphate synthase subunit 2	PDSS2	DLP1_HUMAN	44.1	99.8%	2	2	3	0.00%	5.3%	GLVVLLISK	97.5%	31.1	25	31.1	1	0	0	941.64	113	121
Decaprenyl-diphosphate synthase subunit 2	PDSS2	DLP1_HUMAN	44.1	99.8%	2	2	3	0.00%	5.3%	SALENIVFAVTR	99.7%	56.5	25	50.1	2	0	0	1319.73	386	397
Dedicator of cytokinesis protein 11	DOCK11	DOC11_HUMAN	237.7	99.8%	2	2	2	0.00%	1.3%	FVFEAPYTLSGK	98.8%	34.1	25	31.1	1	0	0	1358.70	1863	1874
Dedicator of cytokinesis protein 11	DOCK11	DOC11_HUMAN	237.7	99.8%	2	2	2	0.00%	1.3%	VVEPLDYENVIAQR	98.4%	33	25	31.5	1	0	0	1644.86	39	52
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	99.8%	2	2	4	0.00%	1.3%	IGCTVSLLNFYK	98.7%	33.8	25	33.2	2	0	0	1414.74	1179	1190
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	99.8%	2	2	4	0.00%	1.3%	TSLYLVQSLPGISR	99.7%	40.2	25	40.2	2	0	0	1533.86	1441	1454
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	7	11	21	0.02%	28.9%	GTIMDTTVDVDKR	99.7%	42.9	25	42.8	4	0	0	1450.72	149	161
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	7	11	21	0.02%	28.9%	HATQAFFDCLR	99.7%	65.7	25	64.1	1	0	0	1365.64	212	222
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	7	11	21	0.02%	28.9%	NAVVVITGATSGLGK	99.7%	115	25	102	2	0	0	1386.80	52	66
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	7	11	21	0.02%	28.9%	SPVEVAQDVLAAVGK	99.7%	112	25	106	2	0	0	1482.82	268	282
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	7	11	21	0.02%	28.9%	TLAPGLFFSLMASR	99.7%	66.5	25	65.7	4	0	0	1510.81	302	315
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	7	11	21	0.02%	28.9%	VMETNYFGPVALTK	99.7%	95.9	25	67.2	4	0	0	1569.80	162	175
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	7	11	21	0.02%	28.9%	YGVMDTTTAQGR	99.7%	78.1	25	72.1	4	0	0	1299.60	256	267
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	5	5	9	0.01%	11.9%	NAAGNFYINDK	99.7%	42.7	25	37.1	2	0	0	1226.58	499	509
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	5	5	9	0.01%	11.9%	SADVESVVSGTLR	99.7%	90	25	84.4	2	0	0	1319.68	326	338
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	5	5	9	0.01%	11.9%	SSPSLTILAGGK	99.7%	42.2	25	29.8	1	0	0	1130.64	409	420
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	5	5	9	0.01%	11.9%	STGSIVGQQPFGGAR	99.7%	63.8	25	63.8	2	0	0	1461.74	510	524
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	5	5	9	0.01%	11.9%	VANEPVLAFTQGSPER	99.7%	65.1	25	65.1	2	0	0	1714.88	32	47
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	30	64	0.06%	34.5%	DLEEAEGR	98.3%	32.6	25	22.8	1	0	0	918.42	410	417
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	30	64	0.06%	34.5%	EAVQLVNTR	99.7%	57.8	25	47.4	2	0	0	1029.57	531	539
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	30	64	0.06%	34.5%	EAVQLVNTREEVEDLCR	99.7%	39.3	25	37.1	0	2	0	2060.01	531	547
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	30	64	0.06%	34.5%	EMAIPVLEAR	99.7%	40.3	25	28.8	2	0	0	1144.60	150	159
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	30	64	0.06%	34.5%	EMMLVTSGAVAFGK	99.7%	51.4	25	14.6	3	0	0	1456.72	111	124
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	30	64	0.06%	34.5%	FASYLTFSPSEVK	99.7%	75.1	25	70.2	2	0	0	1475.74	650	662
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	30	64	0.06%	34.5%	GKDHVVSDFSEHGSLK	99.7%	62.9	25	62.9	0	2	0	1741.85	766	781
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	30	64	0.06%	34.5%	GPVGLEGLLTTK	99.7%	69.3	25	69.3	2	0	0	1184.69	750	761
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	30	64	0.06%	34.5%	HEILLSQSVR	99.7%	56.4	25	47.7	2	0	0	1181.66	129	138
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	30	64	0.06%	34.5%	LAAPLLKR	96.7%	29.9	25	27.3	1	0	0	881.59	418	425
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	30	64	0.06%	34.5%	LASIVEQVSVLQNQGR	99.7%	82.5	25	70.4	4	0	0	1740.96	95	110
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	30	64	0.06%	34.5%	LGSAVVTR	99.7%	75.4	25	55.5	4	0	0	802.48	77	84
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	30	64	0.06%	34.5%	LIDIFYPGDQQSVTFGTK	99.7%	84.8	25	84.8	3	0	0	2029.03	283	300
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	30	64	0.06%	34.5%	LNSLAIGLR	99.7%	77.9	25	61.7	2	0	0	956.59	433	441

Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	30	64	0.06%	34.5%	LRHEILLSQSVR	98.7%	28.1	25	28.1	0	2	0	1450.85	127	138
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	30	64	0.06%	34.5%	MIDLIIPR	99.7%	53.9	25	41	6	0	0	970.58	551	558
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	30	64	0.06%	34.5%	MLATLEPEQR	99.7%	76.5	25	58	5	0	0	1203.60	376	385
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	30	64	0.06%	34.5%	QIAASSQDSVGR	99.7%	75	25	72.7	2	0	0	1218.61	442	453
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	30	64	0.06%	34.5%	SWSNIPFITVPLSR	99.4%	37.6	25	37.6	1	0	0	1616.88	42	55
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	30	64	0.06%	34.5%	TPLFDQIIDMLR	99.7%	75.7	25	72.9	2	0	0	1477.77	627	638
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	30	64	0.06%	34.5%	VGMGGMEAK	99.6%	38.9	25	32.3	2	0	0	879.41	303	311
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	30	64	0.06%	34.5%	VGTFFSEVKPAGPTVEQQGEMAR	99.7%	87.5	25	87.5	0	4	0	2481.21	349	371
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	30	64	0.06%	34.5%	VSGHVITDIVEGK	99.7%	64.2	25	59.3	2	0	0	1353.74	335	347
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	30	64	0.06%	34.5%	VSGHVITDIVEGKK	99.7%	54.4	25	52.3	0	2	0	1481.83	335	348
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	25	30	64	0.06%	34.5%	YLHENLPIPQR	99.5%	38.6	25	34	2	2	0	1379.74	782	792
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	13	19	0.02%	23.0%	ENEITGALLPCLDESR	97.3%	30.8	25	30.8	1	0	0	1816.87	70	85
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	13	19	0.02%	23.0%	EQIVGPLESPVEDSLWPYK	99.4%	37.6	25	37.6	1	0	0	2186.10	270	288
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	13	19	0.02%	23.0%	FAEQLIR	99.7%	41.5	25	21.5	2	0	0	876.49	545	551
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	13	19	0.02%	23.0%	FENLGVSSLGER	99.7%	62	25	59.1	1	0	0	1307.66	86	97
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	13	19	0.02%	23.0%	FIPLARPEVK	97.9%	31.7	25	19.1	2	0	0	1169.70	221	230
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	13	19	0.02%	23.0%	GGFEEPVLLK	99.7%	51.9	25	41.7	1	0	0	1088.60	57	66
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	13	19	0.02%	23.0%	IIDTPQFQR	99.7%	45.6	25	38.2	2	0	0	1117.60	135	143
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	13	19	0.02%	23.0%	ISTAIDDMEAYTK	99.7%	76.9	25	71	1	0	0	1457.68	409	421
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	13	19	0.02%	23.0%	NQVSQLLPEK	99.6%	39.7	25	16.9	2	0	0	1155.64	535	544
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	13	19	0.02%	23.0%	SFLYEIVSNKR	99.6%	39.1	25	36.2	1	0	0	1355.73	295	305
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	13	19	0.02%	23.0%	VGNIIDTMITDAFLK	99.7%	40.8	25	40.8	3	0	0	1650.88	378	392
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	13	19	0.02%	23.0%	YVGETQPTGQIK	99.7%	54.3	25	46.8	2	0	0	1320.68	456	467
Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial	DUT	DUT_HUMAN	26.6	100.0%	3	3	5	0.00%	12.7%	IAQLICER	99.7%	57.6	25	46	2	0	0	1002.54	217	224
Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial	DUT	DUT_HUMAN	26.6	100.0%	3	3	5	0.00%	12.7%	LSEHATAPTR	99.3%	36.6	25	26	2	0	0	1082.56	119	128
Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial	DUT	DUT_HUMAN	26.6	100.0%	3	3	5	0.00%	12.7%	TDIQIALPSGCYGR	98.7%	33.8	25	24.6	1	0	0	1550.76	156	169
Dephospho-CoA kinase domain-containing protein	DCAKD	DCAKD_HUMAN	26.6	100.0%	4	4	6	0.01%	20.8%	INAQLPLTDK	99.7%	57.5	25	53	2	0	0	1112.63	159	168
Dephospho-CoA kinase domain-containing protein	DCAKD	DCAKD_HUMAN	26.6	100.0%	4	4	6	0.01%	20.8%	MFLVGLTGGIASGK	99.7%	85.2	25	85.2	2	0	0	1350.75	1	14
Dephospho-CoA kinase domain-containing protein	DCAKD	DCAKD_HUMAN	26.6	100.0%	4	4	6	0.01%	20.8%	QVILLHTELER	97.6%	31.2	25	25.8	1	0	0	1350.77	188	198
Dephospho-CoA kinase domain-containing protein	DCAKD	DCAKD_HUMAN	26.6	100.0%	4	4	6	0.01%	20.8%	VLGDLIFNQPDRR	97.0%	24.8	25	20.2	0	1	0	1542.84	68	80
Dermcidin	DCD	DCD_HUMAN	11.3	100.0%	3	4	48	0.05%	22.7%	DAVEDLESVGK	99.7%	75.5	25	56.3	17	0	0	1161.56	86	96
Dermcidin	DCD	DCD_HUMAN	11.3	100.0%	3	4	48	0.05%	22.7%	ENAGEDPGLAR	99.7%	83.5	25	74.9	28	0	0	1128.53	43	53
Dermcidin	DCD	DCD_HUMAN	11.3	100.0%	3	4	48	0.05%	22.7%	LGKDAVEDLESVGK	99.7%	77.1	25	68.5	2	1	0	1459.76	83	96
Desmoglein-4	DSG4	DSG4_HUMAN	113.8	99.8%	2	2	4	0.00%	1.7%	EITPLFLIYCR	99.7%	48.7	25	48.7	2	0	0	1424.76	118	128
Desmoglein-4	DSG4	DSG4_HUMAN	113.8	99.8%	2	2	4	0.00%	1.7%	IQVVDVR	99.1%	35.3	25	16.5	2	0	0	828.49	374	380
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	6	6	10	0.01%	2.6%	AELIVQPELK	99.7%	52.4	25	38.7	3	0	0	1139.67	85	94
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	6	6	10	0.01%	2.6%	AITGFDDPFSGK	99.7%	41.1	25	33.3	1	0	0	1254.60	2092	2103
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	6	6	10	0.01%	2.6%	ALLQAILQTEDMLK	99.7%	73	25	73	2	0	0	1602.88	772	785
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	6	6	10	0.01%	2.6%	GFFDPNTEENLTYLQLK	97.7%	31.3	25	31.3	2	0	0	2028.99	2414	2430
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	6	6	10	0.01%	2.6%	IEVLEEELR	99.7%	47.5	25	43.8	1	0	0	1129.61	1034	1042
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	6	6	10	0.01%	2.6%	LNDSILQATEQR	99.3%	36.9	25	29.4	1	0	0	1387.72	1256	1267
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	3	4	7	0.01%	21.9%	INLVLSR	99.7%	46.6	25	30	2	0	0	814.51	72	78
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	3	4	7	0.01%	21.9%	LLPEYPGVLSDVQEEK	99.7%	71.2	25	68.8	2	0	0	1815.94	159	174
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	3	4	7	0.01%	21.9%	VGSLNCIVAVSQNMGIGK	99.7%	49	25	47.3	1	2	0	1862.95	2	19
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	18	29	0.03%	32.6%	ADGGTQVIDTK	99.7%	79.2	25	70.8	2	0	0	1104.55	167	177
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	18	29	0.03%	32.6%	ALLNNSHYYHMAHGK	99.5%	32	25	32	0	1	0	1755.84	90	104
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	18	29	0.03%	32.6%	ALTGGIAHLFK	99.7%	61.9	25	52	2	0	0	1127.66	133	143
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	18	29	0.03%	32.6%	EANLAASFGK	99.7%	65.8	25	59.8	2	0	0	1007.52	496	505
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	18	29	0.03%	32.6%	FPFAANSR	99.7%	48.4	25	37.4	2	0	0	909.46	421	428
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	18	29	0.03%	32.6%	GIEMSEVR	99.7%	45.3	25	40.4	2	0	0	936.45	110	117
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	18	29	0.03%	32.6%	GRIPVNTR	97.8%	31.7	25	20.3	1	0	0	912.54	335	342

Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	18	29	0.03%	32.6%	IPNIYAIGDVVAGPMLAHK	99.7%	82.2	25	82.2	1	3	0	1979.08	347	365
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	18	29	0.03%	32.6%	NETLGGTCLNVGCIPSK	99.7%	119	25	116	2	0	0	1819.87	73	89
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	18	29	0.03%	32.6%	NLGLEELGIELDPR	99.7%	78.9	25	74.7	2	0	0	1567.83	321	334
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	18	29	0.03%	32.6%	SEEQLKEEGIEYK	99.7%	68.6	25	68.6	2	2	0	1581.76	405	417
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	18	29	0.03%	32.6%	TNADTDGMVK	99.7%	47.3	25	45.1	1	0	0	1051.47	431	440
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	18	29	0.03%	32.6%	VCHAHPTLSEAFR	99.7%	39.5	25	34.3	1	2	0	1524.74	483	495
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	18	29	0.03%	32.6%	VVHVNGYGK	97.8%	31.5	25	29.8	1	0	0	972.53	147	155
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	4	4	6	0.01%	8.4%	DVPLGTPLCIIVEK	99.7%	65.9	25	63.1	2	0	0	1553.86	283	296
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	4	4	6	0.01%	8.4%	GVETIANDVVSLATK	99.7%	67.2	25	65.2	2	0	0	1516.82	533	547
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	4	4	6	0.01%	8.4%	ILVAEGTR	98.4%	33	25	24.9	1	0	0	858.50	148	155
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	4	4	6	0.01%	8.4%	VPLPSLSPTMQAGTIAR	99.7%	72	25	72	1	0	0	1738.95	94	110
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	5	6	8	0.01%	10.3%	GMYDGPVYEVPATPK	99.7%	71.2	25	71.2	1	0	0	1639.77	497	511
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	5	6	8	0.01%	10.3%	INCPVYITK	99.4%	37.3	25	23	1	0	0	1107.59	246	254
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	5	6	8	0.01%	10.3%	MDENQFVAVTSTNAAK	99.7%	68.1	25	68.1	2	0	0	1741.81	375	390
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	5	6	8	0.01%	10.3%	SAADIIALAR	99.7%	90.2	25	72.2	2	0	0	1000.58	259	268
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	5	6	8	0.01%	10.3%	VFGLQGVSR	99.7%	47.2	25	32.9	2	0	0	962.54	488	496
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	5	5	8	0.01%	9.8%	GAPAVVISQGR	99.7%	66.8	25	61.4	2	0	0	1054.60	441	451
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	5	5	8	0.01%	9.8%	IFNFYPR	96.8%	30.1	25	0	1	0	0	956.50	391	397
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	5	5	8	0.01%	9.8%	LAEIHGVPR	99.7%	70.6	25	62.8	1	0	0	991.57	488	496
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	5	5	8	0.01%	9.8%	MFVTPGAGR	96.9%	30.2	25	30.2	2	0	0	935.48	459	467
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	5	5	8	0.01%	9.8%	NLHQSGFSLSGSQADDHIAR	99.7%	44.6	25	44.6	0	2	0	2140.02	533	552
Dihydropyrimidinase-related protein 5	DPYSL5	DPYL5_HUMAN	61.4	100.0%	3	3	4	0.00%	6.4%	FVAVTSSNAAK	99.7%	46.1	25	43.3	2	0	0	1094.58	373	383
Dihydropyrimidinase-related protein 5	DPYSL5	DPYL5_HUMAN	61.4	100.0%	3	3	4	0.00%	6.4%	IPHGVSGVQDR	97.6%	31.2	25	21.6	1	0	0	1164.61	344	354
Dihydropyrimidinase-related protein 5	DPYSL5	DPYL5_HUMAN	61.4	100.0%	3	3	4	0.00%	6.4%	VHAENGELVAEGAK	99.1%	35.3	25	35.3	1	0	0	1423.72	190	203
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	3	4	6	0.01%	10.1%	FIPGLQMLSDAAPGK	99.7%	51.2	25	39.5	3	0	0	1560.81	90	104
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	3	4	6	0.01%	10.1%	QLSQNFLLDLR	99.7%	40.7	25	35.4	1	0	0	1346.74	32	42
Dimethyladenosine transferase 1, mitochondrial	TFB1M	TFB1M_HUMAN	39.5	100.0%	3	4	6	0.01%	10.1%	VVQNVFQFR	99.7%	60.6	25	56.5	2	0	0	1136.62	248	256
Dimethyladenosine transferase 2, mitochondrial	TFB2M	TFB2M_HUMAN	45.4	99.9%	2	2	3	0.00%	6.3%	LYLIQMIPR	97.7%	31.4	25	29.7	1	0	0	1146.67	296	304
Dimethyladenosine transferase 2, mitochondrial	TFB2M	TFB2M_HUMAN	45.4	99.9%	2	2	3	0.00%	6.3%	NLGIEAVPWTADIPLK	99.7%	57.7	25	57.7	2	0	0	1736.96	175	190
Diphosphoinositol polyphosphate phosphohydrolase 3-beta	NUDT11	NUD11_HUMAN	18.6	99.8%	2	2	2	0.00%	15.2%	LLGVFEQNQDR	99.7%	40.5	25	34.8	1	0	0	1318.68	79	89
Diphosphoinositol polyphosphate phosphohydrolase 3-beta	NUDT11	NUD11_HUMAN	18.6	99.8%	2	2	2	0.00%	15.2%	SEREDEVLLVSSSR	99.7%	48	25	41.9	1	0	0	1605.81	27	40
DNA damage-binding protein 1	DDB1	DDB1_HUMAN	127.0	100.0%	2	2	2	0.00%	3.5%	IEVQDTSGGTTALRPSASTQALSSSVSSSK	99.7%	65.8	25	65.8	0	1	0	2952.48	740	769
DNA damage-binding protein 1	DDB1	DDB1_HUMAN	127.0	100.0%	2	2	2	0.00%	3.5%	IVVFQYSDGK	99.7%	47.8	25	45.4	1	0	0	1155.60	848	857
DNA ligase 3	LIG3	DNLI3_HUMAN	112.9	100.0%	3	3	4	0.00%	3.0%	LLLPGVIK	97.3%	30.7	25	30.7	1	0	0	852.59	309	316
DNA ligase 3	LIG3	DNLI3_HUMAN	112.9	100.0%	3	3	4	0.00%	3.0%	SEAHTADGISIR	99.6%	39	25	27.2	1	0	0	1256.62	792	803
DNA ligase 3	LIG3	DNLI3_HUMAN	112.9	100.0%	3	3	4	0.00%	3.0%	VLLDIFTGVR	99.7%	75.7	25	74.5	2	0	0	1132.67	933	942
DNA methyltransferase 1-associated protein 1	DMAP1	DMAP1_HUMAN	53.0	100.0%	2	2	3	0.00%	4.7%	LITAADTTAEQR	99.7%	75.4	25	63.3	2	0	0	1289.67	271	282
DNA methyltransferase 1-associated protein 1	DMAP1	DMAP1_HUMAN	53.0	100.0%	2	2	3	0.00%	4.7%	MKLPSSVGQK	95.0%	28.3	25	16.5	1	0	0	1090.59	327	336
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	15.3%	ALNLFQGSVEDTTGSQSLAALLNK	99.7%	117	25	117	2	0	0	2477.29	309	332
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	15.3%	DSLIIIDELGR	99.7%	76.1	25	63.2	2	0	0	1243.69	742	752
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	15.3%	LDSSAQFGYYFR	99.7%	77	25	70.2	2	0	0	1453.67	513	524
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	15.3%	LLLAVFVTPLTDLR	99.7%	64.3	25	64.3	2	0	0	1570.96	431	444
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	15.3%	LNLVEAFVEDAELR	99.7%	116	25	116	2	0	0	1617.85	360	373
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	15.3%	LTSLNEEYTK	99.7%	53.9	25	48.1	2	0	0	1197.60	556	565
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	15.3%	LYQGINQLPNVIQALEK	99.7%	70.8	25	67.3	2	0	0	1941.08	407	423
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	15.3%	NFSTVDIQK	95.7%	28.9	25	19.5	1	0	0	1051.54	538	546
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	15.3%	NLQSVVLSK	99.7%	44.3	25	22.8	2	0	0	987.58	74	82
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	15.3%	NNSFVNEIISR	99.7%	59	25	43.2	2	0	0	1292.66	919	929
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	11	11	20	0.02%	15.3%	QVGVGYVDSIQR	99.7%	70.8	25	69.1	1	0	0	1320.69	160	171
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	18	20	34	0.03%	16.1%	AIMYEETTYSK	99.7%	52.3	25	49.6	2	0	0	1335.61	842	852
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	18	20	34	0.03%	16.1%	AYGVCFVDTSLGK	99.7%	82.3	25	82.3	2	0	0	1416.68	555	567

DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	18	20	34	0.03%	16.1%	EVCLASER	99.4%	37.4	25	25.1	2	0	0	963.46	1335	1342
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	18	20	34	0.03%	16.1%	GTATFDGTAIANAVVK	99.7%	99.9	25	91.6	2	0	0	1535.81	1218	1233
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	18	20	34	0.03%	16.1%	GTQTYSVLEGDPSENYSK	99.7%	99.7	25	99.7	1	0	0	1974.89	520	537
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	18	20	34	0.03%	16.1%	IHNVGSPLK	98.7%	33.8	25	18.7	1	0	0	964.56	825	833
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	18	20	34	0.03%	16.1%	IIDFLSALEGFK	99.7%	67.7	25	61.5	2	0	0	1352.75	855	866
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	18	20	34	0.03%	16.1%	IIGIMEEVADGFK	99.7%	57.4	25	51.4	2	0	0	1421.73	871	883
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	18	20	34	0.03%	16.1%	KLPDLER	96.6%	29.8	25	0	1	0	0	870.50	814	820
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	18	20	34	0.03%	16.1%	LANLINAEER	99.7%	55.4	25	47	2	0	0	1142.62	1015	1024
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	18	20	34	0.03%	16.1%	LANLPEEVIQK	99.7%	53.8	25	38.2	2	0	0	1253.71	1305	1315
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	18	20	34	0.03%	16.1%	LSDGIGVMLPQVLK	99.7%	57.9	25	51.8	4	0	0	1485.83	647	660
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	18	20	34	0.03%	16.1%	STVDAEAVHK	99.6%	40	25	34.4	2	0	0	1056.53	1343	1352
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	18	20	34	0.03%	16.1%	SVAPAAPTSCDFSPGDLVWAK	99.7%	48.4	25	48.4	1	0	0	2176.04	79	99
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	18	20	34	0.03%	16.1%	TLLEEEYFR	99.7%	47.9	25	37.5	2	0	0	1199.59	636	644
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	18	20	34	0.03%	16.1%	VEQTETPEMMEAR	94.7%	28.1	25	28.1	1	0	0	1582.67	483	495
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	18	20	34	0.03%	16.1%	VHVQFFDDSPTR	99.7%	43.4	25	43.4	2	1	0	1447.70	129	140
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	18	20	34	0.03%	16.1%	YQLEIPENFTTR	99.7%	42.7	25	41.3	2	0	0	1510.75	977	988
DNA polymerase alpha catalytic subunit	POLA1	DPOLA_HUMAN	165.9	100.0%	3	3	4	0.00%	2.9%	AAYAGGLVLDPK	99.6%	39.4	25	33.2	1	0	0	1174.65	837	848
DNA polymerase alpha catalytic subunit	POLA1	DPOLA_HUMAN	165.9	100.0%	3	3	4	0.00%	2.9%	DTGNFVIGQILSDQSR	99.7%	77.9	25	69.5	2	0	0	1749.88	1090	1105
DNA polymerase alpha catalytic subunit	POLA1	DPOLA_HUMAN	165.9	100.0%	3	3	4	0.00%	2.9%	DVSPPPLVVMAFSMK	99.6%	39.6	25	35.3	1	0	0	1617.84	531	545
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	16	28	0.03%	17.9%	DLEDQEQLLR	99.7%	46.9	25	38.5	1	0	0	1258.63	1088	1097
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	16	28	0.03%	17.9%	DNCPLVANLVTASLR	99.7%	75.8	25	75.8	2	0	0	1642.86	835	849
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	16	28	0.03%	17.9%	ELNLAISR	99.2%	36	25	14.4	2	0	0	915.53	167	174
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	16	28	0.03%	17.9%	EVSHLNALEER	99.7%	40.4	25	29.2	1	0	0	1296.65	1040	1050
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	16	28	0.03%	17.9%	FGVSSVAEAMALGR	99.7%	107	25	107	2	0	0	1394.71	763	776
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	16	28	0.03%	17.9%	IDISQLVITK	99.7%	85.7	25	54.6	2	0	0	1129.68	876	885
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	16	28	0.03%	17.9%	IFEPILGEGR	99.7%	64.2	25	56.1	2	0	0	1130.62	969	978
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	16	28	0.03%	17.9%	LLEQGIR	94.7%	28.1	25	0	1	0	0	828.49	226	232
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	16	28	0.03%	17.9%	LPCLEISQSVTGFGR	99.7%	82.8	25	82.8	2	0	0	1663.85	711	725
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	16	28	0.03%	17.9%	SEGGEDYTGATVIEPLK	99.7%	90.1	25	90.1	2	0	0	1765.85	575	591
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	16	28	0.03%	17.9%	VGGLLAFAK	99.7%	41.8	25	41.8	2	0	0	875.54	999	1007
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	16	28	0.03%	17.9%	VLSFDIECAGR	99.7%	40.5	25	39.4	1	0	0	1266.61	312	322
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	16	28	0.03%	17.9%	VQMDMLQVLLR	99.7%	71.8	25	58.9	2	0	0	1345.73	455	465
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	16	28	0.03%	17.9%	VSANSVYGFTGAQVGK	99.7%	78	25	68.9	2	0	0	1584.80	695	710
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	16	28	0.03%	17.9%	VTGVPLSYLLSR	99.6%	40	25	11.1	2	0	0	1304.76	538	549
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	16	28	0.03%	17.9%	VYFPYLLISK	98.5%	33.2	25	33.2	2	0	0	1242.71	797	806
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	16	28	0.03%	17.9%	YTVENGYSTSAK	99.7%	46.5	25	46.5	1	0	0	1319.61	739	750
DNA polymerase delta subunit 3	POLD3	DPOD3_HUMAN	51.4	100.0%	3	3	4	0.00%	8.4%	DSGPLFNTDYDILK	99.7%	62.2	25	39	2	0	0	1597.77	110	123
DNA polymerase delta subunit 3	POLD3	DPOD3_HUMAN	51.4	100.0%	3	3	4	0.00%	8.4%	FSAIQCAAAVPR	99.7%	48.5	25	38.5	1	0	0	1290.66	132	143
DNA polymerase delta subunit 3	POLD3	DPOD3_HUMAN	51.4	100.0%	3	3	4	0.00%	8.4%	IVEQPTVSVTEPK	99.7%	83.5	25	82.9	1	0	0	1426.78	262	274
DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	7	7	10	0.01%	3.8%	AIPLAIFQAEPTVR	99.7%	51.8	25	48.9	2	0	0	1525.87	1093	1106
DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	7	7	10	0.01%	3.8%	ASVFVLDTVR	99.1%	35.5	25	31.9	1	0	0	1106.62	1510	1519
DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	7	7	10	0.01%	3.8%	GSTLEEVYGSVAK	99.7%	56.3	25	49.5	1	0	0	1339.67	996	1008
DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	7	7	10	0.01%	3.8%	IFQSSVFEAFLK	98.3%	32.8	25	29.7	2	0	0	1415.76	984	995
DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	7	7	10	0.01%	3.8%	IITIPAALQQVK	99.5%	37.8	25	36.3	2	0	0	1294.81	1144	1155
DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	7	7	10	0.01%	3.8%	SLAQFSYLEPGSIR	99.7%	41.5	25	29.1	1	0	0	1567.81	1472	1485
DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	7	7	10	0.01%	3.8%	VADYWLDVLYSK	99.7%	48.3	25	48.3	1	0	0	1471.75	1009	1020
DNA primase large subunit	PRIM2	PRI2_HUMAN	58.8	100.0%	5	5	6	0.01%	13.0%	DSQLQFEAISDEEK	99.7%	87.5	25	84.1	1	0	0	1638.75	146	159
DNA primase large subunit	PRIM2	PRI2_HUMAN	58.8	100.0%	5	5	6	0.01%	13.0%	IPFADALDLFR	99.7%	71.1	25	66.2	2	0	0	1277.69	186	196
DNA primase large subunit	PRIM2	PRI2_HUMAN	58.8	100.0%	5	5	6	0.01%	13.0%	ISPGGISQILDLVK	98.2%	32.5	25	32.5	1	0	0	1439.85	403	416
DNA primase large subunit	PRIM2	PRI2_HUMAN	58.8	100.0%	5	5	6	0.01%	13.0%	KEPIQPETPQPKPSVQK	98.4%	27.3	25	27.3	0	1	0	1931.06	463	479
DNA primase large subunit	PRIM2	PRI2_HUMAN	58.8	100.0%	5	5	6	0.01%	13.0%	SLPAVQSDER	99.7%	40.9	25	36.8	1	0	0	1101.55	236	245

DNA primase small subunit	PRIM1	PRI1_HUMAN	49.9	100.0%	2	2	4	0.00%	6.2%	LGAFQAQEK	99.7%	45.9	25	35.2	2	0	0	991.52	96	104
DNA primase small subunit	PRIM1	PRI1_HUMAN	49.9	100.0%	2	2	4	0.00%	6.2%	VDQFDPFTVPTISFICR	99.7%	78.1	25	74.6	2	0	0	2042.01	339	355
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	16	26	0.03%	10.4%	DVNGELIAVQR	99.7%	72.8	25	64.7	2	0	0	1213.65	88	98
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	16	26	0.03%	10.4%	EQVSPLETTLEK	99.7%	59.5	25	52.9	2	0	0	1373.72	910	921
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	16	26	0.03%	10.4%	GQDIEYIEIR	99.7%	75.6	25	69.6	2	0	0	1235.63	1157	1166
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	16	26	0.03%	10.4%	LEENIDNIKR	99.7%	42.3	25	42.3	1	1	0	1243.66	1060	1069
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	16	26	0.03%	10.4%	LKEIEHNLSK	99.6%	39.9	25	25.7	1	1	0	1210.68	255	264
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	16	26	0.03%	10.4%	LQGIDLDR	99.7%	55.2	25	39.3	2	0	0	929.51	816	823
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	16	26	0.03%	10.4%	MEVISLQNEK	99.7%	45.3	25	25.2	1	0	0	1190.61	502	511
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	16	26	0.03%	10.4%	NIDQCSEIVK	99.7%	52.1	25	48.5	2	0	0	1205.58	1292	1301
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	16	26	0.03%	10.4%	SELLVEQGR	99.7%	59.7	25	45.5	2	0	0	1030.55	344	352
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	16	26	0.03%	10.4%	TLDQAIMK	97.2%	30.6	25	22.9	1	0	0	935.49	1127	1134
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	16	26	0.03%	10.4%	VIAQLSECEK	99.7%	49.8	25	49.7	2	0	0	1176.59	983	992
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	16	26	0.03%	10.4%	VLASLIIR	99.7%	67.3	25	48.7	2	0	0	884.59	1207	1214
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	16	26	0.03%	10.4%	WLQDNLTLR	99.7%	43.4	25	34.9	2	0	0	1158.63	1017	1025
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	14	16	26	0.03%	10.4%	YELQQLEGSSDR	99.7%	78.8	25	64	2	0	0	1424.67	462	473
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	51	0.05%	35.3%	AILCLLLGGVER	99.7%	69.2	25	59.3	2	0	0	1313.76	316	327
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	51	0.05%	35.3%	ALKDFVASIDATYAK	99.7%	72.3	25	72.2	2	0	0	1612.86	79	93
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	51	0.05%	35.3%	APAGQLPR	99.7%	51.4	25	28.4	2	0	0	809.46	208	215
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	51	0.05%	35.3%	DAQPSFSAEDIAK	99.7%	59.2	25	56.7	2	0	0	1378.65	271	283
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	51	0.05%	35.3%	DLENGSHIR	99.7%	41.2	25	31.7	2	0	0	1040.51	328	336
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	51	0.05%	35.3%	DSEEPFSSVEIQAALSK	99.7%	117	25	101	2	0	0	1836.89	775	791
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	51	0.05%	35.3%	DYLDFLDDEEDQGIYQSK	99.7%	86.2	25	86.2	2	0	0	2192.95	18	35
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	51	0.05%	35.3%	EAHAQSIGMNR	99.7%	77.6	25	66.8	2	1	0	1213.57	757	767
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	51	0.05%	35.3%	ELISDNQYR	99.7%	64.6	25	48.1	2	0	0	1137.55	38	46
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	51	0.05%	35.3%	ESQKVELSESR	99.4%	37.5	25	26.4	1	0	0	1291.65	733	743
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	51	0.05%	35.3%	GGYTSGTFR	98.0%	31.9	25	29.3	2	0	0	945.44	249	257
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	51	0.05%	35.3%	GSSGVGLTAAVTTDQETGER	99.7%	111	25	111	2	0	0	1935.93	372	391
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	51	0.05%	35.3%	IIKPVLTQESATYIAEEYSR	98.7%	28	25	25.2	0	2	0	2311.22	577	596
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	51	0.05%	35.3%	LIVNVNDLR	99.7%	63.6	25	50.9	2	0	0	1055.62	47	55
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	51	0.05%	35.3%	LLNNAFEELVAFQR	99.7%	74.2	25	72.6	2	0	0	1663.88	65	78
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	51	0.05%	35.3%	SKDIFDQLAK	99.7%	53.7	25	46.4	1	0	0	1164.63	292	301
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	51	0.05%	35.3%	SVDVILDDDLVDK	99.7%	72.3	25	66.2	2	0	0	1445.74	216	228
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	51	0.05%	35.3%	SVHYCPATK	98.4%	32.9	25	18.2	2	0	0	1062.50	144	152
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	51	0.05%	35.3%	TAIHEVMEQGR	99.3%	36.5	25	30.6	3	1	0	1286.62	420	430
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	51	0.05%	35.3%	TLETLIR	99.7%	43.4	25	14.6	2	0	0	845.51	617	623
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	51	0.05%	35.3%	TPMENIGLQDSLLSR	99.7%	80.5	25	80.5	4	0	0	1689.85	464	478
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	51	0.05%	35.3%	TVLIACNVK	98.9%	34.4	25	14.3	2	0	0	1017.58	258	266
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	51	0.05%	35.3%	VALLDVFR	99.7%	50.7	25	33.2	2	0	0	932.56	749	756
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	24	28	51	0.05%	35.3%	YVLCTAPR	99.7%	45.3	25	35.8	2	0	0	979.50	357	364
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	12	12	22	0.02%	17.8%	ALADDDFLTVTGK	99.7%	96.2	25	95.7	2	0	0	1365.69	846	858
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	12	12	22	0.02%	17.8%	GILLQLFGGTR	99.7%	89.8	25	86.2	3	0	0	1174.69	479	489
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	12	12	22	0.02%	17.8%	GLQVDLQSDGAAAEDIVASEQSLGQK	99.7%	58.4	25	58.4	0	2	0	2629.30	124	149
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	12	12	22	0.02%	17.8%	IAEPSVCGR	99.7%	42.7	25	22.9	1	0	0	988.49	322	330
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	12	12	22	0.02%	17.8%	LASALAPSIYEHEDIKK	97.8%	25.9	25	22.8	0	1	0	1885.01	462	478
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	12	12	22	0.02%	17.8%	LHGLDEEAEQK	99.7%	41.8	25	39.4	2	0	0	1268.61	429	439
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	12	12	22	0.02%	17.8%	LVIWGTDVNVAACK	99.7%	86.7	25	86.7	2	0	0	1545.81	150	163
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	12	12	22	0.02%	17.8%	QRPDLGSAQK	99.5%	37.9	25	28.5	2	0	0	1099.59	114	123
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	12	12	22	0.02%	17.8%	RLHGLDEEAEQK	99.7%	35.3	25	32.7	0	1	0	1424.71	428	439
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	12	12	22	0.02%	17.8%	TGIVDISILTTGMSATSR	99.7%	94	25	94	2	0	0	1822.96	778	795
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	12	12	22	0.02%	17.8%	TTIENIQLPHTLLSR	99.7%	66.2	25	49.9	2	0	0	1735.97	629	643

DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	12	12	22	0.02%	17.8%	YQQLFEDIR	99.7%	64.5	25	39.3	2	0	0	1211.61	820	828
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	19	20	33	0.03%	30.1%	AGITTTLNSR	99.7%	68.7	25	51.3	2	0	0	1033.56	472	481
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	19	20	33	0.03%	30.1%	AIACLLFGGSR	99.7%	89.9	25	83.4	2	0	0	1164.62	352	362
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	19	20	33	0.03%	30.1%	CSVLAAANSVFGR	99.7%	74.2	25	69	2	0	0	1351.68	482	494
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	19	20	33	0.03%	30.1%	FAIGSQVSEHSIIK	99.7%	72.8	25	51.8	2	0	0	1515.82	683	696
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	19	20	33	0.03%	30.1%	GSSAAGLTASVMR	99.7%	82.6	25	76	2	0	0	1207.61	408	420
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	19	20	33	0.03%	30.1%	HMQLYCDR	99.7%	44.5	25	40.9	3	0	0	1138.48	244	251
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	19	20	33	0.03%	30.1%	IPGIIIAASAVR	99.7%	87.8	25	87.8	2	0	0	1180.74	151	162
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	19	20	33	0.03%	30.1%	LAALPNVYEVISK	99.7%	67.4	25	67.4	2	0	0	1416.81	325	337
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	19	20	33	0.03%	30.1%	LQELPDAVPHGEMPR	96.8%	24.5	25	22.8	0	1	0	1704.84	229	243
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	19	20	33	0.03%	30.1%	LQPFATEADVEEALR	99.7%	112	25	106	2	0	0	1688.85	628	642
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	19	20	33	0.03%	30.1%	QLEAIVR	98.2%	32.5	25	16.3	1	0	0	828.49	612	618
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	19	20	33	0.03%	30.1%	QPAEHLQLLEEAAK	98.1%	26.5	25	26.5	0	1	0	1576.83	91	104
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	19	20	33	0.03%	30.1%	RGDINLLMLGDPGTAK	99.7%	44.3	25	41.4	0	2	0	1670.89	372	387
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	19	20	33	0.03%	30.1%	SFAGAVSPQEEEEFRR	99.5%	38.3	25	38.3	1	0	0	1838.87	309	324
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	19	20	33	0.03%	30.1%	SIAPSIFGGTDMK	99.4%	37	25	32.4	1	0	0	1323.66	338	350
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	19	20	33	0.03%	30.1%	SIAPSIFGGTDMKK	98.2%	32.4	25	32.1	1	0	0	1467.75	338	351
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	19	20	33	0.03%	30.1%	VLGIQVDTDGSGR	99.7%	78.6	25	78.6	2	0	0	1316.68	296	308
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	19	20	33	0.03%	30.1%	VLQLMLR	99.7%	44.6	25	33.6	2	0	0	872.54	711	717
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	19	20	33	0.03%	30.1%	VTIMGIYSIK	99.7%	48.3	25	35.3	2	0	0	1124.64	263	272
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	33	0.03%	24.0%	DFYVAFQDLPTR	99.7%	76	25	60.5	2	0	0	1471.72	109	120
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	33	0.03%	24.0%	EIESEIDSEEELINK	99.7%	94.8	25	79.9	2	0	0	1776.84	755	769
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	33	0.03%	24.0%	ELRDEEQTAESIK	99.7%	68.3	25	59.3	2	0	0	1547.75	314	326
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	33	0.03%	24.0%	ESEDFIVEQYK	99.7%	48	25	48	2	0	0	1386.64	589	599
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	33	0.03%	24.0%	GDINVCIVGDPSTAK	99.7%	58.9	25	52	2	0	0	1545.76	388	402
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	33	0.03%	24.0%	GVLLMLFGGVPK	99.7%	68.9	25	52.1	2	0	0	1230.73	367	378
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	33	0.03%	24.0%	HVEEFSPR	98.5%	33.3	25	30.8	2	0	0	1000.48	408	415
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	33	0.03%	24.0%	IQETQAELPR	99.7%	75.1	25	58.8	2	0	0	1184.63	208	217
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	33	0.03%	24.0%	ISNLIVLHLR	99.7%	58.3	25	55.3	2	0	0	1177.74	723	732
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	33	0.03%	24.0%	LGFSEYCR	99.7%	44.7	25	44.7	2	0	0	1031.46	715	722
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	33	0.03%	24.0%	LVFLACCVAPTNPR	99.7%	88.5	25	87.9	2	0	0	1617.82	296	309
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	33	0.03%	24.0%	MHCCDEVQPK	98.3%	32.6	25	32.6	1	0	0	1319.52	634	643
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	33	0.03%	24.0%	TSILAAANPISGHYDR	99.7%	85.1	25	82.3	2	0	0	1685.86	497	512
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	33	0.03%	24.0%	VSGVDGYETEGIR	99.7%	97	25	86.3	2	0	0	1381.66	270	282
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	33	0.03%	24.0%	VYSLDDIRR	99.7%	45.4	25	35.8	2	0	0	1136.61	566	574
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	33	0.03%	24.0%	YLQLAEELIRPER	99.7%	33.9	25	15.8	2	1	0	1629.90	46	58
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	18	33	0.03%	24.0%	YTQPNICR	98.9%	34.8	25	29	1	0	0	1051.50	174	181
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	21	38	0.04%	30.2%	AGILTTLNAR	99.7%	65.9	25	53.6	2	0	0	1029.61	472	481
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	21	38	0.04%	30.2%	ALLLLLVGGVDQSPR	99.7%	61	25	61	1	0	0	1550.93	353	367
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	21	38	0.04%	30.2%	CSILAAANPAYGR	99.7%	64.8	25	61.4	1	0	0	1363.68	482	494
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	21	38	0.04%	30.2%	DSLLGDKGQTAR	99.7%	56.2	25	49.4	2	0	0	1260.65	642	653
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	21	38	0.04%	30.2%	FLQEFYQDDELGKK	99.7%	60.7	25	53.6	1	0	0	1759.85	16	29
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	21	38	0.04%	30.2%	GNINICLMGDPGVAK	99.7%	48.2	25	48.2	3	0	0	1574.77	373	387
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	21	38	0.04%	30.2%	GSSGVGLTAAVLR	99.7%	83.1	25	62.9	2	0	0	1187.67	408	420
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	21	38	0.04%	30.2%	LAQHITYVHQHSR	99.7%	36.9	25	36.9	0	1	0	1589.83	533	545
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	21	38	0.04%	30.2%	LFADAVQELLPQYK	99.7%	64.8	25	34.1	4	0	0	1634.88	76	89
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	21	38	0.04%	30.2%	QIAEEDFYEK	99.3%	36.5	25	34.5	2	0	0	1271.58	326	335
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	21	38	0.04%	30.2%	SEDDESGAGELTR	99.7%	54.8	25	54.8	2	0	0	1365.58	309	321
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	21	38	0.04%	30.2%	SITVLVEGENTR	99.7%	76.2	25	65.5	2	0	0	1317.70	252	263
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	21	38	0.04%	30.2%	SLEQNIQLPAALLSR	99.7%	89.4	25	86.6	2	0	0	1652.93	500	514
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	21	38	0.04%	30.2%	SPQNQYPAELMR	99.6%	39.4	25	37.7	3	0	0	1433.68	121	132

DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	21	38	0.04%	30.2%	SQLLSYIDR	99.7%	54.3	25	31.3	2	0	0	1094.58	388	396
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	21	38	0.04%	30.2%	TLLAILR	99.7%	46.1	25	17.5	2	0	0	799.54	605	611
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	21	38	0.04%	30.2%	TQRPADVIFATVR	99.7%	40.6	25	29.1	2	2	0	1473.82	654	666
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	18	21	38	0.04%	30.2%	YGNQLVR	99.7%	55.4	25	41.1	2	0	0	849.46	33	39
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	23.3%	AEEVATFFAK	99.7%	65.9	25	52.1	5	0	0	1112.56	253	262
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	23.3%	AVAILCNHQR	99.7%	57.9	25	49.8	2	0	0	1181.62	625	634
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	23.3%	AVALYFIDK	99.7%	50.1	25	27.3	2	0	0	1039.58	476	484
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	23.3%	CDFTQMSQYFK	99.6%	38.9	25	38.9	1	0	0	1454.61	300	310
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	23.3%	DEDDADYKPK	99.7%	40.4	25	35.5	1	0	0	1195.51	141	150
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	23.3%	ELTAPDENIPAK	99.7%	46.6	25	46.6	2	0	0	1297.66	604	615
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	23.3%	GPVFAPPYEPLPENVK	99.7%	59	25	59	6	0	0	1753.92	224	239
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	23.3%	HLQDLMEGLTAK	99.7%	64.8	25	32.8	4	0	0	1355.70	576	587
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	23.3%	IMPEDIIINCSK	99.6%	38.9	25	37.5	1	0	0	1432.72	377	388
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	23.3%	LEEQLMK	99.0%	35.2	25	3.08	1	0	0	906.46	694	700
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	23.3%	LEVQATDREENK	99.7%	62.5	25	58.8	3	0	0	1431.71	701	712
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	23.3%	LNTGILNK	99.7%	48	25	20	3	0	0	872.52	568	575
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	23.3%	MLDHEYTTK	99.7%	52	25	46.9	4	0	0	1137.52	263	271
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	23.3%	NLQLFMENK	99.7%	42.7	25	41.5	2	0	0	1136.58	550	558
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	23.3%	TYNASITLQQQLK	99.7%	85.2	25	73.6	3	0	0	1507.81	591	603
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	23.3%	VPSPPPGHK	94.7%	28.1	25	15	1	0	0	915.50	392	400
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	23.3%	YIMLNPSSR	99.7%	40.3	25	29.8	3	0	0	1096.55	426	434
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	44	0.04%	19.9%	DKYGVFPLR	99.7%	43.9	25	39.8	2	0	0	1094.60	479	487
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	44	0.04%	19.9%	DPALNSGVSQKPDPAK	99.7%	69.6	25	69.2	1	0	0	1623.83	1444	1459
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	44	0.04%	19.9%	EKQDEQVGLPGK	99.7%	59.5	25	43.2	2	0	0	1327.69	1185	1196
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	44	0.04%	19.9%	ELILFSNSDNER	99.7%	77.2	25	71.2	3	0	0	1436.70	702	713
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	44	0.04%	19.9%	EWLLGMLGAESAK	99.7%	42.4	25	42.4	1	0	0	1404.72	1035	1047
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	44	0.04%	19.9%	FLEEFITPIVK	99.7%	55.6	25	51.5	4	0	0	1335.76	569	579
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	44	0.04%	19.9%	FTVETASR	99.7%	52.8	25	46.5	2	0	0	910.46	177	184
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	44	0.04%	19.9%	GFQQISFVNSIATSK	99.7%	104	25	92.4	2	0	0	1626.85	307	321
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	44	0.04%	19.9%	GSVPLSSSPPATHFPDETEITNPVPK	99.2%	30.1	25	30.1	0	1	0	2704.35	1386	1411
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	44	0.04%	19.9%	HVDYVADQIVTK	99.7%	80.6	25	79.8	2	0	0	1387.72	325	336
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	44	0.04%	19.9%	IFDEILVNAADNK	99.7%	106	25	103	4	0	0	1461.76	84	96
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	44	0.04%	19.9%	IVGLQYK	97.2%	30.5	25	24.5	1	0	0	820.49	513	519
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	44	0.04%	19.9%	KPSTSDDSDSNFEK	97.9%	31.8	25	31.8	1	0	0	1556.67	1467	1480
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	44	0.04%	19.9%	LCNIFSTK	96.6%	29.8	25	23.4	1	0	0	982.50	169	176
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	44	0.04%	19.9%	NSTECTLILTEGDSAK	99.7%	95.8	25	75.9	2	0	0	1738.82	451	466
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	44	0.04%	19.9%	SFGSTCQLSEK	99.7%	60	25	51.9	2	0	0	1243.56	387	397
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	44	0.04%	19.9%	SIPSMVDGLKPGQR	97.8%	31.7	25	21.5	1	0	0	1484.79	714	727
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	44	0.04%	19.9%	SVVSDLEADDVK	99.7%	58.8	25	48.9	1	0	0	1276.63	1374	1385
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	44	0.04%	19.9%	TLAVSGLGVVGR	99.7%	89.8	25	78.9	2	0	0	1128.67	467	478
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	44	0.04%	19.9%	TQMAEVLPSPR	97.5%	31	25	22.5	1	0	0	1244.63	1205	1215
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	44	0.04%	19.9%	VTIDPENNLISIWNNGK	99.7%	45.6	25	45.6	1	0	0	1926.99	107	123
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	44	0.04%	19.9%	YDTVLDILR	98.8%	34.1	25	24.9	1	0	0	1107.60	1012	1020
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	44	0.04%	19.9%	YIFTMLSSLAR	99.7%	67	25	60.1	4	0	0	1317.69	805	815
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	44	0.04%	19.9%	YSGPEDDAAISLAFSK	99.7%	79.6	25	72.8	2	0	0	1670.79	640	655
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	21	0.02%	9.4%	DKLDETGVALK	99.7%	51.5	25	38	1	0	0	1188.65	298	308
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	21	0.02%	9.4%	DLIQMLVQR	99.7%	53.9	25	41.4	3	0	0	1115.62	1093	1101
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	21	0.02%	9.4%	ELILFSNSDNER	99.7%	77.2	25	71.2	3	0	0	1436.70	723	734
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	21	0.02%	9.4%	GFQQISFVNSIATTK	99.7%	94.1	25	77.9	1	0	0	1640.86	328	342
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	21	0.02%	9.4%	HVDYVVDQVVGK	99.7%	43.9	25	37.5	1	0	0	1357.71	346	357
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	21	0.02%	9.4%	IFDEILVNAADNK	99.7%	106	25	103	4	0	0	1461.76	105	117

DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	21	0.02%	9.4%	IVGLQYK	97.2%	30.5	25	24.5	1	0	0	820.49	534	540
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	21	0.02%	9.4%	LAQAEAAGLHK	99.7%	54.8	25	53	4	0	0	1108.61	998	1008
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	21	0.02%	9.4%	LCNIFSTK	96.6%	29.8	25	23.4	1	0	0	982.50	190	197
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	21	0.02%	9.4%	LLFPAVDDNLLK	99.7%	62.5	25	53.3	4	0	0	1357.77	837	848
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	21	0.02%	9.4%	NTVEITELPVR	99.7%	50.4	25	44.1	3	0	0	1270.70	940	950
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	21	0.02%	9.4%	SQDFGNLFSFPSYSQK	99.7%	71.9	25	71.9	2	0	0	1851.85	1441	1456
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	21	0.02%	9.4%	YAGPEDDAAITLAFSK	99.7%	89.4	25	89.4	2	0	0	1668.81	661	676
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	AALSALESFLK	99.7%	83.9	25	67.1	2	0	0	1149.65	311	321
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	AQEPESGLSEETQVK	99.7%	78.2	25	66.6	2	0	0	1631.78	4091	4105
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	ATQMPEGGQGAPPMYQLYK	99.7%	63	25	63	3	0	0	2066.97	945	963
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	ATQQQHDFTLTQTADGR	99.7%	84.1	25	78.7	2	2	0	1917.91	2637	2653
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	AYVPALQMAFK	99.7%	43.6	25	40.7	4	0	0	1238.66	747	757
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	CFGTGAAGNR	99.7%	52	25	44.5	1	0	0	1010.45	1312	1321
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	CGAALAGHQLIR	99.7%	67.5	25	67.2	2	0	0	1266.67	25	36
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	CLMDQATDPNILGR	99.7%	86.2	25	86.2	2	0	0	1603.76	4106	4119
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	DCLSIPYR	98.5%	33.2	25	26.7	2	0	0	1023.49	2247	2254
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	DFGLLVFVR	99.7%	65.1	25	53.6	2	0	0	1065.61	62	70
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	DFSAFINLVEFCR	99.7%	52.7	25	44.9	2	0	0	1617.77	619	631
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	DILETHLR	99.7%	51	25	40.8	2	0	0	996.55	1413	1420
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	DILPCLDGYLK	99.7%	61.3	25	45	2	0	0	1306.67	791	801
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	DLCNTHLMR	99.5%	38	25	31.2	2	0	0	1175.53	1362	1370
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	DLLLNTMSQEEK	99.7%	71.1	25	60	2	0	0	1436.69	3814	3825
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	DQNILLGTTYR	99.7%	87.7	25	78.7	4	0	0	1293.68	3325	3335
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	DVDFMYVELIQR	99.7%	81.3	25	70.9	4	0	0	1543.75	380	391
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	EIFNFVLK	99.3%	37	25	18.8	3	0	0	1009.57	247	254
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	ELLNPVVEFVSHPSTTCR	99.7%	70.4	25	69.6	2	2	0	2085.04	2453	2470
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	EQQHVMEELFQSSFR	99.7%	77.6	25	77.6	1	2	0	1910.87	1769	1783
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	FMNAVFFLLPK	99.7%	48.4	25	45.5	2	0	0	1342.72	2378	2388
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	FNNYVDCMK	98.9%	34.7	25	34.5	1	0	0	1190.50	1736	1744
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	FVPLLPGNR	99.0%	35	25	32.4	2	0	0	1012.59	1194	1202
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	FYGELALK	97.8%	31.6	25	26	2	0	0	940.51	156	163
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	FYQGFLFSEKPEK	99.7%	52.2	25	47.1	2	0	0	1619.81	1961	1973
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	GGSWIQEINVAEK	99.7%	73.1	25	58.9	2	0	0	1430.73	4024	4036
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	GIFTSEIGTK	99.7%	70	25	61	2	0	0	1052.56	2941	2950
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	GLSSLLCNFTK	99.7%	66.2	25	57.3	2	0	0	1239.64	226	236
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	GPESESEDHRASGEVR	98.5%	27.6	25	27.6	0	1	0	1741.77	500	515
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	GYGLFAGPCK	99.7%	40.3	25	34.2	2	0	0	1069.51	365	374
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	HGDLPDIQIK	99.7%	63.1	25	53.7	4	0	0	1135.61	2777	2786
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	HNLEIIK	99.7%	41.4	25	15.4	2	0	0	866.51	2233	2239
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	HSSLITPLQAVAQR	99.7%	56.1	25	52.3	2	2	0	1520.85	2787	2800
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	IAPYSVEIK	99.5%	37.8	25	22.9	2	0	0	1019.58	100	108
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	ICSKPVVLPK	99.7%	43.7	25	28.1	1	0	0	1140.68	490	499
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	IIANALSSEPACLAEIEEDKAR	97.3%	25.2	25	25.2	0	1	0	2400.21	3336	3357
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	ILDVMYSR	99.7%	52.5	25	39	4	0	0	996.52	1876	1883
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	ILELSGSSSEDSEK	99.7%	90.2	25	85.9	2	0	0	1480.70	3359	3372
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	IMEFTTTLLNTSPEGWK	99.7%	117	25	109	4	0	0	1983.97	1341	1357
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	INQVFHGSCITEGNELTK	99.7%	88.5	25	88.5	2	2	0	2046.99	1896	1913
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	IPALDLLIK	99.7%	49.6	25	41.9	2	0	0	995.65	125	133
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	KEEENASVIDSAELQAYPALVVEK	99.7%	38.3	25	38.3	0	1	0	2632.34	3426	3449
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	KFIQTFGK	99.5%	38.3	25	20.9	1	0	0	968.56	3631	3638
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	KNILEESLCELVAK	98.8%	34	25	34	1	0	0	1645.88	2334	2347

DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	KQNNFSLAMK	99.7%	65.9	25	55.9	3	0	0	1180.61	3248	3257
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LAAVVSACK	99.7%	47.2	25	39.1	2	0	0	918.51	1448	1456
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LACDVDQVTR	99.7%	62.2	25	43.7	2	0	0	1176.57	972	981
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LAGANPAVITCDELLLGHEK	99.7%	36	25	36	0	1	0	2121.10	4051	4070
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LATTILQHWK	99.7%	47.5	25	47.4	2	0	0	1210.69	1618	1627
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LCYDAFTENMAGENQLLER	99.7%	115	25	115	3	1	0	2290.01	1918	1936
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LGASLAFNNIYR	99.7%	74.4	25	43.6	4	0	0	1338.72	1076	1087
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LGLPGDEVDNK	99.7%	44.7	25	42.8	1	0	0	1156.58	2705	2715
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LGLPGDEVDNKVK	99.7%	56.5	25	53.8	2	0	0	1383.75	2705	2717
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LGNPIVPLNIR	99.7%	62.9	25	62.9	2	0	0	1205.74	2133	2143
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LLEEALLR	99.7%	55.5	25	41.6	4	0	0	956.58	2892	2899
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LLLQGEADQSLLTFIDK	99.7%	74.7	25	74.7	3	0	0	1904.04	3051	3067
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LLNFLMK	99.4%	37.8	25	23.3	3	0	0	878.52	2215	2221
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LLNTWTNR	99.7%	57.6	25	52.6	2	0	0	1017.55	3160	3167
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LLPAELPAKR	98.6%	33.5	25	33.5	1	0	0	1107.69	2900	2909
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LLQDFNR	99.7%	42.2	25	22	2	0	0	905.48	2836	2842
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LLQIIER	99.7%	49.1	25	32.7	4	0	0	884.56	3468	3474
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LLSITVR	99.7%	44.6	25	16.3	2	0	0	801.52	669	675
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LNESTFDTQITK	99.7%	70.2	25	63.9	2	0	0	1396.70	1858	1869
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LNESTFDTQITKK	99.7%	71.5	25	64	2	0	0	1524.79	1858	1870
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LPPDVLR	98.9%	34.6	25	34.6	3	0	0	809.49	2916	2922
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LPVLAGCLK	99.7%	51.9	25	49.1	2	0	0	970.58	217	225
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LQETLSAADR	99.7%	75.7	25	55.2	3	0	0	1103.57	15	24
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LQYFMEQFYGIIR	99.7%	52.3	25	52.3	1	0	0	1723.85	338	350
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LSDFNDITNMLLLK	99.7%	108	25	108	7	0	0	1636.86	3656	3669
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LSFAVPFR	99.7%	51.8	25	44.4	4	0	0	936.53	892	899
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LSLMYAR	99.7%	49	25	40.3	2	0	0	853.46	2739	2745
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LVINTEEVFRPYAK	99.7%	50.9	25	50.9	2	0	0	1678.92	2149	2162
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	LYSLALHPNAFK	99.5%	38.7	25	38.7	2	2	0	1373.76	1063	1074
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	MAVLALLAK	99.7%	75.7	25	65.2	4	0	0	929.59	1643	1651
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	MDPMNIWDDIITNR	99.7%	57.9	25	53.3	2	0	0	1765.79	3173	3186
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	MEVQEQEEDISSLIR	99.7%	85	25	76.1	1	0	0	1805.86	3218	3232
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	MKQDAQVVLYR	99.7%	74.5	25	68.5	2	1	0	1350.72	2763	2773
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	MQLVCCR	99.1%	35.5	25	30.5	1	0	0	966.43	453	459
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	MSPYKDILETHLR	99.7%	57.7	25	56.7	0	2	0	1618.83	1408	1420
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	MSTSPEAFLALR	99.7%	85.9	25	73.4	8	0	0	1322.68	3890	3901
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	MYAALGDPK	99.7%	49.4	25	45.8	4	0	0	965.48	3613	3621
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	NCISTVVHQGLIR	99.7%	74.4	25	65.5	2	2	0	1496.80	477	489
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	NLDLAVLELMQSSVDNTK	99.7%	94.8	25	94.8	3	0	0	2006.01	1574	1591
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	NLLTVTSSDEMMK	99.7%	94.6	25	91.4	6	0	0	1500.69	869	881
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	NLSSNEAISLEEIR	99.7%	106	25	82.4	2	0	0	1574.80	839	852
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	NNWEVSALSR	99.7%	66.4	25	58	3	0	0	1175.58	811	820
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	NVDSNNKELSIAIR	99.7%	91.9	25	91.9	2	0	0	1572.83	351	364
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	QCLPSLDLSCK	99.7%	67.1	25	54.6	2	0	0	1320.63	1498	1508
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	QDAQVVLYR	99.7%	54.1	25	38.2	2	0	0	1091.58	2765	2773
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	QFINLMLPMK	99.4%	37.3	25	28.2	2	0	0	1266.66	3966	3975
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	QGNLSSQVPLK	99.7%	46.7	25	39	1	0	0	1170.65	3148	3158
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	QGNLSSQVPLKR	99.7%	40.9	25	32	2	0	0	1326.75	3148	3159
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	QITQSALLAEAR	99.7%	94.5	25	71.8	4	0	0	1300.72	2951	2962
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	QLFSSLFSGILK	99.7%	45	25	37.8	1	0	0	1339.76	2807	2818
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	QMFLTQTDTGDDR	99.7%	57.1	25	57.1	3	0	0	1527.67	394	406

DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	RLSFAVPFR	97.1%	30.5	25	26	1	0	0	1092.63	891	899
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	SDPGLLTNTMDVFVK	99.7%	104	25	96.8	6	0	0	1636.83	3993	4007
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	SIELFYK	98.2%	32.4	25	15.2	2	0	0	899.49	1187	1193
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	SIGEYDVLR	99.7%	46.6	25	42.3	2	0	0	1051.54	2932	2940
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	SKDFVQVMR	99.7%	54.6	25	40.2	2	0	0	1109.58	2417	2425
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	SLEYCSTASIDSENPPDLNK	99.7%	70.5	25	70.5	2	0	0	2240.00	3010	3029
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	SLGPPQGEEDSVPR	99.7%	76.9	25	75.5	2	0	0	1467.71	2107	2120
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	SLGTIQQCCDAIDHLCR	99.7%	47.8	25	47.8	0	2	0	2046.92	1120	1136
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	SLNSIEFR	99.7%	44.5	25	31.1	2	0	0	965.51	72	79
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	SMEEDPQTSR	96.9%	30.1	25	21.5	2	0	0	1179.49	237	246
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	SPNLWLK	99.7%	40.1	25	24.4	1	0	0	857.49	1203	1209
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	SQGCSEQVLTVLK	99.7%	81.7	25	78.9	4	0	0	1448.74	3290	3302
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	STVLTPMFVETQASQGTLQTR	99.7%	105	25	105	4	1	0	2295.17	2599	2619
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	TETVTSFR	99.7%	42.3	25	36.1	4	0	0	940.47	3865	3872
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	TQMTSAVREPK	99.3%	37	25	23.4	1	0	0	1263.64	206	216
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	TSALSDETKNNWEVSALSR	99.7%	60.9	25	59	0	2	0	2108.03	802	820
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	TVGALQVLGTEAQSSLLK	99.7%	123	25	119	4	0	0	1815.02	1275	1292
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	TVSLLDENNVSSYLSK	99.7%	131	25	124	4	0	0	1768.90	3303	3318
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	TYSVVPMTSR	98.2%	32.4	25	22	2	0	0	1140.57	3790	3799
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	VCLDIIYK	99.7%	47.1	25	28.2	2	0	0	1023.55	2434	2441
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	VFLALAAK	96.8%	30	25	15.8	1	0	0	832.53	464	471
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	VLEQLIVAHFPMQSR	99.2%	30.1	25	30.1	1	1	0	1783.95	1713	1727
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	VPADLLKR	99.0%	35	25	27	1	0	0	911.57	3878	3885
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	VTELALTASDR	99.7%	118	25	106	3	0	0	1175.63	914	924
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	VTVMASLR	99.7%	48	25	31.6	2	0	0	876.50	3726	3733
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	VVQMLGSLGGQINK	99.7%	90.5	25	72.3	4	0	0	1459.79	855	868
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	WPVAGQIR	99.2%	36.1	25	27.4	2	0	0	926.52	2629	2636
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	YAVPSAGLR	99.6%	39.5	25	34.5	2	0	0	933.52	265	273
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	YNFPVEVEVPMER	99.7%	65.6	25	60	4	0	0	1608.77	1988	2000
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	YPEETLSLMTK	99.7%	49.3	25	33.4	3	0	0	1311.65	3475	3485
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	126	157	319	0.31%	34.1%	YSCFALFVK	99.7%	46.6	25	38.7	2	0	0	1134.57	701	709
DNA-directed RNA polymerase I subunit RPA49	POLR1E	RPA49_HUMAN	54.0	100.0%	4	4	5	0.00%	9.8%	AAETIIDTK	97.5%	31	25	26.1	1	0	0	961.52	233	241
DNA-directed RNA polymerase I subunit RPA49	POLR1E	RPA49_HUMAN	54.0	100.0%	4	4	5	0.00%	9.8%	CIWFLDTLIK	99.5%	38	25	28.9	1	0	0	1308.70	338	347
DNA-directed RNA polymerase I subunit RPA49	POLR1E	RPA49_HUMAN	54.0	100.0%	4	4	5	0.00%	9.8%	LSYVGNNFGTGALK	99.5%	38.6	25	37.5	1	0	0	1440.75	129	142
DNA-directed RNA polymerase I subunit RPA49	POLR1E	RPA49_HUMAN	54.0	100.0%	4	4	5	0.00%	9.8%	SALGPGVPHIINTK	99.7%	47	25	44.9	2	0	0	1403.80	358	371
DNA-directed RNA polymerase II subunit RPB1	POLR2A	RPB1_HUMAN	217.2	100.0%	4	4	4	0.00%	2.4%	LLVDSNNPK	98.3%	32.6	25	25.4	1	0	0	999.55	117	125
DNA-directed RNA polymerase II subunit RPB1	POLR2A	RPB1_HUMAN	217.2	100.0%	4	4	4	0.00%	2.4%	NSINQVVQLR	99.7%	50.7	25	36.1	1	0	0	1170.66	881	890
DNA-directed RNA polymerase II subunit RPB1	POLR2A	RPB1_HUMAN	217.2	100.0%	4	4	4	0.00%	2.4%	TPSLTVFLLGQSAR	99.7%	52.8	25	48.2	1	0	0	1489.84	1136	1149
DNA-directed RNA polymerase II subunit RPB1	POLR2A	RPB1_HUMAN	217.2	100.0%	4	4	4	0.00%	2.4%	YSPTSPTYSPTSPK	98.7%	33.9	25	31.5	1	0	0	1512.72	1909	1922
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	6	6	11	0.01%	5.8%	EGEEQLQTQHQK	99.7%	44.8	25	35.3	2	0	0	1454.69	135	146
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	6	6	11	0.01%	5.8%	GPIQILNR	99.7%	60.8	25	49.2	2	0	0	910.55	1065	1072
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	6	6	11	0.01%	5.8%	ITSQIFIGPTYYQR	99.6%	39.4	25	39.4	1	0	0	1686.89	1037	1050
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	6	6	11	0.01%	5.8%	NLTYSAPLYVDITK	99.7%	59.6	25	53.4	2	0	0	1597.85	117	130
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	6	6	11	0.01%	5.8%	QEVPIIIVFR	99.7%	41	25	33.3	2	0	0	1213.73	265	274
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	6	6	11	0.01%	5.8%	VSGDDVIIGK	98.8%	34.2	25	21.9	2	0	0	1002.55	860	869
DNA-directed RNA polymerase II subunit RPB3	POLR2C	RPB3_HUMAN	31.4	100.0%	4	4	8	0.01%	17.5%	FIIENTDLAVANSIR	99.7%	91.5	25	87.9	2	0	0	1675.90	21	35
DNA-directed RNA polymerase II subunit RPB3	POLR2C	RPB3_HUMAN	31.4	100.0%	4	4	8	0.01%	17.5%	ITELTDENVK	99.7%	53.5	25	35.4	2	0	0	1161.60	11	20
DNA-directed RNA polymerase II subunit RPB3	POLR2C	RPB3_HUMAN	31.4	100.0%	4	4	8	0.01%	17.5%	LGLIPLISDDIVDK	99.7%	48.3	25	42.4	2	0	0	1510.87	68	81
DNA-directed RNA polymerase II subunit RPB3	POLR2C	RPB3_HUMAN	31.4	100.0%	4	4	8	0.01%	17.5%	PYANQPTVR	98.9%	34.5	25	34.5	2	0	0	1045.54	2	10
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	8	8	11	0.01%	6.8%	AQENLNPLVVLNLFK	99.7%	61.8	25	61.8	1	0	0	1711.97	214	228
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	8	8	11	0.01%	6.8%	GFSIGIGDVTPGQGLLK	99.7%	45.5	25	45.5	1	0	0	1658.91	695	711

DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	8	8	11	0.01%	6.8%	IDEVAVPVHVAK	99.7%	54.1	25	33.8	1	0	0	1276.73	377	388
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	8	8	11	0.01%	6.8%	LAPVYLSNR	98.4%	32.9	25	27.3	1	0	0	1032.58	686	694
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	8	8	11	0.01%	6.8%	LLVEGDNLR	99.7%	40.7	25	34.4	2	0	0	1028.57	1225	1233
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	8	8	11	0.01%	6.8%	LTEIIFLNDVIK	99.3%	36.6	25	32.7	2	0	0	1417.83	283	294
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	8	8	11	0.01%	6.8%	TVISPDPNLR	96.3%	29.5	25	29.5	1	0	0	1111.61	367	376
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	8	8	11	0.01%	6.8%	VVVQGIPEVSR	99.7%	63.2	25	63.2	2	0	0	1182.68	1199	1209
DNA-directed RNA polymerase III subunit RPC2	POLR3B	RPC2_HUMAN	127.8	100.0%	3	3	4	0.00%	3.4%	GAVGASVTSSTHEK	99.7%	73.7	25	73.7	2	0	0	1330.66	197	210
DNA-directed RNA polymerase III subunit RPC2	POLR3B	RPC2_HUMAN	127.8	100.0%	3	3	4	0.00%	3.4%	LNECPLDPGGYFIVK	99.6%	39.6	25	39.6	1	0	0	1721.86	158	172
DNA-directed RNA polymerase III subunit RPC2	POLR3B	RPC2_HUMAN	127.8	100.0%	3	3	4	0.00%	3.4%	VILIQEQLSK	99.7%	57.2	25	38.3	1	0	0	1170.71	177	186
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	3	3	5	0.00%	2.5%	LSLAQHLR	99.7%	47	25	36.6	2	0	0	937.56	783	790
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	3	3	5	0.00%	2.5%	VAQVLEGFITR	99.7%	71.1	25	64.1	2	0	0	1232.70	977	987
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	3	3	5	0.00%	2.5%	VLDLVLQLFQAK	99.7%	64.4	25	50.7	1	0	0	1386.84	713	724
DNA-directed RNA polymerases I, II, and III subunit RPABC1	POLR2E	RPAB1_HUMAN	24.6	100.0%	3	3	5	0.00%	15.7%	ALIVVQQGMTPSAK	99.7%	66.9	25	63.1	2	0	0	1442.80	102	115
DNA-directed RNA polymerases I, II, and III subunit RPABC1	POLR2E	RPAB1_HUMAN	24.6	100.0%	3	3	5	0.00%	15.7%	IIRPSETAGR	99.7%	49.4	25	31.7	2	0	0	1099.62	193	202
DNA-directed RNA polymerases I, II, and III subunit RPABC1	POLR2E	RPAB1_HUMAN	24.6	100.0%	3	3	5	0.00%	15.7%	IQAGDPVAR	99.7%	41.7	25	40.2	1	0	0	926.51	173	181
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	5	7	13	0.01%	37.3%	ADQFEYVMYGK	99.7%	61.2	25	58.5	2	0	0	1350.60	85	95
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	5	7	13	0.01%	37.3%	IEGDETSTEAATR	99.7%	57.6	25	55.3	2	0	0	1379.63	99	111
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	5	7	13	0.01%	37.3%	LQGDANNLHGFEVDSR	99.7%	79.6	25	74	2	1	0	1771.84	125	140
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	5	7	13	0.01%	37.3%	LSAYVSYGGLLMR	99.7%	86.9	25	79.5	4	0	0	1445.75	112	124
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	5	7	13	0.01%	37.3%	VYRIEGDETSTEAATR	99.7%	65.8	25	60.5	2	0	0	1797.86	96	111
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	5	6	10	0.01%	16.1%	ELYDKGGEQAIK	99.7%	58.8	25	44.2	2	1	0	1350.69	62	73
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	5	6	10	0.01%	16.1%	ETTYYDVLGVKPNATQEELKK	98.8%	28.4	25	28.4	0	1	0	2426.25	4	24
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	5	6	10	0.01%	16.1%	ILEVHIDK	99.7%	50.2	25	15.3	2	0	0	966.56	207	214
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	5	6	10	0.01%	16.1%	NVICDKCEGR	99.5%	37.8	25	37.2	2	0	0	1250.56	131	140
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	5	6	10	0.01%	16.1%	TIVITSHPGQIVK	99.7%	67.8	25	67.8	2	0	0	1392.82	284	296
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	9	9	17	0.02%	25.2%	DGNDLHMTYK	99.7%	44.5	25	39.9	2	0	0	1193.53	263	272
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	9	9	17	0.02%	25.2%	EISFAYEVLSNPEKR	99.7%	73	25	60.8	2	0	0	1781.91	49	63
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	9	9	17	0.02%	25.2%	IGLVEALCGFQFTFK	99.7%	60	25	53.1	1	0	0	1729.90	273	287
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	9	9	17	0.02%	25.2%	ILEVHVDK	99.7%	54.7	25	34.3	2	0	0	952.55	216	223
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	9	9	17	0.02%	25.2%	LYDILGVPPGASENELKK	99.7%	43.6	25	37.8	0	2	0	1943.05	9	26
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	9	9	17	0.02%	25.2%	NVLCSACSGQGGK	99.7%	86.8	25	86.8	2	0	0	1337.59	140	152
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	9	9	17	0.02%	25.2%	VIEPGCVR	99.5%	38.1	25	36	2	0	0	929.49	303	310
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	9	9	17	0.02%	25.2%	VSLEDLYNGK	99.7%	64	25	56.3	2	0	0	1137.58	122	131
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	9	9	17	0.02%	25.2%	YGEQGLR	99.7%	52.7	25	33.3	2	0	0	822.41	69	75
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	5	6	12	0.01%	14.2%	EFTVNIMDTCER	99.7%	78.2	25	78.2	1	0	0	1530.66	227	238
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	5	6	12	0.01%	14.2%	FSQLAEAYEVLSDEVK	99.7%	56.2	25	56.2	1	0	0	1827.90	135	150
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	5	6	12	0.01%	14.2%	GGPTVDPEELFR	99.7%	46.1	25	45.5	3	0	0	1316.65	176	187
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	5	6	12	0.01%	14.2%	GSIIISPCVVCR	99.7%	49.6	25	38.1	4	0	0	1360.71	282	293
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	5	6	12	0.01%	14.2%	VMIPVPAGVEDGQTVR	99.7%	75.1	25	71.1	3	0	0	1683.87	304	319
DnaJ homolog subfamily B member 11	DNAJB11	DJB11_HUMAN	40.5	100.0%	3	3	5	0.00%	11.5%	FQDLGAAYEVLSDSEK	99.7%	109	25	109	2	0	0	1771.84	67	82
DnaJ homolog subfamily B member 11	DNAJB11	DJB11_HUMAN	40.5	100.0%	3	3	5	0.00%	11.5%	KGEGLPNFDNNNIK	99.7%	68	25	53.3	1	0	0	1559.78	302	315
DnaJ homolog subfamily B member 11	DNAJB11	DJB11_HUMAN	40.5	100.0%	3	3	5	0.00%	11.5%	TLEVEIEPGVR	99.7%	72.3	25	60.7	2	0	0	1241.67	207	217
DnaJ homolog subfamily B member 12	DNAJB12	DJB12_HUMAN	41.8	100.0%	3	3	6	0.01%	9.6%	AIGTAYAVLSNPEK	99.7%	67.8	25	61.2	2	0	0	1433.76	153	166
DnaJ homolog subfamily B member 12	DNAJB12	DJB12_HUMAN	41.8	100.0%	3	3	6	0.01%	9.6%	GYTAEQVAAVK	99.7%	49	25	39.3	2	0	0	1136.59	93	103
DnaJ homolog subfamily B member 12	DNAJB12	DJB12_HUMAN	41.8	100.0%	3	3	6	0.01%	9.6%	NVEDDYIANLR	99.7%	66.2	25	66.2	2	0	0	1321.64	316	326
DnaJ homolog subfamily B member 6	DNAJB6	DNJB6_HUMAN	36.1	100.0%	5	5	13	0.01%	20.2%	APGPWDPLASAAGLK	99.7%	42.1	25	42.1	2	0	0	1450.77	288	302
DnaJ homolog subfamily B member 6	DNAJB6	DNJB6_HUMAN	36.1	100.0%	5	5	13	0.01%	20.2%	QVAEAYEVLSDAK	99.7%	75.9	25	71	3	0	0	1422.71	48	60
DnaJ homolog subfamily B member 6	DNAJB6	DNJB6_HUMAN	36.1	100.0%	5	5	13	0.01%	20.2%	SLTINGVADDDALAEER	99.7%	101	25	88	2	0	0	1788.86	226	242
DnaJ homolog subfamily B member 6	DNAJB6	DNJB6_HUMAN	36.1	100.0%	5	5	13	0.01%	20.2%	VDYYEVLGVQR	99.7%	56	25	29.8	4	0	0	1340.68	2	12
DnaJ homolog subfamily B member 6	DNAJB6	DNJB6_HUMAN	36.1	100.0%	5	5	13	0.01%	20.2%	VEVEEDGQLK	99.0%	35.2	25	27.8	2	0	0	1145.57	216	225
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	6	6	13	0.01%	9.0%	ASNLLYGQLK	99.7%	47.7	25	41	2	0	0	1106.62	493	502

DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	6	6	13	0.01%	9.0%	GVNSYPSLFIFR	99.7%	40.2	25	40.2	2	0	0	1399.74	197	208
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	6	6	13	0.01%	9.0%	ILYDILAFAK	99.7%	56.2	25	54.8	4	0	0	1166.68	439	448
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	6	6	13	0.01%	9.0%	NFQEEQINTR	99.7%	54	25	31.8	2	0	0	1278.61	757	766
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	6	6	13	0.01%	9.0%	NSILFLNSLDAK	99.7%	67	25	63.5	2	0	0	1334.73	326	337
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	6	6	13	0.01%	9.0%	YDFGIYDDDPEIITLER	99.7%	42.2	25	42.2	1	0	0	2073.97	120	136
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	3	3	5	0.00%	7.0%	AGFFGTVVEYGAER	99.7%	85.8	25	74.9	2	0	0	1502.73	328	341
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	3	3	5	0.00%	7.0%	GIRPGLTTVLAR	99.4%	37.3	25	30.9	1	0	0	1253.77	249	260
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	3	3	5	0.00%	7.0%	VIDVTVPLQCLVK	99.7%	59.1	25	57.4	2	0	0	1483.86	485	497
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	7	7	10	0.01%	3.9%	AGFLAFTQLPK	99.7%	48.2	25	33	1	0	0	1192.67	440	450
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	7	7	10	0.01%	3.9%	DSLLASLLDGVR	98.7%	33.8	25	28	1	0	0	1258.70	312	323
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	7	7	10	0.01%	3.9%	ENGLEVLQEAFSR	99.7%	76.9	25	70.5	2	0	0	1491.74	1443	1455
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	7	7	10	0.01%	3.9%	IFIAQPAWVLR	99.7%	49.8	25	43.4	2	0	0	1313.77	1987	1997
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	7	7	10	0.01%	3.9%	IVDGPDPENIILILK	99.7%	62	25	61.4	2	0	0	1648.95	1360	1374
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	7	7	10	0.01%	3.9%	LLEGIGLENLDSPAATK	99.7%	67	25	67	1	0	0	1740.94	2140	2156
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	7	7	10	0.01%	3.9%	TELLTEALR	99.7%	43.1	25	19.7	1	0	0	1045.59	91	99
DnaJ homolog subfamily C member 7	DNAJC7	DNJC7_HUMAN	56.4	100.0%	3	3	5	0.00%	6.9%	AVQFFVQALR	99.7%	47	25	39.7	2	0	0	1178.67	229	238
DnaJ homolog subfamily C member 7	DNAJC7	DNJC7_HUMAN	56.4	100.0%	3	3	5	0.00%	6.9%	EALGDAQQSVR	99.7%	66.9	25	63.3	2	0	0	1173.59	80	90
DnaJ homolog subfamily C member 7	DNAJC7	DNJC7_HUMAN	56.4	100.0%	3	3	5	0.00%	6.9%	YPEAQSVASDILR	98.7%	33.7	25	31.7	1	0	0	1448.74	192	204
DnaJ homolog subfamily C member 9	DNAJC9	DNJC9_HUMAN	29.9	100.0%	4	4	7	0.01%	20.0%	ELGLDEGVDSLK	99.7%	46.6	25	46.6	2	0	0	1274.65	206	217
DnaJ homolog subfamily C member 9	DNAJC9	DNJC9_HUMAN	29.9	100.0%	4	4	7	0.01%	20.0%	ISLEDIQAFEK	99.7%	56.4	25	47.7	1	0	0	1292.67	108	118
DnaJ homolog subfamily C member 9	DNAJC9	DNJC9_HUMAN	29.9	100.0%	4	4	7	0.01%	20.0%	NIIQQAIDAGEVPSYNAFVK	99.7%	98.1	25	98.1	2	0	0	2177.12	161	180
DnaJ homolog subfamily C member 9	DNAJC9	DNJC9_HUMAN	29.9	100.0%	4	4	7	0.01%	20.0%	VSLQVHPDR	99.7%	41.8	25	33	2	0	0	1050.57	38	46
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	6	7	13	0.01%	27.7%	EGNFDIVSGTR	99.7%	81.8	25	77.3	2	0	0	1194.58	137	147
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	6	7	13	0.01%	27.7%	GYVFQMEMIVR	99.7%	56.5	25	53	2	0	0	1404.67	206	216
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	6	7	13	0.01%	27.7%	LGGNEIVSFLK	99.7%	72.6	25	68	2	0	0	1176.66	241	251
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	6	7	13	0.01%	27.7%	LGLGTAYIHGMK	99.7%	42.8	25	38.3	4	0	0	1260.68	96	107
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	6	7	13	0.01%	27.7%	QLNYTIGEVPISFVDR	99.7%	68.1	25	66.2	2	0	0	1850.96	219	234
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	6	7	13	0.01%	27.7%	YSVLLPTYNER	99.1%	35.5	25	35.5	1	0	0	1354.70	27	37
Dolichol-phosphate mannosyltransferase subunit 3	DPM3	DPM3_HUMAN	10.1	99.8%	2	2	6	0.01%	23.9%	ELQSQIQEAR	99.7%	66.2	25	52	4	0	0	1201.62	73	82
Dolichol-phosphate mannosyltransferase subunit 3	DPM3	DPM3_HUMAN	10.1	99.8%	2	2	6	0.01%	23.9%	VATFHDCEDAAR	99.7%	46.8	25	46.8	2	0	0	1391.60	61	72
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	9	9	17	0.02%	21.3%	ELGSECGIEFDEEK	99.7%	83	25	76.6	2	0	0	1641.70	140	153
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	9	9	17	0.02%	21.3%	ETHSLFFR	99.7%	42.4	25	39.3	1	0	0	1036.52	58	65
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	9	9	17	0.02%	21.3%	GFELTFK	96.1%	29.3	25	25	1	0	0	841.45	71	77
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	9	9	17	0.02%	21.3%	LPDVYGVFQFK	99.7%	54.5	25	48.9	2	0	0	1312.69	381	391
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	9	9	17	0.02%	21.3%	NTLLIAGLQAR	99.7%	96.1	25	73.8	2	0	0	1169.70	240	250
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	9	9	17	0.02%	21.3%	SSLNPILFR	99.7%	68.6	25	48.2	3	0	0	1046.60	190	198
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	9	9	17	0.02%	21.3%	TADDPSLSLIK	99.6%	39.3	25	32.8	2	0	0	1159.62	78	88
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	9	9	17	0.02%	21.3%	TLVLLDNLNVR	99.7%	71.8	25	53.9	2	0	0	1269.75	47	57
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	9	9	17	0.02%	21.3%	YSQTGNYELAVALSR	99.7%	104	25	102	2	0	0	1671.83	283	297
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	28	0.03%	27.3%	ALTSEIALLQSR	99.7%	84.8	25	71.5	3	0	0	1301.74	525	536
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	28	0.03%	27.3%	ATSFLLALEPELEAR	99.7%	43.2	25	35.8	2	0	0	1659.90	66	80
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	28	0.03%	27.3%	DTYIENEK	96.9%	30.2	25	26.4	1	0	0	1011.46	580	587
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	28	0.03%	27.3%	DVPAYSQDTFK	99.4%	37.5	25	21.3	2	0	0	1270.60	205	215
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	28	0.03%	27.3%	GEDEEENNLEVR	99.7%	61.3	25	51.6	2	0	0	1432.62	90	101
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	28	0.03%	27.3%	HFDETVNR	97.0%	30.3	25	16.8	2	0	0	1017.47	495	502
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	28	0.03%	27.3%	IDHILDAL	99.6%	39.8	25	38.7	2	0	0	909.50	600	607
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	28	0.03%	27.3%	LKTEGSDLCDR	99.7%	46	25	33.2	2	1	0	1293.61	537	547
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	28	0.03%	27.3%	LPVALDPGAK	99.5%	38.6	25	38.6	2	0	0	980.58	117	126
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	28	0.03%	27.3%	NIEIDSPYEISR	99.7%	74.6	25	64.9	2	0	0	1435.71	380	391
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	28	0.03%	27.3%	SEDLLDYGPFR	99.7%	73.3	25	71.5	2	0	0	1311.62	194	204
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	28	0.03%	27.3%	VACITEQVLTLVNK	99.7%	47.7	25	37.6	1	0	0	1587.88	475	488

Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	28	0.03%	27.3%	VHYENNSPFLTITSMTR	99.7%	45.2	25	45.2	0	2	0	2009.97	216	232
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	14	15	28	0.03%	27.3%	VTAEVVLAHLGGGSTSR	99.7%	110	25	106	2	0	0	1653.89	49	65
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	8	9	18	0.02%	20.9%	FELDTSER	99.7%	40.3	25	21.3	2	0	0	996.46	461	468
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	8	9	18	0.02%	20.9%	FPEEEAPSTVLSQNLFTPK	99.7%	62	25	46.5	2	0	0	2134.07	505	523
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	8	9	18	0.02%	20.9%	ISTEVGITNVDLSTVDKDQSIAPK	99.7%	42.5	25	41.4	0	2	0	2530.33	369	392
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	8	9	18	0.02%	20.9%	LQVTNVLSQPLTQATVK	99.7%	113	25	107	4	0	0	1840.05	290	306
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	8	9	18	0.02%	20.9%	TGQEVVFVAEPDNK	99.7%	85.2	25	72.2	2	0	0	1532.76	443	456
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	8	9	18	0.02%	20.9%	TSFTPVGDVFELNFMNVK	99.7%	50.7	25	50.7	3	0	0	2061.00	323	340
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	8	9	18	0.02%	20.9%	YHVPVVVVPEGSASDTHEQAILR	96.2%	23.9	25	23.9	0	1	0	2503.29	267	289
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	8	9	18	0.02%	20.9%	YIANTVELR	99.7%	45.9	25	37.7	2	0	0	1078.59	358	366
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	DAD1	DAD1_HUMAN	12.5	100.0%	3	3	9	0.01%	28.3%	ADFQGISPER	99.7%	60.7	25	47.3	4	0	0	1119.54	83	92
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	DAD1	DAD1_HUMAN	12.5	100.0%	3	3	9	0.01%	28.3%	FLEEYLSSTPQR	99.7%	66.8	25	56.6	2	0	0	1469.73	12	23
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	DAD1	DAD1_HUMAN	12.5	100.0%	3	3	9	0.01%	28.3%	SASVVSVISR	99.7%	59.8	25	51.4	3	0	0	1004.57	2	11
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	8	8	14	0.01%	11.3%	EAYYWLR	99.2%	36.1	25	29.4	1	0	0	1000.49	507	513
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	8	8	14	0.01%	11.3%	EGSPVLLNCLMYK	99.7%	44.2	25	44.2	2	0	0	1523.76	629	641
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	8	8	14	0.01%	11.3%	ENDYYTPTGEFR	99.7%	56.1	25	51.8	2	0	0	1491.64	614	625
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	8	8	14	0.01%	11.3%	FGQVYTEAK	99.7%	55.4	25	51.2	2	0	0	1042.52	647	655
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	8	8	14	0.01%	11.3%	FHNWFDDR	99.7%	44.5	25	40.7	1	0	0	1136.49	68	75
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	8	8	14	0.01%	11.3%	FLAEEGFYK	99.7%	44.2	25	36.1	2	0	0	1103.54	59	67
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	8	8	14	0.01%	11.3%	FYSLLDPSYAK	99.7%	42.2	25	36.5	2	0	0	1303.66	330	340
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	8	8	14	0.01%	11.3%	VGQAMASTEEK	99.7%	42.4	25	36.7	2	0	0	1150.54	555	565
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	STT3B	STT3B_HUMAN	93.7	100.0%	5	6	7	0.01%	7.0%	ESDYFTPQGEFR	99.5%	38.4	25	38.4	1	0	0	1475.64	692	703
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	STT3B	STT3B_HUMAN	93.7	100.0%	5	6	7	0.01%	7.0%	FYSLWDTGYAK	99.7%	64.1	25	58	2	0	0	1350.64	384	394
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	STT3B	STT3B_HUMAN	93.7	100.0%	5	6	7	0.01%	7.0%	SSLNSSPWSGLMALGNSR	99.7%	60.5	25	58.4	2	0	0	1879.90	13	30
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	STT3B	STT3B_HUMAN	93.7	100.0%	5	6	7	0.01%	7.0%	TEEGLGPNIK	98.1%	32.2	25	32.2	1	0	0	1057.55	527	536
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	STT3B	STT3B_HUMAN	93.7	100.0%	5	6	7	0.01%	7.0%	VTNIFPK	98.9%	34.7	25	26.7	1	0	0	818.48	787	793
Dolichyl-phosphate beta-glucosyltransferase	ALG5	ALG5_HUMAN	36.9	99.8%	2	2	4	0.00%	7.7%	ETLPSIWDSPTK	99.7%	55.8	25	49.1	2	0	0	1373.69	54	65
Dolichyl-phosphate beta-glucosyltransferase	ALG5	ALG5_HUMAN	36.9	99.8%	2	2	4	0.00%	7.7%	QLSVVVPSYNEEK	99.7%	47.8	25	46.4	2	0	0	1491.77	66	78
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	12	13	38	0.04%	23.6%	ATVTAMIAR	99.7%	67.4	25	54.3	2	0	0	933.52	449	457
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	12	13	38	0.04%	23.6%	EFVMQVK	99.7%	43.4	25	23.2	4	0	0	880.46	318	324
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	12	13	38	0.04%	23.6%	ELLYGGTSPTAETILK	99.7%	90.4	25	89	4	0	0	1692.91	458	473
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	12	13	38	0.04%	23.6%	LAQIQQAK	99.7%	52	25	42.6	4	0	0	899.53	291	298
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	12	13	38	0.04%	23.6%	LLSELDQQSTEMPR	99.7%	92.5	25	86.7	1	0	0	1646.81	552	565
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	12	13	38	0.04%	23.6%	NAAENMLEILGFK	99.7%	87.1	25	84.9	6	0	0	1449.74	343	355
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	12	13	38	0.04%	23.6%	NAAIAVLEELK	99.7%	51.2	25	44.2	2	0	0	1170.67	240	250
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	12	13	38	0.04%	23.6%	NAAIAVLEELKK	99.7%	48.5	25	32	2	0	0	1298.77	240	251
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	12	13	38	0.04%	23.6%	NLPVNFEVAR	99.7%	41.2	25	33.7	2	0	0	1158.63	197	206
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	12	13	38	0.04%	23.6%	TKPIVKPQTSPEYGQGINPISR	97.6%	25.6	25	25.6	0	1	0	2410.31	269	290
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	12	13	38	0.04%	23.6%	VPQAQPTKPALK	99.7%	49.9	25	44	6	0	0	1277.76	356	367
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	12	13	38	0.04%	23.6%	VSVGEFVGEGEGK	99.7%	98.5	25	89.9	4	0	0	1293.63	220	232
Double-stranded RNA-binding protein Staufen homolog 2	STAU2	STAU2_HUMAN	62.6	100.0%	5	5	13	0.01%	11.6%	ALQALQNEPIPER	99.7%	46.9	25	43.3	4	0	0	1478.80	175	187
Double-stranded RNA-binding protein Staufen homolog 2	STAU2	STAU2_HUMAN	62.6	100.0%	5	5	13	0.01%	11.6%	ASTNLQDQLEK	99.7%	54.4	25	36	3	0	0	1246.63	377	387
Double-stranded RNA-binding protein Staufen homolog 2	STAU2	STAU2_HUMAN	62.6	100.0%	5	5	13	0.01%	11.6%	EFVMQVK	99.7%	43.4	25	23.2	4	0	0	880.46	339	345
Double-stranded RNA-binding protein Staufen homolog 2	STAU2	STAU2_HUMAN	62.6	100.0%	5	5	13	0.01%	11.6%	LAQIQQAK	99.7%	52	25	42.6	4	0	0	899.53	312	319
Double-stranded RNA-binding protein Staufen homolog 2	STAU2	STAU2_HUMAN	62.6	100.0%	5	5	13	0.01%	11.6%	VGNEVATGTGPNK	99.7%	71.1	25	68.5	1	0	0	1243.63	346	358
Double-stranded RNA-binding protein Staufen homolog 2	STAU2	STAU2_HUMAN	62.6	100.0%	5	5	13	0.01%	11.6%	VGNEVATGTGPNKK	99.7%	36.7	25	36.6	0	1	0	1371.72	346	359
Double-stranded RNA-binding protein Staufen homolog 2	STAU2	STAU2_HUMAN	62.6	100.0%	5	5	13	0.01%	11.6%	VISGTTLGYLSPK	99.7%	64.8	25	60.3	4	0	0	1335.75	430	442
Double-stranded RNA-specific adenosine deaminase	ADAR	DSRAD_HUMAN	136.1	100.0%	5	6	10	0.01%	5.3%	AMTILLEEAK	99.7%	52	25	39.5	3	0	0	1118.61	565	574
Double-stranded RNA-specific adenosine deaminase	ADAR	DSRAD_HUMAN	136.1	100.0%	5	6	10	0.01%	5.3%	DINAVLIDMER	99.7%	51.9	25	38.5	1	0	0	1288.66	329	339
Double-stranded RNA-specific adenosine deaminase	ADAR	DSRAD_HUMAN	136.1	100.0%	5	6	10	0.01%	5.3%	LVDQSGPPHEPK	99.7%	56.9	25	56.2	3	0	0	1303.66	746	757
Double-stranded RNA-specific adenosine deaminase	ADAR	DSRAD_HUMAN	136.1	100.0%	5	6	10	0.01%	5.3%	NTNSVPETAPAAIPETK	99.7%	42.4	25	37	1	0	0	1739.88	368	384

Double-stranded RNA-specific adenosine deaminase	ADAR	DSRAD_HUMAN	136.1	100.0%	5	6	10	0.01%	5.3%	YLNTNPVGGLLEYAR	99.7%	75.6	25	70.1	2	0	0	1679.88	722	736
Dual specificity mitogen-activated protein kinase kinase 1	MAP2K1	MP2K1_HUMAN	43.4	99.8%	2	2	3	0.00%	12.7%	DVKPSNILVNSR	99.7%	51.9	25	44.5	2	0	0	1341.75	190	201
Dual specificity mitogen-activated protein kinase kinase 1	MAP2K1	MP2K1_HUMAN	43.4	99.8%	2	2	3	0.00%	12.7%	IPEQILGK	95.6%	28.8	25	25.1	1	0	0	897.54	161	168
Dual specificity mitogen-activated protein kinase kinase 1	MAP2K1	MP2K1_HUMAN	43.4	99.8%	2	2	3	0.00%	12.7%	RLEAFLTQK	99.5%	38.1	25	29.5	2	0	0	1105.64	49	57
Dual specificity mitogen-activated protein kinase kinase 1	MAP2K1	MP2K1_HUMAN	43.4	99.8%	2	2	3	0.00%	12.7%	VSHKPSGLVMAR	99.3%	30.6	25	30.6	0	2	0	1297.70	85	96
Dual specificity mitogen-activated protein kinase kinase 1	MAP2K1	MP2K1_HUMAN	43.4	99.8%	2	2	3	0.00%	12.7%	YPIPPPDAK	99.0%	35.2	25	17.3	1	0	0	997.54	261	269
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	17	0.02%	23.5%	DVKPSNILVNSR	99.7%	51.9	25	44.5	2	0	0	1341.75	194	205
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	17	0.02%	23.5%	ISELGAGNGGVVTK	99.7%	89.7	25	85.8	2	0	0	1301.71	75	88
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	17	0.02%	23.5%	LNQPGTPTR	99.7%	45.8	25	39.7	2	0	0	983.53	389	397
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	17	0.02%	23.5%	MLTNHTFIK	96.8%	30	25	19.4	1	0	0	1104.59	362	370
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	17	0.02%	23.5%	RIPEEILGK	98.4%	32.9	25	25.4	2	0	0	1054.63	164	172
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	17	0.02%	23.5%	RLEAFLTQK	99.5%	38.1	25	29.5	2	0	0	1105.64	53	61
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	17	0.02%	23.5%	VGELKDDDFER	99.7%	47.6	25	45.5	2	2	0	1322.62	64	74
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	17	0.02%	23.5%	VQHRPSGLIMAR	97.4%	25.3	25	21.7	0	1	0	1364.76	89	100
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	17	0.02%	23.5%	YPIPPPDAK	99.0%	35.2	25	17.3	1	0	0	997.54	265	273
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	8	10	16	0.02%	30.3%	DVKPSNVLINK	95.1%	28.4	25	21.3	1	0	0	1226.71	190	200
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	8	10	16	0.02%	30.3%	FPYESWGTPFQQLK	99.4%	37.2	25	37.2	2	0	0	1727.84	266	279
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	8	10	16	0.02%	30.3%	FSPEFVDFTAQCLR	99.7%	79.4	25	79.4	2	0	0	1716.81	294	307
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	8	10	16	0.02%	30.3%	HAQSGTIMAVK	98.7%	33.7	25	25	1	0	0	1158.59	83	93
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	8	10	16	0.02%	30.3%	ISCMSKPPAPNPTPPR	99.0%	29	25	29	0	3	0	1749.88	27	42
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	8	10	16	0.02%	30.3%	KTDIAAFVK	98.8%	34.1	25	18.8	1	0	0	992.58	332	340
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	8	10	16	0.02%	30.3%	MCDFGISGYLVDSVAK	99.7%	79.3	25	77.9	4	0	0	1777.81	206	221
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	MP2K3_HUMAN	39.3	100.0%	8	10	16	0.02%	30.3%	QVVEEPSPQLPADR	99.7%	54.3	25	54.2	2	0	0	1564.80	280	293
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	24	28	49	0.05%	23.3%	AEITDAEGLGLK	99.7%	82.3	25	72.1	2	0	0	1216.64	933	944
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	24	28	49	0.05%	23.3%	AESLQQEVEALK	99.7%	67.9	25	64.3	2	0	0	1344.70	318	329
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	24	28	49	0.05%	23.3%	AFLQGGQEATDIALLLR	99.7%	82.8	25	73.3	2	0	0	1816.00	769	785
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	24	28	49	0.05%	23.3%	ASEQIYGTPSSSPYECLR	99.7%	88.4	25	74.5	2	0	0	2044.93	873	890
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	24	28	49	0.05%	23.3%	DLEEKLETLR	99.7%	51.1	25	39.8	2	0	0	1245.67	226	235
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	24	28	49	0.05%	23.3%	DLETSCSDIR	99.7%	66.8	25	56.3	2	0	0	1195.53	786	795
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	24	28	49	0.05%	23.3%	DQLDETVNVEPLTK	99.7%	54.7	25	41.6	1	0	0	1600.81	709	722
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	24	28	49	0.05%	23.3%	DSPLLLQQISAMR	99.7%	84.9	25	84.9	4	0	0	1471.79	1089	1101
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	24	28	49	0.05%	23.3%	ELTNQQEASVER	99.7%	73.4	25	65.4	2	0	0	1403.68	533	544
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	24	28	49	0.05%	23.3%	FTQSALDCMSVEVGR	99.7%	64.1	25	64.1	2	0	0	1699.78	752	766
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	24	28	49	0.05%	23.3%	GSDGAASSYQLK	99.7%	56.2	25	48.1	2	0	0	1183.56	350	361
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	24	28	49	0.05%	23.3%	GTVAYVGATLFATGK	99.7%	63.4	25	63.4	2	0	0	1455.78	42	56
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	24	28	49	0.05%	23.3%	IKGEELSEANVR	99.7%	75.9	25	69.9	2	1	0	1344.71	961	972
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	24	28	49	0.05%	23.3%	LEETQALLR	99.7%	43.7	25	23.1	1	0	0	1072.60	998	1006
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	24	28	49	0.05%	23.3%	LSHEGPGSELPAGALYR	99.7%	35.4	25	30.2	0	2	0	1753.89	1134	1150
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	24	28	49	0.05%	23.3%	MQEQQADLQR	99.7%	72.9	25	64.5	4	0	0	1246.58	265	274
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	24	28	49	0.05%	23.3%	NQELEVVR	99.7%	51.5	25	36.7	1	0	0	986.53	399	406
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	24	28	49	0.05%	23.3%	QLTAHLQDVNR	98.5%	33.3	25	26.2	1	0	0	1294.69	522	532
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	24	28	49	0.05%	23.3%	QMEVAQANR	98.9%	34.5	25	29.5	1	0	0	1046.50	575	583
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	24	28	49	0.05%	23.3%	SPSAQLMEQVAQLK	99.7%	96.3	25	89.3	4	0	0	1529.80	1180	1193
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	24	28	49	0.05%	23.3%	VDELTTDLEILK	99.7%	95.5	25	67.8	2	0	0	1388.75	332	343
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	24	28	49	0.05%	23.3%	VTFSCAAGFGQR	99.7%	88.2	25	83.5	2	0	0	1300.61	1248	1259
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	24	28	49	0.05%	23.3%	WVGVILDEAK	99.7%	52.7	25	41.1	2	0	0	1129.63	57	66
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	24	28	49	0.05%	23.3%	YEHALSQCSVDVYK	97.8%	25.9	25	25.9	0	1	0	1698.78	670	683
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	8	8	12	0.01%	14.8%	FATEYCNTIEGTAK	99.7%	79	25	70.3	2	0	0	1604.73	340	353
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	8	8	12	0.01%	14.8%	GVSPEPIHLK	97.7%	31.5	25	26.9	1	0	0	1076.61	124	133
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	8	8	12	0.01%	14.8%	IFSPNVVNLTLVDLPGMTK	99.7%	65.4	25	63.8	2	0	0	2074.13	134	152
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	8	8	12	0.01%	14.8%	LGIIGVVNR	99.7%	78.4	25	60.1	2	0	0	940.59	239	247

Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	8	8	12	0.01%	14.8%	SSLLDDLLTESEDMAQR	99.7%	70.7	25	67.3	2	0	0	1938.90	693	709
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	8	8	12	0.01%	14.8%	SYFLIVR	95.2%	28.4	25	20.4	1	0	0	897.52	653	659
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	8	8	12	0.01%	14.8%	TLESVDPLGGLNTIDILTAIR	99.7%	49.7	25	49.7	1	0	0	2211.22	377	397
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	8	8	12	0.01%	14.8%	YIETSELCGGAR	99.7%	65.3	25	51.6	1	0	0	1355.63	354	365
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	38	0.04%	30.5%	AIPNQGEILVIR	98.7%	33.7	25	30.3	1	0	0	1322.78	511	522
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	38	0.04%	30.5%	ALLQMVQQFGVDFEK	99.7%	75.4	25	75.4	3	0	0	1768.89	328	342
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	38	0.04%	30.5%	DMILQFISR	99.7%	54.5	25	26.6	2	0	0	1122.60	158	166
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	38	0.04%	30.5%	ESSLILAVTPANMDLANSDALK	99.7%	65.8	25	65.5	4	0	0	2273.17	167	188
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	38	0.04%	30.5%	FPFELVK	99.7%	51.1	25	0	2	0	0	879.50	370	376
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	38	0.04%	30.5%	GISPVPINLR	98.9%	34.8	25	34.8	2	0	0	1065.64	114	123
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	38	0.04%	30.5%	GMEELIPLVNK	99.7%	51.8	25	42.5	1	0	0	1242.68	5	15
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	38	0.04%	30.5%	GYIGVVNR	99.7%	42	25	35	2	0	0	877.49	230	237
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	38	0.04%	30.5%	IEGSGDQVDTLELSGGAR	99.7%	75.5	25	75.5	1	0	0	1803.87	344	361
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	38	0.04%	30.5%	LDLMDEGTDAR	99.7%	69.1	25	57	1	0	0	1235.56	207	217
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	38	0.04%	30.5%	LQDAFSSIGQSCHLDLPQIAVVGGQSAGK	99.7%	69.5	25	68.6	0	2	0	2983.49	16	44
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	38	0.04%	30.5%	LQSQLLSLEK	99.7%	67.3	25	0	2	0	0	1158.67	300	309
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	38	0.04%	30.5%	NLVDSYVAIINK	99.7%	77.6	25	60.7	3	0	0	1348.75	658	669
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	38	0.04%	30.5%	RPLILQLIFSK	98.8%	34.1	25	34.1	1	0	0	1327.85	67	77
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	38	0.04%	30.5%	SSVLENFVGR	99.7%	64	25	49.8	2	0	0	1107.58	45	54
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	38	0.04%	30.5%	TEHAEFLHCK	99.3%	36.4	25	30.2	2	0	0	1271.58	78	87
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	38	0.04%	30.5%	TGLFTPDLAFEAIVK	99.7%	84	25	74.6	2	0	0	1621.88	400	414
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	38	0.04%	30.5%	TLNQQLTNHIR	99.7%	56.2	25	48.1	2	0	0	1337.73	280	290
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	38	0.04%	30.5%	VPVGDQPPDIEYQIK	99.7%	74.5	25	58	2	0	0	1697.87	143	157
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	20	22	38	0.04%	30.5%	VYSPHVLNLTLIDLPGITK	96.1%	23.8	25	23.8	0	1	0	2093.20	124	142
Dynein light chain 1, cytoplasmic	DYNLL1	DYL1_HUMAN	10.4	100.0%	3	4	11	0.01%	49.4%	NADMSEEMQQDSVECATQALEK	99.7%	74.6	25	74.6	1	4	0	2546.03	10	31
Dynein light chain 1, cytoplasmic	DYNLL1	DYL1_HUMAN	10.4	100.0%	3	4	11	0.01%	49.4%	NFGSYVTHETK	99.7%	55.6	25	45	4	0	0	1282.61	61	71
Dynein light chain 1, cytoplasmic	DYNLL1	DYL1_HUMAN	10.4	100.0%	3	4	11	0.01%	49.4%	YNPTWHCIVGR	99.0%	34.9	25	34.9	2	0	0	1402.67	50	60
Dynein light chain Tctex-type 1	DYNLT1	DYLT1_HUMAN	12.5	99.8%	2	3	5	0.00%	23.0%	EAIESAIGGNAYQHSK	99.7%	81.8	25	81.1	2	0	0	1674.81	23	38
Dynein light chain Tctex-type 1	DYNLT1	DYLT1_HUMAN	12.5	99.8%	2	3	5	0.00%	23.0%	YIVTCVIMQK	99.7%	41.4	25	35.2	3	0	0	1270.65	63	72
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	13	13	17	0.02%	5.5%	EGQWDCSVCLVR	99.7%	54.1	25	49.3	1	0	0	1508.66	1607	1618
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	13	13	17	0.02%	5.5%	ELLQSFDSALQSVK	99.7%	80.4	25	74.8	2	0	0	1564.82	257	270
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	13	13	17	0.02%	5.5%	ELVGPPLAETVFTPK	99.7%	107	25	105	2	0	0	1597.88	1384	1398
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	13	13	17	0.02%	5.5%	FGISEPGNQEK	99.5%	38.3	25	34.5	1	0	0	1205.58	1900	1910
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	13	13	17	0.02%	5.5%	IAVAVLEETTR	99.7%	116	25	112	2	0	0	1201.68	2467	2477
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	13	13	17	0.02%	5.5%	IIDDSDSNLSVVK	99.7%	86.8	25	0	2	0	0	1404.72	721	733
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	13	13	17	0.02%	5.5%	QNQTTSAVSTPASSETSK	99.7%	61.4	25	61.4	1	0	0	1823.86	1635	1652
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	13	13	17	0.02%	5.5%	SGQSALYDALFSSQSPK	99.7%	67	25	61.4	1	0	0	1785.87	380	396
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	13	13	17	0.02%	5.5%	SGSSFVHQASFK	99.7%	53.9	25	47.2	1	0	0	1281.62	1447	1458
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	13	13	17	0.02%	5.5%	SNNSETSSVAQSGSESK	99.7%	77.8	25	77.8	1	0	0	1698.74	2555	2571
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	13	13	17	0.02%	5.5%	STSGEGFQFGK	96.8%	30	25	29.3	1	0	0	1144.53	1953	1963
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	13	13	17	0.02%	5.5%	TGSGLNSFYDQR	99.7%	77.7	25	71.9	1	0	0	1344.62	585	596
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	13	13	17	0.02%	5.5%	YIASVQGSTPSPR	99.7%	68	25	60.2	1	0	0	1362.70	11	23
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	AALPLTTSDTK	99.7%	44.8	25	39.6	2	0	0	1117.61	1498	1508
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	ADGTATAPPPR	99.5%	38.6	25	38.6	2	0	0	1053.53	707	717
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	AGSSTPGDAPPAVAEVQGR	99.7%	67.6	25	62.4	2	0	0	1766.87	2885	2903
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	AIQDPAFSDGIR	99.7%	59.1	25	55.1	2	0	0	1289.65	518	529
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	DGGSGNSTIIVSR	99.5%	38.8	25	27.7	1	0	0	1262.63	2359	2371
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	DSAVAISGADSR	99.7%	63.2	25	59.1	2	0	0	1148.55	2930	2941
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	EMFNPMYALFR	99.7%	47.8	25	42.6	2	0	0	1418.66	4072	4082
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	FLGDEQDQITFVTR	99.7%	92.8	25	84.6	1	0	0	1668.82	418	431
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	FLQFVTGTSK	99.7%	64.5	25	58.6	2	0	0	1127.61	4296	4305

E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	GLQSFVQCQPFER	99.7%	70.3	25	52.7	2	0	0	1595.76	617	629
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	HADHSSLTLGSGSSTTR	99.7%	36.6	25	36.6	0	1	0	1713.82	2522	2538
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	LGSSGLGSASSIQAAVR	99.7%	110	25	101	2	0	0	1560.83	3750	3766
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	LLAELVR	97.5%	31.1	25	22.5	1	0	0	813.52	2074	2080
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	LLECYFTR	99.7%	41.2	25	25.7	1	0	0	1101.54	4123	4130
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	LLSLISIALPENK	99.7%	53.5	25	53.5	2	0	0	1410.86	3456	3468
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	LPGGVQNFPQFSALR	99.7%	66.6	25	66.6	2	0	0	1630.87	1226	1240
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	MVNPTTVLESPHSLPAK	95.6%	23.3	25	13.1	0	1	0	1820.96	1209	1225
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	NLCYHAQTR	99.4%	37.1	25	30.3	1	0	0	1162.54	3211	3219
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	NPDIFTEVANCCIR	99.7%	83.1	25	83.1	2	0	0	1708.78	1881	1894
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	RQQQAATSESSQSEASVR	99.7%	45	25	40.8	0	1	0	1949.93	3787	3804
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	SAATSGAGSTTSGVVSGSLGSR	99.7%	122	25	122	1	0	0	1896.93	1844	1865
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	SILTLSHEPK	98.6%	33.6	25	26.8	2	0	0	1124.63	830	839
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	SLLSILQR	99.7%	42.3	25	19	1	0	0	929.58	3225	3232
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	SSESELCIETPK	99.7%	64	25	58.4	1	0	0	1379.64	3233	3244
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	TLTSIVHLER	99.7%	59.4	25	52.9	2	0	0	1168.67	330	339
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	TPTEAPADCR	99.1%	35.7	25	35.7	2	0	0	1117.49	11	20
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	VLLSPDYLPAMR	99.7%	48.9	25	44.8	3	0	0	1374.75	633	644
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	28	29	45	0.04%	8.2%	VSDGGSSSTDFK	99.7%	58.4	25	58.4	1	0	0	1186.52	3559	3570
E3 ubiquitin-protein ligase MYCBP2	MYCBP2	MYCB2_HUMAN	510.1	100.0%	2	2	4	0.00%	0.5%	ALSVVSTVVR	99.7%	55.6	25	42.9	2	0	0	1030.63	1871	1880
E3 ubiquitin-protein ligase MYCBP2	MYCBP2	MYCB2_HUMAN	510.1	100.0%	2	2	4	0.00%	0.5%	NAIAETIIALTK	99.6%	40	25	40	2	0	0	1257.74	4159	4170
E3 ubiquitin-protein ligase RING2	RNF2	RING2_HUMAN	37.7	99.8%	2	2	2	0.00%	6.9%	TSGNATVDHLSK	99.7%	49.9	25	45.1	1	0	0	1229.61	250	261
E3 ubiquitin-protein ligase RING2	RNF2	RING2_HUMAN	37.7	99.8%	2	2	2	0.00%	6.9%	TWELSLYELQR	96.2%	29.3	25	29.3	1	0	0	1437.74	16	26
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	10	11	20	0.02%	18.7%	ALCWVCAQSR	99.7%	55.9	25	49.6	2	0	0	1250.58	109	118
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	10	11	20	0.02%	18.7%	DLDITSPELR	99.7%	55	25	45.3	2	0	0	1158.60	261	270
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	10	11	20	0.02%	18.7%	EAWDLGVCR	99.7%	66.4	25	63.8	2	0	0	1105.51	352	360
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	10	11	20	0.02%	18.7%	IHAEFVQQK	99.7%	44	25	33.9	2	0	0	1099.59	178	186
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	10	11	20	0.02%	18.7%	LGDTQQSIPGNEER	99.7%	65.1	25	62.6	2	0	0	1543.73	311	324
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	10	11	20	0.02%	18.7%	LQVALGELR	99.7%	53.1	25	25.4	2	0	0	998.60	139	147
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	10	11	20	0.02%	18.7%	LQVALGELRR	98.6%	33.6	25	24.1	2	0	0	1154.70	139	148
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	10	11	20	0.02%	18.7%	NFLVEEEQR	99.7%	47.5	25	23.9	2	0	0	1163.57	187	195
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	10	11	20	0.02%	18.7%	SESWNLKDLDITSPELR	99.7%	42.3	25	42.3	1	1	0	2003.01	254	270
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	10	11	20	0.02%	18.7%	SGFWTIWLWNK	99.7%	57.7	25	38.7	2	0	0	1437.73	375	385
E3 ubiquitin-protein ligase UBR4	UBR4	UBR4_HUMAN	573.8	100.0%	5	5	6	0.01%	1.2%	APSYIEIFGR	99.5%	38.6	25	32.7	1	0	0	1152.60	2364	2373
E3 ubiquitin-protein ligase UBR4	UBR4	UBR4_HUMAN	573.8	100.0%	5	5	6	0.01%	1.2%	ELLEYDLQQR	99.3%	36.5	25	34	1	0	0	1306.66	3827	3836
E3 ubiquitin-protein ligase UBR4	UBR4	UBR4_HUMAN	573.8	100.0%	5	5	6	0.01%	1.2%	GVLPYVGNLITK	96.5%	29.7	25	27.4	1	0	0	1273.75	4204	4215
E3 ubiquitin-protein ligase UBR4	UBR4	UBR4_HUMAN	573.8	100.0%	5	5	6	0.01%	1.2%	IISLDLPVAEVYK	99.7%	60.2	25	58.8	2	0	0	1459.84	4414	4426
E3 ubiquitin-protein ligase UBR4	UBR4	UBR4_HUMAN	573.8	100.0%	5	5	6	0.01%	1.2%	LASAPVPFTVLSLTGNPCK	95.1%	28.3	25	28.3	1	0	0	1972.06	1945	1963
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	13	13	22	0.02%	18.1%	AQFAEATQR	99.1%	35.6	25	27.6	2	0	0	1021.51	18	26
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	13	13	22	0.02%	18.1%	AVFVPDIYSR	99.2%	36.2	25	32.8	2	0	0	1166.62	242	251
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	13	13	22	0.02%	18.1%	CVPQIIAFLNSK	99.5%	38.4	25	33.6	2	0	0	1389.76	708	719
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	13	13	22	0.02%	18.1%	DLQEEVSNLYNNIR	99.7%	51.2	25	39.9	1	0	0	1706.83	539	552
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	13	13	22	0.02%	18.1%	FFADDTQAALTK	99.7%	90.3	25	85.8	2	0	0	1327.65	560	571
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	13	13	22	0.02%	18.1%	GVIFTEAFVAR	99.7%	76.8	25	71.9	2	0	0	1209.66	175	185
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	13	13	22	0.02%	18.1%	IISGHIDLDNR	99.7%	42.1	25	29.9	2	0	0	1252.66	164	174
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	13	13	22	0.02%	18.1%	LAADFQR	99.7%	44.4	25	29.4	2	0	0	820.43	11	17
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	13	13	22	0.02%	18.1%	LGIPDAVSYIK	97.4%	30.9	25	22	1	0	0	1175.67	275	285
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	13	13	22	0.02%	18.1%	NCIEIVNK	97.9%	31.8	25	21.5	1	0	0	989.51	31	38
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	13	13	22	0.02%	18.1%	QISTLESVSTSK	95.9%	29.1	25	21.5	1	0	0	1279.67	403	414
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	13	13	22	0.02%	18.1%	TQSTWVDSFFR	99.3%	36.6	25	35.2	2	0	0	1373.65	252	262
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	13	13	22	0.02%	18.1%	TYDLPGNFLTQALTQR	99.7%	80.2	25	65.1	2	0	0	1837.94	145	160

EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	10	17	0.02%	17.4%	ADQIETQQLMR	99.7%	40.9	25	29.2	2	0	0	1348.65	221	231
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	10	17	0.02%	17.4%	EHQISPGDFPSLR	99.6%	39.2	25	32.2	1	2	0	1482.73	345	357
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	10	17	0.02%	17.4%	ELVNNLGEIYQK	99.7%	63.9	25	63.9	2	0	0	1419.75	330	341
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	10	17	0.02%	17.4%	IINTPEVVR	99.5%	37.8	25	19.9	2	0	0	1040.61	243	251
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	10	17	0.02%	17.4%	KLNDLIK	99.7%	43.8	25	7.77	2	0	0	843.53	293	299
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	10	17	0.02%	17.4%	LLPLEEHYR	99.0%	35	25	27.2	1	0	0	1169.63	33	41
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	10	17	0.02%	17.4%	LNAFGNAFLNR	99.7%	57.2	25	50.8	2	0	0	1236.65	125	135
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	10	17	0.02%	17.4%	SKLPNTVLGK	98.6%	33.5	25	32.1	1	0	0	1056.64	474	483
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	9	10	17	0.02%	17.4%	VYGALMWSLGK	99.7%	50.5	25	44.4	2	0	0	1240.64	232	242
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	3	3	5	0.00%	9.1%	AGGADAVQTVTGGLR	99.7%	75.5	25	69.9	2	0	0	1372.72	15	29
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	3	3	5	0.00%	9.1%	FGNAFLNR	99.7%	60.1	25	48.4	2	0	0	938.48	131	138
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	3	3	5	0.00%	9.1%	KLNDLIK	99.7%	43.8	25	7.77	2	0	0	843.53	296	302
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	3	3	5	0.00%	9.1%	LPNSVLGK	95.7%	28.8	25	21.5	1	0	0	827.50	479	486
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	3	3	5	0.00%	9.1%	VYGALMWSLGK	99.7%	50.5	25	44.4	2	0	0	1240.64	235	245
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	20	65	0.06%	52.8%	AINTLNGLR	99.7%	59.7	25	52.5	6	0	0	971.56	77	85
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	20	65	0.06%	52.8%	DANLYISGLPR	99.7%	79.9	25	75	2	0	0	1218.65	105	115
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	20	65	0.06%	52.8%	DKVAGHSLGYGFVNYVTAK	99.7%	84.6	25	84.6	0	2	0	2026.04	54	72
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	20	65	0.06%	52.8%	DVEDMFSR	99.7%	45.8	25	38.5	3	0	0	998.42	121	128
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	20	65	0.06%	52.8%	FAANPNQNK	99.3%	36.3	25	23.9	4	0	0	1003.50	183	191
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	20	65	0.06%	52.8%	FGGPVHHQAQR	99.7%	47.8	25	41.3	3	4	0	1233.62	207	217
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	20	65	0.06%	52.8%	ILQVSFK	99.7%	52.4	25	0	4	0	0	834.51	314	320
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	20	65	0.06%	52.8%	NVALLSQLYHSPAR	99.7%	80.4	25	67.6	3	2	0	1568.85	192	205
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	20	65	0.06%	52.8%	SEAEEAITSFNGHKPPGSSEPITVK	99.7%	61.8	25	61.8	0	3	0	2612.28	158	182
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	20	65	0.06%	52.8%	SLFSSIGEVESAK	99.7%	93.8	25	82.3	7	0	0	1353.69	38	50
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	20	65	0.06%	52.8%	TMTQKDVEDMFSR	99.7%	40.7	25	40.7	0	2	0	1619.70	116	128
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	20	65	0.06%	52.8%	TNLIVNYLPQNMTQDELR	99.7%	102	25	99.8	9	2	0	2162.09	20	37
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	20	65	0.06%	52.8%	VAGHSLGYGFVNYVTAK	99.7%	48.1	25	48.1	0	2	0	1782.92	56	72
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	20	65	0.06%	52.8%	VLVDQTTGLSR	99.7%	91.8	25	67.6	4	0	0	1188.66	137	147
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	15	20	65	0.06%	52.8%	VSYARPSSEVIK	99.7%	52.9	25	39.5	3	0	0	1335.73	93	104
ELAV-like protein 2	ELAVL2	ELAV2_HUMAN	39.5	100.0%	8	8	22	0.02%	29.0%	AINTLNGLR	99.7%	59.7	25	52.5	6	0	0	971.56	96	104
ELAV-like protein 2	ELAVL2	ELAV2_HUMAN	39.5	100.0%	8	8	22	0.02%	29.0%	DANLYVSGLPK	99.7%	74	25	67.5	2	0	0	1176.63	124	134
ELAV-like protein 2	ELAVL2	ELAV2_HUMAN	39.5	100.0%	8	8	22	0.02%	29.0%	ELEQLFSQYGR	99.7%	58.1	25	58.1	4	0	0	1369.67	140	150
ELAV-like protein 2	ELAVL2	ELAV2_HUMAN	39.5	100.0%	8	8	22	0.02%	29.0%	ILVDQVTGISR	99.7%	87.7	25	81.1	4	0	0	1200.69	156	166
ELAV-like protein 2	ELAVL2	ELAV2_HUMAN	39.5	100.0%	8	8	22	0.02%	29.0%	RIEAEEAIK	96.1%	29.3	25	8.81	1	0	0	1058.58	176	184
ELAV-like protein 2	ELAVL2	ELAV2_HUMAN	39.5	100.0%	8	8	22	0.02%	29.0%	SLFGSIGEIESCK	99.7%	80.7	25	80	4	0	0	1426.69	57	69
ELAV-like protein 2	ELAVL2	ELAV2_HUMAN	39.5	100.0%	8	8	22	0.02%	29.0%	TNLIVNYLPQNMTQEELK	99.7%	57.7	25	57.7	2	0	0	2148.10	39	56
ELAV-like protein 2	ELAVL2	ELAV2_HUMAN	39.5	100.0%	8	8	22	0.02%	29.0%	TNQAILSQLYQSPNR	99.7%	95	25	92.3	4	0	0	1732.90	210	224
ELAV-like protein 2	ELAVL2	ELAV2_HUMAN	39.5	100.0%	8	8	22	0.02%	29.0%	VLQVSFK	97.2%	30.5	25	29.3	1	0	0	820.49	346	352
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	11	14	32	0.03%	46.5%	AAVDAGFVPNDMQVGQTGK	99.7%	105	25	104	4	0	0	1920.91	250	268
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	11	14	32	0.03%	46.5%	ASSTSPVEISEWLDQK	99.7%	78.2	25	69.6	2	0	0	1776.87	188	203
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	11	14	32	0.03%	46.5%	GLLPEELTPLILATQK	99.7%	95.4	25	95.1	4	2	0	1736.02	86	101
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	11	14	32	0.03%	46.5%	GTSFDAAATSGGSASSEK	99.7%	139	25	139	2	0	0	1630.72	170	187
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	11	14	32	0.03%	46.5%	LEVAPISDIIAIK	99.7%	95.1	25	80.2	4	0	0	1381.83	127	139
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	11	14	32	0.03%	46.5%	LGGEVSCLVAGTK	99.7%	89.1	25	86.1	2	0	0	1290.67	47	59
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	11	14	32	0.03%	46.5%	LLYDLADQLHAAVGASR	99.7%	101	25	88.9	2	2	0	1812.96	233	249
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	11	14	32	0.03%	46.5%	QFNYTHICAGASAFGK	99.7%	34.5	25	34.5	0	1	0	1771.82	102	117
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	11	14	32	0.03%	46.5%	SDRPELTGAK	99.7%	54.2	25	43.8	2	0	0	1073.56	207	216
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	11	14	32	0.03%	46.5%	SPDTFVR	99.7%	44.4	25	29.2	2	0	0	821.42	140	146
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	11	14	32	0.03%	46.5%	VLVAQHDVYK	99.7%	58.3	25	42.8	3	0	0	1171.65	76	85
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	20	0.02%	45.5%	EIDGGLETLR	99.7%	84.6	25	77	2	0	0	1102.57	165	174
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	20	0.02%	45.5%	EVIAVSCGPAQCQETIR	99.7%	111	25	107	2	0	0	1917.92	60	76

Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	20	0.02%	45.5%	GIHVEVPPAEAER	99.5%	38.5	25	23.6	1	0	0	1403.73	86	98
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	20	0.02%	45.5%	IEVIKPGDLGVDLTSK	99.7%	60.2	25	60.2	1	0	0	1683.95	206	221
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	20	0.02%	45.5%	LGPLQVAR	99.7%	70.2	25	61.5	2	0	0	853.53	99	106
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	20	0.02%	45.5%	LKLPAVVTADLR	98.1%	32.3	25	30.8	2	0	0	1295.80	175	186
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	20	0.02%	45.5%	LPAVVTADLR	99.7%	44.2	25	35.3	2	0	0	1054.63	177	186
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	20	0.02%	45.5%	LSVISVEDPPQR	99.7%	60.5	25	59.9	2	0	0	1339.72	222	233
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	20	0.02%	45.5%	TALAMGADR	99.5%	38.1	25	18.8	2	0	0	905.45	77	85
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	20	0.02%	45.5%	TGVVTDGVK	98.0%	32	25	22.1	2	0	0	875.48	27	35
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	20	0.02%	45.5%	VETTEDLVAK	99.7%	56.3	25	47	2	0	0	1104.58	239	248
ELMO domain-containing protein 2	ELMOD2	ELMD2_HUMAN	35.0	100.0%	4	5	9	0.01%	13.0%	IENSLTYSK	99.4%	37.5	25	37.3	2	0	0	1054.54	47	55
ELMO domain-containing protein 2	ELMOD2	ELMD2_HUMAN	35.0	100.0%	4	5	9	0.01%	13.0%	IFDTYVGAQR	99.7%	80.4	25	70.2	2	0	0	1169.60	34	43
ELMO domain-containing protein 2	ELMOD2	ELMD2_HUMAN	35.0	100.0%	4	5	9	0.01%	13.0%	LWNLLMPTK	99.7%	43.6	25	43.6	2	0	0	1115.63	134	142
ELMO domain-containing protein 2	ELMOD2	ELMD2_HUMAN	35.0	100.0%	4	5	9	0.01%	13.0%	MCLLQITGYK	99.6%	39.9	25	37.4	3	0	0	1226.63	97	106
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	243	0.24%	56.3%	DGNASGTTLLEALDCILPPTRPTDKPLR	99.7%	77.2	25	77.2	0	2	0	3021.57	220	247
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	243	0.24%	56.3%	EHALLAYTLGVK	99.7%	75.1	25	64.3	24	7	0	1314.74	135	146
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	243	0.24%	56.3%	EVSTYIKK	99.7%	47.1	25	34.2	7	0	0	967.55	173	180
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	243	0.24%	56.3%	FEKEAAEMGK	99.7%	51.2	25	43.2	2	0	0	1139.54	42	51
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	243	0.24%	56.3%	IGGIGTVPVGR	99.7%	84.3	25	79.4	20	0	0	1025.61	256	266
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	243	0.24%	56.3%	LPLQDVYK	99.7%	62.2	25	53.5	16	0	0	975.55	248	255
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	243	0.24%	56.3%	MDSTEPPYSQK	99.7%	42.4	25	37.2	2	0	0	1298.56	155	165
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	243	0.24%	56.3%	NMITGTSQADCAVLIVAAGVGEFEAGISK	99.7%	47.4	25	47.4	0	2	0	2925.43	101	129
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	243	0.24%	56.3%	QLIVGVNK	99.7%	40.9	25	22.7	12	0	0	870.54	147	154
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	243	0.24%	56.3%	QTVAVGVIK	99.7%	60.1	25	39.9	13	0	0	914.57	431	439
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	243	0.24%	56.3%	SGDAAIVDMVPGKPMCVESFSDYPPLGR	99.7%	58.7	25	58.7	0	7	0	3027.39	396	423
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	243	0.24%	56.3%	STTTGHLIYK	99.7%	51.9	25	42.5	30	0	0	1120.60	21	30
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	243	0.24%	56.3%	SVEMHHEALSEALPGDNVGFNVK	99.7%	76.7	25	69.7	0	4	0	2480.19	291	313
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	243	0.24%	56.3%	THINIVVIGHVDSGK	99.7%	120	25	118	9	18	0	1588.88	6	20
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	243	0.24%	56.3%	TIEKFEK	96.9%	30.2	25	23.1	3	0	0	894.49	38	44
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	243	0.24%	56.3%	VETGVLKPGMVVTFAPVNVTTEVK	99.7%	50.7	25	50.7	4	23	0	2531.38	267	290
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	243	0.24%	56.3%	YEEIVKEVSTYIK	99.7%	80.2	25	76.5	2	0	0	1600.85	167	179
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	243	0.24%	56.3%	YYVTIIDAPGHR	99.7%	70.4	25	69.7	23	9	0	1404.73	85	96
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	243	0.24%	56.3%	YYVTIIDAPGHRDFIK	99.7%	65.8	25	65.8	2	2	0	1908.00	85	100
Elongation factor 1-beta	EEF1B2	EF1B_HUMAN	24.8	100.0%	2	2	4	0.00%	12.4%	SIQADGLVWGSSK	99.7%	74.2	25	74.2	2	0	0	1347.69	164	176
Elongation factor 1-beta	EEF1B2	EF1B_HUMAN	24.8	100.0%	2	2	4	0.00%	12.4%	SPAGLQVLNDYLADK	99.7%	98.4	25	98.4	2	0	0	1603.83	8	22
Elongation factor 1-delta	EEF1D	EF1D_HUMAN	31.1	99.8%	2	2	4	0.00%	7.5%	IASLEVENQSLR	99.7%	68.9	25	48.3	2	0	0	1358.73	84	95
Elongation factor 1-delta	EEF1D	EF1D_HUMAN	31.1	99.8%	2	2	4	0.00%	7.5%	LVPVGYGIR	96.7%	29.9	25	23.9	2	0	0	973.58	233	241
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	28	0.03%	28.4%	AKDPFAHLPK	99.1%	35.7	25	26.1	2	0	0	1123.63	276	285
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	28	0.03%	28.4%	ALIAAQYSGAQVR	99.7%	93.6	25	93.6	5	0	0	1347.74	18	30
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	28	0.03%	28.4%	EYFSWEGAFQHVGK	99.7%	42.6	25	41.9	0	2	0	1684.78	415	428
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	28	0.03%	28.4%	FAETQPK	97.9%	31.8	25	18.8	1	0	0	820.42	221	227
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	28	0.03%	28.4%	ILGLLDAYLK	99.7%	60.7	25	53.8	4	0	0	1118.68	138	147
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	28	0.03%	28.4%	KLDPGSEETQTLVR	99.7%	83.5	25	78.3	2	2	0	1572.82	401	414
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	28	0.03%	28.4%	QAFPNTNR	99.5%	38.5	25	28.2	1	0	0	947.47	182	189
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	28	0.03%	28.4%	QATENAKEEVR	95.5%	28.7	25	16.5	1	0	0	1274.63	126	136
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	28	0.03%	28.4%	QVLEPSFR	96.3%	29.4	25	11.6	1	0	0	975.53	174	181
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	28	0.03%	28.4%	STFVLDEFKR	99.7%	44.4	25	36.9	2	1	0	1241.65	286	295
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	28	0.03%	28.4%	TFLVGER	99.7%	44.1	25	32.6	2	0	0	821.45	150	156
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	28	0.03%	28.4%	WFLTCINQPQFR	99.7%	64.5	25	53.1	2	0	0	1609.79	190	201
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	27	50	0.05%	32.9%	ALLELQLEPEELYQTFQR	99.7%	76.8	25	76.8	1	0	0	2220.15	163	180
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	27	50	0.05%	32.9%	ARPFPDGLAEDIDKGEVSAR	99.7%	63.6	25	60	0	2	0	2143.08	606	625
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	27	50	0.05%	32.9%	AYLPVNESFGFTADLR	99.7%	112	25	111	2	0	0	1799.90	786	801

Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	27	50	0.05%	32.9%	CLYASVLTAQPR	99.7%	66.5	25	58.5	2	0	0	1378.71	728	739
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	27	50	0.05%	32.9%	EGALCEENMR	99.7%	70.5	25	56.2	3	0	0	1208.50	689	698
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	27	50	0.05%	32.9%	EGIPALDNFLDKL	99.7%	73.7	25	67.9	3	0	0	1444.77	846	858
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	27	50	0.05%	32.9%	ETVSEESNVLCLSK	99.7%	92.6	25	83.3	2	0	0	1594.76	581	594
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	27	50	0.05%	32.9%	FSVSPVVR	97.6%	31.2	25	27	1	0	0	890.51	499	506
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	27	50	0.05%	32.9%	GEGQLGPAER	99.7%	43.7	25	35.5	3	0	0	1013.50	240	249
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	27	50	0.05%	32.9%	GGGQIIPTAR	99.5%	38.6	25	28.7	6	0	0	969.55	717	726
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	27	50	0.05%	32.9%	GHVFEESQVAGTPMFVVK	99.5%	32	25	32	0	1	0	1961.98	768	785
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	27	50	0.05%	32.9%	GPLMMYISK	99.7%	46.3	25	43.8	2	0	0	1039.53	392	400
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	27	50	0.05%	32.9%	IMGPNYTPGK	99.7%	48	25	43	2	0	0	1077.54	429	438
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	27	50	0.05%	32.9%	IMGPNYTPGKK	97.7%	31.4	25	20.6	1	0	0	1205.63	429	439
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	27	50	0.05%	32.9%	KEDLYLKPIQR	99.7%	51.6	25	44	0	2	0	1402.81	439	449
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	27	50	0.05%	32.9%	NMSVIAHVDHGK	99.7%	44.9	25	43.8	1	0	0	1323.65	21	32
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	27	50	0.05%	32.9%	QFAEMYVAK	99.7%	42.9	25	39.6	1	0	0	1086.53	227	235
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	27	50	0.05%	32.9%	SDPVVSYR	99.7%	42.6	25	32.2	1	0	0	922.46	573	580
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	27	50	0.05%	32.9%	STLTDSLVCK	99.7%	60	25	52.7	2	0	0	1123.57	33	42
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	27	50	0.05%	32.9%	TFCQLILDPIFK	99.7%	54.6	25	54.6	2	0	0	1494.80	288	299
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	27	50	0.05%	32.9%	TGTITTFEHAHNMR	99.3%	30.4	25	30.4	0	3	0	1615.76	482	495
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	27	50	0.05%	32.9%	VFDAIMNFK	99.7%	53.4	25	50	3	0	0	1084.55	300	308
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	27	50	0.05%	32.9%	VFSGLVSTGLK	99.7%	92.1	25	78	4	0	0	1107.64	416	426
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	27	50	0.05%	32.9%	VNFTVDQIR	99.7%	80.2	25	62.8	4	0	0	1091.58	2	10
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	24	27	50	0.05%	32.9%	YEWDVAEAR	99.7%	67.3	25	61	2	0	0	1138.52	639	647
Elongation factor Ts, mitochondrial	TSFM	EFTS_HUMAN	35.4	100.0%	4	4	7	0.01%	20.0%	GFLNSSELSGLPAGPDR	99.7%	46.7	25	45.8	2	0	0	1716.86	162	178
Elongation factor Ts, mitochondrial	TSFM	EFTS_HUMAN	35.4	100.0%	4	4	7	0.01%	20.0%	LGQHVVGMAPLSVGSLDDEPGGEAETK	99.7%	65.5	25	65.5	0	2	0	2709.30	256	282
Elongation factor Ts, mitochondrial	TSFM	EFTS_HUMAN	35.4	100.0%	4	4	7	0.01%	20.0%	TNLEDVGR	99.3%	36.6	25	31.6	1	0	0	903.45	247	254
Elongation factor Ts, mitochondrial	TSFM	EFTS_HUMAN	35.4	100.0%	4	4	7	0.01%	20.0%	YGALVICETSEQK	99.7%	73.4	25	60.1	2	0	0	1497.73	234	246
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	25	34	115	0.11%	69.2%	ADAVQDSEMVELVELEIR	99.7%	74.3	25	62.6	1	0	0	2046.01	183	200
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	25	34	115	0.11%	69.2%	AEAGDNLGALVR	99.7%	101	25	83.4	8	0	0	1185.62	316	327
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	25	34	115	0.11%	69.2%	DKPHVNVGTIGHVDHGK	99.7%	59.7	25	59.7	0	2	0	1809.94	54	70
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	25	34	115	0.11%	69.2%	DLEKPFLLPVEAVYSVPGR	99.7%	68	25	68	7	1	0	2129.16	253	271
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	25	34	115	0.11%	69.2%	EHLLLAR	98.8%	34.3	25	31.5	4	0	0	851.51	163	169
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	25	34	115	0.11%	69.2%	ELAMPGEDLK	98.8%	34.2	25	31.2	2	0	0	1118.54	396	405
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	25	34	115	0.11%	69.2%	ELLTEFGYK	99.7%	49.5	25	47.5	1	0	0	1099.57	201	209
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	25	34	115	0.11%	69.2%	GDECELLGHSK	99.7%	49.3	25	48	2	0	0	1244.56	287	297
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	25	34	115	0.11%	69.2%	GEETPVIVGSALCALEGRDPELGLK	97.6%	25.5	25	24.9	0	2	0	2610.34	210	234
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	25	34	115	0.11%	69.2%	GITINAAHVEYSTAAR	99.7%	102	25	91.1	6	5	0	1673.86	105	120
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	25	34	115	0.11%	69.2%	GLVMVKPGSIKPHQK	96.6%	24.2	25	24.2	0	1	0	1618.95	337	351
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	25	34	115	0.11%	69.2%	GTVVTGTLER	99.7%	67.7	25	46.9	8	0	0	1032.57	272	281
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	25	34	115	0.11%	69.2%	HYAHTDCPGHADYVK	99.7%	62.1	25	61	2	2	0	1770.77	121	135
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	25	34	115	0.11%	69.2%	IILPPEKELAMPGEDLK	99.6%	33.5	25	27.8	0	2	0	1909.04	389	405
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	25	34	115	0.11%	69.2%	KGDECELLGHSK	99.7%	66.2	25	57.6	2	3	0	1372.65	286	297
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	25	34	115	0.11%	69.2%	LLDAVDTYIPVPAR	99.7%	101	25	97.1	10	0	0	1542.85	239	252
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	25	34	115	0.11%	69.2%	NMITGTAPLDGCILVVAANDGPMPQTR	99.7%	54.1	25	54.1	0	2	0	2844.37	136	162
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	25	34	115	0.11%	69.2%	QIGVEHVVVYVNK	99.7%	66.6	25	54.5	2	2	0	1483.83	170	182
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	25	34	115	0.11%	69.2%	TIGTGLVTNTLAMTEEEK	99.7%	119	25	111	11	0	0	1923.96	430	447
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	25	34	115	0.11%	69.2%	TIGTGLVTNTLAMTEEEKNIK	99.3%	30.6	25	29.7	0	1	0	2263.19	430	450
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	25	34	115	0.11%	69.2%	TTLTAAITK	99.7%	65.3	25	50.3	2	0	0	919.55	71	79
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	25	34	115	0.11%	69.2%	TVVTGIEMFHK	99.7%	47.8	25	30.7	10	2	0	1261.66	301	311
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	25	34	115	0.11%	69.2%	VEAQVYILSK	99.7%	72.7	25	64.6	8	0	0	1149.65	352	361
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	25	34	115	0.11%	69.2%	VEAQVYILSKEEGGR	99.7%	74.6	25	74.6	1	1	0	1677.88	352	366
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	25	34	115	0.11%	69.2%	YEEIDNAPEER	99.7%	85.7	25	80.7	2	0	0	1364.60	92	102

Elongator complex protein 1	IKBKAP	ELP1_HUMAN	150.3	100.0%	3	3	5	0.00%	2.6%	IVTVVPQDTK	99.5%	38.4	25	31.1	2	0	0	1099.64	697	706
Elongator complex protein 1	IKBKAP	ELP1_HUMAN	150.3	100.0%	3	3	5	0.00%	2.6%	SVVLQLADGQIFK	99.7%	62.4	25	51.6	2	0	0	1417.81	568	580
Elongator complex protein 1	IKBKAP	ELP1_HUMAN	150.3	100.0%	3	3	5	0.00%	2.6%	VFLGNVETFIK	99.2%	36.2	25	29.5	1	0	0	1266.71	762	772
Emerin	EMD	EMD_HUMAN	29.0	100.0%	7	8	13	0.01%	35.0%	DSAYQSITHYRPVSASR	99.7%	38.1	25	27.5	0	2	0	1937.95	158	174
Emerin	EMD	EMD_HUMAN	29.0	100.0%	7	8	13	0.01%	35.0%	GYNDDYYEESYFTTR	99.7%	98.9	25	98.9	2	0	0	1922.77	89	103
Emerin	EMD	EMD_HUMAN	29.0	100.0%	7	8	13	0.01%	35.0%	KEDALLYQSK	99.7%	56.2	25	40.7	2	0	0	1194.64	79	88
Emerin	EMD	EMD_HUMAN	29.0	100.0%	7	8	13	0.01%	35.0%	LSPPSSSAASSYSFSDLNSTR	99.7%	118	25	118	2	0	0	2161.00	48	68
Emerin	EMD	EMD_HUMAN	29.0	100.0%	7	8	13	0.01%	35.0%	RYNIPHGPVVGSTR	95.1%	23	25	23	0	1	0	1552.83	18	31
Emerin	EMD	EMD_HUMAN	29.0	100.0%	7	8	13	0.01%	35.0%	TYGEPESAGPSR	99.7%	53.4	25	50.2	1	0	0	1250.56	104	115
Emerin	EMD	EMD_HUMAN	29.0	100.0%	7	8	13	0.01%	35.0%	YNIPHGPVVGSTR	99.7%	39.6	25	39	1	2	0	1396.73	19	31
Endonuclease III-like protein 1	NTHL1	NTH_HUMAN	34.4	100.0%	3	3	4	0.00%	11.2%	GLTVDSILQTDDATLGK	99.7%	78.9	25	70.3	2	0	0	1746.91	158	174
Endonuclease III-like protein 1	NTHL1	NTH_HUMAN	34.4	100.0%	3	3	4	0.00%	11.2%	LIYPVGFWR	97.3%	30.7	25	24.9	1	0	0	1150.64	175	183
Endonuclease III-like protein 1	NTHL1	NTH_HUMAN	34.4	100.0%	3	3	4	0.00%	11.2%	SLGPGAGPR	95.1%	28.3	25	23.8	1	0	0	811.44	22	30
Endoplasmic reticulum-Golgi intermediate compartment protein 1	ERGIC1	ERGI1_HUMAN	32.6	99.8%	2	2	4	0.00%	6.9%	EYVAYSHTGR	99.6%	39.8	25	34.4	2	0	0	1182.55	215	224
Endoplasmic reticulum-Golgi intermediate compartment protein 1	ERGIC1	ERGI1_HUMAN	32.6	99.8%	2	2	4	0.00%	6.9%	YSYQYTVANK	99.7%	71.2	25	63.2	2	0	0	1236.59	205	214
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	4	4	4	0.00%	7.1%	DISTNYYASQK	99.7%	41.9	25	41.7	1	0	0	1289.60	672	682
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	4	4	4	0.00%	7.1%	ELISNASDALDK	99.7%	76.3	25	67.3	11	0	0	1275.64	103	114
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	4	4	4	0.00%	7.1%	ELISNASDALDKIR	99.7%	98.3	25	79.8	8	2	0	1544.83	103	116
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	4	4	4	0.00%	7.1%	FAFQAEVNR	99.7%	46.6	25	39	1	0	0	1081.54	76	84
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	4	4	4	0.00%	7.1%	GVVDSDDLPLNVSR	99.7%	60.5	25	50.6	1	0	0	1485.75	435	448
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	4	4	4	0.00%	7.1%	SGTSEFLNK	98.0%	31.9	25	22	1	0	0	982.48	169	177
Enhancer of mRNA-decapping protein 3	EDC3	EDC3_HUMAN	56.1	100.0%	3	3	5	0.00%	7.5%	AAVAWANQNR	96.9%	30.2	25	26.9	1	0	0	1100.56	427	436
Enhancer of mRNA-decapping protein 3	EDC3	EDC3_HUMAN	56.1	100.0%	3	3	5	0.00%	7.5%	KPASSSSAPQNIPK	99.7%	77.6	25	69.4	2	0	0	1411.75	106	119
Enhancer of mRNA-decapping protein 3	EDC3	EDC3_HUMAN	56.1	100.0%	3	3	5	0.00%	7.5%	MLESITNELSLFSK	99.7%	59	25	59	2	0	0	1627.82	374	387
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	6	9	14	0.01%	45.2%	ADTQTYQPYNK	99.7%	50	25	47.1	2	0	0	1328.61	74	84
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	6	9	14	0.01%	45.2%	ADTQTYQPYNKDWIK	97.7%	31.5	25	30.1	1	1	0	1870.90	74	88
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	6	9	14	0.01%	45.2%	IYVLLRR	97.5%	31.1	25	12.6	2	0	0	932.60	91	97
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	6	9	14	0.01%	45.2%	MYEEHLK	96.8%	30.1	25	19.6	1	0	0	949.44	35	41
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	6	9	14	0.01%	45.2%	MYEEHLKR	99.4%	37.1	25	30.8	3	0	0	1105.55	35	42
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	6	9	14	0.01%	45.2%	TYADYESVNECMEGVCK	99.7%	89.9	25	89.9	4	0	0	2054.81	18	34
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	6	8	17	0.02%	26.2%	AFAAGADIK	99.7%	48.9	25	36.8	1	0	0	863.46	93	101
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	6	8	17	0.02%	26.2%	AQFAQPEILIGTIPGAGGTQR	99.7%	80.9	25	76.2	2	1	0	2125.14	158	178
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	6	8	17	0.02%	26.2%	EGMTAFVEK	99.7%	40.4	25	34.2	2	0	0	1011.48	274	282
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	6	8	17	0.02%	26.2%	LFYSTFATDDRK	99.7%	50	25	44.8	1	0	0	1463.72	262	273
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	6	8	17	0.02%	26.2%	NNTVGLIQLNRPK	99.7%	74	25	74	2	0	0	1466.84	44	56
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	6	8	17	0.02%	26.2%	SLAMEMVLTGDR	99.7%	78.3	25	29.6	8	0	0	1338.64	186	197
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	7	7	10	0.01%	8.4%	FASLEFSPGSK	99.7%	57.1	25	48.9	3	0	0	1169.58	42	52
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	7	7	10	0.01%	8.4%	FNVEDGEIVQQVR	99.7%	87.8	25	78.8	1	0	0	1532.77	202	214
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	7	7	10	0.01%	8.4%	NFPQTALVSFATTGEK	99.7%	83.2	25	73.8	1	0	0	1710.87	315	330
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	7	7	10	0.01%	8.4%	NVIAALNSR	97.9%	31.7	25	19.8	1	0	0	957.55	61	69
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	7	7	10	0.01%	8.4%	RPEIPTEQSR	99.5%	38.3	25	23.1	1	0	0	1212.63	882	891
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	7	7	10	0.01%	8.4%	TFIGIFLIDGVTGR	99.7%	91.2	25	78.8	2	0	0	1508.85	755	768
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	7	7	10	0.01%	8.4%	WSQVAPPVLK	96.3%	29.5	25	27.4	1	0	0	1124.65	611	620
ER membrane protein complex subunit 3	EMC3	EMC3_HUMAN	30.0	100.0%	3	3	4	0.00%	16.5%	AGPELLLDSNIR	99.7%	67.6	25	55.8	1	0	0	1297.71	2	13
ER membrane protein complex subunit 3	EMC3	EMC3_HUMAN	30.0	100.0%	3	3	4	0.00%	16.5%	LTQEQVSDSQVLIR	99.7%	76.7	25	55.5	1	0	0	1615.87	44	57
ER membrane protein complex subunit 3	EMC3	EMC3_HUMAN	30.0	100.0%	3	3	4	0.00%	16.5%	SIYSLILGQDNAADQSR	99.7%	108	25	104	2	0	0	1850.92	181	197
ER membrane protein complex subunit 4	EMC4	EMC4_HUMAN	20.1	100.0%	4	4	10	0.01%	27.9%	CWDIALGPLK	98.7%	33.8	25	33.8	1	0	0	1172.61	69	78
ER membrane protein complex subunit 4	EMC4	EMC4_HUMAN	20.1	100.0%	4	4	10	0.01%	27.9%	GSGQGDSLYPVGYLDK	99.7%	67.3	25	67.3	4	0	0	1655.79	35	50
ER membrane protein complex subunit 4	EMC4	EMC4_HUMAN	20.1	100.0%	4	4	10	0.01%	27.9%	QVPDTSVQETDR	99.5%	38.4	25	36.1	1	0	0	1374.65	51	62
ER membrane protein complex subunit 4	EMC4	EMC4_HUMAN	20.1	100.0%	4	4	10	0.01%	27.9%	WAIELSGPGGGSR	99.7%	68.8	25	59.5	4	0	0	1286.65	17	29
ER membrane protein complex subunit 6	EMC6	EMC6_HUMAN	12.0	99.8%	2	2	4	0.00%	20.0%	EGPPFISEAAVR	99.7%	41.2	25	38.1	2	0	0	1272.66	9	20

ER membrane protein complex subunit 6	EMC6	EMC6_HUMAN	12.0	99.8%	2	2	4	0.00%	20.0%	GNAAVLDYCR	99.7%	81	25	73.9	2	0	0	1138.53	21	30
ER membrane protein complex subunit 7	EMC7	EMC7_HUMAN	26.5	99.9%	2	2	2	0.00%	9.5%	SSGPPSYFIK	96.7%	29.9	25	20.2	1	0	0	1082.55	142	151
ER membrane protein complex subunit 7	EMC7	EMC7_HUMAN	26.5	99.9%	2	2	2	0.00%	9.5%	VLVDGEEHVGFLK	99.7%	60	25	60	1	0	0	1441.77	67	79
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	7	10	16	0.02%	34.1%	ADAEYYAAHK	99.7%	49.2	25	49.2	2	0	0	1138.52	258	267
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	7	10	16	0.02%	34.1%	DLNLMAPGLTIQAVR	99.7%	87.2	25	68.9	4	0	0	1627.88	155	169
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	7	10	16	0.02%	34.1%	EALEPSGENVIQNK	99.7%	72.9	25	71.3	2	0	0	1527.77	329	342
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	7	10	16	0.02%	34.1%	ESSLPSKEALEPSGENVIQNK	99.6%	32.7	25	24.6	0	2	0	2256.14	322	342
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	7	10	16	0.02%	34.1%	ISEIEDAAFLAR	99.7%	96	25	82.3	4	0	0	1334.70	242	253
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	7	10	16	0.02%	34.1%	IYFGSNIPNMFVDSSCALK	99.7%	67	25	67	3	0	0	2179.02	295	313
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	7	10	16	0.02%	34.1%	LTPEYLELKK	96.2%	29.4	25	29.4	1	0	0	1233.71	276	285
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	7	10	16	0.02%	34.1%	NFELMEAEK	99.6%	39.7	25	7.74	2	0	0	1126.51	182	190
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	7	10	16	0.02%	34.1%	SVQTTLQTDEVK	99.7%	86.6	25	71.5	4	0	0	1348.70	61	72
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	7	10	16	0.02%	34.1%	VVEKEAETER	99.7%	51.9	25	46.9	2	0	0	1189.61	202	211
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	32	0.03%	50.4%	ADAECYTAMK	99.7%	58.7	25	58.7	1	0	0	1159.48	258	267
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	32	0.03%	50.4%	DIPNMFMDSAGSVSK	99.7%	108	25	101	3	0	0	1598.72	300	314
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	32	0.03%	50.4%	GGALLTSTSGPGFHLMLPFITSYK	97.0%	24.8	25	21	0	1	0	2511.30	37	60
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	32	0.03%	50.4%	IEEGHIGVYYR	99.7%	50	25	40.1	2	0	0	1335.67	26	36
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	32	0.03%	50.4%	IEVVNFLVPNAVYDIVK	95.5%	28.7	25	28.7	1	0	0	1932.08	89	105
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	32	0.03%	50.4%	ISEIEDAAFLAR	99.7%	96	25	82.3	4	0	0	1334.70	242	253
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	32	0.03%	50.4%	KISEIEDAAFLAR	99.7%	104	25	96.3	2	0	0	1462.79	241	253
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	32	0.03%	50.4%	LSFGLEDEPLETATKEN	99.7%	59.8	25	59.8	1	0	0	1892.91	323	339
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	32	0.03%	50.4%	LTPEYLQLMK	99.7%	44.8	25	36.2	4	0	0	1251.67	276	285
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	32	0.03%	50.4%	NYELMESEK	97.3%	30.8	25	30.8	1	0	0	1142.50	182	190
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	32	0.03%	50.4%	SVQTTLQTDEVK	99.7%	86.6	25	71.5	4	0	0	1348.70	61	72
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	32	0.03%	50.4%	VAQVAEITYGQK	99.7%	100	25	98	4	0	0	1306.70	221	232
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	32	0.03%	50.4%	VTKPNIPEAIR	99.0%	35	25	31.5	2	0	0	1237.73	170	180
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	14	16	32	0.03%	50.4%	VVEKEAETER	99.7%	51.9	25	46.9	2	0	0	1189.61	202	211
Estradiol 17-beta-dehydrogenase 11	HSD17B11	DHB11_HUMAN	32.9	99.9%	2	2	3	0.00%	5.3%	FAAVGFHK	99.7%	50	25	16.7	2	0	0	876.47	190	197
Estradiol 17-beta-dehydrogenase 11	HSD17B11	DHB11_HUMAN	32.9	99.9%	2	2	3	0.00%	5.3%	FDAVIGYK	99.7%	52.2	25	45.4	1	0	0	912.48	289	296
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	10	13	30	0.03%	45.2%	GVFVQSVLPYFVATK	99.7%	87.8	25	87.8	5	0	0	1654.92	224	238
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	10	13	30	0.03%	45.2%	ISYSLFTALR	99.7%	101	25	86.4	3	0	0	1170.65	26	35
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	10	13	30	0.03%	45.2%	KPTLDKPSPETFVK	99.7%	59.5	25	58.6	1	2	0	1586.88	244	257
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	10	13	30	0.03%	45.2%	LDQVSSEIKEK	99.7%	52.5	25	37.7	2	0	0	1275.68	87	97
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	10	13	30	0.03%	45.2%	MININILSVCK	99.7%	81.8	25	76.2	4	0	0	1304.71	157	167
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	10	13	30	0.03%	45.2%	MTQLVLPGMVER	99.7%	67.8	25	58.1	7	0	0	1373.73	168	179
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	10	13	30	0.03%	45.2%	SYAEELAK	96.0%	29.1	25	19.9	1	0	0	910.45	65	72
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	10	13	30	0.03%	45.2%	TFVDFFSQCLHEEYR	99.7%	61.1	25	60.9	2	0	0	1977.88	207	221
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	10	13	30	0.03%	45.2%	TIAVDFASEDIYDKIK	99.7%	87.2	25	82.1	2	0	0	1827.94	104	119
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	10	13	30	0.03%	45.2%	VWGVGNEAGVGPGLGEWAVVTGSTDGIGK	98.2%	26.8	25	25.2	0	1	0	2769.38	36	64
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	7	7	17	0.02%	29.0%	DLLGTVWGGPANLEAIAK	99.7%	70.2	25	70.2	4	0	0	1824.99	284	301
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	7	7	17	0.02%	29.0%	ELYLEEALQNER	99.6%	39.4	25	33.4	1	0	0	1506.74	272	283
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	7	7	17	0.02%	29.0%	LVEIIGSR	99.7%	51.5	25	44.8	2	0	0	886.54	199	206
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	7	7	17	0.02%	29.0%	NALNIGMVEEVLQSSDETK	99.7%	95	25	95	1	0	0	2077.01	222	240
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	7	7	17	0.02%	29.0%	QFIQGPPEVIR	99.7%	61.3	25	39.9	3	0	0	1283.71	251	261
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	7	7	17	0.02%	29.0%	SLEEAQEWLK	99.7%	62.9	25	48.4	4	0	0	1232.62	241	250
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	7	7	17	0.02%	29.0%	VIELENWTEGK	99.7%	72.3	25	72.3	2	0	0	1317.67	90	100
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	13	19	42	0.04%	41.6%	ATQALVLAPTR	99.7%	61.3	25	50	2	0	0	1140.67	100	110
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	13	19	42	0.04%	41.6%	DFTVSAMHGDMDQKER	99.7%	37.3	25	37.3	0	4	0	1866.81	296	311
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	13	19	42	0.04%	41.6%	GFKDQIYDIFQK	99.7%	67.3	25	56.7	2	0	0	1501.77	191	202
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	13	19	42	0.04%	41.6%	GIYAYGFEKPSAIQQR	99.7%	88.3	25	85.1	2	0	0	1827.94	46	61
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	13	19	42	0.04%	41.6%	GVAINMVTEEDKR	99.7%	71.9	25	71.9	2	0	0	1461.74	370	382

Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	13	19	42	0.04%	41.6%	GYDVIAQAQSGTGK	99.7%	121	25	111	2	0	0	1394.69	69	82
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	13	19	42	0.04%	41.6%	KEELTLEGIR	99.7%	54	25	35.7	2	0	0	1187.66	238	247
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	13	19	42	0.04%	41.6%	KVDWLTEK	99.7%	40.5	25	25.7	2	0	0	1018.56	284	291
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	13	19	42	0.04%	41.6%	LNSNTQVVLLSATMPSDVLEVTK	99.7%	57.3	25	57.3	4	0	0	2475.30	203	225
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	13	19	42	0.04%	41.6%	LQMEAPHIIVGTPGR	99.7%	63.5	25	51.5	4	4	0	1618.87	147	161
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	13	19	42	0.04%	41.6%	MFVLDEADEMLSR	99.7%	114	25	107	7	0	0	1571.71	178	190
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	13	19	42	0.04%	41.6%	QFYINVER	99.7%	47.7	25	37.9	2	0	0	1068.55	248	255
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	13	19	42	0.04%	41.6%	VLITTDLLAR	99.7%	75.3	25	65.4	3	0	0	1114.68	325	334
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	26	0.03%	32.4%	ELAVQIQK	99.7%	43.3	25	34.2	1	0	0	928.55	117	124
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	26	0.03%	32.4%	EQIYDVYR	99.1%	35.3	25	33.7	1	0	0	1085.53	199	206
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	26	0.03%	32.4%	ETQALILAPTR	99.7%	61.2	25	54.1	2	0	0	1212.69	106	116
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	26	0.03%	32.4%	GFKEQIYDVYR	99.7%	46.8	25	44.1	2	0	0	1417.71	196	206
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	26	0.03%	32.4%	GIYAYGFEKPSAIQQR	99.7%	88.3	25	85.1	2	0	0	1827.94	52	67
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	26	0.03%	32.4%	GRDVIAQSQSGTGK	99.7%	103	25	97.8	2	1	0	1403.72	75	88
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	26	0.03%	32.4%	KGVAINFVK	99.7%	46.2	25	28.4	2	0	0	975.60	374	382
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	26	0.03%	32.4%	KLDYGQHVVAGTPGR	99.4%	31.5	25	18	0	2	0	1597.84	152	166
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	26	0.03%	32.4%	KVDWLTEK	99.7%	40.5	25	25.7	2	0	0	1018.56	289	296
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	26	0.03%	32.4%	LDYGQHVVAGTPGR	99.7%	68.8	25	61.6	1	2	0	1469.75	153	166
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	26	0.03%	32.4%	MLVLDEADEMLNK	99.7%	91.2	25	84.7	4	0	0	1536.73	183	195
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	26	0.03%	32.4%	QFFVAVER	99.7%	54.6	25	44.7	2	0	0	995.53	253	260
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	26	0.03%	32.4%	RDELTLEGIK	99.6%	39.3	25	28.2	2	0	0	1173.65	243	252
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	12	14	26	0.03%	32.4%	VLISTDVWAR	99.7%	52.7	25	44.4	2	0	0	1159.65	330	339
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	5	6	12	0.01%	25.9%	AIVQQWLEYR	99.7%	55.2	25	46.5	4	0	0	1305.70	69	78
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	5	6	12	0.01%	25.9%	EYLLGSTAEEK	99.7%	61.1	25	48.7	3	0	0	1239.61	58	68
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	5	6	12	0.01%	25.9%	FIVDLTVQEKEK	99.7%	43	25	36.6	1	0	0	1448.80	127	138
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	5	6	12	0.01%	25.9%	NDIHTLLK	99.1%	35.6	25	20.8	1	0	0	953.54	89	96
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	5	6	12	0.01%	25.9%	QANKEYLLGSTAEEK	99.7%	77.7	25	75	2	1	0	1680.84	54	68
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	10	11	22	0.02%	33.0%	AGLNCSTENMPIK	99.7%	50.5	25	47.9	2	0	0	1434.67	214	226
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	10	11	22	0.02%	33.0%	GVFNVQMEPK	99.7%	51.2	25	27.9	4	0	0	1164.57	267	276
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	10	11	22	0.02%	33.0%	INLIAPPR	98.3%	32.5	25	31.2	1	0	0	893.56	227	234
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	10	11	22	0.02%	33.0%	NECVVVIR	99.7%	54.9	25	39.9	2	0	0	988.52	68	75
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	10	11	22	0.02%	33.0%	RPGYGAYDAFK	99.7%	40.5	25	27.3	2	0	0	1244.61	144	154
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	10	11	22	0.02%	33.0%	TAWVFDDKYK	99.7%	48.4	25	46.2	2	0	0	1272.63	134	143
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	10	11	22	0.02%	33.0%	TEGLSVLSQAMAVIK	99.7%	54.4	25	51.7	2	0	0	1562.85	245	259
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	10	11	22	0.02%	33.0%	TVYSILR	99.3%	36.4	25	21.8	1	0	0	851.50	107	113
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	10	11	22	0.02%	33.0%	VVTDTDETELAR	99.7%	102	25	96.2	4	0	0	1348.66	277	288
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	10	11	22	0.02%	33.0%	YVMTTTTLER	99.7%	40.2	25	35.9	2	0	0	1230.60	235	244
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	IF2G_HUMAN	51.1	100.0%	3	3	7	0.01%	8.3%	IVLTNPVCTEVGEK	99.7%	82.2	25	82.2	2	0	0	1558.81	427	440
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	IF2G_HUMAN	51.1	100.0%	3	3	7	0.01%	8.3%	LTPLSHEVISR	99.7%	47.6	25	47.2	4	0	0	1251.71	28	38
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	IF2G_HUMAN	51.1	100.0%	3	3	7	0.01%	8.3%	VGQEIEVRPGIVSK	98.7%	28.1	25	23.7	0	1	0	1510.86	290	303
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	ANEFLEVGK	99.7%	56.5	25	49.1	2	0	0	1006.52	15	23
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	ANEFLEVGKK	99.7%	54.2	25	35.2	2	0	0	1134.62	15	24
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	AVEDIHGLFSLSK	99.7%	86.7	25	83.9	4	0	0	1415.75	252	264
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	EDAPIGPHLQSMPSEQIR	99.7%	50.6	25	48.5	1	5	0	2020.98	503	520
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	EEELREYQER	97.6%	31.2	25	27.7	2	0	0	1380.64	838	847
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	ELEIEERER	99.7%	45.1	25	1.01	2	0	0	1202.60	862	870
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	FCLQYTR	99.7%	40.9	25	31.4	3	0	0	987.47	184	190
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	FLWESYR	99.0%	35.2	25	23.2	2	0	0	1000.49	152	158
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	FNVLQYVVPEVK	99.7%	70	25	57.8	6	0	0	1434.80	377	388
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	GLDDDRGPR	96.2%	29.4	25	20.8	1	0	0	1000.48	1072	1080
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	IGLINDMVR	99.7%	62.5	25	52.7	7	0	0	1046.57	368	376

Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	ILQEHEQIK	99.7%	42.3	25	34.2	5	0	0	1137.63	624	632
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	ILQEHEQIKK	98.8%	28.2	25	25.3	0	1	0	1265.72	624	633
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	ITTMQLER	99.7%	56.2	25	38.8	4	0	0	991.52	733	740
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	KIDYFER	99.0%	35.2	25	24	4	0	0	970.50	694	700
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	KQPALDVLYDVMK	98.1%	32.1	25	32.1	1	0	0	1535.81	24	36
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	LATLLGLQAPPTR	99.7%	42.2	25	36	3	0	0	1350.81	355	367
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	LEEIPLIK	99.3%	36.7	25	23.1	2	0	0	954.59	704	711
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	LESLNIQR	99.7%	64.4	25	29.9	4	0	0	972.55	582	589
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	LLDMDGIIVEK	99.7%	82.7	25	75.4	8	0	0	1245.68	341	351
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	LLLTPWVK	99.7%	43.9	25	21.7	1	0	0	969.61	144	151
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	LLQQVSQIYQSIEFSR	99.7%	62.3	25	62.3	4	0	0	1939.03	439	454
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	LTSLVPFVDAFQLER	99.7%	90.4	25	90.4	8	0	0	1734.94	455	469
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	LYHDIAQQAFK	99.7%	51.7	25	38.4	2	0	0	1333.69	173	183
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	MHLSQIQR	99.7%	45	25	37	5	0	0	1028.53	203	210
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	NICQQVNIK	99.7%	40.3	25	21.5	4	0	0	1116.58	76	84
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	NLTQDEMQR	99.0%	34.8	25	30.1	5	0	0	1134.52	309	317
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	NMDDDRLSR	98.8%	34.2	25	23.3	2	0	0	1121.50	1142	1150
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	NQLTAMSSVLAK	99.7%	93.3	25	80.3	10	0	0	1262.68	521	532
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	PAYFQRPENALK	99.7%	40.7	25	30.1	1	0	0	1433.75	2	13
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	QCLDLLR	98.2%	32.5	25	0.35	2	0	0	917.49	159	165
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	QPALDVLYDVMK	98.1%	32.3	25	28.2	2	0	0	1407.72	25	36
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	RGPAEESSSWR	99.7%	46.1	25	45.6	2	0	0	1261.59	1250	1260
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	RLEEIPLIK	99.0%	34.9	25	26.4	2	0	0	1110.69	703	711
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	RLGDSSLSR	95.8%	29	25	9.14	1	0	0	990.53	877	885
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	SGNALFHASTLHR	99.7%	52	25	47	1	4	0	1410.72	286	298
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	SLEDVVR	99.3%	36.4	25	14	1	0	0	817.44	85	91
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	TLSFGSDLNYATR	99.7%	91.2	25	78.6	4	0	0	1444.71	490	502
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	39	48	136	0.13%	26.4%	VLLATLSIPITPER	99.7%	65.7	25	65.7	6	0	0	1522.92	322	335
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	29	72	0.07%	32.2%	AQAVSEDAGGNEGR	99.7%	102	25	102	7	0	0	1360.61	121	134
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	29	72	0.07%	32.2%	DQYSVIFESGDR	99.7%	67.6	25	67	2	0	0	1415.64	304	315
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	29	72	0.07%	32.2%	ETIIAFAWEPNGSK	99.7%	61.9	25	58.5	2	0	0	1562.79	563	576
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	29	72	0.07%	32.2%	FAVLHGEAPR	99.7%	55.9	25	44.8	2	0	0	1096.59	577	586
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	29	72	0.07%	32.2%	FSHQGVQLIDFSPCER	99.7%	76.3	25	76.3	1	2	0	1919.91	371	386
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	29	72	0.07%	32.2%	GIALWGGEK	99.5%	38.6	25	28.8	2	0	0	930.50	356	364
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	29	72	0.07%	32.2%	GTQGVVTNFEIFR	99.7%	64.9	25	64.9	7	0	0	1467.76	536	548
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	29	72	0.07%	32.2%	GTYLATFHQR	99.7%	63.8	25	55.8	5	0	0	1193.61	346	355
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	29	72	0.07%	32.2%	GYIFLEYASPAHAVDAVK	99.7%	106	25	106	2	2	0	1951.00	231	248
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	29	72	0.07%	32.2%	ISVSFYHVK	99.7%	44.8	25	38.6	2	0	0	1079.59	587	595
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	29	72	0.07%	32.2%	ITNDFYPEEDGK	99.7%	56.8	25	56.8	2	0	0	1427.63	217	228
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	29	72	0.07%	32.2%	ITNDFYPEEDGKTK	99.7%	68.4	25	68.4	2	2	0	1656.78	217	230
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	29	72	0.07%	32.2%	MAQELYMEQK	99.7%	77.6	25	44.9	6	0	0	1286.58	763	772
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	29	72	0.07%	32.2%	MTLDTLSIYETPSMGLLDK	99.7%	65.8	25	63.9	2	0	0	2128.06	441	459
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	29	72	0.07%	32.2%	MTLDTLSIYETPSMGLLDKK	99.2%	30.2	25	30.2	0	1	0	2272.15	441	460
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	29	72	0.07%	32.2%	NADGYKLDK	97.7%	31.4	25	27.2	1	0	0	1023.51	249	257
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	29	72	0.07%	32.2%	NLFNVVDCK	99.7%	53.2	25	43.6	3	0	0	1108.55	508	516
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	29	72	0.07%	32.2%	QVPVDVVEMK	99.4%	37.5	25	32.7	2	0	0	1143.61	553	562
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	29	72	0.07%	32.2%	TMMEDFRK	94.8%	28.2	25	21.2	1	0	0	1057.48	752	759
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	29	72	0.07%	32.2%	TSIFWNDVKDPVSIEER	99.7%	51.4	25	50.1	0	2	0	2035.01	316	332
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	29	72	0.07%	32.2%	VDNAYWLWTFQGR	99.7%	51.8	25	49.6	2	0	0	1655.80	677	689
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	29	72	0.07%	32.2%	VNLFTDFDK	99.7%	46.8	25	44.3	2	0	0	1098.55	263	271
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	29	72	0.07%	32.2%	VTLMQLPTR	99.7%	56.4	25	42.2	6	0	0	1058.60	493	501

Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	24	29	72	0.07%	32.2%	YWLEEAECR	99.2%	35.9	25	33	2	0	0	1255.54	295	303
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	11	11	18	0.02%	11.2%	DFESHITSYK	99.2%	36.3	25	30.6	2	0	0	1226.57	151	160
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	11	11	18	0.02%	11.2%	ELLGQGLLLR	99.7%	53.2	25	40.3	2	0	0	1111.68	644	653
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	11	11	18	0.02%	11.2%	FEELTNLIR	99.7%	58.9	25	37.3	2	0	0	1134.62	57	65
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	11	11	18	0.02%	11.2%	GCILTLVER	99.7%	53.1	25	37.5	2	0	0	1060.58	442	450
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	11	11	18	0.02%	11.2%	GTEITHAVVIK	99.7%	64	25	46.7	2	0	0	1167.67	321	331
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	11	11	18	0.02%	11.2%	KIQEESLR	99.6%	39.9	25	14.5	1	0	0	1002.56	782	789
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	11	11	18	0.02%	11.2%	KLNEILQAR	98.7%	34	25	21.1	1	0	0	1084.65	332	340
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	11	11	18	0.02%	11.2%	LGSLVENNER	99.7%	60.7	25	44.3	2	0	0	1130.58	863	872
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	11	11	18	0.02%	11.2%	LNEILQAR	96.2%	29.4	25	19.5	1	0	0	956.55	333	340
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	11	11	18	0.02%	11.2%	SIVDKEGVPR	99.6%	39.4	25	30.7	1	0	0	1099.61	95	104
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN	105.3	100.0%	11	11	18	0.02%	11.2%	TEPTAQQNLALQLAEK	99.7%	104	25	103	2	0	0	1754.93	847	862
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	8	9	22	0.02%	16.2%	DMPYQPFSK	96.1%	29.2	25	25.4	1	0	0	1112.51	27	35
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	8	9	22	0.02%	16.2%	GAVIATELK	99.7%	47.2	25	21.9	2	0	0	901.54	418	426
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	8	9	22	0.02%	16.2%	IFHTVTTTDDPVIR	99.7%	70	25	67.3	2	2	0	1614.85	223	236
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	8	9	22	0.02%	16.2%	LGDDIDLIVR	99.7%	100	25	80	4	0	0	1128.63	365	374
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	8	9	22	0.02%	16.2%	SVYSWDIVVQR	99.7%	63.9	25	63.9	4	0	0	1351.70	261	271
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	8	9	22	0.02%	16.2%	VADWTGATYQDKR	99.7%	63.4	25	62.3	3	0	0	1510.73	42	54
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	8	9	22	0.02%	16.2%	WTCCALLAGSEYLK	99.7%	68.1	25	68.1	3	0	0	1671.79	435	448
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	8	9	22	0.02%	16.2%	YLILKDPNK	99.2%	36	25	30.1	1	0	0	1103.65	506	514
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	31	63	0.06%	55.7%	EIYNEKELLQGK	99.7%	61.7	25	33.9	2	0	0	1463.77	30	41
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	31	63	0.06%	55.7%	ETIDNNSVSSPLQSLQQR	99.7%	124	25	122	2	0	0	2016.00	194	211
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	31	63	0.06%	55.7%	HLVFPLLEFLSVK	98.4%	33	25	33	1	0	0	1541.91	17	29
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	31	63	0.06%	55.7%	IAHFLDR	99.7%	41.3	25	27.9	2	0	0	871.48	10	16
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	31	63	0.06%	55.7%	LASEILMQNWDAAMEDLTR	99.7%	95.5	25	95.5	4	0	0	2207.05	173	191
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	31	63	0.06%	55.7%	LDLLSDTNMVDFAMDVYK	99.7%	120	25	69	2	0	0	2105.98	42	59
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	31	63	0.06%	55.7%	LFIFETFCR	99.7%	54.8	25	46.5	7	0	0	1232.61	338	346
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	31	63	0.06%	55.7%	LGHVVMGNNAVSPYQQVIEK	99.7%	87.5	25	87.5	1	3	0	2183.13	388	407
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	31	63	0.06%	55.7%	LKETIDNNSVSSPLQSLQQR	99.7%	55.1	25	51.9	0	2	0	2257.18	192	211
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	31	63	0.06%	55.7%	LNMTPEEAER	99.7%	43.4	25	38.9	2	0	0	1189.55	360	369
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	31	63	0.06%	55.7%	MFEDPETTR	99.7%	44	25	26.5	4	0	0	1141.48	94	102
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	31	63	0.06%	55.7%	MLFDYLADK	99.7%	55.8	25	43	4	0	0	1115.54	112	120
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	31	63	0.06%	55.7%	NALSSLWGK	99.7%	49.7	25	47.9	2	0	0	975.53	164	172
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	31	63	0.06%	55.7%	NLYSDDIPHALR	99.7%	65.2	25	58.5	2	2	0	1413.71	60	71
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	31	63	0.06%	55.7%	QEYLDTLYR	99.7%	54.8	25	41.1	2	0	0	1200.59	125	133
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	31	63	0.06%	55.7%	QLQAETEPIVK	99.7%	64.7	25	50.4	3	0	0	1255.69	83	93
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	31	63	0.06%	55.7%	RTTVVAQLK	99.7%	45.8	25	31.8	1	0	0	1015.63	74	82
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	31	63	0.06%	55.7%	SEAPNWATQDSGFY	99.7%	65.4	25	65.4	2	0	0	1572.66	432	445
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	31	63	0.06%	55.7%	SQMLAMNIEK	99.7%	56.7	25	42.9	5	0	0	1164.58	415	424
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	31	63	0.06%	55.7%	TTVVAQLK	97.7%	31.5	25	15.5	2	0	0	859.52	75	82
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	31	63	0.06%	55.7%	VLVPATDR	99.4%	37.1	25	34.9	1	0	0	870.50	156	163
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	31	63	0.06%	55.7%	WIVNLIR	99.6%	39.6	25	12.8	2	0	0	913.56	370	376
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	31	63	0.06%	55.7%	YLTTAVITNK	99.7%	65.3	25	53.8	2	0	0	1123.64	256	265
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	24	31	63	0.06%	55.7%	YLTTAVITNKDVR	99.7%	59.9	25	52.8	1	0	0	1493.83	256	268
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	9	17	0.02%	22.1%	AYVSTLMGVPGR	99.7%	66.7	25	60.8	4	0	0	1250.66	215	226
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	9	17	0.02%	22.1%	FLMSLVNQVPK	99.7%	74.6	25	54.2	2	0	0	1275.71	307	317
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	9	17	0.02%	22.1%	IGVDLIMK	99.6%	39.2	25	33.5	2	0	0	904.52	247	254
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	9	17	0.02%	22.1%	TMGVMFTPLTVK	99.7%	44.6	25	44.6	3	0	0	1324.70	227	238
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	9	17	0.02%	22.1%	VIGLSSDLQQVGGASAR	99.7%	129	25	128	2	0	0	1657.89	262	278
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	9	17	0.02%	22.1%	VIGTLLGTVDK	99.7%	53.6	25	48.8	2	0	0	1115.67	116	126
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	7	9	17	0.02%	22.1%	YAYYDTER	99.7%	40.6	25	37.9	2	0	0	1080.46	239	246

Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	6	6	12	0.01%	19.7%	EKLPGELEPVQATQNK	99.7%	43.8	25	43.8	0	2	0	1780.94	194	209
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	6	6	12	0.01%	19.7%	ELAEQLGLSTGEK	99.7%	68.8	25	63.9	2	0	0	1374.71	181	193
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	6	6	12	0.01%	19.7%	ETDLQELFRPFGSISR	99.7%	35.6	25	35.6	0	2	0	1894.97	252	267
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	6	6	12	0.01%	19.7%	GFAFISFHR	99.7%	45.1	25	31.7	2	0	0	1081.56	281	289
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	6	6	12	0.01%	19.7%	LPGELEPVQATQNK	99.7%	65.8	25	63.7	2	0	0	1523.81	196	209
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	6	6	12	0.01%	19.7%	VTNLSEDTR	99.7%	42.1	25	25.3	2	0	0	1034.51	243	251
Eukaryotic translation initiation factor 3 subunit H	EIF3H	EIF3H_HUMAN	39.9	100.0%	2	3	5	0.00%	8.8%	EGTGSTATSSSSTAGAAGK	99.7%	61	25	59.9	2	0	0	1627.74	6	24
Eukaryotic translation initiation factor 3 subunit H	EIF3H	EIF3H_HUMAN	39.9	100.0%	2	3	5	0.00%	8.8%	LFMAQALQEYNN	99.7%	53.6	25	53.6	3	0	0	1441.68	341	352
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	12	18	45	0.04%	44.3%	DMTMFVTASK	99.7%	85.8	25	82.4	5	0	0	1130.52	199	208
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	12	18	45	0.04%	44.3%	DPIVNVWYSVNGER	99.7%	67.5	25	66.7	2	0	0	1647.81	31	44
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	12	18	45	0.04%	44.3%	DPSQIDNNEPYMK	99.7%	42	25	22.4	2	0	0	1566.67	129	141
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	12	18	45	0.04%	44.3%	EGDLLFTVAK	99.7%	65.4	25	59.8	4	0	0	1092.59	21	30
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	12	18	45	0.04%	44.3%	GHFGPINSVAFHPDGK	99.7%	73.5	25	73.5	2	2	0	1679.83	283	298
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	12	18	45	0.04%	44.3%	HVLTGSADNSCR	99.7%	66.8	25	66.8	4	1	0	1316.60	66	77
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	12	18	45	0.04%	44.3%	LFDSTTLEHQK	99.7%	66.6	25	50.5	4	2	0	1318.66	214	224
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	12	18	45	0.04%	44.3%	MKPILLQGHER	99.7%	40.5	25	40.5	0	4	0	1337.74	1	11
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	12	18	45	0.04%	44.3%	QINDIQLSR	99.4%	37.8	25	13.2	3	0	0	1086.59	190	198
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	12	18	45	0.04%	44.3%	SGEVLVNVK	99.7%	68.8	25	59.8	2	0	0	944.54	177	185
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	12	18	45	0.04%	44.3%	SYSSGGEDGYVR	99.7%	55.6	25	55.6	4	0	0	1276.54	299	310
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	12	18	45	0.04%	44.3%	TCGFDFGGNIIMFSTDK	99.7%	86.2	25	86.2	4	0	0	1925.84	98	114
Eukaryotic translation initiation factor 3 subunit K	EIF3K	EIF3K_HUMAN	25.1	100.0%	3	4	7	0.01%	13.3%	CMIDQAHQEERPIR	99.7%	34.1	25	34.1	0	1	0	1782.84	87	100
Eukaryotic translation initiation factor 3 subunit K	EIF3K	EIF3K_HUMAN	25.1	100.0%	3	4	7	0.01%	13.3%	GIDRYNPENLATLER	99.7%	54.8	25	54	2	2	0	1760.89	17	31
Eukaryotic translation initiation factor 3 subunit K	EIF3K	EIF3K_HUMAN	25.1	100.0%	3	4	7	0.01%	13.3%	YNPENLATLER	99.7%	53.9	25	43.2	2	0	0	1319.66	21	31
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	19	20	47	0.05%	36.0%	EPFLQQLK	99.7%	47.5	25	14.9	2	0	0	1002.56	438	445
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	19	20	47	0.05%	36.0%	IDESIHLQLR	99.7%	41.3	25	33.5	1	0	0	1223.67	382	391
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	19	20	47	0.05%	36.0%	KSEEEIDFLR	99.7%	54.7	25	46.7	2	0	0	1265.64	207	216
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	19	20	47	0.05%	36.0%	LAGFLDLTEQEFR	99.7%	93.9	25	89.9	5	0	0	1538.79	475	487
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	19	20	47	0.05%	36.0%	LHSLLGDYYQAIK	99.7%	63	25	63	1	2	0	1520.81	280	292
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	19	20	47	0.05%	36.0%	LYTTMPVAK	99.7%	48.7	25	35.3	2	0	0	1039.55	466	474
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	19	20	47	0.05%	36.0%	MLGYFSLVGLLR	99.7%	57	25	56.5	1	0	0	1384.77	268	279
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	19	20	47	0.05%	36.0%	QLEVYTSGGDPESVAGEYGR	99.7%	125	25	125	2	0	0	2113.97	243	262
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	19	20	47	0.05%	36.0%	QYEQQTYQVIPEVIK	99.7%	58.1	25	57.9	2	0	0	1865.96	39	53
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	19	20	47	0.05%	36.0%	SEEEIDFLR	99.7%	64	25	51.3	2	0	0	1137.54	208	216
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	19	20	47	0.05%	36.0%	TTYKYEMINK	99.3%	36.5	25	33.7	2	0	0	1290.64	353	362
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	19	20	47	0.05%	36.0%	TVSDLIDQK	98.9%	34.8	25	25.4	3	0	0	1018.54	62	70
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	19	20	47	0.05%	36.0%	VFSDEVQQQAQLSTIR	99.7%	106	25	105	5	0	0	1848.95	446	461
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	19	20	47	0.05%	36.0%	VLENIELNKK	99.7%	55	25	39.3	2	0	0	1199.70	293	302
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	19	20	47	0.05%	36.0%	VSGGPSLEQR	99.7%	81	25	66.6	2	0	0	1029.53	144	153
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	19	20	47	0.05%	36.0%	VSSDVIDQK	99.7%	60	25	45.7	3	0	0	990.51	79	87
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	19	20	47	0.05%	36.0%	VYEIQDIYENSWTK	99.7%	82	25	75.7	2	0	0	1787.85	88	101
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	19	20	47	0.05%	36.0%	VYELQASR	99.7%	57.8	25	45.8	4	0	0	965.51	71	78
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	19	20	47	0.05%	36.0%	YGDFFIR	99.7%	46.8	25	29.8	2	0	0	917.45	539	545
Eukaryotic translation initiation factor 3 subunit M	EIF3M	EIF3M_HUMAN	42.5	99.8%	2	3	5	0.00%	5.6%	LLTFMGMAVENK	99.7%	65	25	49	3	0	0	1353.69	279	290
Eukaryotic translation initiation factor 3 subunit M	EIF3M	EIF3M_HUMAN	42.5	99.8%	2	3	5	0.00%	5.6%	YTVYCSLIK	99.7%	43	25	37.3	2	0	0	1146.59	121	129
Eukaryotic translation initiation factor 4 gamma 1	EIF4G1	IF4G1_HUMAN	175.5	100.0%	2	2	2	0.00%	1.2%	ALPSEELNR	96.3%	29.5	25	24.6	1	0	0	1028.54	1437	1445
Eukaryotic translation initiation factor 4 gamma 1	EIF4G1	IF4G1_HUMAN	175.5	100.0%	2	2	2	0.00%	1.2%	GGPPGPPISR	97.1%	30.4	25	19.4	1	0	0	934.51	1033	1042
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	7	7	12	0.01%	7.5%	FLLQDTVELR	99.7%	51.3	25	33.5	2	0	0	1233.68	296	305
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	7	7	12	0.01%	7.5%	GLSFLFPLLK	99.7%	80.9	25	80.6	2	0	0	1134.69	723	732
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	7	7	12	0.01%	7.5%	LEVDIPLVK	99.2%	35.9	25	35.9	2	0	0	1025.62	632	640
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	7	7	12	0.01%	7.5%	SYLAQFAAR	99.7%	55.5	25	50.3	2	0	0	1026.54	641	649
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	7	7	12	0.01%	7.5%	TAGNSEFLGK	98.7%	33.9	25	33	1	0	0	1023.51	32	41

Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	7	7	12	0.01%	7.5%	TNPPLIQEKPAK	99.7%	50.7	25	50.7	2	0	0	1335.76	521	532
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	7	7	12	0.01%	7.5%	VIILSLDR	99.3%	36.6	25	33.3	1	0	0	928.58	585	592
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	4	5	21	0.02%	8.8%	AASIFGGAKPVDTAAR	99.7%	74.6	25	72.1	4	3	0	1531.82	357	372
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	4	5	21	0.02%	8.8%	GLNISAVR	99.7%	61.2	25	29.7	4	0	0	829.49	118	125
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	4	5	21	0.02%	8.8%	SQSSDTEQQSPTSGGGK	99.7%	86.7	25	86.7	4	0	0	1680.73	495	511
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	4	5	21	0.02%	8.8%	VAPAQPSEEGPGR	99.7%	54	25	54	6	0	0	1294.64	512	524
Eukaryotic translation initiation factor 5B	EIF5B	IF2P_HUMAN	138.8	100.0%	3	3	4	0.00%	3.2%	HFEATDILVSK	99.7%	43.1	25	37.8	2	0	0	1259.66	1175	1185
Eukaryotic translation initiation factor 5B	EIF5B	IF2P_HUMAN	138.8	100.0%	3	3	4	0.00%	3.2%	LLQAQGVEVPSK	99.7%	53.7	25	52.4	1	0	0	1268.72	425	436
Eukaryotic translation initiation factor 5B	EIF5B	IF2P_HUMAN	138.8	100.0%	3	3	4	0.00%	3.2%	TSEVPYAGINIGPVHK	99.5%	37.8	25	37.8	1	0	0	1681.89	1000	1015
Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	ECSIT	ECSIT_HUMAN	49.1	100.0%	3	3	5	0.00%	10.7%	ALVPFEDLFGQAPGGER	99.7%	55.9	25	54.6	2	0	0	1802.91	68	84
Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	ECSIT	ECSIT_HUMAN	49.1	100.0%	3	3	5	0.00%	10.7%	DLAVYNQLLNIFPK	99.7%	60	25	60	1	0	0	1647.91	125	138
Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	ECSIT	ECSIT_HUMAN	49.1	100.0%	3	3	5	0.00%	10.7%	DLPQDPVELAMFGLR	99.7%	79	25	72.2	2	0	0	1700.87	218	232
Exocyst complex component 2	EXOC2	EXOC2_HUMAN	104.1	100.0%	3	3	5	0.00%	4.0%	ASNTADTLFQEVLGR	99.7%	82.4	25	81.3	2	0	0	1621.82	249	263
Exocyst complex component 2	EXOC2	EXOC2_HUMAN	104.1	100.0%	3	3	5	0.00%	4.0%	FLFNLPLNIER	99.7%	43.7	25	36.5	2	0	0	1375.77	282	292
Exocyst complex component 2	EXOC2	EXOC2_HUMAN	104.1	100.0%	3	3	5	0.00%	4.0%	VIEAVSEELSR	99.7%	57.8	25	40.9	1	0	0	1231.65	828	838
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	4	4	7	0.01%	5.8%	DASVPLIDVTNLPTPR	99.7%	68.8	25	57.1	2	0	0	1707.93	224	239
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	4	4	7	0.01%	5.8%	ESEVLIGNLGDK	99.7%	47.1	25	41.8	1	0	0	1273.66	682	693
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	4	4	7	0.01%	5.8%	NIFVLQQNLTNITMSR	99.7%	80.4	25	80.4	2	0	0	1892.01	873	888
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	4	4	7	0.01%	5.8%	STTQVADSGYQR	99.7%	61.6	25	59.5	2	0	0	1312.61	314	325
Exosome complex component CSL4	EXOSC1	EXOS1_HUMAN	21.5	100.0%	4	4	6	0.01%	29.7%	ETESQLLPDVGAIVTCK	99.7%	41.3	25	40.6	1	0	0	1859.94	58	74
Exosome complex component CSL4	EXOSC1	EXOS1_HUMAN	21.5	100.0%	4	4	6	0.01%	29.7%	LCNLEEGSPGSGTYTR	99.7%	74.6	25	74.6	1	0	0	1740.79	14	29
Exosome complex component CSL4	EXOSC1	EXOS1_HUMAN	21.5	100.0%	4	4	6	0.01%	29.7%	SFRPGDIVLAK	99.7%	41.5	25	23.8	2	0	0	1202.69	121	131
Exosome complex component CSL4	EXOSC1	EXOS1_HUMAN	21.5	100.0%	4	4	6	0.01%	29.7%	SSENGALPVVSVVR	99.7%	72	25	72	2	0	0	1413.77	44	57
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	5	5	7	0.01%	22.8%	ELALALQEALEPAVR	98.9%	34.7	25	34.7	1	0	0	1622.91	121	135
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	5	5	7	0.01%	22.8%	GGGPAGAGGEAPAALR	99.7%	59.7	25	59.7	2	0	0	1308.67	78	93
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	5	5	7	0.01%	22.8%	GSAYLEAGGTK	99.7%	65.2	25	55.8	1	0	0	1053.52	51	61
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	5	5	7	0.01%	22.8%	LYPVLQQSLVR	99.7%	62.1	25	60.5	2	0	0	1315.77	251	261
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	5	5	7	0.01%	22.8%	VLCAVSGPR	99.7%	67.8	25	50	1	0	0	958.51	62	70
Exosome complex component RRP4	EXOSC2	EXOS2_HUMAN	32.8	100.0%	4	4	8	0.01%	16.4%	LGQGVLVQVSPSLVK	99.7%	78.4	25	64	2	0	0	1523.92	166	180
Exosome complex component RRP4	EXOSC2	EXOS2_HUMAN	32.8	100.0%	4	4	8	0.01%	16.4%	LIASVAGSVER	99.7%	71.4	25	59.6	2	0	0	1101.63	52	62
Exosome complex component RRP4	EXOSC2	EXOS2_HUMAN	32.8	100.0%	4	4	8	0.01%	16.4%	NCIISLVTQR	99.7%	81.4	25	72.7	2	0	0	1203.65	239	248
Exosome complex component RRP4	EXOSC2	EXOS2_HUMAN	32.8	100.0%	4	4	8	0.01%	16.4%	YIGEVGDIVVGR	99.7%	79.6	25	76	2	0	0	1276.69	76	87
Exosome complex component RRP40	EXOSC3	EXOS3_HUMAN	29.6	99.8%	2	2	2	0.00%	9.8%	LLAPDCEIIQEVGK	99.7%	40.5	25	38.9	1	0	0	1584.83	210	223
Exosome complex component RRP40	EXOSC3	EXOS3_HUMAN	29.6	99.8%	2	2	2	0.00%	9.8%	LYPLEIVFGMNGR	99.7%	45.3	25	45.3	1	0	0	1508.79	224	236
Exosome complex component RRP41	EXOSC4	EXOS4_HUMAN	26.4	99.8%	2	2	4	0.00%	9.0%	ALAVVYGPHEIR	99.7%	47.8	25	41.1	2	0	0	1324.74	48	59
Exosome complex component RRP41	EXOSC4	EXOS4_HUMAN	26.4	99.8%	2	2	4	0.00%	9.0%	VLEAAAQAAR	99.7%	77.8	25	56.7	2	0	0	999.56	213	222
Exosome complex component RRP46	EXOSC5	EXOS5_HUMAN	25.2	100.0%	2	2	3	0.00%	11.1%	AVLTFALDSVER	99.7%	88.2	25	54	2	0	0	1320.72	179	190
Exosome complex component RRP46	EXOSC5	EXOS5_HUMAN	25.2	100.0%	2	2	3	0.00%	11.1%	NTCEAVVLGTLHPR	99.7%	91	25	91	1	0	0	1566.81	100	113
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	23	0.02%	17.4%	ASLTYAEAQLR	99.7%	43.8	25	32.5	1	0	0	1222.64	586	596
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	23	0.02%	17.4%	GALTLSSPEVR	94.9%	28.2	25	14	1	0	0	1129.62	628	638
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	23	0.02%	17.4%	IDSANMNDDITTSLR	98.7%	33.8	25	33.8	1	0	0	1665.78	597	611
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	23	0.02%	17.4%	IEDTVFHVFDK	99.7%	51.2	25	44.4	2	0	0	1349.67	896	906
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	23	0.02%	17.4%	IIFSEHLPLSK	99.7%	44.5	25	36.5	1	0	0	1283.74	226	236
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	23	0.02%	17.4%	IIVAIDGWPR	99.7%	47.4	25	36.8	1	0	0	1139.66	398	407
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	23	0.02%	17.4%	IMLDSSNLQHQK	99.7%	40.7	25	34.8	1	0	0	1413.72	911	922
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	23	0.02%	17.4%	LACLSEEGNEIESGK	99.7%	111	25	111	2	0	0	1635.75	211	225
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	23	0.02%	17.4%	LLAVAIGADCTYPELTDK	99.7%	81.3	25	78.1	2	0	0	1949.99	790	807
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	23	0.02%	17.4%	NAIVVLIPK	99.5%	38	25	38	2	0	0	966.63	858	866
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	23	0.02%	17.4%	NVIVLQTVLQEVR	99.7%	88.2	25	88.2	4	0	0	1510.90	87	99
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	23	0.02%	17.4%	SLTANPELIDR	99.2%	36.2	25	18.4	1	0	0	1228.65	200	210
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	23	0.02%	17.4%	YADVIVHR	99.7%	47	25	41.4	2	0	0	972.53	782	789

Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	14	14	23	0.02%	17.4%	YGLEGTVFFEEK	99.7%	89.3	25	84.9	2	0	0	1418.68	867	878
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	7	7	11	0.01%	8.9%	AAAEQAISVR	99.7%	60.1	25	34.3	2	0	0	1015.55	759	768
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	7	7	11	0.01%	8.9%	ASGGLPQFGDEYDFYR	99.7%	41.2	25	41.2	1	0	0	1821.81	49	64
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	7	7	11	0.01%	8.9%	FALGSVVAVTK	99.7%	78.9	25	74.1	2	0	0	1091.65	38	48
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	7	7	11	0.01%	8.9%	LAQVQVQK	99.2%	35.9	25	15.9	1	0	0	913.55	726	733
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	7	7	11	0.01%	8.9%	LYCNVDSNK	99.3%	36.9	25	28.1	2	0	0	1112.50	409	417
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	7	7	11	0.01%	8.9%	TEDFIIDTLELR	99.7%	102	25	93.2	2	0	0	1464.76	335	346
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	7	7	11	0.01%	8.9%	VGILLDEASGVNK	99.7%	67.9	25	62.7	1	0	0	1314.73	124	136
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	AIIASNIMYIVGQYPR	99.7%	82.8	25	71.1	4	2	0	1824.97	538	553
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	AVGHPFVIQLGR	99.7%	42	25	34.9	2	2	0	1293.74	701	712
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	DFEEYPEHR	94.7%	28.1	25	28.1	1	0	0	1221.52	837	845
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	EFAGEDTSDLFLEER	99.7%	99.8	25	84.8	2	0	0	1757.79	1024	1038
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	EPEVLSTMAIIVNK	99.7%	79.6	25	74.8	4	0	0	1559.84	797	810
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	ETLVYLTHLDYVDTER	99.7%	97.2	25	97.2	2	2	0	1966.98	459	474
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	FLNVPMFR	94.6%	28	25	24	1	0	0	1039.54	254	261
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	FLVTVIK	99.6%	39.8	25	15.4	2	0	0	819.53	516	522
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	HWPTFISDIVGASR	99.7%	53.7	25	53.7	2	2	0	1585.81	145	158
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	IYLDMLNVYK	99.7%	69.7	25	64.8	5	0	0	1271.67	713	722
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	KYVVGLIIK	94.8%	28.2	25	28.2	1	0	0	1032.68	104	112
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	LDINLLDNVVNCLYHGEGAQQR	99.7%	60.8	25	54.1	0	1	0	2541.25	23	44
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	LISGWVSR	99.7%	64.2	25	43.8	2	0	0	917.52	758	765
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	LISTLIYK	99.7%	54.5	25	48.8	2	0	0	950.59	246	253
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	LLSEEVFDFSSGQITQVK	99.7%	133	25	133	4	1	0	2027.03	173	190
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	LNMILVQILK	99.7%	75.8	25	63.8	4	0	0	1184.74	130	139
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	LVLDSIIWAFK	99.7%	86.2	25	86.2	3	0	0	1304.76	873	883
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	MAKPEEVLVVENDQGEVVR	99.7%	68.3	25	65.7	0	4	0	2157.09	424	442
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	MAQEVLTHLK	99.7%	63.2	25	40.8	4	0	0	1169.63	45	54
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	NVDILKDPETVK	99.7%	56.7	25	52.4	2	1	0	1370.75	675	686
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	PAIMTMLADHAAR	99.7%	47.3	25	47.3	0	1	0	1397.70	2	14
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	QLLDFSQK	98.8%	34.4	25	25.9	1	0	0	978.53	15	22
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	QLYLPMLFK	95.3%	28.6	25	15.8	1	0	0	1152.65	407	415
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	QMLPLNTNIR	99.7%	47.1	25	35.5	4	0	0	1199.66	296	305
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	SAFPHLQDAQVK	99.7%	60.4	25	50.8	2	0	0	1340.70	984	995
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	TSESLCQNNMVILK	99.7%	91.9	25	80.5	4	0	0	1636.80	159	172
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	TSSDPTCVEK	99.7%	53.2	25	33.8	2	0	0	1123.49	113	122
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	TSSDPTCVEKEK	99.7%	64.9	25	52.2	2	0	0	1380.63	113	124
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	VDTILEFSQNMNTK	99.7%	101	25	99.9	4	0	0	1655.79	63	76
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	YMLLPNQVWDSIIQQATK	98.6%	33.7	25	29.8	1	0	0	2164.11	657	674
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	YVVGLIIK	99.7%	45.8	25	34.9	2	0	0	904.59	105	112
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	32	47	88	0.09%	34.5%	YYGLQILENVIK	99.7%	93.7	25	93.7	2	0	0	1452.81	77	88
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	AACDLVR	99.7%	43.1	25	29.5	2	0	0	804.40	385	391
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	AADEEAFEDNSEEYIR	99.7%	124	25	124	2	0	0	1887.79	356	371
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	AADEEAFEDNSEEYIRR	99.7%	44.2	25	44.2	1	2	0	2043.89	356	372
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	ALTLPGSSENEYIMK	99.7%	92.6	25	83.4	4	0	0	1652.82	560	574
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	ANIVHLMLSSPEQIQK	99.7%	82.8	25	80.5	2	4	0	1807.97	94	109
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	ATIELCSTHANDASALR	99.7%	108	25	108	2	2	0	1829.88	190	206
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	DAAIYLVTSLASK	99.7%	95.3	25	92.3	2	0	0	1351.75	428	440
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	DLEGSDIDTR	99.7%	55.5	25	49.1	2	0	0	1120.51	373	382
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	DLEGSDIDTRR	99.7%	48.2	25	31.1	2	0	0	1276.61	373	383
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	EHDPVGQMVNNPK	99.7%	60.3	25	59.4	2	0	0	1480.69	913	925
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	GSNTIASAAADK	99.7%	64.9	25	54.1	1	0	0	1105.55	715	726

Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	GSNTIASAAADKIPGLLGVFQK	99.7%	63.2	25	61.4	2	2	0	2158.19	715	736
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	HKDAAIYLVTSLASK	99.7%	53.9	25	49.6	0	2	0	1616.90	426	440
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	IHLAQSLHK	99.7%	42.5	25	40.2	2	0	0	1046.61	926	934
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	IIIPEIQK	97.2%	30.6	25	0	1	0	0	953.60	825	832
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	ILFSSLILISK	99.7%	90.2	25	90.2	3	0	0	1233.78	207	217
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	IVEDEPNKICEADR	99.7%	88.9	25	88.9	2	2	0	1687.80	76	89
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	KICAVGITK	99.7%	51.4	25	40.8	2	0	0	989.58	840	848
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	LLQAFLER	99.7%	58	25	40.9	7	0	0	989.58	707	714
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	LLQTDDEEEAGLLELLK	99.7%	130	25	121	4	0	0	1929.01	252	268
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	LLTECPPMMDTEYTK	99.7%	75.8	25	75.8	4	0	0	1828.82	849	863
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	LSTACPGR	95.6%	28.8	25	20.2	1	0	0	861.42	935	942
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	LVLDAFALPLTNLFK	99.7%	78.4	25	78.4	2	0	0	1674.98	175	189
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	MFGMVLEK	99.6%	39.2	25	32	3	0	0	970.47	817	824
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	NLFEDQNTLTSICEK	99.7%	89.9	25	89.9	2	0	0	1811.85	332	346
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	QIFILLFQR	99.7%	46.5	25	45	2	0	0	1177.71	769	777
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	QLSDAISIIGR	99.7%	79.9	25	62.1	2	0	0	1172.66	110	120
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	SANVNEFPVLK	99.7%	50.5	25	34.2	2	0	0	1217.65	471	481
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	SNELWTEIK	99.7%	61.7	25	48.8	2	0	0	1119.57	166	174
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	SQICDNAALYAQK	99.7%	83.1	25	63.3	2	0	0	1481.71	269	281
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	TGNIPALVR	99.7%	57.3	25	54.3	4	0	0	940.56	698	706
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	TLDPDPAIR	99.7%	40.2	25	40.2	1	0	0	997.53	18	26
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	VCASVTFK	96.9%	30.2	25	24.1	1	0	0	911.47	60	67
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	VIVPNMEFR	98.0%	32	25	30.5	1	0	0	1104.59	347	355
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	WPDLLTEMVNR	99.7%	55.4	25	55.4	2	0	0	1373.69	127	137
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	YDEEFQR	99.7%	46.2	25	45.2	3	0	0	986.42	282	288
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	YGALALQEIFDGIQPK	99.7%	101	25	101	6	0	0	1762.94	801	816
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	47	100	0.10%	41.0%	YIMIFR	95.3%	28.5	25	17.7	1	0	0	842.46	487	492
Exportin-4	XPO4	XPO4_HUMAN	130.1	99.7%	2	2	2	0.00%	2.0%	LVFDMLVLQK	94.9%	28.2	25	12.4	1	0	0	1205.70	1056	1065
Exportin-4	XPO4	XPO4_HUMAN	130.1	99.7%	2	2	2	0.00%	2.0%	SPPLNFLSSPVQR	99.7%	65.1	25	62.8	1	0	0	1441.78	737	749
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	17	19	31	0.03%	16.4%	AGGFVVGYTSSGNPIFR	99.7%	115	25	115	2	0	0	1728.87	746	762
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	17	19	31	0.03%	16.4%	ALDMLDAEK	97.1%	30.4	25	29.8	1	0	0	1021.49	802	810
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	17	19	31	0.03%	16.4%	AVMEQIPEIQK	99.7%	61.1	25	56.9	2	0	0	1285.68	1113	1123
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	17	19	31	0.03%	16.4%	AVTVMMDPNSTQR	99.7%	62.9	25	62.9	3	0	0	1481.67	16	28
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	17	19	31	0.03%	16.4%	DIQQTLTQNMER	99.7%	45.1	25	43.5	2	0	0	1476.71	177	188
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	17	19	31	0.03%	16.4%	DPLLLAIIPK	99.7%	50	25	50	4	0	0	1092.70	387	396
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	17	19	31	0.03%	16.4%	IFSFLLNTLQENVNK	99.7%	80.7	25	70.9	2	0	0	1779.96	189	203
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	17	19	31	0.03%	16.4%	IVVEMIK	96.0%	29.2	25	19.4	1	0	0	831.50	119	125
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	17	19	31	0.03%	16.4%	IVVEMIKR	98.4%	33.1	25	19.6	1	0	0	987.60	119	126
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	17	19	31	0.03%	16.4%	LFSSVTFETVEESK	99.7%	89.3	25	89.3	2	0	0	1602.79	577	590
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	17	19	31	0.03%	16.4%	LLDNLLALIR	99.7%	74.6	25	54.4	2	0	0	1153.73	772	781
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	17	19	31	0.03%	16.4%	LLNPSLQK	98.7%	34	25	2.6	1	0	0	912.55	1133	1140
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	17	19	31	0.03%	16.4%	NPCTEQILK	96.9%	30.2	25	23.8	1	0	0	1102.56	763	771
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	17	19	31	0.03%	16.4%	QLLSNELLLTQMEK	99.7%	79	25	73.5	2	0	0	1659.90	632	645
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	17	19	31	0.03%	16.4%	SAILGLPQPLLELNDSPVFK	99.7%	83.1	25	83.1	1	0	0	2151.21	811	830
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	17	19	31	0.03%	16.4%	TDSPSCEYSR	99.6%	39.4	25	39.3	2	0	0	1201.48	414	423
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	17	19	31	0.03%	16.4%	VLSDVDAFIAYVGTDQK	99.7%	91.7	25	86.6	2	0	0	1840.93	688	704
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	4	4	4	0.00%	3.6%	DLSSLLQAVGR	99.7%	47.7	25	41	1	0	0	1158.65	556	566
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	4	4	4	0.00%	3.6%	FNDALTVVER	99.7%	58.5	25	47.1	1	0	0	1163.61	580	589
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	4	4	4	0.00%	3.6%	MFQQTFYLLQK	99.7%	46.8	25	42	1	0	0	1446.75	336	346
Exportin-6	XPO6	XPO6_HUMAN	128.9	100.0%	4	4	4	0.00%	3.6%	STVLASVQR	99.7%	48.3	25	25.7	1	0	0	960.55	956	964
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	19	19	31	0.03%	20.6%	AALSGSYVNFGVFR	99.7%	99	25	95.3	2	0	0	1487.76	841	854

Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	19	19	31	0.03%	20.6%	ALVEFTNSPDCLSK	99.7%	56	25	51.6	1	0	0	1580.76	33	46
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	19	19	31	0.03%	20.6%	DSSLFDIFTLSCNLLK	99.7%	84.2	25	82	1	0	0	1872.94	183	198
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	19	19	31	0.03%	20.6%	GIAFAFNAK	99.6%	40	25	27.2	2	0	0	938.51	728	736
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	19	19	31	0.03%	20.6%	GSSSYSQLLAATCLTK	99.7%	79.2	25	74.3	2	0	0	1686.84	54	69
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	19	19	31	0.03%	20.6%	IYIGDQVQK	96.7%	29.9	25	20.1	1	0	0	1063.58	560	568
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	19	19	31	0.03%	20.6%	LATFVTQALIQLYAR	99.7%	48.3	25	48.3	1	0	0	1707.98	100	114
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	19	19	31	0.03%	20.6%	LESVHIILR	99.7%	68.3	25	68.3	2	0	0	1079.66	418	426
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	19	19	31	0.03%	20.6%	LMAELVHNR	99.7%	53.3	25	49	1	0	0	1082.58	774	782
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	19	19	31	0.03%	20.6%	LQFDVSSPNGILLFR	99.7%	80.6	25	74.6	2	0	0	1705.93	786	800
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	19	19	31	0.03%	20.6%	LYGDDALDNALQTFIK	99.7%	108	25	106	2	0	0	1796.91	855	870
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	19	19	31	0.03%	20.6%	NSIVNSQPPEK	99.7%	46.1	25	41.5	2	0	0	1212.62	1021	1031
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	19	19	31	0.03%	20.6%	NYVLNYLATRPK	99.7%	60.1	25	60.1	2	0	0	1451.80	88	99
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	19	19	31	0.03%	20.6%	SNYQLGELVK	99.7%	43.4	25	37.1	2	0	0	1150.61	339	348
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	19	19	31	0.03%	20.6%	TNNPLPLEQR	99.7%	53	25	44	2	0	0	1181.63	74	83
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	19	19	31	0.03%	20.6%	TTFYTALGR	99.4%	37.2	25	24.5	1	0	0	1029.54	666	674
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	19	19	31	0.03%	20.6%	TTPLNQESDR	99.0%	35.2	25	28.1	1	0	0	1160.55	958	967
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	19	19	31	0.03%	20.6%	VENYPEVIR	99.6%	38.9	25	38.2	2	0	0	1118.58	349	357
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	19	19	31	0.03%	20.6%	VLQLMNLTDSR	99.7%	54.4	25	48.8	2	0	0	1289.69	527	537
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.4%	ALAYFEQLK	99.7%	60.7	25	60	2	0	0	1082.59	21	29
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.4%	ANVEAIMLAVMK	99.7%	97.7	25	89.4	3	0	0	1289.70	370	381
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.4%	DGPVGFADFVYK	99.7%	59	25	59	2	0	0	1314.64	860	871
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.4%	DLQEFIPLINQITAK	99.7%	115	25	114	2	0	0	1742.97	738	752
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.4%	DVVHTSEEAR	99.7%	41.8	25	35.9	2	0	0	1142.54	157	166
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.4%	EEACDCLFEVVNK	99.7%	73.6	25	73.6	1	0	0	1612.70	241	253
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.4%	FFCFQVLEHQVK	99.7%	57.5	25	57.5	2	2	0	1581.79	54	65
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.4%	FMEVEVAIR	99.7%	54.8	25	46.7	3	0	0	1109.57	443	451
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.4%	GVDLYLR	99.7%	41.2	25	33.9	1	0	0	835.47	138	144
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.4%	ILMAIDSELVDR	99.7%	61.9	25	60.2	1	0	0	1374.73	145	156
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.4%	ISPDAWQVCAEALAQR	99.7%	75.2	25	75.2	1	0	0	1814.89	30	45
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.4%	LAQVSPELLLASVR	99.7%	103	25	103	6	0	0	1495.88	415	428
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.4%	LMLAQDEER	99.4%	37.1	25	20	1	0	0	1104.54	635	643
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.4%	NAQEALQAIETK	99.7%	73.1	25	61.6	2	0	0	1315.69	317	328
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.4%	QASLADCLNHAVGFASR	99.4%	31.2	25	31.2	0	2	0	1816.88	644	660
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.4%	QMNPFIEDILNR	99.7%	63.4	25	54.7	2	0	0	1489.75	558	569
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.4%	TCFIILSK	99.7%	46.8	25	36.5	2	0	0	981.54	844	851
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.4%	VFSSTLQNWQTTR	99.7%	80.3	25	75.1	2	0	0	1567.79	430	442
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.4%	VLVTVIQGAVEYPDPIAQK	99.7%	90.5	25	90.5	2	2	0	2040.14	825	843
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	20	23	45	0.04%	25.4%	YSELTTVQQQLIR	99.7%	74.6	25	74.6	2	0	0	1578.85	68	80
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	4	4	6	0.01%	5.7%	ITVPLVSEVQIAQLR	99.7%	90.2	25	90.2	2	0	0	1665.99	365	379
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	4	4	6	0.01%	5.7%	LLDEWFTLDEVPK	99.7%	57.2	25	54.4	2	0	0	1604.82	484	496
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	4	4	6	0.01%	5.7%	SSSSLLASPGHISVK	99.0%	35	25	22.6	1	0	0	1469.80	736	750
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	4	4	6	0.01%	5.7%	VYTENVDKR	98.8%	34.3	25	22.4	1	0	0	1123.57	254	262
FACT complex subunit SPT16	SUPT16H	SP16H_HUMAN	119.9	100.0%	4	4	7	0.01%	5.4%	APGEQTVPALNLQNAFR	99.7%	58	25	57.7	2	0	0	1825.96	607	623
FACT complex subunit SPT16	SUPT16H	SP16H_HUMAN	119.9	100.0%	4	4	7	0.01%	5.4%	GDKVDILYNNIK	99.7%	41.5	25	37.7	1	0	0	1391.75	694	705
FACT complex subunit SPT16	SUPT16H	SP16H_HUMAN	119.9	100.0%	4	4	7	0.01%	5.4%	LTEQKGEQQIQK	96.8%	30	25	20	1	0	0	1429.76	493	504
FACT complex subunit SPT16	SUPT16H	SP16H_HUMAN	119.9	100.0%	4	4	7	0.01%	5.4%	NEGNIFPNPEATFVK	99.7%	65.5	25	54.4	3	0	0	1676.83	582	596
FACT complex subunit SSRP1	SSRP1	SSRP1_HUMAN	81.1	100.0%	2	2	4	0.00%	3.7%	ADVIQATGDAICIFR	99.7%	74.7	25	71.1	2	0	0	1649.83	189	203
FACT complex subunit SSRP1	SSRP1	SSRP1_HUMAN	81.1	100.0%	2	2	4	0.00%	3.7%	FDEISFVNFAR	99.7%	76.7	25	69.3	2	0	0	1344.66	371	381
F-actin-capping protein subunit alpha-1	CAPZA1	CAZA1_HUMAN	32.9	99.8%	2	2	4	0.00%	8.7%	FTITPPTAQVVGVLK	99.7%	41.2	25	41.2	2	0	0	1570.92	179	193
F-actin-capping protein subunit alpha-1	CAPZA1	CAZA1_HUMAN	32.9	99.8%	2	2	4	0.00%	8.7%	LLLNNDNLLR	99.7%	79.6	25	56.1	2	0	0	1197.70	38	47
Fanconi anemia group D2 protein	FANCD2	FACD2_HUMAN	166.5	100.0%	4	4	5	0.00%	3.1%	GILDYLDNISPQQIR	96.9%	30.1	25	25.5	1	0	0	1744.92	516	530

Fanconi anemia group D2 protein	FANCD2	FACD2_HUMAN	166.5	100.0%	4	4	5	0.00%	3.1%	LVSPLCLAPYFR	99.5%	38.5	25	38.5	2	0	0	1435.78	724	735
Fanconi anemia group D2 protein	FANCD2	FACD2_HUMAN	166.5	100.0%	4	4	5	0.00%	3.1%	NSDEINIPR	99.2%	36	25	26.5	1	0	0	1057.53	166	174
Fanconi anemia group D2 protein	FANCD2	FACD2_HUMAN	166.5	100.0%	4	4	5	0.00%	3.1%	SESPSLTQER	99.3%	36.9	25	22.1	1	0	0	1133.54	590	599
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	17	17	29	0.03%	15.2%	CLSQQADVR	95.6%	28.7	25	17.3	1	0	0	1076.52	594	602
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	17	17	29	0.03%	15.2%	DVPLTAEEVEFVVEK	99.7%	89.9	25	82.9	2	0	0	1703.87	183	197
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	17	17	29	0.03%	15.2%	EGDLTNLLQNQAVK	99.7%	80.1	25	66.7	2	0	0	1542.81	26	39
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	17	17	29	0.03%	15.2%	ETGHVSGPDGQNPEK	99.7%	45.8	25	43.6	2	0	0	1551.70	855	869
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	17	17	29	0.03%	15.2%	FVSSLLTALFR	99.6%	39.6	25	39.6	1	0	0	1253.73	809	819
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	17	17	29	0.03%	15.2%	GSPCSEEAGTLR	99.7%	57.7	25	57.7	1	0	0	1263.56	53	64
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	17	17	29	0.03%	15.2%	IFQNLCDITR	99.7%	54.2	25	36.8	1	0	0	1279.65	870	879
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	17	17	29	0.03%	15.2%	IFSAVQQFYQPK	99.7%	64.6	25	46.6	2	0	0	1455.76	915	926
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	17	17	29	0.03%	15.2%	IQQFLR	96.0%	29.1	25	0	2	0	0	804.47	927	932
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	17	17	29	0.03%	15.2%	SADFSQSTSIGIK	99.7%	71.9	25	65.8	2	0	0	1340.67	726	738
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	17	17	29	0.03%	15.2%	SAVAGFLLLLK	99.7%	84.5	25	84.5	2	0	0	1131.71	535	545
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	17	17	29	0.03%	15.2%	SISLLCLEGLQK	99.7%	66.3	25	39.6	2	0	0	1360.75	903	914
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	17	17	29	0.03%	15.2%	SLLNLLSSQEEDFNSK	99.7%	90.3	25	89.5	2	0	0	1823.90	965	980
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	17	17	29	0.03%	15.2%	TAAPTVCLLVLSQAEK	99.7%	85.8	25	85.8	2	0	0	1700.93	1079	1094
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	17	17	29	0.03%	15.2%	TIETSPSLSR	96.8%	30	25	20.1	2	0	0	1090.57	403	412
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	17	17	29	0.03%	15.2%	VLEEVDWLITK	98.2%	32.4	25	5.89	1	0	0	1344.74	1095	1105
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	17	17	29	0.03%	15.2%	YAVNVALQK	99.7%	44.5	25	39.3	2	0	0	1005.57	841	849
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	37	0.04%	34.1%	AAQVMGPPDR	99.7%	60.5	25	55.7	3	0	0	1057.51	300	309
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	37	0.04%	34.1%	AEGFVDALHR	99.7%	52.1	25	45.1	2	0	0	1114.56	16	25
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	37	0.04%	34.1%	DGFGGLAAAR	99.7%	59.1	25	20.8	2	0	0	934.47	328	337
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	37	0.04%	34.1%	EMVLEIIR	99.7%	51	25	0	4	0	0	1002.57	226	233
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	37	0.04%	34.1%	FAVGIVIGR	99.7%	64.7	25	50.4	2	0	0	931.57	263	271
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	37	0.04%	34.1%	GDWSVGAPGGVQEITYTVPADK	99.7%	64.2	25	61.7	2	0	0	2247.09	344	365
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	37	0.04%	34.1%	GVPQQIEVAR	99.7%	45.2	25	35.2	2	0	0	1096.61	409	418
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	37	0.04%	34.1%	IDSIPHLNNSTPLVDPSVYGYGVQK	99.7%	36	25	36	0	1	0	2713.38	33	57
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	37	0.04%	34.1%	IQFKPDDGISPER	99.7%	52.3	25	42.4	2	2	0	1501.76	287	299
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	37	0.04%	34.1%	LLGQIVDR	99.7%	49.4	25	38.3	2	0	0	913.55	140	147
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	37	0.04%	34.1%	MGGGSIEVSVPR	99.7%	83.8	25	76.5	4	0	0	1204.60	251	262
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	37	0.04%	34.1%	MVGFIIGR	99.7%	40.1	25	37.2	2	0	0	908.50	88	95
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	37	0.04%	34.1%	MVMIQDGPLPTGADKPLR	99.7%	38.4	25	38.4	0	2	0	1939.01	196	213
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	37	0.04%	34.1%	RPLDDGVGNQLGALVHQR	99.7%	66.6	25	66.6	0	2	0	1945.04	58	75
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	15	18	37	0.04%	34.1%	SINQQSGAHVELQR	99.7%	66.3	25	65.1	3	0	0	1566.80	379	392
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	6	10	20	0.02%	17.4%	ATPEQYQILK	99.7%	63.2	25	56.5	2	0	0	1190.64	344	353
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	6	10	20	0.02%	17.4%	CSWLVVQCLQR	99.7%	70	25	60.3	2	0	0	1448.71	333	343
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	6	10	20	0.02%	17.4%	IGTDIQDNK	99.7%	53.5	25	32.9	2	0	0	1003.51	324	332
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	6	10	20	0.02%	17.4%	LKEVLEYNAIGGK	99.7%	77.2	25	62.1	2	2	0	1433.80	111	123
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	6	10	20	0.02%	17.4%	QDFVQHFSQIVR	99.7%	41	25	36	0	2	0	1503.77	81	92
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	6	10	20	0.02%	17.4%	VLTEDEMGHPEIGDAIAR	99.7%	68.9	25	62	4	4	0	1968.93	93	110
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	5	6	11	0.01%	13.7%	AHPVFYQGTYSQALNDAKR	96.7%	24.4	25	24.4	0	1	0	2166.07	150	168
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	5	6	11	0.01%	13.7%	DLTQEQTEK	99.7%	43.8	25	28.2	2	0	0	1091.52	8	16
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	5	6	11	0.01%	13.7%	FQIEANFPR	99.7%	43.4	25	20	2	0	0	1121.57	401	409
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	5	6	11	0.01%	13.7%	IYSYVVSRPQPR	99.7%	34.1	25	32.9	2	2	0	1464.80	78	89
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	5	6	11	0.01%	13.7%	QQQDEAYLASLR	99.7%	87.9	25	77.7	2	0	0	1421.70	291	302
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	4	4	6	0.01%	8.6%	DIISELLTSDDMK	99.7%	58.6	25	46	2	0	0	1495.72	523	535
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	4	4	6	0.01%	8.6%	IYSVEALPVAAVNVQSTQ	99.7%	86.5	25	80.2	1	0	0	1889.00	693	710
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	4	4	6	0.01%	8.6%	NQVLPLSDVDTTSATDIQR	99.7%	126	25	126	1	0	0	2073.05	615	633
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	4	4	6	0.01%	8.6%	SAYCLGSSHPR	99.7%	42.1	25	35.6	2	0	0	1234.56	642	652
FAST kinase domain-containing protein 5	FASTKD5	FAKD5_HUMAN	86.6	99.8%	2	2	3	0.00%	3.0%	AAVPLGGFLCNVADK	99.7%	49	25	43.8	2	0	0	1531.79	661	675

FAST kinase domain-containing protein 5	FASTKD5	FAKD5_HUMAN	86.6	99.8%	2	2	3	0.00%	3.0%	LAVQFTNR	99.7%	48.1	25	27.4	1	0	0	948.53	697	704
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	18	18	34	0.03%	7.8%	AALQEELQLCK	99.7%	46.8	25	29.2	2	0	0	1302.67	1132	1142
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	18	18	34	0.03%	7.8%	ADEASELACPTPK	99.7%	62.2	25	62.2	1	0	0	1388.64	2194	2206
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	18	18	34	0.03%	7.8%	AGLYGLPR	99.6%	40	25	35.3	2	0	0	846.48	42	49
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	18	18	34	0.03%	7.8%	AQVADVVVSR	99.7%	65.4	25	46.3	1	0	0	1043.58	1073	1082
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	18	18	34	0.03%	7.8%	EDGLAQQQTQLNLR	99.7%	63.6	25	58	2	0	0	1613.82	2207	2220
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	18	18	34	0.03%	7.8%	FDASFFGVHPK	99.7%	54.5	25	45.5	2	0	0	1251.62	60	70
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	18	18	34	0.03%	7.8%	GLVQALQTK	99.7%	53.5	25	34.3	2	0	0	957.57	1143	1151
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	18	18	34	0.03%	7.8%	HGLYLPTR	97.4%	30.9	25	28.6	1	0	0	956.53	1044	1051
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	18	18	34	0.03%	7.8%	LLEQGLR	94.7%	28.1	25	0	1	0	0	828.49	437	443
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	18	18	34	0.03%	7.8%	LPEDPLLSGLLDSPALK	99.7%	73.8	25	73.8	3	0	0	1778.00	1209	1225
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	18	18	34	0.03%	7.8%	LQVVDQPLPVR	99.7%	56.4	25	56.4	2	0	0	1263.74	374	384
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	18	18	34	0.03%	7.8%	QEPLLIGSTK	95.8%	29	25	27.8	1	0	0	1085.62	317	326
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	18	18	34	0.03%	7.8%	SDEAVKPFGLK	99.7%	41.5	25	35.2	2	0	0	1190.64	523	533
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	18	18	34	0.03%	7.8%	SEGVVAVLLTK	99.7%	59.9	25	55	2	0	0	1115.67	225	235
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	18	18	34	0.03%	7.8%	SFYGSTLFLCR	99.7%	59.3	25	50	2	0	0	1350.65	1394	1404
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	18	18	34	0.03%	7.8%	TGTVSLEVR	99.7%	58.5	25	50.2	2	0	0	961.53	928	936
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	18	18	34	0.03%	7.8%	VLEALLPLK	99.7%	53	25	53	2	0	0	995.65	2383	2391
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	18	18	34	0.03%	7.8%	VVVQVLAEEPEAVLK	99.7%	85.7	25	61	4	0	0	1622.94	1852	1866
Fermitin family homolog 2	FERMT2	FERM2_HUMAN	77.9	99.8%	2	2	2	0.00%	3.5%	GCEVTPDVNISGQK	99.7%	46.2	25	45.3	1	0	0	1503.71	425	438
Fermitin family homolog 2	FERMT2	FERM2_HUMAN	77.9	99.8%	2	2	2	0.00%	3.5%	YYSFFDLNPK	99.7%	61.7	25	53.9	1	0	0	1293.62	276	285
Filaggrin-2	FLG2	FILA2_HUMAN	248.1	99.8%	2	2	6	0.01%	1.0%	FSNSSSSNEFSK	99.1%	35.3	25	35.3	2	0	0	1320.57	404	415
Filaggrin-2	FLG2	FILA2_HUMAN	248.1	99.8%	2	2	6	0.01%	1.0%	SVVTVIDVFYK	99.7%	50	25	45	4	0	0	1269.71	7	17
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	27	0.03%	9.3%	AFGPGLQGGSAGSPAR	99.7%	66.6	25	66.6	2	0	0	1429.72	1072	1087
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	27	0.03%	9.3%	AGVAPLQVK	94.9%	28.2	25	20.9	1	0	0	882.54	1478	1486
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	27	0.03%	9.3%	ALTQTGGPHVK	99.5%	38.8	25	32.8	2	0	0	1108.61	1284	1294
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	27	0.03%	9.3%	AWGPGLEGGVVGK	99.7%	50.4	25	43.8	2	0	0	1226.65	581	593
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	27	0.03%	9.3%	DAPQDFHPDR	97.5%	31	25	29.5	1	0	0	1197.53	665	674
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	27	0.03%	9.3%	EGPYSISVLYGDEEVPR	99.7%	70.8	25	70.8	1	0	0	1909.92	1516	1532
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	27	0.03%	9.3%	LLGWIQNK	99.0%	34.8	25	25.2	1	0	0	971.57	172	179
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	27	0.03%	9.3%	LPQLPITNFSR	97.8%	31.5	25	22.2	2	0	0	1285.73	180	190
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	27	0.03%	9.3%	LSPFMADIR	97.1%	30.5	25	22.2	1	0	0	1049.54	656	664
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	27	0.03%	9.3%	SPFSVAVSPSLDLSK	99.7%	57.9	25	51.7	2	0	0	1533.82	959	973
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	27	0.03%	9.3%	TGVELGKPTHFTVNAK	99.3%	30.5	25	30.5	0	2	0	1698.92	885	900
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	27	0.03%	9.3%	TPCEEILVK	98.5%	33.2	25	23	1	0	0	1088.57	2599	2607
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	27	0.03%	9.3%	VANPSGNLTETYVQDR	99.7%	85.2	25	85.2	1	0	0	1763.86	1297	1312
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	27	0.03%	9.3%	VNVGAGSHPNK	99.0%	35.2	25	30.9	2	0	0	1079.56	761	771
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	27	0.03%	9.3%	VPVHDVTDASK	99.7%	47.6	25	38.7	1	0	0	1167.60	1440	1450
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	27	0.03%	9.3%	VTAQGPGLEPSGNIANK	99.7%	90.4	25	87.8	2	0	0	1652.86	384	400
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	27	0.03%	9.3%	VTVLFAGQHIAK	99.7%	49.4	25	45.8	1	0	0	1283.75	356	367
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	27	0.03%	9.3%	YGGDEIPFSPYR	99.7%	42.1	25	24.8	1	0	0	1400.65	1622	1633
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	19	19	27	0.03%	9.3%	YTPVQQGPVGVNVTYGGDPIPK	99.7%	63.5	25	63.5	1	0	0	2286.18	937	958
Flap endonuclease 1	FEN1	FEN1_HUMAN	42.6	100.0%	3	4	7	0.01%	10.0%	KLPIQEFHLSR	99.4%	31.4	25	30.5	0	2	0	1367.78	201	211
Flap endonuclease 1	FEN1	FEN1_HUMAN	42.6	100.0%	3	4	7	0.01%	10.0%	LIADVAPSAIR	99.7%	52.3	25	39.9	2	0	0	1125.66	9	19
Flap endonuclease 1	FEN1	FEN1_HUMAN	42.6	100.0%	3	4	7	0.01%	10.0%	QLQQAQAAGAEQEVEK	99.7%	123	25	116	2	1	0	1727.86	110	125
Fragile X mental retardation protein 1	FMR1	FMR1_HUMAN	71.2	100.0%	4	4	7	0.01%	10.3%	EDLMGLAIGTHGANIQQAR	99.7%	48.2	25	39.7	0	1	0	1995.01	227	245
Fragile X mental retardation protein 1	FMR1	FMR1_HUMAN	71.2	100.0%	4	4	7	0.01%	10.3%	ENSTHFSQPNSTK	99.7%	47.2	25	33.9	1	0	0	1476.67	360	372
Fragile X mental retardation protein 1	FMR1	FMR1_HUMAN	71.2	100.0%	4	4	7	0.01%	10.3%	LDVPEDLR	95.6%	28.8	25	12.1	2	0	0	956.50	131	138
Fragile X mental retardation protein 1	FMR1	FMR1_HUMAN	71.2	100.0%	4	4	7	0.01%	10.3%	LIQEIVDK	99.1%	35.7	25	22.1	2	0	0	957.56	303	310
Fragile X mental retardation protein 1	FMR1	FMR1_HUMAN	71.2	100.0%	4	4	7	0.01%	10.3%	LQIDEQLR	99.7%	47.4	25	36.3	2	0	0	1014.56	435	442
Fragile X mental retardation protein 1	FMR1	FMR1_HUMAN	71.2	100.0%	4	4	7	0.01%	10.3%	VRIEAENEK	99.7%	40.5	25	26.2	2	0	0	1087.57	316	324

Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	11	12	19	0.02%	22.9%	AGYSTDESSSSSLHATR	99.7%	85.1	25	76.1	1	1	0	1755.78	407	423
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	11	12	19	0.02%	22.9%	EDLMGLAIGTHGANIQQAR	99.7%	48.2	25	39.7	0	1	0	1995.01	237	255
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	11	12	19	0.02%	22.9%	EEGMVPFIFVGTR	99.7%	49.3	25	48.1	2	0	0	1497.74	339	351
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	11	12	19	0.02%	22.9%	IYGETPEACR	99.7%	50	25	39.7	2	0	0	1195.54	274	283
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	11	12	19	0.02%	22.9%	LQIDEQLR	99.7%	47.4	25	36.3	2	0	0	1014.56	379	386
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	11	12	19	0.02%	22.9%	LRPVNPNPLATK	99.7%	49	25	49	2	0	0	1319.78	122	133
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	11	12	19	0.02%	22.9%	SYLEFSEDSVQVPR	99.7%	53.9	25	51.6	2	0	0	1655.79	287	300
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	11	12	19	0.02%	22.9%	TDGSISGDRQPVTVADYISR	99.7%	60.1	25	60.1	0	1	0	2137.05	598	617
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	11	12	19	0.02%	22.9%	TGGPAYGPSSDVSTASETESEKR	99.7%	64.8	25	64.7	0	2	0	2313.05	438	460
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	11	12	19	0.02%	22.9%	VIQEIVDK	99.3%	36.8	25	21	2	0	0	943.55	313	320
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	11	12	19	0.02%	22.9%	VTMAVPEDLR	99.7%	52	25	38.4	1	0	0	1130.59	139	148
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	6	6	9	0.01%	21.2%	AAQEEYVKR	99.7%	70.3	25	60.6	2	0	0	1093.56	323	331
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	6	6	9	0.01%	21.2%	ADDGRPFPQVIK	99.7%	45.3	25	31.6	1	0	0	1342.71	88	99
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	6	6	9	0.01%	21.2%	ALQASALK	94.6%	28	25	0	1	0	0	801.48	305	312
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	6	6	9	0.01%	21.2%	GILAADESTGSIAK	99.7%	83.1	25	81.4	2	0	0	1332.70	29	42
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	6	6	9	0.01%	21.2%	PYQYPALTPEQK	99.7%	45.8	25	36.9	1	0	0	1434.73	2	13
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	6	6	9	0.01%	21.2%	YTPSGQAGAAASESLFVSNHAY	99.7%	117	25	117	2	0	0	2228.03	343	364
Fumarylacetoacetate hydrolase domain-containing protein 2A	FAHD2A	FAH2A_HUMAN	34.6	100.0%	3	3	5	0.00%	14.3%	ATDAMAHVAGFTVAHDVSAR	99.7%	49.3	25	49.3	0	1	0	2026.98	175	194
Fumarylacetoacetate hydrolase domain-containing protein 2A	FAHD2A	FAH2A_HUMAN	34.6	100.0%	3	3	5	0.00%	14.3%	DSVADPHNLK	99.7%	42.3	25	36.4	2	0	0	1095.54	225	234
Fumarylacetoacetate hydrolase domain-containing protein 2A	FAHD2A	FAH2A_HUMAN	34.6	100.0%	3	3	5	0.00%	14.3%	TFDTFCPLGPALVTK	99.7%	73	25	67	2	0	0	1666.85	210	224
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	10	11	18	0.02%	29.3%	AFREEFGAEPELAVSAPGR	99.7%	50.8	25	47.9	1	1	0	2033.01	19	37
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	10	11	18	0.02%	29.3%	EEFGAEPELAVSAPGR	99.7%	71.7	25	71.7	2	0	0	1658.80	22	37
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	10	11	18	0.02%	29.3%	EVQLEELEAAR	99.7%	94.6	25	84.4	2	0	0	1286.66	257	267
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	10	11	18	0.02%	29.3%	GHALLIDCR	99.7%	48.7	25	46.4	2	0	0	1054.55	196	204
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	10	11	18	0.02%	29.3%	HSLASSEYPVR	99.7%	54.8	25	45.8	2	0	0	1245.62	229	239
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	10	11	18	0.02%	29.3%	KDGLVSLLTTSEGADEPQR	99.7%	97.6	25	89.6	1	0	0	2016.02	69	87
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	10	11	18	0.02%	29.3%	LAVLITNSNVR	97.6%	31.3	25	21.3	1	0	0	1199.71	218	228
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	10	11	18	0.02%	29.3%	LQFPLPTAQR	99.5%	37.8	25	22.7	2	0	0	1170.66	88	97
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	10	11	18	0.02%	29.3%	QPQVAELLAEAR	99.7%	73.4	25	70.3	2	0	0	1324.72	6	17
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	10	11	18	0.02%	29.3%	SLETSLVPLSDPK	99.7%	71.3	25	71.3	2	0	0	1385.75	205	217
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	5	5	8	0.01%	6.2%	AASAPYFEVLEK	99.7%	40.1	25	38.5	1	0	0	1324.68	382	393
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	5	5	8	0.01%	6.2%	NLDPLVYLLSK	99.7%	63.8	25	62.4	2	0	0	1274.74	77	87
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	5	5	8	0.01%	6.2%	VLLDFLMEEK	99.7%	55.7	25	42.3	2	0	0	1236.65	498	507
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	5	5	8	0.01%	6.2%	WPLSLIINR	99.7%	47.2	25	47.2	2	0	0	1111.66	624	632
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	5	5	8	0.01%	6.2%	YTIVQQQIPSFLQK	99.7%	88.3	25	87.9	1	0	0	1692.93	432	445
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	5	5	11	0.01%	13.7%	FYQASTSELYGK	99.7%	65.4	25	53.6	3	0	0	1393.66	150	161
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	5	5	11	0.01%	13.7%	GYEVHGIVR	99.6%	39.7	25	36.8	2	0	0	1029.55	47	55
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	5	5	11	0.01%	13.7%	LHYGDLTDSTCLVK	99.7%	63.4	25	57.6	2	0	0	1621.79	82	95
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	5	5	11	0.01%	13.7%	VAFDELVR	99.7%	43.5	25	34.2	2	0	0	948.51	349	356
GDP-mannose 4,6 dehydratase	GMDS	GMDS_HUMAN	42.0	100.0%	5	5	11	0.01%	13.7%	VHVTVDLK	99.5%	38.7	25	29	2	0	0	910.54	315	322
Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	3	3	3	0.00%	3.7%	ALEDITASIAMAVIQQK	99.7%	41.3	25	41	1	0	0	1817.97	398	414
Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	3	3	3	0.00%	3.7%	LVIVHPEVTVK	94.7%	22.7	25	17.3	0	1	0	1233.76	552	562
Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	3	3	3	0.00%	3.7%	SIAEGIGPEER	99.7%	52.1	25	46.7	1	0	0	1157.58	1037	1047
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	8	8	15	0.01%	6.3%	GVLQTAAER	99.7%	50.9	25	26.9	2	0	0	944.52	934	942
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	8	8	15	0.01%	6.3%	LSGEAFDINK	99.7%	49.7	25	41	2	0	0	1093.55	515	524
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	8	8	15	0.01%	6.3%	SIFSLDTPEQYQEAFQK	99.6%	38.9	25	38.9	1	0	0	2030.97	1166	1182
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	8	8	15	0.01%	6.3%	SLEAFFLYGR	99.7%	61.4	25	57.8	5	0	0	1202.62	1275	1284
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	8	8	15	0.01%	6.3%	TVIESSPESPVTITEPYR	99.7%	71.3	25	71.3	1	0	0	2005.01	616	633
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	8	8	15	0.01%	6.3%	VIGELVGHTER	99.7%	50.3	25	46.7	1	0	0	1209.66	56	66
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	8	8	15	0.01%	6.3%	VYEAVELLK	98.9%	34.4	25	29.2	1	0	0	1063.60	991	999
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	8	8	15	0.01%	6.3%	YPSATNNTPAK	99.7%	41.3	25	27	2	0	0	1163.57	1188	1198

General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	7	7	12	0.01%	3.4%	DMLTQTYDLIER	99.7%	59	25	53.6	2	0	0	1497.73	367	378
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	7	7	12	0.01%	3.4%	IASNVLNTK	98.7%	34	25	23.3	2	0	0	959.55	1278	1286
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	7	7	12	0.01%	3.4%	NLIIEAVTNLR	99.7%	51.2	25	47.8	2	0	0	1255.74	619	629
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	7	7	12	0.01%	3.4%	NLSEEGLLR	99.6%	40	25	30.9	2	0	0	1030.55	665	673
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	7	7	12	0.01%	3.4%	NPQAYLNYK	99.7%	40.6	25	40.6	1	0	0	1110.56	1326	1334
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	7	7	12	0.01%	3.4%	VCLAEVYQDK	98.9%	34.7	25	28	2	0	0	1224.59	1335	1344
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	7	7	12	0.01%	3.4%	VLAIGDEKDQTR	99.7%	41.4	25	33.4	1	0	0	1344.71	1402	1413
General transcription factor 3C polypeptide 2	GTF3C2	TF3C2_HUMAN	100.7	100.0%	3	3	4	0.00%	3.3%	DLDRPESQSPK	99.1%	35.5	25	28.1	1	0	0	1271.62	159	169
General transcription factor 3C polypeptide 2	GTF3C2	TF3C2_HUMAN	100.7	100.0%	3	3	4	0.00%	3.3%	EGLPEDGTLYR	98.5%	33.3	25	28.6	1	0	0	1249.61	363	373
General transcription factor 3C polypeptide 2	GTF3C2	TF3C2_HUMAN	100.7	100.0%	3	3	4	0.00%	3.3%	SPLFSVQR	99.7%	52.6	25	38.8	2	0	0	933.52	355	362
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	4	4	7	0.01%	5.5%	AIFAVLTSVLTK	99.7%	100	25	100	2	0	0	1262.77	611	622
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	4	4	7	0.01%	5.5%	ELEYFGLSAAILDK	99.7%	66.4	25	45.7	2	0	0	1568.82	667	680
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	4	4	7	0.01%	5.5%	ISFEEFER	96.7%	30	25	23.8	1	0	0	1056.50	16	23
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	4	4	7	0.01%	5.5%	ISLSTLQQQLGQPEK	99.7%	57.6	25	48.1	2	0	0	1669.91	494	508
General transcription factor 3C polypeptide 4	GTF3C4	TF3C4_HUMAN	92.0	99.9%	2	2	3	0.00%	3.2%	NEAPEGNLGDFAEFQR	99.7%	61.9	25	61.8	1	0	0	1793.81	226	241
General transcription factor 3C polypeptide 4	GTF3C4	TF3C4_HUMAN	92.0	99.9%	2	2	3	0.00%	3.2%	NYQVQFVTLK	99.7%	51.7	25	51.7	2	0	0	1239.67	507	516
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	9	10	15	0.01%	20.6%	DPYCHPVCANR	97.5%	31	25	29.4	1	0	0	1388.58	68	78
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	9	10	15	0.01%	20.6%	EGYNNPPISGENLIGLSR	99.7%	63.7	25	62.1	1	0	0	1929.97	192	209
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	9	10	15	0.01%	20.6%	FSTSSLLLR	99.7%	53.9	25	40.5	2	0	0	1023.58	79	87
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	9	10	15	0.01%	20.6%	HGYAPSDLPVK	99.7%	41	25	40.4	2	0	0	1183.61	329	339
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	9	10	15	0.01%	20.6%	IYQVLDFR	99.7%	53.6	25	45.3	2	0	0	1053.57	315	322
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	9	10	15	0.01%	20.6%	LDAPVDYFYRPETQHR	98.8%	28.4	25	28.4	0	1	0	2006.97	176	191
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	9	10	15	0.01%	20.6%	LKDSVYIFR	97.9%	31.7	25	31.7	1	0	0	1140.64	388	396
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	9	10	15	0.01%	20.6%	MLPTLGGEEGVSR	99.7%	58.9	25	49.9	3	0	0	1361.67	39	51
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	9	10	15	0.01%	20.6%	STYNYSLPITVK	99.7%	45.2	25	41.6	2	0	0	1385.73	343	354
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	DSEQVAELKQELATLK	99.7%	70.8	25	68.3	2	0	0	1801.95	783	798
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	EQDDLLVLLADQDQK	99.7%	102	25	77.6	2	0	0	1742.88	905	919
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	EQDLQLEELR	96.3%	29.4	25	3.82	1	0	0	1272.64	661	670
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	GVMGGQSAGPQHTEAETIQK	99.1%	29.6	25	29.6	0	1	0	2041.96	6	25
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	IVAFENAFER	99.7%	70.4	25	68.5	2	0	0	1195.61	203	212
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	LMDLLADSR	99.7%	72.5	25	54.4	4	0	0	1033.53	171	179
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	LSALLQETK	99.7%	51.4	25	41.8	2	0	0	1002.58	850	858
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	NDGVLLLQALTR	99.7%	109	25	99.5	2	0	0	1312.76	184	195
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	NQELLQSQLTEK	99.7%	59.2	25	53.8	1	0	0	1430.75	745	756
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	QSEDLGSQFTEIFIK	99.7%	112	25	111	2	0	0	1741.86	105	119
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	SQLNSQSVEITK	99.7%	63.5	25	60	2	0	0	1333.70	799	810
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	SSQTSGTNEQSSAIVSAR	99.7%	132	25	119	1	0	0	1809.86	765	782
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	SVEVQGETETIIATK	99.7%	102	25	88	2	0	0	1604.84	828	842
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	VASSTLLDDRR	95.5%	28.7	25	15.4	1	0	0	1232.66	30	40
Glucose-6-phosphate isomerase	GPI	G6PI_HUMAN	63.1	99.8%	2	2	3	0.00%	5.7%	TLAQLNPESSLFIIASK	99.2%	36.3	25	36.3	1	0	0	1832.02	195	211
Glucose-6-phosphate isomerase	GPI	G6PI_HUMAN	63.1	99.8%	2	2	3	0.00%	5.7%	VFEGNRPTNSIVFTK	97.6%	31.3	25	17.4	2	0	0	1708.90	467	481
Glutamate--cysteine ligase regulatory subunit	GCLM	GSH0_HUMAN	30.7	99.8%	2	2	2	0.00%	9.1%	INPDEREEMK	98.0%	32.1	25	32.1	1	0	0	1260.59	81	90
Glutamate--cysteine ligase regulatory subunit	GCLM	GSH0_HUMAN	30.7	99.8%	2	2	2	0.00%	9.1%	TLNEWSSQINPDLVR	99.7%	43.4	25	41.6	1	0	0	1771.90	50	64
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	6	6	11	0.01%	14.1%	AQTGAPCLSFDIVR	99.7%	55.7	25	54.9	2	0	0	1534.77	60	73
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	6	6	11	0.01%	14.1%	EPFLLSGGDDGALK	99.7%	41.7	25	38	2	0	0	1418.72	320	333
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	6	6	11	0.01%	14.1%	GQVEVFALR	99.7%	54.8	25	44.1	2	0	0	1018.57	173	181
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	6	6	11	0.01%	14.1%	LLQVVEEPQALAAFLR	99.7%	98.9	25	93.6	2	0	0	1797.03	183	198
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	6	6	11	0.01%	14.1%	REPFLLSGGDDGALK	99.7%	49.5	25	48.1	0	2	0	1574.82	319	333
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	6	6	11	0.01%	14.1%	SGSPVATFK	97.7%	31.5	25	26.7	1	0	0	893.47	342	350
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	6	6	7	0.01%	10.0%	EIFEQPESVVNTMR	99.7%	46.7	25	33.1	1	0	0	1678.81	346	359
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	6	6	7	0.01%	10.0%	EILETLIK	99.7%	42.1	25	31.5	1	0	0	958.58	18	25

Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	6	6	7	0.01%	10.0%	GYDFESETDTETIAK	99.7%	59.5	25	59.5	1	0	0	1705.74	140	154
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	6	6	7	0.01%	10.0%	GYDVDFPR	99.5%	38.4	25	34.9	2	0	0	968.45	683	690
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	6	6	7	0.01%	10.0%	LATELYHQK	99.7%	47.2	25	27.6	1	0	0	1102.59	548	556
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	6	6	7	0.01%	10.0%	VIFLEDDDVAAVVDGR	99.7%	44.4	25	42.8	1	0	0	1732.88	291	306
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	18	29	0.03%	26.5%	AINFNFGYAK	99.7%	50.8	25	37.5	2	0	0	1144.58	283	292
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	18	29	0.03%	26.5%	ANNGICFLR	99.7%	51.2	25	39.2	1	0	0	1064.53	293	301
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	18	29	0.03%	26.5%	ATGILLYGLASR	99.7%	55.4	25	35.5	1	0	0	1234.72	51	62
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	18	29	0.03%	26.5%	DVLNDTAPR	99.7%	41.8	25	34.7	2	0	0	1000.51	559	567
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	18	29	0.03%	26.5%	EAATQAQQTLGSTIDK	99.7%	107	25	106	2	0	0	1661.83	35	50
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	18	29	0.03%	26.5%	FDDTNPEKEEAK	99.7%	76.6	25	68.4	2	0	0	1422.64	302	313
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	18	29	0.03%	26.5%	FSEGEATLR	99.7%	56.8	25	41.2	2	0	0	1009.49	395	403
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	18	29	0.03%	26.5%	GFHQVPFAPIVFIER	99.5%	32.5	25	32.5	0	1	0	1756.95	602	616
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	18	29	0.03%	26.5%	GLAYVCHQR	99.6%	39.7	25	27.4	1	0	0	1103.54	353	361
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	18	29	0.03%	26.5%	GPSGCVESLEVTCR	99.7%	82.2	25	82.2	1	0	0	1550.69	653	666
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	18	29	0.03%	26.5%	HTGYVIELQHVVK	99.7%	53.3	25	53.3	0	2	0	1522.84	640	652
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	18	29	0.03%	26.5%	ILQLVATGAVR	99.7%	77	25	74.9	2	0	0	1140.71	499	509
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	18	29	0.03%	26.5%	LAWGQPVGLR	99.7%	55.9	25	39.7	2	0	0	1096.63	630	639
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	18	29	0.03%	26.5%	LFTLTALR	99.7%	61.4	25	45.1	2	0	0	934.57	516	523
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	18	29	0.03%	26.5%	LGYFSVDPDSHQGK	99.7%	41.8	25	41.8	1	0	0	1549.73	746	759
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	18	29	0.03%	26.5%	LSFLVSYIASK	99.7%	81.3	25	81.3	2	0	0	1227.70	69	79
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	18	29	0.03%	26.5%	NSALSAQLR	99.7%	76.2	25	64.9	2	0	0	959.53	26	34
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	18	18	29	0.03%	26.5%	SHPLDPIDTVDFER	99.7%	71.2	25	70.3	1	0	0	1640.79	96	109
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	9	10	21	0.02%	20.9%	ELRVPLIGSLPEAR	98.0%	32	25	31.1	1	0	0	1549.91	67	80
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	9	10	21	0.02%	20.9%	FLEATLR	99.3%	36.5	25	24.2	2	0	0	849.48	118	124
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	9	10	21	0.02%	20.9%	GLMEPLLPPK	99.2%	36.1	25	22	3	0	0	1110.62	17	26
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	9	10	21	0.02%	20.9%	HLAQLMESIPHSPGPTR	99.7%	35.9	25	35.9	0	2	0	1886.95	242	258
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	9	10	21	0.02%	20.9%	HLTLACHYDSK	99.7%	41.8	25	40.6	2	0	0	1344.64	162	172
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	9	10	21	0.02%	20.9%	KFLEATLR	99.7%	42.3	25	19.4	2	0	0	977.58	117	124
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	9	10	21	0.02%	20.9%	TPGSPGNLQVR	99.7%	69.8	25	54.7	4	0	0	1125.60	106	116
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	9	10	21	0.02%	20.9%	VPLIGSLPEAR	99.7%	58.1	25	58.1	3	0	0	1151.68	70	80
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	9	10	21	0.02%	20.9%	VVGQLDPQR	99.7%	42.1	25	42.1	2	0	0	1011.56	84	92
Glutathione S-transferase kappa 1	GSTK1	GSTK1_HUMAN	25.5	100.0%	3	3	4	0.00%	18.6%	AGMSAEQAQGLLEK	99.7%	80.7	25	70.6	2	0	0	1432.71	145	158
Glutathione S-transferase kappa 1	GSTK1	GSTK1_HUMAN	25.5	100.0%	3	3	4	0.00%	18.6%	DSGNKPPGLLPR	95.6%	28.8	25	28.1	1	0	0	1250.69	50	61
Glutathione S-transferase kappa 1	GSTK1	GSTK1_HUMAN	25.5	100.0%	3	3	4	0.00%	18.6%	NEDITEPQSILAAAEK	99.7%	73.9	25	73	1	0	0	1728.87	129	144
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	11	16	32	0.03%	41.5%	GALQNIIPASTGAAK	99.7%	73.3	25	71.5	5	0	0	1411.79	201	215
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	11	16	32	0.03%	41.5%	IISNASCTTNCLAPLAK	99.7%	108	25	100	2	0	0	1833.92	146	162
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	11	16	32	0.03%	41.5%	LISWYDNEFGYSNR	99.7%	76.1	25	76.1	2	0	0	1763.80	310	323
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	11	16	32	0.03%	41.5%	LTGMAFR	99.2%	35.8	25	28.6	1	0	0	811.41	228	234
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	11	16	32	0.03%	41.5%	LVINGNPITIFQER	99.7%	83.2	25	79.2	2	0	0	1613.90	67	80
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	11	16	32	0.03%	41.5%	LVINGNPITIFQERDPSK	98.0%	26.4	25	24.7	0	2	0	2041.11	67	84
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	11	16	32	0.03%	41.5%	VIISAPSADAPMFVMGVNHEK	99.7%	36.3	25	30.4	0	4	0	2213.11	119	139
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	11	16	32	0.03%	41.5%	VPTANVSVVDLTCR	99.7%	92.6	25	89.5	2	2	0	1530.79	235	248
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	11	16	32	0.03%	41.5%	VVDLMAHMASK	99.7%	57.2	25	44.5	1	0	0	1201.61	324	334
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	11	16	32	0.03%	41.5%	VVDLMAHMASKE	99.7%	64	25	55	6	1	0	1330.65	324	335
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	11	16	32	0.03%	41.5%	WGDAGAEYVVESTGVFTTMEK	99.7%	110	25	110	2	0	0	2277.04	87	107
Glycerol kinase	GK	GLPK3_HUMAN	61.2	99.8%	2	2	2	0.00%	3.6%	FEPQINAEESEIR	99.7%	53.5	25	51	1	0	0	1561.75	493	505
Glycerol kinase	GK	GLPK3_HUMAN	61.2	99.8%	2	2	2	0.00%	3.6%	WLLDNVR	97.6%	31.3	25	7.59	1	0	0	915.50	156	162
Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	GPD1L_HUMAN	38.4	100.0%	5	5	7	0.01%	12.5%	GIDEGPEGLK	96.4%	29.6	25	27.5	2	0	0	1014.51	123	132
Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	GPD1L_HUMAN	38.4	100.0%	5	5	7	0.01%	12.5%	ICDEITGR	99.7%	61.5	25	55.9	1	0	0	963.46	103	110
Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	GPD1L_HUMAN	38.4	100.0%	5	5	7	0.01%	12.5%	KLTDIINNDHENVK	98.7%	28	25	28	0	1	0	1652.86	51	64
Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	GPD1L_HUMAN	38.4	100.0%	5	5	7	0.01%	12.5%	LQGPQTSAEVYR	99.7%	67	25	66.2	2	0	0	1348.69	299	310

Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	GPD1L_HUMAN	38.4	100.0%	5	5	7	0.01%	12.5%	LTDIINNDHENVK	99.7%	43.1	25	36.8	1	0	0	1524.77	52	64
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	3	3	6	0.01%	5.8%	LPFAAAQIGNSFR	99.7%	72.3	25	65.2	2	0	0	1391.74	319	331
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	3	3	6	0.01%	5.8%	SPITGNDLSPPVSFNLMFK	99.7%	41.7	25	41.7	2	0	0	2064.05	265	283
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	3	3	6	0.01%	5.8%	TVNVVQFEPSK	99.7%	59.9	25	52	2	0	0	1247.66	491	501
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	15.4%	DYFFALAHTVR	99.7%	58	25	51	2	0	0	1339.68	51	61
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	15.4%	EYYDHLPELK	97.6%	31.2	25	15.8	1	0	0	1306.63	731	740
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	15.4%	GLAGLGDVAEVR	99.7%	86.6	25	77.6	2	0	0	1156.63	18	29
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	15.4%	IGEEFLTDLSQLK	99.7%	96.2	25	86.2	1	0	0	1492.79	508	520
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	15.4%	IGEEFLTDLSQLKK	99.6%	32.7	25	32.7	0	1	0	1620.88	508	521
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	15.4%	LLPLVSDEVFIR	99.7%	62.3	25	62.3	3	0	0	1400.81	522	533
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	15.4%	LVTSIGDVVNHDPVVGDR	99.7%	41.2	25	41.2	0	2	0	1891.99	623	640
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	15.4%	NLAENISR	99.4%	37.5	25	16.2	3	0	0	916.48	271	278
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	15.4%	VIFLENYR	99.7%	50.4	25	40.5	3	0	0	1053.57	643	650
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	15.4%	VLYPNDNFFEGK	99.7%	51.5	25	49.3	2	0	0	1442.70	279	290
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	15.4%	WLLLCNPGLADTIVEK	99.7%	66.9	25	66.9	2	0	0	1841.98	492	507
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	16	0.02%	15.4%	YEFGIFNQK	99.7%	41.5	25	29.1	2	0	0	1145.56	162	170
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	APNDFNLR	99.7%	44.1	25	29.1	2	0	0	946.47	249	256
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	DFNVGDYIQAVLDR	99.7%	95.9	25	85.2	2	0	0	1624.80	257	270
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	DFSELEPDKFQNK	99.7%	52.2	25	47.2	2	0	0	1596.75	471	483
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	DYYFALAHTVR	99.7%	57.5	25	44.8	2	0	0	1355.67	51	61
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	EYAQNIWNVEPSDLK	99.7%	58	25	53.5	2	0	0	1805.87	820	834
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	EYYEALPELK	99.7%	41.9	25	40.4	2	0	0	1254.63	731	740
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	FSQFLETEYK	99.7%	74.8	25	68.7	2	0	0	1291.62	546	555
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	GIVGVENVAELK	99.7%	51.6	25	39	2	0	0	1227.69	18	29
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	GIVGVENVAELKK	99.7%	73.1	25	69.7	2	0	0	1355.79	18	30
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	HLEIIYEINQK	99.7%	64.6	25	54.4	2	0	0	1399.76	400	410
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	IDDVAALDK	99.7%	41.4	25	30.2	1	0	0	959.50	716	724
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	IDDVAALDKK	99.7%	54.1	25	37.6	2	0	0	1087.60	716	725
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	IFVDIEK	99.2%	36.3	25	24.9	1	0	0	863.49	353	359
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	INPSSMFDVQVK	99.7%	68.9	25	50.5	3	0	0	1364.69	558	569
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	LHSFLGDDVFLR	99.7%	71.9	25	59.7	2	2	0	1418.74	522	533
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	LITSVADVVNNDPMVGSK	99.7%	105	25	102	5	0	0	1874.95	623	640
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	LVIDQIDNGFFSPK	99.7%	83.9	25	83.9	2	0	0	1592.83	741	754
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	MSLIEEEGSKR	99.7%	58.7	25	44.2	2	0	0	1278.64	429	439
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	NLAENISR	99.4%	37.5	25	16.2	3	0	0	916.48	271	278
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	SRPEFMLPVHFYGK	99.7%	36.2	25	28.8	0	4	0	1723.86	193	206
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	TFAYTNHTVLPEALER	99.7%	42.3	25	40.7	0	2	0	1861.94	372	387
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	VFADYEAYVK	99.7%	55.1	25	52	2	0	0	1204.59	774	783
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	VIFLENYR	99.7%	50.4	25	40.5	3	0	0	1053.57	643	650
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	VIPATDLSEQISTAGTEASGTGNMK	99.7%	106	25	106	1	3	0	2478.20	657	681
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	VLYPNDNFFEGK	99.7%	51.5	25	49.3	2	0	0	1442.70	279	290
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	VSQLYMNPK	99.7%	61.2	25	52.7	4	0	0	1079.56	788	796
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	WLLLCNPGLAELIAEK	99.7%	66.2	25	63.9	1	0	0	1840.00	492	507
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	WPVDLVEK	99.2%	36	25	27	2	0	0	985.54	388	395
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	29	36	69	0.07%	38.3%	YEYGIFNQK	99.1%	35.4	25	35.4	2	0	0	1161.56	162	170
Glyoxylate reductase/hydroxypyruvate reductase	GRHPR	GRHPR_HUMAN	35.7	100.0%	3	4	8	0.01%	11.0%	ILDAAGANLK	99.7%	69.3	25	56	2	0	0	985.57	67	76
Glyoxylate reductase/hydroxypyruvate reductase	GRHPR	GRHPR_HUMAN	35.7	100.0%	3	4	8	0.01%	11.0%	NTMSLLAANNLLAGLR	99.7%	88.4	25	75.6	4	0	0	1687.92	303	318
Glyoxylate reductase/hydroxypyruvate reductase	GRHPR	GRHPR_HUMAN	35.7	100.0%	3	4	8	0.01%	11.0%	RLPEAIEEVK	99.7%	46.5	25	31.3	2	0	0	1183.67	125	134
Golgi phosphoprotein 3	GOLPH3	GOLP3_HUMAN	33.8	99.8%	2	2	3	0.00%	9.4%	QLLDLDPEVECLK	99.7%	46.6	25	46.6	1	0	0	1571.80	270	282
Golgi phosphoprotein 3	GOLPH3	GOLP3_HUMAN	33.8	99.8%	2	2	3	0.00%	9.4%	SDAPTGDVLLDEALK	99.7%	108	25	108	2	0	0	1543.79	124	138
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	10	10	16	0.02%	6.2%	AASSSSPGSPVASSPSR	99.7%	50.2	25	50.2	2	0	0	1531.73	1776	1792

Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	10	10	16	0.02%	6.2%	GATPEGIFLR	99.7%	48.7	25	22.6	2	0	0	1060.58	907	916
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	10	10	16	0.02%	6.2%	LLEAFTER	98.7%	33.7	25	21.9	2	0	0	978.53	801	808
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	10	10	16	0.02%	6.2%	LLITGTEQFNQKPK	99.7%	58.2	25	57.9	1	0	0	1616.90	702	715
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	10	10	16	0.02%	6.2%	LMEIITVENPK	99.7%	59.4	25	46.1	2	0	0	1286.70	502	512
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	10	10	16	0.02%	6.2%	LNLYAASLR	95.8%	29	25	29	1	0	0	1020.58	470	478
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	10	10	16	0.02%	6.2%	MQALTYLQR	99.7%	42.1	25	25.5	1	0	0	1123.59	1562	1570
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	10	10	16	0.02%	6.2%	SEDTTGPITGLALTSVNK	99.7%	83.9	25	83.9	2	0	0	1803.93	74	91
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	10	10	16	0.02%	6.2%	SLEETIIQK	99.3%	37	25	29	1	0	0	1060.59	945	953
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	10	10	16	0.02%	6.2%	VLNSLTQQEK	99.6%	39.8	25	31.5	2	0	0	1159.63	596	605
GPI transamidase component PIG-T	PIGT	PIGT_HUMAN	65.7	100.0%	4	4	5	0.00%	7.4%	ALGQLISK	98.7%	33.8	25	24.9	1	0	0	829.51	72	79
GPI transamidase component PIG-T	PIGT	PIGT_HUMAN	65.7	100.0%	4	4	5	0.00%	7.4%	LYVHTLTITSK	99.7%	49	25	43.6	1	0	0	1275.73	395	405
GPI transamidase component PIG-T	PIGT	PIGT_HUMAN	65.7	100.0%	4	4	5	0.00%	7.4%	RPPENEAPPVPFLHAQR	99.3%	30.8	25	30.8	0	1	0	1955.02	340	356
GPI transamidase component PIG-T	PIGT	PIGT_HUMAN	65.7	100.0%	4	4	5	0.00%	7.4%	VSIQFER	99.7%	44.2	25	15.7	2	0	0	878.47	442	448
G-rich sequence factor 1	GRSF1	GRSF1_HUMAN	53.1	99.8%	2	2	4	0.00%	4.6%	SSPVVNDGVVR	99.7%	53.4	25	47.2	2	0	0	1128.60	243	253
G-rich sequence factor 1	GRSF1	GRSF1_HUMAN	53.1	99.8%	2	2	4	0.00%	4.6%	YIELFLNSCPK	99.4%	37.2	25	32.8	2	0	0	1383.70	468	478
Growth arrest and DNA damage-inducible proteins-interacting protein 1	GADD45GIP1	G45IP_HUMAN	25.4	100.0%	3	3	4	0.00%	16.7%	FQELLQDLEK	99.7%	58.5	25	29.1	2	0	0	1262.66	175	184
Growth arrest and DNA damage-inducible proteins-interacting protein 1	GADD45GIP1	G45IP_HUMAN	25.4	100.0%	3	3	4	0.00%	16.7%	LQAEAQELLGYQVDPR	99.2%	36	25	36	1	0	0	1829.94	156	171
Growth arrest and DNA damage-inducible proteins-interacting protein 1	GADD45GIP1	G45IP_HUMAN	25.4	100.0%	3	3	4	0.00%	16.7%	WPDPEDLLTPR	99.6%	39	25	39	1	0	0	1338.67	39	49
GTPase Era, mitochondrial	ERAL1	ERAL1_HUMAN	48.3	100.0%	3	3	4	0.00%	9.4%	EIFMLSALSQEDVK	97.4%	30.9	25	28.5	1	0	0	1609.81	304	317
GTPase Era, mitochondrial	ERAL1	ERAL1_HUMAN	48.3	100.0%	3	3	4	0.00%	9.4%	ETQVILLDTPGIISPGK	99.7%	49.1	25	49.1	1	0	0	1781.01	160	176
GTPase Era, mitochondrial	ERAL1	ERAL1_HUMAN	48.3	100.0%	3	3	4	0.00%	9.4%	STLSNQLLGR	99.7%	72.8	25	31.8	2	0	0	1088.61	127	136
GTPase-activating protein and VPS9 domain-containing protein 1	GAPVD1	GAPD1_HUMAN	165.0	100.0%	2	2	6	0.01%	2.0%	AVETPPLSSVNLLEGLSR	99.7%	65.6	25	65.6	5	0	0	1882.03	387	404
GTPase-activating protein and VPS9 domain-containing protein 1	GAPVD1	GAPD1_HUMAN	165.0	100.0%	2	2	6	0.01%	2.0%	VQEMVESNEAK	96.4%	29.6	25	29.6	1	0	0	1279.58	247	257
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	28	0.03%	50.5%	DGYYIQAQCAIIMFDVTSR	99.7%	86.6	25	86.6	1	0	0	2251.05	77	95
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	28	0.03%	50.5%	FNVWDTAGQEK	99.7%	64.4	25	51.9	4	0	0	1294.61	61	71
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	28	0.03%	50.5%	GPIKFNVWDTAGQEK	99.7%	77	25	76.9	2	2	0	1689.86	57	71
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	28	0.03%	50.5%	HLTGEFEK	98.7%	33.8	25	20.6	1	0	0	960.48	30	37
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	28	0.03%	50.5%	KYVATLGVEVHPLVFHTNR	99.7%	61.4	25	53.2	0	1	0	2180.20	38	56
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	28	0.03%	50.5%	LVLVGDGGTGK	99.7%	88.3	25	25.9	2	0	0	1015.58	13	23
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	28	0.03%	50.5%	NLQYYDISAK	99.7%	51.6	25	47.2	8	0	0	1214.61	143	152
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	28	0.03%	50.5%	SNYNFEKPFLWLAR	99.7%	52.8	25	45.3	1	2	0	1784.91	153	166
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	28	0.03%	50.5%	VCENIPIVLCGNK	99.7%	66.6	25	66.6	2	0	0	1515.77	111	123
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	12	28	0.03%	50.5%	YVATLGVEVHPLVFHTNR	99.7%	45.6	25	45.6	0	2	0	2052.10	39	56
GTP-binding protein 10	GTPBP10	GTPBA_HUMAN	42.9	100.0%	2	2	4	0.00%	5.2%	LLTNFLPLK	99.7%	54.2	25	47	2	0	0	1058.66	127	135
GTP-binding protein 10	GTPBP10	GTPBA_HUMAN	42.9	100.0%	2	2	4	0.00%	5.2%	TAFETIILLTK	99.4%	37.6	25	34.5	2	0	0	1249.74	249	259
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	7	11	17	0.02%	33.7%	ALAESWNAAFLESSAK	99.7%	96.6	25	96.6	2	0	0	1694.84	136	151
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	7	11	17	0.02%	33.7%	ENQTAVDVFR	99.7%	75.6	25	60.4	2	0	0	1178.58	152	161
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	7	11	17	0.02%	33.7%	IAILGYR	94.8%	28.2	25	25.9	1	0	0	805.49	9	15
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	7	11	17	0.02%	33.7%	IILEAEKMDGAASQGK	99.7%	78.1	25	78.1	4	2	0	1660.86	163	178
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	7	11	17	0.02%	33.7%	KIAILGYR	99.7%	43.5	25	28	2	0	0	933.59	8	15
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	7	11	17	0.02%	33.7%	VQIPIMLVGNK	98.2%	32.5	25	25.9	1	0	0	1211.72	110	120
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	7	11	17	0.02%	33.7%	VQIPIMLVGNKK	99.4%	37.6	25	34.5	2	1	0	1355.81	110	121
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	GBB2_HUMAN	37.3	100.0%	5	5	8	0.01%	17.4%	ACGDSTLTQITAGLDPVGR	99.7%	61.6	25	60.3	1	0	0	1931.95	24	42
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	GBB2_HUMAN	37.3	100.0%	5	5	8	0.01%	17.4%	LIIWDSYTTNK	99.7%	61.6	25	56.8	2	0	0	1353.71	79	89
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	GBB2_HUMAN	37.3	100.0%	5	5	8	0.01%	17.4%	LLVSASQDGK	99.7%	66.4	25	61.7	2	0	0	1017.56	69	78
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	GBB2_HUMAN	37.3	100.0%	5	5	8	0.01%	17.4%	TFVSGACDASIK	99.7%	63	25	56.8	2	0	0	1255.60	198	209
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	GBB2_HUMAN	37.3	100.0%	5	5	8	0.01%	17.4%	VHAIPLR	95.4%	28.6	25	28.6	1	0	0	805.50	90	96
Guanine nucleotide-binding protein G(k) subunit alpha	GNAI3	GNAI3_HUMAN	40.5	99.8%	2	2	3	0.00%	10.7%	ISQSNYIPTQQDVLR	99.7%	50.6	25	38.5	2	0	0	1761.91	162	176
Guanine nucleotide-binding protein G(k) subunit alpha	GNAI3	GNAI3_HUMAN	40.5	99.8%	2	2	3	0.00%	10.7%	LLLLGAGESGK	99.7%	73.4	25	0	5	0	0	1057.63	36	46
Guanine nucleotide-binding protein G(k) subunit alpha	GNAI3	GNAI3_HUMAN	40.5	99.8%	2	2	3	0.00%	10.7%	TTGIVETHFTFK	99.7%	48	25	38.2	1	0	0	1380.72	181	192
Guanine nucleotide-binding protein subunit alpha-11	GNA11	GNA11_HUMAN	42.1	100.0%	3	3	6	0.01%	10.9%	IATLGYLPTQQDVLR	99.7%	51.9	25	49.8	2	0	0	1687.94	167	181

Guanine nucleotide-binding protein subunit alpha-11	GNA11	GNA11_HUMAN	42.1	100.0%	3	3	6	0.01%	10.9%	LLLLGTGESGK	99.7%	63.5	25	38	2	0	0	1087.64	42	52
Guanine nucleotide-binding protein subunit alpha-11	GNA11	GNA11_HUMAN	42.1	100.0%	3	3	6	0.01%	10.9%	VTTFEHQYVSAIK	98.6%	33.4	25	33.4	2	0	0	1522.79	121	133
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	50	0.05%	60.3%	DETNYGIPQR	99.7%	68.9	25	58.6	3	0	0	1192.56	48	57
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	50	0.05%	60.3%	DGQAMLWDLNEGK	99.7%	105	25	96.1	4	0	0	1492.67	213	225
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	50	0.05%	60.3%	DKTIIMWK	99.4%	37.6	25	26.2	4	0	0	1034.57	37	44
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	50	0.05%	60.3%	DVLSVAFSSDNR	99.7%	82.2	25	82	5	0	0	1309.64	107	118
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	50	0.05%	60.3%	FSPNSSNPIIVSCGWDK	99.7%	68.7	25	62.6	2	0	0	1907.90	156	172
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	50	0.05%	60.3%	HLYTLDGGDIINALCFSPNR	99.7%	89.8	25	89.8	2	2	0	2276.11	226	245
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	50	0.05%	60.3%	IIVDELKQEVISTSSK	99.7%	104	25	104	5	2	0	1789.00	265	280
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	50	0.05%	60.3%	LTRDETNYGIPQR	99.7%	54.2	25	41.8	2	0	0	1562.79	45	57
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	50	0.05%	60.3%	LWDLTTGTTTR	99.7%	82.7	25	81.9	3	0	0	1264.65	89	99
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	50	0.05%	60.3%	LWNTLGVCK	99.7%	60	25	55.4	3	0	0	1090.57	131	139
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	50	0.05%	60.3%	TNHIGHTGYLNTVTVSPDGSLCASGGK	99.7%	92.7	25	92.1	0	2	0	2743.31	186	212
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	50	0.05%	60.3%	VWNLANCK	99.7%	40.3	25	40.3	1	0	0	1004.50	176	183
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	50	0.05%	60.3%	VWQVTIGTR	99.7%	76	25	68.4	4	0	0	1059.59	309	317
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	50	0.05%	60.3%	YTVQDESHSEWVSCVR	99.7%	96.3	25	96.3	2	2	0	1981.87	140	155
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	15	20	50	0.05%	60.3%	YWLCAATGPSIK	99.7%	73.1	25	66.8	2	0	0	1366.68	246	257
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	7	7	17	0.02%	14.2%	ELPTVVFR	98.8%	34.3	25	31.5	2	0	0	960.55	198	205
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	7	7	17	0.02%	14.2%	GGIPNVEGAAK	99.6%	39.6	25	35.5	2	0	0	1012.54	378	388
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	7	7	17	0.02%	14.2%	KDPGVPNSAPFK	99.2%	36.3	25	32.7	2	0	0	1256.66	46	57
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	7	7	17	0.02%	14.2%	LLGGFQETCSK	99.7%	56.2	25	56.2	2	0	0	1239.60	243	253
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	7	7	17	0.02%	14.2%	SGFNLEELEK	99.7%	57.3	25	45.2	2	0	0	1165.57	425	434
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	7	7	17	0.02%	14.2%	VGVIGFPNVGK	99.7%	50.6	25	40.1	5	0	0	1086.63	257	267
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	7	7	17	0.02%	14.2%	VIEASDVVLEVLDAR	99.7%	57.6	25	51.3	2	0	0	1627.89	137	151
H/ACA ribonucleoprotein complex subunit 1	GAR1	GAR1_HUMAN	22.3	100.0%	3	3	5	0.00%	10.6%	DFYFSVK	95.5%	28.7	25	20.6	1	0	0	905.44	122	128
H/ACA ribonucleoprotein complex subunit 1	GAR1	GAR1_HUMAN	22.3	100.0%	3	3	5	0.00%	10.6%	FYIDPYK	99.6%	39.1	25	34.7	2	0	0	945.47	144	150
H/ACA ribonucleoprotein complex subunit 1	GAR1	GAR1_HUMAN	22.3	100.0%	3	3	5	0.00%	10.6%	VDEIFGQLR	99.7%	65.8	25	50.7	2	0	0	1076.57	113	121
H/ACA ribonucleoprotein complex subunit 2	NHP2	NHP2_HUMAN	17.2	99.8%	2	3	11	0.01%	19.0%	NLPYVYIPSK	99.7%	42.8	25	35.5	3	0	0	1193.66	102	111
H/ACA ribonucleoprotein complex subunit 2	NHP2	NHP2_HUMAN	17.2	99.8%	2	3	11	0.01%	19.0%	TYQELLVNQNPIAQPLASR	99.7%	76.1	25	75.4	4	4	0	2155.15	23	41
H/ACA ribonucleoprotein complex subunit 3	NOP10	NOP10_HUMAN	7.7	100.0%	2	3	5	0.00%	37.5%	MFLQYYLNEQGDR	98.2%	32.4	25	32.4	1	0	0	1692.77	1	13
H/ACA ribonucleoprotein complex subunit 3	NOP10	NOP10_HUMAN	7.7	100.0%	2	3	5	0.00%	37.5%	VLMTQQPRPVL	99.4%	37.8	25	37.8	4	0	0	1297.73	54	64
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	10	11	18	0.02%	19.6%	APQVVAEAAK	99.7%	44.6	25	38	2	0	0	983.55	434	443
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	10	11	18	0.02%	19.6%	DSAVNAICYGAK	99.7%	58.8	25	52.9	2	0	0	1268.59	303	314
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	10	11	18	0.02%	19.6%	EIGDYIR	99.4%	37.3	25	23.3	1	0	0	865.44	82	88
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	10	11	18	0.02%	19.6%	EVVAEVVK	99.7%	44.4	25	36.4	2	0	0	872.51	426	433
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	10	11	18	0.02%	19.6%	HGKPTDSTPATWK	99.7%	48.6	25	48.6	1	2	0	1425.71	401	413
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	10	11	18	0.02%	19.6%	IMLPGVLR	98.1%	32.2	25	17.5	2	0	0	914.55	315	322
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	10	11	18	0.02%	19.6%	LDTSQWPLLLK	99.7%	84.2	25	74.7	2	0	0	1313.75	47	57
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	10	11	18	0.02%	19.6%	LHNAIEGGTQLSR	99.7%	84	25	83.5	2	0	0	1395.73	159	171
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	10	11	18	0.02%	19.6%	QEYVDYSESAK	97.8%	31.6	25	31.6	1	0	0	1318.58	414	424
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	10	11	18	0.02%	19.6%	RVVYPLEK	94.7%	28	25	7.75	1	0	0	1003.59	284	291
HCLS1-associated protein X-1	HAX1	HAX1_HUMAN	31.6	100.0%	6	7	12	0.01%	27.2%	FHDNFGFDDLVR	99.7%	41.2	25	34.9	2	1	0	1481.68	75	86
HCLS1-associated protein X-1	HAX1	HAX1_HUMAN	31.6	100.0%	6	7	12	0.01%	27.2%	GFFGFPGPR	99.7%	43.3	25	28.2	2	0	0	981.49	9	17
HCLS1-associated protein X-1	HAX1	HAX1_HUMAN	31.6	100.0%	6	7	12	0.01%	27.2%	IFGGVLESDAR	99.7%	95.8	25	78.9	2	0	0	1163.61	140	150
HCLS1-associated protein X-1	HAX1	HAX1_HUMAN	31.6	100.0%	6	7	12	0.01%	27.2%	ITKPDGIVEER	99.7%	40.1	25	33.5	1	0	0	1256.68	216	226
HCLS1-associated protein X-1	HAX1	HAX1_HUMAN	31.6	100.0%	6	7	12	0.01%	27.2%	TREDNDLDSQVSQEGLGPVLQPQPK	99.7%	66.2	25	66.2	0	2	0	2750.36	181	205
HCLS1-associated protein X-1	HAX1	HAX1_HUMAN	31.6	100.0%	6	7	12	0.01%	27.2%	YPDSHQPR	98.1%	32.2	25	20.1	2	0	0	999.46	132	139
HEAT repeat-containing protein 1	HEATR1	HEAT1_HUMAN	242.4	100.0%	4	4	6	0.01%	2.2%	GWEEALENVIK	98.8%	34.1	25	25.6	1	0	0	1287.66	639	649
HEAT repeat-containing protein 1	HEATR1	HEAT1_HUMAN	242.4	100.0%	4	4	6	0.01%	2.2%	LVPDLLAIVQR	99.6%	39.5	25	39.5	2	0	0	1236.77	1644	1654
HEAT repeat-containing protein 1	HEATR1	HEAT1_HUMAN	242.4	100.0%	4	4	6	0.01%	2.2%	NLLSCVYSCPSYIAK	99.7%	44.2	25	43.8	1	0	0	1774.85	1002	1016
HEAT repeat-containing protein 1	HEATR1	HEAT1_HUMAN	242.4	100.0%	4	4	6	0.01%	2.2%	TLATTLAPR	99.7%	52.7	25	45.4	2	0	0	943.56	1812	1820

HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	13	13	21	0.02%	20.5%	AIQDAILEVLK	99.7%	71.3	25	63	2	0	0	1212.72	804	814
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	13	13	21	0.02%	20.5%	ALAVHLLDLGLR	99.7%	70	25	70	2	0	0	1290.79	94	105
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	13	13	21	0.02%	20.5%	ATDTINSQGQFPSYLETVTK	99.7%	83.8	25	83.8	1	0	0	2200.08	636	655
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	13	13	21	0.02%	20.5%	CSLLDPFAAVR	99.7%	41.9	25	41.9	1	0	0	1248.64	173	183
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	13	13	21	0.02%	20.5%	DVQETLMPQVLTTLEEDSK	99.7%	61.6	25	61.6	1	0	0	2176.07	697	715
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	13	13	21	0.02%	20.5%	EGSGLFPDLLVR	99.7%	47	25	40.7	2	0	0	1302.71	815	826
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	13	13	21	0.02%	20.5%	LFDDVPQVR	99.7%	44.8	25	40.1	2	0	0	1088.57	254	262
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	13	13	21	0.02%	20.5%	LIPLLLSSLNDEVPEVR	99.7%	66.6	25	65.1	2	0	0	1907.09	286	302
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	13	13	21	0.02%	20.5%	LLPALAAR	98.2%	32.4	25	25.5	1	0	0	824.54	117	124
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	13	13	21	0.02%	20.5%	LLPGLEADSKPGR	99.7%	65.6	25	58.6	2	0	0	1352.75	34	46
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	13	13	21	0.02%	20.5%	SAELVGTFVSPEVFLK	99.7%	78.1	25	76	2	0	0	1722.93	423	438
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	13	13	21	0.02%	20.5%	SVDDVLSHFAQR	99.7%	45.6	25	36.5	1	0	0	1373.68	242	253
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	13	13	21	0.02%	20.5%	TPSASGLLVLASAMR	99.7%	101	25	101	2	0	0	1473.81	447	461
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	37.1%	AFYPEEISSMVLTK	99.7%	98.5	25	90.6	6	0	0	1614.81	113	126
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	37.1%	AQIHDLVLVGGSTR	99.7%	87.3	25	79	3	2	0	1465.81	329	342
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	37.1%	ARFEELCSDLFR	99.7%	43.8	25	38.3	2	0	0	1542.74	300	311
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	37.1%	ATAGDTHLGGEDFDNR	99.7%	78.7	25	78.7	2	3	0	1675.73	221	236
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	37.1%	DAGVIAGLNVLR	99.7%	96.2	25	82.6	4	0	0	1197.70	160	171
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	37.1%	DNNLLGR	98.3%	32.6	25	24.2	2	0	0	801.42	452	458
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	37.1%	FEELCSDLFR	99.7%	58	25	58	2	0	0	1315.60	302	311
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	37.1%	FGDPVVQSDMK	99.7%	51.6	25	51.6	3	0	0	1222.58	78	88
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	37.1%	GGSGSGPTIEEVD	96.4%	29.6	25	26.2	1	0	0	1204.53	629	641
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	37.1%	IINEPTAAAIAYGLDR	99.7%	105	25	90.3	4	3	0	1687.90	172	187
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	37.1%	ITITNDKGR	99.7%	50.4	25	40.8	2	0	0	1017.57	501	509
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	37.1%	KFGDPVVQSDMK	99.7%	42.3	25	36.4	2	0	0	1350.67	77	88
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	37.1%	LLQDFFNGR	99.7%	60.3	25	47.5	2	0	0	1109.57	349	357
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	37.1%	LSKEEIER	99.7%	53.6	25	33.7	2	0	0	1003.54	510	517
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	37.1%	LVNHFVEEFK	98.8%	34.3	25	29.5	2	0	0	1261.66	237	246
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	37.1%	LVNHFVEEFKR	99.7%	37.9	25	36.8	0	2	0	1417.76	237	247
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	37.1%	MVQEAEKYK	98.8%	34.2	25	26.9	2	0	0	1125.56	518	526
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	37.1%	NALESYAFNMK	99.7%	87.8	25	87.3	5	0	0	1287.60	540	550
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	37.1%	NQVALNPQNTVFDAK	99.7%	111	25	106	2	0	0	1658.85	57	71
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	37.1%	SAVEDEGLK	98.9%	34.5	25	30.8	2	0	0	947.47	551	559
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	37.1%	TTPSYVAFTDTER	99.7%	85.4	25	80.7	5	0	0	1487.70	37	49
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	37.1%	VEIIANDQGNR	99.7%	72.3	25	0	2	0	0	1228.63	26	36
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	37.1%	VQVSYKGETK	99.7%	41.3	25	34.3	1	0	0	1138.61	103	112
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	20	26	59	0.06%	37.1%	YKAEDEVQR	99.7%	46.7	25	37.7	2	0	0	1137.55	525	533
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	11	0.01%	13.9%	AFSDPFVEAEK	99.7%	43.6	25	36.4	2	0	0	1239.59	74	84
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	11	0.01%	13.9%	AGGIETIANEYSDR	99.7%	68.1	25	68.1	1	0	0	1495.70	20	33
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	11	0.01%	13.9%	EFSITDVVPYPISLR	99.7%	47.6	25	47.6	1	0	0	1735.93	391	405
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	11	0.01%	13.9%	FQESEERPK	99.7%	49.6	25	38.6	2	0	0	1149.55	689	697
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	11	0.01%	13.9%	GCALQCAILSPAFK	99.7%	88.9	25	77.3	2	0	0	1535.77	375	388
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	11	0.01%	13.9%	MIMQDKLEK	98.1%	32.3	25	21.9	1	0	0	1135.59	604	612
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	11	0.01%	13.9%	NFTTEQVTAMLLSK	99.7%	90.4	25	82.7	1	0	0	1582.81	111	124
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	11	0.01%	13.9%	SNLAYDIVQLPTGLTGIK	99.7%	102	25	102	2	0	0	1903.05	85	102
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	7	7	11	0.01%	13.9%	VLATAFDTTLGGR	99.7%	102	25	93.9	2	0	0	1321.71	222	234
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	DAGTIAGLNVLR	99.7%	92.7	25	80.3	4	0	0	1199.67	160	171
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	EIAEAYLGK	99.7%	55.6	25	39.3	2	0	0	993.53	129	137
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	FDDAVVQSDMK	99.7%	52.9	25	52.9	2	0	0	1254.57	78	88
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	FEELNADLFR	99.7%	65.8	25	57.8	2	0	0	1253.62	302	311
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	IINEPTAAAIAYGLDK	99.7%	112	25	111	2	0	0	1659.90	172	187

Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	IINEPTAAAIAYGLDKK	99.7%	99.8	25	99.8	2	2	0	1787.99	172	188
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	ITITNDKGR	99.7%	50.4	25	40.8	2	0	0	1017.57	501	509
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	LDKSQIHDIVLVGGSTR	99.7%	42.1	25	42.1	0	2	0	1838.01	326	342
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	LLQDFFNGK	99.7%	50.3	25	33.5	2	0	0	1081.57	349	357
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	LSKEDIER	99.7%	62	25	18.7	2	0	0	989.53	510	517
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	MKEIAEAYLGK	99.7%	66.7	25	54.9	4	1	0	1268.66	127	137
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	MVNHFIAEFK	99.7%	49.8	25	37.2	4	0	0	1235.62	237	246
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	MVQEAEKYK	98.8%	34.2	25	26.9	2	0	0	1125.56	518	526
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	NQTAEKEEFEHQQK	99.5%	31.8	25	31.8	0	2	0	1745.81	584	597
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	NQVAMNPTNTVFDAK	99.7%	110	25	104	4	0	0	1649.80	57	71
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	NQVAMNPTNTVFDAKR	96.2%	23.9	25	23.9	0	1	0	1805.90	57	72
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	NSLESYAFNMK	99.7%	66.6	25	66.6	2	0	0	1319.59	540	550
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	RFDDAVVQSDMK	99.7%	63.1	25	55.9	3	0	0	1410.67	77	88
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	SFYPEEVSSMVLTK	99.7%	104	25	104	4	0	0	1616.79	113	126
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	SINPDEAVAYGAAVQAAILSGDK	99.7%	100	25	100	2	0	0	2260.15	362	384
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	SQIHDIVLVGGSTR	99.7%	77.2	25	75.1	2	2	0	1481.81	329	342
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	STAGDTHLGGEDFDNR	99.7%	72.8	25	72.8	2	1	0	1691.73	221	236
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	TTPSYVAFTDTER	99.7%	85.4	25	80.7	5	0	0	1487.70	37	49
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	TVTNAVVTVPAYFNDSQR	99.7%	72.7	25	72.7	2	2	0	1982.00	138	155
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	VCNPIITK	99.0%	35	25	12.4	2	0	0	944.52	602	609
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	VEIIANDQGNR	99.7%	72.3	25	0	2	0	0	1228.63	26	36
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	37	75	0.07%	43.0%	VQVEYKGETK	99.7%	47.2	25	40.9	2	0	0	1180.62	103	112
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	15	25	0.02%	20.9%	DISTTLNADEAVAR	99.7%	91	25	86.4	2	0	0	1475.73	361	374
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	15	25	0.02%	20.9%	DKLCGPYEK	97.7%	31.3	25	31.3	1	0	0	1109.53	647	655
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	15	25	0.02%	20.9%	FQEAEERPK	99.7%	54.9	25	38	2	0	0	1133.56	706	714
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	15	25	0.02%	20.9%	GCALQCAILSPAFK	99.7%	88.9	25	77.3	2	0	0	1535.77	375	388
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	15	25	0.02%	20.9%	IEVPLYSLLEQTHLK	99.7%	68.6	25	68.3	1	0	0	1783.00	317	331
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	15	25	0.02%	20.9%	LKETAENSLK	99.7%	42.3	25	15.2	2	0	0	1132.62	125	134
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	15	25	0.02%	20.9%	LMNDMTAVALNYGIYK	99.7%	110	25	104	1	0	0	1816.90	170	185
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	15	25	0.02%	20.9%	MFEELGQR	97.3%	30.7	25	28.8	1	0	0	1009.48	715	722
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	15	25	0.02%	20.9%	MIMQDKLEK	98.1%	32.3	25	21.9	1	0	0	1135.59	621	629
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	15	25	0.02%	20.9%	SLDQDPVVR	99.3%	36.6	25	29.6	2	0	0	1028.54	773	781
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	15	25	0.02%	20.9%	SQFEELCAELLQK	99.7%	52.2	25	47.8	2	0	0	1594.78	304	316
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	15	25	0.02%	20.9%	SVLDAAQIVGLNCLR	99.7%	97.3	25	92.2	2	0	0	1628.88	155	169
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	15	25	0.02%	20.9%	VEDVSAVEIVGGATR	99.7%	125	25	110	1	0	0	1501.79	332	346
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	15	25	0.02%	20.9%	VLGTAFDPFLGGK	99.7%	87	25	66.5	4	0	0	1321.72	222	234
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	15	15	25	0.02%	20.9%	YNHIDESEMK	98.3%	32.8	25	26.4	1	0	0	1281.54	740	749
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	8	8	15	0.01%	16.2%	AFLDALQNQAEASSK	99.7%	114	25	106	2	0	0	1592.79	182	196
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	8	8	15	0.01%	16.2%	AQLLQPTLEINPR	99.7%	73.6	25	73.6	2	0	0	1492.85	635	647
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	8	8	15	0.01%	16.2%	ELGSSVALYSR	99.7%	57.9	25	57.9	2	0	0	1181.62	358	368
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	8	8	15	0.01%	16.2%	ELISNASDALEK	99.7%	78.7	25	64.8	2	0	0	1289.66	115	126
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	8	8	15	0.01%	16.2%	ELLQESALIR	99.7%	68.7	25	55.7	2	0	0	1171.67	403	412
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	8	8	15	0.01%	16.2%	GVVDSEDIPLNLSR	99.7%	111	25	0	15	0	0	1513.79	389	402
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	8	8	15	0.01%	16.2%	SDCKEFSSEAR	99.6%	40	25	39.1	1	0	0	1315.56	259	269
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	8	8	15	0.01%	16.2%	TDAPLNIR	99.7%	43.2	25	35.1	2	0	0	899.49	333	340
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	8	8	15	0.01%	16.2%	YESSALPSGQLTSLSEYASR	99.7%	98.9	25	98.9	2	0	0	2146.03	470	489
Heat shock protein beta-1	HSPB1	HSPB1_HUMAN	22.8	100.0%	2	2	4	0.00%	13.2%	LATQSNEITIPVTFESR	99.7%	48.9	25	48.9	2	0	0	1905.99	172	188
Heat shock protein beta-1	HSPB1	HSPB1_HUMAN	22.8	100.0%	2	2	4	0.00%	13.2%	LFDQAFGLPR	99.7%	70.6	25	60.8	2	0	0	1163.62	28	37
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	ADLINNLGTIAK	99.7%	74.9	25	69.1	27	0	0	1242.71	101	112
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	ALLFVPR	99.7%	46.7	25	0	4	0	0	815.51	339	345
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	DNSTMGYMAAK	99.7%	58.1	25	52.7	4	0	0	1188.50	621	631

Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	DQVANSAFVER	99.7%	73.8	25	67.1	8	0	0	1235.60	500	510
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	EDQTEYLEER	99.7%	70	25	63.3	4	0	0	1311.57	192	201
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	EGLELPEDEEEK	98.6%	33.5	25	33.5	1	0	0	1416.64	547	558
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	EGLELPEDEEEKK	99.7%	44.7	25	43.4	2	0	0	1544.73	547	559
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	EKYIDQEELNK	99.7%	60.8	25	44.3	2	0	0	1408.70	282	292
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	ELHINLIPNKQDR	99.7%	55.6	25	52.4	2	2	0	1589.88	75	87
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	ELISNSSDALDK	99.7%	75	25	62.6	2	0	0	1291.64	47	58
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	ELISNSSDALDKIR	99.7%	93.9	25	83.2	2	1	0	1560.82	47	60
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	FENLCK	98.3%	32.8	25	20.4	2	0	0	810.38	568	573
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	FYEQFSK	99.7%	41.8	25	22.7	3	0	0	948.45	437	443
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	GVVDSEDLPLNISR	99.7%	111	25	0	15	0	0	1513.79	387	400
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	HFSVEGQLEFR	99.7%	71.6	25	70.8	11	2	0	1348.66	328	338
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	HIYYITGETK	99.7%	51.2	25	48.3	2	0	0	1224.63	490	499
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	HLEINPDHSIIETLR	99.7%	83.5	25	83.5	2	2	0	1786.94	633	647
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	HNDDEQYAWESSAGGSFTVR	99.7%	121	25	121	2	5	0	2255.96	154	173
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	HSQFIGYPITLFVEK	99.7%	74.8	25	74.8	4	2	0	1778.95	210	224
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	IRYESLTDPSK	99.7%	41.3	25	30.4	2	2	0	1308.68	59	69
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	KHLEINPDHSIIETLR	99.7%	44.5	25	44.5	0	2	0	1915.04	632	647
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	LGIHEDSQNR	99.7%	60.8	25	52.5	4	0	0	1168.57	447	456
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	LGIHEDSQNRK	98.5%	27.5	25	27	0	1	0	1296.67	447	457
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	LVTSPCCIVTSTYGWTANMER	99.7%	100	25	100	5	0	0	2462.12	592	612
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	NPDDITNEEYGEFYK	99.7%	103	25	94.1	2	0	0	1833.78	300	314
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	RAPFDLFENR	99.7%	49.5	25	43.8	2	0	0	1264.64	346	355
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	SLTNDWEDHLAVK	99.7%	89.8	25	74.1	7	2	0	1527.74	315	327
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	TKFENLCK	99.1%	35.7	25	26.8	1	0	0	1039.52	566	573
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	TLTIVDTGIGMTK	99.7%	112	25	0	24	0	0	1349.73	88	100
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	VILHLKEDQTEYLEER	99.7%	79.2	25	74.9	4	5	0	2015.04	186	201
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	YESLTDPSK	99.7%	64	25	58	4	0	0	1039.49	61	69
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	YESLTDPSKLDSGK	99.7%	70.2	25	58.1	4	1	0	1539.75	61	74
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	YIDQEELNK	99.7%	63.7	25	45.7	16	0	0	1151.56	284	292
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	18	25	61	0.06%	43.7%	YYTSASGDEMVSLK	99.7%	88.8	25	88.8	4	0	0	1566.70	465	478
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	ADLINNLGTIAK	99.7%	74.9	25	69.1	27	0	0	1242.71	96	107
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	AKFENLCK	98.2%	32.4	25	22.9	1	0	0	1009.51	558	565
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	ALLFIPR	99.7%	46.7	25	16.3	9	0	0	829.53	331	337
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	APFDLFENK	99.7%	44.3	25	35.8	4	0	0	1080.54	339	347
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	APFDLFENKK	99.7%	46.8	25	39	2	0	0	1208.63	339	348
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	CLELFSELAEDKENYK	98.8%	28.2	25	28	0	1	0	1987.93	412	427
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	DNSTMGYMMAK	99.7%	90.7	25	89.5	14	0	0	1248.51	613	623
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	EDQTEYLEER	99.7%	70	25	63.3	4	0	0	1311.57	187	196
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	EGLELPEDEEEK	98.6%	33.5	25	33.5	1	0	0	1416.64	539	550
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	EGLELPEDEEEKK	99.7%	44.7	25	43.4	2	0	0	1544.73	539	551
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	EKYIDQEELNK	99.7%	60.8	25	44.3	2	0	0	1408.70	274	284
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	ELISNASDALDK	99.7%	76.3	25	67.3	11	0	0	1275.64	42	53
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	ELISNASDALDKIR	99.7%	98.3	25	79.8	8	2	0	1544.83	42	55
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	ELKIDIIPNPQER	99.7%	41.3	25	32.9	2	0	0	1564.87	70	82
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	EQVANSAFVER	99.7%	72.9	25	66.2	15	0	0	1249.62	492	502
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	FENLCK	98.3%	32.8	25	20.4	2	0	0	810.38	560	565
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	FYEAFSK	99.3%	36.7	25	25.7	4	0	0	891.42	429	435
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	GFEVVYMTEPIDEYCVQQLK	99.7%	103	25	50.8	8	4	0	2464.14	507	526
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	GVVDSEDLPLNISR	99.7%	111	25	0	15	0	0	1513.79	379	392
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	HFSVEGQLEFR	99.7%	71.6	25	70.8	11	2	0	1348.66	320	330

Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	HLEINPDHPIVETLR	99.7%	78.1	25	70.9	2	4	0	1782.95	625	639
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	HNDDEQYAWESSAGGSFTVR	99.7%	121	25	121	2	5	0	2255.96	149	168
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	HSQFIGYPITLYLEK	99.7%	62.3	25	0	6	6	0	1808.96	205	219
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	IDIIPNPQER	99.7%	50.3	25	40.9	4	0	0	1194.65	73	82
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	IRYESLTDPSK	99.7%	41.3	25	30.4	2	2	0	1308.68	54	64
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	KFYEAFSK	96.2%	29.4	25	17	2	0	0	1019.52	428	435
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	KHLEINPDHPIVETLR	99.7%	61.4	25	53.9	1	2	0	1911.04	624	639
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	LGIHEDSTNR	99.7%	58.2	25	55.3	6	0	0	1141.56	439	448
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	LGIHEDSTNRR	99.7%	39.8	25	38.6	0	2	0	1297.66	439	449
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	LVSSPCCIVTSTYGWTANMER	99.7%	100	25	100	4	4	0	2448.10	584	604
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	NPDDITQEEYGEFYK	99.7%	98.7	25	98.7	10	0	0	1847.80	292	306
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	RAPFDLFENK	99.7%	46.1	25	31.1	6	0	0	1236.64	338	347
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	RLSELLR	99.7%	40	25	14.3	2	0	0	886.55	450	456
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	SIYYITGESK	99.7%	80.9	25	73.3	8	0	0	1160.58	482	491
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	SLTNDWEDHLAVK	99.7%	89.8	25	74.1	7	2	0	1527.74	307	319
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	TLTLVDTGIGMTK	99.7%	112	25	0	24	0	0	1349.73	83	95
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	VFIMDSCDELIPEYLNFIR	99.7%	73.6	25	73.6	2	0	0	2390.14	360	378
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	VILHLKEDQTEYLEER	99.7%	79.2	25	74.9	4	5	0	2015.04	181	196
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	YESLTDPSK	99.7%	64	25	58	4	0	0	1039.49	56	64
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	YESLTDPSKLDSGK	99.7%	70.2	25	58.1	4	1	0	1539.75	56	69
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	YHTSQSGDEMTSLSEYVSR	99.7%	115	25	115	4	9	0	2176.95	457	475
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	313	0.31%	53.7%	YIDQEELNK	99.7%	63.7	25	45.7	16	0	0	1151.56	276	284
Helicase-like transcription factor	HLTF	HLTF_HUMAN	113.9	100.0%	3	3	4	0.00%	3.0%	ELAAGAFGTK	99.2%	36	25	30.6	1	0	0	964.51	979	988
Helicase-like transcription factor	HLTF	HLTF_HUMAN	113.9	100.0%	3	3	4	0.00%	3.0%	MSELSSSRPK	99.6%	39.4	25	35.6	1	0	0	1121.56	377	386
Helicase-like transcription factor	HLTF	HLTF_HUMAN	113.9	100.0%	3	3	4	0.00%	3.0%	VILDEGHAIR	99.7%	60	25	47.7	2	0	0	1122.63	554	563
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	8	8	17	0.02%	16.5%	ALPLIVGAQLIHADK	99.7%	65.1	25	64.8	1	0	0	1558.93	15	29
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	8	8	17	0.02%	16.5%	GASGSFVVVQK	99.7%	54.7	25	45.9	2	0	0	1078.59	223	233
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	8	8	17	0.02%	16.5%	GQLEQITGK	98.9%	34.8	25	8.82	2	0	0	973.53	312	320
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	8	8	17	0.02%	16.5%	KYVSQYYPK	99.7%	56.1	25	39.6	2	0	0	1175.61	283	291
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	8	8	17	0.02%	16.5%	LEDVLPLAFTR	99.7%	62.5	25	44.3	5	0	0	1273.72	259	269
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	8	8	17	0.02%	16.5%	MDAILTEAIK	98.2%	32.4	25	24.3	1	0	0	1120.59	161	170
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	8	8	17	0.02%	16.5%	SSAVDPEPQVK	99.7%	54.6	25	36.6	2	0	0	1156.58	248	258
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	8	8	17	0.02%	16.5%	TIPSWATLSASQLAR	99.7%	71.6	25	67.1	2	0	0	1601.86	132	146
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	8	11	36	0.04%	25.9%	DLKDYFTK	99.2%	35.8	25	23.9	3	0	0	1029.53	84	91
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	8	11	36	0.04%	25.9%	EVYQQQQYGSGGR	99.7%	90.9	25	84.5	13	0	0	1499.69	233	245
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	8	11	36	0.04%	25.9%	EYFGEFGEIEAIELPMDPK	99.7%	61.6	25	61.6	4	0	0	2214.03	172	190
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	8	11	36	0.04%	25.9%	FGEVVDCTIK	99.7%	67	25	0	18	0	0	1167.57	92	101
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	8	11	36	0.04%	25.9%	FGEVVDCTIKMDPNTGR	99.2%	30.2	25	25.5	0	1	0	1954.90	92	108
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	8	11	36	0.04%	25.9%	GFGFILFK	99.7%	40.8	25	33.3	6	0	0	928.53	111	118
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	8	11	36	0.04%	25.9%	GFVFITFK	99.7%	41.1	25	41.1	2	0	0	958.54	196	203
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	8	11	36	0.04%	25.9%	MFVGGLSWDTSK	99.7%	73.3	25	69.3	2	0	0	1343.63	71	82
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	8	11	36	0.04%	25.9%	MFVGGLSWDTSKK	99.7%	79.8	25	65.6	4	1	0	1455.73	71	83
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	6	9	28	0.03%	28.5%	AEIIADKQSGK	99.7%	60.9	25	41.8	2	0	0	1159.63	127	137
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	6	9	28	0.03%	28.5%	AVPKEDIYSGGGGGGSR	99.7%	94.9	25	89.2	4	1	0	1606.78	173	189
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	6	9	28	0.03%	28.5%	EDIYSGGGGGGSR	99.7%	103	25	99.5	4	0	0	1211.53	177	189
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	6	9	28	0.03%	28.5%	GDVAEGDLIEHFSQFGTVEK	99.7%	87.9	25	86.6	4	4	0	2178.04	107	126
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	6	9	28	0.03%	28.5%	GFGFVYFQNHDAADK	99.7%	77.2	25	77.2	2	3	0	1715.78	140	154
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	6	9	28	0.03%	28.5%	KLFVGGLK	99.1%	35.5	25	0	8	0	0	861.56	99	106
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	6	9	28	0.03%	28.5%	LFIGGLNVQTSESGLR	99.7%	136	25	129	4	0	0	1690.91	9	24
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	16	29	147	0.14%	44.1%	DYFEQYGK	99.7%	50	25	50	4	0	0	1049.46	123	130
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	16	29	147	0.14%	44.1%	EDSQRPGAHLTVK	99.7%	61.1	25	41.5	12	0	0	1437.74	93	105

Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	16	29	147	0.14%	44.1%	EDSQRPGAHLTVKK	99.7%	49.2	25	37.7	2	1	0	1565.84	93	106
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	16	29	147	0.14%	44.1%	EDTEEHHLRDYFEQYGK	99.7%	38	25	38	1	1	0	2195.96	114	130
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	16	29	147	0.14%	44.1%	GFAFVTFDDHDSVDK	99.7%	107	25	101	6	3	0	1699.76	147	161
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	16	29	147	0.14%	44.1%	GFAFVTFDDHDSVDKIVIQK	99.7%	34.4	25	18.3	0	2	0	2281.15	147	166
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	16	29	147	0.14%	44.1%	IEVIEIMTDR	99.7%	76.4	25	71.9	16	0	0	1218.64	131	140
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	16	29	147	0.14%	44.1%	IFVGGIKEDTEEHHLR	99.7%	89.8	25	0	2	8	0	1879.97	107	122
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	16	29	147	0.14%	44.1%	KIFVGGIK	99.1%	35.5	25	0	8	0	0	861.56	106	113
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	16	29	147	0.14%	44.1%	KLFIGGLSFETTDESLR	99.7%	103	25	94.7	1	2	0	1913.00	15	31
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	16	29	147	0.14%	44.1%	LFIGGLSFETTDESLR	99.7%	126	25	113	23	0	0	1784.91	16	31
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	16	29	147	0.14%	44.1%	NQGGYGGSSSSSSYGSGR	99.7%	135	25	135	13	0	0	1694.70	353	370
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	16	29	147	0.14%	44.1%	RGFAFVTFDDHDSVDK	99.7%	62.7	25	50.1	2	2	0	1855.86	146	161
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	16	29	147	0.14%	44.1%	SESPKEPEQLR	99.7%	48.3	25	28.2	7	4	0	1299.65	4	14
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	16	29	147	0.14%	44.1%	SHFEQWGTLTDCVVMR	99.7%	110	25	110	4	8	0	1981.89	32	47
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	16	29	147	0.14%	44.1%	SHFEQWGTLTDCVVMRDPNTK	99.0%	29.2	25	26.2	0	2	0	2537.16	32	52
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	16	29	147	0.14%	44.1%	SSGPYGGGGQYFAKPR	99.7%	111	25	106	17	7	0	1628.78	337	352
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	16	29	147	0.14%	44.1%	YHTVNGHNCEVR	99.7%	65.3	25	59.8	4	3	0	1485.67	167	178
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	16	31	99	0.10%	39.4%	EDSVKPGAHLTVK	99.7%	60.9	25	55	4	0	0	1380.75	114	126
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	16	31	99	0.10%	39.4%	EDSVKPGAHLTVKK	99.7%	37.3	25	32.5	2	1	0	1508.84	114	127
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	16	31	99	0.10%	39.4%	EDTEEYNLR	99.7%	64.4	25	64.4	4	0	0	1168.51	135	143
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	16	31	99	0.10%	39.4%	EDTEEYNLRDYFEK	99.7%	64.3	25	53.2	2	1	0	1850.81	135	148
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	16	31	99	0.10%	39.4%	GEEGHDPKEPEQLR	99.7%	45.3	25	41	2	2	0	1620.76	22	35
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	16	31	99	0.10%	39.4%	GFAFVTFDDHDTVDK	99.7%	85.8	25	83.8	6	3	0	1713.78	168	182
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	16	31	99	0.10%	39.4%	GFAFVTFDDHDTVDKIVVQK	99.1%	29.4	25	13.9	0	2	0	2281.15	168	187
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	16	31	99	0.10%	39.4%	IETIEVMEDR	99.7%	87.8	25	66.6	17	0	0	1234.60	152	161
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	16	31	99	0.10%	39.4%	IFVGGIKEDTEEYNLR	99.7%	96.6	25	91.4	5	6	0	1882.95	128	143
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	16	31	99	0.10%	39.4%	KIFVGGIK	99.1%	35.5	25	0	8	0	0	861.56	127	134
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	16	31	99	0.10%	39.4%	LFIGGLSFETTDDSLR	99.7%	114	25	112	6	0	0	1770.89	37	52
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	16	31	99	0.10%	39.4%	SSGSPYGGGYGSGGGSGGYGSR	99.7%	147	25	147	6	0	0	1910.79	355	376
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	16	31	99	0.10%	39.4%	WGTLTDCVVMR	99.7%	67.3	25	47	6	0	0	1337.63	58	68
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	16	31	99	0.10%	39.4%	WGTLTDCVVMRDPQTK	99.7%	59.8	25	57	4	8	0	1922.91	58	73
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	16	31	99	0.10%	39.4%	YGKIETIEVMEDR	99.7%	71.3	25	70.2	4	3	0	1582.78	149	161
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	16	31	99	0.10%	39.4%	YHTINGHNCEVK	99.7%	52.8	25	52.8	2	1	0	1471.67	188	199
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	16	31	99	0.10%	39.4%	YHTINGHNCEVKK	99.3%	36.8	25	36.5	1	1	0	1599.77	188	200
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	18	26	104	0.10%	42.3%	DLKDYFSK	99.3%	36.8	25	28.4	2	0	0	1015.51	112	119
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	18	26	104	0.10%	42.3%	ESESVDKVMDQK	99.7%	62.9	25	50.7	7	0	0	1394.65	147	158
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	18	26	104	0.10%	42.3%	EYFGGFGEVESIELPMDNK	99.7%	85	25	85	8	0	0	2176.97	200	218
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	18	26	104	0.10%	42.3%	EYFGGFGEVESIELPMDNKTNK	99.7%	51.4	25	51.4	0	2	0	2520.16	200	221
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	18	26	104	0.10%	42.3%	FGEVVDCTLK	99.7%	67	25	0	18	0	0	1167.57	120	129
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	18	26	104	0.10%	42.3%	FGEVVDCTLKLDPITGR	99.7%	86.5	25	84.9	2	4	0	1919.99	120	136
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	18	26	104	0.10%	42.3%	GFCFITFK	96.3%	29.5	25	23.9	1	0	0	1019.50	224	231
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	18	26	104	0.10%	42.3%	GFCFITFKEEEPVK	99.7%	63.6	25	60.8	2	0	0	1730.85	224	237
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	18	26	104	0.10%	42.3%	GFGFVLFK	99.7%	48.5	25	42.3	14	0	0	914.51	139	146
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	18	26	104	0.10%	42.3%	HSEAATAQREEWK	99.7%	71.5	25	67.9	2	0	0	1542.73	86	98
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	18	26	104	0.10%	42.3%	IDASKNEEDEGHSNSSPR	99.7%	112	25	112	2	4	0	1971.86	68	85
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	18	26	104	0.10%	42.3%	IFVGGLSPDTPEEK	99.7%	84.9	25	76.7	12	0	0	1488.76	184	197
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	18	26	104	0.10%	42.3%	IFVGGLSPDTPEEKIR	99.7%	96.1	25	82.2	1	2	0	1757.94	184	199
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	18	26	104	0.10%	42.3%	IREYFGGFGEVESIELPMDNK	98.2%	26.7	25	26.7	0	2	0	2430.16	198	218
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	18	26	104	0.10%	42.3%	KYHNVGLSK	99.6%	39.8	25	29	4	0	0	1045.58	243	251
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	18	26	104	0.10%	42.3%	MFIGGLSWDTTK	99.7%	99.8	25	96.5	4	0	0	1355.67	99	110
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	18	26	104	0.10%	42.3%	MFIGGLSWDTTKK	99.7%	71.4	25	65.5	6	1	0	1483.76	99	111
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	18	26	104	0.10%	42.3%	YHNVGLSK	99.6%	39.6	25	18.8	4	0	0	917.48	244	251

Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	13	31	0.03%	24.0%	DAASVDKVLELK	99.7%	61.2	25	50.3	2	0	0	1287.72	198	209
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	13	31	0.03%	24.0%	DLTEYLSR	99.7%	50	25	37.8	6	0	0	996.50	163	170
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	13	31	0.03%	24.0%	EYFGAFGEIENIELPMDTK	99.7%	74.3	25	73.4	4	0	0	2203.03	251	269
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	13	31	0.03%	24.0%	FGEVVDCTIK	99.7%	67	25	0	18	0	0	1167.57	171	180
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	13	31	0.03%	24.0%	GFCFITYTDEEPVK	99.7%	74.4	25	74.4	2	0	0	1705.78	275	288
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	13	31	0.03%	24.0%	GFCFITYTDEEPVKK	99.7%	90.3	25	90.2	4	2	0	1833.87	275	289
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	13	31	0.03%	24.0%	GFGFVLFK	99.7%	48.5	25	42.3	14	0	0	914.51	190	197
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	13	31	0.03%	24.0%	MFIGGLSWDTSK	99.7%	72.2	25	68.4	4	0	0	1357.65	150	161
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	13	31	0.03%	24.0%	MFIGGLSWDTSKK	99.7%	66.2	25	58.7	4	1	0	1469.75	150	162
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	13	31	0.03%	24.0%	VFVGGLSPDTSEEQIK	99.7%	66.5	25	63.1	2	0	0	1705.86	235	250
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	8	11	31	0.03%	34.7%	ATENDIYNFFSPLNPVR	99.7%	71.9	25	71.9	20	4	0	1996.98	300	316
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	8	11	31	0.03%	34.7%	DLSYCLSGMYDHR	99.7%	68.5	25	68.5	4	0	0	1616.68	263	275
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	8	11	31	0.03%	34.7%	HSGPNSADSANDGFVR	99.7%	101	25	99.9	4	3	0	1630.72	99	114
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	8	11	31	0.03%	34.7%	ITGEAFVQFASQELAEK	99.7%	119	25	112	7	0	0	1867.94	151	167
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	8	11	31	0.03%	34.7%	QSGEAFVELGSEDDVK	99.7%	122	25	122	3	0	0	1709.79	53	68
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	8	11	31	0.03%	34.7%	RYIGIVK	96.8%	30	25	16.9	1	0	0	848.54	218	224
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	8	11	31	0.03%	34.7%	TEMDWVLK	98.5%	33.2	25	14.8	2	0	0	1021.50	91	98
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	8	11	31	0.03%	34.7%	VHIEIGPDGR	99.7%	56.5	25	55.1	11	0	0	1092.58	317	326
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	8	11	31	0.03%	34.7%	VTGEADVEFATHEEAVAAMSK	99.7%	42.7	25	42.7	0	3	0	2208.01	327	347
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	8	11	31	0.03%	34.7%	YGDSEFTVQSTTGHCVHMR	99.7%	59.8	25	59.8	0	4	0	2211.95	276	294
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	19	113	0.11%	42.5%	ATENDIYNFFSPLNPVR	99.7%	71.9	25	71.9	20	4	0	1996.98	300	316
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	19	113	0.11%	42.5%	DLNYCFSGMSDHR	99.7%	65.7	25	65.7	8	0	0	1601.65	263	275
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	19	113	0.11%	42.5%	EGRPSGEAFVELESEDEVK	99.7%	107	25	106	4	5	0	2106.98	50	68
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	19	113	0.11%	42.5%	GAYGGGYGGYDDYNGYNDGYGFGSDR	99.7%	97.2	25	97.2	2	0	0	2717.05	234	259
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	19	113	0.11%	42.5%	GLPWSCSADEVQR	99.7%	81.6	25	78.9	4	0	0	1504.69	17	29
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	19	113	0.11%	42.5%	HTGPNSPDTANDGFVR	99.7%	94	25	94	6	10	0	1684.77	99	114
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	19	113	0.11%	42.5%	IQNGAQGIR	99.7%	60	25	44	5	0	0	956.53	36	44
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	19	113	0.11%	42.5%	SNNVEMDWVLK	99.7%	70.2	25	66.3	9	0	0	1350.64	88	98
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	19	113	0.11%	42.5%	STGEAFVQFASQEIAEK	99.7%	112	25	112	11	0	0	1841.89	151	167
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	19	113	0.11%	42.5%	VHIEIGPDGR	99.7%	56.5	25	55.1	11	0	0	1092.58	317	326
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	19	113	0.11%	42.5%	VTGEADVEFATHEDAVAAMSK	99.7%	46.1	25	46.1	0	5	0	2194.00	327	347
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	12	19	113	0.11%	42.5%	YGDGGSTFQSTTGHCVHMR	99.7%	63.5	25	63.5	1	8	0	2097.89	276	294
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	7	19	0.02%	30.1%	ATENDIYNFFSPLNPMR	99.7%	62.9	25	62.9	5	0	0	2044.94	300	316
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	7	19	0.02%	30.1%	DLNYCFSGMSDHR	99.7%	65.7	25	65.7	8	0	0	1601.65	263	275
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	7	19	0.02%	30.1%	EGRPSGEAFVELESEEEVK	99.7%	37.3	25	34.7	0	2	0	2121.00	50	68
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	7	19	0.02%	30.1%	GLPWSCSADEVMR	99.7%	54.4	25	53.1	1	0	0	1523.66	17	29
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	7	19	0.02%	30.1%	HTGPNSPDTANDGFVR	99.7%	94	25	94	6	10	0	1684.77	99	114
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	7	19	0.02%	30.1%	SNSVEMDWVLK	99.7%	42.6	25	35.3	4	0	0	1307.63	88	98
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	7	19	0.02%	30.1%	STGEAFVQFASQEIAEK	99.7%	112	25	112	11	0	0	1841.89	151	167
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	7	19	0.02%	30.1%	VHIEIGPDGR	99.7%	56.5	25	55.1	11	0	0	1092.58	317	326
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	5	7	19	0.02%	30.1%	YGDGGSSFQSTTGHCVHMR	99.7%	80.7	25	80.7	0	7	0	2083.87	276	294
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	16	47	0.05%	37.0%	ATENDIANFFSPLNPIR	99.7%	72.5	25	66.2	5	2	0	1918.97	206	222
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	16	47	0.05%	37.0%	ATGEADVEFVTHEDAVAAMSK	99.7%	86.6	25	61.3	2	4	0	2194.00	233	253
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	16	47	0.05%	37.0%	DGMDNQGGYGSVGR	99.7%	80.7	25	78.4	6	0	0	1412.59	288	301
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	16	47	0.05%	37.0%	EIAENALGK	99.7%	51.7	25	46.3	4	0	0	944.50	68	76
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	16	47	0.05%	37.0%	HNGPNDASDGTVR	99.7%	45.8	25	38.2	2	0	0	1339.60	7	19
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	16	47	0.05%	37.0%	STGEAFVQFASK	99.7%	86.4	25	80.6	10	0	0	1271.63	56	67
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	16	47	0.05%	37.0%	VHIDIGADGR	99.7%	60	25	51.1	4	0	0	1052.55	223	232
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	16	47	0.05%	37.0%	YIEIFR	99.3%	36.4	25	0	2	0	0	840.46	85	90
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	16	47	0.05%	37.0%	YIELFLNSTPGGGSGMGGSGMGGYGR	99.7%	82.8	25	82.8	4	2	0	2554.13	262	287
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	21	89	0.09%	37.4%	DLAGSIIGK	99.7%	55.1	25	32.2	4	0	0	873.50	397	405

Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	21	89	0.09%	37.4%	DYDDMSPR	99.4%	37.6	25	37.6	2	0	0	998.39	279	286
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	21	89	0.09%	37.4%	GGDLMAYDR	99.7%	49.8	25	42.2	6	0	0	997.44	317	325
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	21	89	0.09%	37.4%	GGDLMAYDRR	99.1%	35.6	25	21.9	2	0	0	1153.54	317	326
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	21	89	0.09%	37.4%	GSDFDCELR	99.7%	55.1	25	50.6	4	0	0	1098.45	140	148
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	21	89	0.09%	37.4%	GSYGDLGGPIITTQVTIPK	99.7%	94.3	25	88.8	6	0	0	1917.03	378	396
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	21	89	0.09%	37.4%	IDEPLEGSEDR	99.7%	79.4	25	70.6	4	0	0	1259.58	423	433
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	21	89	0.09%	37.4%	IILDLISESPIK	99.7%	89.9	25	87.5	15	0	0	1340.80	208	219
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	21	89	0.09%	37.4%	IITITGTQDQIQNAQYLLQNSVK	99.7%	73.6	25	73.6	2	4	0	2589.39	434	456
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	21	89	0.09%	37.4%	LFQECCPHSTDR	99.7%	83.1	25	83.1	4	3	0	1549.65	180	191
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	21	89	0.09%	37.4%	LLIHQSLAGGIIGVK	99.7%	72.8	25	72.8	0	4	0	1518.94	149	163
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	21	89	0.09%	37.4%	NLPLPPPPPPR	97.6%	31.3	25	21.1	2	0	0	1194.70	306	316
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	21	89	0.09%	37.4%	NTDEMVELR	99.7%	78.9	25	64.2	8	0	0	1106.51	38	46
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	21	89	0.09%	37.4%	RDYDDMSPR	98.7%	33.8	25	26.8	1	0	0	1154.49	278	286
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	21	89	0.09%	37.4%	RPAEDMEEEQAFKR	99.7%	98.2	25	98.2	0	9	0	1735.81	22	35
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	16	21	89	0.09%	37.4%	VVLIGGKPDR	99.7%	53.3	25	53.3	9	0	0	1053.64	192	201
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	18	30	130	0.13%	43.8%	AITHLNNNFMFGQK	99.7%	75.9	25	74.2	8	6	0	1650.81	435	448
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	18	30	130	0.13%	43.8%	ASLNGADIYSGCCTLK	99.7%	87.6	25	85.1	5	0	0	1729.79	249	264
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	18	30	130	0.13%	43.8%	IEYAKPTR	99.7%	54.5	25	45.1	10	0	0	977.54	265	272
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	18	30	130	0.13%	43.8%	ISRPGDSDDSR	99.7%	44.5	25	41.4	4	6	0	1204.56	179	189
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	18	30	130	0.13%	43.8%	LCFSTAQHAS	99.7%	56.7	25	56.7	5	0	0	1121.50	580	589
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	18	30	130	0.13%	43.8%	LNVCVSK	99.7%	42	25	31.9	4	0	0	819.44	449	455
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	18	30	130	0.13%	43.8%	MGPPVGGHR	99.7%	40.2	25	22.5	5	0	0	907.46	345	353
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	18	30	130	0.13%	43.8%	NDQDTWDYTNPNLSGQGDPGSNPNKR	99.7%	125	25	125	0	4	0	2890.26	278	303
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	18	30	130	0.13%	43.8%	NGVQAMVEFDSVQSAQR	99.7%	125	25	125	4	0	0	1881.88	230	246
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	18	30	130	0.13%	43.8%	NPNGPYPYTLK	98.7%	33.9	25	24.9	2	0	0	1263.64	569	579
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	18	30	130	0.13%	43.8%	QPAIMPGQSYGLEDGSCSYK	99.7%	73.5	25	73.5	2	0	0	2187.97	456	475
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	18	30	130	0.13%	43.8%	QPAIMPGQSYGLEDGSCSYKDFSESR	98.9%	28.9	25	28.9	0	1	0	2925.27	456	481
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	18	30	130	0.13%	43.8%	SDALETLGFLNHYQMK	99.7%	62.8	25	62.8	8	4	0	1866.91	553	568
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	18	30	130	0.13%	43.8%	SKPGAAMVEMADGYAVDR	99.7%	90	25	37	8	13	0	1883.86	417	434
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	18	30	130	0.13%	43.8%	SSSGLLEWESK	99.7%	63.9	25	50.7	6	0	0	1222.60	542	552
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	18	30	130	0.13%	43.8%	TDNAGDQHGGGGGGGGGAGAAGGGGGGENYDDPHK	99.7%	40.1	25	40.1	0	1	0	2981.20	63	97
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	18	30	130	0.13%	43.8%	TPASPVVHIR	99.7%	60.1	25	54.7	6	0	0	1076.62	98	107
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	18	30	130	0.13%	43.8%	VFNVFCLYGNVEK	99.7%	100	25	89.6	18	0	0	1588.78	399	411
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	ACQIFVR	99.4%	37.1	25	24.4	2	0	0	893.47	652	658
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	ADILEDKDGK	99.7%	54	25	42.3	6	0	0	1103.56	233	242
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	AFITNIPFDVK	99.7%	74.8	25	57.6	14	0	0	1264.69	73	83
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	DKFNECGHVLYADIK	99.7%	71.4	25	60.7	2	2	0	1808.86	671	685
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	EVFSMAGVVVR	99.7%	66.6	25	57.7	2	0	0	1193.63	222	232
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	FESPEVAER	99.7%	60	25	44.6	4	0	0	1063.51	699	707
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	FGSGMNMGR	99.7%	59.3	25	12.4	9	0	0	972.40	363	371
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	FNECGHVLYADIK	99.7%	55.8	25	53	1	0	0	1565.74	673	685
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	GCAVVEFK	99.7%	48.1	25	22	3	0	0	909.45	113	120
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	GGNRFEPYANPTK	99.7%	55.8	25	51.7	2	2	0	1450.71	57	69
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	GIGMGNIGPAGMGMEGIGFGINK	99.7%	115	25	115	10	3	0	2226.04	323	345
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	GNFGGSFAGSFGGAGGHAPGVAR	99.7%	106	25	106	2	5	0	2034.95	628	650
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	INEILSNALK	99.7%	73.3	25	59.4	9	0	0	1114.65	372	381
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	INEILSNALKR	99.7%	57.1	25	50.5	2	0	0	1270.75	372	382
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	KACQIFVR	99.7%	54	25	40.7	2	0	0	1021.56	651	658
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	LGSTVFVANLDYK	99.7%	81.8	25	77.3	7	0	0	1426.76	202	214
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	LKEVFSMAGVVVR	99.7%	80.8	25	75.4	2	5	0	1450.81	220	232
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	MGAGLGHGMDR	99.7%	87	25	80.5	10	0	0	1117.49	419	429

Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	MGAGMGFGLER	99.7%	89.3	25	47.2	13	0	0	1141.51	486	496
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	MGANNLER	99.7%	71.3	25	61	4	0	0	904.43	558	565
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	MGANSLER	99.7%	70.7	25	60	6	0	0	877.42	571	578
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	MGGMEGPFGGGMENMGR	99.7%	82	25	82	9	0	0	1714.68	346	362
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	MGLAMGGGGGASFDR	99.7%	93.1	25	47.8	11	0	0	1399.61	607	621
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	MGLSMER	99.7%	56.6	25	44.1	6	0	0	823.38	525	531
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	MGLVMDR	99.7%	57	25	51	6	0	0	821.40	437	443
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	MGPAMGPALGAGIER	99.7%	75	25	62.4	11	0	0	1427.71	592	606
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	MGPLGLDHMASSIER	99.7%	95.7	25	95.7	8	6	0	1613.78	457	471
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	MGPVMDR	98.9%	34.5	25	25.8	2	0	0	821.36	544	550
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	MVPAGMGAGLER	99.5%	38.8	25	36	5	0	0	1188.59	532	543
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	QGGGGGGGSVPGIER	99.7%	86.5	25	83.6	6	0	0	1284.63	389	403
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	VGEVTYVELLMDAEGK	99.7%	93.3	25	89.9	7	0	0	1768.87	95	110
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	VGQTIER	99.7%	48.4	25.2	18.3	2	0	0	802.44	504	510
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	33	54	210	0.21%	47.4%	WQSLKDLVK	98.0%	32	25	23.2	2	0	0	1116.64	84	92
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	23	31	172	0.17%	39.5%	AGPIWDLR	99.7%	58	25	44.7	6	0	0	927.50	185	192
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	23	31	172	0.17%	39.5%	AIEALKEFNEDGALAVLQQFK	96.1%	23.8	25	23.8	0	1	0	2334.23	61	81
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	23	31	172	0.17%	39.5%	DLFEDELVPLFEK	99.7%	97.8	25	91.1	15	0	0	1593.80	172	184
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	23	31	172	0.17%	39.5%	DSDLSHVQNK	99.7%	44.5	25	36.7	3	0	0	1142.54	82	91
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	23	31	172	0.17%	39.5%	DYAFIHFDER	99.7%	59.3	25	46.5	2	0	0	1312.60	372	381
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	23	31	172	0.17%	39.5%	EFNEDGALAVLQQFK	99.7%	82.8	25	82	8	1	0	1708.85	67	81
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	23	31	172	0.17%	39.5%	EQILEEFSK	99.5%	38.4	25	18.1	6	0	0	1122.57	257	265
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	23	31	172	0.17%	39.5%	GFCFLEYEDHK	99.7%	53.2	25	53.2	8	2	0	1444.62	287	297
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	23	31	172	0.17%	39.5%	GYAFVTFCTK	99.7%	64.3	25	64.3	6	0	0	1193.57	204	213
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	23	31	172	0.17%	39.5%	HIGVCISVANNR	99.7%	63.1	25	0	7	2	0	1339.69	233	244
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	23	31	172	0.17%	39.5%	KYGGPPPDSVYSGQQPSVGTEIFVGK	99.7%	64.8	25	64.8	0	2	0	2694.34	143	168
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	23	31	172	0.17%	39.5%	LDEIYVAGLVAHSDLDER	99.7%	84.7	25	84.7	2	0	0	2015.01	43	60
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	23	31	172	0.17%	39.5%	LFVGSIPK	99.7%	44.8	25	29.3	4	0	0	860.52	245	252
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	23	31	172	0.17%	39.5%	LKDYAFIHFDER	99.7%	44.2	25	39.1	0	2	0	1553.77	370	381
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	23	31	172	0.17%	39.5%	LMMDPLTGLNR	99.7%	80.6	25	73.8	23	0	0	1260.64	193	203
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	23	31	172	0.17%	39.5%	LYNNHEIR	99.7%	53.5	25	40.4	8	0	0	1058.54	222	229
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	23	31	172	0.17%	39.5%	NLANTVTEEILEK	99.7%	108	25	101	12	0	0	1473.78	344	356
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	23	31	172	0.17%	39.5%	SAFLCGVMK	99.7%	57.4	25	55.2	12	0	0	1012.50	92	100
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	23	31	172	0.17%	39.5%	SENQEFYQDTFGQQWK	99.7%	92.1	25	92.1	2	0	0	2034.88	608	623
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	23	31	172	0.17%	39.5%	TGYTLDVTTGQR	99.7%	75.2	25	70.1	10	0	0	1311.65	131	142
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	23	31	172	0.17%	39.5%	TKEQILEEFSK	99.7%	76.6	25	76.6	10	2	0	1351.71	255	265
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	23	31	172	0.17%	39.5%	VTEGLTDVILYHQPDDK	99.7%	64.3	25	64.3	6	6	0	1942.98	266	282
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	23	31	172	0.17%	39.5%	YGGPPPDSVYSGQQPSVGTEIFVGK	99.7%	73.1	25	73.1	2	2	0	2566.25	144	168
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	148	0.15%	38.2%	AGPIWDLR	99.7%	58	25	44.7	6	0	0	927.50	188	195
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	148	0.15%	38.2%	DLYEDELVPLFEK	99.7%	85	25	82.9	18	0	0	1609.80	175	187
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	148	0.15%	38.2%	DYAFVHFEDR	99.7%	47.7	25	47.7	4	0	0	1298.58	375	384
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	148	0.15%	38.2%	EFNEEGALSVLQQFK	99.7%	113	25	100	4	0	0	1738.86	70	84
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	148	0.15%	38.2%	ENILEEFSK	99.7%	46.4	25	42.2	2	0	0	1108.55	260	268
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	148	0.15%	38.2%	GFCFLEYEDHK	99.7%	53.2	25	53.2	8	2	0	1444.62	290	300
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	148	0.15%	38.2%	GYAFITFCGK	99.7%	77.8	25	70.8	7	0	0	1163.56	207	216
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	148	0.15%	38.2%	HLGVCISVANNR	99.7%	63.1	25	0	7	2	0	1339.69	236	247
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	148	0.15%	38.2%	KYGGPPPDSVYSGVQPGIGTEVFVGK	99.7%	35.6	25	29	0	3	0	2635.34	146	171
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	148	0.15%	38.2%	LCDSYEIRPGK	99.7%	62.5	25	46.2	7	1	0	1337.65	225	235
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	148	0.15%	38.2%	LFVGSIPK	99.7%	44.8	25	29.3	4	0	0	860.52	248	255
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	148	0.15%	38.2%	LKDYAFVHFEDR	99.7%	72.4	25	72.4	2	4	0	1539.76	373	384
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	148	0.15%	38.2%	LMMDPLSGQNR	99.7%	59.1	25	39.8	20	0	0	1261.60	196	206

Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	148	0.15%	38.2%	NLATTVTEEILEK	99.7%	115	25	104	23	0	0	1460.78	347	359
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	148	0.15%	38.2%	SAFLCGVMK	99.7%	57.4	25	55.2	12	0	0	1012.50	95	103
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	148	0.15%	38.2%	SFSEFGK	97.9%	31.8	25	28.7	1	0	0	801.38	360	366
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	148	0.15%	38.2%	STAYEDYYYHPPPR	99.7%	63.7	25	63.7	4	8	0	1758.78	428	441
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	148	0.15%	38.2%	TGYTLDVTTGQR	99.7%	75.2	25	70.1	10	0	0	1311.65	134	145
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	148	0.15%	38.2%	TKENILEEFSK	99.7%	70.1	25	58.4	10	2	0	1337.69	258	268
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	148	0.15%	38.2%	TLIEAGLPQK	99.7%	60.9	25	57.1	4	0	0	1069.63	32	41
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	148	0.15%	38.2%	VQESTKGPDEAK	99.7%	63	25	52.7	5	0	0	1288.64	115	126
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	148	0.15%	38.2%	VTEGLVDVILYHQPDDK	99.7%	71.7	25	70.9	6	6	0	1941.00	269	285
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	17	24	148	0.15%	38.2%	YGGPPPDSVYSGVQPGIGTEVFVGK	99.7%	72.5	25	72.5	2	5	0	2507.25	147	171
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	AEGGGGGGRPGAPAAGDGK	99.7%	48	25	41.2	2	2	0	1538.73	216	234
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	AEGGGGGGRPGAPAAGDGKTEQK	99.7%	51.8	25	51.8	0	2	0	2024.97	216	238
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	AEVEGKDLPEHAVLK	98.1%	26.5	25	22.5	0	2	0	1634.88	621	635
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	DCEVVMMIGLPGAGK	99.7%	110	25	86.7	7	0	0	1576.75	496	510
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	DIDIHEVR	99.7%	47	25	38.2	10	0	0	996.51	353	360
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	DLPEHAVLK	99.5%	38	25	28.4	5	0	0	1021.57	627	635
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	EKPYFPIPEEYTFIQNVPLEDR	99.7%	34.7	25	34.7	0	2	0	2724.36	463	484
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	FIEIAAR	99.7%	46.2	25	26.7	12	0	0	819.47	566	572
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	GKVCFEMK	98.8%	34.3	25	25.2	2	0	0	998.48	332	339
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	GYFEYIEENK	99.7%	60.9	25	56.3	5	0	0	1291.58	256	265
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	GYFEYIEENKYSR	99.7%	64.5	25	61.4	7	2	0	1697.78	256	268
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	KAEGGGGGGRPGAPAAGDGK	99.7%	41.8	25	41.8	1	1	0	1666.83	215	234
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	KAVVVCPK	97.6%	31.3	25	23.6	1	0	0	900.53	602	609
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	KDCEVVMMIGLPGAGK	99.7%	88.1	25	88.1	7	5	0	1704.85	495	510
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	KMCLFAGFQR	99.7%	58.2	25	47.9	3	2	0	1273.62	592	601
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	LLEQYKEESK	99.7%	60	25	53.8	10	0	0	1266.66	665	674
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	LNTLLQR	99.7%	53.3	25	23.7	6	0	0	857.52	552	558
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	LQAALDDEEAGGRPAMEPGNGSLDLGGDSAGR	99.7%	95.2	25	90.4	0	4	0	3126.44	38	69
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	MCLFAGFQR	99.7%	67.1	25	63	14	0	0	1145.52	593	601
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	MMVAGFK	98.4%	32.9	25	18.9	3	0	0	815.38	537	543
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	NFILDQTNVSAAAQR	99.7%	138	25	127	17	2	0	1647.84	576	590
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	NGQDLGVAFK	99.7%	64.2	25	61	8	0	0	1048.54	424	433
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	RNFILDQTNVSAAAQR	99.7%	44.9	25	33.3	0	2	0	1803.95	575	590
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	SSGPTSLFAVTVAPPGAR	99.7%	56	25	49.5	11	2	0	1714.91	187	204
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	TCNCETEDYGEK	99.7%	64.9	25	64.9	2	0	0	1505.55	388	399
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	VCFEMK	97.3%	30.8	25	17.7	1	0	0	813.36	334	339
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	VSELKEELK	99.7%	44	25	21.4	2	0	0	1074.60	13	21
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	VTEKIPVR	99.7%	54.8	25	51	2	0	0	941.58	340	347
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	29	43	187	0.18%	33.0%	YNILGTNTIMDK	99.7%	81.9	25	68.2	21	0	0	1398.69	525	536
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	10	11	42	0.04%	15.7%	EALGGQALYPHVLVK	99.7%	76.5	25	60.4	6	0	0	1594.90	361	375
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	10	11	42	0.04%	15.7%	HLPSTEPDPHVVR	99.7%	52.5	25	52.5	0	6	0	1483.77	271	283
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	10	11	42	0.04%	15.7%	INEEISVK	99.2%	36.3	25	23.6	2	0	0	931.51	263	270
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	10	11	42	0.04%	15.7%	NCAVEFNFGQR	99.7%	68.4	25	68.4	5	0	0	1341.60	376	386
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	10	11	42	0.04%	15.7%	NPPGASTYNK	99.6%	39.1	25	35.5	3	0	0	1048.51	722	731
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	10	11	42	0.04%	15.7%	NYILDQTNVYGSAQR	99.7%	131	25	123	6	0	0	1741.85	501	515
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	10	11	42	0.04%	15.7%	QGAPTSFLPPEASQLKPDR	99.7%	34.8	25	34.1	0	3	0	2039.06	147	165
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	10	11	42	0.04%	15.7%	QNQFYDTQVIK	99.7%	51.5	25	43.2	1	0	0	1383.69	107	117
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	10	11	42	0.04%	15.7%	VCFEMK	97.3%	30.8	25	17.7	1	0	0	813.36	257	262
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	10	11	42	0.04%	15.7%	WDVLIQQATQCLNR	99.7%	92.4	25	92.4	6	0	0	1744.88	477	490
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	10	11	42	0.04%	15.7%	YNILGTNAIMDK	99.7%	45.3	25	41.8	4	0	0	1352.69	450	461
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	21	42	0.04%	22.6%	ANFSLPEK	99.7%	57.6	25	39.4	2	0	0	905.47	594	601

Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	21	42	0.04%	22.6%	DLLVQQASQCLSK	99.7%	128	25	123	3	0	0	1489.77	509	521
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	21	42	0.04%	22.6%	DRYGGQPLFSEK	99.7%	52.3	25	45.6	1	0	0	1396.69	262	273
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	21	42	0.04%	22.6%	EGCTEVSLLR	99.7%	70	25	52	3	0	0	1163.57	306	315
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	21	42	0.04%	22.6%	EVEGDDVPESIMLEMK	99.7%	89.7	25	89.7	3	0	0	1820.83	578	593
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	21	42	0.04%	22.6%	FPTLWSGAR	99.7%	40.5	25	29.1	2	0	0	1034.54	274	282
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	21	42	0.04%	22.6%	GLEEPEMDPK	99.7%	51.1	25	44.8	4	0	0	1144.52	497	506
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	21	42	0.04%	22.6%	MKGLEEPEMDPK	97.8%	31.6	25	28.2	1	0	0	1435.64	495	506
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	21	42	0.04%	22.6%	NCVVELNFGQK	99.7%	78.9	25	65.7	2	0	0	1307.64	407	417
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	21	42	0.04%	22.6%	NFILDQCNVYNSGQR	99.7%	101	25	96.9	2	0	0	1827.84	532	546
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	21	42	0.04%	22.6%	NYYGYQGYR	99.7%	50.8	25	46.2	2	0	0	1183.52	739	747
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	21	42	0.04%	22.6%	SGDETPGSEVPGDK	99.7%	70.7	25	70.7	3	0	0	1374.60	161	174
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	21	42	0.04%	22.6%	TIEECEVILMVGLPGSGK	99.7%	73.9	25	70.2	4	0	0	1931.98	448	465
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	21	42	0.04%	22.6%	VTQNLPMK	99.7%	49.3	25	25.4	4	0	0	930.51	298	305
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	21	42	0.04%	22.6%	YGGQPLFSEK	99.7%	48.6	25	39.1	2	0	0	1125.56	264	273
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	21	42	0.04%	22.6%	YNVLGAETVLNQMR	99.7%	101	25	95.1	4	0	0	1607.82	481	494
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	37	225	0.22%	61.5%	DYFEEYGK	99.7%	44.9	25	44.9	3	0	0	1050.44	130	137
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	37	225	0.22%	61.5%	DYFEEYGKIDTIEIITDR	99.7%	51.7	25	51.2	2	2	0	2220.07	130	147
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	37	225	0.22%	61.5%	EESGKPGAHVTVK	99.7%	66.3	25	59.2	9	0	0	1338.70	100	112
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	37	225	0.22%	61.5%	EESGKPGAHVTVKK	99.7%	48	25	39.8	3	0	0	1466.80	100	113
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	37	225	0.22%	61.5%	GFGDGYNGYGGGPGGGNFGGSPGYGGGR	99.7%	138	25	138	4	4	0	2495.04	239	266
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	37	225	0.22%	61.5%	GFGFVTFDDHDPVDK	99.7%	93.6	25	93.6	12	9	0	1695.77	154	168
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	37	225	0.22%	61.5%	GFGFVTFDDHDPVDKIVLQK	99.7%	45.8	25	45.8	2	2	0	2277.16	154	173
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	37	225	0.22%	61.5%	GGGGNFGPGPGSNFR	99.7%	61.5	25	61.2	16	1	0	1377.63	214	228
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	37	225	0.22%	61.5%	GGNFGFGDSR	99.7%	65.4	25	25.2	19	0	0	1013.44	204	213
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	37	225	0.22%	61.5%	IDTIEIITDR	99.7%	101	25	93.6	9	0	0	1188.65	138	147
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	37	225	0.22%	61.5%	KLFIGGLSFETTEESLR	99.7%	56.2	25	56.2	0	3	0	1927.02	22	38
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	37	225	0.22%	61.5%	KLFVGGIK	99.1%	35.5	25	0	8	0	0	861.56	113	120
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	37	225	0.22%	61.5%	LFIGGLSFETTEESLR	99.7%	131	25	130	21	0	0	1798.92	23	38
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	37	225	0.22%	61.5%	LFVGGIKEDTEEHHLR	99.7%	89.8	25	0	2	8	0	1879.97	114	129
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	37	225	0.22%	61.5%	LTDCVVMR	99.7%	59.6	25	48.8	14	0	0	993.49	47	54
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	37	225	0.22%	61.5%	LTDCVVMRDPASK	99.7%	61.1	25	50.5	6	0	0	1491.73	47	59
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	37	225	0.22%	61.5%	NMGGPYGGGNYGPGGSGGSGGYGGR	99.7%	154	25	154	12	8	0	2205.90	326	350
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	37	225	0.22%	61.5%	NYYEQWGK	99.7%	40.2	25	40.2	6	0	0	1087.48	39	46
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	37	225	0.22%	61.5%	QEMQEVQSSR	99.7%	82.2	25	80.1	9	0	0	1221.55	191	200
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	37	225	0.22%	61.5%	RGFGFVTFDDHDPVDK	99.7%	42.7	25	42.7	0	3	0	1851.87	153	168
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	37	225	0.22%	61.5%	TLETVPLER	99.7%	48.1	25	46.9	16	0	0	1057.59	4	12
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	37	225	0.22%	61.5%	YHTINGHNAEVR	99.7%	82.7	25	68.5	4	4	0	1410.69	174	185
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	23	37	225	0.22%	61.5%	YHTINGHNAEVRK	99.7%	46.4	25	46.4	1	3	0	1538.78	174	186
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	18	24	216	0.21%	44.1%	AAVAGEDGR	99.5%	38.2	25	38.2	2	0	0	845.41	65	73
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	18	24	216	0.21%	44.1%	GDDLQAIKK	99.7%	48.3	25	42.8	3	0	0	987.55	190	198
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	18	24	216	0.21%	44.1%	GDDQLELIK	99.7%	54.6	25	38.9	2	0	0	1030.54	276	284
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	18	24	216	0.21%	44.1%	GDDQLELIKDDEK	99.7%	42.4	25	39.3	2	0	0	1517.73	276	288
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	18	24	216	0.21%	44.1%	GFAFVQYVNER	99.7%	91.3	25	91.2	35	0	0	1329.66	51	61
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	18	24	216	0.21%	44.1%	IVGCSVHK	96.3%	29.5	25	24.8	2	0	0	899.48	43	50
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	18	24	216	0.21%	44.1%	KSDVEAIFSK	99.7%	69.1	25	55.4	14	0	0	1123.60	30	39
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	18	24	216	0.21%	44.1%	LKGDDLQAIK	99.7%	47.1	25	22.1	4	0	0	1100.63	188	197
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	18	24	216	0.21%	44.1%	MIAGQVLDINLAAEPK	99.7%	134	25	134	49	6	0	1682.91	74	89
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	18	24	216	0.21%	44.1%	MYSYPAR	99.7%	41.9	25	36.4	9	0	0	903.40	136	142
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	18	24	216	0.21%	44.1%	NDKSEEEQSSSSVK	99.7%	70.8	25	67.8	2	0	0	1553.69	230	243
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	18	24	216	0.21%	44.1%	QKVDSLLENLEK	99.7%	62	25	50.8	11	3	0	1415.77	205	216
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	18	24	216	0.21%	44.1%	SDVEAIFSK	99.7%	69.7	25	64.1	15	0	0	995.50	31	39

Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	18	24	216	0.21%	44.1%	VDSLLENLEK	99.7%	61.5	25	46.7	5	0	0	1159.62	207	216
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	18	24	216	0.21%	44.1%	VDSLLENLEKIEK	99.7%	49.1	25	49.1	2	0	0	1529.84	207	219
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	18	24	216	0.21%	44.1%	VFIGNLNTLVVK	99.7%	93.6	25	90.5	39	0	0	1316.79	18	29
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	18	24	216	0.21%	44.1%	VFIGNLNTLVVKK	99.7%	70.4	25	70.4	2	2	0	1444.89	18	30
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	18	24	216	0.21%	44.1%	VPPPPPIAR	99.0%	35.1	25	31	7	0	0	943.57	143	151
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	16	27	0.03%	18.5%	AAQLCGAGMAAVVDK	99.7%	63	25	56.2	1	0	0	1461.72	830	844
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	16	27	0.03%	18.5%	AILQQLGLNSTCDDSILVK	99.7%	41.1	25	41.1	1	0	0	2088.10	802	820
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	16	27	0.03%	18.5%	ASGVEGADVVK	99.2%	35.8	25	24.5	2	0	0	1031.54	177	187
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	16	27	0.03%	18.5%	ATDCVGHDVVTLLR	99.4%	37.3	25	32	1	0	0	1555.79	625	638
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	16	27	0.03%	18.5%	FLLSESGSGK	99.7%	45.6	25	33.7	2	0	0	1024.53	442	451
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	16	27	0.03%	18.5%	FLSQIESDR	99.7%	58.6	25	43.8	2	0	0	1094.55	786	794
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	16	27	0.03%	18.5%	GAALITAVGVR	99.7%	80.2	25	68.4	2	0	0	1027.63	900	910
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	16	27	0.03%	18.5%	GAAMVTAVAYR	99.7%	95.9	25	87.6	3	0	0	1109.58	452	462
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	16	27	0.03%	18.5%	GDFIALDLGGSSFR	99.7%	78.2	25	71.5	2	0	0	1454.73	78	91
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	16	27	0.03%	18.5%	IDEAILITWTK	99.7%	62.3	25	60.9	2	0	0	1302.73	163	173
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	16	27	0.03%	18.5%	LALLQVR	99.7%	43.3	25	23.7	2	0	0	812.54	795	801
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	16	27	0.03%	18.5%	LSDETLIDIMTR	99.7%	73	25	67.2	2	0	0	1406.72	31	42
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	16	27	0.03%	18.5%	LVDEYSLNAGK	99.7%	52.3	25	44.6	2	0	0	1208.62	728	738
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	16	27	0.03%	18.5%	SANLVAATLGAILNR	99.7%	89.6	25	79.4	2	1	0	1483.86	382	396
Histidine triad nucleotide-binding protein 2, mitochondrial	HINT2	HINT2_HUMAN	17.2	99.8%	2	2	3	0.00%	19.0%	AQQATPGGAAPTIFSR	99.7%	43.5	25	42.2	2	0	0	1572.81	43	58
Histidine triad nucleotide-binding protein 2, mitochondrial	HINT2	HINT2_HUMAN	17.2	99.8%	2	2	3	0.00%	19.0%	DVAPQAPVHFLVIPK	95.7%	28.9	25	27.9	1	0	0	1630.93	80	94
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	16	0.02%	16.2%	ISICSSDKR	96.2%	29.4	25	24.1	1	0	0	1065.54	405	413
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	16	0.02%	16.2%	LGCFNLTIK	99.7%	55.5	25	38.8	2	0	0	1065.58	271	279
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	16	0.02%	16.2%	LHISPSNMTNQNTNEYLEK	99.7%	35	25	35	0	1	0	2249.05	343	361
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	16	0.02%	16.2%	SIRPDNMSEYSK	99.7%	48.7	25	40.6	3	0	0	1426.66	78	89
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	16	0.02%	16.2%	VMTVSFHK	99.7%	54.1	25	48.8	2	0	0	948.50	193	200
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	16	0.02%	16.2%	YGEYFPGTGDLR	99.7%	65.4	25	64.7	4	0	0	1374.63	201	212
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	7	8	16	0.02%	16.2%	YYAVNYPLR	99.7%	43.5	25	32.9	3	0	0	1158.59	221	229
Histone deacetylase complex subunit SAP18	SAP18	SAP18_HUMAN	17.6	100.0%	4	6	10	0.01%	15.7%	EIGSTMSGR	95.6%	28.8	25	24.1	1	0	0	937.44	105	113
Histone deacetylase complex subunit SAP18	SAP18	SAP18_HUMAN	17.6	100.0%	4	6	10	0.01%	15.7%	GTDDSMTLQSQK	99.7%	56.3	25	44.9	3	0	0	1310.59	115	126
Histone deacetylase complex subunit SAP18	SAP18	SAP18_HUMAN	17.6	100.0%	4	6	10	0.01%	15.7%	KGTDDSMTLQSQK	99.7%	73	25	62.2	3	0	0	1438.68	114	126
Histone deacetylase complex subunit SAP18	SAP18	SAP18_HUMAN	17.6	100.0%	4	6	10	0.01%	15.7%	VKEIGSTMSGR	99.7%	51	25	36.4	3	0	0	1164.60	103	113
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	9	12	126	0.12%	30.1%	ALAAAGYDVEK	99.7%	77	25	68.3	28	0	0	1107.57	65	75
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	9	12	126	0.12%	30.1%	ALAAAGYDVEKNNSR	99.7%	102	25	102	6	1	0	1578.79	65	79
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	9	12	126	0.12%	30.1%	ASGPPVSELITK	99.7%	72.2	25	64.9	21	0	0	1198.67	35	46
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	9	12	126	0.12%	30.1%	KALAAAGYDVEK	99.7%	79.6	25	72.3	3	2	0	1235.66	64	75
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	9	12	126	0.12%	30.1%	KASGPPVSELITK	99.7%	82.5	25	76.3	21	3	0	1326.76	34	46
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	9	12	126	0.12%	30.1%	SETAPAAPAAPAPAEK	99.7%	83.7	25	4.82	2	0	0	1478.75	2	17
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	9	12	126	0.12%	30.1%	SGVSLAALK	99.7%	66.2	25	36.2	6	0	0	845.51	55	63
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	9	12	126	0.12%	30.1%	SGVSLAALKK	99.7%	76.2	25	74.7	32	0	0	973.60	55	64
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	9	12	126	0.12%	30.1%	SLVSKGTLVQTK	99.7%	49.9	25	45.4	1	0	0	1260.75	86	97
Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	5	6	24	0.02%	18.3%	ALVQNDTLLQVK	99.7%	86.4	25	74.4	6	0	0	1341.77	95	106
Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	5	6	24	0.02%	18.3%	GAPAAATAPAPTAHK	99.7%	78.3	25	78.2	7	0	0	1331.71	129	143
Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	5	6	24	0.02%	18.3%	RGAPAAATAPAPTAHK	99.7%	48.4	25	48.4	2	2	0	1487.81	128	143
Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	5	6	24	0.02%	18.3%	YSQLVVETIR	99.7%	85.4	25	65	6	0	0	1207.67	48	57
Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	5	6	24	0.02%	18.3%	YSQLVVETIRR	97.0%	30.3	25	22.6	1	0	0	1363.77	48	58
Histone H2A type 1-B/E	HIST1H2AB	H2A1B_HUMAN	14.1	100.0%	4	5	31	0.03%	35.4%	AGLQFPVGR	99.7%	68.2	25	48.5	20	0	0	944.53	22	30
Histone H2A type 1-B/E	HIST1H2AB	H2A1B_HUMAN	14.1	100.0%	4	5	31	0.03%	35.4%	HLQLAIR	99.5%	38.3	25	27.8	2	0	0	850.53	83	89
Histone H2A type 1-B/E	HIST1H2AB	H2A1B_HUMAN	14.1	100.0%	4	5	31	0.03%	35.4%	NDEELNKLLGR	99.7%	64.8	25	53.5	2	0	0	1300.69	90	100
Histone H2A type 1-B/E	HIST1H2AB	H2A1B_HUMAN	14.1	100.0%	4	5	31	0.03%	35.4%	VTIAQGGVLPNIQAVLLPK	99.7%	51.8	25	51.8	5	2	0	1931.17	101	119
Histone H2B type 1-B	HIST1H2BB	H2B1B_HUMAN	14.0	99.8%	2	2	3	0.00%	35.7%	AMGIMNSFVNDIFER	99.7%	92.8	25	32	16	0	0	1759.81	59	73

Histone H2B type 1-B	HIST1H2BB	H2B1B_HUMAN	14.0	99.8%	2	2	3	0.00%	35.7%	ESYSIYVYK	99.3%	36.9	25	35.1	1	0	0	1151.56	36	44
Histone H2B type 1-B	HIST1H2BB	H2B1B_HUMAN	14.0	99.8%	2	2	3	0.00%	35.7%	KESYSIYVYK	99.7%	55.4	25	49.2	2	0	0	1279.66	35	44
Histone H2B type 1-B	HIST1H2BB	H2B1B_HUMAN	14.0	99.8%	2	2	3	0.00%	35.7%	LLLPGELAK	99.7%	48.5	25	11.9	11	0	0	953.60	101	109
Histone H2B type 1-B	HIST1H2BB	H2B1B_HUMAN	14.0	99.8%	2	2	3	0.00%	35.7%	QVHPDTGISSK	98.7%	33.7	25	24.7	2	0	0	1168.60	48	58
Histone H2B type 1-C/E/F/G/I	HIST1H2BC	H2B1C_HUMAN	13.9	100.0%	5	6	37	0.04%	35.7%	AMGIMNSFVNDIFER	99.7%	92.8	25	32	16	0	0	1759.81	59	73
Histone H2B type 1-C/E/F/G/I	HIST1H2BC	H2B1C_HUMAN	13.9	100.0%	5	6	37	0.04%	35.7%	ESYSVYVYK	99.4%	37.6	25	37.6	3	0	0	1137.55	36	44
Histone H2B type 1-C/E/F/G/I	HIST1H2BC	H2B1C_HUMAN	13.9	100.0%	5	6	37	0.04%	35.7%	KESYSVYVYK	99.7%	60.8	25	58.5	5	0	0	1265.64	35	44
Histone H2B type 1-C/E/F/G/I	HIST1H2BC	H2B1C_HUMAN	13.9	100.0%	5	6	37	0.04%	35.7%	LLLPGELAK	99.7%	48.5	25	11.9	11	0	0	953.60	101	109
Histone H2B type 1-C/E/F/G/I	HIST1H2BC	H2B1C_HUMAN	13.9	100.0%	5	6	37	0.04%	35.7%	QVHPDTGISSK	98.7%	33.7	25	24.7	2	0	0	1168.60	48	58
Histone H3.1t	HIST3H3	H31T_HUMAN	15.5	100.0%	4	4	16	0.02%	19.9%	EIAQDFK	99.1%	35.6	25	29.1	1	0	0	850.43	74	80
Histone H3.1t	HIST3H3	H31T_HUMAN	15.5	100.0%	4	4	16	0.02%	19.9%	EIAQDFKTDLR	99.7%	46.7	25	31.2	5	0	0	1335.69	74	84
Histone H3.1t	HIST3H3	H31T_HUMAN	15.5	100.0%	4	4	16	0.02%	19.9%	STELLIR	99.7%	49.1	25	37.5	8	0	0	831.49	58	64
Histone H3.1t	HIST3H3	H31T_HUMAN	15.5	100.0%	4	4	16	0.02%	19.9%	YRPGTVALR	97.5%	31.1	25	29.2	2	0	0	1032.59	42	50
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	8	56	0.06%	51.5%	DAVTYTEHAK	99.7%	52.5	25	49.2	10	0	0	1134.54	69	78
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	8	56	0.06%	51.5%	DNIQGITKPAIR	99.7%	61.8	25	46	9	4	0	1325.75	25	36
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	8	56	0.06%	51.5%	ISGLIYEETR	99.7%	66.5	25	58.1	10	0	0	1180.62	47	56
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	8	56	0.06%	51.5%	TVTAMDVVYALK	99.7%	62.4	25	57.2	9	0	0	1310.70	81	92
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	8	56	0.06%	51.5%	TVTAMDVVYALKR	99.7%	59.2	25	59.2	2	0	0	1466.80	81	93
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	8	56	0.06%	51.5%	VFLENVIR	99.7%	57.2	25	46.2	12	0	0	989.58	61	68
Histone-binding protein RBBP4	RBBP4	RBBP4_HUMAN	47.7	100.0%	2	2	4	0.00%	3.5%	LMIWDTR	99.7%	44.9	25	32	2	0	0	934.48	252	258
Histone-binding protein RBBP4	RBBP4	RBBP4_HUMAN	47.7	100.0%	2	2	4	0.00%	3.5%	TVALWDLR	99.7%	62.4	25	41.1	2	0	0	973.55	297	304
Hornerin	HRNR	HORN_HUMAN	282.4	100.0%	3	4	22	0.02%	2.0%	GEQHGSSSGSSSSYGQHGSGSR	97.6%	25.6	25	25.6	0	1	0	2122.88	1910	1931
Hornerin	HRNR	HORN_HUMAN	282.4	100.0%	3	4	22	0.02%	2.0%	GPYESGSGHSSGLGHR	99.7%	78.6	25	78.6	3	16	0	1584.72	1038	1053
Hornerin	HRNR	HORN_HUMAN	282.4	100.0%	3	4	22	0.02%	2.0%	QSLGHGQHGSGSGQSPSPSR	98.9%	28.6	25	28.6	0	2	0	1947.90	992	1011
Huntingtin	HTT	HD_HUMAN	347.6	100.0%	3	3	5	0.00%	1.2%	AALPSLTNPPSLSPIR	99.7%	46.4	25	46.4	2	0	0	1633.93	1167	1182
Huntingtin	HTT	HD_HUMAN	347.6	100.0%	3	3	5	0.00%	1.2%	LFEPLVIK	97.8%	31.6	25	19.2	2	0	0	958.60	1424	1431
Huntingtin	HTT	HD_HUMAN	347.6	100.0%	3	3	5	0.00%	1.2%	NSAASGLFIQAIQSR	99.7%	57.3	25	57.3	1	0	0	1562.83	1946	1960
Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	HMGCL_HUMAN	34.4	99.8%	2	2	2	0.00%	7.4%	AAQSANISVR	99.7%	59.3	25	48	1	0	0	1016.55	156	165
Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	HMGCL_HUMAN	34.4	99.8%	2	2	2	0.00%	7.4%	FPGINYPVLTPNLK	99.7%	63	25	59.6	1	0	0	1572.88	98	111
Hydroxysteroid dehydrogenase-like protein 2	HSDL2	HSDL2_HUMAN	45.4	100.0%	3	3	9	0.01%	9.6%	LAGCTVFITGASR	99.7%	104	25	80.4	3	0	0	1352.70	8	20
Hydroxysteroid dehydrogenase-like protein 2	HSDL2	HSDL2_HUMAN	45.4	100.0%	3	3	9	0.01%	9.6%	LLGTIYTAAEEIEAVGGK	99.7%	71.5	25	65.9	4	0	0	1834.98	50	67
Hydroxysteroid dehydrogenase-like protein 2	HSDL2	HSDL2_HUMAN	45.4	100.0%	3	3	9	0.01%	9.6%	SGAVEETFR	99.7%	64.5	25	56.2	2	0	0	995.48	307	315
Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	HPRT_HUMAN	24.6	100.0%	4	6	11	0.01%	20.2%	SIPMTVDFIR	99.7%	48.3	25	38.8	1	0	0	1178.62	92	101
Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	HPRT_HUMAN	24.6	100.0%	4	6	11	0.01%	20.2%	TMQTLLSLVR	99.7%	79.7	25	58	3	0	0	1161.67	142	151
Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	HPRT_HUMAN	24.6	100.0%	4	6	11	0.01%	20.2%	VFIPHGLIMDR	99.7%	40.4	25	37.3	0	4	0	1297.71	35	45
Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	HPRT_HUMAN	24.6	100.0%	4	6	11	0.01%	20.2%	VIGGDDLSTLTGK	99.7%	107	25	97.9	3	0	0	1275.68	116	128
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	20	36	0.04%	23.1%	AANSLEAFIFETQDK	99.7%	87.7	25	78.9	2	2	0	1683.82	739	753
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	20	36	0.04%	23.1%	AEAGPEGVAPAPEGEK	99.7%	88.7	25	79.3	2	0	0	1508.72	670	685
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	20	36	0.04%	23.1%	AEAGPEGVAPAPEGEKK	99.7%	56.1	25	53.3	2	0	0	1636.82	670	686
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	20	36	0.04%	23.1%	DAVVYPILVEFTR	99.7%	67	25	66.9	2	0	0	1521.83	439	451
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	20	36	0.04%	23.1%	EAGMQPQLQIR	98.8%	34.4	25	30	2	0	0	1270.66	252	262
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	20	36	0.04%	23.1%	EVEEEPGIHSLK	99.7%	47.8	25	34.9	2	0	0	1366.69	452	463
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	20	36	0.04%	23.1%	EVQYLLNK	95.4%	28.6	25	18.1	1	0	0	1006.56	901	908
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	20	36	0.04%	23.1%	FFGDSAASMAIK	99.7%	74.4	25	64.6	2	0	0	1244.60	80	91
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	20	36	0.04%	23.1%	LAGLFNEQR	99.7%	67.1	25	55.7	2	0	0	1047.56	283	291
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	20	36	0.04%	23.1%	LGNTISSLFGGGTTPDAK	99.7%	108	25	104	2	0	0	1735.89	577	594
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	20	36	0.04%	23.1%	LYQPEYQEVSTEEQREEISGK	99.7%	48.3	25	43.4	0	2	0	2542.19	754	774
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	20	36	0.04%	23.1%	TLGGLEMELR	99.7%	60.8	25	50.2	3	0	0	1118.59	269	278
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	20	36	0.04%	23.1%	TPVIVTLK	98.5%	33.2	25	30.3	1	0	0	870.57	68	75
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	20	36	0.04%	23.1%	VAIVKPGVPMEIVLNK	96.7%	24.4	25	21.2	0	1	0	1723.02	47	62
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	20	36	0.04%	23.1%	VEFEELCADLFER	99.7%	75.2	25	75.2	2	0	0	1656.76	346	358

Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	20	36	0.04%	23.1%	VESVFETLVEDSAEEESTLTK	99.7%	92.7	25	92.7	2	0	0	2342.11	556	576
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	20	36	0.04%	23.1%	VLQLINDNTATALSYGVFR	99.7%	90.2	25	89.9	2	0	0	2095.12	199	217
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	18	20	36	0.04%	23.1%	YFQHLLGK	99.0%	34.8	25	28.1	2	0	0	1005.55	99	106
Ig kappa chain V-II region RPMI 6410	IGKV2-30	KV206_HUMAN	14.7	99.8%	2	3	292	0.29%	12.0%	FSGSGSGTDFTLK	99.7%	101	25	0	273	0	0	1303.62	87	99
Ig kappa chain V-II region RPMI 6410	IGKV2-30	KV206_HUMAN	14.7	99.8%	2	3	292	0.29%	12.0%	FSGSGSGTDFTLKISR	99.7%	100	25	0	8	11	0	1659.83	87	102
Immunoglobulin-binding protein 1	IGBP1	IGBP1_HUMAN	39.2	100.0%	2	2	2	0.00%	5.9%	LPELFETGR	99.7%	56.2	25	54.6	1	0	0	1061.56	12	20
Immunoglobulin-binding protein 1	IGBP1	IGBP1_HUMAN	39.2	100.0%	2	2	2	0.00%	5.9%	YGALPDQGIAK	97.5%	31	25	26	1	0	0	1132.60	277	287
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	7	8	13	0.01%	18.1%	ASLSLIEK	99.7%	50.3	25	42.9	2	0	0	860.51	487	494
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	7	8	13	0.01%	18.1%	EATWTMSNITAGR	99.7%	64.2	25	56.8	2	0	0	1437.68	354	366
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	7	8	13	0.01%	18.1%	EKQPPIDNIIR	96.0%	23.7	25	15.2	0	1	0	1322.74	107	117
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	7	8	13	0.01%	18.1%	GINSSNVENQLQATQAAR	99.7%	111	25	105	2	0	0	1900.95	84	101
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	7	8	13	0.01%	18.1%	NLTWTLSNLCR	99.7%	70.2	25	0	2	0	0	1377.69	228	238
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	7	8	13	0.01%	18.1%	NPAPPIDAVEQILPTLVR	99.7%	69.4	25	69.4	2	0	0	1943.10	241	258
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	7	8	13	0.01%	18.1%	NVSSFPDDATSPLQENR	99.7%	108	25	106	2	0	0	1876.87	52	68
Importin subunit alpha-4	KPNA3	IMA4_HUMAN	57.8	99.8%	2	2	3	0.00%	5.2%	DSQVVQVVLDGLK	99.7%	44.1	25	35.7	1	0	0	1399.78	424	436
Importin subunit alpha-4	KPNA3	IMA4_HUMAN	57.8	99.8%	2	2	3	0.00%	5.2%	EAAWAISNLTISGR	99.7%	51.8	25	43.9	2	0	0	1488.78	387	400
Importin subunit alpha-5	KPNA1	IMA5_HUMAN	60.2	100.0%	3	3	5	0.00%	8.0%	EACWTISNITAGNR	99.7%	65.2	25	61.4	2	0	0	1592.75	357	370
Importin subunit alpha-5	KPNA1	IMA5_HUMAN	60.2	100.0%	3	3	5	0.00%	8.0%	EPNPPIDEVISTPGVVAR	99.7%	58.5	25	58.5	1	0	0	1890.00	113	130
Importin subunit alpha-5	KPNA1	IMA5_HUMAN	60.2	100.0%	3	3	5	0.00%	8.0%	NAVWALSNLCR	99.7%	45.9	25	45.3	2	0	0	1303.66	231	241
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	23	49	0.05%	27.9%	AAVENLPTFLVELSR	99.7%	112	25	109	4	0	0	1658.91	28	42
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	23	49	0.05%	27.9%	DTAAWTVGR	99.7%	63.5	25	49	1	0	0	976.48	426	434
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	23	49	0.05%	27.9%	ESCLEAYTGIVQGLK	99.7%	97	25	91.4	2	0	0	1667.83	763	777
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	23	49	0.05%	27.9%	GALQYLVPILTQTLTK	99.7%	79.2	25	79.2	2	0	0	1759.04	317	332
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	23	49	0.05%	27.9%	GDQENVHPDVMLVQPR	99.7%	50.1	25	50.1	0	3	0	1849.89	778	793
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	23	49	0.05%	27.9%	LAATNALLNSLEFTK	99.7%	108	25	102	6	0	0	1605.88	192	206
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	23	49	0.05%	27.9%	LLETTDRPDGHQNNLR	99.7%	45.2	25	41.1	0	2	0	1878.94	510	525
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	23	49	0.05%	27.9%	NSLTSKDPDIK	99.6%	39.9	25	16.9	2	0	0	1217.64	63	73
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	23	49	0.05%	27.9%	SDYDMVDYLNELR	99.7%	83.2	25	83.2	2	0	0	1632.72	750	762
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	23	49	0.05%	27.9%	SNEILTAIIQGMR	99.7%	95.7	25	89.3	4	0	0	1445.78	170	182
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	23	49	0.05%	27.9%	SSAYESLMEIVK	99.7%	79.2	25	68.8	3	0	0	1356.67	526	537
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	23	49	0.05%	27.9%	TTLVIMER	99.7%	61.2	25	54.8	4	0	0	962.53	550	557
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	23	49	0.05%	27.9%	TVSPDRLELEAAQK	99.7%	50.9	25	41.3	2	0	0	1556.83	10	23
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	23	49	0.05%	27.9%	VAAGLQIK	99.7%	40.4	25	31.3	2	0	0	799.50	55	62
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	23	49	0.05%	27.9%	VAALQNLVK	99.6%	39.1	25	33.4	2	0	0	955.59	235	243
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	23	49	0.05%	27.9%	VLANPGNSQVAR	99.7%	79.7	25	70.5	2	0	0	1225.66	43	54
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	23	49	0.05%	27.9%	WLAIDANAR	97.5%	31.1	25	25.5	2	0	0	1029.55	80	88
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	23	49	0.05%	27.9%	YLEVVLNTLQQASQAQVDK	99.7%	133	25	133	2	0	0	2147.13	731	749
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	19	23	49	0.05%	27.9%	YMEAFKPFLGIGLK	99.7%	45.2	25	45.2	2	0	0	1613.88	646	659
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	8	8	11	0.01%	9.2%	ALLTFYHVTK	99.6%	39.3	25	33.5	1	0	0	1192.67	147	156
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	8	8	11	0.01%	9.2%	FIVQCMNLIK	99.7%	46.9	25	39.5	1	0	0	1265.67	316	325
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	8	8	11	0.01%	9.2%	LTVDDFEFR	99.7%	52.7	25	48.3	2	0	0	1141.55	541	549
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	8	8	11	0.01%	9.2%	MAFFTYPTLTEICR	98.2%	32.4	25	29.1	2	0	0	1749.83	354	367
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	8	8	11	0.01%	9.2%	NFEDSSPETLEAHK	99.7%	65.6	25	62.2	2	0	0	1603.72	338	351
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	8	8	11	0.01%	9.2%	NQLLPELQVIHNR	99.7%	56.5	25	45.3	1	0	0	1573.88	476	488
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	8	8	11	0.01%	9.2%	SIGTDNVCR	99.7%	46.2	25	42	1	0	0	1021.47	255	263
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	8	8	11	0.01%	9.2%	VAPHALSEEEK	97.2%	30.6	25	23.8	1	0	0	1209.61	77	87
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	23	42	0.04%	22.5%	ACYALENFVENLGPK	99.7%	94.2	25	94.2	2	0	0	1724.83	458	472
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	23	42	0.04%	22.5%	APAALPALCDLLASAADPQIR	99.7%	71.6	25	71	1	0	0	2134.13	34	54
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	23	42	0.04%	22.5%	AQELQAVLGLS	99.7%	52.3	25	52	2	0	0	1128.63	1071	1081
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	23	42	0.04%	22.5%	ATEQLQIVLR	99.7%	64.8	25	44.5	2	0	0	1170.68	24	33
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	23	42	0.04%	22.5%	DNICGALAR	99.7%	43.9	25	36.9	1	0	0	989.48	959	967

Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	23	42	0.04%	22.5%	ELLLPDTER	98.9%	34.6	25	28.7	1	0	0	1085.58	12	20
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	23	42	0.04%	22.5%	EVMPLLLAYLK	99.7%	67.1	25	54.5	6	0	0	1289.75	435	445
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	23	42	0.04%	22.5%	GLEDPSQVVR	99.7%	52.2	25	40.7	2	0	0	1099.57	402	411
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	23	42	0.04%	22.5%	ICSLILADNK	99.7%	52.9	25	45.3	1	0	0	1146.62	1026	1035
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	23	42	0.04%	22.5%	ILCCLTFLVK	99.7%	44.3	25	42.8	2	0	0	1266.70	267	276
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	23	42	0.04%	22.5%	LAELCGVLK	99.7%	53	25	43.3	2	0	0	1002.57	793	801
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	23	42	0.04%	22.5%	LIMAMQTLIPIDEAK	99.7%	69.5	25	68.7	4	0	0	1686.92	206	220
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	23	42	0.04%	22.5%	LLNETLGEVGSPGLLFYSLR	99.7%	64.8	25	64.8	1	0	0	2178.18	163	182
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	23	42	0.04%	22.5%	LLPPLLQIVCK	97.3%	30.8	25	30.8	2	0	0	1293.80	391	401
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	23	42	0.04%	22.5%	LLPVLLSTAQEADPEVR	99.7%	88	25	87.1	2	0	0	1851.02	900	916
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	23	42	0.04%	22.5%	NVALGNAIR	98.9%	34.8	25	28.1	1	0	0	927.54	256	264
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	23	42	0.04%	22.5%	QFAAVLTR	99.5%	38.3	25	12.2	2	0	0	905.52	55	62
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	23	42	0.04%	22.5%	SLILTALQR	99.7%	59.3	25	38.9	2	0	0	1014.63	82	90
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	23	42	0.04%	22.5%	TLTTMAPYLSTEDVPLAR	99.7%	90.4	25	90.1	4	0	0	1979.02	183	200
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	23	42	0.04%	22.5%	VVPSYMQAVNR	99.7%	50.4	25	44.1	2	0	0	1263.65	751	761
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	24	71	0.07%	24.1%	ATAAFILANEHNVALFK	99.7%	101	25	96	2	0	0	1829.99	196	212
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	24	71	0.07%	24.1%	EFQQYLPVVMGPLMK	99.7%	48.7	25	45.9	2	0	0	1779.92	618	632
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	24	71	0.07%	24.1%	EGFVEYTEQVVK	99.7%	69.2	25	60.4	2	0	0	1427.71	694	705
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	24	71	0.07%	24.1%	FLFDSVSSQNVGLR	99.7%	102	25	98.1	9	0	0	1568.81	135	148
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	24	71	0.07%	24.1%	FMQDASDVMQLLLK	99.7%	119	25	110	4	0	0	1638.82	573	586
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	24	71	0.07%	24.1%	FVPYYDLFMPSLK	99.7%	49.6	25	0	7	0	0	1635.81	527	539
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	24	71	0.07%	24.1%	HIVENAVQK	94.9%	28.2	25	26.4	1	0	0	1037.57	540	548
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	24	71	0.07%	24.1%	LQELIQK	99.5%	37.8	25	8.15	2	0	0	871.52	497	503
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	24	71	0.07%	24.1%	LVLEQVVTSIASVADTAEEK	99.7%	112	25	105	2	4	0	2102.12	507	526
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	24	71	0.07%	24.1%	QAEETYENIPGQSK	99.7%	51.2	25	43.5	1	0	0	1593.74	28	41
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	24	71	0.07%	24.1%	QMAAVLLR	95.3%	28.5	25	10.9	1	0	0	901.53	60	67
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	24	71	0.07%	24.1%	SLLIPYLDNLVK	99.7%	44.4	25	26	2	0	0	1387.82	476	487
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	24	71	0.07%	24.1%	SLVEIADTVPK	99.7%	107	25	92.8	8	0	0	1171.66	239	249
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	24	71	0.07%	24.1%	STACQMLVCYAK	99.7%	51.1	25	51.1	2	0	0	1431.64	679	690
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	24	71	0.07%	24.1%	TIECISLIGLAVGK	99.7%	99.2	25	94.7	6	0	0	1473.83	557	570
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	24	71	0.07%	24.1%	VAAAESMPLLLECAR	99.7%	68.5	25	63.6	2	0	0	1630.83	721	735
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	24	71	0.07%	24.1%	VCDIAAELAR	99.7%	54.5	25	40.9	6	0	0	1117.57	109	118
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	24	71	0.07%	24.1%	VIAALLQTMEDQGNQR	99.7%	120	25	112	2	0	0	1786.91	442	457
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	24	71	0.07%	24.1%	VQAHAAAALINFTEDCPK	99.7%	50.8	25	50.8	0	2	0	1955.96	458	475
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	20	24	71	0.07%	24.1%	VSDILHSIFSSYK	99.7%	70.1	25	65.8	2	2	0	1495.78	842	854
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	18	21	58	0.06%	21.2%	AFAVGVQQVLLK	99.7%	84.2	25	70.4	6	0	0	1272.77	295	306
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	18	21	58	0.06%	21.2%	AIFQTIQNR	99.7%	52.7	25	43.5	8	0	0	1090.60	964	972
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	18	21	58	0.06%	21.2%	DGALHMIGSLAEILLK	99.7%	39.2	25	35.2	0	1	0	1696.93	430	445
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	18	21	58	0.06%	21.2%	ENIVEAIIHSPELIR	99.7%	79.8	25	66.8	1	2	0	1732.96	93	107
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	18	21	58	0.06%	21.2%	ETENDDLTNVIQK	99.7%	71.5	25	64.3	4	0	0	1518.73	552	564
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	18	21	58	0.06%	21.2%	EYNEFAEVFLK	99.7%	68	25	64.9	4	0	0	1388.67	284	294
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	18	21	58	0.06%	21.2%	FIQLLSDQSDQSVLIQK	99.7%	114	25	105	3	0	0	1962.05	185	201
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	18	21	58	0.06%	21.2%	FKSDQNLQTALELTR	99.2%	30	25	28.7	0	1	0	1763.93	488	502
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	18	21	58	0.06%	21.2%	GIDQCIPLFVEAALER	99.7%	75.2	25	71.3	3	0	0	1830.94	753	768
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	18	21	58	0.06%	21.2%	GTMDPALR	99.7%	48.6	25	38.2	2	0	0	876.42	12	19
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	18	21	58	0.06%	21.2%	LLEVIILQCK	99.7%	69.6	25	69.6	4	0	0	1228.73	741	750
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	18	21	58	0.06%	21.2%	QLQDIATLADQR	98.9%	34.6	25	26	2	0	0	1371.72	991	1002
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	18	21	58	0.06%	21.2%	SDQNLQTALELTR	99.7%	74.3	25	61.4	4	0	0	1488.77	490	502
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	18	21	58	0.06%	21.2%	SPLVAAMQHFLPVLK	99.7%	86.8	25	86.8	2	0	0	1650.94	168	182
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	18	21	58	0.06%	21.2%	TMGFCYQILTEPNADPR	99.7%	66.3	25	66.3	2	0	0	2012.92	411	427
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	18	21	58	0.06%	21.2%	VLTGVAGEDAECHAAK	99.7%	88	25	88	4	0	0	1627.77	725	740

Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	18	21	58	0.06%	21.2%	WALHILAR	99.7%	45	25	40.5	2	0	0	979.58	263	270
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	18	21	58	0.06%	21.2%	YLEMIYSMCK	99.7%	52.5	25	50.2	3	0	0	1337.59	714	723
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	4	4	6	0.01%	5.3%	EYFEFSEFFLK	98.0%	32.1	25	32.1	1	0	0	1485.69	285	295
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	4	4	6	0.01%	5.3%	IAAENELNQSYK	99.7%	60.2	25	60.2	1	0	0	1379.68	20	31
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	4	4	6	0.01%	5.3%	IINFAPSLLR	99.7%	48.1	25	40	2	0	0	1143.69	32	41
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	4	4	6	0.01%	5.3%	LLEVIILQCK	99.7%	69.6	25	69.6	4	0	0	1228.73	741	750
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	4	4	6	0.01%	5.3%	TYAVGIQQVLLK	99.7%	82.4	25	80.5	2	0	0	1332.79	296	307
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	10	13	25	0.02%	13.1%	EALVDTLTGILSPVQEVR	99.7%	77.9	25	73.4	2	0	0	1940.07	23	40
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	10	13	25	0.02%	13.1%	ELGENLDQILR	99.7%	52.9	25	46.3	1	0	0	1299.69	777	787
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	10	13	25	0.02%	13.1%	EVTDTQMPLVAPVILPEMYK	99.7%	66.5	25	50.4	4	0	0	2290.17	176	195
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	10	13	25	0.02%	13.1%	IFTMAEVYGIR	99.7%	53.4	25	49.2	2	0	0	1299.68	196	206
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	10	13	25	0.02%	13.1%	LIINELSNVMEANAAR	99.7%	107	25	106	4	0	0	1773.92	920	935
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	10	13	25	0.02%	13.1%	LIPTLVSIMQAPADK	99.7%	75.2	25	75.2	4	0	0	1612.90	647	661
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	10	13	25	0.02%	13.1%	LLQHGINADDKR	96.7%	29.9	25	21.6	1	0	0	1379.74	866	877
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	10	13	25	0.02%	13.1%	QLASVILK	99.7%	54.3	25	25.8	1	0	0	871.56	75	82
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	10	13	25	0.02%	13.1%	WTNIPLLVK	99.7%	40.9	25	23.3	2	0	0	1083.66	908	916
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	10	13	25	0.02%	13.1%	YSNDPVVASLAQDIFK	99.7%	111	25	100	4	0	0	1766.90	616	631
Inactive hydroxysteroid dehydrogenase-like protein 1	HSDL1	HSDL1_HUMAN	37.0	100.0%	4	4	7	0.01%	11.8%	AYAEELASR	99.7%	54.5	25	46.8	2	0	0	1009.49	82	90
Inactive hydroxysteroid dehydrogenase-like protein 1	HSDL1	HSDL1_HUMAN	37.0	100.0%	4	4	7	0.01%	11.8%	AYLDHFSR	99.2%	36	25	30.4	2	0	0	1008.49	223	230
Inactive hydroxysteroid dehydrogenase-like protein 1	HSDL1	HSDL1_HUMAN	37.0	100.0%	4	4	7	0.01%	11.8%	GLNIILISR	99.7%	68.1	25	63.1	2	0	0	998.64	91	99
Inactive hydroxysteroid dehydrogenase-like protein 1	HSDL1	HSDL1_HUMAN	37.0	100.0%	4	4	7	0.01%	11.8%	WAVVSGATDGIGK	99.7%	41.8	25	36.7	1	0	0	1260.66	69	81
Inorganic pyrophosphatase	PPA1	IPYR_HUMAN	32.7	99.8%	2	2	4	0.00%	6.6%	DKDFAIDIIK	99.5%	38.6	25	29.1	2	0	0	1177.65	212	221
Inorganic pyrophosphatase	PPA1	IPYR_HUMAN	32.7	99.8%	2	2	4	0.00%	6.6%	YVANLFPYK	96.9%	30.2	25	0	2	0	0	1114.59	80	88
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	4	4	8	0.01%	24.2%	IDLPEYQGEPDEISIQK	99.7%	73.7	25	66.8	2	0	0	1973.97	40	56
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	4	4	8	0.01%	24.2%	IVFVTGNAK	99.7%	52.5	25	44.9	2	0	0	948.55	10	18
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	4	4	8	0.01%	24.2%	KIVFVTGNAK	99.3%	36.4	25	36.4	2	0	0	1076.65	9	18
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	4	4	8	0.01%	24.2%	SAYALCTFALSTGDPSQPVR	99.7%	88.8	25	88.8	2	0	0	2141.03	111	130
Inosine-5'-monophosphate dehydrogenase 2	IMPDH2	IMDH2_HUMAN	55.8	99.8%	2	2	3	0.00%	3.9%	EANEILQR	98.7%	33.7	25	6.72	1	0	0	972.51	196	203
Inosine-5'-monophosphate dehydrogenase 2	IMPDH2	IMDH2_HUMAN	55.8	99.8%	2	2	3	0.00%	3.9%	VAQGVSGAVQDK	99.7%	74.9	25	62	2	0	0	1158.61	439	450
Insulin receptor substrate 4	IRS4	IRS4_HUMAN	133.8	100.0%	8	8	18	0.02%	7.6%	AAVSAFPTDSLER	99.7%	55	25	45.7	2	0	0	1363.69	1098	1110
Insulin receptor substrate 4	IRS4	IRS4_HUMAN	133.8	100.0%	8	8	18	0.02%	7.6%	ANPLSLDSAR	99.7%	68.4	25	59	2	0	0	1043.55	985	994
Insulin receptor substrate 4	IRS4	IRS4_HUMAN	133.8	100.0%	8	8	18	0.02%	7.6%	DAEIPEGAAR	99.7%	45.3	25	37.5	2	0	0	1028.50	675	684
Insulin receptor substrate 4	IRS4	IRS4_HUMAN	133.8	100.0%	8	8	18	0.02%	7.6%	GAQDVAGGSNPGAHNPSANLAR	99.4%	31.1	25	31.1	0	2	0	2060.99	1177	1198
Insulin receptor substrate 4	IRS4	IRS4_HUMAN	133.8	100.0%	8	8	18	0.02%	7.6%	LAPSPARPR	99.7%	57.9	25	57.9	4	0	0	964.57	436	444
Insulin receptor substrate 4	IRS4	IRS4_HUMAN	133.8	100.0%	8	8	18	0.02%	7.6%	LEYYENAR	98.1%	32.3	25	26	2	0	0	1057.49	109	116
Insulin receptor substrate 4	IRS4	IRS4_HUMAN	133.8	100.0%	8	8	18	0.02%	7.6%	LLQEEEQER	99.7%	52.3	25	35.7	3	0	0	1173.57	1074	1082
Insulin receptor substrate 4	IRS4	IRS4_HUMAN	133.8	100.0%	8	8	18	0.02%	7.6%	WFQPVANAADAEAVR	99.7%	60.8	25	53.3	1	0	0	1644.81	1162	1176
Insulin-degrading enzyme	IDE	IDE_HUMAN	118.0	99.8%	2	2	5	0.00%	2.2%	NLYVTFPIPDLQK	99.6%	39.3	25	39.3	2	0	0	1547.85	312	324
Insulin-degrading enzyme	IDE	IDE_HUMAN	118.0	99.8%	2	2	5	0.00%	2.2%	QDDKFFLPK	95.5%	28.7	25	6.58	3	0	0	1137.59	563	571
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	22	36	137	0.14%	46.4%	AIETFSGK	99.7%	52.7	25	47.4	2	0	0	852.45	53	60
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	22	36	137	0.14%	46.4%	AISVHSTPEGCSSACK	99.7%	76.7	25	76.7	4	4	0	1690.75	243	258
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	22	36	137	0.14%	46.4%	DQTPDENDQVIVK	99.7%	76.3	25	68.7	5	0	0	1500.72	526	538
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	22	36	137	0.14%	46.4%	EEVKLETHIR	99.7%	55.4	25	48.1	3	2	0	1253.68	484	493
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	22	36	137	0.14%	46.4%	IIGHFYASQMAQR	99.7%	63.7	25	61.7	8	8	0	1521.76	539	551
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	22	36	137	0.14%	46.4%	ILAHNNFVGR	99.7%	57.8	25	50.3	4	0	0	1140.63	281	290
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	22	36	137	0.14%	46.4%	IRDILAQVK	99.7%	50.2	25	26.9	4	0	0	1055.66	553	561
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	22	36	137	0.14%	46.4%	ISYSGQFLVK	99.7%	81.5	25	75.1	3	0	0	1141.63	27	36
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	22	36	137	0.14%	46.4%	ITISSLQDLTLYNPER	99.7%	89.4	25	86.9	4	0	0	1862.99	310	325
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	22	36	137	0.14%	46.4%	LKEENFFGPK	99.7%	53.6	25	52.3	2	1	0	1208.63	474	483
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	22	36	137	0.14%	46.4%	LLVPTQYVGAIIGK	99.7%	106	25	106	16	1	0	1471.89	200	213
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	22	36	137	0.14%	46.4%	LNGHQLENHALK	99.7%	43.1	25	37.7	2	2	0	1373.73	139	150

Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	22	36	137	0.14%	46.4%	LYIGNLNESVTPADLEK	99.7%	89.5	25	81.2	6	0	0	1875.97	4	20
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	22	36	137	0.14%	46.4%	MILEIMHK	99.7%	44	25	39.5	4	0	0	1014.55	259	266
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	22	36	137	0.14%	46.4%	MVIITGPPEAQFK	99.7%	67	25	56.8	11	0	0	1430.77	453	465
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	22	36	137	0.14%	46.4%	QGSPVAAGAPAK	99.7%	70.4	25	63.8	4	0	0	1053.57	179	190
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	22	36	137	0.14%	46.4%	QQQVDIPLR	99.7%	58.8	25	48	7	0	0	1096.61	191	199
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	22	36	137	0.14%	46.4%	RLEIEHSVPK	99.6%	33.3	25	33.3	2	4	0	1207.68	67	76
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	22	36	137	0.14%	46.4%	SGYAFVDCPDEHWAMK	99.7%	80.4	25	77.6	4	2	0	1912.80	37	52
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	22	36	137	0.14%	46.4%	TADEVPLK	99.7%	52.8	25	40.2	4	0	0	872.47	273	280
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	22	36	137	0.14%	46.4%	TVNELQNLTAAEVVVPR	99.7%	96.1	25	86.8	6	4	0	1853.01	509	525
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	22	36	137	0.14%	46.4%	VSYIPDEQIAQGPENGR	99.7%	76.8	25	76.8	4	0	0	1872.91	151	167
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	12	13	37	0.04%	31.2%	DQTPDENEEVIVR	99.7%	73.2	25	58.4	3	0	0	1543.72	548	560
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	12	13	37	0.04%	31.2%	IAPAEGPDVSER	99.7%	52.8	25	46.3	4	0	0	1240.62	463	474
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	12	13	37	0.04%	31.2%	IIGHFFASQTAQR	99.7%	54.1	25	50.4	2	0	0	1475.78	561	573
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	12	13	37	0.04%	31.2%	ILVPTQFVGAIIGK	99.7%	90.7	25	0	6	0	0	1455.89	198	211
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	12	13	37	0.04%	31.2%	ISYIPDEEVSSPSPPQR	99.7%	70.8	25	68.9	3	0	0	1900.93	152	168
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	12	13	37	0.04%	31.2%	ITISSLQDLSIYNPER	99.7%	50.1	25	44.3	1	0	0	1848.97	308	323
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	12	13	37	0.04%	31.2%	KLPLAGQVLLK	95.6%	28.8	25	23.7	1	0	0	1179.78	27	37
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	12	13	37	0.04%	31.2%	LAEEIPLK	99.2%	35.9	25	30.7	3	0	0	912.54	271	278
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	12	13	37	0.04%	31.2%	LSGHQFENYSFK	99.7%	43	25	40.8	3	4	0	1456.69	140	151
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	12	13	37	0.04%	31.2%	LYIGNLSPAVTADDLR	99.7%	66.9	25	66.9	3	0	0	1717.91	5	20
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	12	13	37	0.04%	31.2%	MVIITGPPEAQFK	99.7%	67	25	56.8	11	0	0	1430.77	475	487
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	12	13	37	0.04%	31.2%	SGYAFVDYPDQNWAIR	99.7%	84	25	84	4	0	0	1901.88	38	53
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	12	13	37	0.04%	31.2%	TVNELQNLTSAEVIVPR	99.6%	39.4	25	39.4	2	0	0	1883.02	531	547
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	12	13	37	0.04%	31.2%	YPQGVASQR	99.7%	53	25	39.7	4	0	0	1005.51	589	597
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	17	21	51	0.05%	42.0%	ALQSGPPQSR	99.7%	42.6	25	29.9	2	0	0	1040.55	568	577
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	17	21	51	0.05%	42.0%	DQTPDENDQVVVK	99.7%	73.7	25	63.4	2	0	0	1486.70	526	538
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	17	21	51	0.05%	42.0%	FTEEIPLK	99.7%	41.8	25	31.3	2	0	0	976.54	273	280
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	17	21	51	0.05%	42.0%	IAPAEAPDAK	99.7%	57.3	25	57.3	4	0	0	982.52	441	450
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	17	21	51	0.05%	42.0%	IKEENFVSPK	99.7%	53.4	25	38.8	2	0	0	1190.64	474	483
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	17	21	51	0.05%	42.0%	ILAHNNFVGR	99.7%	57.8	25	50.3	4	0	0	1140.63	281	290
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	17	21	51	0.05%	42.0%	IPVSGPFLVK	99.6%	39.6	25	39.6	4	0	0	1056.65	27	36
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	17	21	51	0.05%	42.0%	ITGHFYACQVAQR	99.7%	71.2	25	68	2	2	0	1550.75	539	551
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	17	21	51	0.05%	42.0%	ITISPLQELTLYNPER	99.7%	73.9	25	73.9	5	0	0	1887.02	310	325
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	17	21	51	0.05%	42.0%	LLVPTQFVGAIIGK	99.7%	90.7	25	0	6	0	0	1455.89	200	213
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	17	21	51	0.05%	42.0%	LNGFQLENFTLK	99.7%	55.2	25	48.2	2	0	0	1423.76	139	150
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	17	21	51	0.05%	42.0%	LYIGNLSENAAPSDLESIFK	99.7%	76.6	25	76.6	2	0	0	2181.11	4	23
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	17	21	51	0.05%	42.0%	MVIITGPPEAQFK	99.7%	67	25	56.8	11	0	0	1430.77	453	465
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	17	21	51	0.05%	42.0%	SILEIMHK	99.4%	37.5	25	34	2	0	0	970.54	259	266
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	17	21	51	0.05%	42.0%	SITILSTPEGTSAACK	99.7%	93.3	25	88.8	2	0	0	1635.83	243	258
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	17	21	51	0.05%	42.0%	TGYAFVDCPDESWALK	99.7%	86.2	25	86.2	2	0	0	1858.83	37	52
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	17	21	51	0.05%	42.0%	TVNELQNLSSAEVVVPR	99.7%	88.6	25	78.8	2	2	0	1854.99	509	525
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	17	21	51	0.05%	42.0%	VAYIPDEMAAQQNPLQQPR	99.7%	80.1	25	80.1	3	1	0	2169.08	151	169
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	17	21	51	0.05%	42.0%	VPSFAAGR	99.7%	54.5	25	44.3	2	0	0	804.44	494	501
Integral membrane protein GPR180	GPR180	GP180_HUMAN	49.4	99.8%	2	2	2	0.00%	6.4%	GSFSSTAAQDAQGQR	99.7%	80.8	25	77.4	1	0	0	1510.69	27	41
Integral membrane protein GPR180	GPR180	GP180_HUMAN	49.4	99.8%	2	2	2	0.00%	6.4%	LQQSSHGYSCSEK	97.7%	31.5	25	27.9	1	0	0	1510.66	82	94
Integrator complex subunit 11	CPSF3L	INT11_HUMAN	67.7	100.0%	2	2	2	0.00%	4.0%	VPIYFSTGLTEK	99.7%	45.5	25	43.9	1	0	0	1354.73	263	274
Integrator complex subunit 11	CPSF3L	INT11_HUMAN	67.7	100.0%	2	2	2	0.00%	4.0%	VTPLGAGQDVGR	99.7%	63.4	25	52.6	1	0	0	1169.63	6	17
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	100.0%	8	8	16	0.02%	17.2%	DLKPSNIFLVDTK	99.7%	57.1	25	51.7	2	0	0	1489.83	414	426
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	100.0%	8	8	16	0.02%	17.2%	EIELIGSGGFGQVFK	99.7%	106	25	102	2	0	0	1580.83	269	283
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	100.0%	8	8	16	0.02%	17.2%	GVDYIHSK	99.3%	36.5	25	22.2	2	0	0	918.47	401	408
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	100.0%	8	8	16	0.02%	17.2%	IGDFGLVTSLK	99.7%	79	25	67.5	2	0	0	1149.65	430	440

Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	100.0%	8	8	16	0.02%	17.2%	LAVEILNK	99.7%	45.4	25	30.1	2	0	0	899.56	70	77
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	100.0%	8	8	16	0.02%	17.2%	LAYLQILSEETSVK	99.7%	83.1	25	83.1	2	0	0	1593.87	160	173
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	100.0%	8	8	16	0.02%	17.2%	VLALELFEQITK	99.7%	64.7	25	64.7	3	0	0	1403.81	389	400
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	100.0%	8	8	16	0.02%	17.2%	YMSPEQISSQDYGK	99.7%	62	25	62	1	0	0	1632.72	454	467
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	13	21	65	0.06%	45.0%	AAEAAINILK	99.7%	62.1	25	44.7	10	0	0	1013.60	91	100
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	13	21	65	0.06%	45.0%	ANASICFAVPDPLMPDPSK	99.7%	73.7	25	72.2	8	0	0	2029.97	101	119
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	13	21	65	0.06%	45.0%	EDSGTFSLGK	99.7%	59.5	25	51.9	3	0	0	1040.49	16	25
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	13	21	65	0.06%	45.0%	HRAEAPPLER	97.7%	31.4	25	28.6	2	0	0	1175.63	6	15
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	13	21	65	0.06%	45.0%	LESFMETGK	99.7%	55	25	47.5	5	0	0	1041.49	165	173
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	13	21	65	0.06%	45.0%	LPEYTLSQEGGPAHK	99.7%	77.6	25	77.6	2	4	0	1626.81	142	156
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	13	21	65	0.06%	45.0%	LPEYTLSQEGGPAHKR	99.7%	85.6	25	81.9	2	2	0	1782.91	142	157
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	13	21	65	0.06%	45.0%	REYTTICR	98.7%	33.7	25	26.8	2	0	0	1098.54	157	164
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	13	21	65	0.06%	45.0%	SDVQIHVPTFTFR	99.7%	65.6	25	63.1	4	4	0	1546.80	57	69
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	13	21	65	0.06%	45.0%	SLLSIPNTDYIQLLSEIAK	99.7%	55.2	25	55.2	1	0	0	2118.17	232	250
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	13	21	65	0.06%	45.0%	TPIQVLHEYGMK	99.7%	71.3	25	66.8	6	4	0	1415.74	34	45
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	13	21	65	0.06%	45.0%	VTVGDITCTGEGTSK	99.7%	111	25	111	4	0	0	1524.72	70	84
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	13	21	65	0.06%	45.0%	VTVGDITCTGEGTSKK	99.7%	71.1	25	69.5	2	0	0	1652.82	70	85
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	19	29	125	0.12%	47.9%	AQDPSEVLTMLTNETGFEISSSDATVK	99.6%	32.7	25	32.7	0	2	0	2870.36	148	174
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	19	29	125	0.12%	47.9%	GTMTTGHNVADLVVILK	99.7%	85.7	25	75.4	5	4	0	1768.96	111	127
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	19	29	125	0.12%	47.9%	ILITTVPPNLR	99.7%	50.3	25	48.3	12	0	0	1236.77	175	185
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	19	29	125	0.12%	47.9%	ILITTVPPNLRK	99.1%	35.3	25	35.3	2	1	0	1364.86	175	186
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	19	29	125	0.12%	47.9%	ILPTLEAVAALGNK	99.7%	102	25	95.1	13	2	0	1409.84	128	141
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	19	29	125	0.12%	47.9%	ILPTLEAVAALGNKVVESLR	99.7%	62.6	25	62.6	2	0	0	2093.23	128	147
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	19	29	125	0.12%	47.9%	ILSHGGFR	99.7%	50.8	25	37.3	2	0	0	886.49	320	327
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	19	29	125	0.12%	47.9%	ILSHGGFRK	97.2%	30.5	25	15.2	1	0	0	1014.58	320	328
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	19	29	125	0.12%	47.9%	KGTMTTGHNVADLVVILK	99.1%	29.6	25	29.6	0	2	0	1913.05	110	127
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	19	29	125	0.12%	47.9%	KLDPELHLDIK	99.7%	61.3	25	35.5	2	5	0	1320.75	186	196
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	19	29	125	0.12%	47.9%	LDPELHLDIK	99.7%	52.3	25	46.3	2	0	0	1192.66	187	196
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	19	29	125	0.12%	47.9%	NQDLAPNSAEQASILSLVTK	99.7%	124	25	124	14	8	0	2099.10	61	80
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	19	29	125	0.12%	47.9%	QPLALNVAYR	99.7%	68.1	25	56.1	12	0	0	1144.65	260	269
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	19	29	125	0.12%	47.9%	RNQDLAPNSAEQASILSLVTK	99.7%	70.6	25	67.6	0	2	0	2255.20	60	80
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	19	29	125	0.12%	47.9%	VHTVMTLEQQDMVCYTAQTLVR	99.7%	73.3	25	73.3	0	2	0	2655.26	298	319
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	19	29	125	0.12%	47.9%	VKPAPDETSFSEALLK	99.7%	80	25	68.6	5	7	0	1731.92	44	59
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	19	29	125	0.12%	47.9%	VKPAPDETSFSEALLKR	99.7%	69.3	25	67.5	2	0	0	1888.02	44	60
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	19	29	125	0.12%	47.9%	VLQSALAAIR	99.7%	96.7	25	87.3	11	0	0	1041.64	197	206
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	19	29	125	0.12%	47.9%	WFEENASQSTVK	99.7%	68.9	25	68.9	5	0	0	1425.66	210	221
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	AEPPQAMNALMR	99.7%	59.3	25	59.3	9	0	0	1328.65	397	408
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	AVSDWIDEQEK	99.7%	70.7	25	57.7	4	0	0	1319.61	44	54
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	AYAALAALEK	99.7%	87.8	25	62.4	18	0	0	1020.57	578	587
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	CLAALASLR	99.7%	63.8	25	45.6	7	0	0	974.55	203	211
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	EATDAIGHLDR	99.7%	74.4	25	56.2	10	0	0	1197.59	298	308
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	EDITQSAQHALR	99.7%	82.4	25	70	10	5	0	1368.69	312	323
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	EPPLSLTIHLTSPVVR	99.7%	97.6	25	95.6	2	4	0	1759.01	162	177
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	EPPLSLTIHLTSPVVREEMEK	95.5%	23.2	25	23.2	0	1	0	2421.27	162	182
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	FNYSGSGGR	99.7%	63.7	25	49.7	4	0	0	944.42	807	815
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	FVMEVEVDGQK	99.7%	68.9	25	52.2	12	0	0	1280.62	555	565
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	GDLDLELVLLCK	99.7%	74.6	25	71.4	2	0	0	1387.75	106	117
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	GEDSAEETEAKPAVVAPAPVVEAVSTPSAAFPSDATAEQGPILTK	95.6%	23.4	25	23.4	0	1	0	4435.20	479	523
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	GWPLELLCEK	99.7%	67.2	25	0	9	0	0	1244.63	248	257
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	GYNHGQGSYSYSNSYNSPGGGGGSDYNYESK	99.7%	87.1	25	87.1	0	2	0	3253.30	776	806
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	HGKNPVMELNEK	95.3%	23.1	25	20.2	0	1	0	1411.70	524	535

Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	HSSVYPTQEELEAVQNMVSHTER	99.7%	51.1	25	51.1	0	4	0	2671.24	18	40
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	IFVNDDR	99.7%	43	25	28.1	2	0	0	878.44	6	12
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	IFVNDDRHVMAK	99.7%	58.1	25	47.2	4	4	0	1444.74	6	17
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	LAAFGQLHK	99.7%	52.1	25	38.5	16	0	0	984.56	324	332
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	LFPDTPLALDANK	99.7%	75.8	25	67.8	11	0	0	1414.76	588	600
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	LFPDTPLALDANKK	99.7%	69.8	25	60.6	8	0	0	1542.85	588	601
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	LNQLKPGLQYK	99.7%	44.1	25	35.7	8	3	0	1301.76	409	419
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	LVSQTGPVHAPIFTMSVEVDGNSFEASGPSK	99.7%	77	25	77	0	2	0	3204.55	420	450
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	NADHSMNYQYR	99.7%	53.3	25	53.2	6	4	0	1398.59	884	894
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	NENPVDYTVQIPPSTTYAITPMK	99.7%	78.3	25	78.3	4	2	0	2595.27	349	371
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	NPVMELNEK	99.7%	51.6	25	46.5	12	0	0	1089.52	527	535
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	NPVMELNEKR	99.7%	54.3	25	41.3	4	0	0	1229.63	527	536
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	NTKEPPLSLTIHLTSPVVR	99.7%	58.8	25	58.8	0	2	0	2102.20	159	177
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	RPMEEDGEEKSPSK	99.7%	56.8	25	56.8	1	8	0	1618.74	372	385
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	SCVIVIR	99.7%	44.8	25	0	2	0	0	846.49	225	231
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	SGGNSYGSGGASYNPGSHGGYGGGSGGGSSYQGK	99.7%	79.6	25	79.6	0	4	0	3012.24	816	849
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	SIGTANRPMGAGEALR	99.7%	53.1	25	44.5	6	3	0	1600.82	258	273
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	SIGTANRPMGAGEALRR	99.7%	45	25	41	0	2	0	1756.92	258	274
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	VLAGETLSVNDPPDVLDR	99.7%	116	25	116	12	1	0	1909.99	183	200
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	VLECLASGIVMPDGSGIYDPCEK	99.7%	98.4	25	98.4	4	1	0	2526.16	275	297
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	VLGMDPLPSK	99.7%	52.8	25	43.6	11	0	0	1056.58	333	342
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	VLQDMGLPTGAEGR	99.7%	94.9	25	87.7	16	0	0	1443.73	461	474
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	VPTWGPLR	99.7%	55.7	25	27.3	2	0	0	925.53	240	247
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	YELISETGGSHDK	99.7%	78.1	25	68.1	2	1	0	1435.67	541	553
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	40	68	281	0.28%	57.4%	YELISETGGSHDKR	99.7%	73.9	25	70.1	6	2	0	1591.77	541	554
Intraflagellar transport protein 27 homolog	IFT27	IFT27_HUMAN	20.5	99.8%	2	2	3	0.00%	15.6%	SQAPGISLPGVLVGNK	99.7%	78.2	25	78.2	2	0	0	1536.87	109	124
Intraflagellar transport protein 27 homolog	IFT27	IFT27_HUMAN	20.5	99.8%	2	2	3	0.00%	15.6%	SYTLTTGMDLVVK	99.7%	40.1	25	37.4	1	0	0	1443.74	35	47
Iron-sulfur protein NUBPL	NUBPL	NUBPL_HUMAN	34.1	99.8%	2	2	4	0.00%	10.7%	AIGLLDVDVYGPSVPK	99.7%	86.7	25	86.7	2	0	0	1642.91	100	115
Iron-sulfur protein NUBPL	NUBPL	NUBPL_HUMAN	34.1	99.8%	2	2	4	0.00%	10.7%	STTAVNLALALAANDSSK	99.7%	50.6	25	50.6	2	0	0	1746.92	82	99
Isobutyryl-CoA dehydrogenase, mitochondrial	ACAD8	ACAD8_HUMAN	45.1	100.0%	3	3	3	0.00%	8.9%	AVIFEDCAVPVANR	96.8%	30.1	25	30.1	1	0	0	1560.78	245	258
Isobutyryl-CoA dehydrogenase, mitochondrial	ACAD8	ACAD8_HUMAN	45.1	100.0%	3	3	3	0.00%	8.9%	IGSEGQGFLIAVR	99.7%	56.6	25	45.1	1	0	0	1346.74	259	271
Isobutyryl-CoA dehydrogenase, mitochondrial	ACAD8	ACAD8_HUMAN	45.1	100.0%	3	3	3	0.00%	8.9%	NAAVALQEER	99.7%	44	25	38.4	1	0	0	1100.57	335	344
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	10	13	26	0.03%	30.3%	APIQWEER	99.7%	66.8	25	57.5	2	0	0	1028.52	59	66
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	10	13	26	0.03%	30.3%	CSDFTEEICR	99.7%	67.8	25	57.5	2	0	0	1316.52	351	360
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	10	13	26	0.03%	30.3%	DMANPTALLLSAVMMLR	99.7%	83.3	25	77.3	2	0	0	1894.94	300	316
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	10	13	26	0.03%	30.3%	IAEFAFEYAR	99.7%	76.9	25	69.7	2	0	0	1216.60	179	188
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	10	13	26	0.03%	30.3%	IEAACFATIK	99.7%	65.8	25	59.8	2	0	0	1123.58	327	336
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	10	13	26	0.03%	30.3%	LITEGASKR	99.3%	37	25	21.9	2	0	0	974.56	170	178
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	10	13	26	0.03%	30.3%	MSDGLFLQK	99.7%	55.3	25	47	4	0	0	1038.53	206	214
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	10	13	26	0.03%	30.3%	NVTAIQGPGGK	99.7%	67.6	25	64	2	0	0	1041.57	67	77
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	10	13	26	0.03%	30.3%	TPIAAGHPSMNLLLR	99.7%	67.6	25	67.6	4	2	0	1590.88	101	115
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	10	13	26	0.03%	30.3%	TPYTDVNIVTIR	99.7%	73.9	25	65	2	0	0	1391.75	135	146
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	11	15	30	0.03%	33.5%	DMGGYSTTTDFIK	99.7%	77.1	25	76.3	4	0	0	1435.64	362	374
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	11	15	30	0.03%	33.5%	EQTEGEYSSLEHESAR	99.7%	85.2	25	82	2	1	0	1851.80	165	180
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	11	15	30	0.03%	33.5%	FAFDYATKK	99.3%	36.6	25	34.3	2	0	0	1090.56	200	208
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	11	15	30	0.03%	33.5%	GELASYDMR	99.7%	43.7	25	41.5	4	0	0	1041.47	123	131
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	11	15	30	0.03%	33.5%	HLNLEYHSSMIADAVK	95.0%	22.9	25	22.9	0	1	0	1843.90	335	350
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	11	15	30	0.03%	33.5%	HNNLDLVIIR	99.7%	54.2	25	40.3	2	0	0	1206.70	155	164
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	11	15	30	0.03%	33.5%	HPFAQAVGR	98.4%	32.9	25	28.3	1	0	0	982.52	309	317
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	11	15	30	0.03%	33.5%	LGDGLFLQCCEEVAELYPK	99.7%	86.6	25	86.6	2	0	0	2241.06	224	242
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	11	15	30	0.03%	33.5%	NIANPTAMLLSASNMLR	99.7%	130	25	88.8	7	0	0	1832.94	318	334

Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	11	15	30	0.03%	33.5%	SVIGHLQTK	98.1%	32.2	25	32.2	2	0	0	982.57	375	383
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	11	15	30	0.03%	33.5%	TRDMGGYSTTTDFIK	99.2%	35.8	25	35.3	2	0	0	1708.79	360	374
Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G	IDH3G_HUMAN	42.8	100.0%	4	4	7	0.01%	10.4%	LGDGLFLQCCR	99.7%	63.7	25	63.7	2	0	0	1338.63	227	237
Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G	IDH3G_HUMAN	42.8	100.0%	4	4	7	0.01%	10.4%	LHSYATSIR	95.4%	28.6	25	14.4	1	0	0	1047.56	341	349
Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G	IDH3G_HUMAN	42.8	100.0%	4	4	7	0.01%	10.4%	SLPGVVTR	99.3%	37	25	27.4	2	0	0	828.49	150	157
Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G	IDH3G_HUMAN	42.8	100.0%	4	4	7	0.01%	10.4%	TSLDLYANVIHCK	99.7%	55.1	25	51.1	2	0	0	1533.77	137	149
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	17	22	42	0.04%	42.9%	ATDFVADR	99.7%	40.2	25	37.7	2	0	0	894.43	181	188
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	17	22	42	0.04%	42.9%	CATITPDEAR	99.7%	45.5	25	42.6	2	0	0	1133.53	113	122
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	17	22	42	0.04%	42.9%	DQTDDQVTIDSALATQK	99.7%	150	25	150	2	0	0	1848.88	90	106
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	17	22	42	0.04%	42.9%	FKDIFQEIFDK	99.7%	62.1	25	50.1	2	0	0	1429.74	262	272
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	17	22	42	0.04%	42.9%	GKLDGNQDLIR	99.7%	62.4	25	52	2	1	0	1228.66	383	393
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	17	22	42	0.04%	42.9%	GRPTSTNPIASIFAWTR	99.7%	42.8	25	42.8	0	2	0	1874.99	361	377
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	17	22	42	0.04%	42.9%	IIWQFIK	98.3%	32.8	25	27.4	2	0	0	947.57	61	67
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	17	22	42	0.04%	42.9%	LIDDMVAQVLK	99.7%	82.4	25	69.3	4	0	0	1244.69	289	299
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	17	22	42	0.04%	42.9%	LILPHVDIQLK	99.7%	46.3	25	30.4	2	1	0	1288.80	70	80
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	17	22	42	0.04%	42.9%	LNEHFLNTTDFLDTIK	99.7%	64.4	25	59.1	2	3	0	1920.97	427	442
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	17	22	42	0.04%	42.9%	NILGGTVFR	99.1%	35.5	25	29.1	2	0	0	976.56	141	149
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	17	22	42	0.04%	42.9%	NILGGTVFREPIICK	99.7%	57.3	25	57.3	2	0	0	1716.95	141	155
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	17	22	42	0.04%	42.9%	SSGGFVWACK	99.7%	65.8	25	55.9	2	0	0	1098.50	300	309
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	17	22	42	0.04%	42.9%	TIEAEAAHGTVTR	99.7%	87.6	25	83.4	2	0	0	1355.69	341	353
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	17	22	42	0.04%	42.9%	VAKPVVEMDGDEMTR	99.7%	56.7	25	56.7	0	1	0	1708.79	46	60
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	17	22	42	0.04%	42.9%	VCVETVESGAMTK	99.7%	120	25	110	4	0	0	1410.66	401	413
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	17	22	42	0.04%	42.9%	YFDLGLPNR	99.7%	51.9	25	44.1	2	0	0	1094.56	81	89
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	26	30	60	0.06%	24.6%	AEPDHMVLGK	97.2%	30.7	25	26	1	0	0	1112.54	894	903
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	26	30	60	0.06%	24.6%	APLKPYPVSPSDK	99.7%	58.2	25	50.3	2	2	0	1398.76	1039	1051
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	26	30	60	0.06%	24.6%	AVPSWFVR	99.3%	36.7	25	28.5	2	0	0	961.53	411	418
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	26	30	60	0.06%	24.6%	CNLVPTDEITVYYK	99.6%	39.6	25	30	1	0	0	1714.84	1001	1014
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	26	30	60	0.06%	24.6%	DVLLPWYNAYR	98.7%	33.9	25	33.9	1	0	0	1409.72	651	661
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	26	30	60	0.06%	24.6%	EFEDAFPADFIAEGIDQTR	99.7%	120	25	120	2	0	0	2170.99	547	565
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	26	30	60	0.06%	24.6%	EIVVIHQDPEALK	99.7%	62.6	25	48.3	2	0	0	1490.82	849	861
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	26	30	60	0.06%	24.6%	ESVDHLTIPSR	99.7%	48.5	25	29.2	2	0	0	1253.65	501	511
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	26	30	60	0.06%	24.6%	FLIQNVLR	99.7%	44.3	25	31.5	4	0	0	1002.61	662	669
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	26	30	60	0.06%	24.6%	FVDILTNWYVR	99.7%	70.1	25	64.1	4	0	0	1425.75	726	736
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	26	30	60	0.06%	24.6%	GSELEITLTR	99.7%	77.2	25	50.1	2	0	0	1118.61	1062	1071
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	26	30	60	0.06%	24.6%	LESDYEILER	99.7%	79	25	68.4	2	0	0	1266.62	269	278
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	26	30	60	0.06%	24.6%	LFLNETQTQEITEDIPVK	99.7%	115	25	106	2	0	0	2118.10	1227	1244
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	26	30	60	0.06%	24.6%	LLILMEAR	99.7%	53.6	25	28.1	4	0	0	958.58	255	262
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	26	30	60	0.06%	24.6%	LYLINSPVVR	99.7%	58.1	25	50.6	3	0	0	1173.70	625	634
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	26	30	60	0.06%	24.6%	MGITEYNNQCR	99.7%	60.3	25	60.3	3	0	0	1401.59	111	121
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	26	30	60	0.06%	24.6%	NNDLCYWVPELVR	99.7%	58.9	25	53.4	2	0	0	1677.81	429	441
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	26	30	60	0.06%	24.6%	NVIVNGLVLASDGQK	99.7%	104	25	104	2	0	0	1526.85	586	600
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	26	30	60	0.06%	24.6%	QLSSEELEQFQK	99.7%	65.9	25	61.4	2	0	0	1465.72	918	929
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	26	30	60	0.06%	24.6%	TESAVSQMQSVIELGR	99.7%	111	25	106	4	0	0	1734.87	818	833
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	26	30	60	0.06%	24.6%	TGTIVVEGHELHDEDIR	99.7%	39.4	25	38	0	2	0	1919.95	930	946
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	26	30	60	0.06%	24.6%	TVYVSVLPTTADF	99.3%	36.7	25	34.7	1	0	0	1412.73	1250	1262
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	26	30	60	0.06%	24.6%	VCMDFNIIR	99.7%	45.4	25	42.3	2	0	0	1183.56	335	343
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	26	30	60	0.06%	24.6%	VENMVDQLLR	99.7%	94.7	25	81.1	2	0	0	1216.64	419	428
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	26	30	60	0.06%	24.6%	YAHQSGFHVDR	98.4%	27.2	25	27.2	0	1	0	1316.61	71	81
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	26	30	60	0.06%	24.6%	YIIEELNVR	99.7%	52.9	25	10.8	3	0	0	1148.63	869	877
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	18	23	44	0.04%	21.5%	ASPLLPANHVTMAK	99.7%	43.6	25	39	3	0	0	1449.79	373	386
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	18	23	44	0.04%	21.5%	AVLEEGTDVVIK	99.7%	98.3	25	91.1	3	0	0	1272.70	434	445

Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	18	23	44	0.04%	21.5%	DQLGGWFQSSLLTSVAAR	99.7%	89.8	25	89.8	2	0	0	1935.99	626	643
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	18	23	44	0.04%	21.5%	DSFLGSIPGK	99.7%	66.3	25	50.8	2	0	0	1020.54	887	896
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	18	23	44	0.04%	21.5%	EAQNLSAMEIR	99.7%	74	25	61.4	4	0	0	1261.62	171	181
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	18	23	44	0.04%	21.5%	ELSNFYFSIIK	99.7%	77.5	25	65.2	2	0	0	1360.71	793	803
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	18	23	44	0.04%	21.5%	EMTADVIELK	99.7%	50.9	25	27.5	2	0	0	1148.59	948	957
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	18	23	44	0.04%	21.5%	EPPYGADVLR	99.7%	42.5	25	33.5	2	0	0	1116.57	688	697
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	18	23	44	0.04%	21.5%	FLINLEGGDIR	99.7%	70.1	25	51.3	2	0	0	1246.68	960	970
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	18	23	44	0.04%	21.5%	FLINLEGGDIREESSYK	99.7%	35.9	25	29.3	0	2	0	1969.99	960	976
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	18	23	44	0.04%	21.5%	FPLLKPSPK	99.7%	43.8	25	36.3	2	0	0	1026.63	273	281
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	18	23	44	0.04%	21.5%	SCQTALVEILDVIVR	99.7%	95.7	25	92.1	2	1	0	1715.94	818	832
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	18	23	44	0.04%	21.5%	SGDLYVLAADK	99.7%	88.4	25	78.7	2	0	0	1151.59	326	336
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	18	23	44	0.04%	21.5%	SYKPVFWSPSSR	99.7%	40.1	25	26	2	0	0	1440.73	239	250
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	18	23	44	0.04%	21.5%	TALAEAELEYNPEHVSR	99.7%	84.2	25	75.8	2	2	0	1928.93	251	267
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	18	23	44	0.04%	21.5%	TKDEYLINSQTTEHIVK	99.7%	49.4	25	48.2	0	2	0	2019.04	539	555
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	18	23	44	0.04%	21.5%	TVIVHGFTLGEK	99.7%	71.5	25	61.6	2	1	0	1300.73	650	661
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	18	23	44	0.04%	21.5%	YTAESSDTLCPR	99.7%	73.7	25	70.2	2	0	0	1399.62	993	1004
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	6	6	8	0.01%	9.3%	ALMGSPQLVAAVVR	99.7%	41.4	25	34.6	1	0	0	1411.81	178	191
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	6	6	8	0.01%	9.3%	ISEDKNPDYR	98.9%	34.7	25	33.1	1	0	0	1236.59	652	661
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	6	6	8	0.01%	9.3%	LAEPSQLLK	98.9%	34.5	25	20.9	1	0	0	998.59	116	124
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	6	6	8	0.01%	9.3%	LLNDEDPVVVTK	99.7%	48.2	25	44.2	1	0	0	1341.73	150	161
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	6	6	8	0.01%	9.3%	LNYGIPAIVK	99.4%	37.1	25	20.7	2	0	0	1087.65	478	487
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	6	6	8	0.01%	9.3%	NEGTATYAAAVLFR	99.7%	77.5	25	67.8	2	0	0	1483.75	638	651
Katanin p60 ATPase-containing subunit A1	KATNA1	KTNA1_HUMAN	56.0	100.0%	2	2	4	0.00%	3.9%	DIISQNPNVR	99.7%	54.7	25	45.7	2	0	0	1155.61	198	207
Katanin p60 ATPase-containing subunit A1	KATNA1	KTNA1_HUMAN	56.0	100.0%	2	2	4	0.00%	3.9%	SVSAADIER	99.7%	50.9	25	27.7	2	0	0	947.48	472	480
Keratin-associated protein 19-5	KRTAP19-5	KR195_HUMAN	7.6	99.8%	2	2	3	0.00%	52.8%	LGYGGGYGGYGYGSGFGGYGYR	99.7%	87.5	25	87.5	1	0	0	2184.94	35	56
Keratin-associated protein 19-5	KRTAP19-5	KR195_HUMAN	7.6	99.8%	2	2	3	0.00%	52.8%	SCRPSCYGGYGFSGFY	99.7%	60.7	25	60.7	2	0	0	1864.74	57	72
Keratin-associated protein 24-1	KRTAP24-1	KR241_HUMAN	27.7	99.8%	2	2	4	0.00%	9.1%	SLSYIPSTFPPLR	99.7%	48.8	25	48.8	3	0	0	1477.81	230	242
Keratin-associated protein 24-1	KRTAP24-1	KR241_HUMAN	27.7	99.8%	2	2	4	0.00%	9.1%	YLCSGSRPLK	95.9%	29	25	20.9	1	0	0	1180.61	243	252
KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	KHDR1_HUMAN	48.2	100.0%	3	4	8	0.01%	8.6%	ILGPQGNTIK	99.3%	36.4	25	27.2	2	0	0	1040.61	176	185
KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	KHDR1_HUMAN	48.2	100.0%	3	4	8	0.01%	8.6%	KDDEENYLDLFSHK	99.7%	40.1	25	29.1	0	2	0	1752.81	139	152
KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	KHDR1_HUMAN	48.2	100.0%	3	4	8	0.01%	8.6%	SGSMDPSGAHPSVR	99.7%	51	25	41.1	2	2	0	1400.62	18	31
Kidney mitochondrial carrier protein 1	SLC25A30	KMCP1_HUMAN	32.5	99.8%	2	2	3	0.00%	9.6%	AAIVVGVELPVYDITK	99.7%	46.5	25	46.5	2	0	0	1686.97	172	187
Kidney mitochondrial carrier protein 1	SLC25A30	KMCP1_HUMAN	32.5	99.8%	2	2	3	0.00%	9.6%	ALYSGIAPAMLR	99.7%	50.2	25	41.6	1	0	0	1278.69	67	78
Kinesin-like protein KIF22	KIF22	KIF22_HUMAN	73.3	99.8%	2	2	3	0.00%	3.8%	ALMDLLQLTR	99.6%	39.5	25	22.4	1	0	0	1173.67	150	159
Kinesin-like protein KIF22	KIF22	KIF22_HUMAN	73.3	99.8%	2	2	3	0.00%	3.8%	VLDLLDPASGDLVIR	99.2%	36.2	25	32.3	2	0	0	1595.90	184	198
Kinesin-like protein KIF23	KIF23	KIF23_HUMAN	110.1	99.8%	2	2	2	0.00%	2.8%	AGSQLGPGYQHHAQPK	99.3%	30.6	25	30.6	0	1	0	1675.83	941	956
Kinesin-like protein KIF23	KIF23	KIF23_HUMAN	110.1	99.8%	2	2	2	0.00%	2.8%	STEEAFEVFWR	99.7%	60.5	25	60.5	1	0	0	1400.65	272	282
Kinetochore-associated protein 1	KNTC1	KNTC1_HUMAN	250.8	100.0%	3	3	4	0.00%	1.5%	LGISFQPVFR	99.2%	36.2	25	29.2	2	0	0	1163.66	1414	1423
Kinetochore-associated protein 1	KNTC1	KNTC1_HUMAN	250.8	100.0%	3	3	4	0.00%	1.5%	SGTEAVLIAHK	99.5%	38.5	25	25.9	1	0	0	1125.63	1746	1756
Kinetochore-associated protein 1	KNTC1	KNTC1_HUMAN	250.8	100.0%	3	3	4	0.00%	1.5%	VLAPELIPSILEK	97.3%	30.8	25	30.8	1	0	0	1421.86	727	739
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	5	5	10	0.01%	14.7%	GLLEESSFATLFPK	99.7%	79.5	25	77.5	2	0	0	1538.81	53	66
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	5	5	10	0.01%	14.7%	ILQDDVACDIIK	99.7%	75.4	25	59.1	2	0	0	1402.73	135	146
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	5	5	10	0.01%	14.7%	LGALTAEEIALK	99.7%	90.2	25	65.4	2	0	0	1228.71	358	369
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	5	5	10	0.01%	14.7%	SVSFEQAVR	99.3%	36.9	25	29	2	0	0	1022.53	126	134
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	5	5	10	0.01%	14.7%	TFDPYIIIR	99.7%	66.4	25	56.2	2	0	0	1137.63	107	115
Kynurenine--oxoglutarate transaminase 3	CCBL2	KAT3_HUMAN	51.4	99.8%	2	2	2	0.00%	4.6%	GFGHPSLVK	99.6%	39	25	25.6	1	0	0	941.52	100	108
Kynurenine--oxoglutarate transaminase 3	CCBL2	KAT3_HUMAN	51.4	99.8%	2	2	2	0.00%	4.6%	IAAIDSLNQYTR	99.7%	50.7	25	46.2	1	0	0	1364.72	88	99
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	6	6	10	0.01%	15.1%	FIPEITISDILR	99.7%	65.6	25	62.8	2	0	0	1416.81	388	399
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	6	6	10	0.01%	15.1%	GDYLLLKPEK	96.1%	29.2	25	25.7	1	0	0	1175.67	283	292
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	6	6	10	0.01%	15.1%	ISELSGCTPDPR	99.7%	56.1	25	46.3	2	0	0	1331.63	266	277
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	6	6	10	0.01%	15.1%	LIQQEDIK	98.7%	33.7	25	18.5	2	0	0	986.55	166	173

L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	6	6	10	0.01%	15.1%	LIVAVEQEEIPR	99.7%	49.1	25	35.4	2	0	0	1395.78	137	148
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	6	6	10	0.01%	15.1%	MDGSIWLGPNAVLAFK	99.7%	48.1	25	48.1	1	0	0	1734.89	319	334
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	4	5	9	0.01%	17.4%	IAWALSR	99.6%	39	25	23.1	2	0	0	816.47	89	95
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	4	5	9	0.01%	17.4%	KSLDFYTR	99.7%	57.6	25	31.2	2	0	0	1029.54	44	51
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	4	5	9	0.01%	17.4%	RFEELGVK	99.7%	40.6	25	18.1	2	0	0	977.54	141	148
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	4	5	9	0.01%	17.4%	VLGMTLIQK	99.7%	52.7	25	45.1	3	0	0	1002.60	52	60
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	20	0.02%	13.5%	ENDIKPLTSFR	97.0%	30.3	25	23.1	1	0	0	1319.70	51	61
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	20	0.02%	13.5%	KFADGEVVR	98.4%	32.9	25	21.7	1	0	0	1020.55	5	13
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	20	0.02%	13.5%	LTPLILKPFGNSISR	99.7%	45.5	25	45.5	2	0	0	1655.98	117	131
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	20	0.02%	13.5%	NDLSPASSGNAVYDFFIGR	99.7%	91.9	25	91.9	8	0	0	2029.96	354	372
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	20	0.02%	13.5%	TFEVTPIR	99.4%	37.6	25	36.9	2	0	0	962.53	196	203
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	20	0.02%	13.5%	VVEGTPLIDGR	99.7%	77.5	25	65	3	0	0	1155.64	280	290
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	20	0.02%	13.5%	YNGEPEHIER	99.7%	51.4	25	40.8	2	1	0	1243.57	132	141
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	22	24	48	0.05%	34.1%	AGGPTTPLSPTR	99.7%	59.3	25	56.9	4	0	0	1154.62	15	26
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	22	24	48	0.05%	34.1%	ALYETELADAR	99.7%	72.5	25	54.3	2	0	0	1251.62	80	90
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	22	24	48	0.05%	34.1%	DAALATALGDKK	99.7%	73	25	58.2	2	0	0	1173.65	146	157
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	22	24	48	0.05%	34.1%	DQMQQQLNDYEQLLDVK	99.7%	79.8	25	71.8	2	0	0	2108.00	351	367
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	22	24	48	0.05%	34.1%	IESLSSQLSNLQK	99.7%	85.9	25	74.9	2	0	0	1446.78	300	312
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	22	24	48	0.05%	34.1%	IGDTSVSYK	99.7%	64.5	25	57.4	2	0	0	969.49	475	483
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	22	24	48	0.05%	34.1%	IQELEDLLAK	99.7%	73.4	25	41.4	4	0	0	1171.66	321	330
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	22	24	48	0.05%	34.1%	KESDLNGAQIK	99.7%	40.6	25	28.7	2	0	0	1202.64	124	134
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	22	24	48	0.05%	34.1%	KIGDTSVSYK	97.6%	31.2	25	26.6	1	0	0	1097.58	474	483
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	22	24	48	0.05%	34.1%	KLLEGEEER	99.7%	61.4	25	39.8	2	0	0	1102.57	379	387
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	22	24	48	0.05%	34.1%	KQLADETLLK	98.6%	33.5	25	27.5	1	0	0	1158.67	182	191
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	22	24	48	0.05%	34.1%	LAQALHEMR	99.7%	59.6	25	54.6	2	0	0	1084.56	242	250
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	22	24	48	0.05%	34.1%	LLEGEEERLK	99.7%	48	25	36	1	0	0	1215.66	380	389
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	22	24	48	0.05%	34.1%	LQEKEELR	99.4%	37.5	25	13.4	2	0	0	1044.57	30	37
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	22	24	48	0.05%	34.1%	LQIELGK	95.6%	28.7	25	0	1	0	0	800.49	103	109
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	22	24	48	0.05%	34.1%	LREYEAALNSK	99.7%	47.2	25	32	2	0	0	1293.68	135	145
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	22	24	48	0.05%	34.1%	LSSEMNTSTVNSAR	99.7%	112	25	106	4	0	0	1512.70	277	290
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	22	24	48	0.05%	34.1%	LYKEELEQTYHAK	99.7%	69.5	25	63.2	2	4	0	1651.83	259	271
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	22	24	48	0.05%	34.1%	MRIESLSSQLSNLQK	97.6%	25.6	25	25	0	1	0	1749.92	298	312
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	22	24	48	0.05%	34.1%	NQNSWGTGEDVK	99.5%	38.3	25	37.1	2	0	0	1334.60	517	528
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	22	24	48	0.05%	34.1%	QIEYEYK	96.6%	29.8	25	28.1	1	0	0	972.47	235	241
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	22	24	48	0.05%	34.1%	QLADETLLK	99.7%	49.8	25	35.7	2	0	0	1030.58	183	191
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	8	8	17	0.02%	18.8%	AGGPATPLSPTR	99.7%	49.8	25	41.1	2	0	0	1124.61	9	20
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	8	8	17	0.02%	18.8%	ALYESELADAR	99.7%	56.4	25	46.2	2	0	0	1237.61	74	84
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	8	8	17	0.02%	18.8%	ATSSSSGSLSATGR	99.7%	103	25	98.7	2	0	0	1268.61	397	410
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	8	8	17	0.02%	18.8%	EGELTVAQGR	99.7%	57.9	25	33.4	4	0	0	1059.54	119	128
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	8	8	17	0.02%	18.8%	GLESDVAELR	99.7%	84	25	62.4	2	0	0	1088.56	152	161
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	8	8	17	0.02%	18.8%	ISEKEEVTTR	99.7%	71.9	25	48.3	2	0	0	1191.62	58	67
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	8	8	17	0.02%	18.8%	KLLEGEEER	99.7%	61.4	25	39.8	2	0	0	1102.57	373	381
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	8	8	17	0.02%	18.8%	LLEGEEERLK	99.7%	48	25	36	1	0	0	1215.66	374	383
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	8	8	17	0.02%	18.8%	LQEKEELR	99.4%	37.5	25	13.4	2	0	0	1044.57	24	31
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	8	8	17	0.02%	18.8%	LQIEIGK	95.6%	28.7	25	0	1	0	0	800.49	97	103
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	8	8	17	0.02%	18.8%	QVLEGEEIAYK	99.7%	65.9	25	57.3	2	0	0	1278.66	486	496
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	8	8	17	0.02%	18.8%	RLVEVDSSR	95.9%	29.1	25	18.6	1	0	0	1060.57	220	228
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	19	23	42	0.04%	20.5%	DYEAGQLYGLEK	99.7%	72.3	25	37.3	1	0	0	1385.66	981	992
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	19	23	42	0.04%	20.5%	ETESAPGSPR	99.3%	36.8	25	34.4	3	0	0	1030.48	514	523
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	19	23	42	0.04%	20.5%	FEPEYSQIK	99.3%	36.7	25	24	1	0	0	1140.56	695	703
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	19	23	42	0.04%	20.5%	FQHPSHELLK	97.1%	30.4	25	15.4	2	0	0	1235.65	872	881

La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	19	23	42	0.04%	20.5%	FQQVPTDALANK	99.7%	64.3	25	54.3	4	0	0	1331.70	742	753
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	19	23	42	0.04%	20.5%	FSHLTSLPQQLPSQQLMSK	99.7%	36.5	25	36.5	0	2	0	2186.13	579	597
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	19	23	42	0.04%	20.5%	GLSASLPDLDSENWIEVK	99.7%	64.9	25	63.4	2	0	0	1972.99	544	561
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	19	23	42	0.04%	20.5%	ILIVTQTPHYMR	99.7%	74.7	25	67.5	4	2	0	1471.81	643	654
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	19	23	42	0.04%	20.5%	KFDGVEGPR	99.4%	37.4	25	26.9	2	0	0	1004.52	367	375
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	19	23	42	0.04%	20.5%	LFGAPEPSTIAR	99.7%	41	25	14.2	2	0	0	1258.68	754	765
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	19	23	42	0.04%	20.5%	LGIGQSQEMNTLFR	99.7%	85.1	25	83.4	4	0	0	1593.81	904	917
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	19	23	42	0.04%	20.5%	LQEYLGK	99.6%	39	25	23	2	0	0	850.47	1011	1017
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	19	23	42	0.04%	20.5%	QIEYYFSVDNLER	99.7%	68.9	25	62.1	2	0	0	1675.80	410	422
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	19	23	42	0.04%	20.5%	SLPTTVPESPNYR	99.7%	41.8	25	38.3	2	0	0	1460.74	766	778
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	19	23	42	0.04%	20.5%	SVQPQSHKPQPTR	94.7%	28.1	25	23.8	1	0	0	1489.79	186	198
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	19	23	42	0.04%	20.5%	THFDYQFGYR	99.5%	37.9	25	37.7	2	0	0	1333.60	357	366
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	19	23	42	0.04%	20.5%	VQALTTDISLIFAALK	99.4%	37.5	25	37.5	1	0	0	1703.99	447	462
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	19	23	42	0.04%	20.5%	VVEIVDEK	99.7%	40.8	25	33	1	0	0	930.51	466	473
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	19	23	42	0.04%	20.5%	YGLECLFR	99.7%	57.3	25	54.9	2	0	0	1057.51	949	956
La-related protein 7	LARP7	LARP7_HUMAN	66.9	100.0%	8	8	11	0.01%	16.5%	AIEFLNNPPEEAPR	99.7%	74.9	25	74.9	2	0	0	1596.80	182	195
La-related protein 7	LARP7	LARP7_HUMAN	66.9	100.0%	8	8	11	0.01%	16.5%	DRVEASSLPEVR	97.1%	30.4	25	30	1	0	0	1357.71	280	291
La-related protein 7	LARP7	LARP7_HUMAN	66.9	100.0%	8	8	11	0.01%	16.5%	EENMDTSNTSISK	99.7%	41	25	41	1	0	0	1471.62	238	250
La-related protein 7	LARP7	LARP7_HUMAN	66.9	100.0%	8	8	11	0.01%	16.5%	GFAFVEFETK	99.7%	58.8	25	56.1	2	0	0	1174.58	167	176
La-related protein 7	LARP7	LARP7_HUMAN	66.9	100.0%	8	8	11	0.01%	16.5%	LEILSGDHEQR	99.7%	62.1	25	52.5	1	0	0	1296.65	521	531
La-related protein 7	LARP7	LARP7_HUMAN	66.9	100.0%	8	8	11	0.01%	16.5%	SSSEDAESLAPR	99.7%	58	25	54.4	1	0	0	1248.57	298	309
La-related protein 7	LARP7	LARP7_HUMAN	66.9	100.0%	8	8	11	0.01%	16.5%	TVYVELLPK	99.7%	41.3	25	40.5	1	0	0	1061.62	126	134
La-related protein 7	LARP7	LARP7_HUMAN	66.9	100.0%	8	8	11	0.01%	16.5%	VNATGPQFVSGVIVK	99.7%	76.7	25	66.4	2	0	0	1515.85	444	458
Large neutral amino acids transporter small subunit 1	SLC7A5	LAT1_HUMAN	55.0	100.0%	3	4	8	0.01%	9.5%	ALAAPAAEEKEEAR	99.7%	75.2	25	75.2	2	2	0	1455.74	10	23
Large neutral amino acids transporter small subunit 1	SLC7A5	LAT1_HUMAN	55.0	100.0%	3	4	8	0.01%	9.5%	GDVSNLDPNFSFEGTK	99.7%	42.9	25	35.7	1	0	0	1726.79	222	237
Large neutral amino acids transporter small subunit 1	SLC7A5	LAT1_HUMAN	55.0	100.0%	3	4	8	0.01%	9.5%	SADGSAPAGEGEGVTLQR	99.7%	96.7	25	96.7	3	0	0	1701.80	31	48
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	AFAETHIK	98.8%	34.3	25	20.7	1	0	0	916.49	1091	1098
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	AGDMENAENILTVMR	99.7%	84.7	25	81	4	0	0	1663.78	245	259
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	AGYPQYVSEILEK	99.7%	77	25	66.8	2	0	0	1496.76	315	327
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	CVANNQVETLEK	99.7%	72	25	60	2	0	0	1404.68	930	941
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	DAGIEPGPDTYLALLNAYAEK	98.7%	33.8	25	31.4	1	0	0	2221.10	260	280
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	DAHLLVESK	99.7%	52.7	25	42.5	2	0	0	1011.55	641	649
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	DLPVTEAVFSALVTGHAR	99.7%	87.7	25	87.7	2	0	0	1883.00	227	244
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	EKDIQEESTFSSR	99.7%	76.1	25	68.9	2	0	0	1555.72	65	77
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	EQNIVFNAETYSNLIK	99.7%	94.5	25	94.5	2	0	0	1882.95	1060	1075
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	GAYDIFLNAK	99.7%	60.1	25	54.6	2	0	0	1111.58	1050	1059
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	GDLSTALEVAIDCYEK	99.7%	48.8	25	46.2	2	0	0	1783.84	836	851
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	GDVENIEVVQK	99.7%	57.4	25	43.8	2	0	0	1229.64	1153	1163
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	GFTLNDAANSR	99.7%	73.5	25	60.5	2	0	0	1165.56	1099	1109
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	IPENIYR	96.3%	29.5	25	10.8	2	0	0	904.49	618	624
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	IQEENVIPR	99.7%	59.7	25	47.3	2	0	0	1097.60	981	989
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	KIIETPGIR	99.7%	42	25	36	2	0	0	1026.63	909	917
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	LDDLFLKR	99.7%	59	25	44.9	2	0	0	1019.59	1351	1358
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	LDSSAVLDTGK	99.7%	70.9	25	64.4	2	0	0	1105.57	740	750
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	LGAVYDVSHYNALLK	99.7%	82.8	25	78.7	2	0	0	1662.89	156	170
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	LIASYCNVGDIEGASK	99.7%	119	25	114	2	0	0	1696.82	203	218
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	LIITQVR	98.3%	32.8	25	13.4	2	0	0	842.55	1110	1116
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	LLMSEDYFTQAMEVK	99.7%	82.7	25	82.7	5	0	0	1804.85	1076	1090
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	LQDAINILK	99.7%	51	25	42.4	2	0	0	1027.61	764	772
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	LVEKGETDLIQK	99.7%	53.8	25	45.6	2	0	0	1372.77	865	876
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	MEEANIQPNR	99.7%	55.2	25	49.1	2	0	0	1201.56	188	197

Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	MLNGLEDSIGLSK	99.7%	70.4	25	64.4	2	0	0	1376.71	1164	1176
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	MVFINNIALAQIK	99.7%	83.8	25	82.9	4	0	0	1490.84	1177	1189
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	NVQGIIEILK	99.7%	60.8	25	49.4	2	0	0	1126.68	454	463
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	SCGSLLPELK	99.7%	62.4	25	46.3	2	0	0	1103.58	129	138
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	SEAANGNLDFVLSFLK	99.7%	96.9	25	88.3	2	0	0	1724.89	514	529
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	SGGLGGSHALLLLR	99.7%	74.7	25	67.4	2	2	0	1350.79	115	128
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	SNTLPISLQSIR	99.7%	89	25	67.7	2	0	0	1328.75	530	541
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	SYVSEKDVTSAK	99.7%	63.4	25	58.8	2	0	0	1313.66	1327	1338
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	TVLDQQQTPSR	99.7%	72.2	25	58.2	2	0	0	1272.65	1129	1139
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	TVQLTSSELESTLETLK	99.7%	88.7	25	85.7	2	0	0	1878.99	656	672
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	VIEPQYFGLAYLFR	99.2%	36.1	25	36.1	1	0	0	1715.92	1210	1223
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	37	42	80	0.08%	32.4%	VYLQNEYK	99.7%	41.8	25	30.5	2	0	0	1056.54	171	178
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	7	7	13	0.01%	12.8%	FLPEFPSCSLLK	99.3%	36.7	25	24.5	2	0	0	1437.74	257	268
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	7	7	13	0.01%	12.8%	GTAAILEYLR	99.7%	66.6	25	48.1	2	0	0	1106.62	588	597
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	7	7	13	0.01%	12.8%	LQTINLSFNR	99.7%	66.9	25	58.8	2	0	0	1205.66	497	506
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	7	7	13	0.01%	12.8%	QATLIPDEVFDAVK	99.6%	38.8	25	31.9	2	0	0	1545.82	410	423
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	7	7	13	0.01%	12.8%	SNIVTSINFSK	99.7%	61	25	54.1	1	0	0	1209.65	424	434
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	7	7	13	0.01%	12.8%	SVPDEIILLR	99.7%	52.1	25	33.8	2	0	0	1154.68	303	312
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	7	7	13	0.01%	12.8%	TLLLDGNPFR	99.7%	57.2	25	44.7	2	0	0	1145.63	569	578
Leucine-rich repeat-containing protein 47	LRRC47	LRC47_HUMAN	63.5	100.0%	4	4	5	0.00%	9.1%	DGPSLLVVEQVR	99.7%	66	25	56.1	1	0	0	1311.73	543	554
Leucine-rich repeat-containing protein 47	LRRC47	LRC47_HUMAN	63.5	100.0%	4	4	5	0.00%	9.1%	ELLLTGPGLEER	99.7%	73.8	25	64.1	1	0	0	1326.73	23	34
Leucine-rich repeat-containing protein 47	LRRC47	LRC47_HUMAN	63.5	100.0%	4	4	5	0.00%	9.1%	NALGPGLSPELGPLPALR	99.7%	73	25	73	1	0	0	1772.01	85	102
Leucine-rich repeat-containing protein 47	LRRC47	LRC47_HUMAN	63.5	100.0%	4	4	5	0.00%	9.1%	TAATLATHELR	99.7%	82.9	25	76.5	2	0	0	1183.64	371	381
Leucine-rich repeat-containing protein 59	LRRC59	LRC59_HUMAN	34.9	99.8%	2	2	3	0.00%	7.2%	LQQLPADFGR	99.7%	41.4	25	30.1	2	0	0	1144.61	74	83
Leucine-rich repeat-containing protein 59	LRRC59	LRC59_HUMAN	34.9	99.8%	2	2	3	0.00%	7.2%	LVTLPVSFAQLK	98.9%	34.7	25	34.7	1	0	0	1315.80	97	108
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	33	0.03%	18.5%	ELAVEGMHR	99.0%	35.1	25	27	1	0	0	1057.51	837	845
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	33	0.03%	18.5%	ELMGEEILGASLSAPLTSYK	99.7%	82.3	25	82.3	2	0	0	2109.08	351	370
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	33	0.03%	18.5%	EVWDYVFFK	95.2%	28.4	25	16.9	1	0	0	1232.60	633	641
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	33	0.03%	18.5%	FDDPLLGPR	99.7%	70.3	25	54.7	2	0	0	1029.54	1118	1126
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	33	0.03%	18.5%	GFYEGIMLVDGFK	99.7%	64.1	25	59.6	4	0	0	1475.72	471	483
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	33	0.03%	18.5%	GTGVVTSVPSDSPDDIAALR	99.7%	74.1	25	74.1	2	0	0	1956.99	385	404
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	33	0.03%	18.5%	ILDLQLEFDEK	99.7%	75.4	25	68.1	2	0	0	1362.72	1007	1017
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	33	0.03%	18.5%	MIDAGDALIYMEPEK	99.7%	80.8	25	77.3	2	0	0	1695.80	498	512
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	33	0.03%	18.5%	QTGEGVGPQEYTLLK	99.7%	72.8	25	66.7	2	0	0	1619.83	254	268
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	33	0.03%	18.5%	SFITTDVNPYYDSFVR	99.7%	89.6	25	89.6	2	0	0	1923.91	204	219
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	33	0.03%	18.5%	STGNFLTLTQAIDK	99.7%	107	25	95.4	2	0	0	1508.80	720	733
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	33	0.03%	18.5%	TGFFEFQAAK	99.7%	57.7	25	56.5	2	0	0	1145.56	823	832
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	33	0.03%	18.5%	VDIGDTIIYLVH	99.7%	86.7	25	84.8	2	0	0	1357.74	1165	1176
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	33	0.03%	18.5%	VFASELNAGIIK	99.7%	93.2	25	80.8	2	0	0	1261.72	796	807
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	33	0.03%	18.5%	VFEVNASNLEK	99.7%	74.3	25	66.5	2	0	0	1249.64	29	39
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	33	0.03%	18.5%	VIASELGSMPELK	99.7%	43.7	25	36.6	1	0	0	1373.73	971	983
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	33	0.03%	18.5%	VIASELGSMPELKK	99.7%	62.9	25	48.5	1	0	0	1501.83	971	984
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	18	20	33	0.03%	18.5%	YTIYSPK	95.1%	28.4	25	16.5	1	0	0	871.46	237	243
Leukotriene A-4 hydrolase	LTA4H	LKHA4_HUMAN	69.3	100.0%	4	4	6	0.01%	9.5%	GSPMEISLPIALSK	97.4%	31	25	26.6	1	0	0	1458.79	84	97
Leukotriene A-4 hydrolase	LTA4H	LKHA4_HUMAN	69.3	100.0%	4	4	6	0.01%	9.5%	LVVDLTDIDPDVAYSSVPYEK	99.7%	50	25	50	2	0	0	2338.17	366	386
Leukotriene A-4 hydrolase	LTA4H	LKHA4_HUMAN	69.3	100.0%	4	4	6	0.01%	9.5%	SAYEFSETESMLK	99.7%	41.8	25	41.8	1	0	0	1521.68	231	243
Leukotriene A-4 hydrolase	LTA4H	LKHA4_HUMAN	69.3	100.0%	4	4	6	0.01%	9.5%	TFGETHPFTK	99.7%	50.1	25	48.5	2	0	0	1164.57	356	365
LINE-1 retrotransposable element ORF1 protein	L1RE1	LORF1_HUMAN	40.1	99.8%	2	2	4	0.00%	6.8%	DFVTTRPALK	98.8%	34.2	25	33.5	2	0	0	1147.65	305	314
LINE-1 retrotransposable element ORF1 protein	L1RE1	LORF1_HUMAN	40.1	99.8%	2	2	4	0.00%	6.8%	LTADLSAETLQAR	99.7%	82.7	25	72	2	0	0	1388.74	249	261
Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	DBT	ODB2_HUMAN	53.5	99.8%	2	3	4	0.00%	4.8%	LSFMPFFLK	96.2%	29.4	25	19.5	1	0	0	1129.61	305	313
Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	DBT	ODB2_HUMAN	53.5	99.8%	2	3	4	0.00%	4.8%	SYLENPAFMLLDLK	99.7%	92	25	85.7	3	0	0	1653.86	469	482

Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	7	7	11	0.01%	3.1%	DLSKPIGALNPK	96.2%	29.4	25	29.4	1	0	0	1252.73	2268	2279
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	7	7	11	0.01%	3.1%	EIFVDFAPFLSR	99.7%	48.8	25	47.6	1	0	0	1440.75	1813	1824
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	7	7	11	0.01%	3.1%	IEPFTTYFLNLQGGK	97.8%	31.5	25	31.3	1	0	0	1727.90	2318	2332
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	7	7	11	0.01%	3.1%	SAAAIALPPIAK	99.7%	48.7	25	39.7	2	0	0	1122.69	213	224
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	7	7	11	0.01%	3.1%	SPVDIVTGGISPVR	99.7%	66.4	25	64.7	2	0	0	1396.78	1488	1501
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	7	7	11	0.01%	3.1%	VGVGTSFGLPQTR	99.7%	41.3	25	40.8	2	0	0	1318.71	2183	2195
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	7	7	11	0.01%	3.1%	YGPDAFFNFPGK	99.7%	58.1	25	54.6	2	0	0	1359.64	201	212
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	153	0.15%	60.5%	DLADELALVDVIEDK	99.7%	115	25	115	3	0	0	1657.85	43	57
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	153	0.15%	60.5%	DLADELALVDVIEDKLK	99.7%	43.4	25	43.4	1	0	0	1899.03	43	59
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	153	0.15%	60.5%	DQLIYNLLK	99.7%	68.4	25	49.7	10	0	0	1119.64	6	14
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	153	0.15%	60.5%	DQLIYNLLKEEQTPQNK	99.7%	72.6	25	72.6	2	2	0	2074.08	6	22
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	153	0.15%	60.5%	DYNVTANSK	99.7%	40.5	25	40.5	7	0	0	1011.47	82	90
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	153	0.15%	60.5%	FIIPNVVK	99.4%	37.1	25	24	4	0	0	929.58	119	126
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	153	0.15%	60.5%	GEMMDLQHGSLFLR	99.7%	75.3	25	74.7	6	6	0	1633.78	60	73
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	153	0.15%	60.5%	GYTSWAIGLSVADLAESIMK	99.7%	93.5	25	93.5	1	0	0	2128.06	246	265
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	153	0.15%	60.5%	ITVVGVGAVGMACAISILMK	99.7%	67.7	25	47.7	5	0	0	2006.08	23	42
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	153	0.15%	60.5%	IVSGKDYNVTANSK	99.7%	44.6	25	44.6	2	1	0	1495.78	77	90
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	153	0.15%	60.5%	LKGEMMDLQHGSLFLR	99.7%	34.3	25	1.72	0	3	0	1890.96	58	73
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	153	0.15%	60.5%	LLIVSNPVDILTYVAWK	99.7%	110	25	0	6	0	0	1944.12	133	149
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	153	0.15%	60.5%	LVIITAGAR	99.7%	74.7	25	56.9	24	0	0	913.58	91	99
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	153	0.15%	60.5%	QVVESAYEVIK	99.7%	74.5	25	67.5	13	0	0	1264.68	233	243
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	153	0.15%	60.5%	RVHPVSTMIK	97.9%	31.9	25	21.9	3	0	0	1167.67	269	278
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	153	0.15%	60.5%	SADTLWGIQK	99.7%	67.1	25	49.6	7	0	0	1118.58	319	328
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	153	0.15%	60.5%	TLHPDLGTDK	98.6%	33.7	25	33.7	2	0	0	1096.56	213	222
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	153	0.15%	60.5%	TLHPDLGTDKDK	98.7%	33.8	25	31.2	1	0	0	1339.69	213	224
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	153	0.15%	60.5%	VIGSGCNLDSAR	99.7%	80.4	25	72.6	22	0	0	1248.60	158	169
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	27	153	0.15%	60.5%	VTLTSEEEAR	99.7%	84	25	77.9	22	0	0	1134.56	306	315
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	16	26	119	0.12%	46.7%	DYSVTANSK	97.7%	31.4	25	20.4	1	0	0	984.46	83	91
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	16	26	119	0.12%	46.7%	EKLIAPVAEEEATVPNNK	99.7%	102	25	97.1	2	2	0	1952.03	6	23
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	16	26	119	0.12%	46.7%	FIIPQIVK	98.0%	32	25	28.4	5	0	0	957.61	120	127
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	16	26	119	0.12%	46.7%	GEMMDLQHGSLFLQTPK	99.7%	80	25	72.3	6	6	0	1931.94	61	77
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	16	26	119	0.12%	46.7%	GLTSVINQK	99.7%	59.8	25	33.3	10	0	0	959.55	300	308
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	16	26	119	0.12%	46.7%	ITVVGVGQVGMACAISILGK	99.7%	118	25	118	11	4	0	1973.09	24	43
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	16	26	119	0.12%	46.7%	IVADKDYSVTANSK	99.7%	86	25	80.9	13	1	0	1510.77	78	91
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	16	26	119	0.12%	46.7%	IVVVTAGVR	99.7%	81.3	25	66.6	7	0	0	913.58	92	100
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	16	26	119	0.12%	46.7%	KSADTLWDIQK	99.7%	61	25	53.9	2	0	0	1304.68	319	329
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	16	26	119	0.12%	46.7%	LIAPVAEEEATVPNNK	99.7%	90.7	25	80.8	10	2	0	1694.90	8	23
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	16	26	119	0.12%	46.7%	LKDDEVAQLK	99.7%	61	25	46.6	3	0	0	1158.64	309	318
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	16	26	119	0.12%	46.7%	LKGEMMDLQHGSLFLQTPK	99.7%	36	25	5.15	0	3	0	2189.11	59	77
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	16	26	119	0.12%	46.7%	MVVESAYEVIK	99.7%	92.3	25	83.1	20	0	0	1267.66	234	244
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	16	26	119	0.12%	46.7%	SADTLWDIQK	99.7%	77.1	25	55.3	7	0	0	1176.59	320	329
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	16	26	119	0.12%	46.7%	SLADELALVDVLEDK	99.7%	111	25	96.3	3	0	0	1629.86	44	58
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	16	26	119	0.12%	46.7%	SLADELALVDVLEDKLK	99.7%	76.3	25	76.3	1	0	0	1871.04	44	60
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	16	26	119	0.12%	46.7%	VIGSGCNLDSAR	99.7%	80.4	25	72.6	22	0	0	1248.60	159	170
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	8	8	13	0.01%	10.2%	DIIALNPLYR	99.7%	50	25	40	2	0	0	1187.68	302	311
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	8	8	13	0.01%	10.2%	EIFDIAFPDEQAEALAVER	99.7%	85.8	25	77.6	2	0	0	2163.06	941	959
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	8	8	13	0.01%	10.2%	FSVGGMTDVAEIK	99.7%	66.9	25	62.4	1	0	0	1353.67	547	559
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	8	8	13	0.01%	10.2%	ILEFIAVSQLR	99.7%	63.6	25	59.3	2	0	0	1288.76	501	511
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	8	8	13	0.01%	10.2%	LAQPYVGVFLK	99.6%	39.9	25	32.5	1	0	0	1234.72	159	169
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	8	8	13	0.01%	10.2%	LSSDVLTLLIK	99.7%	78.7	25	64.6	2	0	0	1201.74	691	701
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	8	8	13	0.01%	10.2%	TENPLILIDEVDK	99.7%	58.1	25	58.1	2	0	0	1498.80	582	594

Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	8	8	13	0.01%	10.2%	YSNENLDLAR	99.7%	53.8	25	31.7	1	0	0	1194.57	473	482
Long-chain fatty acid transport protein 4	SLC27A4	S27A4_HUMAN	72.1	99.8%	2	2	7	0.01%	3.1%	ILSFVYPIR	99.7%	62.6	25	50.8	3	0	0	1107.66	409	417
Long-chain fatty acid transport protein 4	SLC27A4	S27A4_HUMAN	72.1	99.8%	2	2	7	0.01%	3.1%	TVPILFASTVR	99.7%	47.4	25	47.4	4	0	0	1203.71	75	85
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	10	10	17	0.02%	18.5%	AKPVNSKPDSAYR	97.7%	31.4	25	31.4	1	0	0	1432.75	57	69
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	10	10	17	0.02%	18.5%	IGYSSPQTLADQSSK	99.7%	102	25	98.9	2	0	0	1581.78	349	363
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	10	10	17	0.02%	18.5%	LKDIVSLVPR	99.7%	50	25	41.3	2	0	0	1139.71	221	230
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	10	10	17	0.02%	18.5%	LLLCGGAPLSATTQR	99.7%	77.3	25	75.9	2	0	0	1557.84	447	461
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	10	10	17	0.02%	18.5%	LQAGEYVSLGK	99.5%	38.1	25	38.1	1	0	0	1164.63	586	596
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	10	10	17	0.02%	18.5%	LSPEPWTPETGLVTDAFK	99.7%	65.4	25	59.7	2	0	0	1988.00	682	699
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	10	10	17	0.02%	18.5%	NLFILAYNYK	99.7%	56.5	25	38.9	2	0	0	1258.68	407	416
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	10	10	17	0.02%	18.5%	NTPLCDSFVFR	99.7%	40.2	25	36.1	2	0	0	1355.64	425	435
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	10	10	17	0.02%	18.5%	SVNSLDGLASVLYPGCDTLDK	99.6%	39.8	25	39.8	1	0	0	2224.08	70	90
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	10	10	17	0.02%	18.5%	THYQADIER	95.6%	28.8	25	28.8	2	0	0	1132.54	707	715
Low density lipoprotein receptor adapter protein 1	LDLRAP1	ARH_HUMAN	33.9	99.8%	2	2	2	0.00%	9.1%	ETLLEGMLFSLK	99.7%	48.6	25	44.7	1	0	0	1380.74	40	51
Low density lipoprotein receptor adapter protein 1	LDLRAP1	ARH_HUMAN	33.9	99.8%	2	2	2	0.00%	9.1%	SLVATGNLLDLEETAK	99.7%	77.6	25	73.4	1	0	0	1673.90	205	220
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	9	10	21	0.02%	25.0%	EVTWEVLEGEVEK	99.7%	52.9	25	52.9	1	0	0	1546.76	300	312
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	9	10	21	0.02%	25.0%	GSIFVVFDSIESAK	99.7%	89.1	25	80.9	2	0	0	1498.78	152	165
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	9	10	21	0.02%	25.0%	GSIFVVFDSIESAKK	99.7%	66.1	25	66.1	2	0	0	1626.87	152	166
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	9	10	21	0.02%	25.0%	IIEDQQESLNK	99.7%	88.7	25	78.5	4	0	0	1316.67	318	328
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	9	10	21	0.02%	25.0%	KFVETPGQK	96.3%	29.5	25	22.6	1	0	0	1033.57	166	174
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	9	10	21	0.02%	25.0%	LDEGWVPLEIMIK	99.7%	73.9	25	66	3	0	0	1542.82	42	54
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	9	10	21	0.02%	25.0%	LTTDFNVIVEALSK	99.7%	108	25	107	2	0	0	1549.85	61	74
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	9	10	21	0.02%	25.0%	QKLEEDAEMK	99.7%	40.5	25	30.7	3	0	0	1236.58	215	224
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	9	10	21	0.02%	25.0%	SPSKPLPEVTDEYKNDVK	99.7%	42.2	25	42.2	0	3	0	2046.04	92	109
Lymphoid-specific helicase	HELLS	HELLS_HUMAN	97.1	99.8%	2	2	2	0.00%	2.5%	EVVVYAPLSK	99.7%	41.4	25	40.9	1	0	0	1104.63	465	474
Lymphoid-specific helicase	HELLS	HELLS_HUMAN	97.1	99.8%	2	2	2	0.00%	2.5%	IGQTKPVVVYR	99.7%	34.1	25	34.1	0	1	0	1259.75	711	721
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	11	0.01%	15.7%	IAPELYHK	96.8%	30	25	9.42	1	0	0	970.54	298	305
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	11	0.01%	15.7%	ILDDICVAK	96.6%	29.8	25	3.88	1	0	0	1046.56	422	430
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	11	0.01%	15.7%	INMVEELEK	95.4%	28.6	25	19.7	1	0	0	1104.56	394	402
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	11	0.01%	15.7%	LIFYDLR	99.6%	39.4	25	39.4	1	0	0	939.53	142	148
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	11	0.01%	15.7%	MLVVGGIDR	99.7%	59.8	25	54.5	2	0	0	959.53	306	314
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	11	0.01%	15.7%	RGDIIGVQGNPGK	99.7%	52.8	25	45.7	2	0	0	1310.72	178	190
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	11	0.01%	15.7%	SEEEFIHINNK	99.7%	53.8	25	53	1	0	0	1359.65	165	175
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	11	0.01%	15.7%	VAMFLTDSNNIK	99.7%	41.2	25	38.5	1	0	0	1352.69	554	565
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	9	9	11	0.01%	15.7%	YSHLQPGDHLTDITLK	98.4%	27.1	25	27.1	0	1	0	1837.94	112	127
Lysophosphatidylcholine acyltransferase 1	LPCAT1	PCAT1_HUMAN	59.2	100.0%	5	5	7	0.01%	13.1%	LPADTCLLEFAR	99.7%	46	25	45.6	1	0	0	1405.71	325	336
Lysophosphatidylcholine acyltransferase 1	LPCAT1	PCAT1_HUMAN	59.2	100.0%	5	5	7	0.01%	13.1%	NPALYASNVR	99.7%	66.1	25	56.9	1	0	0	1104.58	286	295
Lysophosphatidylcholine acyltransferase 1	LPCAT1	PCAT1_HUMAN	59.2	100.0%	5	5	7	0.01%	13.1%	TALGVAELTVTDLFR	99.7%	83.7	25	79.4	2	0	0	1605.88	447	461
Lysophosphatidylcholine acyltransferase 1	LPCAT1	PCAT1_HUMAN	59.2	100.0%	5	5	7	0.01%	13.1%	TCLITFKPGAFIPGAPVQPVVLR	99.7%	36.7	25	36.7	0	1	0	2481.41	215	237
Lysophosphatidylcholine acyltransferase 1	LPCAT1	PCAT1_HUMAN	59.2	100.0%	5	5	7	0.01%	13.1%	TLDTIQLAFK	99.7%	53.3	25	31	2	0	0	1149.65	417	426
Lysophospholipid acyltransferase 7	MBOAT7	MBOA7_HUMAN	52.8	99.8%	2	2	3	0.00%	5.1%	AASLEYDYETIR	99.3%	36.5	25	29.3	1	0	0	1430.68	289	300
Lysophospholipid acyltransferase 7	MBOAT7	MBOA7_HUMAN	52.8	99.8%	2	2	3	0.00%	5.1%	AASQPTSLAPEK	99.7%	41.7	25	34.9	2	0	0	1199.63	457	468
Macrophage migration inhibitory factor	MIF	MIF_HUMAN	12.5	99.8%	2	3	6	0.01%	17.4%	LLCGLLAER	99.7%	75.4	25	53.8	2	0	0	1044.59	79	87
Macrophage migration inhibitory factor	MIF	MIF_HUMAN	12.5	99.8%	2	3	6	0.01%	17.4%	PMFIVNTNVPR	99.7%	78.8	25	66.9	4	0	0	1287.69	2	12
Magnesium transporter protein 1	MAGT1	MAGT1_HUMAN	38.0	100.0%	4	5	12	0.01%	11.0%	GFSAEQIAR	99.7%	41.6	25	21.5	4	0	0	978.50	160	168
Magnesium transporter protein 1	MAGT1	MAGT1_HUMAN	38.0	100.0%	4	5	12	0.01%	11.0%	RGDTYELQVR	99.7%	42.7	25	37.7	3	1	0	1236.63	150	159
Magnesium transporter protein 1	MAGT1	MAGT1_HUMAN	38.0	100.0%	4	5	12	0.01%	11.0%	VSQLMEWTNK	99.7%	67.7	25	60.1	2	0	0	1235.61	41	50
Magnesium transporter protein 1	MAGT1	MAGT1_HUMAN	38.0	100.0%	4	5	12	0.01%	11.0%	YSSAFTNR	99.7%	49	25	44	2	0	0	945.44	106	113
Malate dehydrogenase, cytoplasmic	MDH1	MDHC_HUMAN	36.4	99.8%	2	2	3	0.00%	5.7%	GEFVTTVQQR	99.7%	51.5	25	46.3	1	0	0	1164.60	221	230
Malate dehydrogenase, cytoplasmic	MDH1	MDHC_HUMAN	36.4	99.8%	2	2	3	0.00%	5.7%	LGVTANDVK	97.1%	30.5	25	11.2	2	0	0	916.51	171	179
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	5	5	9	0.01%	21.9%	GCDVVVIPAGVPR	96.8%	30	25	30	1	0	0	1338.72	92	104

Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	5	5	9	0.01%	21.9%	IFGVTTLDIVR	99.7%	57.1	25	47.6	2	0	0	1233.72	166	176
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	5	5	9	0.01%	21.9%	SQETECTYFSTPLLLGK	99.7%	73.3	25	73.3	2	0	0	1973.95	280	296
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	5	5	9	0.01%	21.9%	VAVLGASGGIGQPLSLLLK	99.7%	80.8	25	80.8	2	0	0	1793.09	27	45
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	5	5	9	0.01%	21.9%	VDFPQDQLTALTGR	99.7%	55.9	25	50.9	2	0	0	1560.80	216	229
Malectin	MLEC	MLEC_HUMAN	32.2	100.0%	3	3	6	0.01%	14.0%	FAEVYFAQSQQK	99.7%	97.9	25	97.9	2	0	0	1445.71	127	138
Malectin	MLEC	MLEC_HUMAN	32.2	100.0%	3	3	6	0.01%	14.0%	LSVQGEVSTFTGK	99.7%	88.6	25	88.6	2	0	0	1352.71	178	190
Malectin	MLEC	MLEC_HUMAN	32.2	100.0%	3	3	6	0.01%	14.0%	VCALYIMAGTVDDVPK	99.7%	85.3	25	73.1	2	0	0	1751.87	205	220
Malonyl-CoA-acyl carrier protein transacylase, mitochondrial	MCAT	FABD_HUMAN	43.0	100.0%	3	3	3	0.00%	7.7%	FNFACLEAR	99.4%	37.7	25	22.3	1	0	0	1127.53	204	212
Malonyl-CoA-acyl carrier protein transacylase, mitochondrial	MCAT	FABD_HUMAN	43.0	100.0%	3	3	3	0.00%	7.7%	LLAQQLVSPVK	99.7%	67.3	25	63.2	1	0	0	1195.74	315	325
Malonyl-CoA-acyl carrier protein transacylase, mitochondrial	MCAT	FABD_HUMAN	43.0	100.0%	3	3	3	0.00%	7.7%	VISGHQEALR	99.7%	62.4	25	58.8	1	0	0	1109.61	237	246
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	6	6	9	0.01%	15.2%	AVILIGGPQK	99.7%	48.6	25	41.3	2	0	0	995.63	4	13
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	6	6	9	0.01%	15.2%	GNVYIHPTAK	98.1%	32.1	25	32.1	1	0	0	1099.59	285	294
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	6	6	9	0.01%	15.2%	GVTVGEGVR	98.5%	33.1	25	21.4	1	0	0	873.48	310	318
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	6	6	9	0.01%	15.2%	LLPAITILGCR	99.7%	44.1	25	43.2	2	0	0	1226.73	380	390
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	6	6	9	0.01%	15.2%	SAGSALYASR	99.7%	43.2	25	39.8	1	0	0	982.50	250	259
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	6	6	9	0.01%	15.2%	VEGTPSDPNPNDPR	99.1%	35.6	25	10.1	2	0	0	1494.68	353	366
Mannose-1-phosphate guanyltransferase beta	GMPPB	GMPPB_HUMAN	39.8	100.0%	4	4	8	0.01%	16.9%	ALILVGGYGTR	99.7%	68.1	25	68.1	2	0	0	1119.65	3	13
Mannose-1-phosphate guanyltransferase beta	GMPPB	GMPPB_HUMAN	39.8	100.0%	4	4	8	0.01%	16.9%	ISMSHEEEPLGTAGPLALAR	99.1%	29.7	25	29.7	0	2	0	2095.05	75	94
Mannose-1-phosphate guanyltransferase beta	GMPPB	GMPPB_HUMAN	39.8	100.0%	4	4	8	0.01%	16.9%	LCSGPGIVGNVLVDPSAR	99.7%	65.2	25	65.2	2	0	0	1810.95	244	261
Mannose-1-phosphate guanyltransferase beta	GMPPB	GMPPB_HUMAN	39.8	100.0%	4	4	8	0.01%	16.9%	YGVVVCEADTGR	99.7%	55.4	25	47.2	2	0	0	1325.62	144	155
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	ALWFQGR	99.3%	36.5	25	20.8	1	0	0	877.47	556	562
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	DDWEEKR	99.1%	35.4	25	6.88	4	0	0	977.43	176	182
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	DLDELSR	99.6%	39.5	25	31.4	1	0	0	847.42	121	127
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	DLDELSRYPEDK	99.7%	67.3	25	60	4	0	0	1479.70	121	132
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	DLSAAGIGLLAAATQSLSMPASLGR	99.7%	92.8	25	92.8	3	1	0	2387.26	20	44
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	DSFDDRGPSLNPVLDYDHGSR	99.7%	53.4	25	53.4	0	4	0	2362.07	187	207
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	EDAMAMVDHCLK	99.7%	68.4	25	62.7	3	0	0	1419.61	543	554
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	EDAMAMVDHCLKK	95.2%	23	25	22.9	0	2	0	1547.70	543	555
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	EWSQHINGASHSR	97.5%	25.5	25	25.3	0	2	0	1508.70	305	317
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	FDQKQELGR	99.7%	51.5	25	39.2	4	0	0	1120.57	488	496
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	FDSEYER	99.7%	42	25	42	4	0	0	945.39	246	252
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	GAPPSSNIEDFHGLLPK	99.7%	76.3	25	73	4	0	0	1778.91	271	287
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	GDADQASNILASFGLSAR	99.7%	96.3	25	96.3	7	2	0	1792.88	103	120
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	GNLGAGNGNLQGPR	99.7%	91.1	25	82.3	6	0	0	1324.67	374	387
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	GPGPLQER	99.7%	52.8	25	40.8	8	0	0	853.45	256	263
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	GPLPLSSQHR	99.7%	54.1	25	51.5	4	0	0	1091.60	93	102
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	GPSLNPVLDYDHGSR	99.7%	95.6	25	92.1	4	4	0	1626.79	193	207
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	GYPHLCSICDLPVHSNK	99.7%	46.4	25	46.4	0	4	0	1996.94	288	304
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	IGPYQPNVPVGIDYVIPK	99.7%	66.6	25	66.6	7	0	0	1969.08	781	798
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	IKNYILMR	99.2%	35.8	25	21.1	4	0	0	1050.61	523	530
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	ITPENLPQILLQLK	99.7%	82.4	25	74.7	5	0	0	1619.97	133	146
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	LCSLFYTNEEVAK	99.7%	79.6	25	72.7	5	0	0	1573.76	805	817
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	MDYEDDRLR	99.7%	46	25	39.2	6	0	0	1212.53	217	225
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	NTHCSSLPHYQK	99.7%	62.5	25	62.5	4	3	0	1471.67	818	829
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	NYILMR	98.2%	32.4	25	14.4	7	0	0	825.43	525	530
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	RTEEGPTLSYGR	99.7%	59	25	44.4	4	2	0	1365.68	149	160
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	SFQQSSLSR	99.7%	68	25	43.2	2	0	0	1039.52	4	12
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	SQAFIEMETR	99.7%	68.4	25	60	10	0	0	1211.57	533	542
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	SQESGYYDR	99.7%	50.2	25	50.2	5	0	0	1104.46	208	216
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	TEEGPTLSYGR	99.7%	72.1	25	62.9	4	0	0	1209.57	150	160
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	VIHLSNLPHSGYSDSAVLK	99.7%	73.7	25	73.7	2	6	0	2037.08	497	515

Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	43	163	0.16%	40.1%	VVHIMDFQR	99.7%	44.5	25	42.4	11	0	0	1144.59	399	407
MAX gene-associated protein	MGA	MGAP_HUMAN	331.8	100.0%	2	2	2	0.00%	0.8%	ISNPSAFSIVPR	99.7%	40.3	25	35.8	1	0	0	1287.71	2208	2219
MAX gene-associated protein	MGA	MGAP_HUMAN	331.8	100.0%	2	2	2	0.00%	0.8%	VGSFIIELASQR	99.7%	43	25	35.4	1	0	0	1319.73	1369	1380
Mediator of DNA damage checkpoint protein 1	MDC1	MDC1_HUMAN	226.7	100.0%	5	5	7	0.01%	3.5%	EGAQVPTGR	96.7%	29.9	25	23.9	1	0	0	914.47	664	672
Mediator of DNA damage checkpoint protein 1	MDC1	MDC1_HUMAN	226.7	100.0%	5	5	7	0.01%	3.5%	NQLVTPEPTSR	98.7%	33.8	25	20.1	2	0	0	1241.65	1585	1595
Mediator of DNA damage checkpoint protein 1	MDC1	MDC1_HUMAN	226.7	100.0%	5	5	7	0.01%	3.5%	TPEPVVPTAPEPHPTTSTDQPVTPK	99.7%	53.6	25	53.6	0	2	0	2623.33	1608	1632
Mediator of DNA damage checkpoint protein 1	MDC1	MDC1_HUMAN	226.7	100.0%	5	5	7	0.01%	3.5%	TPESIVPIAPELQPSTSR	99.0%	35	25	35	1	0	0	1922.02	1567	1584
Mediator of DNA damage checkpoint protein 1	MDC1	MDC1_HUMAN	226.7	100.0%	5	5	7	0.01%	3.5%	TPETLVPTAPK	99.5%	38.5	25	38.5	1	0	0	1153.65	1403	1413
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	3	3	5	0.00%	2.3%	EVGNALLNVVLK	99.7%	48.7	25	32.2	2	0	0	1268.76	1121	1132
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	3	3	5	0.00%	2.3%	FLTEVLLPIVK	99.7%	52.4	25	44.5	2	0	0	1271.80	1230	1240
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	3	3	5	0.00%	2.3%	LFDLLYPEK	98.6%	33.6	25	26.9	1	0	0	1137.62	398	406
Melanoma-associated antigen D2	MAGED2	MAGD2_HUMAN	65.0	100.0%	4	4	7	0.01%	7.3%	EYTDVYPEIIER	99.7%	62	25	56.3	2	0	0	1526.74	312	323
Melanoma-associated antigen D2	MAGED2	MAGD2_HUMAN	65.0	100.0%	4	4	7	0.01%	7.3%	GPIAFWAR	98.9%	34.8	25	31.5	1	0	0	917.50	220	227
Melanoma-associated antigen D2	MAGED2	MAGD2_HUMAN	65.0	100.0%	4	4	7	0.01%	7.3%	LQSSQEPEAPPPR	99.7%	64.8	25	62.4	2	0	0	1435.72	262	274
Melanoma-associated antigen D2	MAGED2	MAGD2_HUMAN	65.0	100.0%	4	4	7	0.01%	7.3%	SSEAVIWEVLR	99.7%	73.1	25	33.9	2	0	0	1288.69	386	396
Melanoma-associated antigen G1	NDNL2	MAGG1_HUMAN	34.3	99.8%	2	2	3	0.00%	9.2%	GPGGSQGSQGPSPQGAR	99.7%	65.9	25	65.9	2	0	0	1524.72	53	69
Melanoma-associated antigen G1	NDNL2	MAGG1_HUMAN	34.3	99.8%	2	2	3	0.00%	9.2%	VSELVQFLLIK	99.7%	40.3	25	33.8	1	0	0	1288.79	89	99
Metaxin-1	MTX1	MTX1_HUMAN	51.5	99.8%	2	2	3	0.00%	6.7%	ISNPWQSPSGTLPALR	99.7%	42.7	25	42.7	1	0	0	1723.91	191	206
Metaxin-1	MTX1	MTX1_HUMAN	51.5	99.8%	2	2	3	0.00%	6.7%	QGADTLAFMSLLEEK	99.7%	55.8	25	53	2	0	0	1652.82	238	252
Metaxin-2	MTX2	MTX2_HUMAN	29.8	99.8%	2	2	4	0.00%	12.2%	LGTQPYFFNK	99.7%	43.3	25	35.9	2	0	0	1214.62	197	206
Metaxin-2	MTX2	MTX2_HUMAN	29.8	99.8%	2	2	4	0.00%	12.2%	VPFIHVGNQVVSELGPIVQFVK	99.7%	64.7	25	64.7	0	2	0	2406.35	72	93
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	28	57	0.06%	36.6%	ADKNEVAAEVAK	99.7%	67.4	25	43.9	2	2	0	1244.65	864	875
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	28	57	0.06%	36.6%	AEVLISTVGPEDCVVPFLTRPK	99.7%	71	25	71	0	2	0	2427.30	26	47
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	28	57	0.06%	36.6%	ALEEGLTPQEICDK	98.5%	33.3	25	33.3	1	0	0	1602.77	322	335
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	28	57	0.06%	36.6%	ALTHIDHSLSR	99.7%	60.5	25	55.3	2	2	0	1249.66	120	130
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	28	57	0.06%	36.6%	FFGGYVPEMVLTPDDQR	99.7%	73.8	25	73.8	4	0	0	1986.93	664	680
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	28	57	0.06%	36.6%	FVEGVCPFCGYEEAR	99.7%	62.5	25	62.5	2	0	0	1819.78	400	414
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	28	57	0.06%	36.6%	GFVLQDTVEQLR	99.7%	95	25	78.7	3	0	0	1404.75	377	388
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	28	57	0.06%	36.6%	GLESLPPLRPQQNPVLPVAGER	99.7%	38.6	25	36.5	0	2	0	2367.31	243	264
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	28	57	0.06%	36.6%	GVGVFGDMAQDTGIPADIWR	99.7%	94.6	25	94.3	4	0	0	2121.01	599	618
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	28	57	0.06%	36.6%	ITQDIFQQLLK	99.7%	73.3	25	57.7	4	0	0	1346.77	365	375
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	28	57	0.06%	36.6%	KGEDVLGSVR	99.7%	54.1	25	43.6	2	0	0	1059.58	109	118
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	28	57	0.06%	36.6%	LENDQIESLR	99.7%	84.6	25	66.2	2	0	0	1216.62	805	814
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	28	57	0.06%	36.6%	LFVSDGVPGCLPVLAAAGR	99.7%	98	25	98	2	0	0	1899.02	3	21
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	28	57	0.06%	36.6%	LINAVELK	99.7%	55.4	25	43.5	2	0	0	899.56	424	431
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	28	57	0.06%	36.6%	NNSELLNNLGNFINR	99.7%	98.2	25	94.1	2	0	0	1731.88	642	656
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	28	57	0.06%	36.6%	NPEQVDLYQFMAK	99.7%	86.6	25	81.6	4	0	0	1598.75	542	554
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	28	57	0.06%	36.6%	QLAVAEGKPPEAPK	99.7%	76.9	25	74.4	2	0	0	1434.80	882	895
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	28	57	0.06%	36.6%	QPQPSPAEGR	99.7%	48.5	25	47	1	0	0	1066.53	205	214
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	28	57	0.06%	36.6%	QQGVLALRPYLQK	99.7%	56.4	25	46.5	2	0	0	1513.89	192	204
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	28	57	0.06%	36.6%	RLEEWLGR	99.4%	37.6	25	21.5	2	0	0	1058.57	460	467
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	28	57	0.06%	36.6%	SCPVVQSSQHLFLDLPK	99.7%	66.4	25	64.1	2	0	0	1955.01	440	456
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	28	57	0.06%	36.6%	TLPGSDWTPNAQFITR	99.7%	75.9	25	75.9	2	0	0	1803.90	468	483
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	23	28	57	0.06%	36.6%	VPVLQLDSGNYLFSTSAICR	99.7%	143	25	143	2	0	0	2240.14	48	67
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	19	182	0.18%	37.7%	AHAAQVTCVAASPHK	99.7%	103	25	99.2	8	10	0	1547.77	165	179
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	19	182	0.18%	37.7%	AHAAQVTCVAASPHKDSVFLSCSEDNR	99.7%	84.9	25	84.9	0	2	0	2957.36	165	191
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	19	182	0.18%	37.7%	CWAGSLWLFK	99.7%	47.4	25	37.1	6	0	0	1267.63	53	62
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	19	182	0.18%	37.7%	DSVFLSCSEDNR	99.7%	73.1	25	64.3	12	0	0	1428.61	180	191
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	19	182	0.18%	37.7%	ETPPPLVPPAAR	99.4%	37.7	25	23.7	6	0	0	1244.70	4	15
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	19	182	0.18%	37.7%	EWNLPPNAPACMER	99.7%	71.1	25	71.1	22	0	0	1684.76	16	29
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	19	182	0.18%	37.7%	FCKYEHDDIVSTVSVLSSGTQAVSGSK	99.7%	101	25	99.7	0	3	0	2901.39	119	145

Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	19	182	0.18%	37.7%	ILLWDTR	99.7%	53.3	25	48.5	19	0	0	916.53	192	198
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	19	182	0.18%	37.7%	KETPPPLVPPAAR	99.7%	53.1	25	46.8	4	1	0	1372.79	3	15
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	19	182	0.18%	37.7%	SDGALLLGASSLSGR	99.7%	135	25	128	32	0	0	1403.75	38	52
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	19	182	0.18%	37.7%	VWDLAQQVVLSSYR	99.7%	124	25	119	18	5	0	1663.88	151	164
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	19	182	0.18%	37.7%	YEHDDIVSTVSVLSSGTQAVSGSK	99.7%	124	25	124	10	12	0	2466.20	122	145
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	19	182	0.18%	37.7%	YRSDGALLLGASSLSGR	99.7%	121	25	116	4	8	0	1722.91	36	52
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	6	9	31	0.03%	44.3%	DRSDCLGEHLYVMVNAK	99.7%	45.6	25	45.6	0	1	0	2006.94	69	85
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	6	9	31	0.03%	44.3%	GLGTGTLYIAESR	99.7%	105	25	98	9	0	0	1337.71	31	43
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	6	9	31	0.03%	44.3%	LEGMLSQSVSSQYNMAGVR	99.7%	115	25	106	6	2	0	2056.98	188	206
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	6	9	31	0.03%	44.3%	QQPDTEAVLNGK	99.7%	59.6	25	56.8	3	0	0	1299.65	19	30
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	6	9	31	0.03%	44.3%	SFPPPGPAEGLLR	99.5%	38.2	25	38.2	7	0	0	1337.72	6	18
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	6	9	31	0.03%	44.3%	TEDSIRDYEDGMEVDTTPTVAGQFEDADVDH	99.7%	75.9	25	75.9	0	3	0	3473.45	207	237
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	8	9	17	0.02%	27.1%	DLADVAAR	98.9%	34.7	25	14.7	2	0	0	830.44	102	109
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	8	9	17	0.02%	27.1%	EAEREGATEEAVR	99.7%	47.9	25	33.7	2	0	0	1446.68	110	122
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	8	9	17	0.02%	27.1%	EIIIEERPGQELTDVNGVR	99.7%	45.2	25	44.6	1	2	0	2167.14	294	312
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	8	9	17	0.02%	27.1%	GSLQILDQLLLPK	99.7%	66	25	57.4	2	0	0	1437.87	11	23
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	8	9	17	0.02%	27.1%	GVSAVVVGADR	99.7%	76	25	61.4	2	0	0	1029.57	239	249
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	8	9	17	0.02%	27.1%	TALTTTISSR	99.7%	80.4	25	73.3	2	0	0	1050.58	351	360
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	8	9	17	0.02%	27.1%	VGTYQLAIVAK	99.7%	77.5	25	70.6	2	0	0	1162.68	260	270
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	8	9	17	0.02%	27.1%	YEAVGSVHQAWEAIR	99.7%	35.8	25	30.8	0	2	0	1715.85	27	41
Methyltransferase-like protein 13	METTL13	MET13_HUMAN	78.8	99.8%	2	2	3	0.00%	3.3%	LAEAVQER	99.4%	37	25	13	1	0	0	915.49	242	249
Methyltransferase-like protein 13	METTL13	MET13_HUMAN	78.8	99.8%	2	2	3	0.00%	3.3%	LATPELLETAQALER	99.7%	105	25	96.8	2	0	0	1654.90	660	674
Microsomal glutathione S-transferase 1	MGST1	MGST1_HUMAN	17.6	100.0%	3	5	14	0.01%	27.1%	IYHTIAYLTPLPQPNR	99.7%	88.4	25	88.4	2	0	0	1897.03	115	130
Microsomal glutathione S-transferase 1	MGST1	MGST1_HUMAN	17.6	100.0%	3	5	14	0.01%	27.1%	KVFANPEDCVAFGK	99.7%	59.5	25	52.3	2	2	0	1581.77	42	55
Microsomal glutathione S-transferase 1	MGST1	MGST1_HUMAN	17.6	100.0%	3	5	14	0.01%	27.1%	MMLMSTATAFYR	99.7%	85.6	25	85.6	8	0	0	1422.66	27	38
Microtubule-associated protein 1B	MAP1B	MAP1B_HUMAN	270.6	100.0%	3	3	3	0.00%	1.4%	AAKPTTTPEVK	96.4%	29.6	25	12.7	1	0	0	1142.64	2299	2309
Microtubule-associated protein 1B	MAP1B	MAP1B_HUMAN	270.6	100.0%	3	3	3	0.00%	1.4%	AVLDALLEGK	99.7%	42.9	25	28.9	1	0	0	1028.60	2400	2409
Microtubule-associated protein 1B	MAP1B	MAP1B_HUMAN	270.6	100.0%	3	3	3	0.00%	1.4%	SVGNTIDPVILFQK	99.7%	74.2	25	71.5	1	0	0	1530.85	401	414
Microtubule-associated protein 1S	MAP1S	MAP1S_HUMAN	112.2	99.9%	2	2	3	0.00%	2.4%	AVLDALLASK	99.4%	37.5	25	34.3	2	0	0	1000.60	991	1000
Microtubule-associated protein 1S	MAP1S	MAP1S_HUMAN	112.2	99.9%	2	2	3	0.00%	2.4%	GDNLETLVLLNPSDK	99.7%	48.4	25	48.4	1	0	0	1627.85	82	96
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	5	5	6	0.01%	1.3%	ALEFGEPVLLVGDTGCGK	99.7%	73.2	25	73.2	2	0	0	1861.94	1379	1396
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	5	5	6	0.01%	1.3%	FLQQEQSVFR	99.6%	38.9	25	33.2	1	0	0	1281.66	155	164
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	5	5	6	0.01%	1.3%	FMLFATQNPPGLYGGR	99.7%	40.4	25	40.4	1	0	0	1768.88	1189	1204
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	5	5	6	0.01%	1.3%	GEPVLLVGETGTGK	99.7%	76.9	25	75.3	1	0	0	1356.74	670	683
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	5	5	6	0.01%	1.3%	ITPYDVQLGYSVLSR	99.7%	55.5	25	54.1	1	0	0	1710.91	2013	2027
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	22	0.02%	17.0%	ADPLALAAEK	99.7%	48	25	32.8	2	0	0	998.55	61	70
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	22	0.02%	17.0%	AMVEAVQLIADGK	99.7%	80.9	25	72.8	1	0	0	1344.72	197	209
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	22	0.02%	17.0%	DLGEEALNEYLK	99.7%	64.2	25	57.2	2	0	0	1393.68	904	915
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	22	0.02%	17.0%	FLFPEGIK	98.3%	32.7	25	22.9	2	0	0	950.53	189	196
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	22	0.02%	17.0%	GVINIIPGSGGIAGQR	99.7%	45.2	25	45.2	2	0	0	1508.85	642	657
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	22	0.02%	17.0%	HGSIIYHPSILPR	99.7%	37.1	25	0	0	2	0	1489.83	122	134
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	22	0.02%	17.0%	IPQPEEGATYEGIQK	99.7%	85.5	25	0	2	0	0	1659.82	213	227
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	22	0.02%	17.0%	LGFTGSTPIGK	99.7%	68.3	25	62	2	0	0	1077.59	667	677
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	22	0.02%	17.0%	LLQYCETGVK	99.7%	41.1	25	36.4	2	0	0	1210.61	779	788
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	22	0.02%	17.0%	SAACLAAGNTLVLKPAQVTPLTALK	99.7%	52.7	25	52.5	0	2	0	2508.42	605	629
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	22	0.02%	17.0%	SPLIIFNDCELDK	99.7%	47.1	25	41.6	1	0	0	1563.77	699	711
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	12	12	22	0.02%	17.0%	VSYASLADVDK	99.7%	67	25	67	2	0	0	1167.59	474	484
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	17	36	0.04%	49.4%	AVIGMTAGATGAFVGTPAEVALIR	99.7%	129	25	129	5	4	0	2289.23	123	146
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	17	36	0.04%	49.4%	AVVVNAAQLASYSQSK	99.7%	105	25	96.9	2	0	0	1635.87	191	206
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	17	36	0.04%	49.4%	EEGVLTLWR	99.6%	39.3	25	30.5	2	0	0	1102.59	174	182
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	17	36	0.04%	49.4%	FLFGGLAGMGATVFVQPLDLVK	99.7%	41.4	25	41.4	1	0	0	2296.24	25	46

Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	17	36	0.04%	49.4%	GIYTGLSAGLLR	99.7%	80.2	25	74.3	2	0	0	1220.70	79	90
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	17	36	0.04%	49.4%	ITREEGVLTLWR	99.7%	34.2	25	33.8	0	1	0	1472.82	171	182
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	17	36	0.04%	49.4%	LGIYTVLFER	99.7%	88.2	25	79.3	6	0	0	1210.68	99	108
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	17	36	0.04%	49.4%	LTGADGTPPGFLLK	99.7%	72.5	25	62.9	2	0	0	1386.76	109	122
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	17	36	0.04%	49.4%	MIDGKPEYK	97.2%	30.6	25	23.1	1	0	0	1080.54	252	260
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	17	36	0.04%	49.4%	NGLDVLFK	99.7%	48.7	25	34.8	2	0	0	905.51	261	268
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	17	36	0.04%	49.4%	NVFNALIR	99.7%	41	25	29.2	2	0	0	946.55	163	170
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	17	36	0.04%	49.4%	TSFHALTSILK	99.7%	55.7	25	47.4	2	1	0	1217.69	63	73
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	13	17	36	0.04%	49.4%	YEGFFSLWK	99.7%	52.5	25	52	3	0	0	1176.57	272	280
Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20	MCAT_HUMAN	32.9	100.0%	2	2	3	0.00%	7.3%	ELIRDEGVTSLYK	99.7%	47.8	25	47.8	2	0	0	1522.81	255	267
Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20	MCAT_HUMAN	32.9	100.0%	2	2	3	0.00%	7.3%	YTGTLDCAK	97.2%	30.6	25	22.1	1	0	0	1028.47	149	157
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	15	27	0.03%	48.4%	FAIYETVR	99.7%	46.6	25	40.5	2	0	0	998.53	79	86
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	15	27	0.03%	48.4%	GALVTVGQLSCYDQAK	99.7%	112	25	112	2	0	0	1709.85	171	186
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	15	27	0.03%	48.4%	GEYQGVFHCAVETAK	99.7%	68.3	25	68.3	2	1	0	1695.78	232	246
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	15	27	0.03%	48.4%	GSQGPLPFHEK	98.8%	34.1	25	25.2	2	0	0	1196.61	92	102
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	15	27	0.03%	48.4%	LFSGATMASSR	99.7%	85.4	25	82.8	2	0	0	1143.55	160	170
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	15	27	0.03%	48.4%	LGPLAFYK	99.7%	43.6	25	36.3	2	0	0	908.52	247	254
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	15	27	0.03%	48.4%	NYAHALDGLYR	99.7%	53.1	25	52.9	2	1	0	1292.64	140	150
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	15	27	0.03%	48.4%	QMTYSLTR	99.7%	40.2	25	31.2	2	0	0	999.49	71	78
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	15	27	0.03%	48.4%	TDGILALYSGLSASLCR	99.7%	105	25	105	2	0	0	1796.92	54	70
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	15	27	0.03%	48.4%	VHLQTQQEVK	99.7%	56.3	25	56.3	2	1	0	1209.66	32	41
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	15	27	0.03%	48.4%	VLLGSVSGLAGGFVGTPADLVNVR	99.7%	108	25	108	2	2	0	2298.28	103	126
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	7	7	15	0.01%	37.3%	KAGEVPSPEAGR	96.1%	29.2	25	22.2	1	0	0	1197.62	62	73
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	7	7	15	0.01%	37.3%	KLYPTVGKPSSS	99.7%	42.7	25	37.7	2	0	0	1263.69	155	166
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	7	7	15	0.01%	37.3%	LYPTVGKPSSS	99.7%	56.7	25	45.4	3	0	0	1135.60	156	166
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	7	7	15	0.01%	37.3%	SVDFLLDSSLR	99.7%	79.4	25	59.4	2	0	0	1251.66	144	154
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	7	7	15	0.01%	37.3%	SVDFLLDSSLRK	99.7%	67.2	25	59.6	2	0	0	1379.75	144	155
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	7	7	15	0.01%	37.3%	VCAASLYVLGTATR	99.7%	104	25	96.8	1	0	0	1481.78	103	116
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	7	7	15	0.01%	37.3%	YLGYANEVGEAFR	99.7%	83.3	25	80	4	0	0	1488.71	21	33
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	7	7	13	0.01%	29.7%	GAAVNLTLVTPEK	99.7%	69.2	25	61.2	2	0	0	1312.75	68	80
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	7	7	13	0.01%	29.7%	GLGATLLR	99.6%	39.8	25	19.4	1	0	0	800.50	189	196
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	7	7	13	0.01%	29.7%	GVNEDTYSGILDCAR	99.7%	84.8	25	84.8	2	0	0	1669.75	259	273
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	7	7	13	0.01%	29.7%	ILAAQGQLSAQGGAQPSVEAPAAPRPTATQLTR	99.7%	140	25	140	0	2	0	3256.74	143	175
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	7	7	13	0.01%	29.7%	IQLQDAGR	99.7%	46.9	25	26.5	2	0	0	900.49	129	136
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	7	7	13	0.01%	29.7%	LAANDFFR	99.7%	55.3	25	45.8	2	0	0	953.48	84	91
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	7	7	13	0.01%	29.7%	VYTSMSDCLIK	99.7%	49.5	25	41.6	2	0	0	1316.62	45	55
Mitochondrial import inner membrane translocase subunit Tim13	TIMM13	TIM13_HUMAN	10.5	100.0%	3	3	4	0.00%	36.8%	LDPGLIMEQVK	99.7%	41.7	25	38.1	1	0	0	1242.68	17	27
Mitochondrial import inner membrane translocase subunit Tim13	TIMM13	TIM13_HUMAN	10.5	100.0%	3	3	4	0.00%	36.8%	VQIAVANAQELLQR	99.7%	103	25	95.4	2	0	0	1552.88	28	41
Mitochondrial import inner membrane translocase subunit Tim13	TIMM13	TIM13_HUMAN	10.5	100.0%	3	3	4	0.00%	36.8%	YMDAWNTVSR	95.5%	28.7	25	28.7	1	0	0	1242.56	73	82
Mitochondrial import inner membrane translocase subunit Tim17-B	TIMM17B	TI17B_HUMAN	18.3	99.8%	2	2	3	0.00%	12.8%	NAPPFLEDPSQLPPK	95.9%	29.1	25	29.1	1	0	0	1649.85	143	157
Mitochondrial import inner membrane translocase subunit Tim17-B	TIMM17B	TI17B_HUMAN	18.3	99.8%	2	2	3	0.00%	12.8%	YTAQQFR	99.3%	36.6	25	33.8	2	0	0	913.45	136	142
Mitochondrial import inner membrane translocase subunit Tim21	TIMM21	TIM21_HUMAN	28.2	99.8%	2	2	3	0.00%	8.5%	ENPGSGEYDFR	99.7%	71.3	25	71.3	2	0	0	1270.53	214	224
Mitochondrial import inner membrane translocase subunit Tim21	TIMM21	TIM21_HUMAN	28.2	99.8%	2	2	3	0.00%	8.5%	FYIEGSEPGK	98.2%	32.4	25	24.6	1	0	0	1126.54	195	204
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	7	9	20	0.02%	26.6%	AQGPQQQPGSEGPSYAK	99.7%	79.5	25	77.6	4	0	0	1729.81	48	64
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	7	9	20	0.02%	26.6%	IPDEFDNDPILVQQLR	99.7%	87.4	25	76.7	2	0	0	1911.98	98	113
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	7	9	20	0.02%	26.6%	QNLFLGSLTSR	99.7%	65.2	25	53.3	3	0	0	1235.67	335	345
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	7	9	20	0.02%	26.6%	RAPDQAAEIGSR	99.7%	53.1	25	48.1	2	1	0	1270.65	32	43
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	7	9	20	0.02%	26.6%	TIALNGVEDVR	99.7%	81.8	25	68.3	2	0	0	1186.64	285	295
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	7	9	20	0.02%	26.6%	TVLEHYALEDDPLAAFK	99.7%	59	25	58.9	2	2	0	1931.98	296	312
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	7	9	20	0.02%	26.6%	VLLDLSAFLK	99.7%	45.4	25	45.4	2	0	0	1118.68	275	284
Mitochondrial import receptor subunit TOM22 homolog	TOMM22	TOM22_HUMAN	15.5	99.8%	2	4	12	0.01%	16.2%	LQMEQQQQLQQR	99.7%	74	25	59.9	8	0	0	1557.78	106	117

Mitochondrial import receptor subunit TOM22 homolog	TOMM22	TOM22_HUMAN	15.5	99.8%	2	4	12	0.01%	16.2%	LWGLTEMFPER	99.7%	40.5	25	30.4	4	0	0	1378.68	48	58
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	6	10	20	0.02%	21.1%	ELFPIQMEGVK	99.7%	48	25	41.7	4	0	0	1290.68	92	102
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	6	10	20	0.02%	21.1%	FVNWQVDGEYR	99.7%	61.2	25	61.2	2	0	0	1412.66	185	195
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	6	10	20	0.02%	21.1%	GSVDSNWIVGATLEK	99.7%	99.4	25	90.5	2	0	0	1575.80	316	330
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	6	10	20	0.02%	21.1%	MAIQTQQSK	99.7%	44.5	25	39.9	2	0	0	1034.53	176	184
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	6	10	20	0.02%	21.1%	MQDTSVSFGYQLDLPK	99.7%	86.1	25	86.1	4	0	0	1828.88	294	309
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	6	10	20	0.02%	21.1%	RPGEEGTVMSLAGK	99.7%	81.2	25	71	4	2	0	1447.72	240	253
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	18	44	0.04%	23.6%	AAMDNSEIAGEKK	99.7%	82.1	25	70.4	4	0	0	1363.65	258	270
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	18	44	0.04%	23.6%	AVDEAADALLK	99.7%	63.8	25	46.9	4	0	0	1115.59	287	297
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	18	44	0.04%	23.6%	ELDSITPEVLPGWK	99.7%	59.5	25	56.4	4	0	0	1583.83	372	385
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	18	44	0.04%	23.6%	ERPPEEVAAR	99.7%	50	25	46.6	4	0	0	1153.60	196	205
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	18	44	0.04%	23.6%	EVAGAKPHITAAEGK	99.7%	59.3	25	53.7	2	2	0	1478.80	316	330
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	18	44	0.04%	23.6%	GIEQAVQSHAVAEEEAR	99.7%	88.1	25	88.1	1	2	0	1823.89	548	564
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	18	44	0.04%	23.6%	ISSVSEVMK	98.3%	32.7	25	22	1	0	0	979.51	111	119
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	18	44	0.04%	23.6%	KAVDEAADALLK	99.7%	49.5	25	44.2	1	0	0	1243.69	286	297
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	18	44	0.04%	23.6%	LFEMVLGPAAYNVPLPK	99.7%	54.3	25	47.4	1	0	0	1859.01	85	101
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	18	44	0.04%	23.6%	LSEQELQFR	99.7%	73.6	25	47	4	0	0	1149.59	517	525
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	18	44	0.04%	23.6%	SEFEQNLSEK	99.7%	47.1	25	40.6	3	0	0	1210.56	507	516
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	18	44	0.04%	23.6%	TSSAETPTIPLGSAVEAIK	99.7%	94	25	85.3	2	0	0	1872.00	582	600
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	18	44	0.04%	23.6%	VAMIDETR	99.7%	41.4	25	27.1	2	0	0	934.47	645	652
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	18	44	0.04%	23.6%	VVSQYHELVVQAR	99.7%	95.1	25	92.1	3	0	0	1527.83	354	366
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	15	18	44	0.04%	23.6%	YSTSGSSGLTTGK	99.7%	68.6	25	66.9	4	0	0	1245.60	33	45
Mitochondrial inner membrane protein OXA1L	OXA1L	OXA1L_HUMAN	48.5	100.0%	4	5	10	0.01%	9.2%	ASSEMALYQK	99.7%	49.5	25	47.2	4	0	0	1127.54	198	207
Mitochondrial inner membrane protein OXA1L	OXA1L	OXA1L_HUMAN	48.5	100.0%	4	5	10	0.01%	9.2%	CLIFPLIVTGQR	99.7%	60.2	25	47.8	2	0	0	1416.80	153	164
Mitochondrial inner membrane protein OXA1L	OXA1L	OXA1L_HUMAN	48.5	100.0%	4	5	10	0.01%	9.2%	LAGDHIEYYK	99.7%	51.1	25	42.9	2	0	0	1208.59	188	197
Mitochondrial inner membrane protein OXA1L	OXA1L	OXA1L_HUMAN	48.5	100.0%	4	5	10	0.01%	9.2%	NQLELAAR	99.7%	40.2	25	11.7	2	0	0	914.51	387	394
Mitochondrial ornithine transporter 1	SLC25A15	ORNT1_HUMAN	32.7	99.9%	2	2	3	0.00%	6.0%	SQNTVWSVIK	99.7%	60.9	25	47.4	2	0	0	1161.63	149	158
Mitochondrial ornithine transporter 1	SLC25A15	ORNT1_HUMAN	32.7	99.9%	2	2	3	0.00%	6.0%	TYSQVGFR	99.6%	39.3	25	22.8	1	0	0	957.48	54	61
Mitochondrial Rho GTPase 2	RHOT2	MIRO2_HUMAN	68.1	100.0%	4	4	5	0.00%	6.6%	ILLLGEAQVGK	99.7%	60	25	34.3	1	0	0	1140.70	7	17
Mitochondrial Rho GTPase 2	RHOT2	MIRO2_HUMAN	68.1	100.0%	4	4	5	0.00%	6.6%	NISELFYYAQK	99.7%	41.6	25	30.2	1	0	0	1375.69	154	164
Mitochondrial Rho GTPase 2	RHOT2	MIRO2_HUMAN	68.1	100.0%	4	4	5	0.00%	6.6%	SAFLQAFLGR	99.7%	50.9	25	48.5	1	0	0	1109.61	430	439
Mitochondrial Rho GTPase 2	RHOT2	MIRO2_HUMAN	68.1	100.0%	4	4	5	0.00%	6.6%	VPIILVGNK	99.7%	44	25	0	2	0	0	952.62	111	119
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	20	23	33	0.03%	55.8%	DSIIYLTADSPNVMTTFR	99.7%	83.3	25	80.6	2	0	0	2044.01	285	302
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	20	23	33	0.03%	55.8%	EFIEMWR	99.3%	36.4	25	36.4	2	0	0	1010.48	96	102
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	20	23	33	0.03%	55.8%	ELQNTVSQLLESEGWNR	99.7%	59.9	25	54.6	1	0	0	2002.98	219	235
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	20	23	33	0.03%	55.8%	ELQNTVSQLLESEGWNRR	99.2%	30	25	30	0	1	0	2159.08	219	236
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	20	23	33	0.03%	55.8%	EVPEHITEEELK	99.7%	42.6	25	31.9	2	0	0	1452.72	107	118
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	20	23	33	0.03%	55.8%	HTGFLEISQHSQEFINR	99.7%	40.7	25	40.7	0	1	0	2043.00	381	397
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	20	23	33	0.03%	55.8%	LLETTEEDKQK	99.7%	64.3	25	52.8	2	0	0	1333.68	165	175
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	20	23	33	0.03%	55.8%	LLLTSTEK	99.2%	36.1	25	25.7	1	0	0	904.54	269	276
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	20	23	33	0.03%	55.8%	LNLATECLPLDK	99.7%	65.6	25	53.8	2	0	0	1386.73	329	340
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	20	23	33	0.03%	55.8%	NESTPPSEELELDKWK	99.7%	64.3	25	60.7	1	0	0	1901.91	52	67
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	20	23	33	0.03%	55.8%	NFLFLR	98.9%	34.7	25	11.2	2	0	0	809.47	176	181
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	20	23	33	0.03%	55.8%	NMDIAMGWK	96.5%	29.7	25	22.4	1	0	0	1065.49	186	194
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	20	23	33	0.03%	55.8%	NNGNWQEALQFVPK	99.7%	58.9	25	53.1	2	0	0	1644.81	365	378
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	20	23	33	0.03%	55.8%	NVDPFHIYFCNLK	99.7%	53.6	25	46.3	2	0	0	1666.80	237	249
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	20	23	33	0.03%	55.8%	SMQPGTSLAK	97.4%	30.9	25	28.5	3	0	0	1019.52	316	325
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	20	23	33	0.03%	55.8%	SSVQEECVSTISSSK	99.7%	74.6	25	74.6	1	0	0	1627.75	72	86
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	20	23	33	0.03%	55.8%	SSVQEECVSTISSSKDEDPLAATR	99.7%	50.2	25	50.2	0	1	0	2596.20	72	95
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	20	23	33	0.03%	55.8%	TLMECVSNTAK	99.7%	48.2	25	41.9	3	0	0	1253.59	119	129
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	20	23	33	0.03%	55.8%	VYVIGSFVDK	99.4%	37.8	25	32.7	2	0	0	1126.61	306	315

Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	20	23	33	0.03%	55.8%	YLQWEIGNK	99.4%	37.8	25	36.5	1	0	0	1150.59	341	349
Mitochondrial ribonuclease P protein 3	KIAA0391	MRRP3_HUMAN	67.3	100.0%	5	5	8	0.01%	10.3%	DIKDDNYSNK	99.5%	38.4	25	34.1	1	0	0	1211.55	291	300
Mitochondrial ribonuclease P protein 3	KIAA0391	MRRP3_HUMAN	67.3	100.0%	5	5	8	0.01%	10.3%	EALLLLEDIKK	99.7%	56.7	25	45.8	2	0	0	1284.78	228	238
Mitochondrial ribonuclease P protein 3	KIAA0391	MRRP3_HUMAN	67.3	100.0%	5	5	8	0.01%	10.3%	ESQLLLNVVSQLAK	99.7%	59.6	25	59.6	2	0	0	1541.89	422	435
Mitochondrial ribonuclease P protein 3	KIAA0391	MRRP3_HUMAN	67.3	100.0%	5	5	8	0.01%	10.3%	LLDILSYLR	99.7%	56.2	25	56.2	2	0	0	1105.66	301	309
Mitochondrial ribonuclease P protein 3	KIAA0391	MRRP3_HUMAN	67.3	100.0%	5	5	8	0.01%	10.3%	SRPPFDVVIDGLNVAK	99.2%	30	25	30	0	1	0	1726.95	400	415
Mitochondrial thiamine pyrophosphate carrier	SLC25A19	TPC_HUMAN	35.5	100.0%	4	4	6	0.01%	9.7%	ALISPFDVIK	99.7%	57	25	52.7	2	0	0	1102.65	31	40
Mitochondrial thiamine pyrophosphate carrier	SLC25A19	TPC_HUMAN	35.5	100.0%	4	4	6	0.01%	9.7%	LQVGGFEHAR	98.5%	33.1	25	23.9	1	0	0	1113.58	244	253
Mitochondrial thiamine pyrophosphate carrier	SLC25A19	TPC_HUMAN	35.5	100.0%	4	4	6	0.01%	9.7%	RLQVGGFEHAR	99.5%	32	25	28.1	0	2	0	1269.68	243	253
Mitochondrial thiamine pyrophosphate carrier	SLC25A19	TPC_HUMAN	35.5	100.0%	4	4	6	0.01%	9.7%	VGYDPKPDGR	98.6%	33.5	25	33.4	1	0	0	1103.55	2	11
Mitochondrial translocator assembly and maintenance protein 41 homolog	TAMM41	TAM41_HUMAN	51.1	99.8%	2	2	3	0.00%	6.4%	ELYGSILQENPQVVYK	99.7%	79.7	25	77.2	2	0	0	1879.98	214	229
Mitochondrial translocator assembly and maintenance protein 41 homolog	TAMM41	TAM41_HUMAN	51.1	99.8%	2	2	3	0.00%	6.4%	LGLSAIVRPSSIR	97.2%	25	25	19	0	1	0	1368.83	291	303
Mitotic checkpoint protein BUB3	BUB3	BUB3_HUMAN	37.2	100.0%	4	4	7	0.01%	14.6%	LNQPPEDGISSVK	99.7%	46.8	25	46.8	2	0	0	1383.71	9	21
Mitotic checkpoint protein BUB3	BUB3	BUB3_HUMAN	37.2	100.0%	4	4	7	0.01%	14.6%	QGYVLSSIEGR	99.5%	38.5	25	30.4	1	0	0	1208.63	192	202
Mitotic checkpoint protein BUB3	BUB3	BUB3_HUMAN	37.2	100.0%	4	4	7	0.01%	14.6%	VAVEYLDPSPEVQK	99.7%	61	25	54.3	2	0	0	1573.81	203	216
Mitotic checkpoint protein BUB3	BUB3	BUB3_HUMAN	37.2	100.0%	4	4	7	0.01%	14.6%	VYTLSVSGDR	99.7%	53	25	47.6	2	0	0	1096.56	140	149
Mitotic spindle assembly checkpoint protein MAD2A	MAD2L1	MD2L1_HUMAN	23.5	100.0%	4	4	5	0.00%	16.6%	EQGITLR	94.8%	28.2	25	18.3	1	0	0	816.46	8	14
Mitotic spindle assembly checkpoint protein MAD2A	MAD2L1	MD2L1_HUMAN	23.5	100.0%	4	4	5	0.00%	16.6%	GIYPSETFTR	99.7%	48.2	25	46.2	2	0	0	1170.58	36	45
Mitotic spindle assembly checkpoint protein MAD2A	MAD2L1	MD2L1_HUMAN	23.5	100.0%	4	4	5	0.00%	16.6%	SFTTTIHK	99.3%	36.6	25	18.3	1	0	0	934.50	185	192
Mitotic spindle assembly checkpoint protein MAD2A	MAD2L1	MD2L1_HUMAN	23.5	100.0%	4	4	5	0.00%	16.6%	WQFDIECDK	99.6%	39.1	25	39.1	1	0	0	1240.53	100	108
Mitotic spindle-associated MMXD complex subunit MIP18	FAM96B	MIP18_HUMAN	17.7	100.0%	3	3	4	0.00%	30.7%	EIFDLIR	98.8%	34.2	25	12.4	1	0	0	905.51	45	51
Mitotic spindle-associated MMXD complex subunit MIP18	FAM96B	MIP18_HUMAN	17.7	100.0%	3	3	4	0.00%	30.7%	SGERPVTAGEEDEQVPDSIDAR	99.7%	38.9	25	35.4	0	1	0	2357.09	23	44
Mitotic spindle-associated MMXD complex subunit MIP18	FAM96B	MIP18_HUMAN	17.7	100.0%	3	3	4	0.00%	30.7%	VGGGGVGGGLLENANPLIYQR	99.7%	67	25	67	2	0	0	2041.08	2	22
MKI67 FHA domain-interacting nucleolar phosphoprotein	NIFK	MK67I_HUMAN	34.2	100.0%	4	4	9	0.01%	17.4%	GIDYDFPSLILQK	99.7%	60.6	25	60.6	4	0	0	1508.80	180	192
MKI67 FHA domain-interacting nucleolar phosphoprotein	NIFK	MK67I_HUMAN	34.2	100.0%	4	4	9	0.01%	17.4%	GYAFVEFESEDVAK	99.7%	77.6	25	72.9	2	0	0	1590.73	87	100
MKI67 FHA domain-interacting nucleolar phosphoprotein	NIFK	MK67I_HUMAN	34.2	100.0%	4	4	9	0.01%	17.4%	IVAETMNNYLFGER	99.6%	39.2	25	39.2	1	0	0	1656.81	101	114
MKI67 FHA domain-interacting nucleolar phosphoprotein	NIFK	MK67I_HUMAN	34.2	100.0%	4	4	9	0.01%	17.4%	VSGTLDTPEK	99.6%	39	25	24.7	2	0	0	1046.54	217	226
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	7	7	10	0.01%	7.7%	AVLASTPR	97.1%	30.5	25	20.6	1	0	0	814.48	247	254
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	7	7	10	0.01%	7.7%	EDLILSLR	99.7%	45.8	25	9.48	1	0	0	958.56	239	246
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	7	7	10	0.01%	7.7%	EVFQTASER	99.7%	49.6	25	45.2	2	0	0	1066.52	308	316
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	7	7	10	0.01%	7.7%	FAEFLLPLLIEK	99.7%	74.9	25	68.2	2	0	0	1432.85	255	266
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	7	7	10	0.01%	7.7%	FLNLSSSPSMAVR	99.7%	45.5	25	41	1	0	0	1424.72	959	971
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	7	7	10	0.01%	7.7%	LLQAAAGASAR	99.7%	76.1	25	70.4	2	0	0	1028.58	374	384
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	7	7	10	0.01%	7.7%	VEAEGLAALHSLTACLSR	99.7%	34.5	25	31.4	0	1	0	1897.98	317	334
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	6	6	16	0.02%	19.4%	AYLEPEHTK	96.7%	29.9	25	24.8	1	0	0	1087.54	24	32
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	6	6	16	0.02%	19.4%	EFPSSFESLVR	99.7%	53.3	25	50.7	2	0	0	1297.64	135	145
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	6	6	16	0.02%	19.4%	ELVVLPR	98.7%	33.9	25	12.5	3	0	0	825.52	42	48
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	6	6	16	0.02%	19.4%	ITDFQFK	99.7%	42.5	25	14.7	3	0	0	898.47	35	41
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	6	6	16	0.02%	19.4%	KAYLEPEHTK	99.7%	35.1	25	35.1	0	3	0	1215.64	23	32
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	6	6	16	0.02%	19.4%	LVTDEDVFPTK	99.7%	69.9	25	58.8	4	0	0	1263.65	121	131
Monocarboxylate transporter 1	SLC16A1	MOT1_HUMAN	53.9	100.0%	3	4	14	0.01%	8.2%	DLHDANTDLIGR	99.7%	60.9	25	55.8	8	2	0	1339.66	225	236
Monocarboxylate transporter 1	SLC16A1	MOT1_HUMAN	53.9	100.0%	3	4	14	0.01%	8.2%	ESKEEETSIDVAGKPNEVTK	99.7%	47.1	25	47.1	0	3	0	2190.08	460	479
Monocarboxylate transporter 1	SLC16A1	MOT1_HUMAN	53.9	100.0%	3	4	14	0.01%	8.2%	LNDMYGDYK	99.5%	38.6	25	38.6	1	0	0	1118.48	412	420
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	44	0.04%	27.4%	AEIDLVCELAK	99.7%	71.7	25	56.3	2	0	0	1260.65	808	818
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	44	0.04%	27.4%	ASGLVPNVVVLVATVR	99.7%	72.1	25	72.1	2	1	0	1593.97	730	745
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	44	0.04%	27.4%	AVIELLEK	99.4%	37.5	25	19.1	2	0	0	914.56	206	213
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	44	0.04%	27.4%	DFILPISDVR	99.7%	56.6	25	50.2	2	0	0	1174.65	926	935
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	44	0.04%	27.4%	DIELSPEAQAK	99.7%	62.8	25	50.9	2	0	0	1200.61	881	891
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	44	0.04%	27.4%	DVDGVTDINLGK	99.7%	75.4	25	61.8	2	0	0	1245.63	178	189
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	44	0.04%	27.4%	EFSEIQLAR	99.7%	54.4	25	30	2	0	0	1092.57	531	539
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	44	0.04%	27.4%	EIGLLADEIEIYGK	99.7%	100	25	94.2	2	0	0	1562.83	380	393

Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	44	0.04%	27.4%	EVLSLLQEK	99.7%	47.6	25	41.5	2	0	0	1058.61	84	92
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	44	0.04%	27.4%	FQFLYDVQVPIVDK	99.7%	91.5	25	89.8	2	0	0	1710.91	855	868
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	44	0.04%	27.4%	GDAHECFVSPVAK	99.6%	33.2	25	33.2	0	1	0	1416.66	193	205
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	44	0.04%	27.4%	IQNMVSSGR	99.5%	37.9	25	32.1	2	0	0	991.50	327	335
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	44	0.04%	27.4%	KITIGQGNTEK	99.7%	45.1	25	31.4	2	0	0	1188.66	586	596
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	44	0.04%	27.4%	LDIDPSTITWQR	99.7%	70.4	25	65.8	2	0	0	1444.74	564	575
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	44	0.04%	27.4%	LQPLSPVPSDIEISR	99.7%	64.9	25	63	2	0	0	1650.91	353	367
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	44	0.04%	27.4%	LVPLVNGVR	99.7%	50.9	25	46	2	0	0	966.61	522	530
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	44	0.04%	27.4%	MHGGGPSVTAGVPLKK	97.3%	25.1	25	18.5	0	2	0	1535.84	749	764
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	44	0.04%	27.4%	SGQPVTADDLGVTGALTVLMK	99.7%	119	25	115	3	0	0	2073.09	639	659
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	44	0.04%	27.4%	TDPSTLTEEEVSK	99.7%	78.9	25	68.9	2	0	0	1435.68	548	560
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	44	0.04%	27.4%	TIAQAVYGAK	99.7%	52.1	25	39.6	2	0	0	1021.57	871	880
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	44	0.04%	27.4%	VLNALKPEK	97.0%	30.3	25	27.4	1	0	0	1011.62	169	177
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	22	24	44	0.04%	27.4%	YVLVAGITPTPLGEGK	99.7%	109	25	109	2	0	0	1614.91	414	429
Motile sperm domain-containing protein 2	MOSPD2	MSPD2_HUMAN	59.7	100.0%	4	4	5	0.00%	8.5%	EISVNDLNESSIPR	99.7%	82	25	82	1	0	0	1572.79	74	87
Motile sperm domain-containing protein 2	MOSPD2	MSPD2_HUMAN	59.7	100.0%	4	4	5	0.00%	8.5%	LIAFWLER	99.7%	54.8	25	43.4	2	0	0	1047.60	128	135
Motile sperm domain-containing protein 2	MOSPD2	MSPD2_HUMAN	59.7	100.0%	4	4	5	0.00%	8.5%	TLIVLTNVTK	99.7%	52	25	52	1	0	0	1101.69	348	357
Motile sperm domain-containing protein 2	MOSPD2	MSPD2_HUMAN	59.7	100.0%	4	4	5	0.00%	8.5%	TWLGPEAVSLLK	95.1%	28.4	25	16.6	1	0	0	1313.75	200	211
mRNA export factor	RAE1	RAE1L_HUMAN	41.0	100.0%	3	4	6	0.01%	10.9%	CYCADVIYPMAVVATAER	96.3%	29.5	25	29.5	1	0	0	2088.96	173	190
mRNA export factor	RAE1	RAE1L_HUMAN	41.0	100.0%	3	4	6	0.01%	10.9%	NAAEELKPR	99.7%	48.9	25	42.5	2	0	0	1027.55	357	365
mRNA export factor	RAE1	RAE1L_HUMAN	41.0	100.0%	3	4	6	0.01%	10.9%	SSNPMMVLQLPER	99.7%	47.6	25	36	3	0	0	1533.74	160	172
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	10	11	17	0.02%	43.9%	EGDVLTPEQAR	99.7%	49.5	25	38.1	2	0	0	1214.60	178	188
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	10	11	17	0.02%	43.9%	GEVGLLFTNR	99.7%	68.8	25	53.7	2	0	0	1105.60	98	107
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	10	11	17	0.02%	43.9%	GVVTLLSDYEVCK	99.7%	84.3	25	78.2	1	0	0	1482.75	165	177
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	10	11	17	0.02%	43.9%	QNLIEELRK	98.2%	32.4	25	13.1	1	0	0	1142.65	24	32
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	10	11	17	0.02%	43.9%	SPSDEYKDNLHQVSK	99.7%	35	25	35	0	2	0	1746.83	80	94
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	10	11	17	0.02%	43.9%	TKEEVNEWFTK	99.7%	54.8	25	50.3	2	0	0	1410.69	108	118
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	10	11	17	0.02%	43.9%	VMMVALGR	98.1%	32.3	25	22	1	0	0	908.47	72	79
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	10	11	17	0.02%	43.9%	YLFIFSVANMR	99.7%	53.2	25	53.2	3	0	0	1360.71	39	49
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	10	11	17	0.02%	43.9%	YMWDSQSGR	98.0%	32	25	32	1	0	0	1129.47	206	214
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	10	11	17	0.02%	43.9%	YTEMDYAR	99.5%	38.6	25	38.6	2	0	0	1064.44	119	126
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	6	6	11	0.01%	16.2%	ACGNFGIPCELR	99.7%	47.2	25	46	2	0	0	1393.64	287	298
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	6	6	11	0.01%	16.2%	ASILNTWISLK	99.7%	55.8	25	47.4	2	0	0	1245.72	404	414
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	6	6	11	0.01%	16.2%	EIVLADVIDNDSWR	99.7%	128	25	122	2	0	0	1644.82	202	215
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	6	6	11	0.01%	16.2%	EVTPEGLQMVK	99.7%	57	25	52.3	2	0	0	1230.64	236	246
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	6	6	11	0.01%	16.2%	NFEWVAER	99.0%	35.1	25	31.1	1	0	0	1050.50	248	255
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	6	6	11	0.01%	16.2%	TKEVYELLDSPGK	99.7%	78.2	25	72.1	2	0	0	1478.77	18	30
Multiple myeloma tumor-associated protein 2	MMTAG2	MMTA2_HUMAN	29.4	99.8%	2	2	2	0.00%	10.3%	LLGLGSASGSVGR	99.7%	57.3	25	51	1	0	0	1173.66	118	130
Multiple myeloma tumor-associated protein 2	MMTAG2	MMTA2_HUMAN	29.4	99.8%	2	2	2	0.00%	10.3%	VESGGPGTSAASAR	99.7%	79.9	25	77.9	1	0	0	1246.60	153	166
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	21	21	59	0.06%	16.3%	AGALHAQVER	98.0%	31.9	25	21.3	1	0	0	1051.56	897	906
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	21	21	59	0.06%	16.3%	ALVDILSEVSK	99.7%	83.9	25	82.1	4	0	0	1173.67	180	190
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	21	21	59	0.06%	16.3%	AQDSSLHMPER	99.2%	35.8	25	29	4	0	0	1286.58	433	443
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	21	21	59	0.06%	16.3%	EIPSATQSPISK	99.7%	56.9	25	51.3	3	0	0	1257.67	1156	1167
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	21	21	59	0.06%	16.3%	EVVEQGLLK	99.7%	47.9	25	34.4	3	0	0	1014.58	287	295
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	21	21	59	0.06%	16.3%	GNTAEGCVHETQEK	99.7%	61.9	25	61.9	4	0	0	1559.68	936	949
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	21	21	59	0.06%	16.3%	HPFSFPLENQAR	98.7%	28	25	25.2	0	1	0	1442.72	499	510
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	21	21	59	0.06%	16.3%	HQACLLLQK	99.4%	37	25	30.6	2	0	0	1110.61	1028	1036
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	21	21	59	0.06%	16.3%	KPTSQIPETK	99.7%	43.5	25	43.5	4	0	0	1128.63	489	498
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	21	21	59	0.06%	16.3%	LITGLGVGR	99.7%	64.1	25	51.4	2	0	0	885.55	77	85
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	21	21	59	0.06%	16.3%	LLEYLR	95.0%	28.3	25	16.6	1	0	0	806.48	57	62
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	21	21	59	0.06%	16.3%	LLGAALPLLTK	99.7%	60.7	25	60.7	6	0	0	1109.73	308	318

Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	21	21	59	0.06%	16.3%	LPAIALDLLR	99.7%	57.5	25	57.5	4	0	0	1094.69	264	273
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	21	21	59	0.06%	16.3%	LVGSVNLFSDENVPR	99.7%	109	25	101	4	0	0	1645.85	232	246
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	21	21	59	0.06%	16.3%	QLMGQVLAK	99.7%	55.2	25	38.8	1	0	0	987.57	1054	1062
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	21	21	59	0.06%	16.3%	SPAPGAPTR	99.5%	38.8	25	23.8	2	0	0	853.45	1232	1240
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	21	21	59	0.06%	16.3%	SPLSALAR	99.7%	57.2	25	29	3	0	0	814.48	1290	1297
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	21	21	59	0.06%	16.3%	SPSLLQSGAK	99.7%	43.6	25	35.5	3	0	0	987.55	1308	1317
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	21	21	59	0.06%	16.3%	TLGVQRPK	98.5%	33.1	25	33.1	1	0	0	898.55	1141	1148
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	21	21	59	0.06%	16.3%	VLDLVEVLVTK	99.7%	65.2	25	65.2	2	0	0	1227.76	828	838
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	21	21	59	0.06%	16.3%	VYSTALSSFLTK	99.7%	92.6	25	83.4	4	0	0	1316.71	977	988
Myosin light polypeptide 6	MYL6	MYL6_HUMAN	16.9	100.0%	5	7	13	0.01%	37.1%	ALGQNPTNAEVLK	99.7%	53.5	25	52	4	0	0	1354.73	38	50
Myosin light polypeptide 6	MYL6	MYL6_HUMAN	16.9	100.0%	5	7	13	0.01%	37.1%	EAFQLFDR	99.7%	59.4	25	57.8	2	0	0	1025.51	14	21
Myosin light polypeptide 6	MYL6	MYL6_HUMAN	16.9	100.0%	5	7	13	0.01%	37.1%	HVLVTLGEK	98.7%	33.9	25	33.9	2	0	0	995.59	111	119
Myosin light polypeptide 6	MYL6	MYL6_HUMAN	16.9	100.0%	5	7	13	0.01%	37.1%	ILYSQCGDVMR	99.7%	56	25	56	3	0	0	1357.62	27	37
Myosin light polypeptide 6	MYL6	MYL6_HUMAN	16.9	100.0%	5	7	13	0.01%	37.1%	NKDQGTYEDYVEGLR	99.7%	65.3	25	65.3	1	1	0	1786.82	80	94
Myosin regulatory light chain 12A	MYL12A	ML12A_HUMAN	19.8	100.0%	3	3	8	0.01%	18.7%	FTDEEVDELYR	99.7%	60	25	60	1	0	0	1415.63	133	143
Myosin regulatory light chain 12A	MYL12A	ML12A_HUMAN	19.8	100.0%	3	3	8	0.01%	18.7%	GNFNYIEFTR	99.7%	67	25	53.6	4	0	0	1260.60	151	160
Myosin regulatory light chain 12A	MYL12A	ML12A_HUMAN	19.8	100.0%	3	3	8	0.01%	18.7%	LNGTDPEDVIR	99.0%	35.2	25	32.9	3	0	0	1228.62	93	103
Myosin-10	MYH10	MYH10_HUMAN	229.0	100.0%	4	4	5	0.00%	2.9%	ALAYDKLEK	98.2%	32.5	25	23.1	1	0	0	1050.58	1412	1420
Myosin-10	MYH10	MYH10_HUMAN	229.0	100.0%	4	4	5	0.00%	2.9%	ALELDPNLYR	99.3%	36.6	25	32.8	1	0	0	1203.64	753	762
Myosin-10	MYH10	MYH10_HUMAN	229.0	100.0%	4	4	5	0.00%	2.9%	LDPHLVLDQLR	99.7%	41	25	33.8	2	0	0	1318.75	690	700
Myosin-10	MYH10	MYH10_HUMAN	229.0	100.0%	4	4	5	0.00%	2.9%	QLLQANPILESFGNAK	99.7%	65.7	25	63.8	1	0	0	1742.94	217	232
Myosin-10	MYH10	MYH10_HUMAN	229.0	100.0%	4	4	5	0.00%	2.9%	SDLLLEGFNNYR	99.7%	46.9	25	46.9	2	0	0	1440.71	297	308
Myosin-9	MYH9	MYH9_HUMAN	226.5	99.9%	2	2	4	0.00%	1.4%	LDPHLVLDQLR	99.7%	41	25	33.8	2	0	0	1318.75	683	693
Myosin-9	MYH9	MYH9_HUMAN	226.5	99.9%	2	2	4	0.00%	1.4%	QLLQANPILEAFGNAK	99.7%	84.6	25	79.5	2	0	0	1726.95	210	225
Myotrophin	MTPN	MTPN_HUMAN	12.9	99.8%	2	2	4	0.00%	25.4%	GPDGLTAFEATDNQAIK	99.7%	58.2	25	53.6	2	0	0	1747.85	98	114
Myotrophin	MTPN	MTPN_HUMAN	12.9	99.8%	2	2	4	0.00%	25.4%	NGDLDEVKDYVAK	99.6%	39.2	25	31.5	2	0	0	1465.72	12	24
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	11	11	17	0.02%	12.4%	AGFVPVYLR	99.7%	44.6	25	40.5	2	0	0	1021.58	726	734
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	11	11	17	0.02%	12.4%	ASEVFLQR	99.7%	72.5	25	51.8	1	0	0	949.51	521	528
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	11	11	17	0.02%	12.4%	EELEALFLPYDLK	99.7%	83	25	76.6	2	0	0	1579.83	811	823
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	11	11	17	0.02%	12.4%	ILIENGVAER	99.7%	59.4	25	44.9	2	0	0	1113.63	12	21
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	11	11	17	0.02%	12.4%	LDYLGVSYGLTPR	99.7%	61.2	25	49.8	2	0	0	1453.77	706	718
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	11	11	17	0.02%	12.4%	QDDPFELFIAATNIR	98.9%	34.5	25	34.5	1	0	0	1749.88	89	103
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	11	11	17	0.02%	12.4%	QQSAQSQVSTTAENK	99.7%	96.1	25	86.8	2	0	0	1606.77	433	447
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	11	11	17	0.02%	12.4%	SLFVVVGDR	99.7%	53.4	25	41.9	2	0	0	991.56	24	32
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	11	11	17	0.02%	12.4%	SMDLSEYIIR	97.2%	30.5	25	29.9	1	0	0	1226.61	957	966
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	11	11	17	0.02%	12.4%	TLSDDLDEAAKEFQEK	99.7%	75.3	25	74.8	1	0	0	1838.87	932	947
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	11	11	17	0.02%	12.4%	YCYYNETHK	94.7%	28.1	25	28.1	1	0	0	1277.53	104	112
N-acetyltransferase 14	NAT14	NAT14_HUMAN	21.7	99.8%	2	2	4	0.00%	14.6%	APSHLSVR	98.1%	32.3	25	21.6	2	0	0	866.48	2	9
N-acetyltransferase 14	NAT14	NAT14_HUMAN	21.7	99.8%	2	2	4	0.00%	14.6%	GSGDVCGVLALAPGTNAGDGAR	99.7%	78.8	25	78.8	2	0	0	2014.96	103	124
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	7	7	11	0.01%	9.2%	AVVLAANHFGR	99.7%	46.1	25	46.1	1	0	0	1154.64	203	213
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	7	7	11	0.01%	9.2%	EANSIIITPGYGLCAAK	99.7%	63.4	25	63.4	2	0	0	1777.92	923	939
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	7	7	11	0.01%	9.2%	FFTGQITAAGK	99.7%	45	25	43.7	2	0	0	1140.60	214	224
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	7	7	11	0.01%	9.2%	GITHIGYTDLPSR	99.7%	40.9	25	34.2	1	0	0	1429.74	367	379
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	7	7	11	0.01%	9.2%	MATQASTLYSNNITK	97.1%	30.4	25	30.4	1	0	0	1658.81	380	394
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	7	7	11	0.01%	9.2%	TSGTLISFIYPAQNPELLNK	99.7%	44.6	25	44.6	2	0	0	2206.18	147	166
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	7	7	11	0.01%	9.2%	VALSPAGVQNLVK	99.7%	70.8	25	68.9	2	0	0	1295.77	72	84
NAD(P)H-hydrate epimerase	APOA1BP	NNRE_HUMAN	31.7	99.9%	2	2	4	0.00%	10.4%	GNAGGIQPDLLISLTAPK	99.7%	42.5	25	42.5	2	0	0	1764.99	228	245
NAD(P)H-hydrate epimerase	APOA1BP	NNRE_HUMAN	31.7	99.9%	2	2	4	0.00%	10.4%	LFGYEPTIYYPK	99.7%	51.6	25	46.2	2	0	0	1490.76	133	144
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	9	9	14	0.01%	20.8%	FDKGPWLK	96.8%	30.1	25	9.28	1	0	0	990.54	278	285
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	9	9	14	0.01%	20.8%	FYDDPR	98.3%	32.8	25	32.8	1	0	0	812.36	117	122
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	9	9	14	0.01%	20.8%	ITSAYLQDIENAYK	99.7%	87.6	25	82.8	2	0	0	1628.82	229	242

NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	9	9	14	0.01%	20.8%	KVVEDIEYLK	99.7%	51.4	25	49.2	2	0	0	1235.69	268	277
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	9	9	14	0.01%	20.8%	LQSWLYSSR	99.7%	48	25	35.1	2	0	0	1139.58	131	139
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	9	9	14	0.01%	20.8%	TFLPEMSEK	98.3%	32.6	25	28.2	1	0	0	1097.52	244	252
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	9	9	14	0.01%	20.8%	TLYHLR	95.0%	28.2	25	7.93	1	0	0	802.46	290	295
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	9	9	14	0.01%	20.8%	VITVDGNICTGK	99.7%	76.3	25	66.6	2	0	0	1276.66	59	70
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	9	9	14	0.01%	20.8%	VVEDIEYLK	99.7%	60	25	53.3	2	0	0	1107.59	269	277
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	100.0%	6	7	14	0.01%	44.8%	FNVTGTPEQYVPYSTTR	99.7%	64.1	25	64.1	2	0	0	1959.94	115	131
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	100.0%	6	7	14	0.01%	44.8%	GLQQITGHGGLR	99.7%	68.6	25	57.5	4	1	0	1236.68	10	21
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	100.0%	6	7	14	0.01%	44.8%	IQEWIPPSTPYK	99.7%	52.5	25	46.9	2	0	0	1458.76	134	145
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	100.0%	6	7	14	0.01%	44.8%	VGTLVGEDK	99.7%	51.9	25	19.7	2	0	0	917.49	35	43
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	100.0%	6	7	14	0.01%	44.8%	VGTLVGEDKYGNK	99.7%	47.8	25	37.8	1	0	0	1379.72	35	47
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	100.0%	6	7	14	0.01%	44.8%	YYEDNKQFFGR	99.7%	64.3	25	64.3	2	0	0	1466.67	48	58
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	NDUAD_HUMAN	16.7	100.0%	4	5	10	0.01%	21.5%	ENLEEEAIIMK	99.7%	75.3	25	58.4	4	0	0	1318.66	89	99
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	NDUAD_HUMAN	16.7	100.0%	4	5	10	0.01%	21.5%	LQIEDFEAR	99.7%	52.4	25	40	2	0	0	1120.56	60	68
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	NDUAD_HUMAN	16.7	100.0%	4	5	10	0.01%	21.5%	RLQIEDFEAR	99.7%	43.8	25	37.4	2	0	0	1276.66	59	68
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	NDUAD_HUMAN	16.7	100.0%	4	5	10	0.01%	21.5%	VGESVFHTTR	99.7%	79.2	25	74.7	2	0	0	1132.57	106	115
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	NDUA5_HUMAN	13.5	100.0%	4	5	9	0.01%	31.0%	ILDVLEEIPK	99.6%	39.6	25	39.6	1	0	0	1168.68	31	40
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	NDUA5_HUMAN	13.5	100.0%	4	5	9	0.01%	31.0%	KYTEQITNEK	99.7%	61.6	25	51.5	2	0	0	1253.64	46	55
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	NDUA5_HUMAN	13.5	100.0%	4	5	9	0.01%	31.0%	TTGLVGLAVCNTPHER	99.7%	47.4	25	41.7	2	2	0	1724.88	8	23
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	NDUA5_HUMAN	13.5	100.0%	4	5	9	0.01%	31.0%	YTEQITNEK	99.7%	54.2	25	41.6	2	0	0	1125.54	47	55
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	NDUFA6	NDUA6_HUMAN	17.9	100.0%	4	4	7	0.01%	18.8%	FFHETEAPRPK	99.7%	48	25	46.8	2	0	0	1358.69	132	142
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	NDUFA6	NDUA6_HUMAN	17.9	100.0%	4	4	7	0.01%	18.8%	GKIELEETIK	99.0%	35	25	20.3	2	0	0	1159.66	112	121
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	NDUFA6	NDUA6_HUMAN	17.9	100.0%	4	4	7	0.01%	18.8%	IELEETIK	96.2%	29.4	25	22.7	1	0	0	974.54	114	121
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	NDUFA6	NDUA6_HUMAN	17.9	100.0%	4	4	7	0.01%	18.8%	VVDLLVIK	99.3%	37	25	37	2	0	0	898.60	104	111
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	17	30	0.03%	48.5%	DAFPEAIIVKPSDIFGR	99.5%	38.5	25	38.5	2	0	0	1875.00	193	209
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	17	30	0.03%	48.5%	FGPIPLGSLGWK	99.6%	39	25	37.4	2	0	0	1271.71	223	234
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	17	30	0.03%	48.5%	FIHVSHLNANIK	99.7%	45.1	25	33.6	2	0	0	1392.77	164	175
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	17	30	0.03%	48.5%	FLNSFASMHR	99.6%	39.2	25	31.5	1	0	0	1209.58	213	222
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	17	30	0.03%	48.5%	IPQAIAQLSK	99.7%	54.9	25	53.9	2	0	0	1068.64	148	157
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	17	30	0.03%	48.5%	MGSQVIIPYR	99.7%	76.9	25	68.3	2	0	0	1163.62	76	85
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	17	30	0.03%	48.5%	NFDFEDVFVK	99.7%	56.3	25	24.2	2	0	0	1259.59	138	147
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	17	30	0.03%	48.5%	QPVYVVDVSK	99.6%	39.1	25	36.1	2	0	0	1133.62	238	247
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	17	30	0.03%	48.5%	SFAFVGPSR	99.7%	51.6	25	38.9	2	0	0	967.50	262	270
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	17	30	0.03%	48.5%	SSVSGIVATVFGATGFLGR	99.7%	78.5	25	78.5	2	0	0	1825.98	49	67
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	17	30	0.03%	48.5%	VFEISPFEPWITR	99.7%	70.8	25	65.9	2	0	0	1620.84	304	316
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	17	30	0.03%	48.5%	VVQHSNVVINLIGR	99.7%	61.7	25	61.7	1	1	0	1547.90	119	132
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	17	30	0.03%	48.5%	WLSAEIEDVKPAK	99.7%	78.4	25	68.3	2	0	0	1485.79	361	373
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	17	30	0.03%	48.5%	YIFAVAHR	95.8%	29	25	18	1	0	0	976.54	279	286
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	17	30	0.03%	48.5%	YLLFHLVK	99.4%	37.5	25	29.6	2	0	0	1032.62	271	278
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	16	17	30	0.03%	48.5%	YVVNHLGR	98.9%	34.5	25	23.8	2	0	0	957.53	68	75
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	NDUFB10	NDUBA_HUMAN	20.8	99.8%	2	2	3	0.00%	14.5%	AFDLIVDRPVTLVR	96.9%	30.2	25	30.2	1	0	0	1613.94	30	43
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	NDUFB10	NDUBA_HUMAN	20.8	99.8%	2	2	3	0.00%	14.5%	YQDLGAYSSAR	99.6%	39.6	25	39.6	2	0	0	1230.57	137	147
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	NDUFB4	NDUB4_HUMAN	15.2	100.0%	3	3	11	0.01%	31.8%	GLIENPALLR	99.7%	63	25	51.8	4	0	0	1095.65	58	67
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	NDUFB4	NDUB4_HUMAN	15.2	100.0%	3	3	11	0.01%	31.8%	TINVYPNFRPTPK	99.5%	38	25	37.2	3	0	0	1546.84	73	85
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	NDUFB4	NDUB4_HUMAN	15.2	100.0%	3	3	11	0.01%	31.8%	TLPETLDPAEYNISPETR	99.7%	65.3	25	65.3	4	0	0	2046.00	13	30
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	7	7	11	0.01%	15.5%	EAYEAGLIGK	99.7%	59.9	25	51.3	2	0	0	1050.55	175	184
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	7	7	11	0.01%	15.5%	GGAGFPTGLK	99.7%	42.9	25	30.6	2	0	0	904.49	89	98
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	7	7	11	0.01%	15.5%	GGTWFAGFGR	99.7%	46.2	25	37.4	2	0	0	1055.51	258	267
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	7	7	11	0.01%	15.5%	GPDWILGEIK	99.7%	45.3	25	44	2	0	0	1127.61	72	81
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	7	7	11	0.01%	15.5%	HFRPELEER	98.3%	27	25	22.9	0	1	0	1212.61	441	449
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	7	7	11	0.01%	15.5%	IFTNLYGR	99.5%	37.9	25	31.4	1	0	0	983.53	41	48

NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	100.0%	7	7	11	0.01%	15.5%	NACGSGYDFDVFVVR	99.7%	93.7	25	93.7	1	0	0	1705.76	185	199
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	4	4	6	0.01%	10.2%	MFEFYER	98.7%	33.7	25	25.1	2	0	0	1021.44	210	216
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	4	4	6	0.01%	10.2%	NITLNFGPQHPAAHGVLR	99.7%	38.5	25	35.1	0	2	0	1942.04	79	96
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	4	4	6	0.01%	10.2%	TSMESLIHHFK	98.1%	26.6	25	22.6	0	1	0	1345.66	373	383
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	4	4	6	0.01%	10.2%	TYLQALPYFDR	99.3%	36.5	25	36.2	1	0	0	1386.71	128	138
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	16	0.02%	39.0%	AANWYER	99.7%	45.5	25	45.5	2	0	0	909.42	162	168
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	16	0.02%	39.0%	DFPLSGYVELR	99.7%	69.4	25	56.7	2	0	0	1295.66	201	211
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	16	0.02%	39.0%	ESAGADTRPTVRPR	99.7%	43.6	25	40.4	0	2	0	1512.79	37	50
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	16	0.02%	39.0%	ILTDYGFEGHPFR	99.7%	87.2	25	87.2	2	0	0	1551.76	187	199
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	16	0.02%	39.0%	QLSAFGEYVAEILPK	99.7%	86.2	25	86.2	2	0	0	1664.89	57	71
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	16	0.02%	39.0%	SLVDLTAVDVPTR	99.7%	86.5	25	84.4	2	0	0	1385.76	110	122
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	16	0.02%	39.0%	TYTDELTPIESAVSVFK	99.7%	48.1	25	46.4	2	0	0	1899.96	145	161
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	16	0.02%	39.0%	VVAEPVELAQEFR	99.7%	71.6	25	67.2	2	0	0	1486.79	219	231
NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	NDUFS6	NDUS6_HUMAN	13.7	99.8%	2	3	5	0.00%	21.8%	TGTCGYCGLQFR	99.5%	38.5	25	38.5	2	0	0	1419.61	109	120
NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	NDUFS6	NDUS6_HUMAN	13.7	99.8%	2	3	5	0.00%	21.8%	VIACDGGGGALGHPK	99.7%	67.5	25	54.4	2	1	0	1408.70	84	98
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	NDUS7_HUMAN	23.6	100.0%	4	6	18	0.02%	15.5%	KVYDQMPEPR	99.4%	37.6	25	37	3	0	0	1278.61	136	145
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	NDUS7_HUMAN	23.6	100.0%	4	6	18	0.02%	15.5%	LDDLVNWAR	99.7%	64.2	25	48.9	4	0	0	1101.57	67	75
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	NDUS7_HUMAN	23.6	100.0%	4	6	18	0.02%	15.5%	QSDVMIVAGTLTNK	99.7%	122	25	115	8	0	0	1476.77	116	129
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	NDUS7_HUMAN	23.6	100.0%	4	6	18	0.02%	15.5%	VYDQMPEPR	99.7%	66.7	25	66.7	3	0	0	1134.52	137	145
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	NDUS8_HUMAN	23.7	100.0%	3	3	6	0.01%	18.6%	LCEAICPAQAITIEAEPR	99.7%	83.6	25	83.6	2	0	0	2042.00	116	133
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	NDUS8_HUMAN	23.7	100.0%	3	3	6	0.01%	18.6%	TLLWTELFR	99.7%	44.6	25	41.7	2	0	0	1178.66	58	66
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	NDUS8_HUMAN	23.7	100.0%	3	3	6	0.01%	18.6%	YVNMQDPEMDMK	99.7%	43.2	25	32.5	2	0	0	1548.60	38	49
NADH-cytochrome b5 reductase 3	CYB5R3	NB5R3_HUMAN	34.2	99.8%	2	2	3	0.00%	10.3%	DILLRPELEELR	98.3%	32.7	25	21.8	1	0	0	1495.85	215	226
NADH-cytochrome b5 reductase 3	CYB5R3	NB5R3_HUMAN	34.2	99.8%	2	2	3	0.00%	10.3%	SVGMIAGGTGITPMLQVIR	99.7%	59.3	25	59.3	2	0	0	1901.04	174	192
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	12	12	19	0.02%	22.3%	ALSEIAGMTLPYDTLDQVR	99.7%	71.3	25	62	2	0	0	2093.06	625	643
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	12	12	19	0.02%	22.3%	FASEIAGVDDLGTTGR	99.7%	129	25	126	2	0	0	1608.79	185	200
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	12	12	19	0.02%	22.3%	FEAPLFNAR	99.7%	54.4	25	45.7	2	0	0	1064.55	409	417
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	12	12	19	0.02%	22.3%	GLLTYTSWEDALSR	99.5%	38.2	25	38.2	1	0	0	1611.80	312	325
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	12	12	19	0.02%	22.3%	ILQDIASGSHPFSQVLK	99.7%	40.8	25	39.3	0	1	0	1840.00	451	467
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	12	12	19	0.02%	22.3%	LVNQQLLADPLVPPQLTIK	99.7%	48.8	25	47.5	1	0	0	2100.24	674	692
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	12	12	19	0.02%	22.3%	NDGAAILAAVSSIAQK	99.7%	102	25	102	2	0	0	1528.83	484	499
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	12	12	19	0.02%	22.3%	SATYVNTEGR	99.7%	59.3	25	47.4	2	0	0	1097.52	593	602
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	12	12	19	0.02%	22.3%	VAGMLQSFQGK	99.7%	69.2	25	60.9	1	0	0	1181.60	326	336
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	12	12	19	0.02%	22.3%	VAVTPPGLAR	98.8%	34.3	25	34.3	2	0	0	980.59	608	617
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	12	12	19	0.02%	22.3%	VLFLLGADGGCITR	99.7%	80.9	25	72.5	2	0	0	1491.80	544	557
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	12	12	19	0.02%	22.3%	VMNILHR	94.7%	28.1	25	16.3	1	0	0	882.50	512	518
NADH-ubiquinone oxidoreductase chain 1	MT-ND1	NU1M_HUMAN	35.7	99.8%	2	3	4	0.00%	8.5%	GPNVVGPYGLLQPFADAMK	99.7%	44	25	44	2	0	0	1990.01	36	54
NADH-ubiquinone oxidoreductase chain 1	MT-ND1	NU1M_HUMAN	35.7	99.8%	2	3	4	0.00%	8.5%	ILGYMQLR	99.7%	51.4	25	44.2	2	0	0	993.56	27	34
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	8	9	22	0.02%	37.4%	AMIENFNAK	99.7%	50.2	25	39.1	2	0	0	1037.51	97	105
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	8	9	22	0.02%	37.4%	DLTQMADELRR	95.0%	28.3	25	22.7	1	0	0	1347.67	150	160
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	8	9	22	0.02%	37.4%	GNSPPSSGEACREEK	97.9%	31.8	25	30.8	1	0	0	1604.70	184	198
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	8	9	22	0.02%	37.4%	HVVLGAIENKVESK	99.7%	40.6	25	40.6	0	4	0	1522.86	170	183
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	8	9	22	0.02%	37.4%	MEEDPDDVPHGHITSLAVK	99.7%	37.8	25	37.8	0	2	0	2105.98	60	78
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	8	9	22	0.02%	37.4%	YVSLHVR	99.2%	36.1	25	20.7	4	0	0	873.49	106	112
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	8	9	22	0.02%	37.4%	YYADGEDAYAMK	99.7%	53.3	25	53.3	3	0	0	1396.57	137	148
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	8	9	22	0.02%	37.4%	YYADGEDAYAMKR	99.7%	55.2	25	54.5	5	0	0	1568.67	137	149
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	29	53	0.05%	23.8%	AIELATTLDESLTNR	99.7%	108	25	90.4	2	0	0	1646.86	783	797
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	29	53	0.05%	23.8%	ALKPANMLER	99.5%	38	25	19.4	3	0	0	1142.64	267	276
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	29	53	0.05%	23.8%	DLSLLQIQMR	99.7%	74	25	62.1	4	0	0	1216.67	119	128
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	29	53	0.05%	23.8%	EALEHLCTYEK	99.7%	56.3	25	41	2	0	0	1392.65	208	218
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	29	53	0.05%	23.8%	EEAYELVR	98.1%	32.2	25	21	1	0	0	1008.50	63	70

N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	29	53	0.05%	23.8%	FAEHGETLAMK	99.7%	53.2	25	44.8	4	2	0	1233.59	42	52
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	29	53	0.05%	23.8%	FLLMLQSVK	99.7%	62.6	25	50.4	4	0	0	1094.63	688	696
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	29	53	0.05%	23.8%	GLTLNCLGK	99.6%	39.9	25	22.1	2	0	0	975.53	53	61
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	29	53	0.05%	23.8%	IAIEIYLK	99.7%	55.8	25	48.9	2	0	0	962.59	560	567
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	29	53	0.05%	23.8%	ILEEFRK	99.7%	46.2	25	39	2	0	0	934.54	170	176
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	29	53	0.05%	23.8%	IYEEAWTK	97.2%	30.5	25	22.6	1	0	0	1039.51	279	286
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	29	53	0.05%	23.8%	KEEAYELVR	99.7%	53.1	25	46.2	2	0	0	1136.59	62	70
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	29	53	0.05%	23.8%	LEDAADVYR	99.7%	78.6	25	70.2	2	0	0	1051.51	240	248
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	29	53	0.05%	23.8%	LFNTAVCESK	99.7%	64.3	25	54.7	2	0	0	1168.57	715	724
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	29	53	0.05%	23.8%	LPLNFLSGEK	99.7%	43.8	25	32.8	2	0	0	1117.63	296	305
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	29	53	0.05%	23.8%	MVYYLDPSSQK	99.7%	55.3	25	50.9	4	0	0	1330.63	771	781
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	29	53	0.05%	23.8%	NPENWAYYK	99.7%	56.2	25	52.3	2	0	0	1184.54	254	262
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	29	53	0.05%	23.8%	RLPLNFLSGEK	99.7%	65.9	25	60	2	0	0	1273.73	295	305
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	29	53	0.05%	23.8%	VAIIEELVVGYETSLK	99.7%	49.9	25	49.9	1	0	0	1762.98	339	354
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	29	53	0.05%	23.8%	VETPLEEAIK	99.7%	42.3	25	32.3	1	0	0	1128.61	650	659
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	29	53	0.05%	23.8%	WDKDNLQILR	99.7%	34.6	25	15	0	2	0	1300.70	109	118
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	22	29	53	0.05%	23.8%	WMDEAQALDTADR	99.7%	90.7	25	85.2	4	0	0	1521.66	430	442
N-alpha-acetyltransferase 20	NAA20	NAA20_HUMAN	20.4	100.0%	3	4	8	0.01%	17.4%	AFTCDDLFR	99.5%	38.1	25	33.7	2	0	0	1144.51	6	14
N-alpha-acetyltransferase 20	NAA20	NAA20_HUMAN	20.4	100.0%	3	4	8	0.01%	17.4%	LMELLEEISER	99.7%	72.8	25	63.7	4	0	0	1361.70	92	102
N-alpha-acetyltransferase 20	NAA20	NAA20_HUMAN	20.4	100.0%	3	4	8	0.01%	17.4%	VSNQVAVNMYK	99.7%	46.5	25	44.1	2	0	0	1252.64	114	124
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	15	26	0.03%	16.2%	ALQQHLCVVQLTR	99.7%	43	25	41.2	0	1	0	1565.86	410	422
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	15	26	0.03%	16.2%	DIQYPFLGPVPTR	99.7%	53	25	47.3	2	0	0	1502.80	748	760
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	15	26	0.03%	16.2%	DTSEYIIQAYK	99.7%	70.4	25	70.3	2	0	0	1330.65	576	586
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	15	26	0.03%	16.2%	FINQLLGVVPLSTPTEDK	99.7%	46.6	25	46.6	2	0	0	1971.08	384	401
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	15	26	0.03%	16.2%	IPEFIAFR	99.7%	52.6	25	28.7	2	0	0	992.56	593	600
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	15	26	0.03%	16.2%	LALPADIR	99.7%	42.4	25	26.8	2	0	0	868.53	402	409
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	15	26	0.03%	16.2%	LLLQQLEATLETGK	99.7%	88.3	25	88.3	1	0	0	1556.89	729	742
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	15	26	0.03%	16.2%	LLLQQLEATLETGKR	99.5%	32.2	25	26.2	0	2	0	1712.99	729	743
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	15	26	0.03%	16.2%	LSLEEETLWLR	99.7%	61.1	25	55.4	2	0	0	1388.74	678	688
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	15	26	0.03%	16.2%	LTSEIQSR	99.3%	36.9	25	22.1	2	0	0	933.50	224	231
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	15	26	0.03%	16.2%	SLLDQLKDVFSK	99.7%	74	25	63.1	2	0	0	1392.77	807	818
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	15	26	0.03%	16.2%	TMFLPLAER	96.6%	29.9	25	23.6	1	0	0	1093.57	171	179
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	15	26	0.03%	16.2%	VFVDLLPATQCTK	99.7%	46.1	25	41.7	2	0	0	1491.79	371	383
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	15	26	0.03%	16.2%	WPECNALSR	99.7%	51.1	25	51.1	1	0	0	1132.52	245	253
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	15	15	26	0.03%	16.2%	YQEALDVIR	99.7%	47.1	25	39	2	0	0	1106.58	209	217
Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACA	NACAM_HUMAN	205.4	100.0%	3	3	6	0.01%	2.0%	IEDLSQQAQLAAAEK	99.7%	104	25	94.2	2	0	0	1614.83	1991	2005
Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACA	NACAM_HUMAN	205.4	100.0%	3	3	6	0.01%	2.0%	NILFVITKPDVYK	99.7%	74.7	25	74.7	2	0	0	1549.90	1964	1976
Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACA	NACAM_HUMAN	205.4	100.0%	3	3	6	0.01%	2.0%	SPASDTYIVFGEAK	99.7%	86	25	86	2	0	0	1484.73	1977	1990
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	5	5	9	0.01%	5.1%	AAEDLFVNIR	99.7%	61.5	25	48	2	0	0	1147.61	306	315
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	5	5	9	0.01%	5.1%	ASLGLADHR	99.7%	64.3	25	54.4	1	0	0	939.50	502	510
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	5	5	9	0.01%	5.1%	ELATVLSDQPGLLGPK	99.7%	71	25	71	2	0	0	1637.91	352	367
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	5	5	9	0.01%	5.1%	NNNQQLAQLQK	99.7%	58.5	25	50.4	2	0	0	1298.68	71	81
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	5	5	9	0.01%	5.1%	SLSELLGPYGMK	99.5%	38.3	25	30.1	2	0	0	1294.67	838	849
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	5	5	9	0.01%	10.1%	DAAAVGNHVAK	99.7%	51.9	25	41.2	2	0	0	1052.55	353	363
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	5	5	9	0.01%	10.1%	EGQGNLPVR	99.5%	37.9	25	30.7	1	0	0	969.51	318	326
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	5	5	9	0.01%	10.1%	LLCSNSAFLR	99.7%	43.8	25	30.6	2	0	0	1180.61	382	391
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	5	5	9	0.01%	10.1%	TYGLVGYMR	99.7%	45.2	25	37.8	2	0	0	1059.53	155	163
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	5	5	9	0.01%	10.1%	YPGVSNYQVEEDIGK	99.7%	65.2	25	65.2	2	0	0	1697.80	442	456
Nesprin-1	SYNE1	SYNE1_HUMAN	1,011.1	100.0%	3	3	4	0.00%	0.3%	QSEADALAVLK	98.0%	32	25	2.88	2	0	0	1144.62	1970	1980
Nesprin-1	SYNE1	SYNE1_HUMAN	1,011.1	100.0%	3	3	4	0.00%	0.3%	SQLEGALSK	95.7%	28.9	25	14.2	1	0	0	932.50	3382	3390
Nesprin-1	SYNE1	SYNE1_HUMAN	1,011.1	100.0%	3	3	4	0.00%	0.3%	VLFTSLADNK	95.2%	28.4	25	27.6	1	0	0	1107.60	6495	6504

Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	3	3	4	0.00%	4.5%	EIEAEIQALR	99.7%	56.7	25	44.5	1	0	0	1171.63	128	137
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	3	3	4	0.00%	4.5%	EYQDLLNVK	99.7%	58.9	25	47.5	6	0	0	1121.58	383	391
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	3	3	4	0.00%	4.5%	LRDDTEAAIR	99.7%	43.7	25	31.5	2	0	0	1159.61	195	204
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	3	3	4	0.00%	4.5%	VQSLQDEVAFLR	99.7%	58.6	25	46.8	1	0	0	1404.75	224	235
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	8	8	31	0.03%	18.9%	EVLDSFLDLAR	99.7%	83.6	25	75.5	9	0	0	1277.67	179	189
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	8	8	31	0.03%	18.9%	GPAGDATVASEK	99.7%	70.3	25	65.2	3	0	0	1102.54	526	537
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	8	8	31	0.03%	18.9%	IVEMEDVGLLFAR	99.7%	74.2	25	72.1	2	0	0	1491.79	289	301
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	8	8	31	0.03%	18.9%	LGPEGELLIR	99.7%	73.9	25	70.8	2	0	0	1096.64	248	257
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	8	8	31	0.03%	18.9%	LSAFVFPGELLLR	99.7%	53	25	53	2	0	0	1461.85	86	98
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	8	8	31	0.03%	18.9%	NIFPSNLVSAAFR	99.7%	47.1	25	41.2	3	0	0	1435.77	190	202
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	8	8	31	0.03%	18.9%	SELPLDPLPVPTEEGNPLLK	99.7%	73.2	25	73.2	6	0	0	2158.16	503	522
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	8	8	31	0.03%	18.9%	STEPELIQVK	99.7%	50	25	36.1	4	0	0	1143.63	493	502
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	9	10	16	0.02%	14.3%	EGLGLDVER	99.7%	45.6	25	37.4	2	0	0	987.51	589	597
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	9	10	16	0.02%	14.3%	FEPVHFVASSSK	97.5%	31	25	25.9	1	0	0	1334.67	57	68
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	9	10	16	0.02%	14.3%	GAVEDVISR	99.7%	54.9	25	33.6	3	0	0	945.50	525	533
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	9	10	16	0.02%	14.3%	LLTDGYACEVR	99.7%	70.4	25	69.5	2	0	0	1296.63	235	245
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	9	10	16	0.02%	14.3%	MTVEYVYER	99.3%	36.7	25	36.7	1	0	0	1189.56	464	472
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	9	10	16	0.02%	14.3%	SESHTDLTFSR	99.7%	41.1	25	40.3	1	1	0	1279.59	616	626
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	9	10	16	0.02%	14.3%	SGEGIREPISVK	97.1%	30.5	25	14.8	1	0	0	1271.70	572	583
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	9	10	16	0.02%	14.3%	TNPEYIYAPLK	99.7%	67.2	25	61.4	2	0	0	1308.68	212	222
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	9	10	16	0.02%	14.3%	VILESEVIAEAVGVK	99.7%	76.4	25	66.6	2	0	0	1555.89	482	496
NHP2-like protein 1	NHP2L1	NH2L1_HUMAN	14.2	100.0%	3	3	5	0.00%	27.3%	AYPLADAHLTK	96.7%	29.9	25	22.2	1	0	0	1199.64	10	20
NHP2-like protein 1	NHP2L1	NH2L1_HUMAN	14.2	100.0%	3	3	5	0.00%	27.3%	LLDLVQQSCNYK	99.7%	55	25	46.2	2	0	0	1480.75	22	33
NHP2-like protein 1	NHP2L1	NH2L1_HUMAN	14.2	100.0%	3	3	5	0.00%	27.3%	QQIQSIQQSIER	99.7%	72.3	25	64.7	2	0	0	1457.77	114	125
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	10	12	20	0.02%	21.1%	AMAAVPQDVVR	99.7%	43.2	25	30.6	1	0	0	1172.61	115	125
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	10	12	20	0.02%	21.1%	AVSDWLIASVEGR	99.7%	54.9	25	40.1	2	0	0	1402.73	195	207
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	10	12	20	0.02%	21.1%	DPEFVFYDQLK	99.7%	64.5	25	56.5	2	0	0	1400.67	501	511
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	10	12	20	0.02%	21.1%	ELETVAAHQFPEVR	99.7%	66.6	25	55	3	2	0	1625.83	340	353
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	10	12	20	0.02%	21.1%	IIAEALTR	99.7%	61.7	25	40.8	1	0	0	886.54	417	424
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	10	12	20	0.02%	21.1%	LLDFSYEQYQK	99.7%	65.9	25	64.3	2	0	0	1433.69	89	99
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	10	12	20	0.02%	21.1%	MQQYDLQGQPYGTR	99.7%	60	25	60	1	0	0	1700.77	51	64
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	10	12	20	0.02%	21.1%	QSAGAVVIILPR	99.7%	58.9	25	40.2	1	0	0	1223.75	103	114
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	10	12	20	0.02%	21.1%	THAAYNLLFFASGGGK	97.7%	31.3	25	31.3	1	0	0	1653.84	264	279
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	10	12	20	0.02%	21.1%	TMAAEVLSR	99.5%	38.6	25	32.1	4	0	0	977.51	74	82
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	15	27	0.03%	39.7%	AVPEGFVIPR	99.7%	52.6	25	44.2	2	0	0	1084.62	118	127
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	15	27	0.03%	39.7%	DVYKEHFQDDVFNEK	99.7%	43.7	25	43.7	0	2	0	1912.87	85	99
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	15	27	0.03%	39.7%	GTDTVAGLALIK	99.7%	93.5	25	60.8	3	0	0	1158.67	217	228
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	15	27	0.03%	39.7%	GVSSQETAGIGASAHLVNFK	99.7%	126	25	121	1	0	0	1973.01	197	216
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	15	27	0.03%	39.7%	GWNYILEK	99.7%	54.4	25	34.9	2	0	0	1022.53	100	107
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	15	27	0.03%	39.7%	KFPVTENSK	98.2%	32.5	25	16.7	2	0	0	1049.56	331	339
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	15	27	0.03%	39.7%	MWSIENIAFGSGGGLLQK	99.7%	71.2	25	69.7	1	0	0	1907.97	372	389
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	15	27	0.03%	39.7%	NAQLNIELEAAHH	99.7%	88.7	25	87	2	0	0	1459.73	479	491
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	15	27	0.03%	39.7%	STQAPLIIRPDSGNPLDTVLK	99.3%	30.4	25	30.4	0	1	0	2235.23	303	323
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	15	27	0.03%	39.7%	SYSFDEIRK	99.7%	40.2	25	27.7	2	0	0	1144.56	470	478
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	15	27	0.03%	39.7%	VIQGDGVDINTLQEIVEGMK	99.7%	123	25	123	4	0	0	2158.11	350	369
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	15	27	0.03%	39.7%	YDGHLPIEIK	99.5%	38.1	25	25.8	2	0	0	1184.63	108	117
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	15	27	0.03%	39.7%	YEETVFYGLQYILNK	99.7%	72.7	25	72.7	1	0	0	1879.95	54	68
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	14	15	27	0.03%	39.7%	YLLETSGNLDGLEYK	99.7%	91.5	25	87.5	2	0	0	1714.85	175	189
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	21	55	0.05%	31.8%	AAPGAEFAPNKR	99.7%	61.1	25	52.8	4	0	0	1228.64	457	468
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	21	55	0.05%	31.8%	AGEVFIHK	99.7%	51.7	25	23.1	5	0	0	900.49	100	107
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	21	55	0.05%	31.8%	AVVIVDDR	99.7%	42	25	22.5	4	0	0	886.50	177	184

Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	21	55	0.05%	31.8%	EKLEMEMEAAR	99.5%	38	25	24.1	2	0	0	1352.62	294	304
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	21	55	0.05%	31.8%	FACHSASLTVR	99.7%	54.8	25	46.4	4	2	0	1248.62	143	153
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	21	55	0.05%	31.8%	FAQPGSFEYEYAMR	99.7%	74.6	25	74.3	4	0	0	1711.74	257	270
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	21	55	0.05%	31.8%	FGQAATMEGIGAIGGTPPAFNR	99.7%	79.8	25	79.8	2	3	0	2179.06	435	456
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	21	55	0.05%	31.8%	GIVEFSGKPAAR	99.7%	51.4	25	51	4	1	0	1231.68	191	202
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	21	55	0.05%	31.8%	LFVGNLPPDITEEEMR	99.7%	51	25	51	4	0	0	1859.92	76	91
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	21	55	0.05%	31.8%	MEELHNQEVQK	99.7%	71.2	25	30.7	4	0	0	1384.65	326	336
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	21	55	0.05%	31.8%	MGQMAMGGAMGINNR	99.7%	61.1	25	60.1	4	0	0	1602.65	384	398
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	21	55	0.05%	31.8%	RMEELHNQEVQK	98.7%	28.2	25	27.8	0	2	0	1540.75	325	336
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	21	55	0.05%	31.8%	VELDNMPLR	99.7%	64.2	25	48.1	6	0	0	1086.56	127	135
NTF2-related export protein 1	NXT1	NXT1_HUMAN	15.8	100.0%	3	4	5	0.00%	21.4%	AAEEFVNVYYTTMDK	99.7%	42	25	42	2	0	0	1796.80	16	30
NTF2-related export protein 1	NXT1	NXT1_HUMAN	15.8	100.0%	3	4	5	0.00%	21.4%	IASDCFR	99.5%	38.1	25	31.6	2	0	0	868.40	128	134
NTF2-related export protein 1	NXT1	NXT1_HUMAN	15.8	100.0%	3	4	5	0.00%	21.4%	TYVDQACR	99.7%	42.4	25	34.4	1	0	0	1012.45	8	15
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	8	8	15	0.01%	11.3%	ANNYNEAVYLVR	99.7%	48.8	25	41.3	2	0	0	1425.71	118	129
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	8	8	15	0.01%	11.3%	ATNDEIFSILK	99.7%	68.9	25	63.1	2	0	0	1250.66	512	522
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	8	8	15	0.01%	11.3%	DGVLEEQIER	99.7%	56.1	25	39.2	2	0	0	1187.59	685	694
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	8	8	15	0.01%	11.3%	IFANTESYLK	99.7%	59.7	25	40	2	0	0	1185.62	195	204
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	8	8	15	0.01%	11.3%	NLFLVIFQR	99.7%	50.3	25	50.3	3	0	0	1149.68	708	716
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	8	8	15	0.01%	11.3%	NYNFGGEFVEAMIR	99.7%	68.8	25	62.9	2	0	0	1646.76	97	110
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	8	8	15	0.01%	11.3%	SFSHSFSALAK	96.8%	30.1	25	19.9	1	0	0	1181.59	558	568
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	8	8	15	0.01%	11.3%	TCAAQLVSYPGK	99.7%	67	25	60.8	1	0	0	1294.65	331	342
Nuclear cap-binding protein subunit 2	NCBP2	NCBP2_HUMAN	18.0	99.9%	2	2	4	0.00%	15.4%	SDSYVELSQYR	99.6%	40	25	34.4	2	0	0	1346.62	11	21
Nuclear cap-binding protein subunit 2	NCBP2	NCBP2_HUMAN	18.0	99.9%	2	2	4	0.00%	15.4%	TACGFCFVEYYSR	99.7%	47.6	25	47.6	2	0	0	1659.69	79	91
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	12	12	19	0.02%	6.6%	AADALEEQQR	99.7%	52.2	25	43.7	1	0	0	1130.54	725	734
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	12	12	19	0.02%	6.6%	AVQAQGGESQQEAQR	99.7%	94.5	25	90.2	2	0	0	1586.75	1574	1588
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	12	12	19	0.02%	6.6%	DSAQTSVTQAQR	99.7%	66.1	25	51.6	2	0	0	1291.62	632	643
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	12	12	19	0.02%	6.6%	EELEQASQAHGAR	99.7%	53.3	25	42.1	1	0	0	1425.67	483	495
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	12	12	19	0.02%	6.6%	HQVEQLSSSLK	99.7%	43.5	25	38.3	2	0	0	1255.66	551	561
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	12	12	19	0.02%	6.6%	LADDLSTLQEK	99.7%	61.8	25	48.3	2	0	0	1232.64	898	908
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	12	12	19	0.02%	6.6%	LDFVCSFLQK	96.9%	30.2	25	24.4	1	0	0	1256.63	61	70
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	12	12	19	0.02%	6.6%	LEILQQQLQVANEAR	99.7%	75.8	25	75.8	2	0	0	1752.96	617	631
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	12	12	19	0.02%	6.6%	LGHELQQAGLK	98.7%	33.7	25	33.6	1	0	0	1193.66	1655	1665
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	12	12	19	0.02%	6.6%	LLQAETASNSAR	99.7%	79.6	25	69.8	2	0	0	1260.65	1271	1282
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	12	12	19	0.02%	6.6%	QELTSQAER	96.8%	30.1	25	19	1	0	0	1061.52	1313	1321
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	12	12	19	0.02%	6.6%	SAPASQASLR	98.9%	34.7	25	28.9	2	0	0	987.52	1840	1849
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	8	8	14	0.01%	10.3%	AIYAALSGNLK	99.7%	61.2	25	41.8	2	0	0	1120.64	426	436
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	8	8	14	0.01%	10.3%	EADLDVATITK	99.7%	80.8	25	72.2	2	0	0	1175.62	627	637
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	8	8	14	0.01%	10.3%	GHLDALTADVK	99.7%	61	25	53.6	2	0	0	1139.61	804	814
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	8	8	14	0.01%	10.3%	IDVIDWLVFDPAQR	99.7%	69.9	25	69.9	2	0	0	1686.89	672	685
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	8	8	14	0.01%	10.3%	SGFGEISSPVIR	99.7%	44.7	25	41.1	2	0	0	1248.66	4	15
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	8	8	14	0.01%	10.3%	TVVEALFQR	99.7%	51	25	46.8	2	0	0	1062.59	251	259
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	8	8	14	0.01%	10.3%	VFEELQATDK	99.7%	75.5	25	64.4	1	0	0	1179.59	492	501
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	8	8	14	0.01%	10.3%	VLLQASQDENFGNTTPR	99.7%	99.3	25	99.3	1	0	0	1889.94	32	48
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	16	16	26	0.03%	16.0%	AAFLQYCR	99.7%	44.8	25	34	1	0	0	1028.50	524	531
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	16	16	26	0.03%	16.0%	DGIQLSEYLPEVK	99.7%	48.6	25	43.6	2	0	0	1490.77	1111	1123
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	16	16	26	0.03%	16.0%	DLLQADQLGSLK	99.7%	76.8	25	63.5	2	0	0	1300.71	1124	1135
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	16	16	26	0.03%	16.0%	DMLQAASHYR	99.3%	36.5	25	34.9	1	0	0	1191.56	734	743
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	16	16	26	0.03%	16.0%	EYEIPSNLTPADVFFR	99.7%	66.4	25	66.4	2	0	0	1897.93	676	691
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	16	16	26	0.03%	16.0%	GLPLGSAVSSPVLFSPVGR	99.7%	80.4	25	80.4	2	0	0	1840.03	36	54
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	16	16	26	0.03%	16.0%	HAYSWDINR	99.0%	34.8	25	20.1	1	0	0	1161.54	306	314
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	16	16	26	0.03%	16.0%	IEEMAEQER	99.7%	62.4	25	32.5	1	0	0	1150.50	992	1000

Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	16	16	26	0.03%	16.0%	LAALASDFSEDMLQEK	99.7%	59.3	25	53.4	2	0	0	1767.85	976	991
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	16	16	26	0.03%	16.0%	LLLCEHAEK	99.4%	37.4	25	36.9	2	0	0	1112.58	638	646
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	16	16	26	0.03%	16.0%	NETIAQEDKIK	99.7%	49.9	25	35.1	1	0	0	1288.67	510	520
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	16	16	26	0.03%	16.0%	NSGLVSITSR	99.7%	68.2	25	68.2	2	0	0	1033.56	467	476
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	16	16	26	0.03%	16.0%	SNPYFEFVLK	99.6%	38.9	25	35.3	2	0	0	1243.64	1136	1145
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	16	16	26	0.03%	16.0%	SSFYSLTSSNISK	99.7%	92.7	25	79.9	2	0	0	1420.70	284	296
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	16	16	26	0.03%	16.0%	TFGSSLPVK	99.7%	42.8	25	35	1	0	0	935.52	83	91
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	16	16	26	0.03%	16.0%	VAYPQADSNLR	99.7%	51.5	25	46.8	2	0	0	1233.62	788	798
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	6	6	12	0.01%	4.5%	DLLILQQLLMR	99.3%	36.7	25	35.5	1	0	0	1355.81	733	743
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	6	6	12	0.01%	4.5%	LLSTYLER	99.7%	62.1	25	45.9	2	0	0	994.56	1291	1298
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	6	6	12	0.01%	4.5%	LPLTPVFEGLAFK	99.7%	60.4	25	49.1	2	0	0	1431.82	1237	1249
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	6	6	12	0.01%	4.5%	SEDGEIVSTPR	99.7%	80.6	25	72.6	3	0	0	1189.57	949	959
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	6	6	12	0.01%	4.5%	SFVELSGAER	99.7%	65.2	25	58.6	1	0	0	1094.55	44	53
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	6	6	12	0.01%	4.5%	TAPLLLSYYLIK	99.7%	61.8	25	53.7	3	0	0	1394.83	766	777
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	23	38	0.04%	12.4%	AQIEQVIANCEHK	99.7%	71.8	25	71.8	2	0	0	1539.76	1207	1219
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	23	38	0.04%	12.4%	ASTEGVAIQGQQGTR	99.7%	78.5	25	71.6	2	0	0	1502.76	70	84
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	23	38	0.04%	12.4%	DACDGHEIGR	99.7%	45.6	25	45.4	2	0	0	1129.47	1484	1493
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	23	38	0.04%	12.4%	DLPSADSVQYR	99.7%	50.5	25	38.3	2	0	0	1250.60	572	582
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	23	38	0.04%	12.4%	EDTLLLIGHLER	99.3%	37	25	34.8	1	0	0	1408.78	244	255
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	23	38	0.04%	12.4%	ENLFMDLLR	99.7%	63.3	25	54.3	2	0	0	1150.59	860	868
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	23	38	0.04%	12.4%	FQDDNVEGDKVSK	99.7%	48.6	25	23.1	2	0	0	1480.69	1733	1745
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	23	38	0.04%	12.4%	FTDELMEQGLTYK	99.7%	82.3	25	81.1	2	0	0	1590.74	173	185
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	23	38	0.04%	12.4%	IQQGALELLR	99.7%	68.3	25	62.7	2	0	0	1140.67	1566	1575
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	23	38	0.04%	12.4%	KPVSTTNLQDPGVLGCPR	99.6%	32.9	25	32.9	0	2	0	1939.01	1013	1030
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	23	38	0.04%	12.4%	LAWALALR	99.7%	57.8	25	45.4	2	0	0	913.56	331	338
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	23	38	0.04%	12.4%	LPGLQATVR	99.7%	49.9	25	46.2	1	0	0	954.57	322	330
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	23	38	0.04%	12.4%	LTAPEDVFSK	98.7%	33.9	25	30.4	2	0	0	1106.57	1452	1461
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	23	38	0.04%	12.4%	LVGDFTHDQSISQK	99.7%	54.8	25	54.5	1	0	0	1574.78	933	946
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	23	38	0.04%	12.4%	MLALALLDR	99.7%	63.5	25	51.9	4	0	0	1015.60	1494	1502
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	23	38	0.04%	12.4%	QLDTYAPFPGK	99.7%	46.7	25	34.2	1	0	0	1236.63	829	839
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	23	38	0.04%	12.4%	QYIATIHSR	99.0%	34.9	25	19.6	2	0	0	1088.58	305	313
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	23	38	0.04%	12.4%	SVSGFLHFDTATK	99.7%	49.2	25	45	2	0	0	1409.71	1165	1177
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	23	38	0.04%	12.4%	TWTLELSPELASMTTR	99.7%	52.2	25	50	1	0	0	1851.92	157	172
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	23	38	0.04%	12.4%	YLYHGNTNPELAFESAK	98.5%	27.4	25	27.4	0	1	0	1953.93	902	918
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	21	23	38	0.04%	12.4%	YSFIQALVR	99.7%	75.6	25	66.6	2	0	0	1096.61	1993	2001
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	5	6	11	0.01%	10.2%	DAAFATLVSDR	99.7%	73.5	25	62	2	0	0	1165.58	495	505
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	5	6	11	0.01%	10.2%	DVDVYSQILR	99.7%	53.9	25	46.5	2	0	0	1207.63	60	69
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	5	6	11	0.01%	10.2%	IMLGDEAALLEQK	99.7%	79.6	25	73.8	2	0	0	1430.76	286	298
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	5	6	11	0.01%	10.2%	SEMVPSCPFIYIIR	99.7%	54	25	45.1	2	0	0	1727.85	45	58
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	5	6	11	0.01%	10.2%	TMPILSPGNTQTLTELELK	99.7%	61.4	25	61.4	3	0	0	2086.11	239	257
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	19	20	38	0.04%	28.0%	AQHQLGEFK	96.8%	30	25	25.5	1	0	0	1057.54	341	349
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	19	20	38	0.04%	28.0%	AVYCIIGR	99.7%	54.5	25	44.3	2	0	0	951.51	389	396
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	19	20	38	0.04%	28.0%	CGDLLAASQVVNR	99.7%	78.1	25	65.3	1	0	0	1402.71	328	340
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	19	20	38	0.04%	28.0%	CVSELVIESR	99.7%	40.5	25	17.7	1	0	0	1191.60	569	578
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	19	20	38	0.04%	28.0%	DNALLSAIEESR	99.7%	108	25	97	2	0	0	1317.66	107	118
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	19	20	38	0.04%	28.0%	EALQYFYFLR	99.7%	45.7	25	29.9	2	0	0	1349.69	546	555
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	19	20	38	0.04%	28.0%	FTSDTKPIINK	99.7%	54.1	25	43.2	2	0	0	1263.69	601	611
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	19	20	38	0.04%	28.0%	GLDISHISQR	99.7%	58.3	25	53.4	4	0	0	1125.60	68	77
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	19	20	38	0.04%	28.0%	LESLSAATTFEPLEPVKDTDIQGFLK	99.7%	58.2	25	58.2	0	2	0	2849.48	78	103
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	19	20	38	0.04%	28.0%	LLMLYTR	99.7%	42.7	25	41.2	2	0	0	909.52	531	537
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	19	20	38	0.04%	28.0%	LLSPVVPQISAPQSNK	99.7%	57.5	25	57.5	2	0	0	1677.95	645	660

Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	19	20	38	0.04%	28.0%	LTLSQFQK	99.7%	56.2	25	43.8	2	0	0	964.55	435	442
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	19	20	38	0.04%	28.0%	LVPLNQESVEER	99.7%	68.7	25	61.2	2	0	0	1412.74	719	730
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	19	20	38	0.04%	28.0%	NLQEIQQAGER	99.7%	73.8	25	37.4	2	0	0	1285.65	32	42
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	19	20	38	0.04%	28.0%	NMALSIAER	97.3%	30.8	25	28.5	1	0	0	1004.52	665	673
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	19	20	38	0.04%	28.0%	QMTDVLLTPATDALK	99.7%	71.5	25	61.6	2	0	0	1616.86	229	243
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	19	20	38	0.04%	28.0%	SSGQSAQLLSHEPGDPPCLR	99.7%	35.1	25	29.1	0	1	0	2136.01	505	524
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	19	20	38	0.04%	28.0%	TLITFAGMIPYR	99.7%	67.1	25	67.1	6	0	0	1398.75	791	802
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	19	20	38	0.04%	28.0%	VIEDRDSQLR	96.1%	29.2	25	17.1	1	0	0	1230.64	777	786
Nuclear pore complex protein Nup98-Nup96	NUP98	NUP98_HUMAN	197.6	100.0%	4	4	6	0.01%	2.8%	GFLEDLAPPER	99.7%	45.9	25	30.5	1	0	0	1243.63	1669	1679
Nuclear pore complex protein Nup98-Nup96	NUP98	NUP98_HUMAN	197.6	100.0%	4	4	6	0.01%	2.8%	LALLLSQFVGSQSVR	99.7%	72.2	25	72.2	2	0	0	1617.93	1358	1372
Nuclear pore complex protein Nup98-Nup96	NUP98	NUP98_HUMAN	197.6	100.0%	4	4	6	0.01%	2.8%	NSPVEAVFSYLTGK	99.7%	88	25	79.5	1	0	0	1511.77	1328	1341
Nuclear pore complex protein Nup98-Nup96	NUP98	NUP98_HUMAN	197.6	100.0%	4	4	6	0.01%	2.8%	SITADPLDYR	99.7%	48.1	25	37.8	2	0	0	1150.57	1514	1523
Nuclear pore membrane glycoprotein 210	NUP210	PO210_HUMAN	205.1	100.0%	3	3	4	0.00%	2.0%	AVDPTSGQLYGLAR	99.7%	55.4	25	41.5	1	0	0	1447.75	1259	1272
Nuclear pore membrane glycoprotein 210	NUP210	PO210_HUMAN	205.1	100.0%	3	3	4	0.00%	2.0%	VFGAPEVLENLEVK	99.7%	52.6	25	48.1	2	0	0	1543.84	1711	1724
Nuclear pore membrane glycoprotein 210	NUP210	PO210_HUMAN	205.1	100.0%	3	3	4	0.00%	2.0%	VGQALELPLR	99.7%	55.8	25	55.8	1	0	0	1095.65	549	558
Nuclear receptor coactivator 5	NCOA5	NCOA5_HUMAN	65.5	100.0%	4	5	8	0.01%	7.6%	DPYGFGDSR	97.9%	31.8	25	23.5	1	0	0	1013.43	14	22
Nuclear receptor coactivator 5	NCOA5	NCOA5_HUMAN	65.5	100.0%	4	5	8	0.01%	7.6%	MADEAILQER	99.7%	76.9	25	59.5	4	0	0	1175.57	316	325
Nuclear receptor coactivator 5	NCOA5	NCOA5_HUMAN	65.5	100.0%	4	5	8	0.01%	7.6%	QYFEEIQR	99.6%	39.6	25	24.5	2	0	0	1112.54	183	190
Nuclear receptor coactivator 5	NCOA5	NCOA5_HUMAN	65.5	100.0%	4	5	8	0.01%	7.6%	RFDAERPVDCSVIVVNK	98.7%	28	25	25.9	0	1	0	2004.03	191	207
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	6	6	9	0.01%	12.8%	AQFFVEDASTASALK	99.7%	99.4	25	92.4	2	0	0	1584.79	159	173
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	6	6	9	0.01%	12.8%	DQSTYISAIR	99.7%	48.2	25	26.2	1	0	0	1153.58	333	342
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	6	6	9	0.01%	12.8%	IIEENIPELLSLNLSNNR	99.6%	39.2	25	39.2	1	0	0	2081.12	259	276
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	6	6	9	0.01%	12.8%	ILNLSGNELK	99.7%	47	25	36.7	2	0	0	1100.63	295	304
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	6	6	9	0.01%	12.8%	LDDMSSIVQK	97.8%	31.7	25	20.6	1	0	0	1151.56	280	289
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	6	6	9	0.01%	12.8%	SDPDLVAQNIDVVLNR	99.7%	63.3	25	56.8	2	0	0	1767.92	234	249
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	13	16	41	0.04%	54.3%	AADPPAENSSAPEAEQGGAE	99.7%	63.7	25	63.7	2	0	0	1897.80	305	324
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	13	16	41	0.04%	54.3%	EDGNEEDKENQGDETQGQQPPQR	99.7%	41.5	25	41.5	0	2	0	2628.10	257	279
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	13	16	41	0.04%	54.3%	EDVFVHQTAIK	99.7%	56.7	25	48.8	2	0	0	1286.67	82	92
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	13	16	41	0.04%	54.3%	EDVFVHQTAIKK	99.7%	46.5	25	33.6	1	1	0	1414.77	82	93
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	13	16	41	0.04%	54.3%	GAEAANVTGPGGVPVQGSK	99.7%	131	25	131	3	0	0	1695.87	119	137
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	13	16	41	0.04%	54.3%	NDTKEDVFVHQTAIK	99.7%	92.1	25	87.9	3	4	0	1744.89	78	92
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	13	16	41	0.04%	54.3%	NEGSESAPEGQAQQR	99.7%	91	25	87.4	2	0	0	1587.70	171	185
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	13	16	41	0.04%	54.3%	NGYGFINR	99.7%	51.5	25	46	5	0	0	940.46	70	77
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	13	16	41	0.04%	54.3%	NYQQNYQNSESGEK	99.7%	72.1	25	72.1	2	0	0	1688.71	157	170
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	13	16	41	0.04%	54.3%	NYQQNYQNSESGEKNEGSESAPEGQAQQR	99.7%	90.2	25	90.2	0	2	0	3257.40	157	185
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	13	16	41	0.04%	54.3%	RPENPKPQDGKETK	99.5%	31.8	25	29.7	0	1	0	1623.85	291	304
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	13	16	41	0.04%	54.3%	RPQYSNPPVQGEVMEGADNQGAGEQGRPVR	99.7%	63.4	25	63.4	0	4	0	3223.53	205	234
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	13	16	41	0.04%	54.3%	SVGDGETVEFDVVEGEK	99.7%	116	25	111	7	0	0	1795.82	102	118
Nucleolar and coiled-body phosphoprotein 1	NOLC1	NOLC1_HUMAN	73.6	99.8%	2	3	6	0.01%	3.4%	DNQLSEVANK	99.5%	38.2	25	4.64	2	0	0	1117.55	24	33
Nucleolar and coiled-body phosphoprotein 1	NOLC1	NOLC1_HUMAN	73.6	99.8%	2	3	6	0.01%	3.4%	VAGGAAPSKPASAK	99.7%	54.5	25	42.5	3	1	0	1211.67	497	510
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	12	21	0.02%	16.4%	DLIGCLQK	98.2%	32.4	25	20	1	0	0	946.50	214	221
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	12	21	0.02%	16.4%	DREIQLEISGK	99.7%	56.9	25	52.5	2	0	0	1287.69	627	637
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	12	21	0.02%	16.4%	EEGTPLTLYYSHWR	99.7%	63.6	25	61.4	2	0	0	1751.84	610	623
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	12	21	0.02%	16.4%	HISVLVPCFLTFPK	94.7%	22.6	25	22.6	0	1	0	1657.91	276	289
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	12	21	0.02%	16.4%	LFHEVVQAFR	99.7%	49.8	25	44.5	2	2	0	1245.67	169	178
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	12	21	0.02%	16.4%	LSNVNLQEK	99.7%	44.7	25	26.3	2	0	0	1044.57	508	516
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	12	21	0.02%	16.4%	MLQPSSSPLWGK	99.7%	45.3	25	34.1	2	0	0	1330.68	234	245
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	12	21	0.02%	16.4%	NSVPVTVAMVER	99.7%	75.3	25	65.6	1	0	0	1301.69	145	156
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	12	21	0.02%	16.4%	SPDKPGGSPSASR	99.6%	32.9	25	31.9	0	1	0	1242.61	49	61
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	12	21	0.02%	16.4%	VLAFLVLSR	99.7%	71.5	25	71.5	3	0	0	1017.65	311	319
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	11	12	21	0.02%	16.4%	VQENSAYICSR	99.7%	83.5	25	80.8	2	0	0	1326.61	577	587

Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	10	10	19	0.02%	16.0%	DLSSSEPVHAK	99.7%	64.2	25	58.2	2	0	0	1169.58	113	123
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	10	10	19	0.02%	16.0%	FAAHLIAGAPSEGSGALKPELSR	99.7%	42.9	25	42.9	0	2	0	2279.21	707	729
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	10	10	19	0.02%	16.0%	FLQGDSFLNEDLNQLIK	99.7%	91.1	25	91.1	2	0	0	1994.02	761	777
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	10	10	19	0.02%	16.0%	FYLENLEQMVK	99.7%	66.1	25	48.8	2	0	0	1413.71	307	317
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	10	10	19	0.02%	16.0%	IRPLTEAEK	99.1%	35.6	25	26.4	2	0	0	1056.60	275	283
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	10	10	19	0.02%	16.0%	KPIPLENPK	98.1%	32.2	25	32.2	1	0	0	1035.62	60	68
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	10	10	19	0.02%	16.0%	LGQASLGVIK	99.7%	72.2	25	33	2	0	0	985.60	394	403
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	10	10	19	0.02%	16.0%	NYEVRPEMLK	96.4%	29.6	25	18.4	2	0	0	1278.65	413	422
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	10	10	19	0.02%	16.0%	SPLLPAVLEGLAK	99.7%	43.8	25	43.8	2	0	0	1307.79	512	524
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	10	10	19	0.02%	16.0%	YSSEVATESPLDFTK	99.7%	86.2	25	86.2	2	0	0	1673.79	779	793
Nucleolar complex protein 4 homolog	NOC4L	NOC4L_HUMAN	58.5	100.0%	3	3	5	0.00%	5.8%	LFGALLER	99.7%	71.1	25	44.1	2	0	0	918.54	56	63
Nucleolar complex protein 4 homolog	NOC4L	NOC4L_HUMAN	58.5	100.0%	3	3	5	0.00%	5.8%	LGELLGHPSFQVK	99.2%	36.3	25	27.8	1	0	0	1424.79	103	115
Nucleolar complex protein 4 homolog	NOC4L	NOC4L_HUMAN	58.5	100.0%	3	3	5	0.00%	5.8%	RLEAVLASR	99.7%	55.3	25	34.6	2	0	0	1014.61	17	25
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	6	6	12	0.01%	9.6%	ADVDVQPYAFTTK	99.7%	84.7	25	84.7	2	0	0	1454.72	191	203
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	6	6	12	0.01%	9.6%	FTQQNYHDR	99.7%	47.4	25	41.2	2	0	0	1208.54	53	61
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	6	6	12	0.01%	9.6%	IAELSEDDQK	99.7%	42.1	25	41.9	2	0	0	1147.55	296	305
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	6	6	12	0.01%	9.6%	LALGQINIAK	99.7%	55.7	25	49.1	2	0	0	1040.65	94	103
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	6	6	12	0.01%	9.6%	LPTIDPNTR	99.6%	38.8	25	31.5	2	0	0	1026.56	161	169
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	6	6	12	0.01%	9.6%	LSQILTDFPK	99.7%	60.3	25	52.2	2	0	0	1161.65	62	71
Nucleolar MIF4G domain-containing protein 1	NOM1	NOM1_HUMAN	96.3	100.0%	3	3	4	0.00%	4.3%	ASGAGSEFQDQTR	99.7%	46.2	25	46.1	1	0	0	1353.60	532	544
Nucleolar MIF4G domain-containing protein 1	NOM1	NOM1_HUMAN	96.3	100.0%	3	3	4	0.00%	4.3%	TRPSAAATAAAR	96.5%	29.7	25	23.2	1	0	0	1143.62	160	171
Nucleolar MIF4G domain-containing protein 1	NOM1	NOM1_HUMAN	96.3	100.0%	3	3	4	0.00%	4.3%	TYNPFYAFLASK	99.7%	47	25	47	2	0	0	1421.71	702	713
Nucleolar protein 16	NOP16	NOP16_HUMAN	21.2	100.0%	5	7	12	0.01%	32.6%	AMEVDIEERPK	99.7%	65.1	25	55.7	3	0	0	1316.65	75	85
Nucleolar protein 16	NOP16	NOP16_HUMAN	21.2	100.0%	5	7	12	0.01%	32.6%	DEKNYYQDTPK	99.7%	45.7	25	45.7	2	0	0	1400.63	136	146
Nucleolar protein 16	NOP16	NOP16_HUMAN	21.2	100.0%	5	7	12	0.01%	32.6%	FGYSVNR	98.6%	33.5	25	25.7	2	0	0	842.42	13	19
Nucleolar protein 16	NOP16	NOP16_HUMAN	21.2	100.0%	5	7	12	0.01%	32.6%	QNLAEMGLAVDPNR	99.7%	70.7	25	70.4	4	0	0	1527.76	51	64
Nucleolar protein 16	NOP16	NOP16_HUMAN	21.2	100.0%	5	7	12	0.01%	32.6%	YMVENHGEDYKAMAR	98.9%	28.8	25	28.8	0	1	0	1845.79	121	135
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	10	18	0.02%	17.3%	ELNEDKLEK	99.4%	37.7	25	21.4	1	0	0	1117.57	222	230
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	10	18	0.02%	17.3%	IDCFSEVPTSVFGEK	99.7%	60.8	25	60.8	2	0	0	1714.80	382	396
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	10	18	0.02%	17.3%	IINDNATYCR	99.7%	46.4	25	46.4	2	0	0	1239.58	203	212
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	10	18	0.02%	17.3%	LAQFIGNR	99.7%	40.4	25	26.7	2	0	0	918.52	213	220
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	10	18	0.02%	17.3%	LREQVEER	98.8%	34.2	25	16.3	2	0	0	1058.56	397	404
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	10	18	0.02%	17.3%	MSQVAPSLSALIGEAVGAR	99.7%	88.8	25	88.5	4	0	0	1872.98	289	307
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	10	18	0.02%	17.3%	STPKEETVNDPEEAGHR	96.7%	24.4	25	24.4	0	1	0	1895.87	537	553
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	10	18	0.02%	17.3%	VLLGVGDPK	99.7%	48.7	25	42.5	2	0	0	897.54	91	99
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	9	10	18	0.02%	17.3%	VVSLSEYR	99.7%	60.7	25	45	2	0	0	952.51	271	278
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	9	10	17	0.02%	22.9%	EAHEPLAVADAK	98.1%	32.2	25	26.6	2	0	0	1250.64	82	93
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	9	10	17	0.02%	22.9%	FQDTAEALAAFTALMEGK	99.7%	53.6	25	53.6	1	0	0	1929.93	50	67
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	9	10	17	0.02%	22.9%	HAASTVQILGAEK	99.7%	85.2	25	77.6	1	0	0	1324.72	311	323
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	9	10	17	0.02%	22.9%	IISDNLTYCK	99.7%	52.5	25	48.4	2	0	0	1226.61	197	206
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	9	10	17	0.02%	22.9%	LSELLPEEVEAEVK	99.7%	61.1	25	58.6	2	0	0	1584.84	222	235
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	9	10	17	0.02%	22.9%	SQMDGLIPGVEPR	99.7%	60.6	25	58.3	4	0	0	1414.70	121	133
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	9	10	17	0.02%	22.9%	TQLYEYLQNR	99.7%	51.5	25	51.5	2	0	0	1327.66	269	278
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	9	10	17	0.02%	22.9%	TYDPSGDSTLPTCSK	99.7%	63.7	25	63.7	2	0	0	1628.71	427	441
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	9	10	17	0.02%	22.9%	YGLIYHASLVGQTSPK	99.7%	53.5	25	48.3	0	1	0	1733.92	338	353
Nucleolar protein 9	NOP9	NOP9_HUMAN	69.4	99.8%	2	2	3	0.00%	4.6%	GSSVDGSPLLLFLR	99.7%	65.7	25	59.2	2	0	0	1460.81	311	324
Nucleolar protein 9	NOP9	NOP9_HUMAN	69.4	99.8%	2	2	3	0.00%	4.6%	TLLQVLGGTILESER	99.7%	42.7	25	40.3	1	0	0	1628.92	209	223
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	AAVIGDVIR	99.7%	61.5	25	48.3	2	0	0	913.55	424	432
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	APQVLVLAPTR	99.7%	73	25	73	4	0	0	1164.71	260	270
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	DFSDITKK	98.9%	34.6	25	23.5	2	0	0	953.49	279	286
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	DSEDNPQTLLFSATCPHWVFNVAK	99.7%	73.9	25	73.9	0	2	0	2776.30	364	387

Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	DVESYIHR	99.7%	43.1	25	32.9	2	0	0	1018.50	517	524
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	EAQELSQNSAIK	99.7%	64.4	25	51	4	0	0	1317.66	450	461
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	EEYQLVQVEQK	99.7%	74.1	25	65.8	2	0	0	1392.70	545	555
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	EGAFSNFPISEETIK	99.7%	59.7	25	59.7	5	0	0	1668.81	185	199
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	ELKEQLGEEIDSK	99.7%	72.2	25	64	2	0	0	1517.77	656	668
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	GAVEALAAALAHISGATSVDQR	99.7%	85.2	25	85.2	2	2	0	2108.11	606	627
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	GRAPQVLVLAPTR	99.7%	54.7	25	54.7	2	0	0	1377.83	258	270
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	GVTFLFPIQAK	99.7%	59.3	25	40.1	2	0	0	1220.70	205	215
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	IGVPSATEIIK	99.7%	53.5	25	53.3	3	0	0	1127.67	563	573
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	KAEPSEVDMNSPK	99.7%	58.8	25	54.2	3	2	0	1431.68	61	73
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	KLSVACFYGGTPYGGQFER	99.7%	43.2	25	34.2	0	2	0	2137.02	286	304
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	LGVCFDVPTASVTEIQEK	99.7%	75.3	25	72.2	2	0	0	1992.99	679	696
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	LLDSVPPTAISHFK	99.4%	37.2	25	25	2	1	0	1524.84	582	595
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	LSVACFYGGTPYGGQFER	99.7%	72.2	25	70.8	2	0	0	2008.92	287	304
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	NEEPSEEEIDAPKPK	99.7%	70.7	25	61.3	2	2	0	1711.80	117	131
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	NGIDILVGTPGR	99.7%	75	25	65.7	4	0	0	1211.67	307	318
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	NGSFGVLVATNVAAR	99.7%	86.7	25	83.8	2	0	0	1475.80	485	499
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	QDAQSLHGDIPQK	99.7%	58.9	25	56.3	2	1	0	1436.71	462	474
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	SDAGLESDTAMK	99.7%	67.7	25	67.7	4	0	0	1240.54	7	18
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	SDAGLESDTAMKK	98.4%	32.8	25	32.8	1	0	0	1368.63	7	19
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	SDKTEEIAEEEETVFPK	99.7%	84.1	25	77	2	2	0	1980.93	38	54
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	STYEQVDLIGK	99.7%	67.3	25	56.7	3	0	0	1252.64	392	402
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	STYEQVDLIGKK	99.7%	79.6	25	56.1	2	0	0	1380.74	392	403
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	TAITVEHLAIK	99.7%	76.7	25	76.7	4	0	0	1195.70	407	417
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	TFSFAIPLIEK	99.7%	64.1	25	62.6	5	0	0	1265.71	237	247
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	TGVCICFYQHK	99.7%	42.5	25	38.3	2	1	0	1412.65	534	544
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	31	40	91	0.09%	46.7%	WQLSVATEQPELEGPR	99.7%	93	25	93	2	0	0	1839.92	703	718
Nucleolar transcription factor 1	UBTF	UBF1_HUMAN	89.4	99.8%	2	2	4	0.00%	3.4%	FLESLPEEEQQR	99.7%	53.3	25	41.4	2	0	0	1504.73	361	372
Nucleolar transcription factor 1	UBTF	UBF1_HUMAN	89.4	99.8%	2	2	4	0.00%	3.4%	TLTELILDAQEHVK	99.7%	75.2	25	75.2	2	0	0	1609.88	84	97
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	24	31	189	0.19%	31.7%	ALELTGLK	99.7%	60.2	25	41.9	7	0	0	844.51	363	370
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	24	31	189	0.19%	31.7%	EAMEDGEIDGNK	99.7%	75	25	75	6	0	0	1307.54	628	639
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	24	31	189	0.19%	31.7%	EAMEDGEIDGNKVTLDWAKPK	99.7%	71.3	25	71.3	0	6	0	2346.13	628	648
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	24	31	189	0.19%	31.7%	ESFDGSVR	99.7%	50.6	25	46.7	3	0	0	896.41	590	597
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	24	31	189	0.19%	31.7%	EVFEDAAEIR	99.7%	70.9	25	53.1	6	0	0	1178.57	411	420
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	24	31	189	0.19%	31.7%	FGYVDFESAEDLEK	99.7%	104	25	96.5	8	0	0	1648.74	349	362
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	24	31	189	0.19%	31.7%	GFGFVDFNSEEDAK	99.7%	90	25	90	17	0	0	1561.68	611	624
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	24	31	189	0.19%	31.7%	GIAYIEFK	99.7%	55.1	25	41.9	5	0	0	940.51	430	437
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	24	31	189	0.19%	31.7%	GLSEDTTEETLK	99.7%	84.6	25	72.6	7	0	0	1322.63	578	589
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	24	31	189	0.19%	31.7%	GLSEDTTEETLKESFDGSVR	99.7%	106	25	106	4	9	0	2200.03	578	597
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	24	31	189	0.19%	31.7%	GYAFIEFASFEDAK	99.7%	114	25	108	10	0	0	1594.74	524	537
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	24	31	189	0.19%	31.7%	KFGYVDFESAEDLEK	99.7%	107	25	92.9	5	2	0	1776.83	348	362
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	24	31	189	0.19%	31.7%	LELQGPR	99.7%	42.5	25	33.7	7	0	0	812.46	555	561
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	24	31	189	0.19%	31.7%	NDLAVVDVR	99.7%	88.8	25	77.5	13	0	0	1000.54	334	342
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	24	31	189	0.19%	31.7%	QKVEGTEPTTAFNLFVGNLNFNK	99.7%	56	25	56	0	4	0	2568.31	296	318
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	24	31	189	0.19%	31.7%	SISLYYTGEK	99.7%	67.6	25	57.9	13	0	0	1160.58	458	467
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	24	31	189	0.19%	31.7%	TEADAEKTFEEK	99.7%	74.8	25	65.6	5	0	0	1397.64	438	449
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	24	31	189	0.19%	31.7%	TGISDVFAK	99.7%	69.1	25	50.5	10	0	0	937.50	325	333
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	24	31	189	0.19%	31.7%	TLVLSNLSYSATEETLQEVFEK	99.7%	129	25	129	5	3	0	2501.27	487	508
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	24	31	189	0.19%	31.7%	VAVATPAKK	98.0%	31.9	25	21.1	2	0	0	884.56	72	80
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	24	31	189	0.19%	31.7%	VEGTEPTTAFNLFVGNLNFNK	99.7%	105	25	105	9	6	0	2312.16	298	318
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	24	31	189	0.19%	31.7%	VFGNEIK	97.1%	30.4	25	10.3	3	0	0	806.44	371	377

Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	24	31	189	0.19%	31.7%	VTLDWAKPK	99.7%	51.5	25	46.2	4	0	0	1057.60	640	648
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	24	31	189	0.19%	31.7%	VTQDELKEVFEDAAEIR	99.7%	99.6	25	94.9	4	6	0	1991.99	404	420
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	8	15	74	0.07%	31.6%	DELHIVEAEAMNYEGSPIK	99.7%	83.2	25	83.2	2	4	0	2161.01	55	73
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	8	15	74	0.07%	31.6%	GPSSVEDIK	99.7%	67	25	59.3	12	0	0	931.47	240	248
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	8	15	74	0.07%	31.6%	GPSSVEDIKAK	99.7%	90.4	25	71.8	9	0	0	1130.61	240	250
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	8	15	74	0.07%	31.6%	LLSISGKR	99.7%	48.9	25	35.3	4	0	0	873.55	135	142
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	8	15	74	0.07%	31.6%	MQASIEK	96.7%	29.9	25	12.1	4	0	0	822.40	251	257
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	8	15	74	0.07%	31.6%	MSVQPTVSLGGFEITPPVVLR	99.7%	93.7	25	93.7	13	6	0	2227.22	81	101
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	8	15	74	0.07%	31.6%	MTDQEAIQDLWQWR	99.7%	66.4	25	66.3	10	0	0	1835.84	278	291
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	8	15	74	0.07%	31.6%	VDNDENEHQLSLR	99.7%	79.6	25	77.3	9	1	0	1568.73	33	45
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	5	5	7	0.01%	3.7%	ALLLVPASVNCLR	99.7%	50.5	25	50.5	2	0	0	1425.82	1142	1154
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	5	5	7	0.01%	3.7%	HTLNPEETSSVVR	99.0%	35.1	25	30.3	1	0	0	1468.74	331	343
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	5	5	7	0.01%	3.7%	LAFSVTNNVIR	99.7%	52.8	25	47.2	1	0	0	1233.69	816	826
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	5	5	7	0.01%	3.7%	LLYPLGGQTNLR	99.6%	39.8	25	31.9	1	0	0	1344.76	501	512
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	5	5	7	0.01%	3.7%	VQRPPSAASAAPSSSK	99.7%	49.5	25	43.8	2	0	0	1540.81	1518	1533
Nucleoporin-like protein 2	NUPL2	NUPL2_HUMAN	44.9	99.8%	2	2	3	0.00%	5.9%	IPLKPPPLELLNV	99.7%	41.1	25	41.1	2	0	0	1442.90	411	423
Nucleoporin-like protein 2	NUPL2	NUPL2_HUMAN	44.9	99.8%	2	2	3	0.00%	5.9%	YSNVIQPSSFSK	99.7%	47.7	25	45.4	1	0	0	1356.68	54	65
Nucleoside diphosphate kinase 6	NME6	NDK6_HUMAN	21.1	100.0%	4	4	6	0.01%	25.3%	EIAAFFPDFSEQR	99.7%	41.3	25	40.7	2	0	0	1556.74	140	152
Nucleoside diphosphate kinase 6	NME6	NDK6_HUMAN	21.1	100.0%	4	4	6	0.01%	25.3%	GSFGLTDTR	99.7%	61.3	25	46.1	1	0	0	953.47	117	125
Nucleoside diphosphate kinase 6	NME6	NDK6_HUMAN	21.1	100.0%	4	4	6	0.01%	25.3%	LVEFMASGPIR	99.1%	35.5	25	32.7	1	0	0	1235.65	72	82
Nucleoside diphosphate kinase 6	NME6	NDK6_HUMAN	21.1	100.0%	4	4	6	0.01%	25.3%	NTTHGSDSVVSASR	99.7%	45.9	25	44.8	2	0	0	1417.67	126	139
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	6	11	29	0.03%	40.1%	GDFCIQVGR	99.7%	66.1	25	58.9	4	0	0	1051.50	106	114
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	6	11	29	0.03%	40.1%	GLVGEIIK	96.3%	29.5	25	25.8	1	0	0	828.52	19	26
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	6	11	29	0.03%	40.1%	GLVGEIIKR	99.6%	39.6	25	36.1	4	0	0	984.62	19	27
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	6	11	29	0.03%	40.1%	NIIHGSDSVESAEK	99.7%	45.6	25	36.7	1	1	0	1485.72	115	128
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	6	11	29	0.03%	40.1%	TFIAIKPDGVQR	99.7%	42.2	25	40.3	4	1	0	1344.76	7	18
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	6	11	29	0.03%	40.1%	VMLGETNPADSKPGTIR	99.7%	61.8	25	56.7	8	5	0	1801.91	89	105
Nucleoside diphosphate kinase, mitochondrial	NME4	NDKM_HUMAN	20.7	100.0%	5	7	12	0.01%	32.1%	AMIGHTDSAEAAPGTIR	99.3%	30.6	25	26.9	1	2	0	1713.82	122	138
Nucleoside diphosphate kinase, mitochondrial	NME4	NDKM_HUMAN	20.7	100.0%	5	7	12	0.01%	32.1%	GDFSVHISR	99.7%	40.4	25	27.6	2	0	0	1017.51	139	147
Nucleoside diphosphate kinase, mitochondrial	NME4	NDKM_HUMAN	20.7	100.0%	5	7	12	0.01%	32.1%	LVGDVIQR	99.6%	39.8	25	30.4	2	0	0	899.53	53	60
Nucleoside diphosphate kinase, mitochondrial	NME4	NDKM_HUMAN	20.7	100.0%	5	7	12	0.01%	32.1%	NVIHASDSVEGAQR	99.7%	54.8	25	42.2	1	2	0	1482.73	148	161
Nucleoside diphosphate kinase, mitochondrial	NME4	NDKM_HUMAN	20.7	100.0%	5	7	12	0.01%	32.1%	TLVAVKPDGVQR	99.7%	42.2	25	38.9	2	0	0	1282.75	40	51
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	5	5	18	0.02%	17.4%	FYEEVHDLER	99.7%	47.6	25	45.1	6	0	0	1336.62	95	104
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	5	5	18	0.02%	17.4%	GIPEFWLTVFK	99.7%	60.9	25	60.9	6	0	0	1336.73	166	176
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	5	5	18	0.02%	17.4%	LDGLVETPTGYIESLPR	99.7%	72.7	25	70.6	5	0	0	1859.98	56	72
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	5	5	18	0.02%	17.4%	NVDLLSDMVQEHDEPILK	97.8%	25.9	25	19.9	0	2	0	2095.04	177	194
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	5	5	18	0.02%	17.4%	YAVLYQPLFDK	99.7%	51.6	25	49.3	3	0	0	1356.72	106	116
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	5	5	18	0.02%	17.4%	YAVLYQPLFDKR	99.7%	45.3	25	42.9	2	0	0	1512.82	106	117
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	7	7	19	0.02%	21.9%	AAATAEEPDPK	99.7%	51.4	25	44.9	3	0	0	1099.53	147	157
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	7	7	19	0.02%	21.9%	FYEEVHDLER	99.7%	47.6	25	45.1	6	0	0	1336.62	84	93
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	7	7	19	0.02%	21.9%	LDNVPHTPSSYIETLPK	97.7%	25.9	25	25.9	0	1	0	1910.99	45	61
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	7	7	19	0.02%	21.9%	LTDQVMQNPR	99.7%	55.6	25	48.5	2	0	0	1201.60	27	36
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	7	7	19	0.02%	21.9%	QVPNESFFNFFNPLK	98.5%	33.3	25	32.9	2	0	0	1827.91	283	297
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	7	7	19	0.02%	21.9%	VLAALQER	99.7%	51.1	25	36.3	3	0	0	899.53	37	44
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	7	7	19	0.02%	21.9%	YAALYQPLFDK	99.7%	43.4	25	40.3	2	0	0	1328.69	95	105
Oligosaccharyltransferase complex subunit OSTC	OSTC	OSTC_HUMAN	16.8	99.8%	2	2	8	0.01%	14.1%	MKLPGYLMG	99.7%	41.2	25	25.4	4	0	0	1025.52	141	149
Oligosaccharyltransferase complex subunit OSTC	OSTC	OSTC_HUMAN	16.8	99.8%	2	2	8	0.01%	14.1%	VPFLVLECPNLK	99.7%	73.2	25	70	4	0	0	1428.79	7	18
Origin recognition complex subunit 3	ORC3	ORC3_HUMAN	82.3	99.8%	2	3	4	0.00%	3.1%	LLLTTQFPFK	99.7%	42.9	25	30.2	2	0	0	1207.71	292	301
Origin recognition complex subunit 3	ORC3	ORC3_HUMAN	82.3	99.8%	2	3	4	0.00%	3.1%	SKEEESVHVTQR	99.7%	60.1	25	55.3	1	1	0	1428.71	164	175
Origin recognition complex subunit 4	ORC4	ORC4_HUMAN	50.4	100.0%	2	2	3	0.00%	5.3%	LDILELLEK	99.5%	38.6	25	38.6	1	0	0	1085.65	196	204
Origin recognition complex subunit 4	ORC4	ORC4_HUMAN	50.4	100.0%	2	2	3	0.00%	5.3%	LLLDNTQIMNALQK	99.7%	68.9	25	68.9	2	0	0	1614.89	404	417

Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	4	4	7	0.01%	9.2%	ESQVSILQSLFGER	99.7%	99.4	25	90.2	2	0	0	1592.83	12	25
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	4	4	7	0.01%	9.2%	LLLEQILNK	99.7%	64.8	25	49.5	2	0	0	1083.68	71	79
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	4	4	7	0.01%	9.2%	TVNFDIIK	99.2%	36.3	25	26.3	1	0	0	949.54	422	429
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	4	4	7	0.01%	9.2%	TYVTQTLLK	99.0%	35.1	25	32.4	2	0	0	1066.61	44	52
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	17	22	58	0.06%	49.0%	AFYNNVLGEYEEYITK	99.7%	77.1	25	69	6	0	0	1952.93	114	129
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	17	22	58	0.06%	49.0%	DNGLLAKPTHGDIIR	99.7%	55.3	25	55.3	0	2	0	1619.89	399	413
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	17	22	58	0.06%	49.0%	FAPPLVIKEDELR	99.7%	71.2	25	68.3	2	1	0	1526.86	414	426
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	17	22	58	0.06%	49.0%	GIYLWDVEGR	99.7%	69.4	25	53.5	4	0	0	1207.61	67	76
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	17	22	58	0.06%	49.0%	GIYLWDVEGRK	99.7%	49.9	25	47.5	2	0	0	1335.71	67	77
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	17	22	58	0.06%	49.0%	GLLNAIVIK	99.7%	62.2	25	57.1	3	0	0	940.62	375	383
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	17	22	58	0.06%	49.0%	HQVLFIADEIQTGLAR	99.7%	38.4	25	28.1	0	2	0	1810.98	256	271
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	17	22	58	0.06%	49.0%	IVFAAGNFWGR	99.7%	67.9	25	67.9	7	0	0	1237.65	170	180
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	17	22	58	0.06%	49.0%	KTVQGPPTSDDIFER	99.7%	75.3	25	75.3	1	2	0	1689.84	32	46
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	17	22	58	0.06%	49.0%	LPSDVVTAVR	99.7%	79.7	25	65.4	5	0	0	1056.60	363	372
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	17	22	58	0.06%	49.0%	SQVDKLTLTSR	99.7%	65.4	25	56.9	3	2	0	1247.70	103	113
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	17	22	58	0.06%	49.0%	TVQGPPTSDDIFER	99.7%	83.3	25	70.9	3	0	0	1561.75	33	46
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	17	22	58	0.06%	49.0%	VAIAALEVLEEENLAENADK	99.7%	119	25	118	2	0	0	2141.10	332	351
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	17	22	58	0.06%	49.0%	VLPMNTGVEAGETACK	99.7%	98.9	25	96.8	4	0	0	1676.80	136	151
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	17	22	58	0.06%	49.0%	WLAVDYENVRPDIVLLGK	99.7%	55.7	25	55.7	2	2	0	2100.15	275	292
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	17	22	58	0.06%	49.0%	YFDFLSSYSAVNQGHCHPK	99.7%	36.6	25	36.6	0	1	0	2257.01	78	96
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	17	22	58	0.06%	49.0%	YGAHNYHPLPVALER	99.7%	58.8	25	58.8	2	0	0	1736.89	50	64
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	13	25	0.02%	32.2%	CQIIYPR	99.7%	42.9	25	26.5	2	0	0	949.49	341	347
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	13	25	0.02%	32.2%	ELEMIGFIENNVSK	99.7%	85.5	25	76.9	2	0	0	1622.81	355	368
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	13	25	0.02%	32.2%	HSNVVILTTSNITEK	99.7%	38.3	25	38.3	0	2	0	1655.90	290	304
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	13	25	0.02%	32.2%	IDVAFVDR	99.7%	61	25	35.9	2	0	0	934.50	305	312
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	13	25	0.02%	32.2%	LSLLLNDISR	99.7%	67	25	46.5	2	0	0	1143.67	369	378
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	13	25	0.02%	32.2%	NVNSNLITWNR	99.7%	68.9	25	64.9	2	0	0	1330.69	163	173
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	13	25	0.02%	32.2%	NVQSVSIIDTELK	99.7%	77.4	25	69.4	2	0	0	1445.78	69	81
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	13	25	0.02%	32.2%	QQLLTLR	99.7%	46.5	25	25	2	0	0	871.54	348	354
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	13	25	0.02%	32.2%	QYIGPPSAAAIFK	99.7%	56.7	25	49.3	2	0	0	1362.74	317	329
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	13	25	0.02%	32.2%	VVLLHGPPGTGK	99.7%	73.7	25	73.7	2	0	0	1174.69	174	185
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	13	25	0.02%	32.2%	VVNAVLTQIDQIKR	99.7%	73.3	25	73.3	2	2	0	1596.94	276	289
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	12	13	25	0.02%	32.2%	YGQLIEINSHSLFSK	99.7%	76.5	25	76.5	1	0	0	1735.90	206	220
Paired amphipathic helix protein Sin3a	SIN3A	SIN3A_HUMAN	145.2	100.0%	2	2	3	0.00%	1.5%	LLFSNTAAQK	99.7%	42.3	25	26.2	2	0	0	1092.60	866	875
Paired amphipathic helix protein Sin3a	SIN3A	SIN3A_HUMAN	145.2	100.0%	2	2	3	0.00%	1.5%	SLLESTYQR	99.7%	43.8	25	35	1	0	0	1096.56	1044	1052
PC4 and SFRS1-interacting protein	PSIP1	PSIP1_HUMAN	60.1	99.8%	2	2	3	0.00%	3.0%	GQEEKQPK	95.8%	28.9	25	23.7	1	0	0	943.48	221	228
PC4 and SFRS1-interacting protein	PSIP1	PSIP1_HUMAN	60.1	99.8%	2	2	3	0.00%	3.0%	IDNLDVNR	99.7%	46.4	25	8.49	2	0	0	958.50	365	372
PCI domain-containing protein 2	PCID2	PCID2_HUMAN	46.0	100.0%	3	3	4	0.00%	10.0%	AVSEGNLLLLHEALAK	99.7%	73.2	25	73.2	1	0	0	1677.95	285	300
PCI domain-containing protein 2	PCID2	PCID2_HUMAN	46.0	100.0%	3	3	4	0.00%	10.0%	DGASCAELVSFK	99.7%	42.1	25	39.4	1	0	0	1283.59	21	32
PCI domain-containing protein 2	PCID2	PCID2_HUMAN	46.0	100.0%	3	3	4	0.00%	10.0%	VFANNADQQLVK	99.7%	46.7	25	42	2	0	0	1346.71	117	128
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	7	8	15	0.01%	11.0%	FIGPDQHR	99.5%	38	25	26.6	2	0	0	969.49	447	454
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	7	8	15	0.01%	11.0%	LFDQPGDPLKR	97.8%	31.5	25	23.7	2	0	0	1285.69	378	388
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	7	8	15	0.01%	11.0%	SAYESQPIR	99.7%	56.6	25	43.5	2	0	0	1050.52	557	565
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	7	8	15	0.01%	11.0%	SELLNELMDSAK	99.7%	85.8	25	85.8	3	0	0	1349.66	608	619
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	7	8	15	0.01%	11.0%	SPALQVLR	99.7%	70.2	25	63.1	2	0	0	883.54	351	358
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	7	8	15	0.01%	11.0%	VEGTDVTGIEEVVIPK	99.7%	105	25	93.6	2	0	0	1684.90	46	61
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	7	8	15	0.01%	11.0%	VMSDFAINQEQK	99.7%	88.1	25	85.8	2	0	0	1409.67	649	660
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	13	22	0.02%	58.2%	EGMNIVEAMER	99.7%	40.3	25	40.3	4	0	0	1278.58	134	144
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	13	22	0.02%	58.2%	FEDENFILK	98.6%	33.6	25	21.2	1	0	0	1154.57	83	91
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	13	22	0.02%	58.2%	IIPGFMCQGGDFTR	99.7%	47.1	25	42.7	3	0	0	1614.74	56	69
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	13	22	0.02%	58.2%	KITIADCGQLE	99.7%	67.3	25	59.1	2	0	0	1247.63	155	165

Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	13	22	0.02%	58.2%	SIYGEKFEDENFILK	99.7%	63.6	25	63.6	2	0	0	1831.91	77	91
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	13	22	0.02%	58.2%	TEWLDGKHVVFGK	99.4%	31	25	25.6	0	2	0	1515.80	119	131
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	13	22	0.02%	58.2%	VKEGMNIVEAMER	99.7%	65	25	65	2	1	0	1505.75	132	144
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	13	22	0.02%	58.2%	VNPTVFFDIAVDGEPLGR	99.7%	65	25	65	1	0	0	1946.00	2	19
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	13	22	0.02%	58.2%	VSFELFADK	99.7%	51.7	25	48.3	2	0	0	1055.54	20	28
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	13	22	0.02%	58.2%	VSFELFADKVPK	99.7%	56.3	25	49.2	2	0	0	1379.76	20	31
Peptidyl-prolyl cis-trans isomerase H	PPIH	PPIH_HUMAN	19.2	100.0%	2	3	6	0.01%	13.0%	IIDGLLVMR	99.7%	49.9	25	40.7	4	0	0	1029.61	144	152
Peptidyl-prolyl cis-trans isomerase H	PPIH	PPIH_HUMAN	19.2	100.0%	2	3	6	0.01%	13.0%	KIENVPTGPNNKPK	99.7%	44.8	25	44.1	0	2	0	1535.85	153	166
Peptidyl-prolyl cis-trans isomerase-like 1	PPIL1	PPIL1_HUMAN	18.2	100.0%	3	8	14	0.01%	26.5%	IIKDFMIQGGDPTGTGR	99.7%	76	25	72	4	4	0	1805.92	56	72
Peptidyl-prolyl cis-trans isomerase-like 1	PPIL1	PPIL1_HUMAN	18.2	100.0%	3	8	14	0.01%	26.5%	VCQGIGMVNR	99.7%	52.6	25	37	2	0	0	1149.55	132	141
Peptidyl-prolyl cis-trans isomerase-like 1	PPIL1	PPIL1_HUMAN	18.2	100.0%	3	8	14	0.01%	26.5%	VGMVETNSQDRPVDDVK	99.5%	38.7	25	38.4	2	2	0	1904.90	142	158
Peptidyl-prolyl cis-trans isomerase-like 3	PPIL3	PPIL3_HUMAN	18.2	99.8%	2	2	3	0.00%	15.5%	GFMVQTGDPTGTGR	99.7%	77	25	75.2	1	0	0	1439.66	48	61
Peptidyl-prolyl cis-trans isomerase-like 3	PPIL3	PPIL3_HUMAN	18.2	99.8%	2	2	3	0.00%	15.5%	KFEDEYSEYLK	98.7%	33.9	25	29.6	2	0	0	1450.67	70	80
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	9	9	21	0.02%	44.2%	ADEGISFR	99.6%	40	25	36	1	0	0	894.43	121	128
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	9	9	21	0.02%	44.2%	ATAVMPDGQFK	98.5%	33.1	25	26.3	2	0	0	1180.57	17	27
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	9	9	21	0.02%	44.2%	DISLSDYKGK	99.7%	42.8	25	40.2	1	0	0	1125.58	28	37
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	9	9	21	0.02%	44.2%	GLFIIDDKGILR	99.7%	54.1	25	54.1	4	0	0	1359.80	129	140
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	9	9	21	0.02%	44.2%	IGHPAPNFK	99.7%	50.3	25	44.7	2	0	0	980.53	8	16
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	9	9	21	0.02%	44.2%	LVQAFQFTDK	99.7%	52.3	25	47.8	2	0	0	1196.63	159	168
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	9	9	21	0.02%	44.2%	QITVNDLPVGR	99.7%	74.4	25	65.9	3	0	0	1211.67	141	151
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	9	9	21	0.02%	44.2%	SVDETLR	98.3%	32.6	25	17.8	1	0	0	819.42	152	158
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	9	9	21	0.02%	44.2%	TIAQDYGVLK	99.7%	46.5	25	39.3	5	0	0	1107.60	111	120
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	4	4	6	0.01%	25.3%	ATAVVDGAFKEVK	99.7%	65.5	25	53	2	0	0	1334.73	17	29
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	4	4	6	0.01%	25.3%	IGKPAPDFK	97.8%	31.6	25	15.2	1	0	0	972.55	8	16
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	4	4	6	0.01%	25.3%	LSEDYGVLK	99.7%	54.9	25	47.8	2	0	0	1023.54	111	119
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	4	4	6	0.01%	25.3%	LSEDYGVLKTDEGIAYR	99.7%	35.8	25	35.8	0	1	0	1928.96	111	127
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	4	4	6	0.01%	25.3%	QITVNDLPVGR	99.7%	74.4	25	65.9	3	0	0	1211.67	140	150
Peroxiredoxin-4	PRDX4	PRDX4_HUMAN	30.5	99.8%	2	2	3	0.00%	15.9%	DYGVYLEDSGHTLR	99.7%	54.5	25	54.5	2	0	0	1624.76	187	200
Peroxiredoxin-4	PRDX4	PRDX4_HUMAN	30.5	99.8%	2	2	3	0.00%	15.9%	GLFIIDDKGILR	99.7%	54.1	25	54.1	4	0	0	1359.80	201	212
Peroxiredoxin-4	PRDX4	PRDX4_HUMAN	30.5	99.8%	2	2	3	0.00%	15.9%	LVQAFQYTDK	98.9%	34.5	25	34.5	1	0	0	1212.63	231	240
Peroxiredoxin-4	PRDX4	PRDX4_HUMAN	30.5	99.8%	2	2	3	0.00%	15.9%	SVDETLR	98.3%	32.6	25	17.8	1	0	0	819.42	224	230
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	9	10	19	0.02%	37.9%	DFTPVCTTELGR	99.7%	56.6	25	47.8	4	0	0	1395.66	42	53
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	9	10	19	0.02%	37.9%	DINAYNCEEPTEK	99.7%	70.7	25	70.7	2	0	0	1582.67	85	97
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	9	10	19	0.02%	37.9%	LPFPIIDDR	99.7%	64.2	25	50.8	2	0	0	1085.60	98	106
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	9	10	19	0.02%	37.9%	LPFPIIDDRNR	96.5%	24.2	25	12.5	0	1	0	1355.74	98	108
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	9	10	19	0.02%	37.9%	LSILYPATTGR	99.7%	43.3	25	32.2	2	0	0	1191.67	145	155
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	9	10	19	0.02%	37.9%	NFDEILR	98.9%	34.7	25	17.1	2	0	0	906.47	156	162
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	9	10	19	0.02%	37.9%	PGGLLLGDVAPNFEANTTVGR	99.7%	80.1	25	79.1	2	1	0	2098.09	2	22
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	9	10	19	0.02%	37.9%	VVFVFGPDK	99.6%	39.9	25	35.3	1	0	0	1007.56	133	141
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	9	10	19	0.02%	37.9%	VVFVFGPDKK	99.7%	47.6	25	47.6	2	0	0	1135.65	133	142
Peroxisomal biogenesis factor 3	PEX3	PEX3_HUMAN	42.1	99.8%	2	2	4	0.00%	5.6%	EAAEYIAQAR	99.7%	62.8	25	55.5	2	0	0	1121.56	44	53
Peroxisomal biogenesis factor 3	PEX3	PEX3_HUMAN	42.1	99.8%	2	2	4	0.00%	5.6%	HSLSLLDLEQK	99.7%	63.9	25	57.2	2	0	0	1282.70	198	208
Peroxisomal multifunctional enzyme type 2	HSD17B4	DHB4_HUMAN	79.7	99.8%	2	2	2	0.00%	3.5%	GALVVVNDLGGDFK	99.7%	61.6	25	60.7	1	0	0	1403.75	33	46
Peroxisomal multifunctional enzyme type 2	HSD17B4	DHB4_HUMAN	79.7	99.8%	2	2	2	0.00%	3.5%	IDVVVNNAGILR	99.7%	42.8	25	35	1	0	0	1282.75	93	104
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	11	0.01%	11.1%	GIYPHEPK	98.2%	32.3	25	27.5	1	0	0	940.49	42	49
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	11	0.01%	11.1%	GSATNYITR	99.7%	65.6	25	57.1	2	0	0	982.50	12	20
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	11	0.01%	11.1%	LAALEEQR	99.7%	41.7	25	32.1	1	0	0	929.51	496	503
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	11	0.01%	11.1%	LAALSASLAR	99.7%	61.3	25	32.3	1	0	0	972.58	276	285
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	11	0.01%	11.1%	LAQEEESEAKR	99.5%	38.5	25	29.2	2	0	0	1289.63	524	534
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	11	0.01%	11.1%	LEGQAQAEAK	99.7%	52.6	25	36.7	2	0	0	1044.53	250	259
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	11	0.01%	11.1%	LQLSLADFR	99.7%	59.9	25	52.3	2	0	0	1062.59	27	35

PHD finger protein 6	PHF6	PHF6_HUMAN	41.3	100.0%	3	3	6	0.01%	7.7%	AEFGDFDIK	98.9%	34.5	25	27.9	2	0	0	1041.49	258	266
PHD finger protein 6	PHF6	PHF6_HUMAN	41.3	100.0%	3	3	6	0.01%	7.7%	TVLQEIKR	99.7%	42.1	25	15	2	0	0	986.60	267	274
PHD finger protein 6	PHF6	PHF6_HUMAN	41.3	100.0%	3	3	6	0.01%	7.7%	TYHYHCALHDK	99.3%	30.7	25	30.7	0	2	0	1444.64	102	112
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	10	11	28	0.03%	23.2%	GSAFSTSISK	98.7%	33.8	25	18.4	2	0	0	984.50	178	187
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	10	11	28	0.03%	23.2%	HWELTAEGEEIAR	99.4%	37.4	25	37.3	1	0	0	1540.74	60	72
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	10	11	28	0.03%	23.2%	LDAEPRPPPTQEAA	99.5%	38.2	25	38.2	1	0	0	1491.74	495	508
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	10	11	28	0.03%	23.2%	LGITQLR	99.7%	56.8	25	40.3	6	0	0	800.50	398	404
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	10	11	28	0.03%	23.2%	QETELSPEMISSGSWR	99.7%	89.3	25	87	1	0	0	1852.84	188	203
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	10	11	28	0.03%	23.2%	SLQALGEVIEAELR	99.7%	110	25	104	4	0	0	1527.84	43	56
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	10	11	28	0.03%	23.2%	THSQGGYGSQGYK	99.7%	69.9	25	69.9	2	0	0	1369.61	299	311
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	10	11	28	0.03%	23.2%	VNLQMVYDSPLCR	99.7%	75.1	25	74.1	2	0	0	1594.77	482	494
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	10	11	28	0.03%	23.2%	VVDSMEDEVQR	99.7%	82.5	25	82.5	6	0	0	1306.59	128	138
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	10	11	28	0.03%	23.2%	YGINNIR	99.7%	41.8	25	27	3	0	0	849.46	469	475
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	12	12	21	0.02%	20.7%	ASEGPAFFPGR	99.7%	81.7	25	65.7	2	0	0	1135.55	537	547
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	12	12	21	0.02%	20.7%	AVHISNPK	97.2%	30.6	25	30.5	1	0	0	865.49	436	443
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	12	12	21	0.02%	20.7%	DLLFQALGR	99.7%	66.2	25	48.2	2	0	0	1032.58	9	17
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	12	12	21	0.02%	20.7%	DRYDSFIELQEK	99.7%	53.4	25	43.7	2	0	0	1542.74	134	145
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	12	12	21	0.02%	20.7%	HLCAVYYNK	94.8%	28.2	25	21.9	1	0	0	1167.56	496	504
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	12	12	21	0.02%	20.7%	LFEISDIVIK	99.7%	50.9	25	34.8	3	0	0	1176.69	474	483
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	12	12	21	0.02%	20.7%	LGVLHPDVITK	99.7%	41	25	41	2	0	0	1191.71	561	571
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	12	12	21	0.02%	20.7%	LIITEETAK	99.7%	46.1	25	34.9	2	0	0	1017.58	108	116
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	12	12	21	0.02%	20.7%	NIFIECTGTDFTK	99.7%	92.6	25	91.9	2	0	0	1545.73	250	262
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	12	12	21	0.02%	20.7%	SHTFPELAYR	95.7%	28.9	25	28.1	1	0	0	1220.61	296	305
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	12	12	21	0.02%	20.7%	TTLLPGLLK	96.8%	30	25	29.6	2	0	0	955.62	452	460
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	12	12	21	0.02%	20.7%	YDLLCLEGLVR	99.7%	64	25	59.7	1	0	0	1350.71	72	82
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	64	0.06%	36.2%	EKGSSASLVLK	97.4%	30.8	25	22.5	2	0	0	1118.64	294	304
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	64	0.06%	36.2%	FACFER	98.8%	34.2	25	29	3	0	0	829.37	235	240
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	64	0.06%	36.2%	FGFYEVFK	97.2%	30.6	25	30.1	4	0	0	1036.51	138	145
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	64	0.06%	36.2%	GIFNGFSVTLK	99.7%	77.2	25	66.5	4	0	0	1182.65	102	112
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	64	0.06%	36.2%	GIFNGFSVTLKEDGVR	99.7%	51.6	25	47.2	2	0	0	1738.91	102	117
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	64	0.06%	36.2%	GSSASLVLK	99.6%	39.6	25	25.1	4	0	0	861.50	296	304
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	64	0.06%	36.2%	GSSASLVLKR	99.7%	55.7	25	29.4	4	0	0	1017.61	296	305
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	64	0.06%	36.2%	GVAPLWMR	99.7%	49.7	25	17.7	7	0	0	929.50	219	226
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	64	0.06%	36.2%	GWAPTFLGYSMQGLCK	99.7%	89.7	25	89.7	7	0	0	1815.86	122	137
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	64	0.06%	36.2%	IQTQPGYANTLR	99.7%	77.8	25	64.2	11	0	0	1361.72	190	201
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	64	0.06%	36.2%	LPRPPPPEMPESLK	99.7%	46.4	25	41.1	1	1	0	1587.86	342	355
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	64	0.06%	36.2%	LPRPPPPEMPESLKK	99.7%	35.6	25	24.5	0	1	0	1715.95	342	356
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	64	0.06%	36.2%	MQVDPQK	97.7%	31.5	25	15	1	0	0	845.42	93	99
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	64	0.06%	36.2%	MYKEEGLK	99.7%	46.6	25	36	5	0	0	997.50	207	214
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	64	0.06%	36.2%	TVEALYK	99.0%	34.9	25	13.1	1	0	0	823.46	241	247
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	16	21	64	0.06%	36.2%	VLYSNMLGEENTYLWR	99.7%	79.2	25	79.2	6	0	0	1987.96	146	161
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	6	6	11	0.01%	34.8%	AATALLEAGLAR	99.7%	83.1	25	62.6	2	0	0	1156.67	2	13
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	6	6	11	0.01%	34.8%	GVITMNEEYETR	99.7%	74.1	25	74.1	2	0	0	1457.66	67	78
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	6	6	11	0.01%	34.8%	IDPTVLLGALPLR	99.7%	67.4	25	67.1	2	0	0	1377.85	41	53
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	6	6	11	0.01%	34.8%	LGVEQLR	99.7%	47.7	25	22.3	2	0	0	814.48	90	96
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	6	6	11	0.01%	34.8%	LSTVDMTGIPTLDNLQK	99.5%	38	25	38	1	0	0	1845.96	97	113
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	6	6	11	0.01%	34.8%	QLVQDENVR	99.7%	47.4	25	38.4	2	0	0	1100.57	58	66
Phosphatidylinositide phosphatase SAC1	SACM1L	SAC1_HUMAN	67.0	99.9%	2	2	4	0.00%	3.4%	ELSAQPEVHR	99.7%	42.7	25	36.2	2	0	0	1165.60	175	184
Phosphatidylinositide phosphatase SAC1	SACM1L	SAC1_HUMAN	67.0	99.9%	2	2	4	0.00%	3.4%	TNVIQSLLAR	99.7%	50.8	25	40.4	2	0	0	1114.66	396	405
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	37	0.04%	30.2%	AALQALGVAEGGER	99.7%	99.3	25	98.7	2	0	0	1341.71	36	49
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	37	0.04%	30.2%	ALGATFGPLLLR	99.7%	51.5	25	47.6	4	0	0	1228.74	245	256

Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	37	0.04%	30.2%	APGPGPPPAAR	99.7%	42.2	25	36.1	2	0	0	987.54	718	728
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	37	0.04%	30.2%	DTPDGTFLVR	99.7%	43	25	39.6	2	0	0	1120.56	346	355
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	37	0.04%	30.2%	EAAGPVGPALEPPTLPLHR	96.1%	23.8	25	23.8	0	1	0	1922.05	200	218
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	37	0.04%	30.2%	EDSVEAVGAQLK	99.7%	67.8	25	56.9	1	0	0	1245.63	436	447
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	37	0.04%	30.2%	ERPEDLELLPGDVLVVSR	99.7%	63	25	63	2	0	0	2036.10	18	35
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	37	0.04%	30.2%	EYDQLYEEYTR	99.4%	37.8	25	37.8	1	0	0	1508.65	459	469
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	37	0.04%	30.2%	FLLQHLGR	99.7%	53	25	47.4	2	0	0	983.58	224	231
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	37	0.04%	30.2%	HESLAQYNAK	99.7%	58.6	25	52.2	2	0	0	1160.57	407	416
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	37	0.04%	30.2%	IAEIHESR	99.7%	54	25	29.7	4	0	0	954.50	532	539
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	37	0.04%	30.2%	IFEEQGQTQEK	99.7%	73.3	25	65.7	2	0	0	1336.64	490	500
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	37	0.04%	30.2%	SFLLALPAPLVTPEASAEAR	99.7%	66.5	25	54.8	4	0	0	2053.13	176	195
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	37	0.04%	30.2%	TAIEAFNETIK	99.7%	59.7	25	55.3	3	0	0	1236.65	479	489
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	37	0.04%	30.2%	TATGFGFAEPYNLYGSLK	99.7%	61.1	25	51.5	2	0	0	1935.95	673	690
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	37	0.04%	30.2%	TGLDSESHYRPELPAPR	99.7%	41.4	25	41.4	0	2	0	1924.95	138	154
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	37	0.04%	30.2%	TQAEEMLSGK	96.2%	29.3	25	29.3	1	0	0	1109.51	630	639
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	99.8%	2	2	4	0.00%	4.5%	GVDASGETTYKK	99.7%	60.4	25	54.9	3	0	0	1255.62	62	73
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	99.8%	2	2	4	0.00%	4.5%	QAQGAQSTSDEKRPVGQK	99.0%	29.1	25	29.1	0	1	0	1914.96	334	351
Phosphatidylserine decarboxylase proenzyme	PISD	PISD_HUMAN	46.7	100.0%	3	3	4	0.00%	8.6%	GSYNDFSFVTHTNR	99.7%	83.1	25	83.1	1	0	0	1644.74	347	360
Phosphatidylserine decarboxylase proenzyme	PISD	PISD_HUMAN	46.7	100.0%	3	3	4	0.00%	8.6%	GVTYSLESFLGPR	99.7%	90.6	25	83.1	2	0	0	1425.74	210	222
Phosphatidylserine decarboxylase proenzyme	PISD	PISD_HUMAN	46.7	100.0%	3	3	4	0.00%	8.6%	ILNFGQVK	94.8%	28.1	25	2.75	1	0	0	918.54	194	201
Phosphatidylserine synthase 1	PTDSS1	PTSS1_HUMAN	55.5	100.0%	3	3	5	0.00%	7.8%	AVLQFTPASWTYVR	99.7%	71.5	25	71.5	2	0	0	1638.86	263	276
Phosphatidylserine synthase 1	PTDSS1	PTSS1_HUMAN	55.5	100.0%	3	3	5	0.00%	7.8%	ILFIGGITAPTVR	99.7%	60	25	58.2	2	0	0	1357.82	324	336
Phosphatidylserine synthase 1	PTDSS1	PTSS1_HUMAN	55.5	100.0%	3	3	5	0.00%	7.8%	TLSKDDVNYK	99.7%	42.4	25	30.1	1	0	0	1182.60	9	18
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	5	5	9	0.01%	9.6%	AFVRPSGTEDVVR	99.7%	55.4	25	53.9	0	2	0	1432.75	493	505
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	5	5	9	0.01%	9.6%	LNHLCGADFVK	99.6%	39.3	25	33.1	2	0	0	1273.64	245	255
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	5	5	9	0.01%	9.6%	MGLLAVLR	99.7%	64	25	48.1	2	0	0	872.54	42	49
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	5	5	9	0.01%	9.6%	VDCANGIGALK	99.7%	53	25	44.2	1	0	0	1117.57	210	220
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	5	5	9	0.01%	9.6%	VISTTDAER	97.0%	30.3	25	26.1	2	0	0	991.51	461	469
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	13	13	29	0.03%	24.5%	AIDTTQLFSLPK	99.7%	87.7	25	75.6	2	0	0	1333.74	589	600
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	13	13	29	0.03%	24.5%	DFVEHSAR	99.7%	41.3	25	35.8	1	0	0	960.45	46	53
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	13	13	29	0.03%	24.5%	EGALDLSGLR	99.7%	50.4	25	36.1	2	0	0	1030.55	579	588
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	13	13	29	0.03%	24.5%	EIISFGSGYGGNSLLGK	99.7%	87	25	87	2	0	0	1698.87	245	261
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	13	13	29	0.03%	24.5%	ETPIGLVPK	96.9%	30.2	25	30.2	1	0	0	953.57	570	578
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	13	13	29	0.03%	24.5%	EVLAELEALER	99.7%	87.2	25	78	2	0	0	1271.68	625	635
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	13	13	29	0.03%	24.5%	GVPLVYEAFNWR	99.7%	47.3	25	42.5	2	0	0	1450.75	458	469
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	13	13	29	0.03%	24.5%	LGTPVLQALGDGDFVK	99.7%	85.1	25	77.6	4	0	0	1629.89	194	209
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	13	13	29	0.03%	24.5%	SYLTEQVNQDLPK	99.7%	102	25	94.7	2	0	0	1534.77	612	624
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	13	13	29	0.03%	24.5%	TLIGHVPDQR	99.7%	49.9	25	23.2	2	0	0	1135.62	235	244
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	13	13	29	0.03%	24.5%	TMYVLPFSMGPVGSPLSR	99.7%	71.1	25	71.1	6	0	0	1970.97	156	173
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	13	13	29	0.03%	24.5%	VLDWICR	98.9%	34.5	25	25.3	1	0	0	961.49	554	560
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	13	13	29	0.03%	24.5%	VLSGDLGQLPTGIR	99.7%	104	25	95.3	2	0	0	1425.81	32	45
Phosphoglycerate kinase 1	PGK1	PGK1_HUMAN	44.6	99.8%	2	2	4	0.00%	6.2%	LGDVYVNDAFGTAHR	99.7%	60	25	55.6	0	2	0	1634.79	157	171
Phosphoglycerate kinase 1	PGK1	PGK1_HUMAN	44.6	99.8%	2	2	4	0.00%	6.2%	VLPGVDALSNI	99.7%	45.4	25	45.4	2	0	0	1097.62	407	417
Phosphoglycerate mutase 1	PGAM1	PGAM1_HUMAN	28.8	100.0%	3	3	4	0.00%	13.8%	ALPFWNEEIVPQIK	99.6%	39.1	25	31.1	1	0	0	1683.91	163	176
Phosphoglycerate mutase 1	PGAM1	PGAM1_HUMAN	28.8	100.0%	3	3	4	0.00%	13.8%	AMEAVAAQGK	98.7%	34	25	29.2	1	0	0	975.49	242	251
Phosphoglycerate mutase 1	PGAM1	PGAM1_HUMAN	28.8	100.0%	3	3	4	0.00%	13.8%	VLIAAHGNSLR	99.7%	51.1	25	51.1	2	0	0	1150.67	181	191
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	7	8	15	0.01%	27.4%	AVVVGFDPHFSYMK	99.7%	55.1	25	55.1	3	0	0	1596.79	167	180
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	7	8	15	0.01%	27.4%	FIAGTGCLVR	99.7%	53.7	25	33.1	2	0	0	1093.58	211	220
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	7	8	15	0.01%	27.4%	FIFDCVSQEYGINPER	99.7%	63.4	25	63	2	0	0	1973.91	239	254
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	7	8	15	0.01%	27.4%	GETAVPGAPEALR	99.7%	60.3	25	40.6	2	0	0	1267.66	42	54
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	7	8	15	0.01%	27.4%	LGFITNNSSK	99.7%	44.8	25	29.5	2	0	0	1080.57	63	72

Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	7	8	15	0.01%	27.4%	QADIIGKPSR	96.3%	29.4	25	18.1	1	0	0	1084.61	229	238
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	7	8	15	0.01%	27.4%	TILTLTGVSTLGDVK	99.7%	98.4	25	98.4	3	0	0	1517.88	276	290
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	6	14	0.01%	32.0%	AGLTHIITMDLHQK	99.7%	64.8	25	0	0	2	0	1577.85	125	138
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	6	14	0.01%	32.0%	EIQGFFSFPVDNLR	99.7%	49.3	25	49.3	4	0	0	1668.84	139	152
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	6	14	0.01%	32.0%	EKPPITVVGDVGGR	99.7%	47.9	25	47.9	1	2	0	1423.79	237	250
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	6	14	0.01%	32.0%	GQDIFIIQTIPR	99.7%	80.9	25	72.8	2	0	0	1400.79	57	68
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	6	14	0.01%	32.0%	IYVMATHGILSAEAPR	99.7%	36.1	25	34.6	0	2	0	1744.91	280	295
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	6	14	0.01%	32.0%	NATVHPGLELPLMMAK	97.1%	24.9	25	24.9	0	1	0	1753.90	221	236
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	6	14	0.01%	32.0%	NIIGVIPYFPYSK	99.7%	46.3	25	46.3	3	0	0	1510.83	91	103
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	100.0%	6	6	14	0.01%	32.0%	VFSANSTAACTELAK	99.7%	91.1	25	85.7	2	0	0	1569.76	10	24
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	11	16	30	0.03%	37.9%	AGLTHLITMDLHQK	99.7%	64.8	25	0	0	2	0	1577.85	137	150
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	11	16	30	0.03%	37.9%	EIQGFFNIPVDNLR	99.7%	65.8	25	51.8	3	0	0	1661.86	151	164
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	11	16	30	0.03%	37.9%	EKPPITVVGDVGGR	99.7%	47.9	25	47.9	1	2	0	1423.79	250	263
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	11	16	30	0.03%	37.9%	GGLVLFSANSNSSCMELSK	99.7%	113	25	106	3	0	0	2000.94	18	36
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	11	16	30	0.03%	37.9%	IFVMATHGLLSSDAPR	99.7%	77.8	25	71.9	4	4	0	1714.89	293	308
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	11	16	30	0.03%	37.9%	IHNGESMSYLFR	95.8%	23.5	25	20.7	0	1	0	1469.68	352	363
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	11	16	30	0.03%	37.9%	LLASMMCK	99.6%	39.2	25	0	2	0	0	969.46	129	136
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	11	16	30	0.03%	37.9%	SIIGVIPYFPYSK	99.2%	35.8	25	30.2	2	0	0	1483.82	103	115
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	11	16	30	0.03%	37.9%	TVDISMILSEAIR	99.7%	72	25	66.8	2	0	0	1463.78	338	350
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	11	16	30	0.03%	37.9%	VQIQESVR	99.7%	61.5	25	40.6	2	0	0	958.53	61	68
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	11	16	30	0.03%	37.9%	VQVYQEPNR	99.7%	41.4	25	34.5	2	0	0	1132.57	49	57
Phosphoribosyltransferase domain-containing protein 1	PRTFDC1	PRDC1_HUMAN	25.7	99.8%	2	2	2	0.00%	10.7%	DIGYSDIMVLCVLK	96.7%	29.9	25	25.9	1	0	0	1625.83	63	76
Phosphoribosyltransferase domain-containing protein 1	PRTFDC1	PRDC1_HUMAN	25.7	99.8%	2	2	2	0.00%	10.7%	FCADLVEHLK	99.7%	59.3	25	56.5	1	0	0	1231.61	81	90
Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform	PHKA1	KPB1_HUMAN	137.3	100.0%	2	2	2	0.00%	2.0%	AALEALDELDLFGVK	99.7%	43.8	25	31.1	1	0	0	1603.86	207	221
Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform	PHKA1	KPB1_HUMAN	137.3	100.0%	2	2	2	0.00%	2.0%	AYELEQSVVK	99.6%	39.1	25	32.7	1	0	0	1165.61	74	83
Pinin	PNN	PININ_HUMAN	81.6	99.8%	2	2	4	0.00%	3.2%	FKQESTVATER	99.7%	54.2	25	34	3	0	0	1295.66	156	166
Pinin	PNN	PININ_HUMAN	81.6	99.8%	2	2	4	0.00%	3.2%	GFSDSGGGPPAK	97.3%	30.8	25	19.5	1	0	0	1076.50	64	75
Plakophilin-1	PKP1	PKP1_HUMAN	82.9	99.9%	2	2	3	0.00%	4.2%	EVVDPEVFFNATGCLR	99.7%	66.1	25	66.1	1	0	0	1852.89	396	411
Plakophilin-1	PKP1	PKP1_HUMAN	82.9	99.9%	2	2	3	0.00%	4.2%	SPNQNVQQAAAGALR	99.7%	74.3	25	68.4	2	0	0	1524.79	298	312
Plasma membrane calcium-transporting ATPase 1	ATP2B1	AT2B1_HUMAN	138.8	100.0%	2	2	4	0.00%	2.8%	EASDIILTDDNFTSIVK	99.7%	52.8	25	52.8	2	0	0	1880.95	824	840
Plasma membrane calcium-transporting ATPase 1	ATP2B1	AT2B1_HUMAN	138.8	100.0%	2	2	4	0.00%	2.8%	YGDLLPADGILIQGNDLK	99.7%	47.3	25	26	2	0	0	1915.02	220	237
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	21	21	31	0.03%	4.7%	ALQALEELR	99.6%	39.2	25	23	2	0	0	1042.59	1671	1679
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	21	21	31	0.03%	4.7%	APVPASELLASGVLSR	99.7%	84.5	25	84.5	2	0	0	1566.89	3447	3462
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	21	21	31	0.03%	4.7%	GLLSAEVAR	97.2%	30.6	25	13.3	1	0	0	915.53	3850	3858
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	21	21	31	0.03%	4.7%	LAAEQELIR	99.3%	36.5	25	25.7	2	0	0	1042.59	1846	1854
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	21	21	31	0.03%	4.7%	LAAIGEATR	99.7%	44.5	25	29	1	0	0	901.51	1976	1984
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	21	21	31	0.03%	4.7%	LKAEATEAAR	99.7%	44.4	25	40.1	2	0	0	1059.58	2349	2358
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	21	21	31	0.03%	4.7%	LQAEEVAQQK	99.7%	45.5	25	32	2	0	0	1143.60	1783	1792
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	21	21	31	0.03%	4.7%	LQEAGILSAEELQR	99.7%	97.3	25	93.2	1	0	0	1556.83	2795	2808
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	21	21	31	0.03%	4.7%	LSVYAALQR	99.7%	44	25	35.3	1	0	0	1020.58	2847	2855
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	21	21	31	0.03%	4.7%	LTVDEAVR	99.0%	34.9	25	19.6	1	0	0	902.49	3213	3220
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	21	21	31	0.03%	4.7%	NLLDEELQR	98.0%	32	25	23.6	1	0	0	1129.58	2340	2348
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	21	21	31	0.03%	4.7%	SDEGQLSPATR	99.7%	49.2	25	36.8	2	0	0	1160.55	714	724
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	21	21	31	0.03%	4.7%	SIQEELQQLR	99.7%	54.6	25	45.1	2	0	0	1243.66	1554	1563
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	21	21	31	0.03%	4.7%	SLVPAAELLESR	99.7%	40.7	25	31.9	2	0	0	1284.72	3116	3127
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	21	21	31	0.03%	4.7%	SQVEEELFSVR	99.7%	65.6	25	57.7	1	0	0	1322.66	2361	2371
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	21	21	31	0.03%	4.7%	SSIAGLLLK	98.6%	33.6	25	21.1	1	0	0	901.57	2833	2841
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	21	21	31	0.03%	4.7%	TPVEVPVGGFK	98.7%	33.7	25	29.6	1	0	0	1129.63	3374	3384
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	21	21	31	0.03%	4.7%	VLADPSDDTK	99.2%	36.1	25	33.4	2	0	0	1060.52	2979	2988
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	21	21	31	0.03%	4.7%	VLALPEPSPAAPTLR	98.6%	33.6	25	33.6	1	0	0	1531.88	1187	1201
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	21	21	31	0.03%	4.7%	VPVDVAYQR	97.7%	31.4	25	26.7	1	0	0	1046.56	3620	3628

Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	21	21	31	0.03%	4.7%	VPVDVAYR	99.1%	35.7	25	25.4	2	0	0	918.50	2961	2968
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	9	12	22	0.02%	22.0%	ASVHTLSGHTNAVATVR	99.7%	65.6	25	65.3	2	2	0	1720.91	321	337
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	9	12	22	0.02%	22.0%	GPQNATDSYVHK	99.7%	60.1	25	53.3	2	2	0	1316.62	69	80
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	9	12	22	0.02%	22.0%	HYTFASGSPDNIK	99.7%	81	25	78.6	2	0	0	1436.68	384	396
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	9	12	22	0.02%	22.0%	LRNEYGPVLHMPTSK	99.7%	37.3	25	36.4	0	2	0	1741.91	48	62
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	9	12	22	0.02%	22.0%	LSLTGHISTVR	99.7%	44.2	25	38.8	1	0	0	1183.68	240	250
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	9	12	22	0.02%	22.0%	LWDLVAGK	99.7%	47.8	25	29.5	2	0	0	901.51	356	363
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	9	12	22	0.02%	22.0%	MPSESAAQSLAVALPLQTK	99.7%	129	25	124	4	0	0	1942.03	117	135
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	9	12	22	0.02%	22.0%	SPYLFSCGEDK	99.7%	61.2	25	61.2	2	0	0	1302.57	258	268
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	9	12	22	0.02%	22.0%	TGYNFQR	99.7%	50.5	25	35.3	1	0	0	885.42	443	449
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	16	18	41	0.04%	19.6%	AEPVEVVAPR	99.6%	39.2	25	35.9	1	0	0	1066.59	487	496
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	16	18	41	0.04%	19.6%	AMVEYEIDLQK	99.7%	67	25	61.5	2	0	0	1338.66	685	695
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	16	18	41	0.04%	19.6%	ELLIFNK	98.5%	33.1	25	21.6	1	0	0	876.52	263	269
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	16	18	41	0.04%	19.6%	GGSDDSSKDPIDVNYEK	99.7%	63.6	25	63.6	1	0	0	1825.81	780	796
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	16	18	41	0.04%	19.6%	GIYFADMVSK	99.7%	41.4	25	26.8	3	0	0	1130.56	894	903
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	16	18	41	0.04%	19.6%	HPDVEVDGFSELR	99.7%	79.2	25	64.6	2	0	0	1499.71	66	78
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	16	18	41	0.04%	19.6%	IAPPEAPVTGYMFGK	99.7%	47.6	25	43.5	2	0	0	1593.80	879	893
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	16	18	41	0.04%	19.6%	KGDEVDGVDEVAK	99.7%	84.5	25	75.6	2	0	0	1360.66	209	221
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	16	18	41	0.04%	19.6%	KPPLLNNADSVQAK	99.7%	67.1	25	65.1	3	1	0	1494.83	748	761
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	16	18	41	0.04%	19.6%	LQLLEDDKENR	99.7%	44.9	25	33.2	3	0	0	1372.71	572	582
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	16	18	41	0.04%	19.6%	MAIMVQSPMFDGK	99.7%	47.5	25	38.7	1	0	0	1454.68	35	47
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	16	18	41	0.04%	19.6%	QQVPSGESAILDR	99.7%	71.7	25	65.8	3	0	0	1399.72	270	282
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	16	18	41	0.04%	19.6%	TLGDFAAEYAK	99.7%	77	25	65.5	4	0	0	1185.58	109	119
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	16	18	41	0.04%	19.6%	TTNFAGILSQGLR	99.7%	100	25	92	4	0	0	1377.75	866	878
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	16	18	41	0.04%	19.6%	VFSATLGLVDIVK	99.7%	90.6	25	69.8	4	0	0	1361.80	552	564
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	16	18	41	0.04%	19.6%	VVSEDFLQDVSASTK	99.7%	119	25	108	4	0	0	1624.81	453	467
Poly(A) RNA polymerase, mitochondrial	MTPAP	PAPD1_HUMAN	66.2	100.0%	3	3	4	0.00%	7.7%	EQNKPDSSPLYIQNPFETSLNISK	99.3%	30.9	25	30.9	0	1	0	2749.37	465	488
Poly(A) RNA polymerase, mitochondrial	MTPAP	PAPD1_HUMAN	66.2	100.0%	3	3	4	0.00%	7.7%	NVSQSQLQK	98.3%	32.7	25	25.6	1	0	0	1031.55	489	497
Poly(A) RNA polymerase, mitochondrial	MTPAP	PAPD1_HUMAN	66.2	100.0%	3	3	4	0.00%	7.7%	SPPILPTLDSLK	99.7%	44.7	25	44.7	2	0	0	1280.75	392	403
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	9	21	0.02%	26.4%	AITIAGVPQSVTECVK	99.7%	51.2	25	47.1	2	0	0	1672.89	145	160
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	9	21	0.02%	26.4%	ESTGAQVQVAGDMLPNSTER	99.7%	110	25	105	7	1	0	2089.98	125	144
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	9	21	0.02%	26.4%	IANPVEGSSGR	99.7%	73.6	25	68.3	2	0	0	1086.55	315	325
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	9	21	0.02%	26.4%	IITLTGPTNAIFK	99.7%	73.1	25	71.8	2	0	0	1388.82	58	70
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	9	21	0.02%	26.4%	INISEGNCPER	99.7%	51.5	25	51.1	4	0	0	1288.60	47	57
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	9	21	0.02%	26.4%	LVVPATQCGSLIGK	99.7%	43.2	25	30.1	2	0	0	1442.80	102	115
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	9	21	0.02%	26.4%	QGANINEIR	99.7%	73.8	25	65.7	1	0	0	1014.53	298	306
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	20	0.02%	23.3%	AITIAGIPQSIIECVK	99.7%	76.2	25	71.8	4	0	0	1712.96	145	160
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	20	0.02%	23.3%	ESTGAQVQVAGDMLPNSTER	99.7%	110	25	105	7	1	0	2089.98	125	144
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	20	0.02%	23.3%	IANPVEGSTDR	99.7%	61.8	25	61.8	4	0	0	1158.58	323	333
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	20	0.02%	23.3%	IITLAGPTNAIFK	99.7%	73.6	25	73.6	8	0	0	1358.80	58	70
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	20	0.02%	23.3%	INISEGNCPER	99.7%	51.5	25	51.1	4	0	0	1288.60	47	57
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	20	0.02%	23.3%	LVVPASQCGSLIGK	99.7%	76.1	25	76.1	4	0	0	1428.79	102	115
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	9	20	0.02%	22.7%	AQSSQDAVSSMNLFDLGGQYLR	99.7%	59.5	25	59.5	2	0	0	2403.12	277	298
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	9	20	0.02%	22.7%	AVTPPMPLLTPATPGGLPPAAAVAAAAATAK	99.3%	30.4	25	30.4	0	1	0	2794.55	302	332
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	9	20	0.02%	22.7%	GYGFIEYEK	99.7%	49.9	25	42.7	4	0	0	1105.52	268	276
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	9	20	0.02%	22.7%	KQESTVMVLR	99.7%	43.7	25	33.4	2	0	0	1190.66	458	467
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	9	20	0.02%	22.7%	KVVAEVYDQER	99.7%	73.8	25	73.8	2	0	0	1335.69	541	551
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	9	20	0.02%	22.7%	LGLPPLTPEQQEALQK	99.7%	45.8	25	44.1	3	0	0	1761.97	54	69
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	9	20	0.02%	22.7%	QGEEEDAEIIVK	99.7%	47.8	25	37	2	0	0	1359.66	503	514
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	9	20	0.02%	22.7%	VVAEVYDQER	99.7%	75.6	25	69.9	2	0	0	1207.60	542	551
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	9	9	20	0.02%	22.7%	VYVGSIYYELGEDTIR	99.7%	81.6	25	75.6	2	0	0	1876.93	131	146

Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	AKEFTNVYIK	99.7%	47.6	25	37	7	6	0	1212.66	187	196
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	ALDTMNFDVIK	99.7%	83.1	25	77.4	31	0	0	1282.64	68	78
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	ALYDTFSAFGNILSCK	99.7%	111	25	106	14	0	0	1806.87	114	129
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	EFSPFGTITSAK	99.7%	62.7	25	56	12	0	0	1284.65	313	324
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	EFTNVYIK	99.7%	49.4	25	34.7	4	0	0	1013.53	189	196
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	EREAELGAR	99.2%	36	25	22	2	0	0	1030.53	178	186
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	FGPALSVK	99.7%	54.8	25	15.8	9	0	0	818.48	214	221
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	FSPAGPILSIR	99.7%	70.1	25	60.5	13	0	0	1157.67	31	41
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	GFGFVCFSSPEEATK	99.7%	82.9	25	82.9	14	0	0	1662.75	334	348
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	GFGFVSFER	99.7%	64.2	25	47.5	10	0	0	1045.51	232	240
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	GYGFVHFETQEAAER	99.7%	102	25	101	6	6	0	1740.80	139	153
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	ITGMLLEIDNSELLHMLESPESLR	99.5%	31.9	25	31.9	0	1	0	2772.38	581	604
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	IVATKPLYVALAQR	99.7%	92.6	25	92.2	12	13	0	1542.94	357	370
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	KEFSPFGTITSAK	99.7%	85.1	25	82.8	8	3	0	1412.74	312	324
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	KSGVGNIFIK	99.7%	41.3	25	34.4	3	0	0	1062.63	95	104
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	LFPLIQAMHPTLAGK	99.7%	85.6	25	83.8	7	0	0	1652.92	566	580
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	LKDLFGK	97.3%	30.7	25	17	2	0	0	820.49	207	213
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	MNGMLLNDR	99.7%	61.8	25	41.7	7	0	0	1095.49	158	166
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	MNGMLLNDRK	99.7%	57.9	25	48.5	2	0	0	1191.60	158	167
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	NFGEDMDDER	99.7%	51.3	25	51.3	4	0	0	1227.46	197	206
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	NFGEDMDDERLK	99.7%	57.8	25	50.1	4	0	0	1468.64	197	208
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	NLDDGIDDER	99.7%	60.5	25	55	8	0	0	1161.50	300	309
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	NLDDGIDDERLR	99.7%	65.2	25	54.9	6	3	0	1430.69	300	311
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	QAHLTNQYMQR	99.7%	73.1	25	65.7	10	10	0	1405.66	375	385
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	RSLGYAYVNFQQPADAER	99.7%	56.7	25	51.6	1	2	0	2085.01	50	67
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	SGVGNIFIK	99.7%	75.5	25	47.8	14	0	0	934.54	96	104
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	SKVDEAVAVLQAHQAK	99.7%	123	25	118	2	6	0	1693.92	605	620
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	SLGYAYVNFQQPADAER	99.7%	112	25	112	15	0	0	1928.91	51	67
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	VANTSTQTMGPRPAAAAAAATPAVR	99.7%	42.2	25	42.2	0	2	0	2397.23	482	506
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	VDEAVAVLQAHQAK	99.7%	82.1	25	82.1	2	2	0	1478.80	607	620
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	31	46	293	0.29%	46.9%	YQGVNLYVK	99.7%	66.4	25	51.4	10	0	0	1083.58	291	299
Polyadenylate-binding protein 2	PABPN1	PABP2_HUMAN	32.7	100.0%	8	10	22	0.02%	19.0%	ELQNEVEK	99.4%	37.6	25	11.5	2	0	0	988.49	138	145
Polyadenylate-binding protein 2	PABPN1	PABP2_HUMAN	32.7	100.0%	8	10	22	0.02%	19.0%	EMEEEAEKLK	99.7%	45.7	25	31.7	2	0	0	1235.58	128	137
Polyadenylate-binding protein 2	PABPN1	PABP2_HUMAN	32.7	100.0%	8	10	22	0.02%	19.0%	GFAYIEFSDK	99.7%	61	25	46.4	2	0	0	1176.56	214	223
Polyadenylate-binding protein 2	PABPN1	PABP2_HUMAN	32.7	100.0%	8	10	22	0.02%	19.0%	GFAYIEFSDKESVR	99.7%	68.7	25	56.2	3	2	0	1647.80	214	227
Polyadenylate-binding protein 2	PABPN1	PABP2_HUMAN	32.7	100.0%	8	10	22	0.02%	19.0%	LKELQNEVEK	95.4%	28.6	25	9.97	1	0	0	1229.67	136	145
Polyadenylate-binding protein 2	PABPN1	PABP2_HUMAN	32.7	100.0%	8	10	22	0.02%	19.0%	TSLALDESLFR	99.7%	75.3	25	71.7	3	0	0	1251.66	228	238
Polyadenylate-binding protein 2	PABPN1	PABP2_HUMAN	32.7	100.0%	8	10	22	0.02%	19.0%	VREMEEEAEK	99.7%	49.7	25	40	2	0	0	1249.57	126	135
Polyadenylate-binding protein 2	PABPN1	PABP2_HUMAN	32.7	100.0%	8	10	22	0.02%	19.0%	VTILCDKFSGHPK	99.7%	62.7	25	55.9	2	3	0	1501.78	201	213
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	21	65	0.06%	38.5%	AHLTNQYMQR	99.7%	51.5	25	43.1	2	0	0	1277.61	376	385
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	21	65	0.06%	38.5%	AKEFTNVYIK	99.7%	47.6	25	37	7	6	0	1212.66	187	196
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	21	65	0.06%	38.5%	ALDTMNFDVIK	99.7%	83.1	25	77.4	31	0	0	1282.64	68	78
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	21	65	0.06%	38.5%	ALYDTFSAFGNILSCK	99.7%	111	25	106	14	0	0	1806.87	114	129
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	21	65	0.06%	38.5%	AVEEMNGKEISGK	99.7%	40.3	25	40.3	2	0	0	1407.68	247	259
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	21	65	0.06%	38.5%	EFSPFGSITSAK	99.7%	73.6	25	71.8	8	0	0	1270.63	313	324
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	21	65	0.06%	38.5%	EFTNVYIK	99.7%	49.4	25	34.7	4	0	0	1013.53	189	196
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	21	65	0.06%	38.5%	FSPAGPVLSIR	99.7%	89.5	25	81.1	13	0	0	1143.65	31	41
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	21	65	0.06%	38.5%	GFGFVCFSSPEEATK	99.7%	82.9	25	82.9	14	0	0	1662.75	334	348
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	21	65	0.06%	38.5%	GFGFVSYEK	99.7%	50.2	25	28.7	2	0	0	1033.50	232	240
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	21	65	0.06%	38.5%	GFGFVSYEKHEDANK	99.7%	36.9	25	32.5	0	2	0	1727.80	232	246
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	21	65	0.06%	38.5%	GYAFVHFETQEAADK	99.7%	74.8	25	74.8	2	2	0	1712.79	139	153

Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	21	65	0.06%	38.5%	ITGMLLEIDNSELLHMLESPESLR	99.5%	31.9	25	31.9	0	1	0	2772.38	590	613
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	21	65	0.06%	38.5%	IVGSKPLYVALAQR	99.7%	69.5	25	52	2	5	0	1514.91	357	370
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	21	65	0.06%	38.5%	KAHLTNQYMQR	99.7%	61.1	25	60.8	4	2	0	1405.70	375	385
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	21	65	0.06%	38.5%	KEFSPFGSITSAK	99.7%	60	25	52.3	2	0	0	1398.73	312	324
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	21	65	0.06%	38.5%	LFPLIQTMHSNLAGK	99.7%	73	25	65.2	4	0	0	1669.91	575	589
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	21	65	0.06%	38.5%	MNGMLLNDR	99.7%	61.8	25	41.7	7	0	0	1095.49	158	166
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	21	65	0.06%	38.5%	MNGMLLNDRK	99.7%	57.9	25	48.5	2	0	0	1191.60	158	167
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	21	65	0.06%	38.5%	NLDDTIDDEK	99.7%	72.4	25	64.9	2	0	0	1177.52	300	309
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	21	65	0.06%	38.5%	NLDDTIDDEKLR	99.7%	71.4	25	66.1	2	0	0	1446.71	300	311
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	21	65	0.06%	38.5%	RSLGYAYVNFQQPADAER	99.7%	56.7	25	51.6	1	2	0	2085.01	50	67
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	21	65	0.06%	38.5%	SGVGNVFIK	99.7%	73.4	25	33.6	2	0	0	920.52	96	104
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	21	65	0.06%	38.5%	SLGYAYVNFQQPADAER	99.7%	112	25	112	15	0	0	1928.91	51	67
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	21	65	0.06%	38.5%	VMLEDGR	99.7%	40.9	25	31.7	2	0	0	835.40	325	331
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	16	21	65	0.06%	38.5%	YQGVNLYIK	99.7%	45.9	25	33.4	5	0	0	1097.60	291	299
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	8	8	12	0.01%	25.8%	FLLYDQTK	95.0%	28.2	25	19	1	0	0	1027.55	200	207
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	8	8	12	0.01%	25.8%	GVVLFPWQAR	99.1%	35.5	25	26.1	2	0	0	1172.66	92	101
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	8	8	12	0.01%	25.8%	IFSLSGTLETVR	99.7%	93.4	25	73	2	0	0	1322.73	286	297
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	8	8	12	0.01%	25.8%	LENLDSDVVQLR	99.7%	94.2	25	89.6	2	0	0	1400.74	269	280
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	8	8	12	0.01%	25.8%	LYDRDVASAAPEK	99.7%	50.4	25	42.8	1	0	0	1434.72	102	114
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	8	8	12	0.01%	25.8%	NHPWLELSDVHR	97.5%	25.5	25	25.3	0	1	0	1502.75	224	235
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	8	8	12	0.01%	25.8%	SQTEAVTFLANHDDSR	99.7%	89.2	25	89.2	1	0	0	1790.83	150	165
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	8	8	12	0.01%	25.8%	VLETVGVFEVPK	99.7%	79.5	25	70.3	2	0	0	1316.75	61	72
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	13	17	40	0.04%	38.6%	AQAALQAVNSVQSGNLALAASAAAVDAGMAMAGQSPVLR	99.7%	38.2	25	38.2	0	1	0	3712.87	147	185
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	13	17	40	0.04%	38.6%	DYGNSPLHR	99.7%	44.8	25	35.9	2	0	0	1058.50	429	437
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	13	17	40	0.04%	38.6%	ELKTDSSPNQAR	99.7%	44.7	25	25	1	0	0	1345.67	135	146
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	13	17	40	0.04%	38.6%	GQPIYIQFSNHK	99.7%	57.2	25	47.5	3	0	0	1431.74	123	134
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	13	17	40	0.04%	38.6%	HQNVQLPR	99.7%	42.9	25	36.4	2	0	0	991.54	411	418
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	13	17	40	0.04%	38.6%	IAIPGLAGAGNSVLLVSNLNPER	99.7%	108	25	108	4	2	0	2275.28	326	348
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	13	17	40	0.04%	38.6%	KLPIDVTEGEVISLGLPFGK	99.7%	102	25	102	2	2	0	2112.20	65	84
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	13	17	40	0.04%	38.6%	LPIDVTEGEVISLGLPFGK	99.7%	99.7	25	99.7	1	0	0	1984.10	66	84
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	13	17	40	0.04%	38.6%	LSLDGQNIYNACCTLR	99.7%	131	25	131	2	0	0	1897.89	239	254
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	13	17	40	0.04%	38.6%	NFQNIFPPSATLHLSNIPPSVSEEDLK	99.7%	39.8	25	37.6	0	5	0	2994.52	445	471
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	13	17	40	0.04%	38.6%	NNQFQALLQYADPVSAQHAK	99.7%	90.3	25	90.3	2	5	0	2243.12	219	238
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	13	17	40	0.04%	38.6%	VLFSSNGGVVK	99.7%	70.5	25	61.6	2	0	0	1106.62	472	482
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	13	17	40	0.04%	38.6%	VTNLLMLK	99.7%	61.9	25	0	4	0	0	947.56	85	92
Polypyrimidine tract-binding protein 3	PTBP3	PTBP3_HUMAN	59.7	100.0%	2	2	3	0.00%	5.1%	HQAVQLPR	99.2%	36	25	31.2	2	0	0	948.54	432	439
Polypyrimidine tract-binding protein 3	PTBP3	PTBP3_HUMAN	59.7	100.0%	2	2	3	0.00%	5.1%	SQPVYIQYSNHR	99.6%	38.8	25	38.3	1	0	0	1491.73	123	134
Polypyrimidine tract-binding protein 3	PTBP3	PTBP3_HUMAN	59.7	100.0%	2	2	3	0.00%	5.1%	VTNLLMLK	99.7%	61.9	25	0	4	0	0	947.56	85	92
Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	FIP1_HUMAN	66.5	100.0%	4	4	7	0.01%	9.6%	AEFTSPPSLFK	99.7%	43.7	25	33.2	2	0	0	1223.63	255	265
Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	FIP1_HUMAN	66.5	100.0%	4	4	7	0.01%	9.6%	ANENSNIQVLSER	99.7%	45.3	25	43	1	0	0	1473.73	332	344
Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	FIP1_HUMAN	66.5	100.0%	4	4	7	0.01%	9.6%	MGLEVIPVTSTTNK	99.7%	69.7	25	64.2	2	0	0	1489.79	197	210
Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	FIP1_HUMAN	66.5	100.0%	4	4	7	0.01%	9.6%	TGAPQYGSYGTAPVNLNIK	99.7%	87.4	25	85.6	2	0	0	1950.99	105	123
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	4	6	15	0.01%	40.8%	GTAYVVYEDIFDAK	99.7%	62.8	25	56.7	4	0	0	1590.77	58	71
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	4	6	15	0.01%	40.8%	ITAEEMYDIFGK	99.7%	96.5	25	81.5	6	0	0	1432.67	30	41
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	4	6	15	0.01%	40.8%	NACDHLSGFNVCNR	99.7%	55	25	55	2	2	0	1663.71	72	85
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	4	6	15	0.01%	40.8%	YLVVLYYNANR	99.7%	41.9	25	34.1	1	0	0	1387.74	86	96
Pre-mRNA-processing factor 17	CDC40	PRP17_HUMAN	65.5	100.0%	2	2	3	0.00%	5.4%	SGEIVQEYDR	99.7%	61.1	25	53.4	2	0	0	1195.56	407	416
Pre-mRNA-processing factor 17	CDC40	PRP17_HUMAN	65.5	100.0%	2	2	3	0.00%	5.4%	TFATYGYALDPSLDNHQVSAK	99.7%	44	25	43.1	0	1	0	2298.10	131	151
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	13	17	33	0.03%	39.5%	ALQDEWDAVMLHSFTLR	99.7%	82.7	25	76	2	1	0	2032.00	77	93
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	13	17	33	0.03%	39.5%	ATVLTTER	99.7%	50.4	25	37.8	2	0	0	890.49	180	187
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	13	17	33	0.03%	39.5%	FIASTGMDR	99.7%	68.6	25	55.2	4	0	0	997.48	489	497

Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	13	17	33	0.03%	39.5%	ILTGGADKNVVVFDK	99.7%	82.2	25	80	2	2	0	1575.87	237	251
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	13	17	33	0.03%	39.5%	IWDLKER	97.6%	31.2	25	15.1	2	0	0	959.53	376	382
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	13	17	33	0.03%	39.5%	IWSVPNASCVQVVR	99.7%	87.3	25	79.1	2	0	0	1614.84	290	303
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	13	17	33	0.03%	39.5%	QELSHALYQHDAACR	99.7%	64.8	25	63.6	0	2	0	1798.83	101	115
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	13	17	33	0.03%	39.5%	SSEQILATLK	99.7%	66.4	25	36.4	2	0	0	1089.62	252	261
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	13	17	33	0.03%	39.5%	TLQLDNNFEVK	99.7%	64.2	25	53.1	2	0	0	1320.68	429	439
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	13	17	33	0.03%	39.5%	TVPEELVKPEELSK	99.7%	76.1	25	69.1	2	0	0	1597.87	193	206
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	13	17	33	0.03%	39.5%	VTDETSGCSLTCAQFHPDGLIFGTGTMDSQIK	99.7%	69.1	25	69.1	0	2	0	3473.57	344	375
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	13	17	33	0.03%	39.5%	VTSVVFHPSQDLVFSASPDATIR	99.7%	46.4	25	46.4	0	2	0	2473.27	267	289
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	13	17	33	0.03%	39.5%	YIAENGTDPINNQPLSEEQLIDIK	99.7%	81.2	25	81.2	2	2	0	2714.35	33	56
Pre-mRNA-processing factor 40 homolog A	PRPF40A	PR40A_HUMAN	108.8	100.0%	5	5	8	0.01%	7.2%	ELEDLEGYQNTIVAGSLITK	99.7%	99.9	25	99.9	2	0	0	2193.13	214	233
Pre-mRNA-processing factor 40 homolog A	PRPF40A	PR40A_HUMAN	108.8	100.0%	5	5	8	0.01%	7.2%	EPAFEDITLESER	99.7%	67.8	25	63.5	2	0	0	1535.72	777	789
Pre-mRNA-processing factor 40 homolog A	PRPF40A	PR40A_HUMAN	108.8	100.0%	5	5	8	0.01%	7.2%	FTNMLGQPGSTALDLFK	99.7%	64.7	25	64.1	2	0	0	1839.93	646	662
Pre-mRNA-processing factor 40 homolog A	PRPF40A	PR40A_HUMAN	108.8	100.0%	5	5	8	0.01%	7.2%	LAFNSLLEK	98.0%	31.9	25	25.1	1	0	0	1034.59	719	727
Pre-mRNA-processing factor 40 homolog A	PRPF40A	PR40A_HUMAN	108.8	100.0%	5	5	8	0.01%	7.2%	STTLDAGNIK	99.6%	39.9	25	26.3	1	0	0	1019.54	709	718
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	27.0%	AAELETDIR	99.7%	47	25	20.8	1	0	0	1017.52	379	387
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	27.0%	AAQDLCEEALR	99.3%	36.6	25	30.3	1	0	0	1275.60	693	703
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	27.0%	AAVELEEPEDAR	99.7%	60.4	25	52.5	2	0	0	1328.63	409	420
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	27.0%	AEVLWLMGAK	99.7%	60.8	25	52.9	2	0	0	1117.61	607	616
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	27.0%	AGSVATCQAVMR	99.7%	48.3	25	38.9	4	0	0	1250.60	516	527
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	27.0%	AIYAYALQVFPSK	96.1%	29.3	25	19.7	1	0	0	1470.80	561	573
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	27.0%	AVIGIGIEEEDRK	99.7%	75.7	25	75.7	2	0	0	1428.77	528	540
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	27.0%	AVVAQAVR	99.2%	36	25	29.7	2	0	0	813.49	360	367
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	27.0%	ESLEALLQR	99.7%	56.4	25	38	2	0	0	1058.58	591	599
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	27.0%	ETNPHHPPAWIASAR	99.7%	47.6	25	47.6	0	1	0	1683.84	303	317
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	27.0%	FELQHGTEEQQEEVR	99.2%	29.9	25	29.9	0	1	0	1858.86	884	898
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	27.0%	HGELWCAVSK	99.7%	48.1	25	38.3	2	0	0	1186.57	908	917
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	27.0%	HIWITAAK	99.5%	38	25	23.6	1	0	0	939.54	465	472
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	27.0%	HLQTGENHTSVDPR	99.4%	37.4	25	35.6	1	0	0	1590.76	190	203
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	27.0%	HYEDFPK	99.0%	35.1	25	28.6	2	0	0	935.43	704	710
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	27.0%	IDSDLGDAWAFFYK	99.7%	95.9	25	95.9	2	0	0	1647.77	870	883
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	27.0%	IQQQFSDLKR	99.7%	35.2	25	29.9	1	2	0	1262.69	138	147
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	27.0%	LESENDEYER	99.7%	55.9	25	55.9	2	0	0	1283.54	651	660
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	27.0%	LETYENAR	95.0%	28.3	25	9.79	1	0	0	995.48	443	450
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	27.0%	LEWVQDNIR	99.7%	47.4	25	32	2	0	0	1172.61	684	692
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	27.0%	LSQVSDSVSGQTVVDPK	99.7%	125	25	114	2	0	0	1745.89	255	271
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	27.0%	NPGLWLESVR	99.7%	49.1	25	44.8	2	0	0	1170.63	776	785
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	23	25	41	0.04%	27.0%	WLAGDVPAAR	99.7%	41.1	25	41.1	2	0	0	1055.56	619	628
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	ADWWTNTAHYNR	99.7%	52.4	25	52.4	1	0	0	1534.68	747	758
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	AISAANLHLR	99.7%	57.2	25	46	2	0	0	1065.62	2077	2086
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	ALDIPLVK	99.7%	41.7	25	30	2	0	0	868.55	421	428
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	ALNMAIPGGPK	98.9%	34.7	25	25	2	0	0	1084.58	268	278
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	ANPALYVLR	99.7%	45.7	25	43.4	2	0	0	1016.59	1736	1744
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	AQIAGYLYGVSPPDNPQVK	99.7%	72	25	68.3	2	0	0	2017.04	2122	2140
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	AVFWDIK	99.7%	43.2	25	26.6	2	0	0	878.48	1152	1158
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	DGVWNLQNEVTK	99.7%	61.7	25	46.7	1	0	0	1402.70	1211	1222
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	DINLQDEDWNEFNDINK	99.7%	104	25	104	2	0	0	2121.94	285	301
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	DLILADYGKK	99.7%	44	25	27.8	2	0	0	1135.64	1985	1994
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	DNPNLLFNMCGFECR	99.7%	66.2	25	66.2	4	0	0	1902.79	1181	1195
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	EAVVNTQELLDLLVK	99.7%	85.6	25	78.6	2	0	0	1683.95	1276	1290
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	EELGLIEQAYDNPHEALSR	99.7%	62.6	25	62.6	0	1	0	2184.06	862	880

Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	EQSQLTATQTR	99.7%	62.6	25	51.5	2	0	0	1262.63	2035	2045
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	FGDLILK	99.7%	45.4	25	27.5	2	0	0	805.48	1902	1908
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	FICISDLR	99.7%	59.7	25	46.9	2	0	0	1023.53	2114	2121
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	FNTGPVGK	99.4%	37.1	25	17.2	2	0	0	819.44	616	623
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	FPPVVFYTPK	99.7%	52.6	25	52.5	5	0	0	1194.66	1311	1320
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	FSPIPFPPLSYK	99.5%	38.2	25	38.2	2	0	0	1392.76	822	833
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	GITPLLER	99.7%	41.4	25	30.9	1	0	0	898.54	643	650
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	GSELQLPFQACLK	99.7%	67.7	25	53.6	2	0	0	1490.77	1886	1898
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	GTYFPTWEGLFWEK	99.7%	40.3	25	40.3	1	0	0	1760.83	1492	1505
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	GYLPSHYER	99.3%	36.4	25	36.4	2	0	0	1121.54	2250	2258
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	HGDEIITSTTSNYETQTFSSK	99.7%	52.7	25	52.7	0	2	0	2346.07	2050	2070
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	IDLTLLNR	99.7%	58.4	25	37.3	2	0	0	957.57	988	995
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	IIHTSVWAGQK	99.7%	50.5	25	43.2	2	0	0	1239.68	1821	1831
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	IMADNPSWDGEK	99.7%	73.4	25	73.4	4	0	0	1378.59	2199	2210
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	ISLIQIFR	99.7%	71.8	25	68.2	3	0	0	989.61	1571	1578
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	LIVDHNIADYMTAK	99.7%	64.2	25	64.2	4	1	0	1619.81	999	1012
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	LKEAYSVK	97.8%	31.5	25	15.9	2	0	0	937.54	846	853
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	LLILALER	99.7%	64.3	25	63.2	4	0	0	940.62	838	845
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	LTLEDLEDSWDR	99.7%	74.7	25	71.7	2	0	0	1491.70	1403	1414
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	LVVDSHVQYR	99.7%	66.9	25	59.5	2	0	0	1215.65	556	565
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	MNSSCADILLFASYK	99.7%	42.1	25	41.8	1	0	0	1719.81	1622	1636
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	NNVNVASLTQSEIR	99.7%	112	25	102	2	0	0	1544.80	1995	2008
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	NNVVINYK	99.7%	52.1	25	47.4	2	0	0	963.53	1013	1020
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	QILMASGSTTFTK	99.7%	62.1	25	56	4	0	0	1400.71	1246	1258
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	QQIAEIEK	99.7%	42.2	25	32.8	2	0	0	958.52	2024	2031
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	QTDVGITHFR	99.7%	65.4	25	51	2	0	0	1173.60	1345	1354
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	RALDIPLVK	99.7%	48.7	25	37.1	2	0	0	1024.65	420	428
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	SGMSHEEDQLIPNLYR	99.5%	38.5	25	38.5	1	1	0	1904.88	1355	1370
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	SLPVEEQPK	97.4%	30.8	25	23.5	1	0	0	1026.55	1851	1859
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	SVTTVQWENSFVSVYSK	99.7%	49	25	41.2	2	0	0	1960.96	1164	1180
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	TAEEVAALIR	99.7%	60.8	25	44.2	2	0	0	1072.60	1841	1850
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	TAQCFLR	99.5%	38	25	25	2	0	0	895.45	1225	1231
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	TGQLFLK	98.2%	32.3	25	22.7	2	0	0	806.48	1814	1820
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	TIIITCSFTPGSCTLTAYK	99.7%	88.2	25	88.2	2	0	0	2134.06	2211	2229
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	TISSYTAFSR	99.7%	71.3	25	66	2	0	0	1132.56	1926	1935
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	TNHIYVSSDDIK	98.9%	34.4	25	25.2	1	0	0	1391.68	2087	2098
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	TSYEEFTHK	98.7%	33.8	25	33.8	2	0	0	1141.52	1202	1210
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	VPGLPTPIENMILR	99.7%	53.8	25	53.8	4	0	0	1565.87	728	741
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	VQMLLSDR	99.7%	55	25	43	2	0	0	961.51	2259	2266
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	VWAEYALKR	98.8%	34	25	27.9	1	0	0	1135.63	1385	1393
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	WLGNLLAR	97.2%	30.6	25	6.05	2	0	0	942.55	651	658
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	WNVSRPSLLADSK	99.7%	47.9	25	36.7	1	2	0	1472.79	1637	1649
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	WQFTLPMMSTLYR	99.7%	44.2	25	44.2	2	0	0	1705.81	228	240
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	YIQPWESEFIDSQR	99.7%	65.1	25	62.6	2	0	0	1797.84	1371	1384
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	YLTEHPDPNNENIVGYNNK	99.7%	36.3	25	36.3	0	2	0	2231.04	1113	1131
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	YLTEHPDPNNENIVGYNNKK	99.7%	36.2	25	36.2	0	1	0	2359.13	1113	1132
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	60	68	128	0.13%	28.6%	YYVLNALK	98.7%	34	25	25.1	2	0	0	983.56	453	460
Pre-mRNA-splicing factor CWC22 homolog	CWC22	CWC22_HUMAN	105.5	100.0%	3	3	4	0.00%	4.0%	LSEETTTSSSR	99.7%	55.8	25	48.2	2	0	0	1197.56	570	580
Pre-mRNA-splicing factor CWC22 homolog	CWC22	CWC22_HUMAN	105.5	100.0%	3	3	4	0.00%	4.0%	SSVAQIKPSSGHDR	99.7%	34	25	32.5	0	1	0	1468.75	3	16
Pre-mRNA-splicing factor CWC22 homolog	CWC22	CWC22_HUMAN	105.5	100.0%	3	3	4	0.00%	4.0%	YTSDKDVPSER	99.7%	49.9	25	43.6	1	0	0	1296.61	784	794
Pre-mRNA-splicing factor ISY1 homolog	ISY1	ISY1_HUMAN	33.0	100.0%	3	3	4	0.00%	13.3%	IKELGGPDYGK	99.0%	35.2	25	35	1	0	0	1176.63	91	101

Pre-mRNA-splicing factor ISY1 homolog	ISY1	ISY1_HUMAN	33.0	100.0%	3	3	4	0.00%	13.3%	VAQIQNAGLGEFR	99.7%	73.1	25	67.7	2	0	0	1402.74	57	69
Pre-mRNA-splicing factor ISY1 homolog	ISY1	ISY1_HUMAN	33.0	100.0%	3	3	4	0.00%	13.3%	YASETLQAQSEEAR	99.7%	82.7	25	80.1	1	0	0	1582.73	267	280
Pre-mRNA-splicing factor RBM22	RBM22	RBM22_HUMAN	46.9	100.0%	3	3	4	0.00%	7.4%	ATSTSDMLLK	99.1%	35.4	25	23.7	2	0	0	1066.55	140	149
Pre-mRNA-splicing factor RBM22	RBM22	RBM22_HUMAN	46.9	100.0%	3	3	4	0.00%	7.4%	NHFYQFGEIR	99.7%	41.9	25	41	1	0	0	1310.63	250	259
Pre-mRNA-splicing factor RBM22	RBM22	RBM22_HUMAN	46.9	100.0%	3	3	4	0.00%	7.4%	YYGINDPVADK	99.7%	48.7	25	38.6	1	0	0	1254.60	202	212
Pre-mRNA-splicing factor SPF27	BCAS2	SPF27_HUMAN	26.1	100.0%	6	6	11	0.01%	26.2%	EAAAALVEEETR	99.7%	74.7	25	57.8	2	0	0	1288.64	30	41
Pre-mRNA-splicing factor SPF27	BCAS2	SPF27_HUMAN	26.1	100.0%	6	6	11	0.01%	26.2%	EAAAALVEEETRR	97.2%	30.5	25	25	2	0	0	1444.74	30	42
Pre-mRNA-splicing factor SPF27	BCAS2	SPF27_HUMAN	26.1	100.0%	6	6	11	0.01%	26.2%	EMESNWVSLVSK	99.7%	69	25	63	2	0	0	1408.68	180	191
Pre-mRNA-splicing factor SPF27	BCAS2	SPF27_HUMAN	26.1	100.0%	6	6	11	0.01%	26.2%	QPIELLSMK	94.6%	28	25	24.7	1	0	0	1058.59	77	85
Pre-mRNA-splicing factor SPF27	BCAS2	SPF27_HUMAN	26.1	100.0%	6	6	11	0.01%	26.2%	RYELPAPSSGQK	99.7%	73.8	25	70.1	2	0	0	1332.69	86	97
Pre-mRNA-splicing factor SPF27	BCAS2	SPF27_HUMAN	26.1	100.0%	6	6	11	0.01%	26.2%	TIVQLENEIYQIK	99.7%	87.8	25	68.1	2	0	0	1590.87	198	210
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	15	16	27	0.03%	20.0%	AEQLAAEAER	99.7%	64.2	25	54.8	2	0	0	1087.54	776	785
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	15	16	27	0.03%	20.0%	AEQLAAEAERDQPLR	99.7%	56.5	25	54.3	2	1	0	1696.86	776	790
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	15	16	27	0.03%	20.0%	AIEVLSDEHAR	99.7%	53.7	25	51.5	2	0	0	1239.63	655	665
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	15	16	27	0.03%	20.0%	ALPITQHSR	96.1%	29.3	25	27.5	2	0	0	1022.57	139	147
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	15	16	27	0.03%	20.0%	AVEPAQQYDMFNIYIK	99.7%	64.9	25	60.7	1	0	0	1929.94	622	637
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	15	16	27	0.03%	20.0%	DLFEQALDGCPPK	99.7%	45.1	25	40	1	0	0	1489.70	578	590
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	15	16	27	0.03%	20.0%	EIINTYTEAVQTVDPFK	99.7%	100	25	100	2	0	0	1968.00	373	389
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	15	16	27	0.03%	20.0%	HENYDEALR	99.6%	39.7	25	39.7	2	0	0	1146.52	446	454
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	15	16	27	0.03%	20.0%	LEQQSVPAAVFGSLKED	99.7%	68	25	65.2	2	0	0	1817.93	839	855
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	15	16	27	0.03%	20.0%	LNQLYER	99.7%	41.7	25	32	2	0	0	935.49	53	59
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	15	16	27	0.03%	20.0%	LSPESAEEYIEYLK	99.7%	77	25	74.3	2	0	0	1670.82	175	188
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	15	16	27	0.03%	20.0%	RPLLLNSVLLR	95.3%	28.5	25	21.9	1	0	0	1293.84	341	351
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	15	16	27	0.03%	20.0%	SHPLPETAVR	97.2%	30.5	25	15.6	1	0	0	1106.60	158	167
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	15	16	27	0.03%	20.0%	SSDRLDEAAQR	99.1%	35.8	25	30.6	2	0	0	1247.60	189	199
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	15	16	27	0.03%	20.0%	VQSLNVDAIIR	99.7%	58	25	29.5	2	0	0	1227.71	235	245
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	5	5	7	0.01%	9.5%	DLSIEEYIR	99.7%	41.2	25	31.7	1	0	0	1137.58	246	254
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	5	5	7	0.01%	9.5%	DSPPEVAGAR	95.1%	28.4	25	20.7	1	0	0	998.49	543	552
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	5	5	7	0.01%	9.5%	IVVEFSSPNVAK	99.7%	49.1	25	37.8	1	0	0	1289.71	127	138
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	5	5	7	0.01%	9.5%	TVLQQVIEDGSK	99.7%	54.7	25	50.4	2	0	0	1316.71	100	111
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	5	5	7	0.01%	9.5%	VGLAALIIQDFK	99.7%	49.5	25	49.5	2	0	0	1287.77	427	438
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	15	16	28	0.03%	33.7%	APILIATDVASR	99.7%	87.8	25	87.8	6	0	0	1226.71	469	480
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	15	16	28	0.03%	33.7%	APLPDLYPFGTMR	99.4%	37.4	25	37.4	2	0	0	1477.75	69	81
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	15	16	28	0.03%	33.7%	DMVGIAQTGSGK	99.7%	70.9	25	64.4	2	0	0	1179.57	210	221
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	15	16	28	0.03%	33.7%	ELAQQVQQVADDYGK	99.7%	99.8	25	98.8	2	0	0	1691.82	255	269
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	15	16	28	0.03%	33.7%	FVINYDYPNSSEDYVHR	99.5%	31.9	25	22.8	0	2	0	2117.96	489	505
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	15	16	28	0.03%	33.7%	GDGPICLVLAPTR	99.7%	55.7	25	53.6	2	0	0	1368.73	242	254
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	15	16	28	0.03%	33.7%	GLDVEDVK	99.7%	44.7	25	36.5	2	0	0	874.45	481	488
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	15	16	28	0.03%	33.7%	GTAYTFFTPGNLK	99.7%	51.8	25	46.1	2	0	0	1416.72	516	528
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	15	16	28	0.03%	33.7%	GVEICIATPGR	99.7%	58.9	25	38.5	3	0	0	1172.61	294	304
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	15	16	28	0.03%	33.7%	KIVDQIRPDR	95.0%	28.3	25	16.1	1	0	0	1239.72	341	350
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	15	16	28	0.03%	33.7%	LIDFLESGK	99.7%	60.6	25	49.1	2	0	0	1021.56	305	313
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	15	16	28	0.03%	33.7%	LMQLVDHR	99.3%	36.8	25	20.2	2	0	0	1027.54	548	555
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	15	16	28	0.03%	33.7%	LTPYEVDELRR	96.7%	30	25	21	1	0	0	1390.73	144	154
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	15	16	28	0.03%	33.7%	MLDMGFEPQIR	99.7%	71.9	25	41.9	8	0	0	1352.63	330	340
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	15	16	28	0.03%	33.7%	NFYVEHPEVAR	99.7%	49.6	25	44.9	2	0	0	1360.66	133	143
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	15	16	28	0.03%	33.7%	QLAEDFLR	99.7%	61.6	25	32	2	0	0	991.52	365	372
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	15	16	28	0.03%	33.7%	QTLMWSATWPK	99.7%	45.4	25	42.8	2	0	0	1348.67	351	361
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	15	16	28	0.03%	33.7%	SSQSSSQQFSGIGR	99.7%	114	25	107	2	0	0	1455.68	671	684
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	15	16	28	0.03%	33.7%	STCIYGGAPK	99.7%	61.1	25	55.9	4	0	0	1053.50	275	284
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	15	16	28	0.03%	33.7%	TIIFVETK	97.2%	30.6	25	30.6	1	0	0	950.56	421	428

Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	15	16	28	0.03%	33.7%	TIIFVETKR	98.0%	32	25	32	2	0	0	1106.66	421	429
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	15	16	28	0.03%	33.7%	VLEEANQAINPK	99.7%	73.7	25	64.4	3	0	0	1325.71	536	547
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	15	16	28	0.03%	33.7%	WDLSELPK	96.6%	29.8	25	18	1	0	0	987.51	122	129
Probable ATP-dependent RNA helicase DDX20	DDX20	DDX20_HUMAN	92.2	100.0%	3	3	4	0.00%	5.5%	AAVHTYGIASVPNQPLKK	99.4%	31	25	31	0	1	0	1894.05	457	474
Probable ATP-dependent RNA helicase DDX20	DDX20	DDX20_HUMAN	92.2	100.0%	3	3	4	0.00%	5.5%	EALPVSLPQIPCLSSFK	99.1%	35.3	25	35.3	2	0	0	1886.01	566	582
Probable ATP-dependent RNA helicase DDX20	DDX20	DDX20_HUMAN	92.2	100.0%	3	3	4	0.00%	5.5%	VLISTDLTSR	99.5%	38.6	25	33.9	1	0	0	1104.63	362	371
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	100.0%	10	10	13	0.01%	12.6%	AQPLSLEELLAK	99.7%	67.4	25	65.4	1	0	0	1311.75	139	150
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	100.0%	10	10	13	0.01%	12.6%	DIIGVAETGSGK	99.7%	49.8	25	46	2	0	0	1146.60	430	441
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	100.0%	10	10	13	0.01%	12.6%	EDSAVFYELK	98.7%	33.7	25	30.9	1	0	0	1200.58	771	780
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	100.0%	10	10	13	0.01%	12.6%	ELAQQIEEETIK	99.7%	55.8	25	55.8	1	0	0	1430.74	479	490
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	100.0%	10	10	13	0.01%	12.6%	GFIAGIDLK	99.7%	51	25	32.6	1	0	0	933.54	302	310
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	100.0%	10	10	13	0.01%	12.6%	HQVQLLGR	99.7%	40.7	25	40.7	1	0	0	950.55	294	301
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	100.0%	10	10	13	0.01%	12.6%	IFREDYSITTK	98.1%	26.5	25	20.7	0	1	0	1372.71	372	382
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	100.0%	10	10	13	0.01%	12.6%	NIEDYIHR	95.6%	28.8	25	18.1	2	0	0	1059.52	744	751
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	100.0%	10	10	13	0.01%	12.6%	QAIPIGLQNR	99.2%	36	25	27.5	1	0	0	1109.64	420	429
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	100.0%	10	10	13	0.01%	12.6%	TLEEKEQEEAR	99.7%	44	25	43	2	0	0	1361.65	329	339
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	6	6	8	0.01%	8.2%	ALQEFDLALR	99.7%	43.1	25	34	1	0	0	1175.64	667	676
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	6	6	8	0.01%	8.2%	EAVVQEPER	99.4%	37.5	25	23.4	1	0	0	1056.53	642	650
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	6	6	8	0.01%	8.2%	ELGIQVHSVTR	99.7%	42.5	25	34.4	2	0	0	1238.69	300	310
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	6	6	8	0.01%	8.2%	IFVNSNTDVAPFLR	99.7%	75.5	25	65.3	2	0	0	1592.84	423	436
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	6	6	8	0.01%	8.2%	SADFNPDFVFTEK	97.9%	31.7	25	29.8	1	0	0	1516.70	79	91
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	6	6	8	0.01%	8.2%	VLVLVPTR	97.2%	30.6	25	30.6	1	0	0	896.59	292	299
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	5	5	8	0.01%	11.1%	GSFADLGLEPR	99.7%	48.5	25	42	2	0	0	1161.59	126	136
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	5	5	8	0.01%	11.1%	LLGQPSLDSLPIPAPR	98.9%	34.6	25	34.6	2	0	0	1673.96	190	205
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	5	5	8	0.01%	11.1%	SPDEPLPVVR	97.5%	31.1	25	31.1	1	0	0	1108.60	28	37
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	5	5	8	0.01%	11.1%	VAELVHILK	99.7%	42	25	38.3	1	0	0	1021.64	378	386
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	5	5	8	0.01%	11.1%	VASPDAVTTITSSK	99.7%	50.5	25	48	2	0	0	1376.73	344	357
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	8	8	11	0.01%	15.0%	DVLVATDVASK	99.7%	52.5	25	38	1	0	0	1117.61	484	494
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	8	8	11	0.01%	15.0%	GVEAVAIHGGKDQEER	96.1%	23.8	25	23.8	0	1	0	1694.85	456	471
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	8	8	11	0.01%	15.0%	ILESVAEGR	96.0%	29.2	25	5.57	1	0	0	973.53	116	124
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	8	8	11	0.01%	15.0%	LLQEDSSPLLR	99.7%	43	25	32.7	2	0	0	1270.70	283	293
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	8	8	11	0.01%	15.0%	SALVKPVTINVGR	99.5%	32.5	25	32.5	0	2	0	1353.82	388	400
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	8	8	11	0.01%	15.0%	SGNTGIATTFINK	99.7%	49	25	49	1	0	0	1323.69	526	538
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	8	8	11	0.01%	15.0%	TPPPVLIFAEK	96.3%	29.5	25	29.5	2	0	0	1211.70	431	441
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	8	8	11	0.01%	15.0%	YLALDEADR	96.8%	30.1	25	22.2	1	0	0	1065.52	340	348
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	5	5	13	0.01%	13.4%	IQIEAIPLALQGR	99.7%	96.3	25	87.6	2	0	0	1421.85	50	62
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	5	5	13	0.01%	13.4%	LFALVLTPTR	99.7%	43.4	25	33	2	0	0	1130.69	93	102
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	5	5	13	0.01%	13.4%	LIDHLENTK	99.7%	43.8	25	40.2	2	0	0	1082.58	153	161
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	5	5	13	0.01%	13.4%	LQQYYIFIPSK	99.7%	40.4	25	17.8	4	0	0	1399.76	238	248
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	5	5	13	0.01%	13.4%	TGAFALPILNALLETPQR	99.7%	69.2	25	69.2	3	0	0	1925.09	75	92
Probable ATP-dependent RNA helicase DDX49	DDX49	DDX49_HUMAN	54.2	99.8%	2	2	4	0.00%	4.4%	ILIATDVASR	99.7%	75.2	25	47.3	2	0	0	1058.62	301	310
Probable ATP-dependent RNA helicase DDX49	DDX49	DDX49_HUMAN	54.2	99.8%	2	2	4	0.00%	4.4%	TAAFVLPILQK	99.7%	45.4	25	45.4	2	0	0	1200.74	53	63
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	26	67	0.07%	37.8%	APILIATDVASR	99.7%	87.8	25	87.8	6	0	0	1226.71	392	403
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	26	67	0.07%	37.8%	DGWPAMGIHGDK	98.5%	33.2	25	27.3	1	0	0	1299.58	364	375
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	26	67	0.07%	37.8%	ELAQQVQQVAAEYCR	99.7%	77.5	25	77.5	3	0	0	1792.86	178	192
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	26	67	0.07%	37.8%	FVINYDYPNSSEDYIHR	99.7%	94	25	84.2	1	2	0	2131.97	412	428
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	26	67	0.07%	37.8%	GDGPICLVLAPTR	99.7%	55.7	25	53.6	2	0	0	1368.73	165	177
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	26	67	0.07%	37.8%	GLDVEDVK	99.7%	44.7	25	36.5	2	0	0	874.45	404	411
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	26	67	0.07%	37.8%	GVEICIATPGR	99.7%	58.9	25	38.5	3	0	0	1172.61	217	227
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	26	67	0.07%	37.8%	KIVDQIRPDR	95.0%	28.3	25	16.1	1	0	0	1239.72	264	273
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	26	67	0.07%	37.8%	LIDFLECGK	99.7%	64.5	25	59	4	0	0	1094.56	228	236

Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	26	67	0.07%	37.8%	LLQLVEDR	99.7%	65.1	25	42.6	4	0	0	985.57	471	478
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	26	67	0.07%	37.8%	LMEEIMSEK	99.7%	41.6	25	31.1	2	0	0	1109.52	332	340
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	26	67	0.07%	37.8%	LMEEIMSEKENK	99.7%	48.5	25	42.4	2	0	0	1480.70	332	343
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	26	67	0.07%	37.8%	MLDMGFEPQIR	99.7%	71.9	25	41.9	8	0	0	1352.63	253	263
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	26	67	0.07%	37.8%	NFYQEHPDLAR	99.7%	55.6	25	43.4	1	0	0	1389.65	57	67
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	26	67	0.07%	37.8%	QTLMWSATWPK	99.7%	45.4	25	42.8	2	0	0	1348.67	274	284
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	26	67	0.07%	37.8%	QVSDLISVLR	99.7%	79	25	63.9	5	0	0	1129.66	452	461
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	26	67	0.07%	37.8%	STCIYGGAPK	99.7%	61.1	25	55.9	4	0	0	1053.50	198	207
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	26	67	0.07%	37.8%	TAQEVETYR	99.7%	80	25	68.2	2	0	0	1096.53	69	77
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	26	67	0.07%	37.8%	TAQEVETYRR	95.8%	23.5	25	23.5	0	1	0	1252.63	69	78
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	26	67	0.07%	37.8%	TGTAYTFFTPNNIK	99.7%	89.3	25	79.2	4	0	0	1574.79	438	451
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	26	67	0.07%	37.8%	TIVFVETK	98.5%	33.3	25	29.1	2	0	0	936.54	344	351
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	26	67	0.07%	37.8%	TIVFVETKR	99.7%	55.4	25	55.1	2	0	0	1092.64	344	352
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	26	67	0.07%	37.8%	TTYLVLDEADR	99.7%	88.7	25	82.6	2	0	0	1295.65	242	252
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	26	67	0.07%	37.8%	WNLDELPK	96.4%	29.5	25	16.1	1	0	0	1014.53	46	53
Probable ATP-dependent RNA helicase DDX52	DDX52	DDX52_HUMAN	67.5	100.0%	3	3	5	0.00%	5.8%	ELASQIHR	99.2%	36.1	25	20.2	2	0	0	953.52	245	252
Probable ATP-dependent RNA helicase DDX52	DDX52	DDX52_HUMAN	67.5	100.0%	3	3	5	0.00%	5.8%	ELLASAPTGSGK	97.9%	31.8	25	31.8	2	0	0	1130.61	204	215
Probable ATP-dependent RNA helicase DDX52	DDX52	DDX52_HUMAN	67.5	100.0%	3	3	5	0.00%	5.8%	GFNPPVLVFVQSIER	99.7%	48.6	25	48.6	1	0	0	1701.93	410	424
Probable ATP-dependent RNA helicase DHX36	DHX36	DHX36_HUMAN	114.8	100.0%	3	3	4	0.00%	3.4%	ASLLDDYQLPEILR	99.7%	76.6	25	67.9	2	0	0	1645.88	620	633
Probable ATP-dependent RNA helicase DHX36	DHX36	DHX36_HUMAN	114.8	100.0%	3	3	4	0.00%	3.4%	AVICAGLYPK	99.5%	38.4	25	31.9	1	0	0	1091.59	833	842
Probable ATP-dependent RNA helicase DHX36	DHX36	DHX36_HUMAN	114.8	100.0%	3	3	4	0.00%	3.4%	LGGIAYFLSR	99.7%	79.4	25	73.2	1	0	0	1096.62	648	657
Probable ATP-dependent RNA helicase DHX37	DHX37	DHX37_HUMAN	129.5	100.0%	2	2	2	0.00%	1.6%	VEDFTQNPR	97.8%	31.6	25	27.4	1	0	0	1105.53	413	421
Probable ATP-dependent RNA helicase DHX37	DHX37	DHX37_HUMAN	129.5	100.0%	2	2	2	0.00%	1.6%	YEGNVTEETR	99.7%	57.3	25	57.3	1	0	0	1197.54	335	344
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	7	9	13	0.01%	5.7%	LAAIAVAER	99.0%	34.8	25	19.9	1	0	0	913.55	251	259
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	7	9	13	0.01%	5.7%	LASNALQEPSSFR	99.7%	74.6	25	66.7	2	0	0	1419.72	1069	1081
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	7	9	13	0.01%	5.7%	LLAPVNCPIADFLMK	99.7%	49.7	25	49	2	0	0	1717.90	782	796
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	7	9	13	0.01%	5.7%	LSQSLGLVSK	99.7%	76.1	25	61.5	2	0	0	1031.61	81	90
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	7	9	13	0.01%	5.7%	SFDALNFVTMLK	99.7%	58.6	25	50.1	3	0	0	1401.71	713	724
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	7	9	13	0.01%	5.7%	SPSPALHPPQK	95.2%	28.4	25	28.4	1	0	0	1158.63	1221	1231
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	7	9	13	0.01%	5.7%	VVLIVGETGSGK	99.7%	44.1	25	43.5	2	0	0	1158.67	211	222
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	6	6	11	0.01%	5.9%	DLEDESTPIVK	99.7%	53.4	25	36.4	1	0	0	1245.62	940	950
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	6	6	11	0.01%	5.9%	DSPTLSNSGIR	99.7%	54.5	25	49.1	2	0	0	1146.58	898	908
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	6	6	11	0.01%	5.9%	GFQEDSEIR	99.6%	39.2	25	25.6	2	0	0	1080.50	208	216
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	6	6	11	0.01%	5.9%	LGDASIAAPFTSK	99.7%	65.7	25	65.2	2	0	0	1277.67	951	963
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	6	6	11	0.01%	5.9%	SIDGSIVLPLAR	99.7%	65.7	25	57.2	2	0	0	1240.73	786	797
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	6	6	11	0.01%	5.9%	SPQENLVPCDVLLLR	99.7%	82.5	25	78.7	2	0	0	1752.93	328	342
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	7	8	13	0.01%	12.6%	DSKPHFTTVFQNSVYK	99.5%	32.3	25	32.3	0	2	0	1897.94	653	668
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	7	8	13	0.01%	12.6%	IMDLIGIQTK	99.7%	62	25	43	3	0	0	1131.64	123	132
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	7	8	13	0.01%	12.6%	LTEYPLVINTLK	99.7%	49.9	25	45.7	2	0	0	1403.81	92	103
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	7	8	13	0.01%	12.6%	TEMGLYYSYFK	99.7%	45.7	25	45.7	1	0	0	1401.64	62	72
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	7	8	13	0.01%	12.6%	TPLCNLLVK	99.7%	50.1	25	45.9	2	0	0	1057.61	644	652
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	7	8	13	0.01%	12.6%	VLEVVKE	99.7%	41.7	25	6.8	2	0	0	815.49	669	675
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	7	8	13	0.01%	12.6%	YSTKPDAVFAGAMPTMASVK	99.7%	41.7	25	38.7	0	1	0	2104.01	544	563
Probable cytosolic iron-sulfur protein assembly protein CIAO1	CIAO1	CIAO1_HUMAN	37.8	100.0%	4	4	6	0.01%	15.6%	EPGLLASCSDDGEVAFWK	99.7%	41	25	41	1	0	0	1980.90	315	332
Probable cytosolic iron-sulfur protein assembly protein CIAO1	CIAO1	CIAO1_HUMAN	37.8	100.0%	4	4	6	0.01%	15.6%	MKDSLVLLGR	99.7%	62.5	25	53.2	2	0	0	1131.66	1	10
Probable cytosolic iron-sulfur protein assembly protein CIAO1	CIAO1	CIAO1_HUMAN	37.8	100.0%	4	4	6	0.01%	15.6%	SVAWAPSGNLLATCSR	99.7%	83.8	25	79	1	0	0	1689.84	110	125
Probable cytosolic iron-sulfur protein assembly protein CIAO1	CIAO1	CIAO1_HUMAN	37.8	100.0%	4	4	6	0.01%	15.6%	SVLSEGHQR	99.7%	42.7	25	23.8	2	0	0	1012.52	54	62
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	8	8	13	0.01%	25.6%	LLHGFNAEGIHFS	99.6%	39.9	25	37.2	1	0	0	1441.72	301	313
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	8	8	13	0.01%	25.6%	LQVLVGDVLK	99.7%	59.1	25	30.8	2	0	0	1083.68	107	116
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	8	8	13	0.01%	25.6%	LSINTQLLAR	99.7%	71	25	57.6	2	0	0	1128.67	175	184
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	8	8	13	0.01%	25.6%	NNFRPPPK	97.8%	31.6	25	16.7	1	0	0	969.53	194	201

Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	8	8	13	0.01%	25.6%	NPLIINSIIDK	99.7%	64.4	25	62.9	2	0	0	1239.73	41	51
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	8	8	13	0.01%	25.6%	SMDIDDFIR	99.7%	47.5	25	37.6	1	0	0	1111.51	292	300
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	8	8	13	0.01%	25.6%	SSAVQQLLEK	99.7%	56.4	25	38	2	0	0	1102.61	244	253
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	8	8	13	0.01%	25.6%	VVACELDPR	99.7%	64.6	25	46.1	2	0	0	1058.53	81	89
Probable global transcription activator SNF2L1	SMARCA1	SMCA1_HUMAN	122.6	99.8%	2	2	3	0.00%	8.1%	ANYAVDAYFR	99.7%	54.6	25	44.9	2	0	0	1189.56	755	764
Probable global transcription activator SNF2L1	SMARCA1	SMCA1_HUMAN	122.6	99.8%	2	2	3	0.00%	8.1%	CNELQDIEK	99.7%	42.8	25	24.8	2	0	0	1148.53	906	914
Probable global transcription activator SNF2L1	SMARCA1	SMCA1_HUMAN	122.6	99.8%	2	2	3	0.00%	8.1%	DFNQFIK	96.8%	30	25	10.3	1	0	0	911.46	864	870
Probable global transcription activator SNF2L1	SMARCA1	SMCA1_HUMAN	122.6	99.8%	2	2	3	0.00%	8.1%	LDSIVIQQGR	99.7%	73.1	25	65.6	2	0	0	1128.64	642	651
Probable global transcription activator SNF2L1	SMARCA1	SMCA1_HUMAN	122.6	99.8%	2	2	3	0.00%	8.1%	LITDNTVEER	99.7%	56.6	25	40	2	0	0	1189.61	622	631
Probable global transcription activator SNF2L1	SMARCA1	SMCA1_HUMAN	122.6	99.8%	2	2	3	0.00%	8.1%	LLNILMQLR	99.7%	84.8	25	65.2	5	0	0	1113.68	449	457
Probable global transcription activator SNF2L1	SMARCA1	SMCA1_HUMAN	122.6	99.8%	2	2	3	0.00%	8.1%	NPDIPNPALAQR	96.3%	29.5	25	18.6	1	0	0	1305.69	818	829
Probable global transcription activator SNF2L1	SMARCA1	SMCA1_HUMAN	122.6	99.8%	2	2	3	0.00%	8.1%	VLIFSQMTR	99.7%	65.2	25	59.1	2	0	0	1094.60	505	513
Probable global transcription activator SNF2L1	SMARCA1	SMCA1_HUMAN	122.6	99.8%	2	2	3	0.00%	8.1%	YLVIDEAHR	99.7%	48.6	25	43.6	2	0	0	1115.58	307	315
Probable glutamate--tRNA ligase, mitochondrial	EARS2	SYEM_HUMAN	58.7	100.0%	3	3	6	0.01%	6.1%	GGPAGPYQQSQR	99.7%	51.8	25	49.2	2	0	0	1245.60	109	120
Probable glutamate--tRNA ligase, mitochondrial	EARS2	SYEM_HUMAN	58.7	100.0%	3	3	6	0.01%	6.1%	NMSQEQVAQK	99.7%	55.4	25	53.5	2	0	0	1162.55	169	178
Probable glutamate--tRNA ligase, mitochondrial	EARS2	SYEM_HUMAN	58.7	100.0%	3	3	6	0.01%	6.1%	TALYNYIFAK	99.7%	55.1	25	40.3	2	0	0	1203.64	56	65
Probable histidine--tRNA ligase, mitochondrial	HARS2	SYHM_HUMAN	56.9	99.8%	2	2	2	0.00%	4.0%	ESPTIVQGR	95.4%	28.6	25	22.1	1	0	0	986.53	160	168
Probable histidine--tRNA ligase, mitochondrial	HARS2	SYHM_HUMAN	56.9	99.8%	2	2	2	0.00%	4.0%	LIAELWDSGIK	99.7%	54.4	25	50	1	0	0	1244.69	428	438
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	9	9	16	0.02%	11.3%	AMQDALADLPEWYGIK	99.7%	45.8	25	40.2	2	0	0	1820.89	251	266
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	9	9	16	0.02%	11.3%	EEVDLTGSVPVHAK	99.7%	63.7	25	52	1	0	0	1480.76	615	628
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	9	9	16	0.02%	11.3%	FYVLSMFPYPSGK	99.7%	72.8	25	72.8	2	0	0	1535.76	84	96
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	9	9	16	0.02%	11.3%	IPVPQQVAR	98.7%	33.8	25	33.5	2	0	0	1007.60	853	861
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	9	9	16	0.02%	11.3%	LPSGQYLQR	99.7%	66.3	25	57.9	2	0	0	1061.57	606	614
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	9	9	16	0.02%	11.3%	LSSSAEFTGMTR	99.7%	71.9	25	70.4	1	0	0	1286.60	408	419
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	9	9	16	0.02%	11.3%	TALINFLVQD	99.7%	54	25	54	2	0	0	1133.62	894	903
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	9	9	16	0.02%	11.3%	TDALPGVLR	99.7%	54.3	25	45.2	2	0	0	941.54	682	690
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	9	9	16	0.02%	11.3%	VYTISDTIAR	99.7%	42.3	25	33	2	0	0	1138.61	104	113
Probable proline--tRNA ligase, mitochondrial	PARS2	SYPM_HUMAN	53.3	100.0%	3	3	4	0.00%	7.4%	DGVMDLLTPVQTV	97.7%	31.5	25	28	1	0	0	1387.71	463	475
Probable proline--tRNA ligase, mitochondrial	PARS2	SYPM_HUMAN	53.3	100.0%	3	3	4	0.00%	7.4%	FGYPFVIIAGK	99.7%	42.2	25	31.6	2	0	0	1211.68	428	438
Probable proline--tRNA ligase, mitochondrial	PARS2	SYPM_HUMAN	53.3	100.0%	3	3	4	0.00%	7.4%	QLPFLLYQVTR	99.4%	37	25	36.1	1	0	0	1377.79	176	186
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	5	5	8	0.01%	16.7%	AVDPEDDFQR	99.7%	71.7	25	69.3	2	0	0	1191.53	95	104
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	5	5	8	0.01%	16.7%	ELQDAFSR	94.7%	28	25	19.7	1	0	0	965.47	22	29
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	5	5	8	0.01%	16.7%	ESYDDVSSFR	99.7%	59.9	25	59.1	2	0	0	1204.51	263	272
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	5	5	8	0.01%	16.7%	QAQAAVLAVLPR	99.7%	45.9	25	45.9	2	0	0	1236.74	111	122
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	100.0%	5	5	8	0.01%	16.7%	RPTDYFAEMAK	98.8%	34	25	34	1	0	0	1344.63	132	142
Probable serine carboxypeptidase CPVL	CPVL	CPVL_HUMAN	54.2	100.0%	4	4	10	0.01%	10.1%	FLSLPEVR	99.7%	41.7	25	35.7	2	0	0	960.55	332	339
Probable serine carboxypeptidase CPVL	CPVL	CPVL_HUMAN	54.2	100.0%	4	4	10	0.01%	10.1%	NNDFYVTGESYAGK	99.7%	93.9	25	93.3	5	0	0	1564.69	195	208
Probable serine carboxypeptidase CPVL	CPVL	CPVL_HUMAN	54.2	100.0%	4	4	10	0.01%	10.1%	SDSEVAGYIR	99.7%	83.1	25	72.8	2	0	0	1096.53	424	433
Probable serine carboxypeptidase CPVL	CPVL	CPVL_HUMAN	54.2	100.0%	4	4	10	0.01%	10.1%	YVPAIAHLIHSLNPVR	99.7%	47.2	25	47	1	0	0	1800.03	209	224
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	5	6	11	0.01%	19.4%	ISNDPSPGYNIEQMAK	99.7%	68.2	25	67.1	3	0	0	1779.82	170	185
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	5	6	11	0.01%	19.4%	LVELPYTVK	99.0%	35.1	25	28	2	0	0	1061.62	190	198
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	5	6	11	0.01%	19.4%	PAVLGFEGSANK	99.7%	77.8	25	69.6	2	0	0	1189.62	2	13
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	5	6	11	0.01%	19.4%	TPLSDSGVTQR	99.7%	51	25	36.5	2	0	0	1160.59	313	323
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	5	6	11	0.01%	19.4%	TYVTPPGTGFLPGDTAR	99.7%	72.7	25	70.9	2	0	0	1749.88	31	47
Probable tRNA pseudouridine synthase 1	TRUB1	TRUB1_HUMAN	37.3	99.9%	2	2	3	0.00%	6.3%	GPTSAELLNR	99.7%	44.7	25	37.5	1	0	0	1057.56	79	88
Probable tRNA pseudouridine synthase 1	TRUB1	TRUB1_HUMAN	37.3	99.9%	2	2	3	0.00%	6.3%	GVLVVGIGSGTK	99.7%	61.1	25	50.2	2	0	0	1086.65	126	137
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	19	20	33	0.03%	7.9%	CLAENAVYLCDR	99.7%	54.6	25	54.6	1	0	0	1483.67	683	694
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	19	20	33	0.03%	7.9%	EIYTNLGPR	99.7%	53.4	25	48	2	0	0	1062.56	795	803
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	19	20	33	0.03%	7.9%	ELDMEPYTVAGVAK	99.7%	42.1	25	41.5	2	0	0	1522.75	1821	1834
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	19	20	33	0.03%	7.9%	ELLAFQTSEK	99.7%	48.9	25	41	2	0	0	1165.61	1436	1445
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	19	20	33	0.03%	7.9%	FLFTTGFHTK	99.7%	41.3	25	34.7	2	0	0	1198.63	2051	2060

Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	19	20	33	0.03%	7.9%	FNDYFEFPR	99.7%	55.9	25	48.2	2	0	0	1234.55	1812	1820
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	19	20	33	0.03%	7.9%	FSEYLLECPSAEVR	99.7%	72.5	25	64.7	1	0	0	1699.80	2100	2113
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	19	20	33	0.03%	7.9%	HSGDYFTLLR	99.3%	36.4	25	32.4	1	0	0	1208.61	1371	1380
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	19	20	33	0.03%	7.9%	IIEDCSNSEETVK	99.6%	39.1	25	11.5	1	0	0	1523.69	2289	2301
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	19	20	33	0.03%	7.9%	LAQQISDEASR	99.7%	77.3	25	70.5	1	0	0	1217.61	1221	1231
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	19	20	33	0.03%	7.9%	LPPVLAIQLK	98.3%	32.5	25	29.9	2	0	0	1091.72	1789	1798
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	19	20	33	0.03%	7.9%	LQYYVPR	97.7%	31.4	25	21	1	0	0	938.51	1659	1665
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	19	20	33	0.03%	7.9%	LVELCVAK	99.4%	37.4	25	13.6	1	0	0	931.53	155	162
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	19	20	33	0.03%	7.9%	LYSVVSQLIR	99.7%	71.3	25	59.1	2	0	0	1177.69	2228	2237
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	19	20	33	0.03%	7.9%	SGGLPLVLSMLTR	99.7%	41.2	25	41.2	4	0	0	1343.77	1120	1132
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	19	20	33	0.03%	7.9%	VISSVSYYTHR	99.7%	62.5	25	56.1	2	0	0	1311.67	361	371
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	19	20	33	0.03%	7.9%	VLGGSFADQK	99.7%	50.9	25	42.9	2	0	0	1021.53	1713	1722
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	19	20	33	0.03%	7.9%	VVIQSNDDIASR	99.7%	63.1	25	63.1	2	0	0	1316.68	777	788
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	19	20	33	0.03%	7.9%	YSHVQEVQER	99.7%	50	25	40.3	2	0	0	1274.61	648	657
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	100.0%	6	7	11	0.01%	10.6%	FLGSGGFIGYAPNLSK	99.7%	91.9	25	87.3	2	0	0	1627.85	151	166
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	100.0%	6	7	11	0.01%	10.6%	FLLEYIAPMTEK	99.7%	63.8	25	63.8	4	0	0	1454.76	615	626
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	100.0%	6	7	11	0.01%	10.6%	IFQNLDGALDEVVLK	96.1%	29.2	25	25.3	1	0	0	1673.91	206	220
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	100.0%	6	7	11	0.01%	10.6%	LTHYHEGLPTTR	97.2%	25	25	20.2	0	1	0	1424.73	704	715
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	100.0%	6	7	11	0.01%	10.6%	SEDYVDIVQGR	99.7%	63.6	25	56.5	2	0	0	1280.61	431	441
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	100.0%	6	7	11	0.01%	10.6%	VGVDYEGGGCR	99.7%	78.3	25	78.3	1	0	0	1168.51	671	681
Profilin-1	PFN1	PROF1_HUMAN	15.1	100.0%	4	4	6	0.01%	35.0%	DSLLQDGEFSMDLR	99.7%	73.4	25	73.4	1	0	0	1641.74	76	89
Profilin-1	PFN1	PROF1_HUMAN	15.1	100.0%	4	4	6	0.01%	35.0%	EGVHGGLINK	98.2%	32.5	25	19	1	0	0	1023.56	117	126
Profilin-1	PFN1	PROF1_HUMAN	15.1	100.0%	4	4	6	0.01%	35.0%	STGGAPTFNVTVTK	99.7%	55.7	25	50.9	2	0	0	1379.72	92	105
Profilin-1	PFN1	PROF1_HUMAN	15.1	100.0%	4	4	6	0.01%	35.0%	TDKTLVLLMGK	99.7%	46	25	46	2	0	0	1234.71	106	116
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	12	12	18	0.02%	18.7%	DTIVLLCKPEPELNAAIPSANPAK	99.7%	35.6	25	35.6	0	1	0	2561.36	518	541
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	12	12	18	0.02%	18.7%	ELPELLQR	99.7%	44.1	25	41.1	2	0	0	997.57	439	446
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	12	12	18	0.02%	18.7%	FLTALAQDGVINEEALSVTELDR	99.7%	103	25	102	2	0	0	2504.29	584	606
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	12	12	18	0.02%	18.7%	FYNELTEILVR	99.7%	71.1	25	63	2	0	0	1396.75	676	686
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	12	12	18	0.02%	18.7%	LANQAADYFGDAFK	99.7%	59.8	25	53.9	1	0	0	1530.72	216	229
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	12	12	18	0.02%	18.7%	LQHAAELIK	99.7%	42.4	25	28.6	1	0	0	1022.60	277	285
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	12	12	18	0.02%	18.7%	NIQVSHQEFSK	99.0%	35.1	25	31.9	1	0	0	1316.66	628	638
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	12	12	18	0.02%	18.7%	SLLSNLDEVKK	99.7%	50.2	25	24.7	2	0	0	1245.71	554	564
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	12	12	18	0.02%	18.7%	STPVNVPISQK	99.7%	47.6	25	47.6	1	0	0	1169.65	340	350
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	12	12	18	0.02%	18.7%	SVIEQGGIQTVDQLIK	99.7%	95.1	25	88.2	2	0	0	1727.95	423	438
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	12	12	18	0.02%	18.7%	TMQGSEVVNVLK	99.7%	46	25	36.9	1	0	0	1320.68	542	553
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	12	12	18	0.02%	18.7%	TSEVDLAKPLVK	99.7%	50.3	25	43.1	2	0	0	1299.75	12	23
Programmed cell death protein 10	PDCD10	PDC10_HUMAN	24.7	100.0%	4	4	7	0.01%	19.8%	AINVFVSANR	99.7%	69.2	25	48.1	2	0	0	1090.60	187	196
Programmed cell death protein 10	PDCD10	PDC10_HUMAN	24.7	100.0%	4	4	7	0.01%	19.8%	ENPGLTQDIIMK	97.3%	30.8	25	26.8	1	0	0	1358.70	54	65
Programmed cell death protein 10	PDCD10	PDC10_HUMAN	24.7	100.0%	4	4	7	0.01%	19.8%	IPDEINDR	99.7%	44.6	25	33	2	0	0	971.48	117	124
Programmed cell death protein 10	PDCD10	PDC10_HUMAN	24.7	100.0%	4	4	7	0.01%	19.8%	SVEVNFTESLLR	99.7%	76.5	25	74.1	2	0	0	1393.73	71	82
Programmed cell death protein 6	PDCD6	PDCD6_HUMAN	21.9	100.0%	5	7	12	0.01%	28.3%	AGVNFSEFTGVWK	99.7%	63.3	25	63.1	2	0	0	1441.71	78	90
Programmed cell death protein 6	PDCD6	PDCD6_HUMAN	21.9	100.0%	5	7	12	0.01%	28.3%	LSDQFHDILIR	99.7%	53.2	25	43.2	2	1	0	1356.73	126	136
Programmed cell death protein 6	PDCD6	PDCD6_HUMAN	21.9	100.0%	5	7	12	0.01%	28.3%	QALSGFGYR	99.7%	76.9	25	60.5	2	0	0	998.51	117	125
Programmed cell death protein 6	PDCD6	PDCD6_HUMAN	21.9	100.0%	5	7	12	0.01%	28.3%	SIISMFDRENK	99.7%	52.5	25	47.2	3	0	0	1339.67	67	77
Programmed cell death protein 6	PDCD6	PDCD6_HUMAN	21.9	100.0%	5	7	12	0.01%	28.3%	YITDWQNVFR	99.7%	59.1	25	53.2	2	0	0	1341.66	91	100
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	18	71	0.07%	56.6%	AAELIANSLATAGDGLIELR	99.7%	102	25	82.9	6	2	0	1998.09	220	239
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	18	71	0.07%	56.6%	AAIISAEGDSK	99.7%	68.3	25	62.5	5	0	0	1061.55	209	219
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	18	71	0.07%	56.6%	AVIFDRFR	96.9%	30.2	25	28.2	2	0	0	1023.57	36	43
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	18	71	0.07%	56.6%	DLQNVNITLR	99.7%	70.3	25	59.4	3	0	0	1185.66	84	93
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	18	71	0.07%	56.6%	EFTEAVEAK	99.7%	59.2	25	48.4	2	0	0	1023.50	178	186
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	18	71	0.07%	56.6%	FDAGELITQR	99.7%	84.1	25	73.8	12	0	0	1149.59	134	143

Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	18	71	0.07%	56.6%	FVVEKAEQQK	99.7%	45.5	25	32	2	0	0	1205.65	198	207
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	18	71	0.07%	56.6%	IFTSIGEDYDER	99.7%	90.1	25	88.1	9	0	0	1444.66	106	117
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	18	71	0.07%	56.6%	ILFRPVASQLPR	99.7%	52.7	25	42.9	4	6	0	1396.84	94	105
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	18	71	0.07%	56.6%	KAAIISAEGDSK	99.7%	66.6	25	59.1	2	0	0	1189.64	208	219
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	18	71	0.07%	56.6%	KLEAAEDIAYQLSR	99.7%	131	25	126	3	2	0	1606.84	240	253
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	18	71	0.07%	56.6%	LEAAEDIAYQLSR	99.7%	55.7	25	51.2	2	0	0	1478.75	241	253
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	18	71	0.07%	56.6%	NITYLPAGQSVLLQLPQ	99.0%	34.8	25	34.8	3	0	0	1855.03	256	272
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	18	71	0.07%	56.6%	QVSDDLTER	99.7%	64.6	25	46.4	2	0	0	1062.51	149	157
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	15	18	71	0.07%	56.6%	VLPSITTEILK	99.7%	67.7	25	56.4	4	0	0	1213.74	118	128
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	108	0.11%	57.5%	AQFLVEK	99.7%	44.3	25	21.1	4	0	0	834.47	210	216
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	108	0.11%	57.5%	AQVSLLIR	99.7%	53.8	25	36.4	6	0	0	899.57	158	165
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	108	0.11%	57.5%	DLQMVNISLR	99.7%	71.8	25	53.7	8	0	0	1188.64	98	107
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	108	0.11%	57.5%	ESVFTVEGGHR	99.7%	79.1	25	63.8	4	4	0	1217.59	38	48
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	108	0.11%	57.5%	EYTAAVEAK	99.7%	57.7	25	54.7	5	0	0	981.49	192	200
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	108	0.11%	57.5%	FNASQLITQR	99.7%	81.1	25	69.4	9	0	0	1177.63	148	157
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	108	0.11%	57.5%	IGGVQQDTILAEGLHFR	99.7%	106	25	106	4	8	0	1853.99	55	71
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	108	0.11%	57.5%	IPWFQYPIIYDIR	99.7%	65.3	25	57.5	4	0	0	1723.92	72	84
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	108	0.11%	57.5%	IVQAEGEAEAAK	99.7%	99.2	25	91.3	4	0	0	1215.62	225	236
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	108	0.11%	57.5%	IYLTADNLVLNLQDESFTR	99.7%	86.9	25	86.9	4	1	0	2225.15	271	289
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	108	0.11%	57.5%	LGLDYEER	99.7%	59.7	25	47	8	0	0	994.48	124	131
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	108	0.11%	57.5%	LLLGAGAVAYGVR	99.7%	89.7	25	77.3	8	0	0	1259.75	25	37
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	108	0.11%	57.5%	MLGEALSK	99.7%	45.6	25	24.6	8	0	0	864.45	237	244
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	108	0.11%	57.5%	VLPSIVNEVLK	99.7%	43	25	34.1	5	0	0	1210.74	132	142
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	23	108	0.11%	57.5%	VLSRPNAQELPSMYQR	99.7%	56.7	25	56.7	6	8	0	1888.97	108	123
Prolactin-inducible protein	PIP	PIP_HUMAN	16.6	100.0%	4	4	11	0.01%	35.6%	ELGICPDDAAVIPIK	99.5%	38.3	25	27.3	2	0	0	1610.85	119	133
Prolactin-inducible protein	PIP	PIP_HUMAN	16.6	100.0%	4	4	11	0.01%	35.6%	FYTIEILKVE	99.7%	52.9	25	44.7	5	0	0	1254.70	137	146
Prolactin-inducible protein	PIP	PIP_HUMAN	16.6	100.0%	4	4	11	0.01%	35.6%	TYLISSIPLQGAFNYK	95.0%	28.3	25	28.3	1	0	0	1814.97	70	85
Prolactin-inducible protein	PIP	PIP_HUMAN	16.6	100.0%	4	4	11	0.01%	35.6%	YTACLCDDNPK	99.7%	44.7	25	44.7	3	0	0	1356.56	86	96
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	12	16	33	0.03%	55.2%	AEDNADTLALVFEAPNQEK	99.7%	101	25	101	2	0	0	2074.99	92	110
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	12	16	33	0.03%	55.2%	ATPLSSTVTLSMSADVPLVVEYK	99.7%	86	25	86	2	2	0	2424.26	218	240
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	12	16	33	0.03%	55.2%	DLSHIGDAVVISCAK	99.7%	76.6	25	76.6	2	0	0	1584.81	150	164
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	12	16	33	0.03%	55.2%	FSASGELGNGNIK	99.7%	113	25	106	2	0	0	1293.64	169	181
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	12	16	33	0.03%	55.2%	IADMGHLK	99.7%	47.1	25	43.3	2	0	0	884.47	241	248
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	12	16	33	0.03%	55.2%	LMDLDVEQLGIPEQEYSCVVK	99.7%	68.1	25	68.1	4	0	0	2481.19	118	138
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	12	16	33	0.03%	55.2%	LVQGSILK	98.8%	34.1	25	13.7	1	0	0	857.55	6	13
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	12	16	33	0.03%	55.2%	LVQGSILKK	99.7%	56.9	25	19.8	2	0	0	985.64	6	14
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	12	16	33	0.03%	55.2%	MPSGEFAR	99.7%	43	25	33.4	4	0	0	910.41	139	146
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	12	16	33	0.03%	55.2%	NLAMGVNLTSMSK	99.7%	114	25	111	6	0	0	1365.69	65	77
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	12	16	33	0.03%	55.2%	SEGFDTYR	99.7%	49	25	41	2	0	0	974.42	54	61
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	12	16	33	0.03%	55.2%	YLNFFTK	99.2%	36.1	25	24	2	0	0	932.49	211	217
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	7	7	12	0.01%	16.3%	DPEGFVGHPVNAFK	99.7%	78.1	25	69	2	0	0	1513.74	73	86
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	7	7	12	0.01%	16.3%	FHDIISDAEIEIVK	99.7%	51.2	25	46.2	1	0	0	1628.85	340	353
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	7	7	12	0.01%	16.3%	GVAVDYLPER	99.7%	58.3	25	46	2	0	0	1118.58	277	286
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	7	7	12	0.01%	16.3%	HAACPVLVGNK	99.7%	44.1	25	36	2	0	0	1165.61	500	510
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	7	7	12	0.01%	16.3%	LLELDPEHQR	99.4%	37.6	25	37.6	2	0	0	1249.65	231	240
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	7	7	12	0.01%	16.3%	LNTEWSELENLVLK	99.7%	50.4	25	44	1	0	0	1687.89	91	104
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	7	7	12	0.01%	16.3%	LQDTYNLDTDTISK	99.7%	94.7	25	94.7	2	0	0	1626.79	137	150
Propionyl-CoA carboxylase beta chain, mitochondrial	PCCB	PCCB_HUMAN	58.2	99.8%	2	2	2	0.00%	5.2%	LLYAFAEATVPK	99.7%	63.5	25	53.4	1	0	0	1322.74	415	426
Propionyl-CoA carboxylase beta chain, mitochondrial	PCCB	PCCB_HUMAN	58.2	99.8%	2	2	2	0.00%	5.2%	SVTNEDVTQEELGGAK	99.7%	104	25	102	1	0	0	1676.80	233	248
Proteasomal ATPase-associated factor 1	PAAF1	PAAF1_HUMAN	42.2	100.0%	3	3	4	0.00%	8.4%	FLAPYTTFSR	99.7%	44.8	25	41.7	1	0	0	1202.62	80	89
Proteasomal ATPase-associated factor 1	PAAF1	PAAF1_HUMAN	42.2	100.0%	3	3	4	0.00%	8.4%	GGILDTAIVDR	99.7%	70.5	25	60	1	0	0	1129.62	177	187

Proteasomal ATPase-associated factor 1	PAAF1	PAAF1_HUMAN	42.2	100.0%	3	3	4	0.00%	8.4%	SGAPVLSLLSVR	99.7%	85.5	25	79.8	2	0	0	1198.72	321	332
Proteasomal ubiquitin receptor ADRM1	ADRM1	ADRM1_HUMAN	42.2	99.8%	2	2	4	0.00%	5.9%	SQSAAVTPSSTTSSTR	99.7%	86.2	25	86.2	2	0	0	1567.76	211	226
Proteasomal ubiquitin receptor ADRM1	ADRM1	ADRM1_HUMAN	42.2	99.8%	2	2	4	0.00%	5.9%	VPQCPSGR	99.5%	38.6	25	36.6	2	0	0	900.44	85	92
Proteasome activator complex subunit 3	PSME3	PSME3_HUMAN	29.5	100.0%	3	3	5	0.00%	16.1%	ITSEAEDLVANFFPK	99.7%	91.2	25	87.5	2	0	0	1680.85	22	36
Proteasome activator complex subunit 3	PSME3	PSME3_HUMAN	29.5	100.0%	3	3	5	0.00%	16.1%	SNQQLVDIIEK	99.7%	66	25	58.4	1	0	0	1286.70	111	121
Proteasome activator complex subunit 3	PSME3	PSME3_HUMAN	29.5	100.0%	3	3	5	0.00%	16.1%	TVESEAASYLDQISR	99.7%	93.4	25	71.8	2	0	0	1668.81	167	181
Proteasome activator complex subunit 4	PSME4	PSME4_HUMAN	211.3	100.0%	3	3	4	0.00%	1.9%	LLYELVSIPK	99.7%	45.9	25	45.9	2	0	0	1174.71	101	110
Proteasome activator complex subunit 4	PSME4	PSME4_HUMAN	211.3	100.0%	3	3	4	0.00%	1.9%	LSTSSYSQVR	99.7%	63	25	50.1	1	0	0	1127.57	974	983
Proteasome activator complex subunit 4	PSME4	PSME4_HUMAN	211.3	100.0%	3	3	4	0.00%	1.9%	SLNLPVGSSQVLVPR	99.3%	36.8	25	24.8	1	0	0	1565.90	286	300
Proteasome inhibitor PI31 subunit	PSMF1	PSMF1_HUMAN	29.8	99.8%	2	2	3	0.00%	10.0%	ALIDPSSGLPNR	99.7%	43.1	25	43.1	2	0	0	1239.67	220	231
Proteasome inhibitor PI31 subunit	PSMF1	PSMF1_HUMAN	29.8	99.8%	2	2	3	0.00%	10.0%	IVSGIITPIHEQWEK	99.7%	42.7	25	34.3	1	0	0	1749.95	134	148
Proteasome subunit alpha type-3	PSMA3	PSA3_HUMAN	28.4	100.0%	4	4	7	0.01%	16.5%	AVENSSTAIGIR	99.7%	64.5	25	44.1	2	0	0	1217.65	30	41
Proteasome subunit alpha type-3	PSMA3	PSA3_HUMAN	28.4	100.0%	4	4	7	0.01%	16.5%	CKDGVVFGVEK	99.2%	36.2	25	21	1	0	0	1237.62	42	52
Proteasome subunit alpha type-3	PSMA3	PSA3_HUMAN	28.4	100.0%	4	4	7	0.01%	16.5%	SNFGYNIPLK	99.6%	39.3	25	39.3	2	0	0	1152.60	101	110
Proteasome subunit alpha type-3	PSMA3	PSA3_HUMAN	28.4	100.0%	4	4	7	0.01%	16.5%	VFQVEYAMK	99.7%	52.3	25	43.8	2	0	0	1114.56	21	29
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	8	10	23	0.02%	34.5%	ATCIGNNSAAAVSMLK	99.7%	113	25	94.4	4	0	0	1607.79	161	176
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	8	10	23	0.02%	34.5%	LLDEVFFSEK	99.7%	73.2	25	69.3	4	0	0	1226.63	55	64
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	8	10	23	0.02%	34.5%	LNEDMACSVAGITSDANVLTNELR	99.7%	49.3	25	49.3	1	0	0	2593.22	68	91
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	8	10	23	0.02%	34.5%	LSAEKVEIATLTR	99.7%	75.6	25	63.8	2	2	0	1430.82	206	218
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	8	10	23	0.02%	34.5%	QAYTQFGGK	99.5%	38.7	25	25.5	2	0	0	999.49	119	127
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	8	10	23	0.02%	34.5%	QKEVEQLIK	99.4%	37.4	25	20.1	2	0	0	1114.65	230	238
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	8	10	23	0.02%	34.5%	TTIFSPEGR	99.7%	46.9	25	32.8	2	0	0	1007.52	9	17
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	8	10	23	0.02%	34.5%	VEIATLTR	99.7%	66.7	25	49.9	4	0	0	902.53	211	218
Proteasome subunit alpha type-5	PSMA5	PSA5_HUMAN	26.4	100.0%	4	5	9	0.01%	22.4%	AIGSASEGAQSSLQEVYHK	99.7%	100	25	100	1	0	0	1961.96	169	187
Proteasome subunit alpha type-5	PSMA5	PSA5_HUMAN	26.4	100.0%	4	5	9	0.01%	22.4%	GVNTFSPEGR	99.7%	40.6	25	28.4	2	0	0	1063.52	11	20
Proteasome subunit alpha type-5	PSMA5	PSA5_HUMAN	26.4	100.0%	4	5	9	0.01%	22.4%	ITSPLMEPSSIEK	99.7%	63.1	25	58.1	4	0	0	1431.74	54	66
Proteasome subunit alpha type-5	PSMA5	PSA5_HUMAN	26.4	100.0%	4	5	9	0.01%	22.4%	LFQVEYAIEAIK	99.7%	82.2	25	71.7	2	0	0	1423.78	21	32
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	6	7	13	0.01%	29.4%	ALLEVVQSGGK	99.7%	84.8	25	78.5	2	0	0	1100.63	194	204
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	6	7	13	0.01%	29.4%	GRDIVVLGVEK	99.7%	61.2	25	56.4	2	0	0	1184.70	37	47
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	6	7	13	0.01%	29.4%	LTVEDPVTVEYITR	99.7%	108	25	95.8	2	0	0	1634.86	96	109
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	6	7	13	0.01%	29.4%	LYQTDPSGTYHAWK	99.7%	59.5	25	53	2	0	0	1666.79	144	157
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	6	7	13	0.01%	29.4%	NIELAVMR	99.7%	44.4	25	36	3	0	0	961.51	205	212
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	6	7	13	0.01%	29.4%	NYTDEAIETDDLTIK	99.7%	137	25	136	2	0	0	1740.82	175	189
Proteasome subunit beta type-5	PSMB5	PSB5_HUMAN	28.5	100.0%	4	4	5	0.00%	14.4%	ATAGAYIASQTVK	99.7%	64.4	25	55.5	1	0	0	1280.68	79	91
Proteasome subunit beta type-5	PSMB5	PSB5_HUMAN	28.5	100.0%	4	4	5	0.00%	14.4%	ATAGAYIASQTVKK	95.4%	28.6	25	28.6	1	0	0	1408.78	79	92
Proteasome subunit beta type-5	PSMB5	PSB5_HUMAN	28.5	100.0%	4	4	5	0.00%	14.4%	DAYSGGAVNLYHVR	99.7%	46.1	25	44.1	1	0	0	1521.74	226	239
Proteasome subunit beta type-5	PSMB5	PSB5_HUMAN	28.5	100.0%	4	4	5	0.00%	14.4%	LLANMVYQYK	99.7%	49.8	25	46.4	2	0	0	1242.66	141	150
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	21	22	40	0.04%	14.1%	AGEQLAPFLPQLVPR	97.7%	31.5	25	24.1	3	0	0	1635.92	1112	1126
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	21	22	40	0.04%	14.1%	AIACVVTACSAELEK	99.7%	91	25	86	2	0	0	1621.79	1591	1605
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	21	22	40	0.04%	14.1%	ALSINTLVK	98.7%	33.8	25	20.5	2	0	0	958.59	1272	1280
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	21	22	40	0.04%	14.1%	AQGAIAMASIAK	99.7%	54.2	25	29.1	1	0	0	1147.61	1545	1556
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	21	22	40	0.04%	14.1%	ELCSLASDLSQPDLVYK	99.7%	49.2	25	47.4	2	0	0	1937.95	1068	1084
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	21	22	40	0.04%	14.1%	HSVATAADLELK	99.7%	51.6	25	46.7	2	0	0	1254.67	274	285
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	21	22	40	0.04%	14.1%	IVAISCAADILK	99.7%	72.1	25	64.7	2	0	0	1273.72	1633	1644
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	21	22	40	0.04%	14.1%	LLLQGLMDSVEAK	99.7%	41.1	25	39.9	1	0	0	1432.77	880	892
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	21	22	40	0.04%	14.1%	LLSMAYSAVGK	99.7%	95.3	25	81.8	3	0	0	1139.61	415	425
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	21	22	40	0.04%	14.1%	LMSALLSGLTDR	99.7%	80.4	25	75	2	0	0	1276.69	1401	1412
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	21	22	40	0.04%	14.1%	LSSTQEGVR	99.7%	42.7	25	26.5	2	0	0	976.51	47	55
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	21	22	40	0.04%	14.1%	MSEQQDLER	99.7%	40.5	25	33.4	2	0	0	1151.50	771	779
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	21	22	40	0.04%	14.1%	NGPLPIPSEGSGFTK	99.7%	44	25	44	2	0	0	1500.77	823	837
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	21	22	40	0.04%	14.1%	SASPFNLAEKPK	99.7%	51	25	45.7	2	0	0	1288.69	157	168

Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	21	22	40	0.04%	14.1%	SVPNQPSTNEILQAVLK	99.7%	42.3	25	38.2	1	0	0	1838.00	1606	1622
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	21	22	40	0.04%	14.1%	TEALSVIELLLK	99.7%	62.6	25	52.1	2	0	0	1328.80	1785	1796
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	21	22	40	0.04%	14.1%	TLMSSGQMAPSSSNK	99.7%	66.2	25	62.7	2	0	0	1557.69	632	646
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	21	22	40	0.04%	14.1%	TPDGQGLSTYK	99.7%	54.2	25	53.6	2	0	0	1166.57	1057	1067
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	21	22	40	0.04%	14.1%	TSCALTIHAIGR	99.7%	71.6	25	68.2	1	0	0	1299.68	1457	1468
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	21	22	40	0.04%	14.1%	VYLGDIPLK	95.7%	28.9	25	22.6	2	0	0	1017.60	305	313
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	21	22	40	0.04%	14.1%	YLLLLAAGDPR	99.7%	68.4	25	61.8	2	0	0	1201.69	517	527
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	AAILPTSIFLTNK	99.7%	107	25	107	33	0	0	1388.81	228	240
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	AAILPTSIFLTNKK	99.7%	54.2	25	53.3	3	6	0	1516.91	228	241
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	DDGVSIPGEYTSFLAPISSSK	99.7%	97.4	25	97.1	17	0	0	2170.06	459	479
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	DDIIENAPTTHTEEYSGEEK	99.7%	92.1	25	92.1	3	6	0	2278.00	165	184
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	DLNCVPEIADTLGAVAK	99.7%	115	25	113	23	2	0	1785.91	19	35
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	DPEAQFEMPYVVR	99.7%	80	25	80	3	0	0	1580.74	493	505
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	DPIKYSQYQQAIYK	99.7%	58.3	25	57.5	1	0	0	1744.89	330	343
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	DPMIDNNR	99.7%	47.9	25	43.3	4	0	0	974.44	527	534
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	DRDPEAQFEMPYVVR	99.7%	63.9	25	62.8	4	4	0	1851.87	491	505
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	DTNVQVLMVLGAGR	99.7%	108	25	92.4	2	0	0	1488.78	355	368
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	DWNTLIVGK	99.7%	60.4	25	45.3	13	0	0	1045.57	77	85
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	EFIQEPAK	99.7%	42.7	25	34.8	13	0	0	961.50	53	60
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	EGQTICVR	99.7%	41.9	25	33	14	0	0	962.47	594	601
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	GPLVNASLR	99.7%	61.2	25	49.8	8	0	0	926.54	369	377
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	IAVALEIGADLPSNHVIDR	99.7%	74.7	25	74.7	3	3	0	2003.09	202	220
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	IKLYAVEK	99.1%	35.5	25	20.3	1	0	0	963.59	386	393
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	KGFPVLSK	99.7%	55.3	25	34	12	0	0	875.54	241	248
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	LSPWIRPDSK	97.8%	31.6	25	29.4	4	0	0	1198.66	86	95
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	QGFDFLCMPVFHPR	99.7%	65.8	25	65.8	5	9	0	1750.82	36	49
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	REFIQEPAK	99.3%	36.9	25	21.4	2	0	0	1117.60	52	60
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	SDLLLSGR	99.7%	53	25	39.9	6	0	0	860.48	69	76
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	TLCDYSK	95.3%	28.5	25	24.3	1	0	0	886.40	194	200
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	TLCDYSKR	99.7%	57	25	41.4	4	0	0	1042.50	194	201
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	TWMWWHNFR	98.2%	32.3	25	30.5	1	0	0	1379.61	185	193
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	VPEEEKDTNVQVLMVLGAGR	99.7%	110	25	108	4	10	0	2184.13	349	368
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	VPLVAPEDLR	99.7%	56.7	25	51.8	14	0	0	1108.64	155	164
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	VPLVAPEDLRDDIIENAPTTHTEEYSGEEK	99.7%	108	25	108	0	3	0	3367.62	155	184
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	WLGEPIK	97.9%	31.8	25	13.1	2	0	0	842.48	221	227
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	29	44	259	0.26%	41.4%	YSQYQQAIYK	99.7%	74.4	25	74.4	16	0	0	1291.63	334	343
Protein BUD31 homolog	BUD31	BUD31_HUMAN	17.0	100.0%	5	5	10	0.01%	34.7%	DTNFGTNCICR	99.7%	61	25	59.5	2	0	0	1357.56	110	120
Protein BUD31 homolog	BUD31	BUD31_HUMAN	17.0	100.0%	5	5	10	0.01%	34.7%	IIECTHCGCR	99.7%	53.7	25	53.7	2	0	0	1305.55	131	140
Protein BUD31 homolog	BUD31	BUD31_HUMAN	17.0	100.0%	5	5	10	0.01%	34.7%	KVESLWPIFR	99.7%	54.1	25	45.8	2	0	0	1274.73	42	51
Protein BUD31 homolog	BUD31	BUD31_HUMAN	17.0	100.0%	5	5	10	0.01%	34.7%	QGYENLCCLR	99.7%	52	25	42	2	0	0	1312.58	95	104
Protein BUD31 homolog	BUD31	BUD31_HUMAN	17.0	100.0%	5	5	10	0.01%	34.7%	YIFDLFYKR	99.7%	42.6	25	35.8	2	0	0	1264.67	59	67
Protein CIP2A	KIAA1524	CIP2A_HUMAN	102.2	100.0%	3	3	4	0.00%	4.1%	ALALAQADR	99.7%	61.6	25	46.3	1	0	0	928.52	648	656
Protein CIP2A	KIAA1524	CIP2A_HUMAN	102.2	100.0%	3	3	4	0.00%	4.1%	KLESVAEEHEILTK	97.4%	25.4	25	25.4	0	1	0	1625.87	716	729
Protein CIP2A	KIAA1524	CIP2A_HUMAN	102.2	100.0%	3	3	4	0.00%	4.1%	LITPLAFALTSDNR	99.7%	94.6	25	94.6	2	0	0	1531.85	509	522
Protein CMSS1	CMSS1	CMS1_HUMAN	31.9	100.0%	4	5	8	0.01%	15.1%	ANDLTHSLSSYLK	99.7%	61.7	25	55.6	2	1	0	1448.74	125	137
Protein CMSS1	CMSS1	CMS1_HUMAN	31.9	100.0%	4	5	8	0.01%	15.1%	ECFLIQPK	95.8%	29	25	18.6	1	0	0	1034.53	54	61
Protein CMSS1	CMSS1	CMS1_HUMAN	31.9	100.0%	4	5	8	0.01%	15.1%	QGGLNLSPLK	99.7%	70.1	25	55.4	2	0	0	1026.59	222	231
Protein CMSS1	CMSS1	CMS1_HUMAN	31.9	100.0%	4	5	8	0.01%	15.1%	VVHLGVGTPGR	99.7%	69.8	25	64.3	2	0	0	1091.63	205	215
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	6	7	15	0.01%	15.5%	LLASANLEEVTMK	99.7%	108	25	99.4	4	0	0	1418.76	332	344
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	6	7	15	0.01%	15.5%	LLYNRPGTVSSLK	99.3%	36.9	25	23.4	1	0	0	1447.83	112	124
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	6	7	15	0.01%	15.5%	NVGQFSGFPFEK	99.7%	48.6	25	48.6	4	0	0	1356.66	126	137

Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	6	7	15	0.01%	15.5%	SGVNSELVK	99.7%	53.8	25	34.1	2	0	0	932.50	169	177
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	6	7	15	0.01%	15.5%	SGVNSELVKR	99.7%	57	25	45.9	2	0	0	1088.61	169	178
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	6	7	15	0.01%	15.5%	SICEVLDLER	99.7%	69	25	57.9	2	0	0	1233.61	159	168
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	6	6	8	0.01%	5.2%	DDAMAAVPAK	98.8%	34.2	25	33.5	1	0	0	1004.47	1240	1249
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	6	6	8	0.01%	5.2%	ELGEYFLFDPK	99.7%	67.1	25	67.1	2	0	0	1357.67	1117	1127
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	6	6	8	0.01%	5.2%	KLDSELTAR	96.8%	30.1	25	24.9	1	0	0	1032.57	487	495
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	6	6	8	0.01%	5.2%	LNAILFK	99.4%	37.4	25	17.2	2	0	0	818.51	937	943
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	6	6	8	0.01%	5.2%	QDLEAEVSQLTGEVAK	97.6%	31.2	25	28.6	1	0	0	1716.87	535	550
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	6	6	8	0.01%	5.2%	TAQNLSIFLGSFR	99.7%	56	25	56	1	0	0	1453.78	856	868
Protein disulfide-isomerase	P4HB	PDIA1_HUMAN	57.1	100.0%	4	4	6	0.01%	7.5%	EADDIVNWLK	99.7%	41.5	25	32.3	2	0	0	1202.61	121	130
Protein disulfide-isomerase	P4HB	PDIA1_HUMAN	57.1	100.0%	4	4	6	0.01%	7.5%	ITEFCHR	99.1%	35.7	25	31.3	2	0	0	962.45	339	345
Protein disulfide-isomerase	P4HB	PDIA1_HUMAN	57.1	100.0%	4	4	6	0.01%	7.5%	LKAEGSEIR	94.6%	28	25	14.2	1	0	0	1002.56	70	78
Protein disulfide-isomerase	P4HB	PDIA1_HUMAN	57.1	100.0%	4	4	6	0.01%	7.5%	YKPESEELTAER	99.4%	37.2	25	37.2	1	0	0	1451.70	327	338
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	11	11	17	0.02%	10.4%	ADLTALFLPR	99.7%	71	25	64.7	2	0	0	1116.64	875	884
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	11	11	17	0.02%	10.4%	AVQGAQQPSLYQIR	99.7%	64.3	25	59.3	2	0	0	1558.83	1047	1060
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	11	11	17	0.02%	10.4%	FVFLLDR	94.8%	28.1	25	26.9	1	0	0	909.52	646	652
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	11	11	17	0.02%	10.4%	GVDLSGNDFK	96.1%	29.3	25	23	1	0	0	1051.51	12	21
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	11	11	17	0.02%	10.4%	KFESLFPGK	97.2%	30.6	25	26.3	1	0	0	1052.58	1007	1015
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	11	11	17	0.02%	10.4%	LAEDILNTMFDTSYSK	99.7%	69	25	69	1	0	0	1847.87	1116	1131
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	11	11	17	0.02%	10.4%	LLQSLLDTR	99.7%	57.6	25	43.6	2	0	0	1058.62	765	773
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	11	11	17	0.02%	10.4%	NAEAVLQSPGLSGK	99.7%	62.5	25	59.6	2	0	0	1370.73	849	862
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	11	11	17	0.02%	10.4%	TGLCYLPEELAALQK	95.9%	29	25	14.9	1	0	0	1705.88	43	57
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	11	11	17	0.02%	10.4%	VGLGLGYLELPQINYK	99.7%	46.7	25	46.7	2	0	0	1776.99	731	746
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	11	11	17	0.02%	10.4%	VPECLYTLPSLR	99.7%	53.1	25	36.3	2	0	0	1447.76	238	249
Protein jagunal homolog 1	JAGN1	JAGN1_HUMAN	21.1	100.0%	4	4	8	0.01%	17.5%	AAGTDGSDFQHR	99.7%	71.2	25	66.1	2	0	0	1261.56	9	20
Protein jagunal homolog 1	JAGN1	JAGN1_HUMAN	21.1	100.0%	4	4	8	0.01%	17.5%	LLDSWFTSTQEK	99.7%	57.2	25	57.2	2	0	0	1454.72	169	180
Protein jagunal homolog 1	JAGN1	JAGN1_HUMAN	21.1	100.0%	4	4	8	0.01%	17.5%	LLDSWFTSTQEKK	98.1%	32.2	25	32.2	2	0	0	1582.81	169	181
Protein jagunal homolog 1	JAGN1	JAGN1_HUMAN	21.1	100.0%	4	4	8	0.01%	17.5%	MSVGHLR	99.0%	35	25	23.5	2	0	0	799.42	55	61
Protein kinase C delta type	PRKCD	KPCD_HUMAN	77.5	99.8%	2	2	3	0.00%	4.7%	ASTFCGTPDYIAPEILQGLK	99.6%	39.8	25	39.8	1	0	0	2181.09	505	524
Protein kinase C delta type	PRKCD	KPCD_HUMAN	77.5	99.8%	2	2	3	0.00%	4.7%	LLAEALNQVTQR	99.7%	72	25	66.7	2	0	0	1355.76	286	297
Protein KRI1 homolog	KRI1	KRI1_HUMAN	82.6	100.0%	5	5	7	0.01%	9.0%	EEAETPAEATGKPQR	99.7%	76.9	25	69.2	1	0	0	1613.78	593	607
Protein KRI1 homolog	KRI1	KRI1_HUMAN	82.6	100.0%	5	5	7	0.01%	9.0%	FEEPDSASVK	94.9%	28.2	25	19.1	1	0	0	1108.52	302	311
Protein KRI1 homolog	KRI1	KRI1_HUMAN	82.6	100.0%	5	5	7	0.01%	9.0%	LLGPTVMLGGCEFSR	99.7%	63.7	25	63.7	2	0	0	1636.82	657	671
Protein KRI1 homolog	KRI1	KRI1_HUMAN	82.6	100.0%	5	5	7	0.01%	9.0%	LQAFGLNPK	94.8%	28.1	25	13.1	1	0	0	987.56	674	682
Protein KRI1 homolog	KRI1	KRI1_HUMAN	82.6	100.0%	5	5	7	0.01%	9.0%	LQETSSQSYVEEQK	99.7%	88.5	25	83.3	2	0	0	1655.78	145	158
Protein lin-28 homolog B	LIN28B	LN28B_HUMAN	27.1	100.0%	4	4	12	0.01%	24.4%	EGSPLDIPVDVFVHQSK	98.9%	34.7	25	34.7	2	0	0	1866.96	52	68
Protein lin-28 homolog B	LIN28B	LN28B_HUMAN	27.1	100.0%	4	4	12	0.01%	24.4%	GGGEEPGKLPEPAEEESQVLR	99.7%	45.3	25	45.3	0	2	0	2208.08	9	29
Protein lin-28 homolog B	LIN28B	LN28B_HUMAN	27.1	100.0%	4	4	12	0.01%	24.4%	MGFGFISMINR	99.7%	66.7	25	63.2	4	0	0	1272.62	41	51
Protein lin-28 homolog B	LIN28B	LN28B_HUMAN	27.1	100.0%	4	4	12	0.01%	24.4%	NVAQPPASSQGR	99.6%	39.2	25	39.2	4	0	0	1211.61	168	179
Protein LSM12 homolog	LSM12	LSM12_HUMAN	21.7	99.8%	2	2	3	0.00%	16.9%	EGSALSHVR	99.7%	47.4	25	26.2	2	0	0	955.50	155	163
Protein LSM12 homolog	LSM12	LSM12_HUMAN	21.7	99.8%	2	2	3	0.00%	16.9%	LSQAYAISAGVSLEGQQLFQTIHK	99.7%	48.8	25	48.2	0	1	0	2589.37	99	122
Protein LYRIC	MTDH	LYRIC_HUMAN	63.8	100.0%	3	3	4	0.00%	6.0%	LSSQISAGEEK	99.7%	53.9	25	26.7	1	0	0	1148.58	293	303
Protein LYRIC	MTDH	LYRIC_HUMAN	63.8	100.0%	3	3	4	0.00%	6.0%	TISTSDPAEVLVK	99.7%	49.8	25	39.4	2	0	0	1359.74	492	504
Protein LYRIC	MTDH	LYRIC_HUMAN	63.8	100.0%	3	3	4	0.00%	6.0%	TVEVAEGEAVR	99.7%	62.1	25	54.4	1	0	0	1159.60	132	142
Protein mago nashi homolog 2	MAGOHB	MGN2_HUMAN	17.3	100.0%	4	5	8	0.01%	23.6%	IGSLIDVNQSK	99.7%	78.9	25	65.9	2	0	0	1173.65	106	116
Protein mago nashi homolog 2	MAGOHB	MGN2_HUMAN	17.3	100.0%	4	5	8	0.01%	23.6%	IGSLIDVNQSKDPEGLR	99.7%	35.1	25	35.1	1	1	0	1840.98	106	122
Protein mago nashi homolog 2	MAGOHB	MGN2_HUMAN	17.3	100.0%	4	5	8	0.01%	23.6%	SVMEELKR	98.6%	33.6	25	25.8	2	0	0	991.52	57	64
Protein mago nashi homolog 2	MAGOHB	MGN2_HUMAN	17.3	100.0%	4	5	8	0.01%	23.6%	VFYYLVQDLK	99.7%	60	25	49.9	2	0	0	1287.70	123	132
Protein misato homolog 1	MSTO1	MSTO1_HUMAN	61.8	100.0%	2	2	3	0.00%	4.0%	AAELLQDEYSGR	99.7%	48.8	25	48.8	2	0	0	1351.65	245	256
Protein misato homolog 1	MSTO1	MSTO1_HUMAN	61.8	100.0%	2	2	3	0.00%	4.0%	TLHGQETYTPR	99.7%	42.5	25	37.3	1	0	0	1302.64	56	66
Protein MON2 homolog	MON2	MON2_HUMAN	190.5	100.0%	2	2	4	0.00%	1.1%	AVAVESIHR	98.8%	34.1	25	17	1	0	0	981.55	353	361

Protein MON2 homolog	MON2	MON2_HUMAN	190.5	100.0%	2	2	4	0.00%	1.1%	LQLLLLNPLK	98.8%	34.2	25	34.2	3	0	0	1164.77	862	871
Protein NipSnap homolog 1	NIPSNAP1	NIPS1_HUMAN	33.3	100.0%	3	4	7	0.01%	13.0%	FSGGYPALMDCMNK	98.5%	33.3	25	33.3	2	0	0	1590.68	128	141
Protein NipSnap homolog 1	NIPSNAP1	NIPS1_HUMAN	33.3	100.0%	3	4	7	0.01%	13.0%	GWDENVYYTVPLVR	99.7%	59.6	25	59	2	0	0	1710.85	255	268
Protein NipSnap homolog 1	NIPSNAP1	NIPS1_HUMAN	33.3	100.0%	3	4	7	0.01%	13.0%	MGPNIYELR	99.7%	56	25	52.7	3	0	0	1108.55	180	188
Protein NipSnap homolog 2	GBAS	NIPS2_HUMAN	33.7	100.0%	3	3	5	0.00%	10.8%	ICQEVLPK	99.7%	41.6	25	16.6	2	0	0	986.53	92	99
Protein NipSnap homolog 2	GBAS	NIPS2_HUMAN	33.7	100.0%	3	3	5	0.00%	10.8%	SGPNIYELR	99.7%	68.3	25	59.5	2	0	0	1048.54	182	190
Protein NipSnap homolog 2	GBAS	NIPS2_HUMAN	33.7	100.0%	3	3	5	0.00%	10.8%	YEGGYPALTEVMNK	99.3%	36.5	25	36.5	1	0	0	1571.74	130	143
Protein Njmu-R1	C17orf75	NJMU_HUMAN	44.6	100.0%	3	3	4	0.00%	7.3%	AIQDTNNLKR	97.4%	30.9	25	21.6	1	0	0	1172.64	326	335
Protein Njmu-R1	C17orf75	NJMU_HUMAN	44.6	100.0%	3	3	4	0.00%	7.3%	GGNPFLFR	99.7%	45.2	25	23.3	1	0	0	907.48	309	316
Protein Njmu-R1	C17orf75	NJMU_HUMAN	44.6	100.0%	3	3	4	0.00%	7.3%	NVIAVLEEFMK	99.7%	50.9	25	45	2	0	0	1292.69	379	389
Protein pelota homolog	PELO	PELO_HUMAN	43.4	100.0%	6	7	10	0.01%	16.9%	ANEAMAIDTLLISDELFR	99.7%	46.7	25	46.7	1	0	0	2022.02	302	319
Protein pelota homolog	PELO	PELO_HUMAN	43.4	100.0%	6	7	10	0.01%	16.9%	FYEQVVQAIQR	99.7%	47.7	25	38	2	0	0	1380.73	185	195
Protein pelota homolog	PELO	PELO_HUMAN	43.4	100.0%	6	7	10	0.01%	16.9%	GTNIQENEYVK	99.7%	41.1	25	35.2	2	0	0	1294.63	85	95
Protein pelota homolog	PELO	PELO_HUMAN	43.4	100.0%	6	7	10	0.01%	16.9%	KQWDSVVLER	99.6%	39	25	32.9	1	0	0	1259.67	115	124
Protein pelota homolog	PELO	PELO_HUMAN	43.4	100.0%	6	7	10	0.01%	16.9%	KVQTESSTGSVGSNR	99.7%	71.2	25	65.9	1	1	0	1536.76	46	60
Protein pelota homolog	PELO	PELO_HUMAN	43.4	100.0%	6	7	10	0.01%	16.9%	VQTESSTGSVGSNR	99.7%	83	25	76.1	2	0	0	1408.67	47	60
Protein PRRC2A	PRRC2A	PRC2A_HUMAN	228.9	100.0%	7	8	13	0.01%	5.1%	EGTLTQVPLAPPPPGAPPSPAPAR	99.0%	29.2	25	29.2	0	1	0	2318.25	1129	1152
Protein PRRC2A	PRRC2A	PRC2A_HUMAN	228.9	100.0%	7	8	13	0.01%	5.1%	GGGTGGPNHPPAPR	99.7%	46.5	25	37.7	3	1	0	1271.62	1067	1080
Protein PRRC2A	PRRC2A	PRC2A_HUMAN	228.9	100.0%	7	8	13	0.01%	5.1%	GVGSGGQGPPPPR	99.7%	87.3	25	75.6	2	0	0	1162.60	905	917
Protein PRRC2A	PRRC2A	PRC2A_HUMAN	228.9	100.0%	7	8	13	0.01%	5.1%	LKAEPAAPPAAPSTPAPPPAVPK	99.5%	32.5	25	26.7	0	2	0	2175.22	504	526
Protein PRRC2A	PRRC2A	PRC2A_HUMAN	228.9	100.0%	7	8	13	0.01%	5.1%	QSSSEISLAVER	99.7%	46.2	25	39.2	2	0	0	1305.66	455	466
Protein PRRC2A	PRRC2A	PRC2A_HUMAN	228.9	100.0%	7	8	13	0.01%	5.1%	SDSGGSSSEPFDR	99.7%	69.1	25	49.9	1	0	0	1327.54	759	771
Protein PRRC2A	PRRC2A	PRC2A_HUMAN	228.9	100.0%	7	8	13	0.01%	5.1%	SEGSEYEEIPK	99.7%	42.1	25	30.8	1	0	0	1267.57	1089	1099
Protein QIL1	QIL1	QIL1_HUMAN	13.1	100.0%	3	3	5	0.00%	28.0%	EGWEYVK	97.2%	30.5	25	18	2	0	0	910.43	108	114
Protein QIL1	QIL1	QIL1_HUMAN	13.1	100.0%	3	3	5	0.00%	28.0%	EYSKEGWEYVK	99.1%	35.6	25	30.8	2	0	0	1417.66	104	114
Protein QIL1	QIL1	QIL1_HUMAN	13.1	100.0%	3	3	5	0.00%	28.0%	GSVAGGAVYLVYDQELLGPSDK	99.7%	90.1	25	90.1	1	0	0	2238.13	15	36
Protein RFT1 homolog	RFT1	RFT1_HUMAN	60.3	99.9%	2	2	2	0.00%	3.9%	GSQEVLGHAAR	99.7%	61.1	25	55.5	1	0	0	1124.58	2	12
Protein RFT1 homolog	RFT1	RFT1_HUMAN	60.3	99.9%	2	2	2	0.00%	3.9%	ITDLLPNITR	99.5%	37.8	25	34.9	1	0	0	1155.67	221	230
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	19	19	32	0.03%	11.9%	AIFENTLSTYPK	99.7%	53.2	25	46.2	2	0	0	1383.72	1782	1793
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	19	19	32	0.03%	11.9%	AINIGQLVDVK	99.7%	66.9	25	53.2	2	0	0	1169.69	632	642
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	19	19	32	0.03%	11.9%	EGKEEAEETNVLPK	97.6%	31.2	25	23.5	1	0	0	1572.78	1506	1519
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	19	19	32	0.03%	11.9%	FAQLEFQLGDAER	99.7%	68.9	25	62.1	1	0	0	1523.75	1767	1779
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	19	19	32	0.03%	11.9%	FYNNVQGLVPK	99.7%	50.7	25	50.6	2	0	0	1278.68	561	571
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	19	19	32	0.03%	11.9%	IPLLLTSLSFK	99.7%	43.6	25	43.6	4	0	0	1231.77	1178	1188
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	19	19	32	0.03%	11.9%	KPALVSTVEGGQDPK	99.7%	42.4	25	36.6	1	0	0	1525.82	707	721
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	19	19	32	0.03%	11.9%	LGPSVVGLAR	99.7%	75.8	25	68.3	2	0	0	968.59	1343	1352
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	19	19	32	0.03%	11.9%	LKDGVLAYAR	98.8%	34	25	25.7	2	0	0	1105.64	386	395
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	19	19	32	0.03%	11.9%	TSIIEAQYLR	99.7%	71	25	65.6	2	0	0	1193.65	437	446
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	19	19	32	0.03%	11.9%	TTEPGVTGLLLAVEGPAAK	99.7%	63.1	25	63.1	2	0	0	1824.01	982	1000
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	19	19	32	0.03%	11.9%	VFYTGQVVK	99.4%	37.4	25	31.7	1	0	0	1040.58	585	593
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	19	19	32	0.03%	11.9%	VGQYLNCIVEK	99.7%	49.7	25	44.2	1	0	0	1322.68	235	245
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	19	19	32	0.03%	11.9%	VIHLSLAPK	98.9%	34.6	25	34.6	1	0	0	977.61	1821	1829
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	19	19	32	0.03%	11.9%	VKDYGCIVK	95.0%	28.3	25	15.1	1	0	0	1081.57	552	560
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	19	19	32	0.03%	11.9%	VLCLSQSEGR	99.6%	39.4	25	32.2	2	0	0	1148.57	692	701
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	19	19	32	0.03%	11.9%	VTPNEGLTVSFPFGK	99.7%	55.9	25	50.5	2	0	0	1592.83	1240	1254
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	19	19	32	0.03%	11.9%	VVVLNCEPSKER	95.4%	28.6	25	28.6	1	0	0	1429.75	594	605
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	19	19	32	0.03%	11.9%	YHDIEPGAVVK	99.7%	50.4	25	44.4	2	0	0	1227.64	447	457
Protein SAAL1	SAAL1	SAAL1_HUMAN	53.6	100.0%	2	3	5	0.00%	5.3%	KPENSAESNTEETKR	99.7%	59.7	25	59.7	0	2	0	1719.81	369	383
Protein SAAL1	SAAL1	SAAL1_HUMAN	53.6	100.0%	2	3	5	0.00%	5.3%	VLQNMEQCQK	98.9%	34.6	25	29.5	3	0	0	1277.60	359	368
Protein SET	SET	SET_HUMAN	33.5	100.0%	4	4	7	0.01%	16.6%	EFHLNESGDPSSK	99.7%	74.1	25	65.2	2	0	0	1446.65	155	167
Protein SET	SET	SET_HUMAN	33.5	100.0%	4	4	7	0.01%	16.6%	IDFYFDENPYFENK	99.7%	65.3	25	56.8	2	0	0	1840.81	137	150

Protein SET	SET	SET_HUMAN	33.5	100.0%	4	4	7	0.01%	16.6%	LNEQASEEILK	99.7%	51.5	25	37.9	1	0	0	1273.66	58	68
Protein SET	SET	SET_HUMAN	33.5	100.0%	4	4	7	0.01%	16.6%	VEVTEFEDIK	99.7%	60.7	25	52.6	2	0	0	1208.60	123	132
Protein SON	SON	SON_HUMAN	263.8	100.0%	4	4	7	0.01%	2.1%	AGIEGPLLASDVGR	99.7%	72.7	25	70	1	0	0	1354.73	1750	1763
Protein SON	SON	SON_HUMAN	263.8	100.0%	4	4	7	0.01%	2.1%	ILDSFAAAPVPTTTLVLK	99.7%	45	25	45	2	0	0	1857.07	241	258
Protein SON	SON	SON_HUMAN	263.8	100.0%	4	4	7	0.01%	2.1%	LGQDPYR	99.7%	46.7	25	40.7	2	0	0	848.43	944	950
Protein SON	SON	SON_HUMAN	263.8	100.0%	4	4	7	0.01%	2.1%	SVESTSPEPSK	99.7%	42.9	25	32.2	2	0	0	1147.55	278	288
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	5	6	11	0.01%	8.7%	DVLLDVAYAYGK	99.7%	82.4	25	82.4	2	0	0	1326.69	293	304
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	5	6	11	0.01%	8.7%	ELQSVEQEVR	99.7%	71.7	25	59.4	1	0	0	1216.62	164	173
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	5	6	11	0.01%	8.7%	LLGSLYALGIPK	99.7%	65.3	25	65.3	2	0	0	1244.76	149	160
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	5	6	11	0.01%	8.7%	LSFHQTQVSQR	99.7%	45	25	32.3	2	0	0	1330.69	305	315
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	5	6	11	0.01%	8.7%	VLVMLAAQSR	99.7%	84.9	25	78.7	4	0	0	1087.63	261	270
Protein THEM6	THEM6	THEM6_HUMAN	23.9	100.0%	3	3	3	0.00%	13.9%	DGFVCALLR	97.3%	30.7	25	15.2	1	0	0	1050.54	142	150
Protein THEM6	THEM6	THEM6_HUMAN	23.9	100.0%	3	3	3	0.00%	13.9%	LLEPFEVR	98.7%	33.7	25	16.2	1	0	0	1002.56	113	120
Protein THEM6	THEM6	THEM6_HUMAN	23.9	100.0%	3	3	3	0.00%	13.9%	MESGLSDVTKDQ	99.7%	41.3	25	35.7	1	0	0	1325.59	197	208
Protein timeless homolog	TIMELESS	TIM_HUMAN	138.7	99.8%	2	2	4	0.00%	1.7%	FGGSYIVQGLK	99.7%	61.2	25	50.5	2	0	0	1168.64	278	288
Protein timeless homolog	TIMELESS	TIM_HUMAN	138.7	99.8%	2	2	4	0.00%	1.7%	LLALGLVAER	99.7%	78.6	25	78.6	2	0	0	1054.66	931	940
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	6	20	0.02%	10.9%	AFSPTTVNTGR	99.7%	62.3	25	45.8	5	0	0	1150.59	195	205
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	6	20	0.02%	10.9%	ETSMVHELNR	99.7%	51.3	25	43	4	0	0	1231.57	406	415
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	6	20	0.02%	10.9%	GQYNTYPIK	99.7%	50.2	25	35.3	4	0	0	1083.55	274	282
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	6	20	0.02%	10.9%	IIEVGDTPK	99.7%	54.9	25	46.3	4	0	0	971.54	99	107
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	6	20	0.02%	10.9%	IIEVGDTPKDR	99.7%	51.1	25	37.2	2	0	0	1242.67	99	109
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	6	6	20	0.02%	10.9%	TWIEVSGSSAK	99.7%	49.9	25	45	1	0	0	1164.59	378	388
Protein tyrosine phosphatase type IVA 1	PTP4A1	TP4A1_HUMAN	19.8	99.8%	2	2	4	0.00%	15.6%	FLITHNPTNATLNK	99.7%	55.3	25	55.3	2	0	0	1583.85	19	32
Protein tyrosine phosphatase type IVA 1	PTP4A1	TP4A1_HUMAN	19.8	99.8%	2	2	4	0.00%	15.6%	VCEATYDTTLVEK	99.7%	52.6	25	39.4	2	0	0	1528.72	48	60
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	12	12	18	0.02%	16.2%	ALIPLALEGTDVGQTK	99.7%	96.4	25	96.4	2	0	0	1625.91	692	707
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	12	12	18	0.02%	16.2%	DNALTLLIK	97.5%	31.1	25	9.85	1	0	0	1000.60	313	321
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	12	12	18	0.02%	16.2%	EVQDLFEAQGNDR	99.0%	35.2	25	35.2	1	0	0	1520.70	807	819
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	12	12	18	0.02%	16.2%	GAVVVLNMVEASR	99.7%	64.4	25	55.7	1	0	0	1344.73	882	894
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	12	12	18	0.02%	16.2%	LDQAVLDLQR	99.7%	73.7	25	55.9	2	0	0	1170.65	108	117
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	12	12	18	0.02%	16.2%	LEDYDKAETEASK	99.7%	62.9	25	62	1	0	0	1498.69	71	83
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	12	12	18	0.02%	16.2%	LGSAGGTDFSMK	99.2%	36.2	25	32.1	1	0	0	1170.55	505	516
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	12	12	18	0.02%	16.2%	LLDMGETDLMLAALR	99.7%	67.1	25	41	2	0	0	1677.86	203	217
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	12	12	18	0.02%	16.2%	LLVLYSGEDDELLQR	99.7%	95	25	83.7	2	0	0	1762.92	822	836
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	12	12	18	0.02%	16.2%	TVATLSILGTR	99.7%	71.7	25	63.2	1	0	0	1131.67	230	240
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	12	12	18	0.02%	16.2%	VEQMFQILLDPEEK	99.7%	63.1	25	47.9	2	0	0	1718.87	153	166
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	12	12	18	0.02%	16.2%	VFLALVEEVEDR	99.7%	77.5	25	74.7	2	0	0	1418.75	670	681
Protein virilizer homolog	KIAA1429	VIR_HUMAN	202.0	100.0%	3	3	4	0.00%	2.1%	DTGELASSFLEFMR	99.7%	71.9	25	61.3	1	0	0	1602.75	1389	1402
Protein virilizer homolog	KIAA1429	VIR_HUMAN	202.0	100.0%	3	3	4	0.00%	2.1%	EESPENLFLELEK	99.7%	44.5	25	31.6	1	0	0	1576.77	1446	1458
Protein virilizer homolog	KIAA1429	VIR_HUMAN	202.0	100.0%	3	3	4	0.00%	2.1%	VVTAGSAILQK	99.3%	36.7	25	29.2	2	0	0	1086.65	546	556
Protein YIF1A	YIF1A	YIF1A_HUMAN	32.0	99.8%	2	2	3	0.00%	9.2%	TAALGPDSMGGPVPR	99.7%	44.5	25	44.1	2	0	0	1441.71	251	265
Protein YIF1A	YIF1A	YIF1A_HUMAN	32.0	99.8%	2	2	3	0.00%	9.2%	YFFAVDTAYVAK	99.7%	83.5	25	80.3	1	0	0	1394.70	93	104
Protein YIPF5	YIPF5	YIPF5_HUMAN	28.0	99.8%	2	2	3	0.00%	8.2%	QYAGYDYSQQGR	99.7%	48.4	25	47.3	1	0	0	1435.62	38	49
Protein YIPF5	YIPF5	YIPF5_HUMAN	28.0	99.8%	2	2	3	0.00%	8.2%	TLTVLHPLK	99.4%	37.6	25	37.6	2	0	0	1021.64	107	115
Pumilio homolog 1	PUM1	PUM1_HUMAN	126.5	100.0%	5	5	8	0.01%	5.1%	DQYANYVVQK	99.7%	44.8	25	31.2	1	0	0	1227.60	1118	1127
Pumilio homolog 1	PUM1	PUM1_HUMAN	126.5	100.0%	5	5	8	0.01%	5.1%	FFEFGSLEQK	99.7%	54	25	37.7	2	0	0	1231.60	905	914
Pumilio homolog 1	PUM1	PUM1_HUMAN	126.5	100.0%	5	5	8	0.01%	5.1%	GNVLVLSQHK	99.4%	37.3	25	31.3	2	0	0	1094.63	1067	1076
Pumilio homolog 1	PUM1	PUM1_HUMAN	126.5	100.0%	5	5	8	0.01%	5.1%	SASSASSLFSPSSTLFSSSR	99.7%	79.7	25	79.7	2	0	0	1992.95	797	816
Pumilio homolog 1	PUM1	PUM1_HUMAN	126.5	100.0%	5	5	8	0.01%	5.1%	YISAAPGAEAK	98.4%	32.8	25	31.5	1	0	0	1077.56	784	794
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	AFFESHPAPSAER	99.7%	50	25	50	2	2	0	1445.68	870	882
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	AGIISTVEVLK	99.7%	76.1	25	62.4	2	0	0	1129.68	628	638
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	ATFDISLVVPK	99.7%	57.2	25	52.5	2	0	0	1189.68	198	208

Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	DAESIHQYLLQR	99.7%	71	25	65.8	2	0	0	1472.75	901	912
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	DVFSPIGER	94.8%	28.1	25	20.8	1	0	0	1019.52	681	689
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	DYFNVPYPLPK	99.7%	55.6	25	52.9	5	0	0	1352.69	294	304
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	ETALLIDPK	99.7%	55.5	25	35.9	2	0	0	999.57	328	336
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	FALEVAAK	99.7%	42.1	25	26.6	2	0	0	848.49	280	287
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	GMNMYLTK	99.5%	38.2	25	32.3	2	0	0	957.45	460	467
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	HGDGTTLDIMLK	99.7%	66.3	25	66.3	3	0	0	1316.65	754	765
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	IDFVGELNDK	99.7%	65.4	25	42	3	0	0	1149.58	146	155
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	IDFVGELNDKMK	99.6%	39.2	25	39.2	1	0	0	1424.71	146	157
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	ILMDKPEMNVVLK	99.2%	36.1	25	29.5	3	0	0	1561.83	559	571
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	KPYPDDENLVEVK	99.7%	71.2	25	60.3	3	0	0	1545.78	222	234
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	LEAAAQVR	99.3%	36.6	25	22.5	2	0	0	857.48	80	87
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	LGLQNDLFSLAR	99.7%	92.5	25	79.7	5	0	0	1346.74	616	627
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	LGWDPKPGEGHLDALLR	99.2%	30	25	30	0	1	0	1873.99	690	706
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	LNLGTVGFYR	99.7%	72.9	25	55.4	5	0	0	1139.62	581	590
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	LSVEGFAVDK	99.7%	43.9	25	39.8	2	0	0	1064.56	854	863
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	QILSADLR	99.7%	46.7	25	30.6	2	0	0	915.53	737	744
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	SKYTTPSGEVR	99.4%	37.7	25	32.5	1	0	0	1224.62	162	172
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	SPVYLTVLK	99.7%	54	25	51.2	2	0	0	1019.61	745	753
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	TIQQCCENILLNAAWLK	99.7%	71.9	25	63.5	2	0	0	2075.04	883	899
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	TQYSSAMLESLLPGIR	99.7%	66	25	41.2	4	0	0	1765.92	591	606
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	VALSNMNVIDR	99.7%	74	25	67.9	4	0	0	1231.65	211	221
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	VLGATLLPDLIQK	99.7%	108	25	108	4	0	0	1380.85	782	794
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	VTLSFPSTLQTGTGTLK	99.7%	69.4	25	69.4	2	0	0	1750.96	129	145
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	YAAVTQFEATDAR	99.7%	105	25	104	3	0	0	1442.69	173	185
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	29	34	76	0.07%	35.1%	YQGGFLISR	99.7%	59.2	25	52.1	2	0	0	1040.55	842	850
Putative ataxin-7-like protein 3B	ATXN7L3B	A7L3B_HUMAN	10.8	99.8%	2	2	3	0.00%	30.9%	DFGIQPVEDK	99.7%	47.6	25	45.5	2	0	0	1147.56	58	67
Putative ataxin-7-like protein 3B	ATXN7L3B	A7L3B_HUMAN	10.8	99.8%	2	2	3	0.00%	30.9%	LPLCSLPGEPGNGPDQQLQR	99.7%	56.5	25	56	1	0	0	2176.08	72	91
Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial	CLPP	CLPP_HUMAN	30.2	99.8%	2	3	6	0.01%	7.9%	AYDIYSR	99.4%	37.3	25	19.4	1	0	0	887.43	72	78
Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial	CLPP	CLPP_HUMAN	30.2	99.8%	2	3	6	0.01%	7.9%	GQATDIAIQAEEIMK	99.7%	78.1	25	76.6	5	0	0	1617.82	186	200
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	AIFQQPPVGVR	99.7%	58.5	25	58.5	4	0	0	1211.69	715	725
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	AIVLAAIFR	99.7%	69	25	69	4	0	0	973.62	886	894
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	ATISLSDSDLLR	99.7%	76.3	25	67.8	2	0	0	1290.69	1116	1127
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	AVAGWEEVLR	99.7%	59.2	25	42.8	2	0	0	1129.60	942	951
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	AVDSPNIK	95.6%	28.8	25	1.52	1	0	0	843.46	839	846
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	CNVIITQPR	99.7%	42.3	25	35.5	2	0	0	1100.59	484	492
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	DPFSSSLQNR	99.7%	46.2	25	37.7	2	0	0	1150.55	909	918
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	DSGPLSDPITGKPYVPLLEAEEVR	99.7%	49.6	25	49.6	0	3	0	2582.34	389	412
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	DVNTDFLLILLK	99.7%	103	25	95.2	4	0	0	1403.81	565	576
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	EHYLEDILAK	96.9%	30.2	25	24.1	1	0	0	1230.64	620	629
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	ENYLEENLLYAPSLR	99.7%	53.5	25	52.8	3	0	0	1823.92	959	973
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	EYLTTLGQR	99.7%	49.8	25	43.3	2	0	0	1080.57	865	873
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	FKPNSVTYR	99.2%	36	25	28.5	2	0	0	1111.59	1041	1049
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	GEPGGILCFLPGWQEIK	99.7%	55	25	49.3	1	0	0	1900.96	666	682
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	GGALLFCTVGILLR	99.7%	67.4	25	58.4	4	0	0	1489.86	529	542
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	GSSFEMTDDDSAIR	99.7%	99	25	99	3	0	0	1530.64	224	237
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	GVLMAGLYPNLIQVR	99.7%	62.5	25	55.7	6	0	0	1659.93	1017	1031
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	IPQLLLER	99.7%	57.5	25	22.3	4	0	0	981.61	467	474
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	ISAVSVAQR	99.7%	73.1	25	32	3	0	0	930.54	494	502
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	LQEALGMHESK	99.7%	64.4	25	57.1	4	0	0	1258.61	688	698
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	LQSDDILPLGK	99.7%	58.8	25	45.2	2	0	0	1198.67	378	388

Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	LSQSLLELWR	99.7%	74.8	25	65.7	2	0	0	1244.70	413	422
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	LVLMSATGDNER	99.7%	88.8	25	74.7	4	0	0	1321.64	587	598
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	MVPFQVPEILR	99.7%	44.6	25	35.4	3	0	0	1328.74	803	813
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	NLLNSVIGR	99.7%	63.5	25	51.5	2	0	0	985.58	55	63
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	NLMQFHTVGTK	99.7%	44.7	25	38.7	4	0	0	1291.65	264	274
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	NVGFQVR	97.6%	31.2	25	21.4	2	0	0	819.45	514	520
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	QAAAAACQLFK	99.7%	52.5	25	47.4	2	0	0	1178.60	112	122
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	QLNPESIRPGGPGGLSR	99.3%	30.6	25	30.6	0	2	0	1734.92	167	183
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	RISAVSVAQR	99.7%	54	25	17	2	0	0	1086.64	493	502
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	RPCTIQVPEPILR	98.3%	26.9	25	26.9	0	2	0	1578.88	344	356
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	SGNILLHK	99.7%	52.5	25	28.8	2	0	0	881.52	1052	1059
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	SVEVEGYGSK	99.7%	56.4	25	55.2	2	0	0	1054.51	96	105
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	TAVEFLSK	94.7%	28.1	25	26.1	1	0	0	894.49	831	838
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	TPLENLVLQAK	99.7%	65.6	25	65.6	4	0	0	1225.72	814	824
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	VIQIATSSSTAK	99.7%	81.7	25	74	3	0	0	1205.67	252	263
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	VSCLETVWVSR	99.7%	73	25	63.5	2	0	0	1335.67	763	773
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	38	43	99	0.10%	35.1%	VSHELGPSLR	99.7%	47.8	25	42.6	1	0	0	1094.60	503	512
Putative ATP-dependent RNA helicase DHX57	DHX57	DHX57_HUMAN	155.6	99.9%	2	2	3	0.00%	1.7%	LLYCTTGVLLR	99.7%	48.7	25	35.9	2	0	0	1308.73	641	651
Putative ATP-dependent RNA helicase DHX57	DHX57	DHX57_HUMAN	155.6	99.9%	2	2	3	0.00%	1.7%	TEESDFLLLVLK	99.7%	62.2	25	59.8	1	0	0	1406.78	674	685
Putative deoxyribose-phosphate aldolase	DERA	DEOC_HUMAN	35.2	100.0%	5	5	10	0.01%	20.1%	DSLAWLSLVK	99.7%	56.7	25	44.9	2	0	0	1131.64	264	273
Putative deoxyribose-phosphate aldolase	DERA	DEOC_HUMAN	35.2	100.0%	5	5	10	0.01%	20.1%	ETVNATFPVAIVMLR	99.7%	71.8	25	68.8	2	0	0	1660.91	224	238
Putative deoxyribose-phosphate aldolase	DERA	DEOC_HUMAN	35.2	100.0%	5	5	10	0.01%	20.1%	GTELDLSWISK	99.7%	53.5	25	32.8	2	0	0	1248.65	7	17
Putative deoxyribose-phosphate aldolase	DERA	DEOC_HUMAN	35.2	100.0%	5	5	10	0.01%	20.1%	IGASTLLSDIER	99.7%	89.1	25	80.2	2	0	0	1274.70	288	299
Putative deoxyribose-phosphate aldolase	DERA	DEOC_HUMAN	35.2	100.0%	5	5	10	0.01%	20.1%	TILATGELGTLTNVYK	99.7%	89.1	25	89.1	2	0	0	1693.94	189	204
Putative GTP-binding protein 6	GTPBP6	GTPB6_HUMAN	56.9	100.0%	3	3	4	0.00%	6.2%	ALTGDAAIQPR	99.7%	59.7	25	44.1	1	0	0	1112.61	313	323
Putative GTP-binding protein 6	GTPBP6	GTPB6_HUMAN	56.9	100.0%	3	3	4	0.00%	6.2%	DVSHPEAELQK	98.0%	31.9	25	26.2	2	0	0	1252.62	383	393
Putative GTP-binding protein 6	GTPBP6	GTPB6_HUMAN	56.9	100.0%	3	3	4	0.00%	6.2%	VIISNSAYGK	98.2%	32.5	25	14.6	1	0	0	1051.58	500	509
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	29.3%	AHILACAPSNSGADLLCQR	99.7%	54.7	25	51.9	0	2	0	2053.99	548	566
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	29.3%	DGQLLIR	98.3%	32.7	25	3.66	2	0	0	814.48	136	142
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	29.3%	EAGQCFESFLVVR	99.7%	71.9	25	63.8	4	0	0	1541.74	12	24
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	29.3%	EGEGGLSLQVEPEWR	99.7%	58.4	25	58.4	2	0	0	1685.81	986	1000
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	29.3%	EGNSPSFFNPEEAATVTSYLK	99.7%	104	25	104	4	0	0	2288.07	788	808
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	29.3%	ETGDPGGQLVLAGDPR	99.7%	87.8	25	87.4	4	0	0	1581.79	667	682
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	29.3%	GPDGYDPQFITK	99.7%	60.9	25	49.3	1	0	0	1337.64	716	727
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	29.3%	HGLGYSLLER	99.7%	45.4	25	39.8	2	0	0	1144.61	696	705
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	29.3%	HGVDVEVQGPHEAR	99.7%	61.3	25	61.2	0	4	0	1529.75	122	135
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	29.3%	IANLAYVTK	99.7%	42.2	25	34.4	2	0	0	992.58	63	71
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	29.3%	IEEGERPDR	95.7%	28.9	25	14.5	1	0	0	1100.53	271	279
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	29.3%	ISFGTPAPGFSSMLYGMK	99.7%	44.6	25	31.6	3	0	0	1890.91	45	62
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	29.3%	KGEYVFPAK	99.6%	39.5	25	33.8	2	0	0	1038.56	602	610
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	29.3%	KGPDGYDPQFITK	95.7%	28.9	25	28.9	1	0	0	1465.73	715	727
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	29.3%	LDLQQGQNLLQGLSK	99.7%	76.5	25	69.1	4	0	0	1654.91	953	967
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	29.3%	LLTLEVPGVTESRPSVLR	99.5%	32.3	25	32.3	0	2	0	1966.13	376	393
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	29.3%	LLTYNSLYK	96.9%	30.2	25	22.3	2	0	0	1114.61	706	714
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	29.3%	RFNVAVTR	99.7%	41.7	25	32.6	3	0	0	962.55	904	911
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	29.3%	SLESNPEQLQAMR	99.7%	75	25	73.8	6	0	0	1502.73	496	508
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	29.3%	SVGVISPYR	99.7%	47.3	25	34.8	4	0	0	977.54	826	834
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	29.3%	SVGVISPYRK	96.9%	30.2	25	20.4	2	0	0	1105.64	826	835
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	29.3%	SVILISTVR	99.7%	60.1	25	41	4	0	0	987.62	874	882
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	29.3%	TVTLVEAIK	99.7%	63.2	25	51.4	4	0	0	973.59	531	539
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	29.3%	VGSVEEFQGQER	99.7%	89.8	25	79.2	4	0	0	1364.64	862	873

Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	29.3%	VLITTLITAGR	99.7%	109	25	100	4	0	0	1157.73	618	628
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	26	27	75	0.07%	29.3%	VNFTFNR	98.8%	34.2	25	31.2	2	0	0	897.46	445	451
Putative mitochondrial import inner membrane translocase subunit Tim23B	TIMM23B	TI23B_HUMAN	28.0	99.8%	2	3	5	0.00%	10.5%	NVQILNMVTR	99.7%	77.3	25	45.3	3	0	0	1187.66	113	122
Putative mitochondrial import inner membrane translocase subunit Tim23B	TIMM23B	TI23B_HUMAN	28.0	99.8%	2	3	5	0.00%	10.5%	YLVQDTDEFILPTGANK	99.7%	72	25	66.1	2	0	0	1923.97	52	68
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	6	6	12	0.01%	15.0%	ALDQSDNDMSAVYR	99.7%	79	25	79	2	0	0	1600.69	536	549
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	6	6	12	0.01%	15.0%	DLTIPESSTVK	96.7%	30	25	25.1	1	0	0	1189.63	180	190
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	6	6	12	0.01%	15.0%	DLVLGPSGVLQGIRPGK	99.7%	76.5	25	76.5	2	0	0	1706.00	339	355
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	6	6	12	0.01%	15.0%	FQQAVDAVEEFLR	99.7%	71.6	25	59.4	3	0	0	1551.78	79	91
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	6	6	12	0.01%	15.0%	GLYEDCSSCFQAMGK	99.7%	55.9	25	55.9	2	0	0	1768.70	408	422
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	6	6	12	0.01%	15.0%	TSFFLGEVGNAAK	99.7%	105	25	102	2	0	0	1340.68	423	435
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	11	14	35	0.03%	15.5%	EAMNDPLLER	99.7%	49.6	25	37.7	4	0	0	1187.57	244	253
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	11	14	35	0.03%	15.5%	FTDILVR	99.7%	42.1	25	27.1	2	0	0	863.50	146	152
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	11	14	35	0.03%	15.5%	HQSFVLVGETGSGK	99.7%	65.5	25	65.5	2	0	0	1445.74	153	166
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	11	14	35	0.03%	15.5%	HRLDLGEDYPSGK	99.7%	43.3	25	36.8	0	1	0	1486.73	5	17
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	11	14	35	0.03%	15.5%	IRVESLLVTAISK	99.7%	64.6	25	64.6	2	0	0	1428.88	451	463
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	11	14	35	0.03%	15.5%	RVAAMSVAQR	96.7%	30	25	13.4	1	0	0	1088.60	195	204
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	11	14	35	0.03%	15.5%	SLMSADNVR	99.7%	40.3	25	29.7	2	0	0	992.48	653	661
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	11	14	35	0.03%	15.5%	SNLGSVVLQLK	99.7%	80.9	25	73.6	6	0	0	1157.69	505	515
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	11	14	35	0.03%	15.5%	TCTDIKPEWLVK	99.7%	60	25	56.7	1	0	0	1489.77	749	760
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	11	14	35	0.03%	15.5%	TLATDILMGVLK	99.7%	93	25	79.1	8	0	0	1290.73	266	277
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	11	14	35	0.03%	15.5%	YGVIILDEAHER	99.7%	73.3	25	64.2	4	2	0	1414.73	254	265
Putative ribonuclease	YBEY	YBEY_HUMAN	19.3	99.8%	2	2	3	0.00%	12.0%	AVLDELGRR	95.6%	28.8	25	20.3	1	0	0	1028.58	143	151
Putative ribonuclease	YBEY	YBEY_HUMAN	19.3	99.8%	2	2	3	0.00%	12.0%	FDLGIICVDNK	99.7%	79.5	25	66	2	0	0	1293.65	35	45
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	10	10	25	0.02%	15.6%	ELLLSAIDSVNATSK	99.7%	117	25	113	4	0	0	1560.85	493	507
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	10	10	25	0.02%	15.6%	GADSELSTVPSVTK	99.7%	61.2	25	49.7	3	0	0	1390.71	656	669
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	10	10	25	0.02%	15.6%	GISAGAVQTAGK	99.7%	75.2	25	68.3	3	0	0	1059.58	80	91
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	10	10	25	0.02%	15.6%	IQDIVGILR	99.7%	67.9	25	50.6	3	0	0	1026.63	243	251
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	10	10	25	0.02%	15.6%	LGVTNTIISHYDGR	99.7%	57.5	25	57.5	2	0	0	1545.80	432	445
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	10	10	25	0.02%	15.6%	LVPTGLDFGQEGFTR	99.7%	94.1	25	87.2	3	0	0	1636.83	539	553
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	10	10	25	0.02%	15.6%	NTGVILANDANAER	99.7%	105	25	102	1	0	0	1457.73	408	421
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	10	10	25	0.02%	15.6%	SPEAKPLPGK	99.5%	37.9	25	32.9	2	0	0	1023.58	67	76
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	10	10	25	0.02%	15.6%	SVVGNLHR	99.1%	35.7	25	24.8	3	0	0	881.50	424	431
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	10	10	25	0.02%	15.6%	TQASSSFQDSSQPAGK	99.7%	89.4	25	78.3	1	0	0	1625.74	670	685
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	7	7	10	0.01%	9.5%	FGVITEVDIK	99.7%	58.5	25	49.9	2	0	0	1120.63	397	406
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	7	7	10	0.01%	9.5%	ISHLSGSGSGDER	99.6%	39.1	25	38.2	2	0	0	1301.61	204	216
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	7	7	10	0.01%	9.5%	LQQLALGR	99.7%	45.9	25	25.3	1	0	0	898.55	307	314
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	7	7	10	0.01%	9.5%	QDGGTAPVASASPK	99.7%	42	25	36.5	1	0	0	1285.64	770	783
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	7	7	10	0.01%	9.5%	SSGAASSAPGGGDGAEYK	99.7%	49.1	25	46.3	1	0	0	1568.68	153	170
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	7	7	10	0.01%	9.5%	SSSSSAASDTATSTQRPLR	97.9%	31.8	25	29.8	1	0	0	1909.92	871	889
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	7	7	10	0.01%	9.5%	VGAGAGAAPFR	99.7%	56.7	25	48.2	2	0	0	973.52	349	359
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	9	9	20	0.02%	27.0%	AMLDQLMGTSR	99.7%	63.4	25	56.4	3	0	0	1254.58	9	19
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	9	9	20	0.02%	27.0%	LADHFGGK	98.4%	33	25	23.5	2	0	0	844.43	206	213
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	9	9	20	0.02%	27.0%	LAETQEEISAEVAAK	99.7%	105	25	99.8	3	0	0	1588.81	108	122
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	9	9	20	0.02%	27.0%	LHLGFIEIR	99.7%	50.6	25	48.5	1	0	0	1097.65	214	222
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	9	9	20	0.02%	27.0%	NSMPASSFQQQK	99.6%	39.8	25	34.1	2	0	0	1352.63	175	186
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	9	9	20	0.02%	27.0%	SHLLNCCPHDVLSGTR	98.5%	27.4	25	27.2	0	2	0	1865.87	38	53
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	9	9	20	0.02%	27.0%	SSEEREAGEI	99.7%	47.1	25	41.4	1	0	0	1106.50	383	392
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	9	9	20	0.02%	27.0%	VEQLGAEGNVEESQK	99.7%	116	25	109	2	0	0	1616.78	140	154
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	9	9	20	0.02%	27.0%	VHELNEEIGK	99.7%	60.6	25	54.1	4	0	0	1167.60	126	135
Pyridoxal phosphate phosphatase	PDXP	PLPP_HUMAN	31.7	100.0%	3	3	4	0.00%	17.2%	LAGDPSAGDGAAPR	99.7%	64.4	25	64.4	2	0	0	1254.61	129	142
Pyridoxal phosphate phosphatase	PDXP	PLPP_HUMAN	31.7	100.0%	3	3	4	0.00%	17.2%	LPGPPDAPGAVFVLGGEGLR	99.7%	36.7	25	32.2	0	1	0	1919.04	100	119

Pyridoxal phosphate phosphatase	PDXP	PLPP_HUMAN	31.7	100.0%	3	3	4	0.00%	17.2%	TPGTGSLAAAVETASGR	99.7%	85.3	25	85.3	1	0	0	1545.79	190	206
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	23	39	0.04%	51.1%	CMTNTPVVVR	99.7%	52.5	25	42.2	2	0	0	1192.58	120	129
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	23	39	0.04%	51.1%	DNVSSPGGATIHALHVLESGGFR	98.9%	28.5	25	28.5	0	2	0	2321.16	229	251
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	23	39	0.04%	51.1%	EGATVYATGTHAQVEDGR	99.7%	93.5	25	93.5	2	2	0	1861.87	130	147
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	23	39	0.04%	51.1%	ELQSMADQEQVSPAAIK	99.7%	101	25	87.2	4	0	0	1860.90	267	283
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	23	39	0.04%	51.1%	ELQSMADQEQVSPAAIKK	99.7%	44.6	25	41.1	1	3	0	1973.00	267	284
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	23	39	0.04%	51.1%	GFTAAGVLAAHK	99.7%	68.8	25	60	2	0	0	1142.63	18	29
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	23	39	0.04%	51.1%	IMASSPDMDLATVSALR	99.7%	128	25	128	3	0	0	1777.88	30	46
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	23	39	0.04%	51.1%	IMASSPDMDLATVSALRK	98.1%	26.5	25	21.4	0	1	0	1937.97	30	47
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	23	39	0.04%	51.1%	LDSPAGTALSPSGHTK	99.7%	62.7	25	56.5	2	1	0	1538.78	292	307
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	23	39	0.04%	51.1%	LGAQALLGAAK	99.7%	77.9	25	68.2	3	0	0	1012.62	205	215
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	23	39	0.04%	51.1%	LSAFRPAPR	98.2%	32.4	25	20.6	1	0	0	1014.58	108	116
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	23	39	0.04%	51.1%	MLLHSEQHPGQLK	99.7%	48.3	25	46.5	3	4	0	1533.78	216	228
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	23	39	0.04%	51.1%	SLLINAVEASCIR	99.7%	90.6	25	83.2	6	0	0	1445.78	252	264
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	13	23	39	0.04%	51.1%	VKLDSPAGTALSPSGHTK	99.7%	90	25	84.9	1	2	0	1765.94	290	307
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	13	16	37	0.04%	43.8%	ELQSMADQEK	99.7%	51.7	25	40	4	0	0	1194.53	267	276
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	13	16	37	0.04%	43.8%	GFTAAGILSAHK	99.7%	62.8	25	53.7	4	0	0	1172.64	18	29
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	13	16	37	0.04%	43.8%	HIVVSCAAGVTISSVEK	99.7%	52	25	52	0	2	0	1756.93	90	106
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	13	16	37	0.04%	43.8%	IIASSPEMNLPTVSALR	99.7%	130	25	130	4	0	0	1798.97	30	46
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	13	16	37	0.04%	43.8%	ISPAALKK	99.3%	36.5	25	28.4	2	0	0	827.54	277	284
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	13	16	37	0.04%	43.8%	KLMAFQPAPK	99.7%	48.9	25	34.1	2	0	0	1130.64	107	116
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	13	16	37	0.04%	43.8%	LAIQLGAQALLGAAK	99.7%	82.8	25	82.8	2	0	0	1437.88	201	215
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	13	16	37	0.04%	43.8%	LESPTVSTLTPSSPGK	99.7%	127	25	100	2	0	0	1600.84	292	307
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	13	16	37	0.04%	43.8%	LMAFQPAPK	99.7%	57.6	25	47.5	1	0	0	1002.54	108	116
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	13	16	37	0.04%	43.8%	MGVNLTR	99.7%	43.5	25	10.3	2	0	0	806.42	48	54
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	13	16	37	0.04%	43.8%	MLLDSEQHPCQLK	99.7%	67.4	25	58.6	4	0	0	1598.77	216	228
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	13	16	37	0.04%	43.8%	SLLINAVEASCIR	99.7%	90.6	25	83.2	6	0	0	1445.78	252	264
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	13	16	37	0.04%	43.8%	VKLESPTVSTLTPSSPGK	99.7%	86.9	25	80.1	2	0	0	1828.01	290	307
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	6	10	16	0.02%	26.3%	AATMSAVEAATCR	99.7%	60.5	25	60.5	2	0	0	1354.61	255	267
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	6	10	16	0.02%	26.3%	IAAQTLLGTAK	99.7%	81.6	25	81.6	2	0	0	1086.65	208	218
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	6	10	16	0.02%	26.3%	MAGAIAQGLIR	99.7%	76.6	25	68.5	4	0	0	1116.62	19	29
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	6	10	16	0.02%	26.3%	MGMPSSLAHR	99.7%	49.2	25	42.6	4	0	0	1086.52	198	207
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	6	10	16	0.02%	26.3%	MLLHEGQHPAQLR	98.0%	26.3	25	26.3	0	1	0	1545.80	219	231
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	6	10	16	0.02%	26.3%	VEAQHILASAPTDR	99.7%	54.8	25	52.9	1	2	0	1507.79	33	46
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	5	5	7	0.01%	6.8%	AEAEAQAEELSFPR	99.7%	81.1	25	75.2	1	0	0	1547.73	929	942
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	5	5	7	0.01%	6.8%	DFTATFGPLDSLNTR	99.7%	82.4	25	71.5	2	0	0	1654.81	1022	1036
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	5	5	7	0.01%	6.8%	GANAVGYTNYPDNVVFK	99.7%	50	25	41.1	2	0	0	1828.89	645	661
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	5	5	7	0.01%	6.8%	LDNASAFQGAVISPHYDSLLVK	99.7%	48.6	25	48.6	0	1	0	2345.21	407	428
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	5	5	7	0.01%	6.8%	TSTAPAASPNVR	99.7%	47	25	39.8	1	0	0	1171.61	19	30
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	10	11	26	0.03%	28.7%	AAASTDYYK	96.7%	30	25	24.3	1	0	0	989.46	236	244
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	10	11	26	0.03%	28.7%	AHGFTFTR	97.0%	30.3	25	26.5	2	0	0	936.47	120	127
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	10	11	26	0.03%	28.7%	EILAELTGR	99.7%	56.1	25	47	2	0	0	1001.56	133	141
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	10	11	26	0.03%	28.7%	GPILMELQTYR	99.7%	62.9	25	62.9	2	0	0	1320.70	278	288
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	10	11	26	0.03%	28.7%	LEEGPPVTTVLTR	99.7%	65.9	25	59.3	7	0	0	1411.78	46	58
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	10	11	26	0.03%	28.7%	LPCIFICENNR	99.7%	61.5	25	61.5	2	0	0	1435.68	216	226
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	10	11	26	0.03%	28.7%	NFYGGNGIVGAQVPLGAGIALACK	99.7%	55	25	55	0	2	0	2347.22	159	182
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	10	11	26	0.03%	28.7%	RGDFIPGLR	99.7%	45.8	25	28.6	1	0	0	1030.58	245	253
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	10	11	26	0.03%	28.7%	TREEIQEVR	99.0%	35	25	11.1	2	0	0	1159.61	303	311
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	10	11	26	0.03%	28.7%	YGMGTSVER	99.7%	50.2	25	41.6	5	0	0	1015.45	227	235
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	18	33	0.03%	34.8%	DAINQGMDEELER	99.4%	37.2	25	37.2	1	0	0	1519.67	37	49
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	18	33	0.03%	34.8%	DAINQGMDEELERDEK	99.7%	69.8	25	69.4	2	2	0	1891.83	37	52

Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	18	33	0.03%	34.8%	DFLIPIGK	99.6%	39	25	23.9	2	0	0	902.53	220	227
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	18	33	0.03%	34.8%	DIIFAIK	99.1%	35.6	25	24.7	2	0	0	819.50	348	354
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	18	33	0.03%	34.8%	DIIFAIKK	99.3%	37	25	26	2	0	0	947.59	348	355
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	18	33	0.03%	34.8%	EGVECEVINMR	99.7%	59.2	25	57	4	0	0	1335.60	259	269
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	18	33	0.03%	34.8%	ILEDNSIPQVK	99.7%	75.1	25	63	2	0	0	1255.69	337	347
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	18	33	0.03%	34.8%	IMEGPAFNFLDAPAVR	99.7%	101	25	93.4	4	0	0	1747.88	309	324
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	18	33	0.03%	34.8%	TYYMSGGLQPVPIVFR	99.7%	103	25	95.9	4	0	0	1827.95	130	145
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	18	33	0.03%	34.8%	VFLLGEEVAQYDGAYK	99.7%	124	25	124	2	0	0	1801.90	53	68
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	18	33	0.03%	34.8%	VTGADVPMPYAK	99.7%	58.6	25	54.3	4	0	0	1264.62	325	336
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	18	33	0.03%	34.8%	VVSPWNSEDAK	99.7%	57.8	25	36.8	2	0	0	1231.60	174	184
Pyruvate dehydrogenase protein X component, mitochondrial	PDHX	ODPX_HUMAN	54.1	99.8%	2	2	3	0.00%	4.6%	HSLDASQGTATGPR	99.7%	62.7	25	59.7	2	0	0	1397.68	195	208
Pyruvate dehydrogenase protein X component, mitochondrial	PDHX	ODPX_HUMAN	54.1	99.8%	2	2	3	0.00%	4.6%	VVDDELATR	99.7%	48.8	25	43.8	1	0	0	1017.52	477	485
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	AEGSDVANAVLDGADCIMLSGETAK	99.7%	106	25	106	4	3	0	2510.14	343	367
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	AGKPVICATQMLESMIK	99.7%	46.8	25	45.7	4	7	0	1908.96	320	336
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	CCSGAIIVLTK	99.7%	66.3	25	59.3	4	0	0	1221.63	423	433
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	CDENILWLDYK	99.7%	80.9	25	79.2	3	0	0	1468.68	152	162
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	DPVQEAWAEDVDLR	99.7%	82.4	25	79.9	2	0	0	1642.77	476	489
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	EAEAAIYHLQLFEELR	97.6%	25.6	25	25.5	1	1	0	1931.99	384	399
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	EAEAAIYHLQLFEELRR	97.7%	25.7	25	25.7	0	1	0	2088.09	384	400
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	FGVEQDVDMVFASFIR	99.7%	105	25	101	5	0	0	1875.89	231	246
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	GADFLVTEVENGGSLGSK	99.7%	125	25	113	9	0	0	1779.88	189	206
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	GADFLVTEVENGGSLGSKK	95.0%	22.9	25	18	0	1	0	1907.97	189	207
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	GDLGIEIPAEK	99.7%	60.8	25	41.3	14	0	0	1141.61	295	305
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	GDVVIVLTGWRPGSGFTNTMR	99.7%	41.3	25	41.3	0	2	0	2279.16	506	526
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	GDYPLEAVR	99.7%	62.8	25	53.2	13	0	0	1019.52	368	376
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	GIFPVLCK	97.7%	31.4	25	11.1	2	0	0	933.52	468	475
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	GSGTAEVELK	99.7%	52.1	25	34	2	0	0	990.51	126	135
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	GSGTAEVELKK	99.7%	65.8	25	46.8	16	0	0	1118.61	126	136
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	GVNLPGAAVDLPAVSEK	99.7%	121	25	119	4	0	0	1636.89	208	224
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	GVNLPGAAVDLPAVSEKDIQDLK	98.1%	26.5	25	26.5	0	1	0	2349.27	208	230
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	ITLDNAYMEK	99.7%	64.3	25	63.5	7	0	0	1213.58	142	151
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	IYVDDGLISLQVK	99.7%	106	25	104	11	0	0	1462.82	174	186
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	KGVNLPGAAVDLPAVSEK	99.7%	96.3	25	96.3	2	2	0	1764.99	207	224
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	LAPITSDPTEATAVGAVEASFK	99.7%	139	25	139	6	4	0	2175.12	401	422
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	LDIDSPPITAR	99.7%	74.1	25	68.4	17	0	0	1197.65	33	43
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	LNFSHGTHEYHAETIK	99.7%	69.5	25	62.3	2	3	0	1883.90	74	89
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	MQHLIAR	99.7%	41.1	25	28.4	7	0	0	868.48	377	383
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	NTGIICTIGPASR	99.7%	87.8	25	87.8	15	0	0	1359.71	44	56
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	RFDEILEASDGIMVAR	99.7%	81	25	76.6	4	5	0	1821.92	279	294
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	SVETLKEMIK	99.5%	38	25	28	4	0	0	1193.64	57	66
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	TATESFASDPILYRPVAVALDTK	99.7%	71.7	25	71.1	2	8	0	2465.29	93	115
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	30	46	205	0.20%	68.4%	VNFAMNVGK	99.7%	68.4	25	60.3	7	0	0	979.50	490	498
Queuine tRNA-ribosyltransferase subunit QTRTD1	QTRTD1	QTRD1_HUMAN	46.7	100.0%	3	3	5	0.00%	8.7%	GVDLFESFFPYQVTER	99.7%	75.2	25	75.2	2	0	0	1933.93	267	282
Queuine tRNA-ribosyltransferase subunit QTRTD1	QTRTD1	QTRD1_HUMAN	46.7	100.0%	3	3	5	0.00%	8.7%	LQEESEVLQK	99.7%	42.7	25	25.1	1	0	0	1202.63	177	186
Queuine tRNA-ribosyltransferase subunit QTRTD1	QTRTD1	QTRD1_HUMAN	46.7	100.0%	3	3	5	0.00%	8.7%	SLLFLDNCLR	99.7%	44.3	25	31.3	2	0	0	1250.66	167	176
Rab-like protein 3	RABL3	RABL3_HUMAN	26.4	99.8%	2	2	3	0.00%	8.1%	WSLEALNR	99.7%	41.5	25	33.2	1	0	0	988.52	109	116
Rab-like protein 3	RABL3	RABL3_HUMAN	26.4	99.8%	2	2	3	0.00%	8.1%	YLAAGSSNAVK	99.7%	46.9	25	26.2	2	0	0	1080.57	185	195
Ragulator complex protein LAMTOR1	LAMTOR1	LTOR1_HUMAN	17.7	100.0%	3	3	5	0.00%	23.6%	IAAYAYSALSQIR	99.7%	58.9	25	45.8	2	0	0	1426.77	135	147
Ragulator complex protein LAMTOR1	LAMTOR1	LTOR1_HUMAN	17.7	100.0%	3	3	5	0.00%	23.6%	LAVLSSSLTHWK	99.7%	65	25	56.6	1	0	0	1341.75	92	103
Ragulator complex protein LAMTOR1	LAMTOR1	LTOR1_HUMAN	17.7	100.0%	3	3	5	0.00%	23.6%	TDEQALLSSILAK	99.7%	89.6	25	87.1	2	0	0	1388.76	48	60
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	9	9	19	0.02%	18.6%	AFNSSSFNSNTFLTR	99.7%	87	25	79.5	2	0	0	1692.80	501	515

Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	9	9	19	0.02%	18.6%	GAVAIADAIR	99.7%	68.2	25	58	4	0	0	956.55	280	289
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	9	9	19	0.02%	18.6%	GAVAMAETLK	99.7%	48.8	25	28	1	0	0	990.53	252	261
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	9	9	19	0.02%	18.6%	ILAAALTECHR	99.7%	51.3	25	51.3	2	0	0	1254.66	161	171
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	9	9	19	0.02%	18.6%	LNTAEDAKDVIK	99.7%	62.9	25	46.7	1	0	0	1316.71	32	43
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	9	9	19	0.02%	18.6%	SSVLIAQQTDTSDPEK	99.7%	99.6	25	95.5	2	0	0	1718.84	453	468
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	9	9	19	0.02%	18.6%	TQVAGGQLSFK	99.7%	58	25	51.5	3	0	0	1135.61	16	26
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	9	9	19	0.02%	18.6%	VINLNDNTFTEK	99.7%	56	25	49.1	2	0	0	1407.71	240	251
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	9	9	19	0.02%	18.6%	VSSVFKDEATVR	99.7%	92.4	25	81.7	2	0	0	1337.71	476	487
Ran-specific GTPase-activating protein	RANBP1	RANG_HUMAN	23.3	99.8%	2	2	4	0.00%	10.0%	FLNAENAQK	99.7%	41	25	23.4	2	0	0	1034.53	142	150
Ran-specific GTPase-activating protein	RANBP1	RANG_HUMAN	23.3	99.8%	2	2	4	0.00%	10.0%	TLEEDEEELFK	99.7%	53.1	25	49.8	2	0	0	1381.64	40	50
Ras GTPase-activating protein-binding protein 1	G3BP1	G3BP1_HUMAN	52.2	100.0%	4	4	6	0.01%	11.6%	EAGEQGDIEPR	99.7%	48.4	25	43	2	0	0	1200.55	321	331
Ras GTPase-activating protein-binding protein 1	G3BP1	G3BP1_HUMAN	52.2	100.0%	4	4	6	0.01%	11.6%	FMQTFVLAPEGSVANK	99.7%	57.9	25	57.9	1	0	0	1738.88	108	123
Ras GTPase-activating protein-binding protein 1	G3BP1	G3BP1_HUMAN	52.2	100.0%	4	4	6	0.01%	11.6%	LPNFGFVVFDDSEPVQK	99.7%	53.7	25	53.7	2	0	0	1937.96	377	393
Ras GTPase-activating protein-binding protein 1	G3BP1	G3BP1_HUMAN	52.2	100.0%	4	4	6	0.01%	11.6%	TFSWASVTSK	98.6%	33.6	25	29.8	1	0	0	1113.56	248	257
Ras GTPase-activating protein-binding protein 2	G3BP2	G3BP2_HUMAN	54.1	100.0%	3	4	7	0.01%	8.5%	LPNFGFVVFDDSEPVQR	99.7%	49	25	49	2	0	0	1965.97	371	387
Ras GTPase-activating protein-binding protein 2	G3BP2	G3BP2_HUMAN	54.1	100.0%	3	4	7	0.01%	8.5%	TEELKPQVEEK	99.7%	49.1	25	34.9	2	0	0	1329.69	206	216
Ras GTPase-activating protein-binding protein 2	G3BP2	G3BP2_HUMAN	54.1	100.0%	3	4	7	0.01%	8.5%	VEAKPEVQSQPPR	99.7%	39.6	25	37.3	1	2	0	1464.78	278	290
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	17	17	30	0.03%	12.3%	ALESGDVNTVWK	99.7%	53.3	25	46.1	1	0	0	1318.66	466	477
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	17	17	30	0.03%	12.3%	ALQSPALGLR	98.8%	34.2	25	31.3	2	0	0	1025.61	327	336
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	17	17	30	0.03%	12.3%	ATFYGEQVDYYK	99.7%	61.4	25	61.4	2	0	0	1483.67	1517	1528
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	17	17	30	0.03%	12.3%	DHINDIIK	97.3%	30.8	25	20.8	1	0	0	967.52	834	841
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	17	17	30	0.03%	12.3%	EEIQSSISGVTAAYNR	99.7%	105	25	98.8	2	0	0	1724.84	723	738
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	17	17	30	0.03%	12.3%	GLQQQNSDWYLK	99.7%	40.5	25	36.1	1	0	0	1479.72	337	348
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	17	17	30	0.03%	12.3%	ILAIGLINEALDEGDAQK	99.7%	85	25	85	3	0	0	1883.01	539	556
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	17	17	30	0.03%	12.3%	ITLQDVVSHSK	99.7%	47.3	25	31.7	2	0	0	1226.67	925	935
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	17	17	30	0.03%	12.3%	LGLAPQIQDLYGK	98.7%	34	25	34	1	0	0	1415.79	162	174
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	17	17	30	0.03%	12.3%	LGNFFSPK	99.7%	46.3	25	39.5	2	0	0	909.48	81	88
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	17	17	30	0.03%	12.3%	LIFQMPQNK	97.6%	31.2	25	25.6	1	0	0	1118.60	989	997
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	17	17	30	0.03%	12.3%	LIVDVIR	98.5%	33.3	25	10.8	2	0	0	827.54	1391	1397
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	17	17	30	0.03%	12.3%	LPYDVTPEQALAHEEVK	99.7%	45.7	25	37	0	2	0	1938.98	1112	1128
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	17	17	30	0.03%	12.3%	LQQTYAALNSK	99.7%	73	25	64.8	2	0	0	1236.66	1506	1516
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	17	17	30	0.03%	12.3%	NVIFEISPTEEVGDFEVK	99.7%	82.7	25	76	2	0	0	2052.02	1587	1604
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	17	17	30	0.03%	12.3%	TLQALQIPAAK	99.7%	69.7	25	64.2	2	0	0	1153.69	557	567
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	17	17	30	0.03%	12.3%	YQELINDIAR	99.7%	51.1	25	45.6	2	0	0	1234.64	1478	1487
Ras suppressor protein 1	RSU1	RSU1_HUMAN	31.5	100.0%	2	2	3	0.00%	9.8%	HMQANPEPPK	96.2%	29.4	25	26.3	1	0	0	1148.55	249	258
Ras suppressor protein 1	RSU1	RSU1_HUMAN	31.5	100.0%	2	2	3	0.00%	9.8%	LTVLPPELGNLDLTGQK	99.7%	61.6	25	60.3	2	0	0	1808.02	192	208
Ras-related protein Rab-13	RAB13	RAB13_HUMAN	22.8	100.0%	3	4	6	0.01%	16.7%	SIKENASAGVER	99.7%	60.2	25	48.4	2	0	0	1260.65	105	116
Ras-related protein Rab-13	RAB13	RAB13_HUMAN	22.8	100.0%	3	4	6	0.01%	16.7%	SSMNVDEAFSSLAR	99.7%	97.6	25	91.7	3	0	0	1529.69	154	167
Ras-related protein Rab-13	RAB13	RAB13_HUMAN	22.8	100.0%	3	4	6	0.01%	16.7%	TITTAYYR	97.5%	31	25	14.2	1	0	0	988.51	72	79
Ras-related protein Rab-18	RAB18	RAB18_HUMAN	23.0	100.0%	4	4	7	0.01%	22.3%	GAQGVILVYDVTR	99.7%	44.6	25	39.3	2	0	0	1390.77	80	92
Ras-related protein Rab-18	RAB18	RAB18_HUMAN	23.0	100.0%	4	4	7	0.01%	22.3%	ILIIGESGVGK	99.7%	49	25	29.4	2	0	0	1085.66	11	21
Ras-related protein Rab-18	RAB18	RAB18_HUMAN	23.0	100.0%	4	4	7	0.01%	22.3%	LAIWDTAGQER	99.7%	47.8	25	43.2	2	0	0	1259.64	59	69
Ras-related protein Rab-18	RAB18	RAB18_HUMAN	23.0	100.0%	4	4	7	0.01%	22.3%	NDIVNMLVGNK	96.0%	29.2	25	22	1	0	0	1232.63	113	123
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	4	4	11	0.01%	30.8%	FADDTYTESYISTIGVDFK	99.7%	108	25	108	2	0	0	2172.00	28	46
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	4	4	11	0.01%	30.8%	LQIWDTAGQER	99.7%	75.1	25	0	6	0	0	1316.66	59	69
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	4	4	11	0.01%	30.8%	MGPGAASGGERPNLK	99.4%	31.5	25	27.6	0	2	0	1457.72	173	187
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	4	4	11	0.01%	30.8%	NATNVEQAFMTMAAEIK	99.7%	50.6	25	11.9	1	0	0	1884.88	154	170
Ras-related protein Rab-2A	RAB2A	RAB2A_HUMAN	23.5	99.8%	2	2	3	0.00%	14.2%	IQEGVFDINNEANGIK	99.7%	45.6	25	40.4	1	0	0	1760.88	171	186
Ras-related protein Rab-2A	RAB2A	RAB2A_HUMAN	23.5	99.8%	2	2	3	0.00%	14.2%	TASNVEEAFINTAK	99.7%	90.1	25	90.1	2	0	0	1494.74	152	165
Ras-related protein Rab-32	RAB32	RAB32_HUMAN	25.0	100.0%	2	2	4	0.00%	9.3%	DNINIEEAAR	99.7%	64.8	25	53	2	0	0	1144.56	177	186
Ras-related protein Rab-32	RAB32	RAB32_HUMAN	25.0	100.0%	2	2	4	0.00%	9.3%	LQLWDIAGQER	99.7%	66.6	25	52.2	2	0	0	1328.70	77	87

Ras-related protein Rab-7a	RAB7A	RAB7A_HUMAN	23.5	99.9%	2	2	3	0.00%	13.0%	DPENFPFVVLGNK	96.0%	29.2	25	26.5	1	0	0	1475.75	114	126
Ras-related protein Rab-7a	RAB7A	RAB7A_HUMAN	23.5	99.9%	2	2	3	0.00%	13.0%	EAINVEQAFQTIAR	99.7%	72.3	25	72.3	2	0	0	1589.83	158	171
Ras-related protein Rab-9A	RAB9A	RAB9A_HUMAN	22.8	99.8%	2	2	4	0.00%	12.4%	DATNVAAAFEEAVR	99.7%	73.8	25	66.8	2	0	0	1463.71	157	170
Ras-related protein Rab-9A	RAB9A	RAB9A_HUMAN	22.8	99.8%	2	2	4	0.00%	12.4%	VILLGDGGVGK	99.7%	52.6	25	35.3	2	0	0	1027.61	10	20
Ras-related protein R-Ras2	RRAS2	RRAS2_HUMAN	23.4	99.8%	2	2	2	0.00%	11.3%	LVVVGGGGVGK	98.4%	33	25	33	1	0	0	941.58	17	27
Ras-related protein R-Ras2	RRAS2	RRAS2_HUMAN	23.4	99.8%	2	2	2	0.00%	11.3%	QVTQEEGQQLAR	99.7%	57.2	25	51.4	1	0	0	1386.70	136	147
Regulation of nuclear pre-mRNA domain-containing protein 1A	RPRD1A	RPR1A_HUMAN	35.7	100.0%	4	4	8	0.01%	19.2%	ALQDLENAASGDAAVHQR	99.7%	88	25	88	2	0	0	1865.91	169	186
Regulation of nuclear pre-mRNA domain-containing protein 1A	RPRD1A	RPR1A_HUMAN	35.7	100.0%	4	4	8	0.01%	19.2%	DFAPVIVEAFK	99.7%	74.9	25	70.8	2	0	0	1235.67	80	90
Regulation of nuclear pre-mRNA domain-containing protein 1A	RPRD1A	RPR1A_HUMAN	35.7	100.0%	4	4	8	0.01%	19.2%	IASLPVEVQEVSLLDK	99.7%	101	25	89.9	2	0	0	1739.98	187	202
Regulation of nuclear pre-mRNA domain-containing protein 1A	RPRD1A	RPR1A_HUMAN	35.7	100.0%	4	4	8	0.01%	19.2%	LTFLYLANDVIQNSK	99.7%	84	25	84	2	0	0	1738.94	57	71
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	ADSVVVLLCR	99.7%	54.1	25	45	2	0	0	1131.62	201	210
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	AGAKPDQIGIITPYEGQR	99.7%	56.2	25	56	1	2	0	1914.01	794	811
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	AGLSQSLFER	99.7%	80.8	25	60.2	2	0	0	1107.58	689	698
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	ANEHQGIGFLNDPR	98.6%	33.6	25	28.8	1	1	0	1567.76	855	868
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	AYQHGGVTGLSQY	99.7%	40.2	25	40.2	2	0	0	1380.65	1117	1129
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	DETGELSSADEKR	99.7%	48	25	48	2	0	0	1436.65	593	605
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	DGPLGETVLECYNCGCR	99.7%	90.2	25	90.2	2	0	0	1999.83	173	189
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	EAIDSPVSFLALHNQIR	99.7%	66.5	25	58.2	2	0	0	1910.01	561	577
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	EAIIPGSVYDR	99.7%	47	25	39.5	2	0	0	1219.63	950	960
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	EKDFIILSCVR	99.7%	61.1	25	56.4	2	0	0	1379.74	844	854
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	ESQTQDNITVR	98.4%	33	25	28.9	2	0	0	1290.63	322	332
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	FTAQGLPDLNHSQVYAVK	99.7%	35.2	25	35.2	0	1	0	1988.02	474	491
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	GNTSGSHIVNHLVR	94.5%	22.5	25	19.9	0	1	0	1490.78	149	162
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	IAYFTLPK	99.7%	43.5	25	38.9	2	0	0	952.55	342	349
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	IPSEQEQLR	99.7%	46.1	25	32.4	2	0	0	1099.57	245	253
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	KLVNTINPGAR	99.7%	63.2	25	54.9	2	0	0	1182.70	929	939
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	LKESQTQDNITVR	97.2%	25	25	21	0	1	0	1531.81	320	332
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	LLGHEVEDVIIK	99.7%	74.3	25	74.1	2	1	0	1364.78	456	467
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	LMQGDEICLR	99.7%	67.9	25	45.7	2	0	0	1234.59	367	376
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	LQVQYR	98.1%	32.1	25	0	1	0	0	806.45	709	714
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	LVNTINPGAR	99.0%	35	25	24.9	2	0	0	1054.60	930	939
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	LYQEVEIASVDAFQGR	99.7%	78.7	25	78.7	2	0	0	1824.91	828	843
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	QITAQQINK	98.6%	33.5	25	27.6	1	0	0	1043.58	256	264
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	QPCASQSSLK	99.7%	41.9	25	33.7	1	0	0	1105.53	211	220
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	SILIDESTQATEPECMVPVVLGAK	99.6%	38.9	25	38.9	2	0	0	2587.30	643	666
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	SQIDVALSQDSTYQGER	99.7%	88.6	25	83	1	0	0	1896.89	1100	1116
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	TFAVDETSVSGYIYHK	99.7%	81.5	25	81.5	1	0	0	1816.88	440	455
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	TVLQRPLSLIQGPPGTGK	99.7%	36.8	25	36.8	0	2	0	1862.09	492	509
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	TVTSATIVYHLAR	99.7%	89.7	25	81.7	2	1	0	1431.80	510	522
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	VLVEGPLNNLR	99.7%	65.7	25	57.4	2	0	0	1223.71	908	918
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	VPDNYGDEIAIELR	99.7%	89.9	25	89.9	2	0	0	1603.80	394	407
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	YEDAYQYQNIFGPLVK	99.7%	98.9	25	98.9	2	0	0	1947.95	296	311
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	33	37	61	0.06%	36.2%	YGVIIVGNPK	99.7%	62.4	25	62.4	2	0	0	1059.62	879	888
Regulator of nonsense transcripts 3B	UPF3B	REN3B_HUMAN	57.8	100.0%	5	6	11	0.01%	12.4%	FLESYATDNEK	99.7%	55.8	25	47.4	2	0	0	1316.60	163	173
Regulator of nonsense transcripts 3B	UPF3B	REN3B_HUMAN	57.8	100.0%	5	6	11	0.01%	12.4%	KAESTESIGSSEK	99.7%	42.5	25	38.9	2	0	0	1352.65	406	418
Regulator of nonsense transcripts 3B	UPF3B	REN3B_HUMAN	57.8	100.0%	5	6	11	0.01%	12.4%	MTSTPETLLEEIEAK	99.7%	81	25	78.9	4	0	0	1691.84	174	188
Regulator of nonsense transcripts 3B	UPF3B	REN3B_HUMAN	57.8	100.0%	5	6	11	0.01%	12.4%	NQEDIILFR	99.7%	58.1	25	45.3	2	0	0	1147.61	103	111
Regulator of nonsense transcripts 3B	UPF3B	REN3B_HUMAN	57.8	100.0%	5	6	11	0.01%	12.4%	VGTIDDDPEYRK	99.7%	43	25	35.5	1	0	0	1407.68	151	162
Regulatory-associated protein of mTOR	RPTOR	RPTOR_HUMAN	149.0	100.0%	4	4	5	0.00%	3.4%	ALETIGANLQK	99.7%	48.5	25	36.9	2	0	0	1157.65	98	108
Regulatory-associated protein of mTOR	RPTOR	RPTOR_HUMAN	149.0	100.0%	4	4	5	0.00%	3.4%	CVSLVPGVTLDLIEK	95.0%	28.3	25	28.3	1	0	0	1642.91	283	297
Regulatory-associated protein of mTOR	RPTOR	RPTOR_HUMAN	149.0	100.0%	4	4	5	0.00%	3.4%	LDDQIFLNR	99.7%	45.9	25	35.3	1	0	0	1133.60	1013	1021

Regulatory-associated protein of mTOR	RPTOR	RPTOR_HUMAN	149.0	100.0%	4	4	5	0.00%	3.4%	QDLLVASLFR	99.7%	53.3	25	30.7	1	0	0	1161.66	339	348
Renin receptor	ATP6AP2	RENR_HUMAN	39.0	100.0%	2	2	3	0.00%	9.1%	IPDVAALSMGFSVK	98.1%	32.1	25	26.2	1	0	0	1434.77	42	55
Renin receptor	ATP6AP2	RENR_HUMAN	39.0	100.0%	2	2	3	0.00%	9.1%	LFQENSVLSSLPLNSLSR	99.7%	68.7	25	68.7	2	0	0	2004.08	158	175
Replication factor C subunit 1	RFC1	RFC1_HUMAN	128.3	100.0%	3	3	6	0.01%	3.1%	AALLSGPPGVGK	99.7%	44.7	25	37	2	0	0	1066.63	646	657
Replication factor C subunit 1	RFC1	RFC1_HUMAN	128.3	100.0%	3	3	6	0.01%	3.1%	AIVAESLNNTSIK	99.7%	70.4	25	62.8	2	0	0	1359.75	688	700
Replication factor C subunit 1	RFC1	RFC1_HUMAN	128.3	100.0%	3	3	6	0.01%	3.1%	GGIQELIGLIK	99.7%	41.9	25	30.4	2	0	0	1140.70	732	742
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	13	16	30	0.03%	42.1%	APGSAGHYELPWVEK	99.7%	53.1	25	49	1	2	0	1640.81	27	41
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	13	16	30	0.03%	42.1%	DAMLELNASNDR	99.7%	71.4	25	62.8	2	0	0	1348.62	100	111
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	13	16	30	0.03%	42.1%	EGNVPNIIIAGPPGTGK	99.7%	64.8	25	55.2	2	0	0	1633.89	66	82
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	13	16	30	0.03%	42.1%	FALACNASDK	99.7%	52.9	25	42.8	2	0	0	1096.51	167	176
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	13	16	30	0.03%	42.1%	FALACNASDKIIEPIQSR	99.7%	46.9	25	46.9	0	2	0	2033.05	167	184
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	13	16	30	0.03%	42.1%	IAEGVNSLLQMAGLLAR	99.7%	65.6	25	58.8	2	0	0	1771.97	327	343
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	13	16	30	0.03%	42.1%	IIEPIQSR	99.7%	43.2	25	25.6	1	0	0	955.56	177	184
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	13	16	30	0.03%	42.1%	IIILDEADSMTDGAQQALR	99.7%	95	25	95	4	0	0	2076.03	137	155
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	13	16	30	0.03%	42.1%	LNEIVGNEDTVSR	99.7%	98.8	25	98.8	2	0	0	1445.72	47	59
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	13	16	30	0.03%	42.1%	LTDAQILTR	99.7%	72.3	25	63.8	4	0	0	1030.59	193	201
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	13	16	30	0.03%	42.1%	TFQMAEYLK	98.0%	31.9	25	25.7	3	0	0	1130.56	305	313
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	13	16	30	0.03%	42.1%	TTSILCLAR	99.7%	43.3	25	30.6	2	0	0	1034.57	83	91
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	13	16	30	0.03%	42.1%	VCDEPHPLLVK	99.7%	48.5	25	36.7	1	0	0	1306.68	254	264
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	11	12	22	0.02%	29.2%	AIYHLEAFVAK	99.7%	57.2	25	40.1	2	0	0	1261.69	328	338
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	11	12	22	0.02%	29.2%	ALLMCEACR	99.7%	46.5	25	46.5	4	0	0	1123.51	226	234
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	11	12	22	0.02%	29.2%	EGLNLPSQLAHR	99.7%	44.9	25	35.7	2	0	0	1334.72	203	214
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	11	12	22	0.02%	29.2%	ETANAIVSQQTPQR	99.7%	89.2	25	78.2	2	0	0	1542.79	257	270
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	11	12	22	0.02%	29.2%	IEHQTITTPSK	99.7%	50.6	25	42	2	0	0	1254.67	69	79
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	11	12	22	0.02%	29.2%	IEHQTITTPSKK	99.7%	52	25	47.3	1	0	0	1382.76	69	80
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	11	12	22	0.02%	29.2%	LDYHKEQAAQLR	95.8%	28.9	25	28.3	1	0	0	1471.77	16	27
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	11	12	22	0.02%	29.2%	TVAQSQQLETNSQR	99.7%	119	25	107	2	0	0	1589.79	114	127
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	11	12	22	0.02%	29.2%	VVIQEMLK	99.7%	41.5	25	27.5	2	0	0	959.56	106	113
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	11	12	22	0.02%	29.2%	VVLLTEVDK	99.7%	43.5	25	43.5	2	0	0	1015.60	131	139
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	11	12	22	0.02%	29.2%	VVLLTEVDKLTK	99.7%	78	25	78	2	0	0	1357.83	131	142
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	17	0.02%	30.9%	AITFLQSATR	99.7%	80.2	25	72.4	2	0	0	1107.62	241	250
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	17	0.02%	30.9%	ELFGPELFR	99.7%	50	25	30	2	0	0	1107.58	94	102
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	17	0.02%	30.9%	ISDEGIAYLVK	99.7%	94.3	25	86	2	0	0	1207.66	222	232
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	17	0.02%	30.9%	IVILDEADSMTSAAQAALR	99.7%	77.9	25	77.3	2	0	0	1975.02	146	164
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	17	0.02%	30.9%	NFAQLTVSGSR	99.2%	35.8	25	4.07	1	0	0	1179.61	125	135
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	17	0.02%	30.9%	SLEGADLPNLLFYGPPGTGK	99.7%	68.1	25	68.1	2	0	0	2046.05	65	84
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	17	0.02%	30.9%	TSTILAAAR	99.6%	39.3	25	28.1	2	0	0	903.53	85	93
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	17	0.02%	30.9%	VITDIAGVIPAEK	99.7%	83.3	25	74.8	2	0	0	1325.77	261	273
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	9	9	17	0.02%	30.9%	VLELNASDER	99.7%	66.5	25	60.9	2	0	0	1145.58	105	114
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	15	30	0.03%	35.9%	ALNILQSTNMAFGK	99.7%	108	25	87	4	0	0	1507.79	216	229
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	15	30	0.03%	35.9%	ALVTLSSGDMR	99.7%	73.6	25	64.4	4	0	0	1149.59	204	214
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	15	30	0.03%	35.9%	FCLICNYLSK	99.7%	57.7	25	57.7	2	0	0	1317.63	151	160
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	15	30	0.03%	35.9%	FGPLTPELMVPR	99.7%	54.7	25	54.2	4	0	0	1356.73	174	185
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	15	30	0.03%	35.9%	GPILSFASTR	99.7%	67.5	25	66.5	3	0	0	1048.58	103	112
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	15	30	0.03%	35.9%	IQLSSLIAAFQVTR	99.7%	113	25	113	2	0	0	1546.90	320	333
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	15	30	0.03%	35.9%	LSVGTNEK	95.7%	28.9	25	17.7	2	0	0	847.45	312	319
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	15	30	0.03%	35.9%	LVILDEADAMTQDAQNALR	99.7%	108	25	101	4	0	0	2087.04	121	139
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	15	30	0.03%	35.9%	MADIEYR	99.7%	46.6	25	38.7	2	0	0	897.41	305	311
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	15	30	0.03%	35.9%	TSTILACAK	99.7%	48.8	25	47.1	2	0	0	964.51	67	75
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	15	30	0.03%	35.9%	VDFPSSVR	99.7%	48.5	25	40	1	0	0	906.47	291	298
Required for meiotic nuclear division protein 1 homolog	RMND1	RMND1_HUMAN	51.6	100.0%	6	6	11	0.01%	14.9%	DAANILVMGVENSAK	99.7%	105	25	103	2	0	0	1531.78	205	219

Required for meiotic nuclear division protein 1 homolog	RMND1	RMND1_HUMAN	51.6	100.0%	6	6	11	0.01%	14.9%	EGAAVFWNVK	99.7%	43.2	25	43.2	2	0	0	1120.58	231	240
Required for meiotic nuclear division protein 1 homolog	RMND1	RMND1_HUMAN	51.6	100.0%	6	6	11	0.01%	14.9%	EGDPGTIFFFR	99.7%	54.9	25	49.9	2	0	0	1285.62	220	230
Required for meiotic nuclear division protein 1 homolog	RMND1	RMND1_HUMAN	51.6	100.0%	6	6	11	0.01%	14.9%	IGELFALR	99.7%	71.4	25	52.7	2	0	0	918.54	353	360
Required for meiotic nuclear division protein 1 homolog	RMND1	RMND1_HUMAN	51.6	100.0%	6	6	11	0.01%	14.9%	LNSELDLDDAILEK	99.7%	97	25	90.4	2	0	0	1587.81	289	302
Required for meiotic nuclear division protein 1 homolog	RMND1	RMND1_HUMAN	51.6	100.0%	6	6	11	0.01%	14.9%	LSHEEVMQK	96.2%	29.4	25	22.7	1	0	0	1100.54	344	352
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	8	14	0.01%	23.3%	AEELHYPLGER	99.7%	50	25	49.5	2	1	0	1313.65	25	35
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	8	14	0.01%	23.3%	EALLGVQEDVDEYVK	99.7%	106	25	106	2	0	0	1706.85	42	56
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	8	14	0.01%	23.3%	QLHDDYFYHDEL	99.7%	56.9	25	54.4	2	2	0	1594.68	306	317
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	8	14	0.01%	23.3%	VIDFDENTALDDAEEESFR	99.7%	84.3	25	84.3	1	0	0	2214.97	130	148
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	8	14	0.01%	23.3%	VIDFDENTALDDAEEESFRK	99.7%	46.2	25	43	0	2	0	2343.06	130	149
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	8	14	0.01%	23.3%	WDPTANEDPEWILVEK	99.7%	66.1	25	62.9	2	0	0	1941.92	217	232
Retinoid-inducible serine carboxypeptidase	SCPEP1	RISC_HUMAN	50.8	100.0%	5	6	7	0.01%	11.9%	DLAMVASDMMVLLK	99.7%	54.3	25	48.3	2	0	0	1536.78	134	147
Retinoid-inducible serine carboxypeptidase	SCPEP1	RISC_HUMAN	50.8	100.0%	5	6	7	0.01%	11.9%	MAAGIGLELYK	99.7%	71.2	25	65.9	1	0	0	1165.63	172	182
Retinoid-inducible serine carboxypeptidase	SCPEP1	RISC_HUMAN	50.8	100.0%	5	6	7	0.01%	11.9%	NLAFYWILK	99.0%	35	25	15.2	1	0	0	1167.66	420	428
Retinoid-inducible serine carboxypeptidase	SCPEP1	RISC_HUMAN	50.8	100.0%	5	6	7	0.01%	11.9%	SLETSAFVK	98.2%	32.3	25	26.4	2	0	0	981.53	408	416
Retinoid-inducible serine carboxypeptidase	SCPEP1	RISC_HUMAN	50.8	100.0%	5	6	7	0.01%	11.9%	VAEQVLNAVNK	99.7%	86	25	79.1	1	0	0	1184.66	233	243
Rho-related GTP-binding protein RhoG	RHOG	RHOG_HUMAN	21.3	100.0%	3	3	4	0.00%	22.0%	AVLNPTPIKR	99.7%	43.8	25	35	2	0	0	1108.68	175	184
Rho-related GTP-binding protein RhoG	RHOG	RHOG_HUMAN	21.3	100.0%	3	3	4	0.00%	22.0%	EYIPTVFDNYSAQSAVDGR	99.7%	85.2	25	85.2	1	0	0	2131.99	31	49
Rho-related GTP-binding protein RhoG	RHOG	RHOG_HUMAN	21.3	100.0%	3	3	4	0.00%	22.0%	YLECSALQQDGVK	99.7%	51.2	25	44.9	1	0	0	1510.72	154	166
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	5	5	9	0.01%	26.8%	AVVLEYFTR	99.7%	52.6	25	50	1	0	0	1097.60	55	63
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	5	5	9	0.01%	26.8%	CPSYVGITGILLQETK	99.7%	67.2	25	67.2	2	0	0	1778.94	147	162
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	5	5	9	0.01%	26.8%	EANDSDVQPSGAQR	99.7%	52.3	25	48	2	0	0	1473.66	13	26
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	5	5	9	0.01%	26.8%	LFDIKPEQQR	99.7%	41	25	35.4	2	0	0	1273.69	86	95
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	5	5	9	0.01%	26.8%	SVIYHALSQK	99.7%	53	25	49.8	2	0	0	1145.63	3	12
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	9	10	21	0.02%	43.7%	AALLHGETR	99.7%	46	25	44.8	2	0	0	967.53	227	235
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	9	10	21	0.02%	43.7%	GLAFELVYSPAIK	99.7%	76.8	25	71.8	2	0	0	1407.79	149	161
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	9	10	21	0.02%	43.7%	GPYDVANLGLLFGLSESDAK	99.7%	81.6	25	81.6	2	0	0	2066.04	199	218
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	9	10	21	0.02%	43.7%	KTAFGIISTVK	99.7%	62.1	25	61.7	2	0	0	1164.70	236	246
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	9	10	21	0.02%	43.7%	LTIIVSDPSHCNVLR	99.7%	49.5	25	45.3	2	0	0	1723.92	77	91
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	9	10	21	0.02%	43.7%	LYDVVAVFPK	99.7%	72.6	25	69.2	4	0	0	1150.65	99	108
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	9	10	21	0.02%	43.7%	NVIISSAAERPLEIR	99.7%	46.9	25	37	2	0	0	1667.94	184	198
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	9	10	21	0.02%	43.7%	RPPINVAIDR	99.5%	38.7	25	21.6	2	0	0	1150.67	139	148
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	9	10	21	0.02%	43.7%	YTISSALNLMQICK	99.7%	115	25	109	3	0	0	1657.83	168	181
Ribonuclease P protein subunit p38	RPP38	RPP38_HUMAN	31.8	100.0%	6	6	10	0.01%	21.9%	ELLLVLVCK	99.7%	55.9	25	54.5	2	0	0	1086.66	128	136
Ribonuclease P protein subunit p38	RPP38	RPP38_HUMAN	31.8	100.0%	6	6	10	0.01%	21.9%	NTTDFVDEVR	99.7%	49.1	25	43	2	0	0	1195.56	185	194
Ribonuclease P protein subunit p38	RPP38	RPP38_HUMAN	31.8	100.0%	6	6	10	0.01%	21.9%	QASVTLQPLK	98.5%	33.1	25	31.8	1	0	0	1084.64	251	260
Ribonuclease P protein subunit p38	RPP38	RPP38_HUMAN	31.8	100.0%	6	6	10	0.01%	21.9%	QLAIGVNEVTR	99.5%	38.5	25	29.3	1	0	0	1199.67	112	122
Ribonuclease P protein subunit p38	RPP38	RPP38_HUMAN	31.8	100.0%	6	6	10	0.01%	21.9%	TSLNNPYIIR	99.7%	57.2	25	49.3	2	0	0	1190.65	23	32
Ribonuclease P protein subunit p38	RPP38	RPP38_HUMAN	31.8	100.0%	6	6	10	0.01%	21.9%	VPSLSVPWLQDR	99.7%	61.1	25	60	2	0	0	1396.76	200	211
Ribonuclease P/MRP protein subunit POP5	POP5	POP5_HUMAN	18.8	100.0%	4	4	6	0.01%	27.0%	FLIQYNR	99.7%	40.4	25	30.5	1	0	0	953.52	113	119
Ribonuclease P/MRP protein subunit POP5	POP5	POP5_HUMAN	18.8	100.0%	4	4	6	0.01%	27.0%	LSLDDRVLSSLVR	98.9%	28.7	25	28.5	0	1	0	1472.84	22	34
Ribonuclease P/MRP protein subunit POP5	POP5	POP5_HUMAN	18.8	100.0%	4	4	6	0.01%	27.0%	YLLCELVSDDPR	99.7%	62	25	56.5	2	0	0	1479.72	8	19
Ribonuclease P/MRP protein subunit POP5	POP5	POP5_HUMAN	18.8	100.0%	4	4	6	0.01%	27.0%	YLNAYTGIVLLR	99.7%	67	25	64.2	2	0	0	1395.80	57	68
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	6	6	12	0.01%	7.4%	AASVHTVGEDTEETPHR	97.7%	25.8	25	25.8	0	2	0	1835.85	449	465
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	6	6	12	0.01%	7.4%	AGPEGTSQEIPK	99.7%	65.9	25	52.1	2	0	0	1213.61	89	100
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	6	6	12	0.01%	7.4%	ISDQDLNR	99.6%	39.2	25	27.3	2	0	0	960.47	567	574
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	6	6	12	0.01%	7.4%	NQPTNVTLSSGFVADR	99.7%	83.9	25	83.9	2	0	0	1705.85	15	30
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	6	6	12	0.01%	7.4%	SSNSLVFQTLPR	99.7%	74.4	25	55.6	2	0	0	1348.72	126	137
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	6	6	12	0.01%	7.4%	YITASTFAQAR	99.7%	52.2	25	47	2	0	0	1228.63	101	111
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	9	12	23	0.02%	36.5%	FSNQETCVEIGESVR	99.7%	80.3	25	80.3	1	0	0	1754.80	35	49
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	9	12	23	0.02%	36.5%	IFSGSSHQDLSQK	99.7%	75.6	25	69.4	2	0	0	1433.70	6	18

Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	9	12	23	0.02%	36.5%	IQVIDISMILAEAIR	99.7%	59.2	25	54.7	2	0	0	1700.96	287	301
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	9	12	23	0.02%	36.5%	MVLVGDVK	99.7%	43.2	25	32.5	2	0	0	876.49	205	212
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	9	12	23	0.02%	36.5%	MVLVGDVKDR	99.7%	61.3	25	57.4	4	0	0	1131.62	205	214
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	9	12	23	0.02%	36.5%	NCTIVSPDAGGAK	99.7%	60.3	25	50.3	2	0	0	1289.62	164	176
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	9	12	23	0.02%	36.5%	VAILVDDMADTCGTICHAADK	99.7%	40.4	25	40.4	0	4	0	2292.03	215	235
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	9	12	23	0.02%	36.5%	VTAVIPCFPYAR	99.4%	37.5	25	36.8	2	0	0	1393.73	85	96
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	9	12	23	0.02%	36.5%	VYAILTHGIFSGPAISR	99.7%	96.3	25	92.9	2	2	0	1802.00	244	260
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	5	6	8	0.01%	47.2%	FSNQETSVEIGESVR	99.7%	94	25	88	2	0	0	1681.80	35	49
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	5	6	8	0.01%	47.2%	INNAAFEAVVVTNTIPQEDK	99.7%	60.8	25	60.2	1	0	0	2173.11	261	280
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	5	6	8	0.01%	47.2%	IQVIDISMILAEAIR	99.7%	59.2	25	54.7	2	0	0	1700.96	287	301
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	5	6	8	0.01%	47.2%	LNVEFALIHK	98.9%	34.7	25	33.4	1	0	0	1183.68	185	194
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	5	6	8	0.01%	47.2%	MVLVGDVK	99.7%	43.2	25	32.5	2	0	0	876.49	205	212
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	5	6	8	0.01%	47.2%	MVLVGDVKDR	99.7%	61.3	25	57.4	4	0	0	1131.62	205	214
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	5	6	8	0.01%	47.2%	NCIIVSPDAGGAK	99.1%	35.7	25	31	1	0	0	1301.65	164	176
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	5	6	8	0.01%	47.2%	PNIVLFSGSSHQDLSQR	99.7%	85.5	25	81	1	2	0	1884.96	2	18
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	5	6	8	0.01%	47.2%	VAILVDDMADTCGTICHAADK	99.7%	40.4	25	40.4	0	4	0	2292.03	215	235
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	5	6	8	0.01%	47.2%	VTAVIPCFPYAR	99.4%	37.5	25	36.8	2	0	0	1393.73	85	96
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	5	6	8	0.01%	47.2%	VYAILTHGIFSGPAISR	99.7%	96.3	25	92.9	2	2	0	1802.00	244	260
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	4	4	7	0.01%	6.8%	FVNLISER	99.7%	56.3	25	38.2	2	0	0	977.54	122	129
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	4	4	7	0.01%	6.8%	GCYFVLDWLQK	99.7%	65.7	25	64	1	0	0	1428.70	172	182
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	4	4	7	0.01%	6.8%	LLDVTGGLGTDELR	99.7%	91.8	25	81	2	0	0	1458.78	99	112
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	4	4	7	0.01%	6.8%	SGNELPLAVASTADLIR	99.7%	107	25	103	2	0	0	1726.93	80	96
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	14	14	27	0.03%	27.8%	AAESETPGKSPEK	99.7%	58.5	25	54.6	2	0	0	1330.65	418	430
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	14	14	27	0.03%	27.8%	ATNESEDEIPQLVPIGK	99.7%	58.6	25	54.5	2	0	0	1839.93	357	373
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	14	14	27	0.03%	27.8%	AVDALLTHCK	99.7%	57.4	25	55.6	2	0	0	1127.59	39	48
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	14	14	27	0.03%	27.8%	DDVAPESGDTTVK	99.7%	62.1	25	62.1	2	0	0	1333.61	319	331
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	14	14	27	0.03%	27.8%	EINDCIGGTVLNISK	99.7%	89.2	25	85.4	2	0	0	1632.83	193	207
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	14	14	27	0.03%	27.8%	KALPASETPK	99.7%	52.5	25	46.8	2	0	0	1041.59	408	417
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	14	14	27	0.03%	27.8%	KVPVSVNLLSK	98.7%	33.9	25	33.9	2	0	0	1183.74	178	188
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	14	14	27	0.03%	27.8%	LLPSLIGR	99.7%	51.3	25	36.7	2	0	0	868.56	164	171
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	14	14	27	0.03%	27.8%	LTLPHSIR	99.7%	40.2	25	40.2	2	0	0	936.56	82	89
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	14	14	27	0.03%	27.8%	TASVLSKDDVAPESGDTTVK	97.6%	25.5	25	25.5	0	1	0	2020.01	312	331
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	14	14	27	0.03%	27.8%	TPANEKVEIQK	99.7%	46.7	25	35	2	0	0	1256.68	375	385
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	14	14	27	0.03%	27.8%	TVSQIISLQTLK	99.7%	64.4	25	64.4	2	0	0	1330.79	125	136
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	14	14	27	0.03%	27.8%	TVSQIISLQTLKK	99.7%	47.7	25	47.7	2	0	0	1458.89	125	137
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	14	14	27	0.03%	27.8%	VPVSVNLLSK	99.7%	51.4	25	45.2	2	0	0	1055.65	179	188
Ribosomal protein S6 kinase alpha-1	RPS6KA1	KS6A1_HUMAN	82.7	100.0%	3	3	4	0.00%	7.8%	DLKPENILLDEEGHIK	99.7%	56.7	25	53.4	0	2	0	1862.99	187	202
Ribosomal protein S6 kinase alpha-1	RPS6KA1	KS6A1_HUMAN	82.7	100.0%	3	3	4	0.00%	7.8%	DPSEEIEILLR	99.7%	64.5	25	59	1	0	0	1313.69	455	465
Ribosomal protein S6 kinase alpha-1	RPS6KA1	KS6A1_HUMAN	82.7	100.0%	3	3	4	0.00%	7.8%	EASFVLHTIGK	99.7%	65.7	25	61.6	2	0	0	1201.66	511	521
Ribosomal protein S6 kinase alpha-1	RPS6KA1	KS6A1_HUMAN	82.7	100.0%	3	3	4	0.00%	7.8%	ICDFGFAK	99.7%	51.8	25	0	2	0	0	957.45	555	562
Ribosomal protein S6 kinase alpha-1	RPS6KA1	KS6A1_HUMAN	82.7	100.0%	3	3	4	0.00%	7.8%	NLVFSDGYVVK	95.7%	28.8	25	7.3	1	0	0	1240.66	411	421
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	6	6	8	0.01%	10.0%	DLKPENILLDEEGHIK	99.7%	56.7	25	53.4	0	2	0	1862.99	193	208
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	6	6	8	0.01%	10.0%	EASAVLFTITK	99.7%	57.2	25	52.4	1	0	0	1179.66	515	525
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	6	6	8	0.01%	10.0%	GAMAATYSALNR	99.7%	69.6	25	63.2	1	0	0	1241.59	701	712
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	6	6	8	0.01%	10.0%	ICDFGFAK	99.7%	51.8	25	0	2	0	0	957.45	559	566
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	6	6	8	0.01%	10.0%	LGMPQFLSPEAQSLLR	99.4%	37.5	25	37.1	1	0	0	1802.95	285	300
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	6	6	8	0.01%	10.0%	NQSPVLEPVGR	98.5%	33.3	25	28.1	1	0	0	1195.64	713	723
Ribosomal RNA processing protein 1 homolog A	RRP1	RRP1_HUMAN	52.8	100.0%	4	4	7	0.01%	8.9%	LAGNEQVTR	99.7%	72.7	25	57.2	2	0	0	987.52	17	25
Ribosomal RNA processing protein 1 homolog A	RRP1	RRP1_HUMAN	52.8	100.0%	4	4	7	0.01%	8.9%	LFEMASR	95.4%	28.6	25	13	1	0	0	869.42	307	313
Ribosomal RNA processing protein 1 homolog A	RRP1	RRP1_HUMAN	52.8	100.0%	4	4	7	0.01%	8.9%	TKDSLVLNNITR	99.7%	76.1	25	72.1	2	0	0	1373.77	204	215
Ribosomal RNA processing protein 1 homolog A	RRP1	RRP1_HUMAN	52.8	100.0%	4	4	7	0.01%	8.9%	VGAEELTADQNLK	99.7%	62.5	25	53.5	2	0	0	1387.71	180	192

Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	10	10	15	0.01%	18.9%	ELLADQNLK	99.7%	41	25	36.4	1	0	0	1043.57	183	191
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	10	10	15	0.01%	18.9%	ETGGFSQEELLK	99.7%	45.2	25	29.6	1	0	0	1337.66	42	53
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	10	10	15	0.01%	18.9%	GVFEAIVDQSPFVPEETMEEQK	97.7%	25.7	25	23.8	0	2	0	2509.18	215	236
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	10	10	15	0.01%	18.9%	HHLQPENPGPGGAAPSLEQNR	99.7%	49.8	25	49	0	2	0	2206.08	407	427
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	10	10	15	0.01%	18.9%	SILVSPTGPSR	99.6%	39.6	25	32.7	2	0	0	1113.63	702	712
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	10	10	15	0.01%	18.9%	SSTATHPPGPAVQLNK	99.7%	52.3	25	49.7	2	0	0	1604.84	661	676
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	10	10	15	0.01%	18.9%	TPTSSPASSPLVAK	99.7%	68.9	25	68.3	2	0	0	1342.72	728	741
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	10	10	15	0.01%	18.9%	VAFDPEQKPLHGVLK	95.8%	23.5	25	23.5	0	1	0	1677.93	713	727
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	10	10	15	0.01%	18.9%	VFCVEEEDSESSLQK	99.7%	98.1	25	87.6	1	0	0	1785.78	384	398
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	10	10	15	0.01%	18.9%	VFLDVLMK	97.8%	31.6	25	27.3	1	0	0	964.55	144	151
Ribosome biogenesis protein BMS1 homolog	BMS1	BMS1_HUMAN	145.8	99.8%	2	2	3	0.00%	1.6%	AFAVQSAVR	99.7%	46.9	25	30	1	0	0	948.53	44	52
Ribosome biogenesis protein BMS1 homolog	BMS1	BMS1_HUMAN	145.8	99.8%	2	2	3	0.00%	1.6%	IAATGVVLDLDK	99.7%	72.7	25	66.6	2	0	0	1214.70	1008	1019
Ribosome biogenesis protein BRX1 homolog	BRIX1	BRX1_HUMAN	41.4	99.8%	2	2	2	0.00%	5.7%	FLVQNIHTLAELK	99.7%	68.8	25	56.7	1	0	0	1525.87	141	153
Ribosome biogenesis protein BRX1 homolog	BRIX1	BRX1_HUMAN	41.4	99.8%	2	2	2	0.00%	5.7%	FVLNLIK	98.7%	33.8	25	31.6	1	0	0	846.54	236	242
Ribosome production factor 2 homolog	RPF2	RPF2_HUMAN	35.6	100.0%	3	3	4	0.00%	8.5%	GPTVSNIR	99.5%	38.3	25	29.5	1	0	0	843.47	169	176
Ribosome production factor 2 homolog	RPF2	RPF2_HUMAN	35.6	100.0%	3	3	4	0.00%	8.5%	KPYGVLYK	99.7%	49.3	25	25.6	1	0	0	967.56	57	64
Ribosome production factor 2 homolog	RPF2	RPF2_HUMAN	35.6	100.0%	3	3	4	0.00%	8.5%	THLASDDLYK	99.7%	49.1	25	44.5	2	0	0	1162.57	228	237
Ribosome-binding protein 1	RRBP1	RRBP1_HUMAN	152.5	100.0%	6	6	9	0.01%	5.3%	DALNQATSQVESK	99.7%	52.6	25	47.1	1	0	0	1390.68	807	819
Ribosome-binding protein 1	RRBP1	RRBP1_HUMAN	152.5	100.0%	6	6	9	0.01%	5.3%	EQEITAVQAR	99.7%	43.9	25	40.1	2	0	0	1144.60	752	761
Ribosome-binding protein 1	RRBP1	RRBP1_HUMAN	152.5	100.0%	6	6	9	0.01%	5.3%	LQSSEAEVR	98.4%	33	25	21.2	1	0	0	1018.52	922	930
Ribosome-binding protein 1	RRBP1	RRBP1_HUMAN	152.5	100.0%	6	6	9	0.01%	5.3%	NTDVAQSPEAPK	99.7%	41.2	25	19.5	2	0	0	1256.61	609	620
Ribosome-binding protein 1	RRBP1	RRBP1_HUMAN	152.5	100.0%	6	6	9	0.01%	5.3%	SIEALLEAGQAR	99.7%	45.8	25	23.7	1	0	0	1257.68	959	970
Ribosome-binding protein 1	RRBP1	RRBP1_HUMAN	152.5	100.0%	6	6	9	0.01%	5.3%	VEPAVSSVVNSIQVLTSK	99.7%	66.2	25	66.2	2	0	0	1857.03	149	166
RING finger protein 219	RNF219	RN219_HUMAN	81.1	99.8%	2	2	4	0.00%	2.5%	FAVAALQSK	99.7%	50.2	25	32.9	2	0	0	934.54	217	225
RING finger protein 219	RNF219	RN219_HUMAN	81.1	99.8%	2	2	4	0.00%	2.5%	NLSLESQIK	95.7%	28.9	25	11.6	2	0	0	1031.57	117	125
RISC-loading complex subunit TARBP2	TARBP2	TRBP2_HUMAN	39.0	99.8%	2	2	3	0.00%	7.7%	SCSLGSLGALGPACCR	99.7%	42.8	25	41.2	1	0	0	1665.75	281	296
RISC-loading complex subunit TARBP2	TARBP2	TRBP2_HUMAN	39.0	99.8%	2	2	3	0.00%	7.7%	TPISLLQEYGTR	99.7%	99.1	25	84.2	2	0	0	1377.74	30	41
RNA 3'-terminal phosphate cyclase	RTCA	RTCA_HUMAN	39.3	100.0%	3	3	6	0.01%	9.3%	AFVAGVLPFK	99.7%	59.7	25	50.6	2	0	0	1048.62	196	205
RNA 3'-terminal phosphate cyclase	RTCA	RTCA_HUMAN	39.3	100.0%	3	3	6	0.01%	9.3%	FGFIFNCDIK	99.7%	57.9	25	43.7	2	0	0	1260.61	147	156
RNA 3'-terminal phosphate cyclase	RTCA	RTCA_HUMAN	39.3	100.0%	3	3	6	0.01%	9.3%	VSTALSCLLGLPLR	99.7%	52.1	25	51	2	0	0	1499.86	22	35
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	4	0.00%	41.8%	ALETVFGK	98.4%	33	25	17.7	2	0	0	864.48	23	30
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	4	0.00%	41.8%	DRDYSDHPSGGSYR	99.7%	70.1	25	70.1	2	2	0	1611.68	269	282
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	4	0.00%	41.8%	DSYESYGNSR	99.7%	79.2	25	74.9	6	0	0	1177.48	283	292
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	4	0.00%	41.8%	DSYGGPPR	99.7%	43.3	25	27.3	2	0	0	848.39	188	195
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	4	0.00%	41.8%	DVYLSPR	94.8%	28.1	25	26.7	1	0	0	849.45	204	210
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	4	0.00%	41.8%	DYAPPPRDYTYR	96.4%	29.6	25	22.9	1	0	0	1513.71	233	244
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	4	0.00%	41.8%	DYGHSSSRDDYPSR	99.6%	33	25	33	2	2	0	1641.69	245	258
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	4	0.00%	41.8%	DYSDHPSGGSYR	99.7%	58.2	25	58.2	2	0	0	1340.55	271	282
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	4	0.00%	41.8%	GFAFVTFESPADAK	99.7%	99.9	25	67.2	14	0	0	1486.72	50	63
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	4	0.00%	41.8%	GFAFVTFESPADAKDAAR	99.7%	103	25	103	2	2	0	1899.92	50	67
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	4	0.00%	41.8%	GGHMDDGGYSMNFNMSSSR	99.7%	65.8	25	39.8	2	11	0	2065.78	126	144
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	4	0.00%	41.8%	GPPPSYGGSSR	99.7%	60.7	25	60.7	10	0	0	1061.50	299	309
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	4	0.00%	41.8%	GRDSYGGPPR	99.7%	48.9	25	12.6	2	0	0	1061.51	186	195
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	4	0.00%	41.8%	LFIGGLNTETNEK	99.7%	93.4	25	84.4	10	0	0	1435.74	10	22
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	4	0.00%	41.8%	RDVYLSPR	97.9%	31.8	25	18.3	2	0	0	1005.55	203	210
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	4	0.00%	41.8%	REPLPSR	96.4%	29.6	25	11.1	1	0	0	854.48	196	202
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	4	0.00%	41.8%	VEQATKPSFER	99.7%	46	25	40.3	2	0	0	1291.66	81	91
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	4	0.00%	41.8%	YDDYSSSR	99.7%	42.5	25	42.5	2	0	0	992.40	310	317
RNA binding protein fox-1 homolog 1	RBFOX1	RFOX1_HUMAN	42.8	100.0%	3	3	6	0.01%	8.6%	GFGFVTFENSADADR	99.7%	66	25	62.9	2	0	0	1632.73	157	171
RNA binding protein fox-1 homolog 1	RBFOX1	RFOX1_HUMAN	42.8	100.0%	3	3	6	0.01%	8.6%	KIEVNNATAR	99.7%	68.2	25	46.3	2	0	0	1115.62	185	194
RNA binding protein fox-1 homolog 1	RBFOX1	RFOX1_HUMAN	42.8	100.0%	3	3	6	0.01%	8.6%	LHGTVVEGR	98.7%	33.9	25	19.4	2	0	0	967.53	176	184

RNA methyltransferase-like protein 1	RNMTL1	RMTL1_HUMAN	47.0	100.0%	4	4	6	0.01%	11.0%	APSTWEESGLR	99.7%	64.8	25	64.8	1	0	0	1232.59	83	93
RNA methyltransferase-like protein 1	RNMTL1	RMTL1_HUMAN	47.0	100.0%	4	4	6	0.01%	11.0%	EKQPLEESASR	99.7%	52.6	25	41.1	2	0	0	1273.64	72	82
RNA methyltransferase-like protein 1	RNMTL1	RMTL1_HUMAN	47.0	100.0%	4	4	6	0.01%	11.0%	KAPSEASAQEQR	99.7%	76.6	25	65.4	2	0	0	1301.64	60	71
RNA methyltransferase-like protein 1	RNMTL1	RMTL1_HUMAN	47.0	100.0%	4	4	6	0.01%	11.0%	VVFPSGEVVEQK	99.7%	56.8	25	48.8	1	0	0	1317.70	40	51
RNA polymerase-associated protein CTR9 homolog	CTR9	CTR9_HUMAN	133.5	99.8%	2	2	2	0.00%	2.2%	DLITQATLLYTMADK	99.7%	47.7	25	47.7	1	0	0	1696.88	108	122
RNA polymerase-associated protein CTR9 homolog	CTR9	CTR9_HUMAN	133.5	99.8%	2	2	2	0.00%	2.2%	FDLALAATEAR	99.7%	52.1	25	43.3	1	0	0	1177.62	805	815
RNA pseudouridylate synthase domain-containing protein 3	RPUSD3	RUSD3_HUMAN	38.5	100.0%	4	4	7	0.01%	13.7%	DTPVELLAPLPPYFSR	99.7%	47.5	25	47.5	2	0	0	1814.97	326	341
RNA pseudouridylate synthase domain-containing protein 3	RPUSD3	RUSD3_HUMAN	38.5	100.0%	4	4	7	0.01%	13.7%	QVLDEALLR	99.7%	41.5	25	25.8	2	0	0	1056.60	288	296
RNA pseudouridylate synthase domain-containing protein 3	RPUSD3	RUSD3_HUMAN	38.5	100.0%	4	4	7	0.01%	13.7%	SGPLGDQPFAGLLPK	99.7%	50.8	25	50.8	2	0	0	1496.81	54	68
RNA pseudouridylate synthase domain-containing protein 3	RPUSD3	RUSD3_HUMAN	38.5	100.0%	4	4	7	0.01%	13.7%	TLQCLGLR	98.0%	32	25	18.4	1	0	0	960.53	342	349
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	121	0.12%	47.6%	AIKVEQATKPSFESGR	99.7%	79.8	25	79.8	2	2	0	1747.93	78	93
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	121	0.12%	47.6%	ALEAVFGK	99.7%	54.8	25	43.6	2	0	0	834.47	23	30
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	121	0.12%	47.6%	DRDYSDHPSGGSYR	99.7%	70.1	25	70.1	2	2	0	1611.68	269	282
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	121	0.12%	47.6%	DSYESYGNSR	99.7%	79.2	25	74.9	6	0	0	1177.48	283	292
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	121	0.12%	47.6%	DSYGGPPR	99.7%	43.3	25	27.3	2	0	0	848.39	188	195
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	121	0.12%	47.6%	DVYLSPR	94.8%	28.1	25	26.7	1	0	0	849.45	204	210
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	121	0.12%	47.6%	DYAPPPRDYTYR	96.4%	29.6	25	22.9	1	0	0	1513.71	233	244
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	121	0.12%	47.6%	DYGHSSSRDDYPSR	99.6%	33	25	33	2	2	0	1641.69	245	258
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	121	0.12%	47.6%	DYSDHPSGGSYR	99.7%	58.2	25	58.2	2	0	0	1340.55	271	282
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	121	0.12%	47.6%	GFAFVTFESPADAK	99.7%	99.9	25	67.2	14	0	0	1486.72	50	63
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	121	0.12%	47.6%	GFAFVTFESPADAKDAAR	99.7%	103	25	103	2	2	0	1899.92	50	67
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	121	0.12%	47.6%	GGHMDDGGYSMNFNMSSSR	99.7%	65.8	25	39.8	2	11	0	2065.78	126	144
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	121	0.12%	47.6%	GPPPSYGGSSR	99.7%	60.7	25	60.7	10	0	0	1061.50	299	309
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	121	0.12%	47.6%	GRDSYGGPPR	99.7%	48.9	25	12.6	2	0	0	1061.51	186	195
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	121	0.12%	47.6%	IVEVLLMK	99.7%	61.4	25	52.2	6	0	0	944.59	34	41
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	121	0.12%	47.6%	IVEVLLMKDR	99.7%	63.7	25	57.4	2	0	0	1231.71	34	43
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	121	0.12%	47.6%	LFIGGLNTETNEK	99.7%	93.4	25	84.4	10	0	0	1435.74	10	22
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	121	0.12%	47.6%	RDVYLSPR	97.9%	31.8	25	18.3	2	0	0	1005.55	203	210
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	121	0.12%	47.6%	REPLPSR	96.4%	29.6	25	11.1	1	0	0	854.48	196	202
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	121	0.12%	47.6%	RGPPPPPR	99.7%	55.1	25	46.1	13	0	0	873.51	94	101
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	121	0.12%	47.6%	VEQATKPSFESGR	99.7%	64.3	25	61.3	11	5	0	1435.72	81	93
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	121	0.12%	47.6%	YDDYSSSR	99.7%	42.5	25	42.5	2	0	0	992.40	310	317
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	25	28	73	0.07%	31.5%	AHLSENELEALEK	99.7%	66.7	25	66.7	2	0	0	1482.74	794	806
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	25	28	73	0.07%	31.5%	ASNIVMLR	99.3%	36.5	25	27.4	1	0	0	903.51	127	134
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	25	28	73	0.07%	31.5%	DGLGSDNIGSR	99.7%	56.9	25	50.7	2	0	0	1090.51	854	864
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	25	28	73	0.07%	31.5%	EKYGIPEPPEPK	99.7%	42.4	25	35.2	2	0	0	1383.72	823	834
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	25	28	73	0.07%	31.5%	ESATADAGYAILEK	99.7%	118	25	112	4	0	0	1438.71	686	699
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	25	28	73	0.07%	31.5%	GDPTGAGPEASLEPGADSVSMQAFSR	99.7%	80.4	25	79.3	1	2	0	2534.15	473	498
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	25	28	73	0.07%	31.5%	GFAFVEFSHLQDATR	99.7%	76.9	25	72.4	2	0	0	1724.84	172	186
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	25	28	73	0.07%	31.5%	GLVAAYSGESDSEEEQER	99.7%	137	25	132	2	0	0	1955.85	727	744
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	25	28	73	0.07%	31.5%	GQLQSHGVQAR	99.7%	70.2	25	56.4	12	0	0	1180.62	147	157
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	25	28	73	0.07%	31.5%	GSSYGVTSTESYK	99.7%	60.5	25	53.7	2	0	0	1365.62	903	915
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	25	28	73	0.07%	31.5%	INEDWLCNK	99.7%	63.5	25	38.1	4	0	0	1191.55	213	221
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	25	28	73	0.07%	31.5%	KYGGISTASVDFEQPTR	99.7%	95.5	25	95.5	1	2	0	1855.92	837	853
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	25	28	73	0.07%	31.5%	LACLLCR	99.7%	46.6	25	30.3	2	0	0	905.47	759	765
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	25	28	73	0.07%	31.5%	LDQQTLPLGGR	99.7%	76.1	25	68.8	6	0	0	1197.66	253	263
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	25	28	73	0.07%	31.5%	MLPQAATEDDIR	99.7%	67.1	25	61.8	5	0	0	1359.66	135	146
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	25	28	73	0.07%	31.5%	NSFQPISSLR	99.7%	48.9	25	19.5	4	0	0	1148.61	671	680
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	25	28	73	0.07%	31.5%	QGIVTPIEAQTR	99.7%	53.6	25	42.2	2	0	0	1312.72	882	893
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	25	28	73	0.07%	31.5%	QNLEIHR	96.5%	29.7	25	11.9	1	0	0	909.49	786	792
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	25	28	73	0.07%	31.5%	SEAEQKLPLGTR	99.7%	47.2	25	30	4	0	0	1328.72	241	252

RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	25	28	73	0.07%	31.5%	TINVEFAK	99.7%	43.1	25	33.5	2	0	0	921.50	376	383
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	25	28	73	0.07%	31.5%	TYVPALEQSADGHK	99.7%	54.6	25	51.3	2	0	0	1515.74	614	627
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	25	28	73	0.07%	31.5%	TYVPALEQSADGHKETGAPSK	97.1%	24.9	25	24.1	0	2	0	2186.07	614	634
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	25	28	73	0.07%	31.5%	VSMHYSDPKPK	95.6%	23.3	25	3.14	0	1	0	1288.64	202	212
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	25	28	73	0.07%	31.5%	WMEANQHSLNILGQK	98.8%	28.3	25	27.1	0	1	0	1768.88	187	201
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	25	28	73	0.07%	31.5%	YGGISTASVDFEQPTR	99.7%	94	25	90.5	2	0	0	1727.82	838	853
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	9	9	16	0.02%	15.8%	AQPSASLGVGYR	99.7%	43.5	25	37.9	2	0	0	1205.63	251	262
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	9	9	16	0.02%	15.8%	AQPSVSLGAPYR	99.7%	42	25	36.5	3	0	0	1245.66	275	286
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	9	9	16	0.02%	15.8%	ASYDDPYKK	99.1%	35.6	25	21.3	1	0	0	1086.51	586	594
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	9	9	16	0.02%	15.8%	ASYVAPLTAQPATYR	99.7%	76.8	25	68.4	2	0	0	1608.84	224	238
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	9	9	16	0.02%	15.8%	IFVGNVSAACTSQELR	99.7%	111	25	111	3	0	0	1751.87	81	96
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	9	9	16	0.02%	15.8%	INVELSTK	97.4%	30.9	25	24.6	1	0	0	903.51	142	149
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	9	9	16	0.02%	15.8%	KGPGLAVQSGDK	99.1%	35.7	25	28.6	1	0	0	1156.63	153	164
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	9	9	16	0.02%	15.8%	TQPMTAQAASYR	99.7%	57.6	25	52.1	1	0	0	1340.63	263	274
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	9	9	16	0.02%	15.8%	YSGSYNDYLR	99.7%	68.2	25	68.2	2	0	0	1237.55	648	657
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	9	16	0.02%	12.5%	AKENDENCGPTTTVFVGNISEK	99.0%	29.2	25	29.2	0	1	0	2410.12	76	97
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	9	16	0.02%	12.5%	EDINAIEMEEDKR	96.4%	29.6	25	28.7	1	0	0	1591.73	262	274
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	9	16	0.02%	12.5%	EKEELEEIR	99.7%	41.4	25	19.1	2	0	0	1174.60	539	547
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	9	16	0.02%	12.5%	FPVAPLIPYPLITK	99.7%	54.6	25	54.6	2	0	0	1568.95	248	261
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	9	16	0.02%	12.5%	GAIEVLIR	99.7%	59.9	25	44.1	2	0	0	870.54	209	216
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	9	16	0.02%	12.5%	LGASNSPGQPNSVK	99.7%	57.1	25	52	2	0	0	1355.69	672	685
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	9	16	0.02%	12.5%	LLAEGHPDPDAELQR	99.7%	50.3	25	46.1	2	2	0	1660.83	550	564
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	9	16	0.02%	12.5%	LLHDLQIGEK	99.7%	40.6	25	34.5	2	0	0	1165.66	146	155
RNA-binding protein 26	RBM26	RBM26_HUMAN	113.6	100.0%	3	3	5	0.00%	3.7%	AEAEAAAVHGAR	99.7%	59	25	19.7	2	0	0	1152.58	936	947
RNA-binding protein 26	RBM26	RBM26_HUMAN	113.6	100.0%	3	3	5	0.00%	3.7%	AISSTEAVLNNR	99.7%	63.2	25	49.8	2	0	0	1274.67	586	597
RNA-binding protein 26	RBM26	RBM26_HUMAN	113.6	100.0%	3	3	5	0.00%	3.7%	EGSTQQLQTTSPK	99.7%	43.7	25	39.2	1	0	0	1404.70	606	618
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	6	7	10	0.01%	9.1%	AAEGVSAADMAK	99.7%	55.7	25	54.2	2	0	0	1136.53	454	465
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	6	7	10	0.01%	9.1%	DTQSVSAIGEEK	99.7%	56.3	25	49.8	1	0	0	1263.61	197	208
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	6	7	10	0.01%	9.1%	FNQLVEQYK	99.7%	45.3	25	22.5	2	0	0	1168.60	730	738
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	6	7	10	0.01%	9.1%	GFGFVQFK	98.3%	32.8	25	24.7	1	0	0	929.49	155	162
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	6	7	10	0.01%	9.1%	LINNNPEIFGPLK	99.7%	45.5	25	36	2	0	0	1468.82	559	571
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	6	7	10	0.01%	9.1%	SEQLEELFSQVGPVK	99.7%	72.9	25	72.9	2	0	0	1689.87	17	31
RNA-binding protein 34	RBM34	RBM34_HUMAN	48.6	100.0%	3	3	5	0.00%	7.4%	ILDDTEDTVVSQR	99.7%	46.5	25	40.3	1	0	0	1490.73	157	169
RNA-binding protein 34	RBM34	RBM34_HUMAN	48.6	100.0%	3	3	5	0.00%	7.4%	IQINQEEER	99.7%	58.4	25	53.6	2	0	0	1158.58	172	180
RNA-binding protein 34	RBM34	RBM34_HUMAN	48.6	100.0%	3	3	5	0.00%	7.4%	LGQVASSLFR	99.7%	62.1	25	57.7	2	0	0	1077.61	35	44
RNA-binding protein 39	RBM39	RBM39_HUMAN	59.4	100.0%	5	5	14	0.01%	11.9%	AAAMANNLQK	98.7%	33.8	25	14.5	2	0	0	1031.53	235	244
RNA-binding protein 39	RBM39	RBM39_HUMAN	59.4	100.0%	5	5	14	0.01%	11.9%	DLEEFFSTVGK	99.7%	68.7	25	56	5	0	0	1271.62	168	178
RNA-binding protein 39	RBM39	RBM39_HUMAN	59.4	100.0%	5	5	14	0.01%	11.9%	TDASSASSFLDSDELER	99.7%	108	25	108	2	0	0	1829.80	330	346
RNA-binding protein 39	RBM39	RBM39_HUMAN	59.4	100.0%	5	5	14	0.01%	11.9%	TGIDLGTTGR	99.7%	45.8	25	11.9	1	0	0	990.52	347	356
RNA-binding protein 39	RBM39	RBM39_HUMAN	59.4	100.0%	5	5	14	0.01%	11.9%	VLGVPIIVQASQAEK	99.7%	64.6	25	63.2	4	0	0	1551.91	218	232
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	8	9	17	0.02%	28.6%	AEDAVEAIR	99.7%	52.1	25	30	2	0	0	973.49	121	129
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	8	9	17	0.02%	28.6%	ATAPVPTVGEGYGYGHESELSQASAAAR	99.7%	53.8	25	53.8	0	2	0	2776.32	314	341
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	8	9	17	0.02%	28.6%	GLDNTEFQGK	99.7%	69.6	25	66.8	2	0	0	1108.53	130	139
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	8	9	17	0.02%	28.6%	LFIGNLPR	99.7%	52.2	25	13.1	2	0	0	929.56	4	11
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	8	9	17	0.02%	28.6%	LHGVNINVEASK	99.7%	62.9	25	54.7	2	1	0	1280.70	60	71
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	8	9	17	0.02%	28.6%	LHVGNISPTCTNK	99.7%	48.5	25	44.9	2	0	0	1440.73	80	92
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	8	9	17	0.02%	28.6%	VADLTEQYNEQYGAVR	99.7%	107	25	104	2	0	0	1855.88	183	198
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	8	9	17	0.02%	28.6%	VLECDIIK	99.7%	45.4	25	30.4	2	0	0	989.53	28	35
RNA-binding protein FUS	FUS	FUS_HUMAN	53.4	99.8%	2	2	4	0.00%	3.0%	GEATVSFDDPPSAK	99.7%	105	25	100	2	0	0	1420.66	335	348
RNA-binding protein FUS	FUS	FUS_HUMAN	53.4	99.8%	2	2	4	0.00%	3.0%	LKGEATVSFDDPPSAK	99.7%	39.1	25	39.1	0	2	0	1661.84	333	348
RNA-binding protein Musashi homolog 1	MSI1	MSI1H_HUMAN	39.1	100.0%	3	4	10	0.01%	11.0%	EYFGQFGEVK	99.7%	48.7	25	43.2	2	0	0	1203.57	38	47

RNA-binding protein Musashi homolog 1	MSI1	MSI1H_HUMAN	39.1	100.0%	3	4	10	0.01%	11.0%	GFGFVTFESEDIVEK	99.7%	64.9	25	62	2	0	0	1703.82	151	165
RNA-binding protein Musashi homolog 1	MSI1	MSI1H_HUMAN	39.1	100.0%	3	4	10	0.01%	11.0%	GFGFVTFMDQAGVDK	99.7%	86.9	25	77.5	6	0	0	1634.75	62	76
RNA-binding protein Musashi homolog 2	MSI2	MSI2H_HUMAN	35.2	100.0%	4	4	12	0.01%	17.7%	GFGFVTFADPASVDK	99.7%	84.5	25	84.2	6	0	0	1557.76	63	77
RNA-binding protein Musashi homolog 2	MSI2	MSI2H_HUMAN	35.2	100.0%	4	4	12	0.01%	17.7%	GFGFVTFENEDVVEK	99.7%	83.6	25	72.6	2	0	0	1716.81	152	166
RNA-binding protein Musashi homolog 2	MSI2	MSI2H_HUMAN	35.2	100.0%	4	4	12	0.01%	17.7%	IFVGGLSANTVVEDVK	99.7%	105	25	105	3	0	0	1647.90	112	127
RNA-binding protein Musashi homolog 2	MSI2	MSI2H_HUMAN	35.2	100.0%	4	4	12	0.01%	17.7%	VLGQPHHELDSK	99.7%	51	25	43.9	1	0	0	1359.70	78	89
RNA-binding protein PNO1	PNO1	PNO1_HUMAN	27.9	100.0%	4	4	6	0.01%	17.5%	AEEGFTQVTR	99.7%	57.8	25	41.9	2	0	0	1137.55	12	21
RNA-binding protein PNO1	PNO1	PNO1_HUMAN	27.9	100.0%	4	4	6	0.01%	17.5%	FTIENVTR	98.0%	31.9	25	24	1	0	0	979.52	192	199
RNA-binding protein PNO1	PNO1	PNO1_HUMAN	27.9	100.0%	4	4	6	0.01%	17.5%	MDTEEARPAK	97.1%	30.5	25	30.1	1	0	0	1147.54	47	56
RNA-binding protein PNO1	PNO1	PNO1_HUMAN	27.9	100.0%	4	4	6	0.01%	17.5%	QAEQLSAAGEGGDAGR	99.7%	82.9	25	78.5	2	0	0	1516.70	31	46
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	12	13	52	0.05%	35.9%	AAVLGENGR	97.9%	31.7	25	31.7	2	0	0	886.47	70	78
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	12	13	52	0.05%	35.9%	GYAFVQYSNER	99.7%	77.1	25	68.4	4	0	0	1333.62	56	66
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	12	13	52	0.05%	35.9%	KSDVETIFSK	99.7%	71.9	25	59.6	2	0	0	1153.61	35	44
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	12	13	52	0.05%	35.9%	LEQIAAEQK	99.7%	62.3	25	49.4	5	0	0	1029.56	208	216
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	12	13	52	0.05%	35.9%	LQASNVTNK	99.7%	65.5	25	50.2	4	0	0	974.53	5	13
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	12	13	52	0.05%	35.9%	LQASNVTNKNDPK	99.7%	42.5	25	30.9	3	0	0	1428.74	5	17
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	12	13	52	0.05%	35.9%	LSPVPVPR	98.9%	34.6	25	29	1	0	0	864.53	134	141
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	12	13	52	0.05%	35.9%	SDVETIFSK	99.7%	49.5	25	30.6	4	0	0	1025.52	36	44
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	12	13	52	0.05%	35.9%	SNIDALLSR	99.7%	85	25	54.5	6	0	0	988.54	199	207
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	12	13	52	0.05%	35.9%	SSELQAIK	99.7%	69.7	25	34.9	4	0	0	875.48	184	191
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	12	13	52	0.05%	35.9%	VFIGNLNTALVK	99.7%	114	25	0	11	0	0	1288.76	23	34
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	12	13	52	0.05%	35.9%	VLAGQTLDINMAGEPKPDRPK	99.7%	64.7	25	64.7	0	6	0	2250.19	79	99
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	13	15	30	0.03%	45.2%	ANCIDSTASAEAVFASEVK	99.7%	130	25	128	2	0	0	1969.92	266	284
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	13	15	30	0.03%	45.2%	ANCIDSTASAEAVFASEVKK	99.4%	31.2	25	31.2	0	2	0	2098.01	266	285
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	13	15	30	0.03%	45.2%	DHAVVVGVYRPPPK	99.7%	78.5	25	73.4	2	2	0	1533.85	305	318
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	13	15	30	0.03%	45.2%	GKEDALVTK	99.5%	38.7	25	34.4	2	0	0	960.54	101	109
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	13	15	30	0.03%	45.2%	HEGVFICR	98.5%	33.1	25	33.1	2	0	0	1017.49	93	100
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	13	15	30	0.03%	45.2%	IVALNAHTFLR	99.7%	81.7	25	76.3	2	2	0	1254.73	245	255
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	13	15	30	0.03%	45.2%	LAAAILGGVDQIHIKPGAK	99.7%	45.6	25	43.8	0	2	0	1872.11	144	162
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	13	15	30	0.03%	45.2%	MQQENMKPQEQLTLEPYER	99.7%	41.6	25	40.4	0	2	0	2424.12	286	304
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	13	15	30	0.03%	45.2%	NLVPGESVYGEK	99.7%	44.5	25	39.5	2	0	0	1291.65	110	121
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	13	15	30	0.03%	45.2%	NLVPGESVYGEKR	99.7%	59.9	25	53.5	2	0	0	1447.75	110	122
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	13	15	30	0.03%	45.2%	NVMVEPHR	99.6%	39.7	25	36.6	2	0	0	997.49	85	92
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	13	15	30	0.03%	45.2%	TNIIPVIEDAR	99.7%	55.7	25	0	2	0	0	1240.69	208	218
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	13	15	30	0.03%	45.2%	VSISEGDDKIEYR	99.7%	65.4	25	59.7	2	0	0	1510.74	123	135
RRP12-like protein	RRP12	RRP12_HUMAN	143.7	100.0%	3	3	4	0.00%	2.0%	RAVLETIR	98.3%	32.8	25	21.4	1	0	0	957.58	711	718
RRP12-like protein	RRP12	RRP12_HUMAN	143.7	100.0%	3	3	4	0.00%	2.0%	SWLLPVIR	99.0%	35.2	25	14.8	2	0	0	983.60	567	574
RRP12-like protein	RRP12	RRP12_HUMAN	143.7	100.0%	3	3	4	0.00%	2.0%	VLATQPGPGR	98.1%	32.2	25	30.1	1	0	0	995.56	1129	1138
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	16	0.02%	19.3%	ALESSIAPIVIFASNR	99.7%	76.5	25	76.5	2	2	0	1687.94	318	333
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	16	0.02%	19.3%	AVLLAGPPGTGK	99.7%	45.7	25	40.2	2	0	0	1080.64	65	76
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	16	0.02%	19.3%	EACGVIVELIK	97.6%	31.2	25	17.2	2	0	0	1230.68	47	57
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	16	0.02%	19.3%	GLGLDESGLAK	99.7%	56.2	25	48.7	2	0	0	1059.57	23	33
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	16	0.02%	19.3%	LDPSIFESLQK	99.7%	50.4	25	41.7	2	0	0	1276.68	172	182
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	16	0.02%	19.3%	QAASGLVGQENAR	99.7%	85.9	25	77.7	2	0	0	1300.66	34	46
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	16	0.02%	19.3%	TALALAIAQELGSK	99.7%	101	25	101	2	0	0	1385.80	77	90
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	12	20	0.02%	29.8%	AAGVVLEMIR	99.7%	70.4	25	58.3	1	0	0	1058.60	55	64
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	12	20	0.02%	29.8%	ALESDMAPVLIMATNR	99.7%	89.6	25	72.7	2	0	0	1731.88	315	330
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	12	20	0.02%	29.8%	AVLIAGQPGTGK	99.7%	72.4	25	58.5	2	0	0	1111.65	72	83
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	12	20	0.02%	29.8%	DKVQAGDVITIDK	99.7%	67.1	25	53.3	2	0	0	1401.76	185	197
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	12	20	0.02%	29.8%	EVVHTVSLHEIDVINSR	99.7%	35.7	25	35.7	0	2	0	1947.03	237	253
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	12	20	0.02%	29.8%	FVQCPDGELQK	99.7%	49.7	25	45.1	2	0	0	1320.63	224	234

RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	12	20	0.02%	29.8%	GTEVQVDDIKR	99.7%	49.5	25	32	2	0	0	1259.66	418	428
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	12	20	0.02%	29.8%	TEALTQAFR	99.7%	43.7	25	33.6	2	0	0	1036.54	116	124
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	12	20	0.02%	29.8%	TQGFLALFSGDTGEIK	99.7%	90.5	25	80.9	2	0	0	1683.86	254	269
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	12	20	0.02%	29.8%	TTEMETIYDLGTK	99.7%	70.9	25	70.9	2	0	0	1501.71	165	177
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	12	20	0.02%	29.8%	VYSLFLDESR	99.7%	52.2	25	42.9	1	0	0	1228.62	429	438
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	5	8	13	0.01%	15.7%	ELLEIVKK	98.3%	32.5	25	21.9	1	0	0	971.61	344	351
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	5	8	13	0.01%	15.7%	FVIGGPQGDAGLTGR	99.7%	107	25	99.3	2	0	0	1444.75	250	264
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	5	8	13	0.01%	15.7%	TGMILLAGEITSR	99.7%	82.8	25	76.5	4	0	0	1361.75	62	74
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	5	8	13	0.01%	15.7%	TQVTVQYMQDR	99.7%	44.2	25	37.4	2	0	0	1384.65	182	192
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	5	8	13	0.01%	15.7%	YLDEDTIYHLQPSGR	99.7%	74.1	25	74.1	2	2	0	1806.87	235	249
SAFB-like transcription modulator	SLTM	SLTM_HUMAN	117.2	99.8%	2	2	2	0.00%	2.1%	ELLSAEENKR	99.3%	36.5	25	24.3	1	0	0	1188.62	141	150
SAFB-like transcription modulator	SLTM	SLTM_HUMAN	117.2	99.8%	2	2	2	0.00%	2.1%	TELHGQLISVEK	99.7%	52.4	25	49.3	1	0	0	1353.74	448	459
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	AEIGIAMGSGTAVAK	99.7%	84.9	25	80.8	4	0	0	1375.73	713	727
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	AMGVVVATGVNTEIGK	99.7%	73.2	25	52	2	0	0	1561.83	219	234
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	CLALATHDNPLR	99.7%	49.2	25	43.7	2	0	0	1380.71	560	571
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	DIVPGDIVEIAVGDK	99.7%	45.6	25	45.6	2	0	0	1539.83	144	158
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	EEMHLEDSANFIK	96.9%	30.2	25	29.5	1	0	0	1562.72	573	585
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	EFDELNPSAQR	99.7%	66.6	25	59.7	2	0	0	1305.61	656	666
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	EFTLEFSR	99.7%	52.9	25	38.1	3	0	0	1028.50	482	489
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	EWGSGSDTLR	99.7%	45.7	25	35	2	0	0	1107.51	550	559
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	GAPEGVIDR	99.7%	42.1	25	34.2	2	0	0	913.47	515	523
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	GTAVAICR	97.8%	31.6	25	20	1	0	0	847.45	629	636
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	HTDPVPDPR	99.5%	37.9	25	33	2	0	0	1033.51	190	198
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	IGIFGQDEDVTSK	99.7%	82.2	25	75.6	4	0	0	1408.70	638	650
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	IRDEMVATEQER	99.7%	62.4	25	49.8	5	1	0	1476.71	235	246
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	ISLPVILMDETLK	99.7%	93.8	25	82.1	4	0	0	1471.84	972	984
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	KAEIGIAMGSGTAVAK	99.7%	54.2	25	52.7	1	1	0	1519.82	712	727
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	LDEFGEQLSK	99.7%	63.1	25	44.5	3	0	0	1165.57	253	262
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	MNVFDTELK	99.7%	46	25	21.2	2	0	0	1112.53	452	460
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	NMLFSGTNIAAGK	99.7%	80.8	25	80.7	4	0	0	1323.67	206	218
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	NYLEPGKECVQPATK	99.5%	38.4	25	32.2	1	0	0	1733.85	989	1003
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	RIGIFGQDEDVTSK	99.1%	29.7	25	28.9	0	2	0	1564.80	637	650
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	SLPSVETLGCTSVICSDK	99.7%	98.2	25	98.2	2	0	0	1952.93	335	352
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	SMSVYCTPNKPSR	99.7%	52.7	25	52.7	2	0	0	1526.71	493	505
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	TGTLTTNQMSVCR	99.7%	67.7	25	67.7	3	0	0	1468.69	353	365
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	VDQSILTGESVSVIK	99.7%	85.3	25	77.6	5	0	0	1574.86	175	189
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	VGEATETALTCLVEK	99.7%	106	25	101	4	0	0	1620.82	437	451
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	VIMITGDNK	99.7%	46.4	25	8.72	3	0	0	990.53	620	628
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	35	72	0.07%	29.6%	WGSNELPAEEGK	99.7%	76.6	25	76	2	0	0	1316.61	36	47
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	22	54	0.05%	23.0%	ADSLLAVVK	99.7%	77.9	25	63.9	4	0	0	915.55	286	294
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	22	54	0.05%	23.0%	AIEDEGGNPDEIEITSEGNK	99.7%	109	25	109	2	0	0	2116.95	64	83
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	22	54	0.05%	23.0%	AIEDEGGNPDEIEITSEGNKK	99.7%	90.7	25	90.7	2	4	0	2245.05	64	84
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	22	54	0.05%	23.0%	CYGFVTMSTAEEATK	99.7%	85	25	85	5	0	0	1710.74	448	462
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	22	54	0.05%	23.0%	DDAYWPEAK	96.0%	29.2	25	25.3	1	0	0	1094.48	720	728
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	22	54	0.05%	23.0%	DGWGGYGSDKR	99.7%	44.5	25	37	2	0	0	1197.53	796	806
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	22	54	0.05%	23.0%	ELPEQLQEHAIEDK	99.7%	55.6	25	39.7	2	0	0	1678.83	173	186
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	22	54	0.05%	23.0%	FHDFDHR	97.2%	30.7	25	20.2	1	0	0	973.43	746	752
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	22	54	0.05%	23.0%	GRYPDHSVDR	99.3%	30.8	25	23.6	1	2	0	1201.57	755	764
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	22	54	0.05%	23.0%	ILDILGETCK	99.7%	84.4	25	73.6	4	0	0	1161.62	217	226
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	22	54	0.05%	23.0%	KFDFDACNEVPPAPK	99.7%	90.1	25	80.9	1	1	0	1734.82	356	370
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	22	54	0.05%	23.0%	MSSPEDDSDTKR	99.7%	49.5	25	47.4	2	0	0	1367.57	382	393

Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	22	54	0.05%	23.0%	NFWVSGLSSTTR	99.7%	62.7	25	52.8	8	0	0	1354.67	407	418
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	22	54	0.05%	23.0%	REPAEQPGDGER	99.7%	45.9	25	44.7	3	0	0	1340.62	295	306
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	22	54	0.05%	23.0%	RPYDLDR	96.9%	30.2	25	16.7	2	0	0	934.47	712	718
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	22	54	0.05%	23.0%	SEPVKEESSELEQPFAQDTSSVGPDR	99.7%	65.7	25	65.7	0	4	0	2848.31	227	252
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	22	54	0.05%	23.0%	SWQGTADGGMMDR	97.2%	30.5	25	30.5	1	0	0	1411.57	832	844
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	18	22	54	0.05%	23.0%	YHSDFNR	98.5%	33.2	25	28.4	2	0	0	938.41	736	742
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.8%	ADSLLAVVK	99.7%	77.9	25	63.9	4	0	0	915.55	285	293
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.8%	AWQGAMDAGAASR	99.7%	45.6	25	39.6	1	0	0	1307.58	861	873
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.8%	DGWGGYGSDKR	99.7%	44.5	25	37	2	0	0	1197.53	820	830
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.8%	DIKPIIKDEK	99.0%	34.8	25	26.7	2	2	0	1198.70	389	398
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.8%	EYVAAQLR	99.7%	42	25	23.6	4	0	0	949.51	164	171
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.8%	FHDFDHR	97.2%	30.7	25	20.2	1	0	0	973.43	765	771
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.8%	GLSGPSGPGHMASR	97.9%	31.7	25	31.7	1	0	0	1326.62	884	897
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.8%	ILDILGETCK	99.7%	84.4	25	73.6	4	0	0	1161.62	216	225
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.8%	KFDFDACNEVPPAPK	99.7%	90.1	25	80.9	1	1	0	1734.82	355	369
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.8%	LEAFHER	99.7%	48	25	38.6	4	0	0	901.45	651	657
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.8%	NLWVSGLSSTTR	99.7%	71.8	25	64.8	3	0	0	1320.69	408	419
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.8%	NTLETSSLNFK	99.7%	79.9	25	72.3	4	0	0	1253.64	189	199
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.8%	REPAEQPGDGER	99.7%	45.9	25	44.7	3	0	0	1340.62	294	305
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.8%	RPYDLDR	96.9%	30.2	25	16.7	2	0	0	934.47	730	736
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.8%	SEPVKEESSELEQPFAQDTSSVGPDR	99.7%	65.7	25	65.7	0	4	0	2848.31	226	251
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.8%	SKGEPVISVK	99.4%	37.2	25	30.7	4	0	0	1043.61	577	586
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	29	0.03%	20.8%	VTPDIEESLLEPENEK	99.7%	89.4	25	86.1	4	0	0	1841.90	200	215
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	10	10	21	0.02%	13.7%	DQIIDSLKR	99.7%	42.9	25	26.5	3	0	0	1087.61	80	88
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	10	10	21	0.02%	13.7%	EPAVLMGILGIYK	99.7%	69.1	25	69.1	1	0	0	1403.80	539	551
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	10	10	21	0.02%	13.7%	LGSSSLTNIPEEVR	99.7%	64.9	25	46	1	0	0	1501.79	288	301
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	10	10	21	0.02%	13.7%	LILPELGPVFK	99.7%	51.7	25	37	2	0	0	1225.76	408	418
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	10	10	21	0.02%	13.7%	LLTVQHPLEESR	99.7%	67	25	58.7	3	0	0	1421.77	101	112
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	10	10	21	0.02%	13.7%	MVHGNITPENIILNK	98.3%	26.9	25	26.9	0	1	0	1692.91	174	188
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	10	10	21	0.02%	13.7%	NACLQTSSLAVR	99.7%	86.7	25	72.8	4	0	0	1319.67	494	505
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	10	10	21	0.02%	13.7%	QQEPIQILLIFLQK	99.7%	45	25	45	1	0	0	1711.02	419	432
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	10	10	21	0.02%	13.7%	VTADVTSAVMGNPVTR	99.7%	88.7	25	78.7	1	0	0	1633.82	15	30
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	10	10	21	0.02%	13.7%	VTNIGNQQIDK	99.7%	65.8	25	50	4	0	0	1229.65	637	647
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	3	3	7	0.01%	6.9%	FGQDIISPLLSVK	99.7%	74.7	25	68.4	3	0	0	1416.81	51	63
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	3	3	7	0.01%	6.9%	LTSAVSSLPELLEK	99.7%	83.7	25	60.8	2	0	0	1486.84	382	395
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	3	3	7	0.01%	6.9%	SLLDIISDPDAGTPEDK	99.7%	69.8	25	64.9	2	0	0	1785.88	437	453
Septin-2	2-Sep	SEPT2_HUMAN	41.5	99.7%	2	2	2	0.00%	6.9%	STLINSLFLTDLYPER	99.6%	40	25	38.8	1	0	0	1882.00	51	66
Septin-2	2-Sep	SEPT2_HUMAN	41.5	99.7%	2	2	2	0.00%	6.9%	VNIVPVIAK	94.8%	28.2	25	12.7	1	0	0	952.62	175	183
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	6	6	11	0.01%	12.5%	LEPKPQPPVAEATPR	99.7%	55.7	25	53.8	0	2	0	1629.90	223	237
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	6	6	11	0.01%	12.5%	QVENAGAIGPSR	99.7%	56	25	44.1	2	0	0	1198.62	118	129
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	6	6	11	0.01%	12.5%	RTELSIDISSK	95.4%	28.6	25	18.2	1	0	0	1248.68	107	117
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	6	6	11	0.01%	12.5%	VPEVPTAPATDAAPK	99.7%	54.4	25	44.2	2	0	0	1463.77	172	186
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	6	6	11	0.01%	12.5%	VVNIVPVIAK	99.7%	50.3	25	50.3	2	0	0	1051.69	436	445
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	6	6	11	0.01%	12.5%	YLQEEVNINR	99.7%	53.9	25	45.3	2	0	0	1277.65	390	399
Serine hydroxymethyltransferase, mitochondrial	SHMT2	GLYM_HUMAN	56.0	100.0%	4	4	6	0.01%	8.5%	HADIVTTTTHK	96.4%	24	25	20.1	0	2	0	1223.64	270	280
Serine hydroxymethyltransferase, mitochondrial	SHMT2	GLYM_HUMAN	56.0	100.0%	4	4	6	0.01%	8.5%	LGAPALTSR	99.7%	55.3	25	45.4	1	0	0	885.52	426	434
Serine hydroxymethyltransferase, mitochondrial	SHMT2	GLYM_HUMAN	56.0	100.0%	4	4	6	0.01%	8.5%	TGLIDYNQLALTAR	99.7%	64	25	58.4	2	0	0	1548.84	201	214
Serine hydroxymethyltransferase, mitochondrial	SHMT2	GLYM_HUMAN	56.0	100.0%	4	4	6	0.01%	8.5%	YSEGYPGKR	98.7%	33.8	25	33.8	1	0	0	1056.51	96	104
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	7	7	12	0.01%	16.9%	AACFAIQK	99.7%	43.4	25	34.7	2	0	0	908.47	190	197
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	7	7	12	0.01%	16.9%	DHPALNYNIVSGPPSHK	99.7%	42.9	25	42.9	0	1	0	1845.92	76	92
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	7	7	12	0.01%	16.9%	EQEIEDQKNPR	99.7%	65.6	25	55.3	2	0	0	1385.67	223	233

Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	7	7	12	0.01%	16.9%	LLQEIVDQCMNR	99.7%	64.2	25	63.7	2	0	0	1518.74	411	422
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	7	7	12	0.01%	16.9%	RGDIVFVDR	99.6%	39.1	25	18.2	2	0	0	1076.58	181	189
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	7	7	12	0.01%	16.9%	VVVTVEQTEEELER	99.7%	92.3	25	92	1	0	0	1659.84	446	459
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	7	7	12	0.01%	16.9%	YGVGTCGPR	99.7%	44	25	38.3	2	0	0	966.45	128	136
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	12	55	0.05%	47.2%	DAEDAVYGR	99.7%	41.8	25	32.6	2	0	0	995.44	66	74
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	12	55	0.05%	47.2%	DGTGVVEFVR	99.7%	76.1	25	56.9	7	0	0	1078.55	155	164
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	12	55	0.05%	47.2%	DGYDYDGYR	99.7%	52.3	25	52.3	6	0	0	1123.43	75	83
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	12	55	0.05%	47.2%	EAGDVCYADVYR	99.7%	68.9	25	68.9	7	0	0	1417.61	143	154
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	12	55	0.05%	47.2%	GGPPFAFVEFEDPR	99.7%	58.5	25	58.5	2	0	0	1564.74	52	65
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	12	55	0.05%	47.2%	GGPPFAFVEFEDPRDAEDAVYGR	99.7%	36.2	25	35.2	0	2	0	2541.17	52	74
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	12	55	0.05%	47.2%	IYVGNLPPDIR	99.7%	71	25	61.7	7	0	0	1256.70	18	28
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	12	55	0.05%	47.2%	KEDMTYAVR	99.7%	60.3	25	51.8	9	0	0	1112.54	165	173
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	12	55	0.05%	47.2%	LRVEFPR	99.4%	37.6	25	19.4	11	0	0	916.54	84	90
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	12	55	0.05%	47.2%	SHEGETAYIR	99.7%	48.8	25	45.8	7	0	0	1162.55	182	191
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	12	55	0.05%	47.2%	TKDIEDVFYK	99.7%	65.4	25	64.4	4	0	0	1257.64	29	38
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	12	55	0.05%	47.2%	VVVSGLPPSGSWQDLK	98.0%	31.9	25	30.8	2	0	0	1668.90	123	138
Serine/arginine-rich splicing factor 10	SRSF10	SRS10_HUMAN	31.3	100.0%	6	8	15	0.01%	23.7%	DAEDALHNLDR	99.4%	37.1	25	31.7	1	0	0	1268.59	63	73
Serine/arginine-rich splicing factor 10	SRSF10	SRS10_HUMAN	31.3	100.0%	6	8	15	0.01%	23.7%	GFAYVQFEDVR	99.7%	59.7	25	54	4	0	0	1330.64	52	62
Serine/arginine-rich splicing factor 10	SRSF10	SRS10_HUMAN	31.3	100.0%	6	8	15	0.01%	23.7%	QIEIQFAQGDR	99.7%	59.1	25	57.9	3	0	0	1304.66	80	90
Serine/arginine-rich splicing factor 10	SRSF10	SRS10_HUMAN	31.3	100.0%	6	8	15	0.01%	23.7%	QIEIQFAQGDRK	99.7%	71.9	25	56.3	2	1	0	1432.75	80	91
Serine/arginine-rich splicing factor 10	SRSF10	SRS10_HUMAN	31.3	100.0%	6	8	15	0.01%	23.7%	YGPIVDVYVPLDFYTR	99.7%	42.3	25	42.3	1	0	0	1916.98	33	48
Serine/arginine-rich splicing factor 10	SRSF10	SRS10_HUMAN	31.3	100.0%	6	8	15	0.01%	23.7%	YLRPPNTSLFVR	99.2%	30.1	25	30.1	1	2	0	1462.82	4	15
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	9	10	47	0.05%	45.7%	AFGYYGPLR	99.7%	55.7	25	50.2	10	0	0	1043.53	29	37
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	9	10	47	0.05%	45.7%	DSCPLDCK	98.3%	32.7	25	32.7	4	0	0	994.40	4	11
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	9	10	47	0.05%	45.7%	GPPPSWGR	98.8%	34.2	25	27.9	3	0	0	853.43	91	98
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	9	10	47	0.05%	45.7%	NPPGFAFVEFEDPR	99.7%	61.1	25	61.1	7	0	0	1621.76	44	57
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	9	10	47	0.05%	45.7%	NPPGFAFVEFEDPRDAADAVR	96.3%	23.9	25	23.9	0	1	0	2320.10	44	64
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	9	10	47	0.05%	45.7%	NRGPPPSWGR	99.6%	39.9	25	34	6	0	0	1123.58	89	98
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	9	10	47	0.05%	45.7%	VRVELSNGEK	99.7%	60.7	25	44.7	4	0	0	1130.62	76	85
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	9	10	47	0.05%	45.7%	VYVGNLGNNGNK	99.7%	67.6	25	67.6	4	0	0	1248.63	12	23
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	9	10	47	0.05%	45.7%	VYVGNLGNNGNKTELER	99.7%	82.5	25	74.9	4	4	0	1876.95	12	28
Serine/arginine-rich splicing factor 5	SRSF5	SRSF5_HUMAN	31.3	100.0%	4	4	7	0.01%	12.9%	LIVENLSSR	99.7%	55.6	25	50.6	2	0	0	1030.59	110	118
Serine/arginine-rich splicing factor 5	SRSF5	SRSF5_HUMAN	31.3	100.0%	4	4	7	0.01%	12.9%	LNEGVVEFASYGDLK	99.7%	117	25	114	2	0	0	1640.82	144	158
Serine/arginine-rich splicing factor 5	SRSF5	SRSF5_HUMAN	31.3	100.0%	4	4	7	0.01%	12.9%	VSWQDLK	99.7%	40.5	25	21.4	1	0	0	875.46	119	125
Serine/arginine-rich splicing factor 5	SRSF5	SRSF5_HUMAN	31.3	100.0%	4	4	7	0.01%	12.9%	VSWQDLKDFMR	99.7%	42.2	25	38	2	0	0	1424.70	119	129
Serine/arginine-rich splicing factor 7	SRSF7	SRSF7_HUMAN	27.4	100.0%	6	7	16	0.02%	26.1%	AFSYYGPLR	99.7%	45.6	25	36.9	2	0	0	1073.54	30	38
Serine/arginine-rich splicing factor 7	SRSF7	SRSF7_HUMAN	27.4	100.0%	6	7	16	0.02%	26.1%	GHYAYDCHR	95.4%	28.6	25	28.3	1	0	0	1178.48	113	121
Serine/arginine-rich splicing factor 7	SRSF7	SRSF7_HUMAN	27.4	100.0%	6	7	16	0.02%	26.1%	NPPGFAFVEFEDPR	99.7%	61.1	25	61.1	7	0	0	1621.76	45	58
Serine/arginine-rich splicing factor 7	SRSF7	SRSF7_HUMAN	27.4	100.0%	6	7	16	0.02%	26.1%	NPPGFAFVEFEDPRDAEDAVR	99.7%	39.5	25	39.5	0	2	0	2378.10	45	65
Serine/arginine-rich splicing factor 7	SRSF7	SRSF7_HUMAN	27.4	100.0%	6	7	16	0.02%	26.1%	VELSTGMPR	99.7%	43.4	25	37.9	3	0	0	989.51	79	87
Serine/arginine-rich splicing factor 7	SRSF7	SRSF7_HUMAN	27.4	100.0%	6	7	16	0.02%	26.1%	VRVELSTGMPR	99.7%	44.8	25	44.8	2	0	0	1244.68	77	87
Serine/arginine-rich splicing factor 7	SRSF7	SRSF7_HUMAN	27.4	100.0%	6	7	16	0.02%	26.1%	VYVGNLGTGAGK	99.7%	95.2	25	91.1	6	0	0	1135.61	13	24
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	63	0.06%	58.8%	DAEDAIYGR	98.8%	34.2	25	29.2	2	0	0	1009.46	64	72
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	63	0.06%	58.8%	DGVGMVEYLR	99.7%	74.2	25	52.5	7	0	0	1138.56	145	154
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	63	0.06%	58.8%	EAGDVCYADVQK	99.7%	77.3	25	72.4	4	0	0	1354.59	133	144
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	63	0.06%	58.8%	EDMEYALR	98.5%	33.2	25	26.8	1	0	0	1026.46	156	163
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	63	0.06%	58.8%	EKDLEDLFYK	99.7%	55.6	25	47.4	2	1	0	1299.65	27	36
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	63	0.06%	58.8%	FEDPRDAEDAIYGR	99.7%	38.2	25	38.2	3	4	0	1653.75	59	72
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	63	0.06%	58.8%	GSPHYFSPFRPY	99.7%	55	25	55	3	3	0	1454.69	210	221
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	63	0.06%	58.8%	HGLVPFAFVR	99.7%	45.5	25	43.6	3	0	0	1142.65	49	58
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	63	0.06%	58.8%	IYVGNLPTDVR	99.7%	61.7	25	47.2	2	0	0	1246.68	16	26

Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	63	0.06%	58.8%	KEDMEYALR	99.7%	50.8	25	44	6	0	0	1170.55	155	163
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	63	0.06%	58.8%	LRVEFPR	99.4%	37.6	25	19.4	11	0	0	916.54	82	88
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	63	0.06%	58.8%	NGYDYGQCR	99.7%	55.7	25	49.4	3	0	0	1132.45	73	81
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	63	0.06%	58.8%	SHEGETSYIR	99.7%	52.6	25	48.5	6	0	0	1178.54	172	181
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	14	19	63	0.06%	58.8%	VLVSGLPPSGSWQDLK	99.7%	43.7	25	32.8	2	0	0	1682.91	113	128
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	9	11	18	0.02%	28.0%	AKDLILR	98.3%	32.8	25	23.7	4	0	0	828.53	353	359
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	9	11	18	0.02%	28.0%	DIKPDNLLLDSK	99.7%	41	25	38.6	2	1	0	1370.75	212	223
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	9	11	18	0.02%	28.0%	DTGHVYAMK	99.6%	38.8	25	27.1	2	0	0	1021.48	110	118
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	9	11	18	0.02%	28.0%	DWVFINYTYK	99.7%	49.7	25	0	2	0	0	1348.66	437	446
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	9	11	18	0.02%	28.0%	FCCEWEHR	99.7%	47.4	25	47.4	1	0	0	1223.47	360	367
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	9	11	18	0.02%	28.0%	IGAPGVEEIK	99.7%	55.9	25	42.5	2	0	0	1012.57	368	377
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	9	11	18	0.02%	28.0%	LGLEDFESLK	99.7%	66	25	59.6	2	0	0	1150.60	84	93
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	9	11	18	0.02%	28.0%	LSDFGLCTGLK	99.7%	80.6	25	78.4	2	0	0	1210.61	228	238
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	9	11	18	0.02%	28.0%	LSDFGLCTGLKK	99.7%	70.9	25	65	3	0	0	1338.71	228	239
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	9	11	18	0.02%	28.0%	NLNHSLPSDFTFQNMNSK	99.7%	42.9	25	42.9	0	2	0	2093.97	248	265
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	9	11	18	0.02%	28.0%	RFEGLTAR	99.7%	42.9	25	31.7	2	0	0	949.52	447	454
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	9	11	18	0.02%	28.0%	SNSFFEGVDWEHIR	98.2%	32.5	25	32.5	1	0	0	1722.79	378	391
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	9	11	18	0.02%	28.0%	VMEEEGLKDEEK	99.7%	59.8	25	48.2	3	0	0	1435.66	51	62
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	13	13	33	0.03%	23.1%	AKDLILR	98.3%	32.8	25	23.7	4	0	0	828.53	354	360
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	13	13	33	0.03%	23.1%	DIKPDNLLLDAK	99.7%	49	25	46.3	4	0	0	1354.76	213	224
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	13	13	33	0.03%	23.1%	DTGHIYAMK	99.3%	36.6	25	25.1	1	0	0	1035.49	111	119
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	13	13	33	0.03%	23.1%	DWVFLNYTYK	99.7%	49.7	25	0	2	0	0	1348.66	435	444
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	13	13	33	0.03%	23.1%	ERPAAIPIEIK	99.7%	48.3	25	38.2	2	0	0	1236.73	393	403
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	13	13	33	0.03%	23.1%	FCIDSENR	99.6%	39	25	39	4	0	0	1040.45	361	368
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	13	13	33	0.03%	23.1%	FEGLTQR	99.7%	40.1	25	11.5	2	0	0	850.44	446	452
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	13	13	33	0.03%	23.1%	LGLDDFESLK	99.7%	63.2	25	63.2	2	0	0	1136.58	85	94
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	13	13	33	0.03%	23.1%	LSDFGLCTGLK	99.7%	80.6	25	78.4	2	0	0	1210.61	229	239
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	13	13	33	0.03%	23.1%	LSDFGLCTGLKK	99.7%	70.9	25	65	3	0	0	1338.71	229	240
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	13	13	33	0.03%	23.1%	NLTHNPPSDFSFQNMNSK	99.7%	58.1	25	58.1	0	2	0	2093.93	249	266
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	13	13	33	0.03%	23.1%	RFEGLTQR	97.9%	31.8	25	20.5	3	0	0	1006.54	445	452
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	13	13	33	0.03%	23.1%	SKDWVFLNYTYK	99.7%	61.4	25	48.4	2	0	0	1563.78	433	444
Serine/threonine-protein kinase Chk1	CHEK1	CHK1_HUMAN	54.4	100.0%	3	3	4	0.00%	6.9%	ILVENPSAR	99.7%	51.3	25	24.2	2	0	0	998.56	245	253
Serine/threonine-protein kinase Chk1	CHEK1	CHK1_HUMAN	54.4	100.0%	3	3	4	0.00%	6.9%	VTSGGVSESPSGFSK	99.7%	69.9	25	67.6	1	0	0	1425.69	278	292
Serine/threonine-protein kinase Chk1	CHEK1	CHK1_HUMAN	54.4	100.0%	3	3	4	0.00%	6.9%	YSSSQPEPR	99.7%	45.6	25	43.5	1	0	0	1050.49	314	322
Serine/threonine-protein kinase MST4	MST4	MST4_HUMAN	46.5	100.0%	2	2	4	0.00%	6.7%	AANVLLSEQGDVK	99.7%	69.6	25	62.3	3	0	0	1343.72	147	159
Serine/threonine-protein kinase MST4	MST4	MST4_HUMAN	46.5	100.0%	2	2	4	0.00%	6.7%	ADIWSLGITAIELAK	99.7%	76.1	25	43.8	1	0	0	1600.89	200	214
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	5	5	8	0.01%	2.2%	DASAVSLSESK	99.7%	56.7	25	48.3	2	0	0	1093.54	911	921
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	5	5	8	0.01%	2.2%	IQSIAPSLQVITSK	95.5%	28.7	25	20.4	1	0	0	1484.87	2153	2166
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	5	5	8	0.01%	2.2%	ISSMEGERLR	94.7%	28.1	25	20.5	1	0	0	1177.60	274	283
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	5	5	8	0.01%	2.2%	LFDAPEAPLPSR	99.7%	65	25	48	2	0	0	1312.69	1121	1132
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	5	5	8	0.01%	2.2%	TLDQSPELR	95.3%	28.5	25	20.9	2	0	0	1058.55	1162	1170
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	5	5	10	0.01%	12.9%	DTAEGVSQELISAGLVDGR	99.7%	64.9	25	58.2	2	0	0	1916.96	459	477
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	5	5	10	0.01%	12.9%	IPISLVLR	99.7%	59	25	58.5	2	0	0	910.61	432	439
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	5	5	10	0.01%	12.9%	LLSGGSVLDIIK	99.7%	45.2	25	34.5	2	0	0	1214.74	94	105
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	5	5	10	0.01%	12.9%	SGVLDESTIATILR	99.7%	64.5	25	64.5	2	0	0	1474.81	115	128
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	5	5	10	0.01%	12.9%	TAQALSSGSGSQETK	99.7%	56	25	49.4	2	0	0	1451.70	417	431
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	76	0.07%	44.2%	AMEIASQR	99.7%	44.8	25	20.7	4	0	0	905.45	402	409
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	76	0.07%	44.2%	ATVEQVLDPR	99.7%	77.9	25	72	6	0	0	1127.61	156	165
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	76	0.07%	44.2%	DCANVNDFFMR	99.7%	73.4	25	73.4	6	0	0	1404.57	360	370
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	76	0.07%	44.2%	DMDIIMK	94.7%	28.1	25	21.3	1	0	0	865.42	443	449
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	76	0.07%	44.2%	EANVYHASTANGESR	99.7%	82.9	25	82.1	4	0	0	1605.73	191	205

Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	76	0.07%	44.2%	ELFEFVTDPSITHENMDAYLSK	99.7%	34.5	25	34.5	0	2	0	2602.20	380	401
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	76	0.07%	44.2%	ELYLQVIQYMR	99.7%	85.3	25	77.6	4	0	0	1455.77	302	312
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	76	0.07%	44.2%	GIITEINGCISTGK	99.7%	64.8	25	59	2	0	0	1462.76	177	190
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	76	0.07%	44.2%	GYVWNGGSNPQANR	99.7%	74.8	25	71.5	2	0	0	1519.70	82	95
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	76	0.07%	44.2%	HSVAVMTVR	99.7%	43.6	25	28.1	6	0	0	999.54	371	379
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	76	0.07%	44.2%	INLDKLNVTDSVINK	99.7%	88.3	25	88.3	3	3	0	1685.94	120	134
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	76	0.07%	44.2%	LKEEDMAMNAQQDNILYQTVTGLK	99.7%	63.7	25	63.7	0	3	0	2785.34	450	473
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	76	0.07%	44.2%	LNTAEIPCPEPIMLR	99.7%	64.8	25	50.1	7	0	0	1753.90	257	271
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	76	0.07%	44.2%	LNVTDSVINK	99.7%	68.5	25	51.1	6	0	0	1102.61	125	134
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	76	0.07%	44.2%	SHVLVMSFIGKDDMPAPLLK	99.7%	36.2	25	36.2	0	1	0	2230.16	272	291
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	76	0.07%	44.2%	SSQDHVDEEVFKR	99.7%	70.7	25	65.9	1	3	0	1575.74	415	427
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	76	0.07%	44.2%	TSILVFK	99.1%	35.6	25	28.7	4	0	0	807.50	212	218
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	76	0.07%	44.2%	VPALLENQVEER	99.7%	87.3	25	86.7	5	0	0	1396.74	482	493
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	76	0.07%	44.2%	VVPGQFDDADSSDSENR	99.7%	103	25	103	2	0	0	1837.78	11	27
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	20	27	76	0.07%	44.2%	YVSGEFR	96.7%	30	25	25.5	1	0	0	857.42	223	229
Serine/threonine-protein kinase VRK1	VRK1	VRK1_HUMAN	45.5	100.0%	5	5	7	0.01%	13.6%	ASNLLLNYK	99.7%	59	25	42.5	2	0	0	1035.58	180	188
Serine/threonine-protein kinase VRK1	VRK1	VRK1_HUMAN	45.5	100.0%	5	5	7	0.01%	13.6%	NPDQVYLVDYGLAYR	99.7%	89.4	25	87.6	1	0	0	1785.88	189	203
Serine/threonine-protein kinase VRK1	VRK1	VRK1_HUMAN	45.5	100.0%	5	5	7	0.01%	13.6%	TVLQLSLR	95.4%	28.6	25	16.8	1	0	0	929.58	153	160
Serine/threonine-protein kinase VRK1	VRK1	VRK1_HUMAN	45.5	100.0%	5	5	7	0.01%	13.6%	VEPSDNGPLFTELK	99.7%	61.4	25	58.5	2	0	0	1545.78	72	85
Serine/threonine-protein kinase VRK1	VRK1	VRK1_HUMAN	45.5	100.0%	5	5	7	0.01%	13.6%	YCPEGVHK	95.8%	28.9	25	26.6	1	0	0	989.45	204	211
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	5	5	8	0.01%	9.6%	ESSLTEPVIVGLLK	99.7%	45.6	25	45.6	2	0	0	1484.86	354	367
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	5	5	8	0.01%	9.6%	FLESPDFQPNIAK	99.7%	59.1	25	53.8	2	0	0	1505.76	220	232
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	5	5	8	0.01%	9.6%	TVETEAVQMLK	99.7%	47.2	25	42.2	2	0	0	1248.65	550	560
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	5	5	8	0.01%	9.6%	VLPIMFPALYR	99.4%	37.2	25	37.2	1	0	0	1319.75	442	452
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	5	5	8	0.01%	9.6%	YSGGPQIVK	97.5%	31	25	25.2	1	0	0	948.52	74	82
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	5	5	6	0.01%	9.0%	ELVSDANQHVK	98.7%	33.9	25	25.4	1	0	0	1239.63	332	342
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	5	5	6	0.01%	9.0%	LAGGDWFTSR	99.7%	41.3	25	5.86	1	0	0	1109.54	135	144
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	5	5	6	0.01%	9.0%	LSTIALALGVER	98.9%	34.7	25	29.9	1	0	0	1242.74	35	46
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	5	5	6	0.01%	9.0%	LTQDQDVDVK	99.7%	57.1	25	50.3	2	0	0	1160.58	567	576
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	5	5	6	0.01%	9.0%	MAGDPVANVR	99.7%	66.3	25	58.2	1	0	0	1045.51	528	537
Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	PPP2CA	PP2AA_HUMAN	35.6	99.8%	2	2	3	0.00%	8.4%	SPDTNYLFMGDYVDR	99.7%	76.4	25	76.4	1	0	0	1792.78	75	89
Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	PPP2CA	PP2AA_HUMAN	35.6	99.8%	2	2	3	0.00%	8.4%	YSFLQFDPAPR	99.7%	57	25	56.3	2	0	0	1340.66	284	294
Serine/threonine-protein phosphatase 4 catalytic subunit	PPP4C	PP4C_HUMAN	35.1	99.8%	2	2	4	0.00%	10.4%	DFIIFEAAPQETR	99.7%	60.2	25	55.2	2	0	0	1536.77	282	294
Serine/threonine-protein phosphatase 4 catalytic subunit	PPP4C	PP4C_HUMAN	35.1	99.8%	2	2	4	0.00%	10.4%	VGGDVPETNYLFMGDFVDR	99.7%	41	25	41	2	0	0	2130.98	68	86
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	7	8	20	0.02%	28.5%	AHQLVHEGYK	99.7%	47.3	25	47.3	3	0	0	1181.61	236	245
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	7	8	20	0.02%	28.5%	APLDLDKYVEIAR	99.7%	94.5	25	83.8	4	1	0	1502.82	2	14
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	7	8	20	0.02%	28.5%	CGNIASIMVFK	96.3%	29.5	25	28.4	1	0	0	1239.62	265	275
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	7	8	20	0.02%	28.5%	GAGWLFGAK	99.7%	45.5	25	25.5	2	0	0	906.48	211	219
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	7	8	20	0.02%	28.5%	LVTVWSAPNYCYR	99.7%	50.8	25	50.6	2	0	0	1628.79	252	264
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	7	8	20	0.02%	28.5%	TGGQVPDTNYIFMGDFVDR	99.7%	69.4	25	64.5	3	0	0	2131.98	67	85
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	7	8	20	0.02%	28.5%	VTNEFVHINNLK	99.7%	65.7	25	65.7	4	0	0	1427.76	220	231
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	11	13	38	0.04%	35.3%	AIETTDIISR	99.7%	67.4	25	54	5	0	0	1118.61	153	162
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	11	13	38	0.04%	35.3%	ALQFPPEGWLR	99.6%	39.9	25	32	6	0	0	1313.70	241	251
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	11	13	38	0.04%	35.3%	EPLSLINVR	99.7%	46.8	25	43.1	2	0	0	1040.61	66	74
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	11	13	38	0.04%	35.3%	EQAELTGLR	99.7%	57.7	25	33.2	6	0	0	1016.54	126	134
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	11	13	38	0.04%	35.3%	HSQYHVDGSLEK	99.7%	62.7	25	62.5	1	1	0	1399.66	105	116
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	11	13	38	0.04%	35.3%	HSQYHVDGSLEKDR	99.7%	45.4	25	38.1	0	2	0	1670.79	105	118
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	11	13	38	0.04%	35.3%	NVESGEEELASK	99.7%	71.6	25	62.6	5	0	0	1291.60	77	88
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	11	13	38	0.04%	35.3%	QEEDSYEIFICHANVIR	99.7%	65.3	25	65.3	0	2	0	2122.99	219	235
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	11	13	38	0.04%	35.3%	REPLSLINVR	99.5%	38.5	25	35.7	2	0	0	1196.71	65	74
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	11	13	38	0.04%	35.3%	TLGDTGFMPPDK	99.7%	46.8	25	39.5	5	0	0	1278.60	274	285

Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	11	13	38	0.04%	35.3%	VSTDLLR	99.2%	36.2	25	12.3	1	0	0	803.46	170	176
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	PP1G_HUMAN	37.0	100.0%	7	8	12	0.01%	29.4%	AHQVVEDGYEFFAK	99.7%	70.3	25	70.3	2	1	0	1639.78	247	260
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	PP1G_HUMAN	37.0	100.0%	7	8	12	0.01%	29.4%	EIFLSQPILLELEAPLK	99.7%	41.8	25	41.8	1	0	0	1953.13	44	60
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	PP1G_HUMAN	37.0	100.0%	7	8	12	0.01%	29.4%	ICGDIHGQYYDLLR	96.4%	24.1	25	20.8	0	1	0	1722.83	61	74
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	PP1G_HUMAN	37.0	100.0%	7	8	12	0.01%	29.4%	NVQLQENEIR	99.7%	45.4	25	41.1	2	0	0	1242.64	27	36
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	PP1G_HUMAN	37.0	100.0%	7	8	12	0.01%	29.4%	QSLETICLLLAYK	99.7%	40.7	25	40.5	1	0	0	1551.85	99	111
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	PP1G_HUMAN	37.0	100.0%	7	8	12	0.01%	29.4%	TFTDCFNCLPIAAIVDEK	99.7%	96.6	25	82.1	2	0	0	2113.99	151	168
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	PP1G_HUMAN	37.0	100.0%	7	8	12	0.01%	29.4%	YPENFFLLR	99.7%	53	25	38.1	2	0	0	1198.63	114	122
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	7	7	13	0.01%	27.7%	EFLVAGGEDFK	99.7%	40.2	25	39.3	2	0	0	1211.59	236	246
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	7	7	13	0.01%	27.7%	FSPDGELYASGSEDGTLR	99.7%	84	25	80.1	2	0	0	1900.86	273	290
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	7	7	13	0.01%	27.7%	IYDLNKPEAEPK	99.7%	51.8	25	48	2	0	0	1416.74	126	137
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	7	7	13	0.01%	27.7%	LWQTVVGK	99.7%	40.9	25	24.6	2	0	0	930.54	291	298
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	7	7	13	0.01%	27.7%	SFEAPATINSASLHPEK	99.7%	60.8	25	60.8	1	0	0	1798.90	219	235
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	7	7	13	0.01%	27.7%	TVDFTQDSNYLLTGGQDK	99.7%	106	25	106	2	0	0	2001.94	105	122
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	7	7	13	0.01%	27.7%	YDYNSGEELESYK	99.7%	75.4	25	75.4	2	0	0	1596.67	250	262
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	13	26	0.03%	34.2%	DQAVENILVSPVVVASSLGLVSLGGK	99.7%	41.2	25	41.2	0	1	0	2551.43	61	86
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	13	26	0.03%	34.2%	DTQSGSLLFIGR	99.7%	93.6	25	79.8	4	0	0	1293.68	394	405
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	13	26	0.03%	34.2%	GVVEVTHDLQK	99.7%	62.1	25	50.3	2	0	0	1224.66	309	319
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	13	26	0.03%	34.2%	HLAGLGLTEAIDK	99.7%	58.8	25	56.2	2	0	0	1337.74	320	332
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	13	26	0.03%	34.2%	HLAGLGLTEAIDKNK	99.7%	63.6	25	63.6	0	2	0	1579.88	320	334
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	13	26	0.03%	34.2%	KPAAAAAPGTAEK	99.3%	36.8	25	33.8	2	0	0	1182.65	23	35
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	13	26	0.03%	34.2%	LFYADHPFIFLVR	99.7%	55.5	25	55.5	2	2	0	1637.88	381	393
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	13	26	0.03%	34.2%	LQIVEMPLAHK	99.7%	52.8	25	41.8	2	0	0	1294.72	253	263
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	13	26	0.03%	34.2%	LYGPSSVSFADDFVR	99.7%	91.7	25	85.5	3	0	0	1659.80	134	148
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	13	26	0.03%	34.2%	SAGLAFSLYQAMAK	99.7%	75.9	25	69.5	2	0	0	1457.75	47	60
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	13	26	0.03%	34.2%	TGLYNYYDDEKEK	99.7%	52.5	25	52.5	1	1	0	1637.73	240	252
Serrate RNA effector molecule homolog	SRRT	SRRT_HUMAN	100.7	99.8%	2	2	2	0.00%	2.3%	ESLSEEEAQK	99.7%	52	25	44.6	1	0	0	1149.53	678	687
Serrate RNA effector molecule homolog	SRRT	SRRT_HUMAN	100.7	99.8%	2	2	2	0.00%	2.3%	VALSEPQPER	99.0%	35.2	25	33.7	1	0	0	1125.59	450	459
Sestrin-2	SESN2	SESN2_HUMAN	54.5	99.8%	2	2	3	0.00%	6.0%	FAPGGVGDSGPGEEQR	99.7%	40.8	25	40.8	1	0	0	1559.71	18	33
Sestrin-2	SESN2	SESN2_HUMAN	54.5	99.8%	2	2	3	0.00%	6.0%	GPSAFIPVEEVLR	99.7%	49.9	25	48.5	2	0	0	1413.77	43	55
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	8	9	18	0.02%	22.9%	ASSTCPLTFENVK	99.7%	61.2	25	57.9	2	0	0	1453.70	257	269
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	8	9	18	0.02%	22.9%	ATYLPQLTTEK	99.7%	46.9	25	46.9	2	0	0	1264.68	160	170
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	8	9	18	0.02%	22.9%	GITSFLVDR	99.6%	39.3	25	26.5	2	0	0	1007.55	231	239
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	8	9	18	0.02%	22.9%	IGTIYEGASNIQLNTIAK	99.7%	100	25	95.7	2	0	0	1906.03	409	426
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	8	9	18	0.02%	22.9%	LLEAGKPFIK	99.7%	53.5	25	36.4	2	0	0	1115.68	356	365
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	8	9	18	0.02%	22.9%	VPEANILGQIGHGYK	99.7%	77.1	25	72.6	2	2	0	1595.85	270	284
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	8	9	18	0.02%	22.9%	YAIGSLNEGR	99.7%	64.3	25	52.5	2	0	0	1079.55	285	294
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	8	9	18	0.02%	22.9%	YYASEIAGQTTSK	99.7%	115	25	105	2	0	0	1418.68	372	384
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	19	34	0.03%	48.8%	ANHFFTVTDPR	99.7%	58.7	25	56.9	2	0	0	1304.64	25	35
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	19	34	0.03%	48.8%	FVPFAAVAAANCINIPLMR	99.7%	52.7	25	52.7	1	3	0	2091.09	179	197
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	19	34	0.03%	48.8%	HVSPLIGR	97.8%	31.6	25	24.5	1	0	0	878.52	171	178
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	19	34	0.03%	48.8%	ILMAAPGMAIPPFIMNTLEK	99.7%	49	25	49	5	0	0	2158.15	234	253
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	19	34	0.03%	48.8%	IQESHPELR	99.7%	63.1	25	45.8	2	0	0	1108.57	306	314
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	19	34	0.03%	48.8%	IQESHPELRR	98.7%	34	25	28.4	1	2	0	1264.68	306	315
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	19	34	0.03%	48.8%	NILLTNEQLESAR	99.7%	102	25	92.7	2	0	0	1500.80	36	48
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	19	34	0.03%	48.8%	NILLTNEQLESARK	99.7%	58	25	53	2	0	0	1628.90	36	49
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	19	34	0.03%	48.8%	QAITQVVVSR	99.7%	88.9	25	85	2	0	0	1100.64	224	233
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	19	34	0.03%	48.8%	QGIVPPGLTENELWR	99.7%	69	25	67.2	2	0	0	1708.90	56	70
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	19	34	0.03%	48.8%	SSMSVTSLEAELQAK	99.7%	99.3	25	96.6	2	0	0	1596.78	291	305
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	19	34	0.03%	48.8%	VGIPVTDENGNR	99.7%	56.6	25	53	2	0	0	1270.64	203	214
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	19	34	0.03%	48.8%	WDQSTFIGR	99.7%	60	25	0	2	0	0	1109.54	16	24

Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	14	19	34	0.03%	48.8%	YIYDSAFHPDTGEK	99.7%	74.5	25	70.9	2	1	0	1642.74	73	86
Sideroflexin-2	SFXN2	SFXN2_HUMAN	36.2	100.0%	4	4	9	0.01%	18.3%	AAAIGITQVVISR	99.7%	64.7	25	52.5	3	0	0	1298.78	220	232
Sideroflexin-2	SFXN2	SFXN2_HUMAN	36.2	100.0%	4	4	9	0.01%	18.3%	ITMSAPGMILLPVIMER	97.7%	31.4	25	24.1	1	0	0	1888.01	233	249
Sideroflexin-2	SFXN2	SFXN2_HUMAN	36.2	100.0%	4	4	9	0.01%	18.3%	MGVVPPGTQVEQLLYAK	95.3%	28.5	25	28.5	1	0	0	1829.98	55	71
Sideroflexin-2	SFXN2	SFXN2_HUMAN	36.2	100.0%	4	4	9	0.01%	18.3%	YGELEPYVYFNK	99.7%	54.3	25	47.6	4	0	0	1521.73	309	320
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	100.0%	5	5	10	0.01%	20.2%	DAVPAFIEPNVR	99.7%	43.4	25	34.3	2	0	0	1327.70	19	30
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	100.0%	5	5	10	0.01%	20.2%	IQSPTEETEIFYHR	99.7%	35.7	25	34.9	0	2	0	1749.84	322	335
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	100.0%	5	5	10	0.01%	20.2%	QLLCTNEDVSSPASADQR	99.7%	102	25	97.9	2	0	0	1990.91	67	84
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	100.0%	5	5	10	0.01%	20.2%	SLATVHPDSSNLIPK	99.7%	56.2	25	48.5	2	0	0	1578.85	92	106
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	100.0%	5	5	10	0.01%	20.2%	YGLTGPWIK	99.5%	38.5	25	26.1	2	0	0	1034.57	189	197
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	5	6	16	0.02%	26.8%	GDLLFLTNR	99.7%	65.9	25	45.7	4	0	0	1048.58	64	72
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	5	6	16	0.02%	26.8%	GDLLFLTNRVEDPIR	99.3%	30.9	25	30.9	0	2	0	1757.95	64	78
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	5	6	16	0.02%	26.8%	GDNNAVDDRGLYK	99.7%	50.8	25	49.9	3	0	0	1436.68	115	127
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	5	6	16	0.02%	26.8%	MLSLDFLDDVRR	99.6%	32.9	25	29.9	1	2	0	1495.76	1	12
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	5	6	16	0.02%	26.8%	VGEIVVFR	99.7%	71.8	25	65.3	4	0	0	918.54	79	86
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	9	18	0.02%	35.4%	FDDKYTLK	99.5%	38.2	25	30	2	0	0	1029.53	166	173
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	9	18	0.02%	35.4%	FFDHSGTLVMDAYEPEISR	99.7%	42.4	25	42.4	0	3	0	2230.01	196	214
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	9	18	0.02%	35.4%	IDDKPVKIDK	99.7%	44.8	25	30.9	2	0	0	1170.67	41	50
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	9	18	0.02%	35.4%	IDKWDGSAVK	99.7%	46.5	25	25.3	2	0	0	1118.58	48	57
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	9	18	0.02%	35.4%	LHDSLAIER	99.7%	53.4	25	42.4	3	0	0	1053.57	215	223
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	9	18	0.02%	35.4%	SGLLDKWK	99.7%	48	25	33.4	2	0	0	946.54	33	40
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	9	18	0.02%	35.4%	SIFLVAHR	99.4%	37.1	25	30	2	0	0	942.55	138	145
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	9	18	0.02%	35.4%	YVENFGLIDGR	99.7%	70.5	25	68	2	0	0	1282.64	74	84
Signal peptidase complex subunit 3	SPCS3	SPCS3_HUMAN	20.3	100.0%	5	5	9	0.01%	25.6%	LLLKDMK	98.2%	32.5	25	20.8	1	0	0	876.52	118	124
Signal peptidase complex subunit 3	SPCS3	SPCS3_HUMAN	20.3	100.0%	5	5	9	0.01%	25.6%	MNTVLSR	99.7%	48.8	25	25	2	0	0	820.43	1	7
Signal peptidase complex subunit 3	SPCS3	SPCS3_HUMAN	20.3	100.0%	5	5	9	0.01%	25.6%	NNALNQVVLWDK	99.7%	59.3	25	47.3	2	0	0	1413.75	97	108
Signal peptidase complex subunit 3	SPCS3	SPCS3_HUMAN	20.3	100.0%	5	5	9	0.01%	25.6%	NVEDFTGPR	99.7%	57.5	25	48.6	2	0	0	1034.49	50	58
Signal peptidase complex subunit 3	SPCS3	SPCS3_HUMAN	20.3	100.0%	5	5	9	0.01%	25.6%	YFFFDDGNGLK	99.7%	48.3	25	38.4	2	0	0	1322.61	127	137
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	9	15	33	0.03%	47.8%	EVNKFQMAYSNLLR	99.7%	67.1	25	52.3	4	3	0	1712.88	75	88
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	9	15	33	0.03%	47.8%	FQMAYSNLLR	99.7%	71.9	25	55.4	6	0	0	1242.63	79	88
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	9	15	33	0.03%	47.8%	GTVEGFEPADNK	99.7%	79	25	79	2	0	0	1263.59	44	55
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	9	15	33	0.03%	47.8%	GTVEGFEPADNKCLLR	99.7%	39.6	25	35.6	1	1	0	1805.89	44	59
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	9	15	33	0.03%	47.8%	ISTVVSSK	99.0%	34.9	25	34.9	1	0	0	820.48	67	74
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	9	15	33	0.03%	47.8%	KGTVEGFEPADNK	99.7%	68	25	55.5	4	1	0	1391.68	43	55
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	9	15	33	0.03%	47.8%	KISTVVSSK	96.0%	29.2	25	19.5	2	0	0	948.57	66	74
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	9	15	33	0.03%	47.8%	TSGSVYITLKK	99.7%	52.5	25	52.5	4	0	0	1196.69	22	32
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	9	15	33	0.03%	47.8%	VLLESEQFLTELTR	99.7%	79.4	25	67.7	4	0	0	1677.91	2	15
Signal recognition particle 19 kDa protein	SRP19	SRP19_HUMAN	16.2	100.0%	2	3	5	0.00%	18.8%	SVMLYAAEMIPK	99.7%	49.5	25	40.9	3	0	0	1384.69	103	114
Signal recognition particle 19 kDa protein	SRP19	SRP19_HUMAN	16.2	100.0%	2	3	5	0.00%	18.8%	TGGADQSLQQGEGSK	99.7%	74	25	65.4	2	0	0	1462.68	122	136
Signal recognition particle 9 kDa protein	SRP9	SRP09_HUMAN	10.1	100.0%	4	5	11	0.01%	37.2%	LYLADPMK	99.2%	35.8	25	22.5	4	0	0	950.50	17	24
Signal recognition particle 9 kDa protein	SRP9	SRP09_HUMAN	10.1	100.0%	4	5	11	0.01%	37.2%	LYLADPMKAR	99.3%	36.6	25	25	1	0	0	1193.63	17	26
Signal recognition particle 9 kDa protein	SRP9	SRP09_HUMAN	10.1	100.0%	4	5	11	0.01%	37.2%	PQYQTWEEFSR	99.7%	66.4	25	66.4	2	0	0	1470.66	2	12
Signal recognition particle 9 kDa protein	SRP9	SRP09_HUMAN	10.1	100.0%	4	5	11	0.01%	37.2%	VTDDLVCLVYK	99.7%	87.9	25	74.2	4	0	0	1324.68	42	52
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	4	7	11	0.01%	6.7%	AGAVEQLR	99.7%	52.3	25	27.3	2	0	0	843.47	459	466
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	4	7	11	0.01%	6.7%	ALADHSMAQTPR	99.7%	60	25	58.3	3	2	0	1297.63	569	580
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	4	7	11	0.01%	6.7%	DAAGIAMEAIAFAR	99.7%	86.1	25	68.7	3	0	0	1406.71	497	510
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	4	7	11	0.01%	6.7%	LIDGIVLTK	97.1%	30.5	25	17	1	0	0	971.61	581	589
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	10	11	28	0.03%	48.3%	AIVFVVDSAAFQR	99.7%	87.2	25	83.9	3	0	0	1422.77	138	150
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	10	11	28	0.03%	48.3%	AVLLVGLCDSGK	99.7%	77.3	25	72	2	0	0	1231.67	66	77
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	10	11	28	0.03%	48.3%	DTQTSITDSCAVYR	99.7%	70.1	25	70.1	4	0	0	1616.72	91	104
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	10	11	28	0.03%	48.3%	GDVGSADIQDLEK	99.7%	86	25	73.4	4	0	0	1346.64	253	265

Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	10	11	28	0.03%	48.3%	GNSLTLIDLPGHESLR	99.7%	66.8	25	66.8	2	2	0	1721.92	110	125
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	10	11	28	0.03%	48.3%	LIQQQLEK	99.6%	39.3	25	16.1	2	0	0	999.58	192	199
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	10	11	28	0.03%	48.3%	LQFLER	99.7%	40.3	25	0	2	0	0	805.46	126	131
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	10	11	28	0.03%	48.3%	NTPSFLIACNK	99.7%	49.3	25	36.9	2	0	0	1264.64	171	181
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	10	11	28	0.03%	48.3%	SAAPSTLDSSSTAPAQLGK	99.7%	73.2	25	73.2	1	0	0	1788.90	209	227
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	10	11	28	0.03%	48.3%	VADGGGAGGTFQPYLDTLR	99.7%	66.7	25	66.7	4	0	0	1894.93	9	27
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	13	13	28	0.03%	23.8%	AAIEAFNK	99.7%	51.4	25	39.2	1	0	0	863.46	206	213
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	13	13	28	0.03%	23.8%	DLPDVQELITQVR	99.7%	52.6	25	43.9	4	0	0	1525.82	509	521
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	13	13	28	0.03%	23.8%	FETFCLDPSLVTK	99.7%	74.2	25	68	2	0	0	1556.77	558	570
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	13	13	28	0.03%	23.8%	GAGGEENKENERPSAGSK	96.0%	23.7	25	23.7	0	1	0	1816.84	32	49
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	13	13	28	0.03%	23.8%	LASAFTEEQAVLYNQR	99.7%	82.7	25	78	3	0	0	1839.92	221	236
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	13	13	28	0.03%	23.8%	LEALITQTR	99.7%	45.9	25	35.7	3	0	0	1044.60	278	286
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	13	13	28	0.03%	23.8%	LFESMLSECR	99.7%	60.2	25	54.3	2	0	0	1271.58	336	345
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	13	13	28	0.03%	23.8%	SPRPQDLIR	95.1%	28.4	25	14.5	1	0	0	1081.61	418	426
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	13	13	28	0.03%	23.8%	VEEISPNIR	99.7%	53.3	25	45.2	4	0	0	1056.57	237	245
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	13	13	28	0.03%	23.8%	VTEELLTDNR	99.7%	76	25	56.7	2	0	0	1189.61	113	122
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	13	13	28	0.03%	23.8%	WSEALVLYDR	99.5%	38.8	25	25.5	1	0	0	1251.64	479	488
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	13	13	28	0.03%	23.8%	YANEVNSDAGAFK	99.7%	69.8	25	55	3	0	0	1385.63	492	504
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	13	13	28	0.03%	23.8%	YLLLVLMDAER	99.1%	35.5	25	34.1	1	0	0	1351.73	123	133
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	10	10	18	0.02%	19.1%	AIELLQEFSDQHPENAAEIK	99.7%	35.5	25	35.5	0	2	0	2282.13	357	376
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	10	10	18	0.02%	19.1%	EALNVINTHTK	99.7%	43.5	25	35.8	2	0	0	1239.67	63	73
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	10	10	18	0.02%	19.1%	ELYGQVLYR	96.4%	29.6	25	20.6	1	0	0	1140.60	113	121
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	10	10	18	0.02%	19.1%	GTQGATAGASSELDASK	99.7%	97.2	25	96.4	2	0	0	1550.73	601	617
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	10	10	18	0.02%	19.1%	SPAHLSLIR	99.7%	64.7	25	56.5	2	0	0	993.58	443	451
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	10	10	18	0.02%	19.1%	TEEALQLYNQIIK	99.7%	74.6	25	64.7	2	0	0	1562.84	242	254
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	10	10	18	0.02%	19.1%	TIESANQQTDKLK	99.7%	77.3	25	70.4	2	0	0	1475.77	100	112
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	10	10	18	0.02%	19.1%	VDVEALENSAGATYIR	99.7%	97.1	25	89.6	1	0	0	1707.85	516	531
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	10	10	18	0.02%	19.1%	VLANNSLSFEK	99.7%	60.5	25	49.3	2	0	0	1221.65	74	84
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	10	10	18	0.02%	19.1%	YGQNGDFTR	99.7%	49.7	25	46.8	2	0	0	1057.47	21	29
Signal transducer and activator of transcription 1-alpha/beta	STAT1	STAT1_HUMAN	87.3	100.0%	2	2	2	0.00%	3.3%	ELSAVTFPDIIR	98.2%	32.5	25	29.2	1	0	0	1360.75	638	649
Signal transducer and activator of transcription 1-alpha/beta	STAT1	STAT1_HUMAN	87.3	100.0%	2	2	2	0.00%	3.3%	TELISVSEVHPSR	99.7%	60	25	51.4	1	0	0	1453.76	704	716
Signal transducer and activator of transcription 3	STAT3	STAT3_HUMAN	88.1	99.9%	2	2	4	0.00%	5.1%	GLSIEQLTTLAEK	99.7%	85.7	25	75.9	2	0	0	1402.78	519	531
Signal transducer and activator of transcription 3	STAT3	STAT3_HUMAN	88.1	99.9%	2	2	4	0.00%	5.1%	LLQTAATAAQQGGQANHPTAAVVTEK	99.7%	84.8	25	84.8	0	2	0	2576.34	115	140
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	5	6	10	0.01%	37.2%	DVAYQYVK	99.5%	38	25	31.5	1	0	0	985.50	96	103
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	5	6	10	0.01%	37.2%	ISVFRPGLR	96.4%	29.6	25	23	1	0	0	1044.63	87	95
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	5	6	10	0.01%	37.2%	NPVTIFSLATNEMWR	99.7%	61.4	25	60.8	4	0	0	1778.89	52	66
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	5	6	10	0.01%	37.2%	SGDSEVYQLGDVSQK	99.7%	104	25	102	2	0	0	1611.75	67	81
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	5	6	10	0.01%	37.2%	VGQDPVLR	99.7%	56.6	25	50.7	2	0	0	883.50	39	46
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	13	13	19	0.02%	13.0%	AAVGQESPGGLEAGNAK	99.7%	65	25	60	1	0	0	1555.77	1299	1315
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	13	13	19	0.02%	13.0%	DLALVNDQLLGFVR	99.7%	86.5	25	84.6	2	0	0	1572.87	391	404
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	13	13	19	0.02%	13.0%	EINSDQATQGNISSDR	99.7%	69.8	25	69.8	1	0	0	1734.79	1220	1235
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	13	13	19	0.02%	13.0%	EVQLAQIFEPLSR	99.7%	85.1	25	79.6	2	0	0	1529.83	751	763
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	13	13	19	0.02%	13.0%	FNDIHVPVR	97.6%	31.3	25	23.4	1	0	0	1096.59	332	340
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	13	13	19	0.02%	13.0%	IAPVHIDSEAISALVK	97.2%	25	25	25	0	1	0	1662.94	618	633
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	13	13	19	0.02%	13.0%	IETDLPQIR	99.7%	54.2	25	32.9	2	0	0	1084.60	709	717
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	13	13	19	0.02%	13.0%	LLVACCLADIFR	99.7%	77.2	25	73.9	1	0	0	1450.75	88	99
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	13	13	19	0.02%	13.0%	LYTVCDVALCVINSK	99.7%	79.1	25	79.1	1	0	0	1754.88	1075	1089
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	13	13	19	0.02%	13.0%	NDDLNKPINK	98.7%	34	25	30.8	2	0	0	1170.61	1285	1294
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	13	13	19	0.02%	13.0%	SIEGTADDEEEGVSPDTAIR	99.7%	69.5	25	61.6	1	0	0	2090.94	638	657
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	13	13	19	0.02%	13.0%	STLIPILHQK	99.7%	43.8	25	14.8	2	0	0	1149.70	718	727
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	13	13	19	0.02%	13.0%	TVTAAGAENIQQK	99.7%	73.8	25	61.5	2	0	0	1330.70	1240	1252

Small nuclear ribonucleoprotein E	SNRPE	RUXE_HUMAN	10.8	100.0%	4	6	15	0.01%	42.4%	GDNITLLQSVSN	99.7%	55	25	47.4	2	0	0	1260.64	81	92
Small nuclear ribonucleoprotein E	SNRPE	RUXE_HUMAN	10.8	100.0%	4	6	15	0.01%	42.4%	IMLKGDNITLLQSVSN	99.7%	54.5	25	54.5	4	0	0	1761.94	77	92
Small nuclear ribonucleoprotein E	SNRPE	RUXE_HUMAN	10.8	100.0%	4	6	15	0.01%	42.4%	IQVWLYEQVNMR	99.7%	65	25	60	2	0	0	1594.80	31	42
Small nuclear ribonucleoprotein E	SNRPE	RUXE_HUMAN	10.8	100.0%	4	6	15	0.01%	42.4%	VMVQPINLIFR	99.7%	49.9	25	46.3	7	0	0	1345.77	13	23
Small nuclear ribonucleoprotein F	SNRPF	RUXF_HUMAN	9.7	100.0%	3	3	7	0.01%	18.6%	CNNVLYIR	99.7%	56.8	25	39.1	4	0	0	1051.54	66	73
Small nuclear ribonucleoprotein F	SNRPF	RUXF_HUMAN	9.7	100.0%	3	3	7	0.01%	18.6%	LKWGMEYK	98.4%	33	25	21.4	1	0	0	1054.54	23	30
Small nuclear ribonucleoprotein F	SNRPF	RUXF_HUMAN	9.7	100.0%	3	3	7	0.01%	18.6%	WGMEYK	98.1%	32.2	25	30.1	2	0	0	813.36	25	30
Small nuclear ribonucleoprotein Sm D1	SNRPD1	SMD1_HUMAN	13.3	100.0%	4	6	23	0.02%	37.8%	EPVQLETLSIR	99.7%	58.4	25	45.3	4	0	0	1284.72	51	61
Small nuclear ribonucleoprotein Sm D1	SNRPD1	SMD1_HUMAN	13.3	100.0%	4	6	23	0.02%	37.8%	LSHETVTIELK	99.7%	48.2	25	38.5	6	0	0	1269.71	10	20
Small nuclear ribonucleoprotein Sm D1	SNRPD1	SMD1_HUMAN	13.3	100.0%	4	6	23	0.02%	37.8%	NGTQVHGTITGVDVSMNTHLK	99.7%	71.3	25	71.3	0	5	0	2225.10	21	41
Small nuclear ribonucleoprotein Sm D1	SNRPD1	SMD1_HUMAN	13.3	100.0%	4	6	23	0.02%	37.8%	NREPVQLETLSIR	99.7%	63.2	25	55.8	6	2	0	1554.86	49	61
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	8	11	25	0.02%	55.9%	EEEEFNTGPLSVLTQSVK	99.7%	65.7	25	65.7	2	0	0	2006.99	20	37
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	8	11	25	0.02%	55.9%	EMWTEVPK	98.9%	34.6	25	25.1	2	0	0	1019.49	72	79
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	8	11	25	0.02%	55.9%	GDSVIVVLR	99.7%	82.1	25	64.7	6	0	0	957.57	103	111
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	8	11	25	0.02%	55.9%	HCNMVLENVK	99.7%	62.2	25	62.2	4	0	0	1243.59	62	71
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	8	11	25	0.02%	55.9%	NNTQVLINCR	99.7%	69.6	25	60.6	4	0	0	1231.62	38	47
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	8	11	25	0.02%	55.9%	REEEEFNTGPLSVLTQSVK	99.7%	47.2	25	47.2	1	1	0	2163.09	19	37
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	8	11	25	0.02%	55.9%	SEMTPEELQK	99.7%	49.8	25	43.4	4	0	0	1191.56	9	18
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	8	11	25	0.02%	55.9%	SEMTPEELQKR	99.3%	36.9	25	29.7	1	0	0	1347.66	9	19
Small nuclear ribonucleoprotein Sm D3	SNRPD3	SMD3_HUMAN	13.9	100.0%	3	4	8	0.01%	31.7%	FLILPDMLK	99.7%	46.9	25	26.5	4	0	0	1105.63	70	78
Small nuclear ribonucleoprotein Sm D3	SNRPD3	SMD3_HUMAN	13.9	100.0%	3	4	8	0.01%	31.7%	VAQLEQVYIR	99.7%	75.1	25	61.3	2	0	0	1218.68	55	64
Small nuclear ribonucleoprotein Sm D3	SNRPD3	SMD3_HUMAN	13.9	100.0%	3	4	8	0.01%	31.7%	VLHEAEGHIVTCETNTGEVYR	99.7%	74.6	25	74.6	0	2	0	2414.14	9	29
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN	24.6	100.0%	7	10	27	0.03%	24.6%	GENLVSMTVEGPPPK	99.7%	66.8	25	63.9	4	0	0	1570.78	74	88
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN	24.6	100.0%	7	10	27	0.03%	24.6%	GENLVSMTVEGPPPKDTGIAR	99.7%	49.6	25	49.6	0	4	0	2184.10	74	94
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN	24.6	100.0%	7	10	27	0.03%	24.6%	HMNLILCDCDEFRK	99.7%	39.5	25	39.5	0	1	0	1850.83	37	50
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN	24.6	100.0%	7	10	27	0.03%	24.6%	IFIGTFK	99.7%	40.5	25	24.4	2	0	0	825.49	26	32
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN	24.6	100.0%	7	10	27	0.03%	24.6%	MLQHIDYR	99.6%	39.1	25	31.9	3	0	0	1091.53	9	16
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN	24.6	100.0%	7	10	27	0.03%	24.6%	RVLGLVLLR	99.7%	43.7	25	32.5	2	0	0	1038.71	65	73
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN	24.6	100.0%	7	10	27	0.03%	24.6%	VLGLVLLR	99.7%	64	25	64	11	0	0	882.61	66	73
SNW domain-containing protein 1	SNW1	SNW1_HUMAN	61.5	100.0%	7	7	10	0.01%	13.4%	DISEVIALGVPNPR	99.0%	35.2	25	31.5	2	0	0	1479.82	387	400
SNW domain-containing protein 1	SNW1	SNW1_HUMAN	61.5	100.0%	7	7	10	0.01%	13.4%	DMAQSIYRPSK	99.7%	40.1	25	40.1	1	0	0	1295.64	442	452
SNW domain-containing protein 1	SNW1	SNW1_HUMAN	61.5	100.0%	7	7	10	0.01%	13.4%	GLQTVHINENFAK	99.7%	68.4	25	68.4	1	0	0	1470.77	274	286
SNW domain-containing protein 1	SNW1	SNW1_HUMAN	61.5	100.0%	7	7	10	0.01%	13.4%	IKYDAIAR	99.2%	36.2	25	26.3	1	0	0	949.55	96	103
SNW domain-containing protein 1	SNW1	SNW1_HUMAN	61.5	100.0%	7	7	10	0.01%	13.4%	LAEALYIADR	99.7%	79.1	25	71.9	2	0	0	1134.62	287	296
SNW domain-containing protein 1	SNW1	SNW1_HUMAN	61.5	100.0%	7	7	10	0.01%	13.4%	LAPAQYIR	96.9%	30.2	25	9.46	1	0	0	931.54	171	178
SNW domain-containing protein 1	SNW1	SNW1_HUMAN	61.5	100.0%	7	7	10	0.01%	13.4%	VAAAMPVR	99.3%	36.9	25	34.4	2	0	0	814.46	159	166
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	69	0.07%	29.9%	AAVPDAVGK	97.0%	30.3	25	25.5	1	0	0	827.46	597	605
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	69	0.07%	29.9%	ADIGVAMGIAGSDVSK	99.7%	111	25	108	4	0	0	1490.75	728	743
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	69	0.07%	29.9%	AVAGDASESALLK	99.7%	90.9	25	79.4	5	0	0	1231.65	446	458
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	69	0.07%	29.9%	AVFQANQENLPILK	99.7%	87.9	25	71.3	4	0	0	1584.87	431	444
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	69	0.07%	29.9%	CIELCCGSVK	99.7%	57.6	25	43.8	2	0	0	1225.54	459	468
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	69	0.07%	29.9%	DGPNALTPPPTTPEWIK	99.6%	39.1	25	37	2	0	0	1833.94	75	91
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	69	0.07%	29.9%	GIVVYTGDR	99.7%	53.9	25	53.4	3	0	0	979.52	256	264
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	69	0.07%	29.9%	GVGIISEGNETVEDIAAR	99.7%	146	25	140	2	0	0	1829.92	630	647
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	69	0.07%	29.9%	IVEIPFNSTNK	99.7%	48	25	42.4	2	0	0	1261.68	477	487
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	69	0.07%	29.9%	LIFDNLKK	99.7%	42.9	25	29.7	2	0	0	990.60	767	774
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	69	0.07%	29.9%	LIIVEGCQR	99.7%	50.2	25	41.2	4	0	0	1087.59	699	707
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	69	0.07%	29.9%	LNIPVSQVNPR	99.7%	66.8	25	65.1	7	0	0	1236.71	648	658
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	69	0.07%	29.9%	MSINAEEVVVGDLVEVK	99.7%	63.3	25	63.3	1	0	0	1846.95	178	194
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	69	0.07%	29.9%	NIAFFSTNCVEGTAR	99.7%	96.5	25	96.5	2	0	0	1686.79	241	255
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	69	0.07%	29.9%	NLEAVETLGSTSTICSDK	99.7%	59.3	25	59.3	2	0	0	1924.92	360	377

Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	69	0.07%	29.9%	NMVPQQALVIR	99.7%	53.7	25	44.3	3	0	0	1284.71	163	173
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	69	0.07%	29.9%	NPNTSEPQHLLVMK	99.7%	56.9	25	50.5	3	0	0	1607.82	495	508
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	69	0.07%	29.9%	QGAIVAVTGDGVNDSPALK	99.7%	114	25	114	2	0	0	1811.95	708	726
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	69	0.07%	29.9%	SPDFTNENPLETR	99.7%	77.6	25	68.7	4	0	0	1519.70	228	240
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	69	0.07%	29.9%	TSATWLALSR	99.7%	87.2	25	74.2	4	0	0	1105.60	414	423
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	69	0.07%	29.9%	VDNSSLTGESEPQTR	99.7%	95.5	25	85.9	3	0	0	1619.75	213	227
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	69	0.07%	29.9%	VIMVTGDHPITAK	99.7%	77.8	25	77.8	4	0	0	1381.75	613	625
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	69	0.07%	29.9%	YGTDLSR	99.7%	40.7	25	24.9	2	0	0	811.39	55	61
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	24	28	69	0.07%	29.9%	YHTEIVFAR	99.7%	49.1	25	39.3	1	0	0	1135.59	684	692
Sorting and assembly machinery component 50 homolog	SAMM50	SAM50_HUMAN	52.0	100.0%	6	6	10	0.01%	15.4%	GMSAEYSFPIWK	99.7%	52.2	25	40.5	1	0	0	1415.67	210	221
Sorting and assembly machinery component 50 homolog	SAMM50	SAM50_HUMAN	52.0	100.0%	6	6	10	0.01%	15.4%	ICDGVQFGAGIR	99.7%	69	25	63.6	2	0	0	1292.64	456	467
Sorting and assembly machinery component 50 homolog	SAMM50	SAM50_HUMAN	52.0	100.0%	6	6	10	0.01%	15.4%	SSLSHAMVIDSR	99.7%	62.8	25	50.7	2	0	0	1302.65	256	267
Sorting and assembly machinery component 50 homolog	SAMM50	SAM50_HUMAN	52.0	100.0%	6	6	10	0.01%	15.4%	TKDDIIICEIGDVFK	99.7%	77.9	25	72.1	1	0	0	1765.90	58	72
Sorting and assembly machinery component 50 homolog	SAMM50	SAM50_HUMAN	52.0	100.0%	6	6	10	0.01%	15.4%	VTFQFSYGTK	99.7%	57.7	25	48.6	2	0	0	1177.59	159	168
Sorting and assembly machinery component 50 homolog	SAMM50	SAM50_HUMAN	52.0	100.0%	6	6	10	0.01%	15.4%	VTGQFPWSSLR	99.4%	37.2	25	29	2	0	0	1277.66	195	205
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	SPTN1_HUMAN	284.5	99.8%	2	2	3	0.00%	0.8%	DVTGAEALLER	99.6%	39	25	31.3	2	0	0	1173.61	1370	1380
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	SPTN1_HUMAN	284.5	99.8%	2	2	3	0.00%	0.8%	LFGAAEVQR	99.2%	36	25	22.4	1	0	0	990.54	251	259
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	2	2	3	0.00%	1.6%	ALVADSHPESER	99.7%	42.8	25	42.7	1	0	0	1310.63	1657	1668
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	2	2	3	0.00%	1.6%	LQQFLR	96.0%	29.1	25	0	2	0	0	804.47	1064	1069
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	2	2	3	0.00%	1.6%	LVSQDNFGFDLPAVEAATK	99.7%	40.5	25	40.5	2	0	0	2022.02	444	462
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	13	15	25	0.02%	27.7%	AIDLMNALMR	99.7%	57.3	25	50.1	3	0	0	1147.60	385	394
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	13	15	25	0.02%	27.7%	ASAALAALEK	99.7%	89.1	25	62.8	2	0	0	944.54	564	573
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	13	15	25	0.02%	27.7%	DKPTETLLNTVK	99.2%	35.9	25	27.2	2	0	0	1358.75	111	122
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	13	15	25	0.02%	27.7%	DNLPIQIQK	99.7%	41.5	25	36.2	1	0	0	1068.61	123	131
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	13	15	25	0.02%	27.7%	EDITHSAQHALR	99.7%	48	25	40	1	0	0	1377.69	304	315
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	13	15	25	0.02%	27.7%	FPTYPVPHYSFF	99.7%	57.7	25	57.6	2	0	0	1501.72	661	672
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	13	15	25	0.02%	27.7%	FVMEVEVDGQK	99.7%	68.9	25	52.2	12	0	0	1280.62	541	551
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	13	15	25	0.02%	27.7%	GWPLELICEK	99.7%	67.2	25	0	9	0	0	1244.63	240	249
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	13	15	25	0.02%	27.7%	LFSGPNAANNK	99.7%	53	25	41.2	3	0	0	1132.57	574	584
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	13	15	25	0.02%	27.7%	LFSGPNAANNKK	99.7%	47.1	25	32.7	1	0	0	1260.67	574	585
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	13	15	25	0.02%	27.7%	LNQIRPGLQYK	99.7%	51	25	41.7	2	1	0	1329.76	395	405
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	13	15	25	0.02%	27.7%	LSAFGQIYK	99.7%	47.7	25	41.8	2	0	0	1026.56	316	324
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	13	15	25	0.02%	27.7%	NPVMELNEK	99.7%	51.6	25	46.5	12	0	0	1089.52	513	521
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	13	15	25	0.02%	27.7%	NPVMELNEKR	99.7%	54.3	25	41.3	4	0	0	1229.63	513	522
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	13	15	25	0.02%	27.7%	NTKEPTLTLK	99.7%	44.9	25	31.3	2	0	0	1144.66	152	161
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	13	15	25	0.02%	27.7%	SCVIVLR	99.7%	44.8	25	0	2	0	0	846.49	217	223
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	13	15	25	0.02%	27.7%	SIGTCNRPLGAGEALR	96.4%	24	25	18.5	0	1	0	1671.86	250	265
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	13	15	25	0.02%	27.7%	TQGPILTASGK	98.5%	33.4	25	28.3	2	0	0	1072.60	502	512
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	13	15	25	0.02%	27.7%	YELISETGGSHDK	99.7%	78.1	25	68.1	2	1	0	1435.67	527	539
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	13	15	25	0.02%	27.7%	YELISETGGSHDKR	99.7%	73.9	25	70.1	6	2	0	1591.77	527	540
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	5	5	7	0.01%	20.9%	AAFVLPEFAR	99.0%	34.9	25	32.4	1	0	0	1120.61	286	295
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	5	5	7	0.01%	20.9%	NPSTNFQEPVQPLTQQQVAQMQLK	99.6%	33.5	25	33.5	0	1	0	2754.39	254	277
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	5	5	7	0.01%	20.9%	VLIIGGGDGGVLR	99.7%	66.2	25	66.2	2	0	0	1225.73	97	109
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	5	5	7	0.01%	20.9%	YQDILVFR	99.7%	62.6	25	58.8	2	0	0	1053.57	48	55
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	5	5	7	0.01%	20.9%	YYNSDVHR	99.4%	37.4	25	37.4	1	0	0	1053.47	278	285
Sphingosine-1-phosphate lyase 1	SGPL1	SGPL1_HUMAN	63.5	99.9%	2	2	3	0.00%	4.6%	ALPSQGLSSSAVLEK	99.7%	82.8	25	76.4	2	0	0	1486.81	115	129
Sphingosine-1-phosphate lyase 1	SGPL1	SGPL1_HUMAN	63.5	99.9%	2	2	3	0.00%	4.6%	ASGTVYSGEEK	97.2%	30.6	25	26.7	1	0	0	1127.52	145	155
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	3	4	13	0.01%	15.3%	GTVLDQVPVNPSLYLIK	99.7%	56.8	25	40	4	0	0	1856.05	74	90
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	3	4	13	0.01%	15.3%	SSVGPSKPVSQPR	99.7%	56.7	25	35.8	4	3	0	1325.72	38	50
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	3	4	13	0.01%	15.3%	VSALEVLPDR	99.7%	75	25	54.6	2	0	0	1098.62	108	117
Spliceosome RNA helicase DDX39B	DDX39B	DX39B_HUMAN	49.0	99.8%	2	3	4	0.00%	23.6%	DFLLKPELLR	98.8%	34.2	25	20.3	1	0	0	1243.74	49	58

Spliceosome RNA helicase DDX39B	DDX39B	DX39B_HUMAN	49.0	99.8%	2	3	4	0.00%	23.6%	DVQEIFR	99.1%	35.6	25	16	2	0	0	906.47	210	216
Spliceosome RNA helicase DDX39B	DDX39B	DX39B_HUMAN	49.0	99.8%	2	3	4	0.00%	23.6%	ELAFQISK	99.4%	37.6	25	29.8	2	0	0	935.52	124	131
Spliceosome RNA helicase DDX39B	DDX39B	DX39B_HUMAN	49.0	99.8%	2	3	4	0.00%	23.6%	GLAITFVSDENDAK	99.7%	83.3	25	79.2	2	0	0	1479.73	385	398
Spliceosome RNA helicase DDX39B	DDX39B	DX39B_HUMAN	49.0	99.8%	2	3	4	0.00%	23.6%	GSYVSIHSSGFR	99.7%	58.5	25	47.7	2	0	0	1296.63	37	48
Spliceosome RNA helicase DDX39B	DDX39B	DX39B_HUMAN	49.0	99.8%	2	3	4	0.00%	23.6%	ILNDVQDR	99.7%	44.5	25	31	2	0	0	972.51	399	406
Spliceosome RNA helicase DDX39B	DDX39B	DX39B_HUMAN	49.0	99.8%	2	3	4	0.00%	23.6%	ILVATNLFGR	99.7%	85	25	67.8	4	0	0	1103.66	340	349
Spliceosome RNA helicase DDX39B	DDX39B	DX39B_HUMAN	49.0	99.8%	2	3	4	0.00%	23.6%	NCPHIVVGTPGR	99.7%	55.3	25	47	1	1	0	1306.67	164	175
Spliceosome RNA helicase DDX39B	DDX39B	DX39B_HUMAN	49.0	99.8%	2	3	4	0.00%	23.6%	VAVFFGGLSIK	99.7%	48.2	25	48.2	2	0	0	1137.67	145	155
Spliceosome RNA helicase DDX39B	DDX39B	DX39B_HUMAN	49.0	99.8%	2	3	4	0.00%	23.6%	YQQFKDFQR	97.8%	31.7	25	31.7	1	0	0	1259.62	330	338
Spliceosome-associated protein CWC15 homolog	CWC15	CWC15_HUMAN	26.6	99.9%	2	2	3	0.00%	15.3%	MENILSGNPLLNLTGPSQPQANFK	98.0%	26.3	25	26.3	0	1	0	2583.32	160	183
Spliceosome-associated protein CWC15 homolog	CWC15	CWC15_HUMAN	26.6	99.9%	2	2	3	0.00%	15.3%	QTTQDAPEEVR	99.7%	49.2	25	36	2	0	0	1273.60	45	55
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	AAGLATMISTMRPDIDNMDEYVR	99.7%	50.8	25	50.8	0	2	0	2618.19	603	625
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	AIVNVIGMHK	99.7%	44.5	25	38.2	4	0	0	1097.61	999	1008
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	ATVNTFGYIAK	99.7%	81.7	25	79.9	2	0	0	1184.63	1076	1086
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	DTPGHGSGWAETPR	98.0%	26.3	25	25.9	0	1	0	1467.66	302	315
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	EFQSPDEEMKK	97.2%	30.6	25	29.4	1	0	0	1367.61	776	786
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	EIISNLAK	97.9%	31.9	25	10.5	1	0	0	887.52	595	602
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	EVMLILIR	99.7%	59.5	25	35.2	4	0	0	986.61	768	775
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	GDTPGHATPGHGGATSSAR	99.7%	76.9	25	76.9	1	2	0	1733.80	271	289
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	GGDSIGETPTPGASK	99.7%	64.1	25	59.2	2	0	0	1373.65	319	333
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	ILVVIEPLLIDEDYYAR	99.7%	86.5	25	86.5	2	0	0	2034.12	574	590
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	IWDPTPSHTPAGAATPGR	99.7%	49.2	25	47.9	0	1	0	1831.91	253	270
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	IYNDDKNTYIR	99.7%	68.2	25	62.2	2	2	0	1414.70	1287	1297
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	LLVDVDESTLSPEEQK	99.7%	88.2	25	83.5	2	0	0	1801.91	478	493
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	LLVDVDESTLSPEEQKER	99.7%	111	25	106	1	2	0	2087.05	478	495
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	QCCGTDGVEANYIK	97.5%	31	25	31	1	0	0	1614.69	794	807
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	QLVDTTVELANK	99.7%	89.7	25	87.4	2	0	0	1330.72	832	843
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	QQAADLISR	99.7%	59	25	41.4	2	0	0	1001.54	949	957
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	SLVEIIEHGLVDEQQK	99.7%	52.8	25	38.5	2	0	0	1836.97	685	700
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	SRWDETPASQMGGSTPVLTPGK	97.3%	25.1	25	25.1	0	1	0	2318.11	336	357
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	SVNDQPSGNLPFLKPDDIQYFDK	99.7%	36.8	25	36.1	0	2	0	2637.28	455	477
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	TEILPPFFK	99.1%	35.5	25	24.7	1	0	0	1091.61	808	816
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	THEDIEAQIR	99.7%	59.4	25	53.4	2	0	0	1211.60	7	16
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	TMIISPER	99.7%	42	25	30.9	2	0	0	962.50	125	132
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	VGAAEIISR	99.7%	72	25	36.7	2	0	0	915.53	844	852
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	VPELNVQNGVLK	99.7%	65.2	25	59.3	2	0	0	1309.75	1138	1149
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	VQENCIDLVGR	99.7%	67.1	25	61.8	2	0	0	1302.65	1031	1041
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	VVNGAAASQPPSKR	99.6%	39.7	25	36.9	2	0	0	1381.75	183	196
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	WDETPASQMGGSTPVLTPGK	99.7%	94.1	25	94.1	2	0	0	2074.98	338	357
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	29	34	59	0.06%	28.1%	WDQTADQTPGATPK	99.7%	63.6	25	58	2	0	0	1515.71	200	213
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	12	12	20	0.02%	16.0%	AAVLLEQER	99.7%	47.9	25	43.2	2	0	0	1028.57	184	192
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	12	12	20	0.02%	16.0%	GIEKPPFELPDFIK	95.5%	28.7	25	24.4	1	0	0	1629.89	516	529
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	12	12	20	0.02%	16.0%	GPPPPPGDENR	97.0%	30.3	25	30.3	1	0	0	1132.54	248	258
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	12	12	20	0.02%	16.0%	ISLGMPVGPNAHK	99.7%	45.1	25	34.5	2	0	0	1320.71	615	627
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	12	12	20	0.02%	16.0%	KPGDLSDELR	99.7%	54.2	25	40	2	0	0	1129.59	605	614
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	12	12	20	0.02%	16.0%	LAEIGAPIQGNR	99.7%	60.9	25	60.9	2	0	0	1238.69	36	47
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	12	12	20	0.02%	16.0%	LAEIGAPIQGNREELVER	95.9%	23.6	25	23.6	0	2	0	1994.07	36	53
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	12	12	20	0.02%	16.0%	LAQQQAALLMQQEER	99.7%	100	25	99.2	1	0	0	1756.90	149	163
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	12	12	20	0.02%	16.0%	SSLGQSASETEEDTVSVSK	99.7%	88.8	25	88.8	2	0	0	1940.89	302	320
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	12	12	20	0.02%	16.0%	VGEPVALSEEER	99.7%	77.1	25	68.6	2	0	0	1314.65	135	146
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	12	12	20	0.02%	16.0%	VPPPWLIAMQR	95.6%	28.8	25	27.3	1	0	0	1307.73	628	638

Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	12	12	20	0.02%	16.0%	YGPPPSYPNLK	96.7%	30	25	23.4	2	0	0	1232.63	639	649
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	13	13	32	0.03%	13.5%	DYIVVGSDSGR	99.7%	80.1	25	67.2	2	0	0	1167.56	76	86
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	13	13	32	0.03%	13.5%	FGNICVVR	99.7%	49.2	25	39.3	2	0	0	964.50	1050	1057
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	13	13	32	0.03%	13.5%	FLAVGLVDNTVR	99.7%	85	25	71.6	3	0	0	1303.74	604	615
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	13	13	32	0.03%	13.5%	FSNTGEDWYVLVGVAK	99.7%	64.3	25	64.3	3	0	0	1784.89	896	911
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	13	13	32	0.03%	13.5%	IVILEYQPSK	99.7%	60.6	25	53.9	2	0	0	1189.68	87	96
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	13	13	32	0.03%	13.5%	LGAVFNQVAFPLQYTPR	99.7%	117	25	117	4	0	0	1921.03	770	786
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	13	13	32	0.03%	13.5%	MFLYNLTLQR	99.7%	59.5	25	54.6	2	0	0	1298.69	1	10
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	13	13	32	0.03%	13.5%	NENQLIIFADDTYPR	99.7%	98.2	25	98.2	2	0	0	1808.88	1017	1031
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	13	13	32	0.03%	13.5%	NFGDQPDIR	99.7%	42.5	25	33.7	2	0	0	1061.50	260	268
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	13	13	32	0.03%	13.5%	SVAGGFVYTYK	99.7%	59.8	25	50.2	2	0	0	1191.60	919	929
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	13	13	32	0.03%	13.5%	TPVEEVPAAIAPFQGR	99.7%	79.2	25	69.9	2	0	0	1681.89	943	958
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	13	13	32	0.03%	13.5%	TVLDPVTGDLSDTR	99.7%	92.2	25	90.2	4	0	0	1488.75	677	690
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	13	13	32	0.03%	13.5%	YFDTVPVAAAMCVLK	99.7%	59.6	25	59.6	2	0	0	1684.84	329	343
Splicing factor 45	RBM17	SPF45_HUMAN	45.0	99.9%	2	2	3	0.00%	5.5%	IIVGDATEKDASK	99.7%	68.1	25	51.2	2	0	0	1346.72	277	289
Splicing factor 45	RBM17	SPF45_HUMAN	45.0	99.9%	2	2	3	0.00%	5.5%	LLQSQLQVK	97.0%	30.3	25	25	1	0	0	1056.64	25	33
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	7	11	20	0.02%	39.2%	AVIDLNNR	99.7%	47	25	29.8	2	0	0	914.51	126	133
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	7	11	20	0.02%	39.2%	GGFCNFMHLKPISR	99.7%	40.8	25	40.4	1	4	0	1663.82	166	179
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	7	11	20	0.02%	39.2%	NPQNSSQSADGLR	99.7%	78.2	25	78.2	2	0	0	1373.64	54	66
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	7	11	20	0.02%	39.2%	QYEMGECTR	99.7%	49.8	25	42.3	3	0	0	1173.47	157	165
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	7	11	20	0.02%	39.2%	VNCSFYFK	99.7%	53.8	25	52.3	2	0	0	1064.49	16	23
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	7	11	20	0.02%	39.2%	WFNGQPIHAELSPVTDFR	99.7%	46.8	25	46.8	2	2	0	2114.05	134	151
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	7	11	20	0.02%	39.2%	YGEVEEMNVCDNLGDHLVGNVYVK	99.7%	76	25	76	0	2	0	2769.25	93	116
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	15	29	0.03%	26.9%	ELLTSFGPLK	99.7%	47.2	25	29.3	2	0	0	1104.63	277	286
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	15	29	0.03%	26.9%	GAKEEHGGLIR	99.7%	52	25	46.3	2	0	0	1166.63	68	78
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	15	29	0.03%	26.9%	IFVEFTSVFDCQK	99.7%	63.2	25	59.5	2	0	0	1619.78	432	444
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	15	29	0.03%	26.9%	LFIGGLPNYLNDDQVK	99.7%	68.8	25	60.3	2	0	0	1805.94	261	276
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	15	29	0.03%	26.9%	LGGLTQAPGNPVLAVQINQDK	99.7%	73.5	25	73.5	2	1	0	2133.17	175	195
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	15	29	0.03%	26.9%	NFAFLEFR	99.7%	47.1	25	40.9	2	0	0	1043.53	196	203
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	15	29	0.03%	26.9%	SIEIPRPVDGVEVPGCGK	99.7%	73.7	25	68.7	2	2	0	1908.99	414	431
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	15	29	0.03%	26.9%	SVDETTQAMAFDGIIFQGQSLK	99.7%	83.3	25	81.7	4	4	0	2402.15	204	225
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	9	15	29	0.03%	26.9%	YCDPDSYHR	99.7%	55.6	25	55.6	2	2	0	1212.47	463	471
Splicing factor, arginine/serine-rich 15	SCAF4	SFR15_HUMAN	125.9	99.8%	2	2	4	0.00%	2.4%	DLSIGNPIPTVVSGAR	99.7%	46.4	25	46.4	2	0	0	1595.88	778	793
Splicing factor, arginine/serine-rich 15	SCAF4	SFR15_HUMAN	125.9	99.8%	2	2	4	0.00%	2.4%	VPGLYVIDSIVR	99.7%	57.8	25	57.8	2	0	0	1330.77	60	71
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	4	4	6	0.01%	8.5%	AELDDTPMR	98.8%	34.1	25	33.8	1	0	0	1063.47	350	358
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	4	4	6	0.01%	8.5%	AVVIVDDR	99.7%	42	25	22.5	4	0	0	886.50	400	407
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	4	4	6	0.01%	8.5%	FATHAAALSVR	99.7%	41.8	25	32.9	1	0	0	1143.63	366	376
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	4	4	6	0.01%	8.5%	FGQGGAGPVGGQGPR	99.7%	70.7	25	68.9	2	0	0	1341.67	667	681
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	4	4	6	0.01%	8.5%	LFVGNLPADITEDEFKR	99.7%	38.8	25	37	0	2	0	1964.01	299	315
SRA stem-loop-interacting RNA-binding protein, mitochondrial	SLIRP	SLIRP_HUMAN	12.3	99.8%	2	2	3	0.00%	22.9%	IPWTAASSQLK	97.8%	31.6	25	25.9	1	0	0	1201.66	26	36
SRA stem-loop-interacting RNA-binding protein, mitochondrial	SLIRP	SLIRP_HUMAN	12.3	99.8%	2	2	3	0.00%	22.9%	NALQQENHIIDGVK	99.7%	59.9	25	56.6	2	0	0	1578.82	75	88
SRSF protein kinase 1	SRPK1	SRPK1_HUMAN	74.3	100.0%	4	4	8	0.01%	7.5%	HFTEDIQTR	99.3%	36.6	25	24.5	4	0	0	1146.55	507	515
SRSF protein kinase 1	SRPK1	SRPK1_HUMAN	74.3	100.0%	4	4	8	0.01%	7.5%	IADLGNACWVHK	99.7%	41.8	25	6.28	2	0	0	1383.68	495	506
SRSF protein kinase 1	SRPK1	SRPK1_HUMAN	74.3	100.0%	4	4	8	0.01%	7.5%	SAEHYTETALDEIR	99.7%	67.2	25	58	1	0	0	1634.77	113	126
SRSF protein kinase 1	SRPK1	SRPK1_HUMAN	74.3	100.0%	4	4	8	0.01%	7.5%	STAGNFLVNPLEPK	99.2%	36.2	25	25.8	1	0	0	1486.79	473	486
SRSF protein kinase 2	SRPK2	SRPK2_HUMAN	77.5	99.8%	2	2	4	0.00%	6.5%	AADLLVNPLDPR	99.7%	49.1	25	45.1	2	0	0	1293.72	508	519
SRSF protein kinase 2	SRPK2	SRPK2_HUMAN	77.5	99.8%	2	2	4	0.00%	6.5%	HFTEDIQTR	99.3%	36.6	25	24.5	4	0	0	1146.55	540	548
SRSF protein kinase 2	SRPK2	SRPK2_HUMAN	77.5	99.8%	2	2	4	0.00%	6.5%	IADLGNACWVHK	99.7%	41.8	25	6.28	2	0	0	1383.68	528	539
SRSF protein kinase 2	SRPK2	SRPK2_HUMAN	77.5	99.8%	2	2	4	0.00%	6.5%	TVSASSTGDLPK	99.7%	43.5	25	30.3	2	0	0	1162.60	492	503
Stathmin	STMN1	STMN1_HUMAN	17.3	99.8%	2	2	3	0.00%	15.4%	AIEENNNFSK	99.7%	47	25	0	2	0	0	1165.55	86	95
Stathmin	STMN1	STMN1_HUMAN	17.3	99.8%	2	2	3	0.00%	15.4%	ASGQAFELILSPR	99.7%	40.6	25	29.2	1	0	0	1388.75	15	27

Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	NSDHL	NSDHL_HUMAN	41.9	100.0%	3	3	5	0.00%	11.0%	DPQLVPILIEAAR	98.9%	34.7	25	28.8	1	0	0	1434.83	208	220
Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	NSDHL	NSDHL_HUMAN	41.9	100.0%	3	3	5	0.00%	11.0%	FFLGDLCSR	99.6%	39.6	25	39.6	2	0	0	1114.54	80	88
Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	NSDHL	NSDHL_HUMAN	41.9	100.0%	3	3	5	0.00%	11.0%	GYAVNVFDIQQGFDNPQVR	99.7%	63.7	25	63.7	2	0	0	2167.06	61	79
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	9	17	0.02%	35.1%	AEQINQAAGEASAVLAK	99.7%	131	25	129	2	0	0	1670.87	234	250
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	9	17	0.02%	35.1%	APVPGTPDSLSSGSSR	99.7%	52.7	25	49.4	2	0	0	1514.74	322	337
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	9	17	0.02%	35.1%	ASYGVEDPEYAVTQLAQTTMR	99.7%	74.5	25	72.9	3	0	0	2330.10	115	135
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	9	17	0.02%	35.1%	DVQGTDASLDEELDRVK	99.7%	62.9	25	62.9	2	0	0	1889.91	338	354
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	9	17	0.02%	35.1%	ESAINVAEGKK	99.5%	38	25	31.9	2	0	0	1145.62	212	222
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	9	17	0.02%	35.1%	ILEPGLNILIPVLDR	99.7%	53.8	25	53.8	3	0	0	1675.02	58	72
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	9	17	0.02%	35.1%	NTVVLFVPQQEAWVVER	99.7%	52.1	25	52.1	2	0	0	2014.08	35	51
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	8	9	17	0.02%	35.1%	QAQILASEAEK	99.7%	40.9	25	28	1	0	0	1187.63	223	233
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	16	16	39	0.04%	31.8%	AQFEGIVTDLIR	99.7%	86.4	25	82.1	4	0	0	1361.74	349	360
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	16	16	39	0.04%	31.8%	ASNGDAWVEAHGK	99.7%	58.9	25	58.9	1	0	0	1341.62	147	159
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	16	16	39	0.04%	31.8%	DAGQISGLNVLR	99.7%	80	25	66.6	3	0	0	1242.68	207	218
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	16	16	39	0.04%	31.8%	LLGQFTLIGIPPAPR	99.7%	59	25	59	4	0	0	1592.95	499	513
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	16	16	39	0.04%	31.8%	LYSPSQIGAFVLMK	99.7%	61.5	25	61.5	2	0	0	1569.83	160	173
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	16	16	39	0.04%	31.8%	NAVITVPAYFNDSQR	99.7%	80.2	25	76.9	2	0	0	1694.85	188	202
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	16	16	39	0.04%	31.8%	QAASSLQQASLK	99.7%	64.2	25	60.6	1	0	0	1231.66	635	646
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	16	16	39	0.04%	31.8%	QAVTNPNNTFYATK	99.7%	91	25	90.9	2	0	0	1568.77	108	121
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	16	16	39	0.04%	31.8%	RYDDPEVQK	99.7%	45.4	25	35.9	2	0	0	1149.55	127	135
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	16	16	39	0.04%	31.8%	SDIGEVILVGGMTR	99.7%	90.8	25	82.7	2	0	0	1446.76	378	391
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	16	16	39	0.04%	31.8%	SQVFSTAADGQTQVEIK	99.7%	105	25	105	2	0	0	1808.90	469	485
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	16	16	39	0.04%	31.8%	STNGDTFLGGEDFDQALLR	99.7%	87.4	25	81.9	3	0	0	2055.96	266	284
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	16	16	39	0.04%	31.8%	TTPSVVAFTADGER	99.7%	113	25	109	4	0	0	1450.72	86	99
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	16	16	39	0.04%	31.8%	VINEPTAAALAYGLDK	99.7%	117	25	116	3	0	0	1645.88	219	234
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	16	16	39	0.04%	31.8%	VLENAEGAR	99.7%	52	25	37.4	2	0	0	958.50	77	85
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	16	16	39	0.04%	31.8%	VQQTVQDLFGR	99.7%	49.9	25	46	2	0	0	1290.68	395	405
Striatin-interacting protein 1	STRIP1	STRP1_HUMAN	95.6	99.9%	2	2	3	0.00%	2.4%	ILLAAAPTSK	99.7%	41.2	25	33	2	0	0	984.61	527	536
Striatin-interacting protein 1	STRIP1	STRP1_HUMAN	95.6	99.9%	2	2	3	0.00%	2.4%	NLFSCINLLR	98.6%	33.4	25	24.9	1	0	0	1249.67	664	673
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	ADQDRLDLEER	98.9%	34.4	25	27.7	1	0	0	1359.65	402	412
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	AEEDTQFNYHR	99.7%	64.5	25	57.3	2	0	0	1409.61	178	188
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	AFVSMVYSEEGAEDR	99.7%	105	25	101	2	0	0	1689.74	78	92
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	DCIQYIK	99.4%	37.1	25	0.66	1	0	0	939.46	555	561
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	DKFQETSDEFEAAR	99.7%	80.8	25	80.8	2	1	0	1672.75	1036	1049
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	DLIHGAPVGKPAANR	98.5%	27.4	25	27.4	0	1	0	1515.84	63	77
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	DLTLEENQVK	99.7%	71.5	25	52.8	2	0	0	1188.61	364	373
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	DLTLEENQVKK	99.3%	36.4	25	30.9	1	0	0	1316.71	364	374
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	ELNQVMEQLGDAR	99.7%	79.9	25	73.3	2	0	0	1502.73	476	488
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	FNACFESVATNIDEIYK	99.7%	94.3	25	93.9	2	0	0	2020.93	1070	1086
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	GEPETFLPLDYLEVKPTDEK	99.7%	49.3	25	49.3	1	0	0	2320.16	565	584
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	HLALNLQEK	99.1%	35.5	25	28.1	1	0	0	1065.61	726	734
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	IIDETMAQLQDLK	99.7%	83.7	25	77.8	2	0	0	1533.78	862	874
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	LEEYITTSK	97.2%	30.6	25	30.6	1	0	0	1083.56	438	446
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	LGIQLDFEK	99.7%	51.5	25	41.1	2	0	0	1062.58	817	825
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	LNEQQSVLQR	99.7%	70.1	25	47.6	2	0	0	1214.65	1010	1019
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	LTEELKEQMK	99.7%	40.9	25	39.6	2	0	0	1248.65	681	690
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	LYHNEVEIEK	99.7%	43.4	25	35.2	2	1	0	1273.64	228	237
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	NFLVFQGAVESIAMK	99.7%	102	25	90.4	4	0	0	1669.86	132	146
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	NMDAIIVDSEK	99.7%	56.5	25	46.8	2	0	0	1250.59	541	551
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	QIIGPFQR	97.4%	30.9	25	19.8	1	0	0	958.55	19	26
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	SGELAQEYDKR	99.7%	54.8	25	45.9	2	0	0	1295.62	161	171

Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	SGVISGGASDLK	99.7%	58.4	25	36.8	2	0	0	1090.57	649	660
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	SKLESELANFGPR	99.3%	30.9	25	30.9	0	1	0	1447.75	735	747
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	SNLMDAISFVLGEK	99.7%	75.9	25	71.2	4	0	0	1539.77	39	52
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	TALFEEISR	99.7%	68.9	25	63.8	2	0	0	1065.56	152	160
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	TVALDGTLFQK	99.7%	55.9	25	43.6	2	0	0	1192.66	638	648
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	VIVGGSSEYK	98.2%	32.3	25	28.3	1	0	0	1038.55	97	106
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	VLTFDLTKYPDANPNPNEQ	99.7%	46.4	25	46.1	1	0	0	2176.06	1215	1233
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	VVQLHEYSEELEK	99.7%	65.5	25	65.5	2	0	0	1602.80	111	123
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	31	36	57	0.06%	29.2%	YSQSDLEQTK	99.7%	65.9	25	52.3	2	0	0	1198.56	714	723
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	ALNHEIEELEK	99.7%	41.2	25	39.5	1	1	0	1324.67	276	286
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	AMNVLTEAEER	99.7%	59.4	25	53.3	2	0	0	1278.60	987	997
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	ASNLQDLVYK	98.3%	32.7	25	24.1	1	0	0	1150.61	59	68
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	ASVSITFDNSDKK	99.7%	45.3	25	38.8	2	0	0	1411.71	77	89
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	DQEALEAVKR	99.6%	38.8	25	31.8	2	0	0	1158.61	447	456
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	DTSATTALELVAGER	99.7%	90.9	25	78.1	2	0	0	1533.78	534	548
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	EGMFNNANVLFK	99.3%	36.8	25	28.4	1	0	0	1383.67	1147	1158
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	ENLTELSGGQR	99.7%	81.5	25	69.1	2	0	0	1203.60	1080	1090
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	EVITAQDTVIK	99.7%	47.1	25	43.1	1	0	0	1216.68	880	890
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	FQELKDVQDELR	99.7%	53.2	25	41.4	1	0	0	1519.78	678	689
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	FVDGVSTVAR	99.7%	79.9	25	65.6	2	0	0	1050.56	1161	1170
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	GLVASLISVK	99.7%	55.5	25	52.9	2	0	0	986.62	524	533
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	HLFGQPNSAYDFK	99.7%	59.6	25	58.7	2	0	0	1523.73	946	958
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	IKELDHNISK	99.7%	43.3	25	27.7	2	0	0	1196.66	910	919
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	ILTTIEDLDQKK	99.7%	64.4	25	16.1	2	0	0	1416.79	1015	1026
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	LKETYEALLAR	99.7%	60.6	25	47.8	2	0	0	1306.74	492	502
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	LQEELSENDKK	99.7%	59.6	25	51.6	2	0	0	1332.66	263	273
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	LYNVVVDTEVTGK	99.7%	102	25	99.4	2	0	0	1436.76	549	561
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	QQLEAVNEAIK	99.7%	40.4	25	34	2	0	0	1242.67	838	848
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	SAEELKEMQDK	98.9%	34.5	25	29.2	3	0	0	1307.61	249	259
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	SIILEGFK	99.7%	45.9	25	45.9	2	0	0	906.53	5	12
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	SLEDALAEAQR	99.7%	95.5	25	83.4	2	0	0	1202.60	298	308
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	SQAASILTK	99.7%	50.8	25	42	2	0	0	918.53	669	677
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	SSYLEYQK	98.6%	33.5	25	29.4	1	0	0	1017.49	215	222
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	TIEESEETLK	99.7%	40.6	25	31.8	2	0	0	1178.58	751	760
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	TILEEEITPTIQK	99.7%	75.9	25	61.4	2	0	0	1514.83	197	209
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	27	29	50	0.05%	25.6%	TVTLGGDVFDPHGTLSGGAR	99.7%	42.5	25	42.5	0	2	0	1956.98	649	668
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	AELGTDLLSQLSLEDQK	99.7%	77.3	25	77.3	2	0	0	1859.96	779	795
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	AILNGIDSINK	99.7%	48.1	25	38.2	2	0	0	1157.65	504	514
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	AKLDELSAK	99.7%	40.6	25	20.3	1	0	0	974.55	237	245
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	ALDQFVNFSEQK	99.7%	76.7	25	71.5	2	0	0	1425.70	986	997
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	ALEYTIYNQELNETR	99.7%	80.2	25	61.2	2	0	0	1856.90	222	236
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	DLEDTEANKEK	99.7%	45.7	25	42	2	0	0	1291.60	419	429
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	DLQDELAGNSEQR	99.7%	63	25	56.4	1	0	0	1474.68	311	323
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	DQTIVDPFSSK	99.7%	52.7	25	22.8	2	0	0	1236.61	16	26
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	DTAYPETNDAIPMISK	99.0%	34.9	25	34.9	1	0	0	1765.83	597	612
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	EENAEQQALAAK	99.7%	84.7	25	76.8	2	0	0	1301.63	475	486
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	ELGSLPQEAFEK	99.7%	48.8	25	41.5	2	0	0	1347.68	945	956
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	GALTGGYYDTR	99.7%	77.8	25	70.3	2	0	0	1173.55	662	672
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	IKLEGIITR	98.1%	32.2	25	9.63	2	0	0	1042.66	819	827
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	INQMATAPDSQR	99.7%	53.9	25	43.6	4	0	0	1331.64	144	155
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	KAEEELGELEAK	99.7%	87.2	25	67.7	2	0	0	1345.68	684	695

Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	KYEAIQLTFK	98.9%	34.7	25	34.7	1	0	0	1240.69	1025	1034
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	LALLHEGTGPR	99.7%	63.3	25	56.3	2	0	0	1163.65	62	72
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	LFYHIVDSDEVSTK	99.2%	30.2	25	30.2	0	1	0	1652.82	558	571
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	MNLPGEVTFLPLNK	99.7%	69.8	25	58	4	0	0	1588.84	579	592
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	NDVMNLLESAGFSR	99.7%	116	25	116	4	0	0	1552.74	119	132
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	NFSEVFQK	99.4%	37.5	25	19	2	0	0	998.49	1039	1046
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	QKELAETEPK	99.5%	37.8	25	30.2	1	0	0	1172.62	341	350
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	QVIIQGFR	99.7%	55.5	25	38.6	2	0	0	960.56	5	12
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	SEDLDNSIDKTEAGIK	99.7%	74.7	25	71.6	1	0	0	1734.84	880	895
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	SIMELMNVLELR	99.3%	36.8	25	29.8	1	0	0	1479.75	1013	1024
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	SLDQAINDK	99.0%	34.8	25	24.4	2	0	0	1003.51	401	409
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	SMEVSTQLAR	99.7%	51.7	25	43	4	0	0	1121.56	635	644
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	VDALNDEIR	99.7%	53.8	25	27.9	1	0	0	1044.53	797	805
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	VETYLNENLR	99.7%	68.8	25	43.3	2	0	0	1250.64	828	837
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	30	34	59	0.06%	28.8%	VSHIDVITAEMAK	99.7%	65.9	25	57.8	2	0	0	1413.74	1195	1207
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	23	24	40	0.04%	19.8%	DTLVADNLDQATR	99.7%	69.9	25	65.1	2	0	0	1431.71	714	726
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	23	24	40	0.04%	19.8%	ELEANVLATAPDK	99.7%	62.5	25	62.5	1	0	0	1370.72	841	853
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	23	24	40	0.04%	19.8%	FTASIQR	96.4%	29.6	25	18.9	1	0	0	822.45	821	827
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	23	24	40	0.04%	19.8%	FTQLDLEDVQVR	99.7%	102	25	94.4	2	0	0	1462.75	390	401
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	23	24	40	0.04%	19.8%	IAEMETQKEK	99.2%	36	25	26.7	2	0	0	1206.60	334	343
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	23	24	40	0.04%	19.8%	IFNLSGGEK	99.0%	34.9	25	20.2	2	0	0	964.51	1188	1196
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	23	24	40	0.04%	19.8%	IHEDTKEINEK	99.7%	68.1	25	61.2	2	0	0	1355.68	344	354
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	23	24	40	0.04%	19.8%	LGDLGAIDEK	97.5%	31.1	25	28.1	1	0	0	1030.54	619	628
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	23	24	40	0.04%	19.8%	LHNTIVEINNHK	99.3%	36.7	25	36.3	1	0	0	1431.77	887	898
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	23	24	40	0.04%	19.8%	LLEENVSAFK	99.7%	71.3	25	60.2	2	0	0	1149.62	858	867
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	23	24	40	0.04%	19.8%	LTQEETNFK	99.7%	56.9	25	49.8	2	0	0	1109.55	565	573
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	23	24	40	0.04%	19.8%	NAQFIIISLR	99.7%	48.6	25	48.6	1	0	0	1174.69	1243	1252
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	23	24	40	0.04%	19.8%	NTNAAEESLPEIQK	99.7%	97.8	25	89.8	2	0	0	1543.76	975	988
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	23	24	40	0.04%	19.8%	QAFYFALR	99.6%	39.2	25	22.7	2	0	0	1015.54	706	713
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	23	24	40	0.04%	19.8%	QLDECASAITK	99.7%	59.7	25	53.1	2	0	0	1235.59	912	922
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	23	24	40	0.04%	19.8%	QNIGVATFIGLDK	99.7%	41.6	25	39.2	2	0	0	1375.76	661	673
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	23	24	40	0.04%	19.8%	SLEDKAAEVVK	99.7%	45.3	25	37.1	1	0	0	1188.65	964	974
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	23	24	40	0.04%	19.8%	SLVHDLFQK	96.3%	29.5	25	22.6	1	0	0	1086.59	574	582
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	23	24	40	0.04%	19.8%	SNNIINETTTR	99.7%	66	25	58.7	3	0	0	1262.63	435	445
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	23	24	40	0.04%	19.8%	VAELDKITYER	99.7%	48	25	42.6	2	0	0	1336.71	1107	1117
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	23	24	40	0.04%	19.8%	VIQENEHALQK	99.7%	70.5	25	63.6	2	0	0	1308.69	999	1009
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	23	24	40	0.04%	19.8%	VLDAIIQEK	99.7%	49.4	25	40.7	2	0	0	1028.60	599	607
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	23	24	40	0.04%	19.8%	VVTLQGQIIEQSGTMTGGGSK	99.7%	124	25	120	2	0	0	2091.08	737	757
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	SDHB	SDHB_HUMAN	31.6	100.0%	2	2	3	0.00%	9.3%	DLVPDLSNFYAQYK	99.0%	34.8	25	32.6	2	0	0	1672.82	138	151
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	SDHB	SDHB_HUMAN	31.6	100.0%	2	2	3	0.00%	9.3%	YLGPAVLMQAYR	99.7%	42	25	35.3	1	0	0	1381.73	206	217
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	8	11	25	0.02%	31.8%	GGQTHLGLPVFNTVK	99.7%	70.4	25	70.4	3	2	0	1567.86	91	105
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	8	11	25	0.02%	31.8%	IGIMPGHIHK	99.1%	35.7	25	35.2	2	0	0	1102.62	183	192
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	8	11	25	0.02%	31.8%	IICQGFTGK	99.6%	38.9	25	30.5	2	0	0	1023.53	58	66
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	8	11	25	0.02%	31.8%	ISALQSAGVVVSMSPAQLGTTIYK	99.7%	59.9	25	59.9	0	2	0	2437.30	315	338
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	8	11	25	0.02%	31.8%	LIGPNCPGVINPGECK	99.7%	94.8	25	89.4	2	0	0	1724.85	167	182
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	8	11	25	0.02%	31.8%	LVGGTTPGK	99.7%	44.4	25	35.8	2	0	0	829.48	82	90
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	8	11	25	0.02%	31.8%	MGHAGAIIAGGK	99.7%	70.6	25	69.4	6	0	0	1098.57	297	308
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	8	11	25	0.02%	31.8%	QGTFHSQQALEYGTK	99.7%	42.5	25	38.9	2	2	0	1694.81	67	81
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	11	20	0.02%	25.7%	CDVIAQGIVMAVK	99.7%	111	25	95.8	2	0	0	1403.74	384	396
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	11	20	0.02%	25.7%	DLEIKIPVVVR	98.3%	32.8	25	32.8	1	0	0	1280.79	397	407
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	11	20	0.02%	25.7%	EPIDIEEGIKK	99.7%	44.1	25	35.6	1	0	0	1270.69	206	216

Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	11	20	0.02%	25.7%	EQALQLAQK	99.7%	51.5	25	43.1	2	0	0	1028.57	217	225
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	11	20	0.02%	25.7%	ICNQVLVCER	99.7%	67.7	25	62.5	2	0	0	1290.63	151	160
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	11	20	0.02%	25.7%	ILACDDLDEAAR	99.7%	87.8	25	77	2	0	0	1361.64	427	438
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	11	20	0.02%	25.7%	INFDSNSAYR	99.7%	66.8	25	63.7	2	0	0	1186.55	275	284
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	11	20	0.02%	25.7%	LSEIVTLAK	99.7%	60.8	25	40.6	2	0	0	973.59	443	451
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	11	20	0.02%	25.7%	LYSLFLK	99.7%	41.2	25	32.7	2	0	0	883.53	243	249
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	11	20	0.02%	25.7%	MGFPPNIVESAAENMVK	99.7%	70.2	25	65.9	2	0	0	1833.89	226	242
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	11	11	20	0.02%	25.7%	SPDEAYAIAK	99.7%	66.1	25	63.8	2	0	0	1064.53	79	88
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	13	25	0.02%	28.9%	DPNVVGQLAK	98.9%	34.7	25	28.4	1	0	0	1040.57	109	118
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	13	25	0.02%	28.9%	EAQVYQAFK	99.7%	42.7	25	38.4	2	0	0	1083.55	339	347
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	13	25	0.02%	28.9%	ETYLAILMDR	99.7%	55.1	25	50.3	4	0	0	1240.62	151	160
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	13	25	0.02%	28.9%	FFVADTANEALEAAK	99.7%	111	25	111	2	0	0	1596.79	59	73
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	13	25	0.02%	28.9%	ILNNSGLPITSAIDLEDAAK	99.7%	98.6	25	98.6	2	0	0	2055.10	404	423
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	13	25	0.02%	28.9%	INFDDNAEFR	99.7%	69	25	62.1	2	0	0	1240.56	260	269
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	13	25	0.02%	28.9%	LEGTNVQEAQK	99.7%	74.5	25	59.8	2	0	0	1216.62	393	403
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	13	25	0.02%	28.9%	LYNLFLK	99.7%	45.8	25	34.6	2	0	0	910.54	228	234
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	13	25	0.02%	28.9%	MAENLGFVGPLK	99.7%	88.2	25	76.7	4	0	0	1275.68	207	218
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	13	25	0.02%	28.9%	QMIGYNLATK	99.7%	46.8	25	35.1	2	0	0	1154.59	119	128
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	11	13	25	0.02%	28.9%	VMVAEALDISR	99.7%	84.2	25	74.2	2	0	0	1203.64	140	150
SUMO-conjugating enzyme UBC9	UBE2I	UBC9_HUMAN	18.0	99.9%	2	2	2	0.00%	8.2%	DHPFGFVAVPTK	99.7%	44	25	42.6	1	0	0	1314.68	19	30
SUMO-conjugating enzyme UBC9	UBE2I	UBC9_HUMAN	18.0	99.9%	2	2	2	0.00%	8.2%	KDHPFGFVAVPTK	96.8%	24.5	25	23.5	0	1	0	1442.78	18	30
SUN domain-containing protein 2	SUN2	SUN2_HUMAN	80.3	99.8%	2	2	2	0.00%	4.2%	DSSPHFQAEQR	99.7%	57.1	25	49	1	0	0	1301.59	265	275
SUN domain-containing protein 2	SUN2	SUN2_HUMAN	80.3	99.8%	2	2	2	0.00%	4.2%	IGLADYALESGGASVISTR	99.7%	85.3	25	85.3	1	0	0	1879.98	544	562
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	33	0.03%	16.6%	AIGNTELENK	99.7%	49.7	25	39.7	2	0	0	1088.56	1013	1022
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	33	0.03%	16.6%	DVDFEGTDEPIFGK	99.7%	67.8	25	67.8	2	0	0	1568.71	65	78
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	33	0.03%	16.6%	EIEEYIHKPK	99.6%	38.8	25	24.3	1	0	0	1285.68	639	648
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	33	0.03%	16.6%	EYPFILDAFQR	99.7%	54.9	25	47.3	4	0	0	1398.71	135	145
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	33	0.03%	16.6%	GIVILMVDEK	99.7%	46.8	25	36.2	1	0	0	1116.63	533	542
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	33	0.03%	16.6%	IVIPNEESVVIYYK	99.7%	51.4	25	50.3	2	0	0	1665.91	615	628
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	33	0.03%	16.6%	LDFNTDEEKK	99.5%	37.9	25	28.6	1	0	0	1238.59	409	418
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	33	0.03%	16.6%	LGFATSSDVIEMK	99.7%	76	25	54.4	2	0	0	1397.70	861	873
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	33	0.03%	16.6%	LTEQLAGPLR	99.7%	73.9	25	60.6	2	0	0	1097.63	924	933
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	33	0.03%	16.6%	MTDVFEGSIIR	99.7%	74.4	25	67.2	3	0	0	1267.64	985	995
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	33	0.03%	16.6%	NFQPVIIFSFSK	99.7%	54.7	25	48.2	4	0	0	1426.77	385	396
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	33	0.03%	16.6%	RLEELLR	99.7%	44.9	25	11	2	0	0	928.56	999	1005
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	33	0.03%	16.6%	SFYQFQHYR	99.6%	39.7	25	31	2	0	0	1275.59	588	596
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	33	0.03%	16.6%	TVLQMDELK	99.6%	38.9	25	28.6	2	0	0	1076.57	844	852
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	33	0.03%	16.6%	WISSGEYIQMSGR	99.7%	66.1	25	66.1	1	0	0	1513.71	511	523
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	33	0.03%	16.6%	YCLPFLQPGR	99.5%	38.3	25	34.9	2	0	0	1250.64	649	658
Suppressor of SWI4 1 homolog	PPAN	SSF1_HUMAN	53.2	100.0%	2	2	4	0.00%	5.5%	LPGGPTLTFQVK	99.7%	76.1	25	69.9	2	0	0	1257.72	102	113
Suppressor of SWI4 1 homolog	PPAN	SSF1_HUMAN	53.2	100.0%	2	2	4	0.00%	5.5%	VGGSDEEASGIPSR	99.7%	95.8	25	90.2	2	0	0	1360.63	356	369
Surfeit locus protein 4	SURF4	SURF4_HUMAN	30.4	100.0%	3	3	6	0.01%	15.2%	GQNDLMGTAEDFADQFLR	99.7%	68.5	25	68.5	2	0	0	2043.91	2	19
Surfeit locus protein 4	SURF4	SURF4_HUMAN	30.4	100.0%	3	3	6	0.01%	15.2%	LCLISTFLEDGIR	99.7%	77	25	70.6	2	0	0	1536.81	31	43
Surfeit locus protein 4	SURF4	SURF4_HUMAN	30.4	100.0%	3	3	6	0.01%	15.2%	SMFAGVPTMR	99.7%	40.2	25	31	2	0	0	1128.52	140	149
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	4	4	7	0.01%	4.9%	ALNIVDQEGSLLGK	99.7%	80.1	25	78.2	2	0	0	1456.80	215	228
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	4	4	7	0.01%	4.9%	ATTGTQTLLSSGTR	99.7%	76.8	25	71.5	2	0	0	1393.73	696	709
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	4	4	7	0.01%	4.9%	GADQKPTSADCAVR	99.7%	50.4	25	45.3	2	0	0	1475.69	646	659
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	4	4	7	0.01%	4.9%	YSLSGSVAHSR	99.7%	61.4	25	55.1	1	0	0	1163.58	63	73
Survival motor neuron protein	SMN1	SMN_HUMAN	31.8	100.0%	3	3	4	0.00%	13.9%	ETCVVVYTGYGNR	99.7%	83.3	25	82.9	2	0	0	1517.71	121	133
Survival motor neuron protein	SMN1	SMN_HUMAN	31.8	100.0%	3	3	4	0.00%	13.9%	NTAASLQQWK	99.7%	48	25	37.9	1	0	0	1146.59	84	93
Survival motor neuron protein	SMN1	SMN_HUMAN	31.8	100.0%	3	3	4	0.00%	13.9%	SAPWNSFLPPPPPMPGPR	96.9%	30.2	25	30.2	1	0	0	1944.98	187	204

SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	19	35	0.03%	18.0%	ANYAVDAYFR	99.7%	54.6	25	44.9	2	0	0	1189.56	740	749
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	19	35	0.03%	18.0%	CNELQDIEK	99.7%	42.8	25	24.8	2	0	0	1148.53	891	899
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	19	35	0.03%	18.0%	DFNQFIK	96.8%	30	25	10.3	1	0	0	911.46	849	855
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	19	35	0.03%	18.0%	DIDILNSAGK	99.7%	67.9	25	33.3	2	0	0	1045.55	431	440
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	19	35	0.03%	18.0%	EIQEPDPTYEEK	99.7%	54	25	43.9	2	0	0	1477.67	72	83
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	19	35	0.03%	18.0%	ENMELEEKEK	94.7%	28.1	25	10.1	1	0	0	1278.59	1011	1020
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	19	35	0.03%	18.0%	ESEITDEDIDGILER	99.7%	107	25	107	2	0	0	1733.81	666	680
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	19	35	0.03%	18.0%	FITDNTVEER	99.7%	54.2	25	43.4	2	0	0	1223.59	607	616
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	19	35	0.03%	18.0%	LDGQTPHDER	99.7%	48.5	25	47.2	1	0	0	1167.54	529	538
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	19	35	0.03%	18.0%	LDSIVIQQGR	99.7%	73.1	25	65.6	2	0	0	1128.64	627	636
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	19	35	0.03%	18.0%	LLNILMQLR	99.7%	84.8	25	65.2	5	0	0	1113.68	446	454
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	19	35	0.03%	18.0%	NPELPNAAQAQK	99.7%	68.3	25	61.9	2	0	0	1280.66	803	814
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	19	35	0.03%	18.0%	QNLLSVGDYR	99.7%	69.8	25	40.4	2	0	0	1164.60	133	142
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	19	35	0.03%	18.0%	SVCLIGDKEQR	99.7%	50.7	25	28.3	2	0	0	1304.66	257	267
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	19	35	0.03%	18.0%	TEQEEDEELLTESSK	99.7%	85.2	25	85.2	2	0	0	1766.78	146	160
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	19	35	0.03%	18.0%	VLIFSQMTR	99.7%	65.2	25	59.1	2	0	0	1094.60	502	510
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	19	35	0.03%	18.0%	WGRDDIENIAR	94.7%	22.7	25	14	0	1	0	1344.67	860	870
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	18	19	35	0.03%	18.0%	YLVIDEAHR	99.7%	48.6	25	43.6	2	0	0	1115.58	304	312
Symplekin	SYMPK	SYMPK_HUMAN	141.2	99.8%	2	2	5	0.00%	2.3%	AEVLSFILEDVR	99.7%	47.5	25	46.2	1	0	0	1390.76	602	613
Symplekin	SYMPK	SYMPK_HUMAN	141.2	99.8%	2	2	5	0.00%	2.3%	VVLEAPLITESALEVVR	99.7%	92.4	25	92.4	4	0	0	1838.06	667	683
Syntaxin-18	STX18	STX18_HUMAN	38.7	99.7%	2	2	2	0.00%	5.4%	LQEIFTEK	94.9%	28.2	25	15	1	0	0	1007.54	266	273
Syntaxin-18	STX18	STX18_HUMAN	38.7	99.7%	2	2	2	0.00%	5.4%	TCSEAIQQLR	99.7%	50.3	25	26.1	1	0	0	1205.59	106	115
Syntaxin-binding protein 2	STXBP2	STXB2_HUMAN	66.5	100.0%	5	5	6	0.01%	11.1%	ADTPSLGEGPEK	97.1%	30.4	25	24.3	1	0	0	1200.57	214	225
Syntaxin-binding protein 2	STXBP2	STXB2_HUMAN	66.5	100.0%	5	5	6	0.01%	11.1%	DFQGTPTFTYK	94.5%	27.9	25	22.7	1	0	0	1304.62	90	100
Syntaxin-binding protein 2	STXBP2	STXB2_HUMAN	66.5	100.0%	5	5	6	0.01%	11.1%	EPIPSLEAIYLLSPTEK	98.4%	32.9	25	32.9	1	0	0	1900.03	66	82
Syntaxin-binding protein 2	STXBP2	STXB2_HUMAN	66.5	100.0%	5	5	6	0.01%	11.1%	LIVPVLLDAAVPAYDK	99.7%	74.1	25	71.3	2	0	0	1696.99	388	403
Syntaxin-binding protein 2	STXBP2	STXB2_HUMAN	66.5	100.0%	5	5	6	0.01%	11.1%	YETTGLSEAR	99.6%	39.5	25	37.9	1	0	0	1126.54	266	275
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	6	8	16	0.02%	15.2%	FGGNPGGFGNQGGFGNSR	99.7%	111	25	102	2	0	0	1726.77	276	293
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	6	8	16	0.02%	15.2%	FTEYETQVK	99.7%	45	25	18.9	3	0	0	1144.55	152	160
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	6	8	16	0.02%	15.2%	GISVHISNAEPK	99.7%	63.9	25	59.9	1	0	0	1251.67	252	263
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	6	8	16	0.02%	15.2%	KMDETDASSAVK	99.7%	71.9	25	58.6	4	0	0	1281.60	84	95
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	6	8	16	0.02%	15.2%	MDETDASSAVK	99.7%	42.1	25	40.7	2	0	0	1169.50	85	95
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	6	8	16	0.02%	15.2%	TSDLIVLGLPWK	99.7%	88.9	25	82.5	4	0	0	1341.78	103	114
Target of EGR1 protein 1	TOE1	TOE1_HUMAN	56.5	100.0%	3	3	6	0.01%	6.7%	ALLNLPGTQTSGEAK	98.7%	33.8	25	22.1	2	0	0	1499.81	348	362
Target of EGR1 protein 1	TOE1	TOE1_HUMAN	56.5	100.0%	3	3	6	0.01%	6.7%	SILSLGLACFK	99.7%	54.5	25	46.7	2	0	0	1208.67	96	106
Target of EGR1 protein 1	TOE1	TOE1_HUMAN	56.5	100.0%	3	3	6	0.01%	6.7%	YAAEFHAR	99.7%	45.3	25	40.2	2	0	0	964.46	231	238
TATA-binding protein-associated factor 172	BTAF1	BTAF1_HUMAN	206.9	100.0%	5	5	9	0.01%	2.9%	AVTLAVQPR	95.7%	28.9	25	21.1	1	0	0	954.57	745	753
TATA-binding protein-associated factor 172	BTAF1	BTAF1_HUMAN	206.9	100.0%	5	5	9	0.01%	2.9%	FGDFVSDEVVAPVR	99.7%	49.2	25	49.2	2	0	0	1536.77	355	368
TATA-binding protein-associated factor 172	BTAF1	BTAF1_HUMAN	206.9	100.0%	5	5	9	0.01%	2.9%	IAAGQAVEAIVK	99.7%	83.3	25	76	2	0	0	1169.69	60	71
TATA-binding protein-associated factor 172	BTAF1	BTAF1_HUMAN	206.9	100.0%	5	5	9	0.01%	2.9%	IPVPINAELR	99.7%	40.1	25	37.6	2	0	0	1121.67	1258	1267
TATA-binding protein-associated factor 172	BTAF1	BTAF1_HUMAN	206.9	100.0%	5	5	9	0.01%	2.9%	LLCVFALDR	98.3%	32.6	25	20.1	2	0	0	1106.60	346	354
TBC1 domain family member 4	TBC1D4	TBCD4_HUMAN	146.6	100.0%	2	2	3	0.00%	2.1%	IQALESNLENLLTR	99.7%	85.5	25	85.5	2	0	0	1613.89	1227	1240
TBC1 domain family member 4	TBC1D4	TBCD4_HUMAN	146.6	100.0%	2	2	3	0.00%	2.1%	QAFSTAAALQSAK	98.9%	34.6	25	27.2	1	0	0	1293.68	435	447
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	26	34	135	0.13%	52.0%	AFHNEAQVNPER	99.7%	76.2	25	76.2	4	4	0	1411.67	469	480
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	26	34	135	0.13%	52.0%	AFHNEAQVNPERK	99.7%	59.7	25	50.7	3	4	0	1539.77	469	481
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	26	34	135	0.13%	52.0%	DCLINAAK	99.7%	41.7	25	26.5	4	0	0	904.46	146	153
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	26	34	135	0.13%	52.0%	DDKHGSYEDAVHSGALND	99.7%	75.5	25	75.5	2	3	0	1929.82	539	556
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	26	34	135	0.13%	52.0%	EQLAIAEFAR	99.7%	79.2	25	70.2	12	0	0	1147.61	434	443
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	26	34	135	0.13%	52.0%	EVGDGTTSVVIIAAELLK	99.7%	105	25	105	2	0	0	1815.01	85	102
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	26	34	135	0.13%	52.0%	FATEAAITILR	99.7%	86.5	25	67.6	9	0	0	1205.69	516	526
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	26	34	135	0.13%	52.0%	GANDFMCDEMER	99.7%	85.4	25	85.4	12	0	0	1474.54	379	390

T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	26	34	135	0.13%	52.0%	HGSYEDAVHSGALND	99.7%	89.5	25	89	2	0	0	1571.67	542	556
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	26	34	135	0.13%	52.0%	IACLDFSLQK	99.7%	73	25	67.7	5	0	0	1194.62	234	243
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	26	34	135	0.13%	52.0%	ICDDELILIK	99.7%	60.4	25	52.4	5	0	0	1231.66	356	365
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	26	34	135	0.13%	52.0%	IHPTSVISGYR	99.7%	42.3	25	39.6	2	0	0	1229.66	112	122
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	26	34	135	0.13%	52.0%	LGVQVVITDPEK	99.7%	77.6	25	72.8	2	0	0	1297.74	248	259
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	26	34	135	0.13%	52.0%	LGVQVVITDPEKLDQIR	99.7%	49.6	25	47.7	0	4	0	1923.09	248	264
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	26	34	135	0.13%	52.0%	LLEVEHPAAK	99.7%	68.4	25	58.7	7	0	0	1106.62	64	73
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	26	34	135	0.13%	52.0%	MLVDDIGDVTITNDGATILK	99.7%	127	25	121	4	0	0	2120.08	44	63
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	26	34	135	0.13%	52.0%	QAGVFEPTIVK	99.7%	58.4	25	53.3	3	0	0	1188.66	500	510
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	26	34	135	0.13%	52.0%	SLHDALCVVK	99.7%	51.9	25	38.7	4	0	0	1141.60	391	400
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	26	34	135	0.13%	52.0%	SLLVIPNTLAVNAAQDSTDLVAK	99.7%	91.1	25	91.1	14	0	0	2353.30	444	466
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	26	34	135	0.13%	52.0%	SQNVMAAASIANIVK	99.7%	129	25	122	5	0	0	1516.82	19	33
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	26	34	135	0.13%	52.0%	SSLGPVGLDK	99.7%	57.6	25	34.2	4	0	0	972.54	34	43
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	26	34	135	0.13%	52.0%	TSASIILR	99.7%	66.5	25	55	2	0	0	860.52	371	378
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	26	34	135	0.13%	52.0%	VLCELADLQDK	99.7%	85.5	25	78.9	2	0	0	1303.66	74	84
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	26	34	135	0.13%	52.0%	WIGLDLSNGKPR	99.7%	63.4	25	62.1	2	2	0	1355.74	485	496
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	26	34	135	0.13%	52.0%	YFVEAGAMAVR	99.7%	75.5	25	66.9	4	0	0	1213.60	299	309
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	26	34	135	0.13%	52.0%	YPVNSVNILK	99.7%	55	25	39	3	0	0	1146.65	190	199
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	14	19	31	0.03%	35.1%	AAHSEGNTTAGLDMR	99.7%	72	25	68.2	1	2	0	1546.69	467	481
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	14	19	31	0.03%	35.1%	AGADEERAETAR	97.9%	31.8	25	21.1	1	0	0	1275.59	14	25
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	14	19	31	0.03%	35.1%	DASLMVTNDGATILK	99.7%	87.6	25	80.2	2	0	0	1548.79	58	72
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	14	19	31	0.03%	35.1%	EALLSSAVDHGSDEVK	99.7%	99.9	25	92.2	2	1	0	1656.81	139	154
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	14	19	31	0.03%	35.1%	EAVAMESYAK	99.7%	67.6	25	62	2	0	0	1098.51	432	441
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	14	19	31	0.03%	35.1%	GATQQILDEAER	99.7%	80.2	25	76.1	2	0	0	1330.66	377	388
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	14	19	31	0.03%	35.1%	HGINCFINR	99.7%	49.7	25	42.6	2	0	0	1130.55	285	293
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	14	19	31	0.03%	35.1%	ILIANTGMDTDKIK	99.7%	91.9	25	79.3	4	1	0	1532.84	237	250
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	14	19	31	0.03%	35.1%	LAVEAVLR	99.7%	50.5	25	16.1	2	0	0	870.54	182	189
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	14	19	31	0.03%	35.1%	LTSFIGAIAIGDLVK	99.7%	85.2	25	81.8	2	0	0	1517.89	26	40
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	14	19	31	0.03%	35.1%	MLPTIIADNAGYDSADLVAQLR	99.7%	74.2	25	74.2	1	0	0	2347.20	445	466
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	14	19	31	0.03%	35.1%	VAEIEHAEKEK	99.7%	44.1	25	34	2	0	0	1282.66	264	274
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	14	19	31	0.03%	35.1%	VLVDMSR	98.2%	32.4	25	24.2	1	0	0	819.44	83	89
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	14	19	31	0.03%	35.1%	VQDDEVGDGTTSVTVLAAELLR	99.7%	133	25	133	2	1	0	2288.16	90	111
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	32	132	0.13%	58.8%	AFADAMEVIPSTLAENAGLNPISTVTELR	99.1%	29.7	25	29.6	0	1	0	3030.55	453	481
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	32	132	0.13%	58.8%	ALIAGGGAPEIELALR	99.7%	100	25	100	13	0	0	1550.89	420	435
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	32	132	0.13%	58.8%	AQDIEAGDGTTSVVIIAGSLLDSCTK	99.7%	114	25	114	2	4	0	2621.30	97	122
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	32	132	0.13%	58.8%	AYILNLVK	99.3%	36.5	25	28.4	5	0	0	933.58	281	288
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	32	132	0.13%	58.8%	DALSDLALHFLNK	99.7%	97.6	25	85.5	13	2	0	1456.78	307	319
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	32	132	0.13%	58.8%	DIEREDIEFICK	99.7%	50.5	25	48.9	6	0	0	1566.75	327	338
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	32	132	0.13%	58.8%	ETLLNSATTSLNSK	99.7%	111	25	111	2	0	0	1478.77	161	174
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	32	132	0.13%	58.8%	FSNISAAK	99.7%	46	25	33.9	2	0	0	837.45	35	42
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	32	132	0.13%	58.8%	GAYQDRDKPAQIR	99.5%	32.3	25	28.8	0	2	0	1517.78	22	34
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	32	132	0.13%	58.8%	GDVTITNDGATILK	99.7%	102	25	91.9	3	0	0	1417.75	66	79
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	32	132	0.13%	58.8%	GIHPTIISESFQK	99.7%	41.4	25	41.4	4	2	0	1456.78	127	139
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	32	132	0.13%	58.8%	IDDVVNTR	99.7%	49	25	42.4	4	0	0	931.48	532	539
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	32	132	0.13%	58.8%	IGLIQFCLSAPK	99.7%	70	25	68.3	10	0	0	1346.75	246	257
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	32	132	0.13%	58.8%	KTGCNVLLIQK	99.5%	38.7	25	26.2	1	0	0	1273.73	292	302
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	32	132	0.13%	58.8%	LGGTIDDCELVEGLVLTQK	99.7%	98	25	98	2	0	0	2060.06	214	232
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	32	132	0.13%	58.8%	LVIEEAER	99.7%	55.7	25	50.7	7	0	0	958.52	396	403
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	32	132	0.13%	58.8%	MIQDGKGDVTITNDGATILK	99.7%	97.4	25	91.9	2	6	0	2106.08	60	79
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	32	132	0.13%	58.8%	MLVELSK	98.0%	31.9	25	5.37	2	0	0	835.46	90	96
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	32	132	0.13%	58.8%	QMQVLHPAAR	99.7%	55.5	25	46	4	0	0	1150.62	80	89

T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	32	132	0.13%	58.8%	SIHDALCVIR	99.7%	59.4	25	0	5	0	0	1183.63	404	413
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	32	132	0.13%	58.8%	TDMDNQIVVSDYAQMDR	99.7%	98.4	25	98.4	5	0	0	2032.86	258	274
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	32	132	0.13%	58.8%	TGCNVLLIQK	99.7%	70.2	25	44.8	6	0	0	1145.63	293	302
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	32	132	0.13%	58.8%	TLSGMESYCVR	99.7%	69.3	25	65.2	8	0	0	1318.58	442	452
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	32	132	0.13%	58.8%	VIDPATATSVDLR	99.7%	111	25	106	10	0	0	1357.73	194	206
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	32	132	0.13%	58.8%	VVSQYSSLLSPMSVNAVMK	99.7%	96.2	25	95.1	4	0	0	2072.04	175	193
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	25	37	84	0.08%	41.2%	AVTIFIR	99.7%	42.1	25	16.6	3	0	0	819.51	382	388
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	25	37	84	0.08%	41.2%	CPTLEQYAMR	98.7%	33.9	25	30.7	1	0	0	1284.57	440	449
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	25	37	84	0.08%	41.2%	DTEPLIQTAK	98.3%	32.7	25	32	2	0	0	1115.59	161	170
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	25	37	84	0.08%	41.2%	DVDFELIK	99.5%	38.2	25	16.6	2	0	0	978.51	203	210
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	25	37	84	0.08%	41.2%	DVDFELIKVEGK	99.7%	73.4	25	64.8	2	0	0	1391.74	203	214
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	25	37	84	0.08%	41.2%	EKFEEMIQQIK	99.7%	46.6	25	39.8	2	2	0	1438.72	283	293
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	25	37	84	0.08%	41.2%	EMNPALGIDCLHK	99.7%	72.3	25	65.2	4	2	0	1513.71	484	496
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	25	37	84	0.08%	41.2%	FEEMIQQIK	99.7%	42.1	25	31.7	2	0	0	1181.59	285	293
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	25	37	84	0.08%	41.2%	GVIVDKDFSHPQMPK	99.7%	49.7	25	47.3	3	4	0	1697.87	227	241
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	25	37	84	0.08%	41.2%	HKLDVTSVEDYK	99.7%	34.5	25	31.8	0	2	0	1433.73	264	275
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	25	37	84	0.08%	41.2%	IADGYEQAAR	99.7%	88.1	25	81.5	6	0	0	1093.53	133	142
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	25	37	84	0.08%	41.2%	IAILTCPFEPPKPK	99.7%	56.7	25	56.7	2	1	0	1610.90	248	261
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	25	37	84	0.08%	41.2%	IDDIRKPGESEE	99.7%	48	25	42.3	2	0	0	1387.67	530	541
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	25	37	84	0.08%	41.2%	KQQISLATQMVR	99.7%	62.8	25	58.4	2	2	0	1418.78	514	525
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	25	37	84	0.08%	41.2%	LDVTSVEDYK	99.7%	68.3	25	63	2	0	0	1168.57	266	275
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	25	37	84	0.08%	41.2%	LGFAGLVQEISFGTTK	99.7%	115	25	115	6	0	0	1667.90	353	368
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	25	37	84	0.08%	41.2%	LMGLEALK	99.7%	41.9	25	20.3	4	0	0	874.51	28	35
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	25	37	84	0.08%	41.2%	LMVELSK	99.7%	47.9	25	9.22	4	0	0	835.46	90	96
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	25	37	84	0.08%	41.2%	MIIEEAKR	99.7%	54.8	25	38.7	4	0	0	989.54	393	400
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	25	37	84	0.08%	41.2%	MLVIEQCK	99.4%	37.1	25	20.1	2	0	0	1036.52	371	378
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	25	37	84	0.08%	41.2%	QQISLATQMVR	99.7%	57	25	51.4	4	0	0	1290.68	515	525
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	25	37	84	0.08%	41.2%	RDVDFELIK	99.0%	35	25	4.82	2	0	0	1134.62	202	210
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	25	37	84	0.08%	41.2%	SLHDALCVIR	99.7%	59.4	25	0	5	0	0	1183.63	401	410
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	25	37	84	0.08%	41.2%	TSLGPNGLDK	99.7%	55.2	25	46.4	2	0	0	1001.53	50	59
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	25	37	84	0.08%	41.2%	WVGGPEIELIAIATGGR	99.7%	82	25	74.3	3	0	0	1738.95	324	340
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	18	22	56	0.06%	39.6%	ALEIIPR	99.7%	45.7	25	36	4	0	0	811.50	441	447
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	18	22	56	0.06%	39.6%	ATISNDGATILK	99.7%	59.4	25	40.3	2	0	0	1203.66	56	67
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	18	22	56	0.06%	39.6%	CQVFEETQIGGER	99.7%	83.6	25	77.7	2	0	0	1552.71	345	357
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	18	22	56	0.06%	39.6%	GGAEQFMEETER	99.7%	80.7	25	75.9	6	0	0	1383.58	376	387
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	18	22	56	0.06%	39.6%	IKEIAVTVK	98.9%	34.6	25	17.6	1	0	0	1000.64	136	144
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	18	22	56	0.06%	39.6%	LLDVVHPAAK	99.7%	65.2	25	56.6	4	0	0	1062.63	68	77
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	18	22	56	0.06%	39.6%	LPIGDVATQYFADR	99.7%	88.9	25	87	4	0	0	1565.80	293	306
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	18	22	56	0.06%	39.6%	NDSVVAGGGAIEMELSK	99.7%	105	25	105	2	0	0	1692.81	402	418
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	18	22	56	0.06%	39.6%	QLCDNAGFDATNILNK	99.7%	86.2	25	79	2	0	0	1793.85	448	463
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	18	22	56	0.06%	39.6%	QQLLIGAYAK	99.7%	44	25	37.5	1	0	0	1104.64	431	440
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	18	22	56	0.06%	39.6%	SLHDAIMIVR	99.7%	59.6	25	49.3	4	0	0	1154.64	388	397
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	18	22	56	0.06%	39.6%	SQDAEVGDGTTSVTLLAAEFLK	99.7%	128	25	128	4	1	0	2252.13	85	106
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	18	22	56	0.06%	39.6%	TATQLAVNK	99.7%	60.9	25	50.6	4	0	0	945.54	127	135
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	18	22	56	0.06%	39.6%	TCTFILR	99.7%	41.4	25	12.8	2	0	0	910.48	369	375
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	18	22	56	0.06%	39.6%	TFSYAGFEMQPK	99.7%	80.1	25	77.2	4	0	0	1405.65	219	230
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	18	22	56	0.06%	39.6%	VPEEDLKR	99.7%	52.2	25	43	4	0	0	985.53	314	321
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	18	22	56	0.06%	39.6%	VQGGALEDSQLVAGVAFK	99.7%	111	25	111	2	0	0	1788.95	200	217
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	18	22	56	0.06%	39.6%	YNFFTGCPK	99.7%	52.3	25	43.4	3	0	0	1133.51	358	366
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	ACTILLR	99.7%	53.3	25	34.9	2	0	0	846.49	371	377
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	ALDDMISTLK	99.7%	74.4	25	68.1	6	0	0	1106.58	129	138

T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	ALDDMISTLKK	99.7%	56.1	25	46.7	4	1	0	1234.67	129	139
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	AMTGVEQWPYR	99.7%	53.9	25	53.8	4	0	0	1337.63	428	438
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	AVAQALEVIPR	99.7%	101	25	79.5	15	0	0	1166.69	439	449
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	EILSEVER	99.7%	55.2	25	17.8	7	0	0	974.52	382	389
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	EIQVQHPAAK	99.7%	56.2	25	45.2	10	0	0	1120.61	69	78
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	ELGIWEPLAVK	99.7%	69.1	25	61.3	5	0	0	1254.71	492	502
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	GISDLAQHYLMR	99.7%	73.8	25	70.1	10	2	0	1403.71	295	306
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	IDDIVSGHK	99.7%	54.3	25	40.1	6	0	0	983.52	519	527
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	IDDIVSGHKK	97.8%	31.6	25	19.9	1	0	0	1111.61	519	528
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	IGDEYFTFITDCK	99.7%	62.9	25	54.1	2	0	0	1608.73	355	367
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	IGDEYFTFITDCKDPK	99.7%	49.3	25	48.5	2	1	0	1948.90	355	370
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	IPGGIIEDSCVLR	99.7%	94.9	25	85.4	6	0	0	1428.75	204	216
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	IVLLDSSLEYK	99.7%	75.2	25	70.7	9	0	0	1279.71	238	248
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	IVLLDSSLEYKK	99.7%	58.7	25	55.5	2	1	0	1407.81	238	249
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	IVSRPEELREDDVGTGAGLLEIK	99.7%	52.6	25	51.9	0	2	0	2496.33	331	353
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	KGESQTDIEITR	99.7%	86.7	25	56	2	2	0	1376.70	249	260
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	MLLDPMGGIVMTNDGNAILR	99.7%	94.7	25	94.7	10	1	0	2179.06	49	68
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	MVQFEENGR	99.7%	53.4	25	50.2	2	0	0	1109.50	182	190
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	MVQFEENGRK	99.7%	48.3	25	35.2	3	0	0	1237.60	182	191
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	NLQDAMQVCR	99.7%	73.1	25	72.8	11	0	0	1250.56	390	399
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	NVLLDPQLVPGGGASEMAVAHALTEK	99.7%	43.4	25	41.4	0	5	0	2617.37	400	425
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	SMIEISR	99.7%	45.8	25	31.7	3	0	0	835.43	79	85
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	TAVETAVLLLR	99.7%	107	25	98.2	6	0	0	1185.72	508	518
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	TLIQNCGASTIR	99.7%	73.4	25	64.2	5	0	0	1333.69	450	461
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	27	41	153	0.15%	50.6%	WSSLACNIALDAVK	99.7%	108	25	101	5	0	0	1547.79	168	181
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	7	7	13	0.01%	15.9%	AIADTGANVVVTGGK	99.7%	71.6	25	63.2	2	0	0	1372.74	282	296
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	7	7	13	0.01%	15.9%	AVDDGVNTFK	99.7%	66.1	25	53.9	2	0	0	1065.52	391	400
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	7	7	13	0.01%	15.9%	DIDEVSSLLR	99.7%	57.3	25	48.2	2	0	0	1146.60	156	165
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	7	7	13	0.01%	15.9%	FAEAFEAIPR	99.7%	74	25	63.5	2	0	0	1150.59	441	450
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	7	7	13	0.01%	15.9%	IAVYSCPFDGMITETK	99.7%	53.4	25	53.4	2	0	0	1847.86	239	254
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	7	7	13	0.01%	15.9%	LFVTNDAATILR	99.7%	104	25	91.3	2	0	0	1333.75	63	74
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	7	7	13	0.01%	15.9%	LVPGGGATEIELAK	94.9%	28.2	25	10.8	1	0	0	1354.76	408	421
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	105	0.10%	48.8%	ALQFLEEVK	99.7%	61.3	25	56.4	3	0	0	1076.60	130	138
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	105	0.10%	48.8%	AQAALAVNISAAR	99.7%	93.2	25	88.4	2	0	0	1255.71	16	28
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	105	0.10%	48.8%	AQLGVQAFADALLIIPK	99.7%	68.9	25	67.4	4	0	0	1768.04	433	449
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	105	0.10%	48.8%	DGNVLLHEMQIQHPTASLIAK	99.7%	55.3	25	55.3	0	4	0	2315.22	59	79
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	105	0.10%	48.8%	EMDRETLIDVAR	99.7%	50.5	25	39.5	5	4	0	1447.72	142	153
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	105	0.10%	48.8%	ETLIDVAR	99.4%	37.8	25	29.4	2	0	0	916.51	146	153
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	105	0.10%	48.8%	GFVVINQK	99.3%	36.5	25	24	2	0	0	904.53	288	295
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	105	0.10%	48.8%	GIDPFSLDALSK	99.7%	89.3	25	32.9	11	0	0	1262.66	296	307
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	105	0.10%	48.8%	GLQDVLR	99.7%	44.3	25	16.7	2	0	0	800.46	29	35
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	105	0.10%	48.8%	GLVLDHGAR	99.7%	53.4	25	36.8	10	0	0	937.52	209	217
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	105	0.10%	48.8%	HKSETDTSLIR	99.7%	47.8	25	47.8	2	1	0	1286.67	198	208
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	105	0.10%	48.8%	HTLTQIK	98.8%	34.1	25	14.1	1	0	0	840.49	382	388
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	105	0.10%	48.8%	IITEGFEAAK	99.7%	68.1	25	30.6	6	0	0	1078.58	118	127
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	105	0.10%	48.8%	KQDEPIDLFMIEIMEMK	99.7%	42.6	25	34.7	0	2	0	2158.01	181	197
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	105	0.10%	48.8%	MLVSGAGDIK	99.7%	57.1	25	33.5	7	0	0	990.53	46	55
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	105	0.10%	48.8%	NAIDDGCVVPGAGAVEVAMAEALIK	99.7%	65.4	25	65.3	0	2	0	2470.23	400	424
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	105	0.10%	48.8%	QADLYISEGLHPR	99.7%	68.8	25	57.3	7	5	0	1498.77	105	117
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	105	0.10%	48.8%	SETDTSLIR	99.7%	65.3	25	52.3	5	0	0	1021.52	200	208
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	105	0.10%	48.8%	TEVNSGFFYK	99.7%	59.9	25	57.7	4	0	0	1191.57	242	251

T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	105	0.10%	48.8%	VATAQDDITGDGTTSNVLIIGELLK	99.7%	89	25	89	2	2	0	2544.34	80	104
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	105	0.10%	48.8%	VCGDSDKGFVVINQK	99.7%	60.6	25	59.3	2	2	0	1665.83	281	295
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	22	31	105	0.10%	48.8%	VLAQNSGFDLQETLVK	99.7%	118	25	112	6	0	0	1761.94	450	465
Telomere length regulation protein TEL2 homolog	TELO2	TELO2_HUMAN	91.7	99.8%	2	2	2	0.00%	2.8%	AVLICLAQLGEPELR	98.8%	34.2	25	34.2	1	0	0	1681.93	363	377
Telomere length regulation protein TEL2 homolog	TELO2	TELO2_HUMAN	91.7	99.8%	2	2	2	0.00%	2.8%	LVEQVPDR	98.7%	34	25	25.1	1	0	0	955.52	255	262
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	6	6	13	0.01%	3.8%	IGISDISSLSEK	99.7%	52.8	25	50.5	2	0	0	1248.67	1700	1711
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	6	6	13	0.01%	3.8%	ITSELSEANALELLSK	99.7%	74.7	25	74.7	2	0	0	1717.92	88	103
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	6	6	13	0.01%	3.8%	LIAEQTLQENLIEK	99.7%	94.8	25	92.6	2	0	0	1641.91	1468	1481
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	6	6	13	0.01%	3.8%	LVSDIIDPVALEIPLSK	99.7%	52.1	25	52.1	4	0	0	1822.06	2399	2415
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	6	6	13	0.01%	3.8%	SLIDNFALNPDILCSAK	99.3%	36.6	25	36.6	1	0	0	1890.96	299	315
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	6	6	13	0.01%	3.8%	YAEYSFTSLPVPESNLR	99.7%	51	25	51	2	0	0	1972.97	1659	1675
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	6	6	11	0.01%	8.4%	AVYTLYQQR	99.7%	52.5	25	41.2	2	0	0	1141.60	505	513
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	6	6	11	0.01%	8.4%	LAAVQLLQFLAPK	99.7%	70.2	25	70.2	2	0	0	1411.87	116	128
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	6	6	11	0.01%	8.4%	LLLQHAPLR	99.7%	49.5	25	45.3	2	0	0	1060.66	866	874
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	6	6	11	0.01%	8.4%	SQNFDILQSAISK	99.7%	94.3	25	89.5	2	0	0	1450.75	747	759
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	6	6	11	0.01%	8.4%	VGPEELPVVGQLLR	99.7%	49.1	25	49.1	2	0	0	1505.87	852	865
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	6	6	11	0.01%	8.4%	YLVGGLSGVDEGLSSTENLK	99.7%	70.2	25	66.6	1	0	0	2038.03	299	318
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	5	5	9	0.01%	4.1%	ASELNPESIYSVFK	99.7%	52	25	52	2	0	0	1583.80	624	637
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	5	5	9	0.01%	4.1%	SGPGLIGLGIK	99.7%	63.7	25	44.8	2	0	0	1011.62	271	281
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	5	5	9	0.01%	4.1%	SNPDQPAVILLLR	98.5%	33.3	25	33.3	1	0	0	1435.83	1355	1367
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	5	5	9	0.01%	4.1%	TLDQISDADNIPGLLVLK	99.7%	71.1	25	67	2	0	0	1925.06	375	392
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	5	5	9	0.01%	4.1%	VVAQYAQR	99.7%	49.9	25	41.9	2	0	0	934.51	1202	1209
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	5	5	10	0.01%	11.7%	IHSDTFASGGER	99.7%	45	25	41.9	1	0	0	1276.59	337	348
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	5	5	10	0.01%	11.7%	LSQLGLDAGK	99.7%	55.7	25	40.2	1	0	0	1001.56	218	227
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	5	5	10	0.01%	11.7%	SFLESIDDALAEK	99.7%	85.9	25	78.7	2	0	0	1437.71	116	128
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	5	5	10	0.01%	11.7%	VLLQAFDVVER	99.7%	81.7	25	72.4	4	0	0	1288.73	105	115
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	5	5	10	0.01%	11.7%	YGYTDIDLLSAAK	99.7%	73.5	25	73.5	2	0	0	1429.72	250	262
Thioredoxin	TXN	THIO_HUMAN	11.7	100.0%	4	4	8	0.01%	31.4%	EKLEATINELV	99.7%	58.1	25	58.1	2	0	0	1258.69	95	105
Thioredoxin	TXN	THIO_HUMAN	11.7	100.0%	4	4	8	0.01%	31.4%	TAFQEALDAAGDK	99.7%	71.8	25	71.8	1	0	0	1336.64	9	21
Thioredoxin	TXN	THIO_HUMAN	11.7	100.0%	4	4	8	0.01%	31.4%	VGEFSGANK	99.6%	38.9	25	29.9	3	0	0	908.45	86	94
Thioredoxin	TXN	THIO_HUMAN	11.7	100.0%	4	4	8	0.01%	31.4%	VGEFSGANKEK	98.8%	34.3	25	24.5	2	0	0	1165.58	86	96
Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3	PRDX3_HUMAN	27.7	99.8%	2	2	4	0.00%	10.2%	DYGVLLEGSGLALR	99.7%	98.2	25	81.5	2	0	0	1462.79	171	184
Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3	PRDX3_HUMAN	27.7	99.8%	2	2	4	0.00%	10.2%	GLFIIDPNGVIK	99.7%	51.9	25	42.2	2	0	0	1285.75	185	196
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	12	12	22	0.02%	8.8%	ADQLDYENFR	99.7%	50.4	25	50.4	1	0	0	1270.57	1085	1094
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	12	12	22	0.02%	8.8%	AEGGYFGQIR	99.7%	69	25	60.2	2	0	0	1097.54	711	720
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	12	12	22	0.02%	8.8%	ASVHCLETGEYTHIR	98.5%	27.4	25	27.4	0	1	0	1772.84	1107	1121
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	12	12	22	0.02%	8.8%	CIFSAIDAVYCAR	99.7%	53.8	25	52.5	1	0	0	1545.72	986	998
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	12	12	22	0.02%	8.8%	FLCCMLETVTR	99.7%	57.3	25	49.5	2	0	0	1429.66	1042	1052
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	12	12	22	0.02%	8.8%	FVELVHQQK	99.7%	42.6	25	38.4	2	0	0	1127.62	999	1007
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	12	12	22	0.02%	8.8%	GEFLHLCR	99.7%	49.4	25	39.5	1	0	0	1031.51	22	29
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	12	12	22	0.02%	8.8%	GSPVNALQNK	96.5%	29.7	25	22.1	1	0	0	1027.55	406	415
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	12	12	22	0.02%	8.8%	LDPETLESLGLIK	99.7%	80.7	25	68.2	3	0	0	1427.80	127	139
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	12	12	22	0.02%	8.8%	TPNFSTLLCYDR	99.7%	64.1	25	62.6	2	0	0	1486.70	1008	1019
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	12	12	22	0.02%	8.8%	VFSDIIYTVASCTENEASR	99.7%	64.8	25	64.8	2	0	0	2162.01	1020	1038
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	12	12	22	0.02%	8.8%	VLNLGQALER	99.7%	54.7	25	44.6	4	0	0	1112.64	1137	1146
THO complex subunit 3	THOC3	THOC3_HUMAN	38.8	100.0%	3	4	7	0.01%	6.0%	TASVFLLEK	98.1%	32.2	25	24.7	2	0	0	1007.58	78	86
THO complex subunit 3	THOC3	THOC3_HUMAN	38.8	100.0%	3	4	7	0.01%	6.0%	TASVFLLEKDR	99.7%	51.4	25	48.4	2	0	0	1278.71	78	88
THO complex subunit 3	THOC3	THOC3_HUMAN	38.8	100.0%	3	4	7	0.01%	6.0%	YVLGMQELFR	99.7%	54.7	25	50.3	3	0	0	1271.65	34	43
THO complex subunit 4	ALYREF	THOC4_HUMAN	26.9	100.0%	5	7	17	0.02%	35.0%	MDMSLDDIIK	99.7%	53.3	25	43.2	2	0	0	1180.56	5	14
THO complex subunit 4	ALYREF	THOC4_HUMAN	26.9	100.0%	5	7	17	0.02%	35.0%	QLPDKWQHDLFDSGFGGGAGVETGGK	99.7%	38.1	25	38.1	0	1	0	2703.28	82	107
THO complex subunit 4	ALYREF	THOC4_HUMAN	26.9	100.0%	5	7	17	0.02%	35.0%	QQLSAEELDAQLDAYNAR	99.7%	124	25	122	2	2	0	2034.97	236	253

THO complex subunit 4	ALYREF	THOC4_HUMAN	26.9	100.0%	5	7	17	0.02%	35.0%	QYNGVPLDGRPMNIQLVTSQIDAQR	99.6%	33.5	25	31.4	0	2	0	2829.43	165	189
THO complex subunit 4	ALYREF	THOC4_HUMAN	26.9	100.0%	5	7	17	0.02%	35.0%	SLGTADVHFER	99.7%	80.1	25	69.1	6	2	0	1231.61	145	155
THO complex subunit 6 homolog	THOC6	THOC6_HUMAN	37.5	100.0%	4	4	6	0.01%	15.8%	AVPLAVPLGQTEVFQALQR	99.7%	60.1	25	60.1	1	0	0	2037.15	4	22
THO complex subunit 6 homolog	THOC6	THOC6_HUMAN	37.5	100.0%	4	4	6	0.01%	15.8%	AWLWAEMLK	97.9%	31.7	25	16.1	1	0	0	1147.60	99	107
THO complex subunit 6 homolog	THOC6	THOC6_HUMAN	37.5	100.0%	4	4	6	0.01%	15.8%	TSLEVPEINALLLVPK	99.7%	41	25	40.9	2	0	0	1736.02	122	137
THO complex subunit 6 homolog	THOC6	THOC6_HUMAN	37.5	100.0%	4	4	6	0.01%	15.8%	VDVFTNLGYR	99.7%	69.7	25	59.6	2	0	0	1183.61	326	335
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	4	4	7	0.01%	6.8%	GFQEVVTPNIFNSR	99.7%	50.7	25	50.7	2	0	0	1607.82	368	381
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	4	4	7	0.01%	6.8%	LADFGVLHR	99.7%	42.9	25	33.4	2	0	0	1027.57	434	442
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	4	4	7	0.01%	6.8%	MGGEEKPIGAGEEK	97.1%	30.4	25	12.1	1	0	0	1447.67	13	26
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	4	4	7	0.01%	6.8%	NELSGALTGLTR	99.7%	86	25	64.1	2	0	0	1231.66	443	454
Threonine--tRNA ligase, mitochondrial	TARS2	SYTM_HUMAN	81.0	100.0%	4	4	6	0.01%	5.4%	AEASGGLGGLTR	99.7%	54.5	25	45.5	1	0	0	1088.57	439	450
Threonine--tRNA ligase, mitochondrial	TARS2	SYTM_HUMAN	81.0	100.0%	4	4	6	0.01%	5.4%	LADFGALHR	99.7%	61.6	25	48.8	2	0	0	999.54	430	438
Threonine--tRNA ligase, mitochondrial	TARS2	SYTM_HUMAN	81.0	100.0%	4	4	6	0.01%	5.4%	LVELQNTR	99.1%	35.5	25	22	1	0	0	972.55	703	710
Threonine--tRNA ligase, mitochondrial	TARS2	SYTM_HUMAN	81.0	100.0%	4	4	6	0.01%	5.4%	VYNALVAFIR	99.7%	69.9	25	65.4	2	0	0	1165.67	331	340
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	3	3	5	0.00%	6.9%	AANNIASLLTK	99.7%	52.7	25	47.4	2	0	0	1115.64	359	369
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	3	3	5	0.00%	6.9%	STLAYGMLR	99.3%	36.4	25	23.3	1	0	0	1027.52	305	313
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	3	3	5	0.00%	6.9%	TGSVDIIVTDLPFGK	99.7%	64.2	25	59.3	2	0	0	1561.85	397	411
Thymidine kinase, cytosolic	TK1	KITH_HUMAN	25.5	100.0%	2	3	5	0.00%	11.5%	GQIQVILGPMFSGK	99.0%	35.2	25	31.9	3	0	0	1474.81	19	32
Thymidine kinase, cytosolic	TK1	KITH_HUMAN	25.5	100.0%	2	3	5	0.00%	11.5%	TVIVAALDGTFQR	99.7%	82.8	25	81.2	2	0	0	1390.77	118	130
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	13	14	44	0.04%	15.0%	ASAVSELSPR	99.7%	70.2	25	63	4	0	0	1016.54	236	245
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	13	14	44	0.04%	15.0%	DSRPSQAAGDNQGDEAK	99.7%	40.4	25	38	0	2	0	1745.77	186	202
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	13	14	44	0.04%	15.0%	EESAASGGAAYTK	99.7%	72.1	25	67.8	4	0	0	1241.56	334	346
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	13	14	44	0.04%	15.0%	EQTFSGGTSQDTK	99.7%	72.8	25	66.9	3	0	0	1385.62	203	215
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	13	14	44	0.04%	15.0%	GSFSDTGLGDGK	99.7%	78	25	77.9	6	0	0	1140.52	376	387
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	13	14	44	0.04%	15.0%	IDISPSTFR	98.7%	33.7	25	21.7	1	0	0	1035.55	679	687
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	13	14	44	0.04%	15.0%	KTEELEEESFPER	96.9%	24.6	25	21.1	0	2	0	1622.75	486	498
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	13	14	44	0.04%	15.0%	SIFQHIQSAQSQR	99.7%	87	25	69.9	7	4	0	1529.78	609	621
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	13	14	44	0.04%	15.0%	SPLQSVVVR	99.7%	53.1	25	43	5	0	0	984.58	253	261
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	13	14	44	0.04%	15.0%	SPPSTGSTYGSSQK	99.7%	76.6	25	76.6	2	0	0	1383.64	320	333
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	13	14	44	0.04%	15.0%	TEELEEESFPER	99.7%	41.8	25	25.8	1	0	0	1494.66	487	498
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	13	14	44	0.04%	15.0%	WEGLVYAPPGK	99.7%	42.2	25	31	1	0	0	1216.64	471	481
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	13	14	44	0.04%	15.0%	YKDDPVDLR	99.7%	44.2	25	26.6	2	0	0	1120.56	710	718
Tight junction protein ZO-1	TJP1	ZO1_HUMAN	195.5	99.9%	2	2	4	0.00%	1.4%	EEAVLFLLDLPK	99.2%	35.8	25	35.8	1	0	0	1386.79	481	492
Tight junction protein ZO-1	TJP1	ZO1_HUMAN	195.5	99.9%	2	2	4	0.00%	1.4%	SVASSQPAKPTK	99.7%	52	25	50.1	3	0	0	1200.66	175	186
Tight junction protein ZO-2	TJP2	ZO2_HUMAN	134.0	99.8%	2	2	3	0.00%	2.4%	EDAVLYLLEIPK	99.7%	58	25	56.6	2	0	0	1402.78	569	580
Tight junction protein ZO-2	TJP2	ZO2_HUMAN	134.0	99.8%	2	2	3	0.00%	2.4%	SNPSAVAGNETPGASTK	99.7%	58.4	25	57.7	1	0	0	1587.76	1017	1033
Torsin-1A-interacting protein 1	TOR1AIP1	TOIP1_HUMAN	66.2	100.0%	3	3	5	0.00%	6.7%	FESFPAGSTLIFYK	99.0%	35.1	25	32.3	1	0	0	1606.82	481	494
Torsin-1A-interacting protein 1	TOR1AIP1	TOIP1_HUMAN	66.2	100.0%	3	3	5	0.00%	6.7%	SELGNQSPSTSSR	99.7%	62	25	62	2	0	0	1349.63	309	321
Torsin-1A-interacting protein 1	TOR1AIP1	TOIP1_HUMAN	66.2	100.0%	3	3	5	0.00%	6.7%	SQPAILLLTAAR	99.7%	48.7	25	44.7	2	0	0	1253.76	405	416
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	6	7	12	0.01%	26.9%	ATTPADGEEPAPEAEALAAAR	99.7%	95.9	25	95.9	2	2	0	2037.97	6	26
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	6	7	12	0.01%	26.9%	DYIQSTMETEK	98.6%	33.4	25	30.1	1	0	0	1360.59	124	134
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	6	7	12	0.01%	26.9%	FLSGLELVK	99.6%	39.6	25	24.5	2	0	0	1005.60	32	40
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	6	7	12	0.01%	26.9%	GVDLYVLEK	99.7%	66.2	25	49.6	2	0	0	1035.57	197	205
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	6	7	12	0.01%	26.9%	TIGQVLAR	98.7%	34	25	9.16	1	0	0	857.52	145	152
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	6	7	12	0.01%	26.9%	TPQGLSNLAK	99.7%	63.1	25	52.5	2	0	0	1028.57	135	144
Trafficking protein particle complex subunit 1	TRAPPC1	TPPC1_HUMAN	16.8	100.0%	4	5	8	0.01%	26.9%	DGFLAFQTSR	99.7%	61	25	49.4	2	0	0	1141.56	59	68
Trafficking protein particle complex subunit 1	TRAPPC1	TPPC1_HUMAN	16.8	100.0%	4	5	8	0.01%	26.9%	LHYYETPTGIK	99.3%	36.5	25	31	1	0	0	1321.68	71	81
Trafficking protein particle complex subunit 1	TRAPPC1	TPPC1_HUMAN	16.8	100.0%	4	5	8	0.01%	26.9%	SRLDSYVR	99.7%	42.9	25	34.8	2	0	0	995.53	128	135
Trafficking protein particle complex subunit 1	TRAPPC1	TPPC1_HUMAN	16.8	100.0%	4	5	8	0.01%	26.9%	TVHNLYLFDR	99.7%	55.4	25	42.5	2	1	0	1277.66	2	11
Trafficking protein particle complex subunit 6B	TRAPPC6B	TPC6B_HUMAN	18.0	99.8%	2	2	3	0.00%	11.4%	VGQGLIER	99.7%	49.9	25	29.1	2	0	0	871.50	43	50
Trafficking protein particle complex subunit 6B	TRAPPC6B	TPC6B_HUMAN	18.0	99.8%	2	2	3	0.00%	11.4%	YLAFTCGLIR	98.8%	34.4	25	25	1	0	0	1213.64	118	127

Transaldolase	TALDO1	TALDO_HUMAN	37.5	99.8%	2	2	3	0.00%	7.1%	ALAGCDFLTISPK	99.7%	53.6	25	53.6	1	0	0	1392.72	246	258
Transaldolase	TALDO1	TALDO_HUMAN	37.5	99.8%	2	2	3	0.00%	7.1%	LLGELLQDNAK	99.7%	73.5	25	64.6	2	0	0	1213.68	259	269
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	12	12	20	0.02%	8.6%	AIEEGTLEEIEEEVR	99.7%	65.2	25	61.8	1	0	0	1745.84	1391	1405
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	12	12	20	0.02%	8.6%	AVATYHANTER	99.7%	54.1	25	40.4	2	0	0	1232.60	503	513
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	12	12	20	0.02%	8.6%	DSDAGSSTPTTSTR	99.7%	59	25	56.5	2	0	0	1382.60	1416	1429
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	12	12	20	0.02%	8.6%	DTALETALNAK	99.7%	63.4	25	54.8	2	0	0	1146.60	427	437
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	12	12	20	0.02%	8.6%	ELPEYYELIR	99.7%	57	25	52	2	0	0	1324.68	1493	1502
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	12	12	20	0.02%	8.6%	GLDPVEILQER	99.7%	78.2	25	68.8	2	0	0	1268.68	360	370
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	12	12	20	0.02%	8.6%	IQELENLPGSLAGDLR	99.7%	65.2	25	59.6	2	0	0	1724.92	382	397
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	12	12	20	0.02%	8.6%	LCTVNSVEEK	98.9%	34.4	25	22.6	1	0	0	1178.57	1204	1213
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	12	12	20	0.02%	8.6%	LLLTGTPLQNK	99.7%	64.2	25	0	2	0	0	1197.72	907	917
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	12	12	20	0.02%	8.6%	QLSEVFIQLPSR	99.0%	34.8	25	34.3	2	0	0	1416.78	1480	1491
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	12	12	20	0.02%	8.6%	TLMNTIMQLR	99.0%	35	25	18.8	1	0	0	1252.64	1034	1043
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	12	12	20	0.02%	8.6%	VIQAGMFDQK	99.7%	45	25	39.5	1	0	0	1136.58	1228	1237
Transcription elongation factor B polypeptide 1	TCEB1	ELOC_HUMAN	12.5	100.0%	3	3	5	0.00%	41.1%	AMLSGPGQFAENETNEVNFR	99.7%	59.6	25	59.6	2	0	0	2227.01	44	63
Transcription elongation factor B polypeptide 1	TCEB1	ELOC_HUMAN	12.5	100.0%	3	3	5	0.00%	41.1%	LISSDGHEFIVK	99.7%	48.9	25	47.2	1	0	0	1344.72	21	32
Transcription elongation factor B polypeptide 1	TCEB1	ELOC_HUMAN	12.5	100.0%	3	3	5	0.00%	41.1%	TYGGCEGPDAMYVK	99.7%	54	25	54	2	0	0	1563.65	7	20
Transcription elongation regulator 1	TCERG1	TCRG1_HUMAN	123.9	100.0%	3	3	5	0.00%	2.9%	EALFNEFVAAAR	99.7%	89.8	25	89.8	2	0	0	1337.68	770	781
Transcription elongation regulator 1	TCERG1	TCRG1_HUMAN	123.9	100.0%	3	3	5	0.00%	2.9%	LFNEHIEALTK	96.4%	29.6	25	24.6	1	0	0	1314.71	945	955
Transcription elongation regulator 1	TCERG1	TCRG1_HUMAN	123.9	100.0%	3	3	5	0.00%	2.9%	VFFYNPTTR	99.7%	41	25	38.2	2	0	0	1144.58	544	552
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	8	10	15	0.01%	26.8%	AEWQVYKEEISR	99.7%	69	25	68.5	2	2	0	1537.76	105	116
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	8	10	15	0.01%	26.8%	EQLPIFK	99.6%	38.8	25	21.6	1	0	0	874.50	63	69
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	8	10	15	0.01%	26.8%	FSKEQLPIFK	99.3%	36.4	25	34.6	1	1	0	1236.70	60	69
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	8	10	15	0.01%	26.8%	IYQDAYR	99.5%	38.3	25	33.5	2	0	0	928.45	98	104
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	8	10	15	0.01%	26.8%	NLSDSEKELYIQHAK	99.7%	40.9	25	37.4	0	1	0	1774.90	191	205
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	8	10	15	0.01%	26.8%	SAYNVYVAER	99.7%	65.8	25	58.3	2	0	0	1171.57	160	169
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	8	10	15	0.01%	26.8%	SWEEQMIEVGR	99.7%	52.8	25	51.8	2	0	0	1363.63	217	227
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	8	10	15	0.01%	26.8%	SWEEQMIEVGRK	99.7%	53.6	25	53.6	1	0	0	1491.73	217	228
Transcriptional activator protein Pur-alpha	PURA	PURA_HUMAN	34.9	100.0%	3	4	9	0.01%	18.0%	FFFDVGSNK	99.7%	54.8	25	53.3	2	0	0	1060.51	231	239
Transcriptional activator protein Pur-alpha	PURA	PURA_HUMAN	34.9	100.0%	3	4	9	0.01%	18.0%	GPGLGSTQGQTIALPAQGLIEFR	99.7%	72.5	25	72.5	4	1	0	2311.24	177	199
Transcriptional activator protein Pur-alpha	PURA	PURA_HUMAN	34.9	100.0%	3	4	9	0.01%	18.0%	LIDDYGVEEEPAELPEGTSLTVDNKR	99.7%	50.1	25	49.5	0	2	0	2889.40	205	230
Transcriptional activator protein Pur-beta	PURB	PURB_HUMAN	33.2	100.0%	3	3	5	0.00%	11.5%	GGGEQETQELASK	99.7%	71.2	25	62.9	2	0	0	1333.62	25	37
Transcriptional activator protein Pur-beta	PURB	PURB_HUMAN	33.2	100.0%	3	3	5	0.00%	11.5%	GGGGGPCGFQPASR	98.0%	32	25	27.6	1	0	0	1304.58	11	24
Transcriptional activator protein Pur-beta	PURB	PURB_HUMAN	33.2	100.0%	3	3	5	0.00%	11.5%	VSEVKPSYR	99.7%	44.1	25	37	2	0	0	1064.57	247	255
Transducin beta-like protein 3	TBL3	TBL3_HUMAN	89.0	100.0%	3	3	8	0.01%	5.1%	AALEALLPYTER	98.2%	32.4	25	29.6	2	0	0	1346.73	755	766
Transducin beta-like protein 3	TBL3	TBL3_HUMAN	89.0	100.0%	3	3	8	0.01%	5.1%	SPGLYFLTAGDQGTLR	99.7%	69	25	69	2	0	0	1695.87	257	272
Transducin beta-like protein 3	TBL3	TBL3_HUMAN	89.0	100.0%	3	3	8	0.01%	5.1%	VNILEVASGAVLR	99.7%	104	25	95.2	4	0	0	1340.79	47	59
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	16	18	37	0.04%	25.0%	AVLGTSNFK	99.1%	35.4	25	28.1	1	0	0	936.51	487	495
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	16	18	37	0.04%	25.0%	DSAQNSVIIVDK	99.7%	83.2	25	73.8	2	0	0	1288.67	194	205
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	16	18	37	0.04%	25.0%	GFVEPDHYVVVGAQR	99.7%	72.8	25	67.2	1	2	0	1672.84	395	409
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	16	18	37	0.04%	25.0%	ILNIFGVIK	99.7%	59.1	25	44.8	2	0	0	1016.65	386	394
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	16	18	37	0.04%	25.0%	LAQMFSDMVLK	99.7%	47.5	25	42.3	2	0	0	1282.65	429	439
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	16	18	37	0.04%	25.0%	LAVDEEENADNNTK	99.7%	83.2	25	69.9	2	0	0	1561.70	40	53
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	16	18	37	0.04%	25.0%	LLNENSYVPR	99.7%	68.1	25	58	2	0	0	1204.63	146	155
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	16	18	37	0.04%	25.0%	LTTDFGNAEK	99.7%	55.9	25	42.5	2	0	0	1095.53	656	665
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	16	18	37	0.04%	25.0%	LTVSNVLK	99.4%	37.6	25	18.8	2	0	0	873.54	375	382
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	16	18	37	0.04%	25.0%	LVYLVENPGGYVAYSK	99.7%	91.6	25	91.6	2	0	0	1771.93	209	224
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	16	18	37	0.04%	25.0%	SAFSNLFGGEPLSYTR	99.7%	101	25	101	2	0	0	1745.85	7	22
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	16	18	37	0.04%	25.0%	SGVGTALLLK	99.7%	46.9	25	33.4	2	0	0	958.59	419	428
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	16	18	37	0.04%	25.0%	SSGLPNIPVQTISR	99.7%	57.8	25	53.9	2	0	0	1468.81	326	339
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	16	18	37	0.04%	25.0%	VEYHFLSPYVSPK	99.7%	56.4	25	56.4	2	2	0	1565.80	681	693

Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	16	18	37	0.04%	25.0%	VSASPLLYTLIEK	99.7%	105	25	104	5	0	0	1433.83	496	508
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	16	18	37	0.04%	25.0%	YNSQLLSFVR	99.7%	60.2	25	60.2	2	0	0	1226.65	614	623
Transformation/transcription domain-associated protein	TRRAP	TRRAP_HUMAN	437.6	100.0%	4	4	5	0.00%	1.3%	ELYADFIAAQIK	99.7%	51.8	25	44.7	1	0	0	1381.74	275	286
Transformation/transcription domain-associated protein	TRRAP	TRRAP_HUMAN	437.6	100.0%	4	4	5	0.00%	1.3%	LGFTPSVTIEQR	99.7%	52.6	25	44.3	2	0	0	1347.73	1992	2003
Transformation/transcription domain-associated protein	TRRAP	TRRAP_HUMAN	437.6	100.0%	4	4	5	0.00%	1.3%	LVEDNPSSLSLVEIYK	99.7%	69.9	25	65.3	1	0	0	1805.95	3583	3598
Transformation/transcription domain-associated protein	TRRAP	TRRAP_HUMAN	437.6	100.0%	4	4	5	0.00%	1.3%	TIPNVIISHR	99.7%	40.2	25	36.8	1	0	0	1149.67	997	1006
Transformer-2 protein homolog alpha	TRA2A	TRA2A_HUMAN	32.7	100.0%	5	7	21	0.02%	25.5%	ANPDPNTCLGVFGLSLYTTER	99.7%	59.4	25	59.4	2	1	0	2325.12	113	133
Transformer-2 protein homolog alpha	TRA2A	TRA2A_HUMAN	32.7	100.0%	5	7	21	0.02%	25.5%	GFAFVYFER	99.7%	61.8	25	43.8	6	0	0	1135.56	161	169
Transformer-2 protein homolog alpha	TRA2A	TRA2A_HUMAN	32.7	100.0%	5	7	21	0.02%	25.5%	IDDSKEAMER	99.7%	57.5	25	43.7	3	0	0	1193.55	170	179
Transformer-2 protein homolog alpha	TRA2A	TRA2A_HUMAN	32.7	100.0%	5	7	21	0.02%	25.5%	IRVDYSITK	99.7%	51.5	25	36.8	3	0	0	1094.62	190	198
Transformer-2 protein homolog alpha	TRA2A	TRA2A_HUMAN	32.7	100.0%	5	7	21	0.02%	25.5%	RSPSPYYSR	99.7%	48.5	25	32.2	2	0	0	1112.55	259	267
Transformer-2 protein homolog alpha	TRA2A	TRA2A_HUMAN	32.7	100.0%	5	7	21	0.02%	25.5%	SPSPYYSR	98.2%	32.4	25	21.3	1	0	0	956.45	260	267
Transformer-2 protein homolog alpha	TRA2A	TRA2A_HUMAN	32.7	100.0%	5	7	21	0.02%	25.5%	YGPLSGVNVVYDQR	99.7%	76.6	25	68.1	6	0	0	1566.79	142	155
Transformer-2 protein homolog beta	TRA2B	TRA2B_HUMAN	33.7	100.0%	7	7	18	0.02%	27.8%	AAQDRDQIYR	98.5%	33.2	25	28.5	1	0	0	1235.61	252	261
Transformer-2 protein homolog beta	TRA2B	TRA2B_HUMAN	33.7	100.0%	7	7	18	0.02%	27.8%	ANPDPNCCLGVFGLSLYTTER	99.7%	64.6	25	64.6	2	0	0	2384.10	112	132
Transformer-2 protein homolog beta	TRA2B	TRA2B_HUMAN	33.7	100.0%	7	7	18	0.02%	27.8%	GFAFVYFENVDDAK	99.7%	94.2	25	79.1	5	0	0	1621.75	160	173
Transformer-2 protein homolog beta	TRA2B	TRA2B_HUMAN	33.7	100.0%	7	7	18	0.02%	27.8%	GYDDRDYYSR	98.5%	33.1	25	29.1	3	0	0	1309.54	229	238
Transformer-2 protein homolog beta	TRA2B	TRA2B_HUMAN	33.7	100.0%	7	7	18	0.02%	27.8%	RSPSPYYSR	99.7%	48.5	25	32.2	2	0	0	1112.55	263	271
Transformer-2 protein homolog beta	TRA2B	TRA2B_HUMAN	33.7	100.0%	7	7	18	0.02%	27.8%	SPSPYYSR	98.2%	32.4	25	21.3	1	0	0	956.45	264	271
Transformer-2 protein homolog beta	TRA2B	TRA2B_HUMAN	33.7	100.0%	7	7	18	0.02%	27.8%	YGPIADVSIVYDQQSR	99.7%	106	25	104	4	0	0	1810.90	141	156
Transgelin-2	TAGLN2	TAGL2_HUMAN	22.4	99.9%	2	2	3	0.00%	14.1%	DDGLFSGDPNWFPK	97.6%	31.2	25	31.2	1	0	0	1594.72	140	153
Transgelin-2	TAGLN2	TAGL2_HUMAN	22.4	99.9%	2	2	3	0.00%	14.1%	GASQAGMTGYGMPR	99.7%	55.2	25	55.2	2	0	0	1415.60	183	196
Transitional endoplasmic reticulum ATPase	VCP	TERA_HUMAN	89.3	100.0%	2	2	3	0.00%	3.6%	GILLYGPPGTGK	99.7%	44.1	25	0	1	0	0	1172.67	240	251
Transitional endoplasmic reticulum ATPase	VCP	TERA_HUMAN	89.3	100.0%	2	2	3	0.00%	3.6%	NAPAIIFIDELDAIAPK	99.7%	87.4	25	73.7	2	0	0	1811.00	296	312
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	5	5	9	0.01%	19.3%	AQNKPFYVVAESFK	99.7%	39.1	25	39.1	0	1	0	1627.85	221	234
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	5	5	9	0.01%	19.3%	DGATILTHAYSR	99.7%	58.9	25	51.3	2	0	0	1304.66	121	132
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	5	5	9	0.01%	19.3%	DKGETIQGLR	99.7%	48.8	25	38.1	2	0	0	1116.60	37	46
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	5	5	9	0.01%	19.3%	FISLASLEYSDYSK	99.7%	110	25	105	2	0	0	1622.79	75	88
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	5	5	9	0.01%	19.3%	VLEAAVAAK	99.7%	53.3	25	35	2	0	0	871.52	137	145
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	7	9	14	0.01%	26.8%	AVTGTHTLALAAK	99.7%	74.6	25	67.1	2	0	0	1253.72	247	259
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	7	9	14	0.01%	26.8%	FVAPEEVLPFTEGDILEK	98.8%	34.4	25	34.4	1	0	0	2033.05	288	305
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	7	9	14	0.01%	26.8%	IESFVETLK	98.7%	33.8	25	22.8	2	0	0	1065.58	15	23
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	7	9	14	0.01%	26.8%	LSPQFPNEEDSFHK	99.7%	41.1	25	39.8	1	0	0	1674.78	274	287
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	7	9	14	0.01%	26.8%	MTAAQPSETTVGNMVR	99.7%	70.5	25	70.5	4	0	0	1724.79	68	83
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	7	9	14	0.01%	26.8%	SDESDQQESLHK	99.7%	56.4	25	48.4	2	0	0	1402.61	100	111
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	100.0%	7	9	14	0.01%	26.8%	WSNAGELMELIR	99.7%	64.6	25	58.8	2	0	0	1434.70	51	62
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	8	9	17	0.02%	17.2%	ASPSTAGETPSGVK	99.7%	76.9	25	72.4	4	0	0	1288.64	129	142
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	8	9	17	0.02%	17.2%	ASPSTAGETPSGVKR	99.7%	49.9	25	49.9	1	0	0	1444.74	129	143
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	8	9	17	0.02%	17.2%	ILQEAWTEGR	99.7%	82.6	25	66.6	2	0	0	1202.62	345	354
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	8	9	17	0.02%	17.2%	LGLQYSQGLVSGSNAR	99.7%	103	25	97.9	2	0	0	1649.86	210	225
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	8	9	17	0.02%	17.2%	LPEYPQVDDLLLR	99.7%	58.8	25	54.5	2	0	0	1570.85	144	156
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	8	9	17	0.02%	17.2%	VGTAQLALVAR	99.7%	93.4	25	74.2	2	0	0	1098.66	418	428
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	8	9	17	0.02%	17.2%	VSLFSHLPQYSR	99.6%	39	25	39	1	1	0	1433.75	177	188
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	8	9	17	0.02%	17.2%	VVVVDSRPWLEGR	98.7%	33.8	25	22.7	2	0	0	1511.83	358	370
Translation initiation factor eIF-2B subunit epsilon	EIF2B5	EI2BE_HUMAN	80.4	100.0%	4	4	7	0.01%	5.8%	GYNPAEVGAAGK	99.7%	53.1	25	41.5	2	0	0	1133.56	482	493
Translation initiation factor eIF-2B subunit epsilon	EIF2B5	EI2BE_HUMAN	80.4	100.0%	4	4	7	0.01%	5.8%	IITSELYR	99.7%	41.1	25	22.3	1	0	0	994.56	122	129
Translation initiation factor eIF-2B subunit epsilon	EIF2B5	EI2BE_HUMAN	80.4	100.0%	4	4	7	0.01%	5.8%	VFQNEVLGTLQR	99.7%	81.5	25	74.1	2	0	0	1403.76	552	563
Translation initiation factor eIF-2B subunit epsilon	EIF2B5	EI2BE_HUMAN	80.4	100.0%	4	4	7	0.01%	5.8%	YCALLLPLLK	99.7%	45.3	25	45.3	2	0	0	1203.72	617	626
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	4	4	6	0.01%	13.9%	DFIGVDSTGKR	99.7%	55.3	25	46.5	2	0	0	1194.61	156	166
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	4	4	6	0.01%	13.9%	HLVGVDSLIGPETQIGEK	99.4%	31.4	25	31.4	0	1	0	1892.01	350	367
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	4	4	6	0.01%	13.9%	KGQDSIEPVPGQK	99.7%	74.9	25	74.9	2	0	0	1382.73	134	146

Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	4	4	6	0.01%	13.9%	LLSALCPEEPPVHSSAQIVSK	98.9%	28.7	25	28.7	0	1	0	2262.18	329	349
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	AALLETLSLLLAK	99.7%	69.7	25	69.7	2	0	0	1355.85	2324	2336
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	ADYTSHLR	99.7%	44.6	25	30.7	1	0	0	962.47	2184	2191
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	AGSVELLGAMAYCAPK	99.7%	82.8	25	73.8	2	0	0	1637.80	1515	1530
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	AIITALGVER	99.7%	59.9	25	44.5	2	0	0	1042.63	1872	1881
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	ALADENEFVR	99.7%	64.2	25	51.8	2	0	0	1163.57	1785	1794
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	ALCDPLEEVR	98.2%	32.5	25	27.8	1	0	0	1201.59	2013	2022
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	ALGTLVSHVTLR	99.7%	76.9	25	68.6	1	0	0	1266.75	915	926
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	ALQAAIQQLAEAQPEATAK	99.7%	77.2	25	77.2	2	0	0	1952.04	69	87
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	ALVAVLLSR	99.7%	67.9	25	56.7	4	0	0	941.61	568	576
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	ASLLDPVPEVR	99.2%	35.9	25	30.7	2	0	0	1195.67	1664	1674
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	AVMSNLSAHGVK	99.7%	47.2	25	40.7	3	0	0	1213.64	1485	1496
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	AYSDQAIVNLLK	99.7%	86.5	25	66.8	2	0	0	1334.73	2610	2621
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	DLAPYLPSVTPGLK	97.9%	31.7	25	23.5	1	0	0	1470.82	1650	1663
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	EEFAIMQTPAGELYDK	99.7%	49	25	45.3	1	0	0	1841.86	761	776
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	FDKEEEIR	96.5%	29.7	25	6.66	1	0	0	1065.52	1135	1142
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	GAAYGLAGLVK	99.7%	63.8	25	52	2	0	0	1019.59	1396	1406
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	GIKEEVQLTSK	99.7%	46.4	25	32.6	2	0	0	1231.69	819	829
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	GLGILSLK	95.0%	28.2	25	5.33	1	0	0	800.52	1407	1414
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	GVTSILPVLR	99.7%	44.9	25	44.9	2	0	0	1054.66	2260	2269
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	HHIETGGGQLPAK	99.7%	57.9	25	55.3	1	2	0	1344.70	2538	2550
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	HLDQIIPR	99.7%	43.3	25	35.1	2	0	0	991.57	705	712
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	HLFAILGGSEGK	99.2%	35.8	25	34.9	1	0	0	1228.67	341	352
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	IDPEAFITR	99.0%	35.1	25	29	2	0	0	1061.56	696	704
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	ILPEIIPILEEGLR	99.7%	58.4	25	58.4	2	0	0	1604.96	1960	1973
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	LFCLTLHR	97.8%	31.7	25	18.7	1	0	0	1059.58	53	60
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	LMDEAVLALR	99.7%	78.6	25	62	4	0	0	1130.62	314	323
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	LMEIYQEK	99.3%	36.6	25	34.4	2	0	0	1053.53	1201	1208
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	LMPEIVATASK	98.7%	33.7	25	22.1	1	0	0	1159.64	1735	1745
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	LMQQLLESDKYAER	99.3%	30.6	25	25.8	0	1	0	1723.87	1381	1394
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	LTEVLTDSHVK	99.7%	58.2	25	48.6	2	0	0	1241.67	1543	1553
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	LYRPPPVLDALGR	99.7%	52	25	43.3	1	2	0	1466.85	1209	1221
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	NAPNDASYDAVR	99.7%	64.6	25	64.6	2	0	0	1292.59	1305	1316
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	NLLHSLQSSGIGSK	99.7%	77.4	25	67.3	2	1	0	1440.78	88	101
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	QAGAEALSQAVAR	99.7%	84.2	25	68.3	2	0	0	1271.67	1177	1189
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	QGEEVFQSLSK	96.6%	29.8	25	28.5	1	0	0	1251.62	2624	2634
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	QLSSCLPNIVPK	99.1%	35.7	25	30.6	1	0	0	1355.74	1531	1542
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	SALLDFYMK	99.7%	61.9	25	55	3	0	0	1087.55	221	229
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	SDTQLVVR	99.3%	36.4	25	8.82	1	0	0	917.51	1894	1901
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	SGAAQGLAEVMAGLGVEK	99.7%	101	25	87.6	2	0	0	1687.87	1714	1731
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	SIIQSAQQDSIK	99.7%	49.9	25	38.7	2	0	0	1317.70	777	788
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	SIIQSAQQDSIKK	99.7%	55.1	25	50.5	2	0	0	1445.80	777	789
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	SLVSGLIR	99.4%	37.4	25	9.4	2	0	0	844.53	2192	2199
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	VDENGPELLPR	99.7%	53.7	25	47.6	2	0	0	1238.64	1027	1037
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	VISESPPDQWEAR	99.7%	55.4	25	52.2	2	0	0	1513.73	1222	1234
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	VLAFLSSVAGDALTR	99.7%	75.7	25	75.7	4	0	0	1519.85	2093	2107
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	VLAGLYMGR	99.7%	50.9	25	43.7	1	0	0	979.54	1885	1893
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	VLPLEALVTDAGEVTEAGK	99.7%	93.2	25	93.2	3	3	0	1912.03	617	635
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	48	55	96	0.09%	20.5%	YLLDSCAPLLR	99.7%	64.1	25	60.6	2	0	0	1320.70	241	251
Translocation protein SEC63 homolog	SEC63	SEC63_HUMAN	88.0	100.0%	3	3	5	0.00%	3.8%	AYAALTDEESR	99.7%	56.4	25	42.2	1	0	0	1225.57	148	158
Translocation protein SEC63 homolog	SEC63	SEC63_HUMAN	88.0	100.0%	3	3	5	0.00%	3.8%	VLLLSHLAR	99.7%	55.2	25	55.2	2	0	0	1021.65	303	311

Translocation protein SEC63 homolog	SEC63	SEC63_HUMAN	88.0	100.0%	3	3	5	0.00%	3.8%	YSGDQILIR	99.7%	44.6	25	33.4	2	0	0	1064.57	218	226
Translocator protein	TSPO	TSPOA_HUMAN	18.8	99.8%	2	2	5	0.00%	9.5%	ELGGFTEK	99.7%	53.7	25	24	4	0	0	880.44	70	77
Translocator protein	TSPO	TSPOA_HUMAN	18.8	99.8%	2	2	5	0.00%	9.5%	FVHGEGLR	98.1%	32.2	25	25.2	1	0	0	914.48	25	32
Translocon-associated protein subunit alpha	SSR1	SSRA_HUMAN	32.2	99.8%	2	2	4	0.00%	9.1%	GEDFPANNIVK	99.7%	62.6	25	57.8	2	0	0	1203.60	92	102
Translocon-associated protein subunit alpha	SSR1	SSRA_HUMAN	32.2	99.8%	2	2	4	0.00%	9.1%	GTEDFIVESLDASFR	99.7%	77.4	25	77.4	2	0	0	1685.80	111	125
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	6	8	23	0.02%	37.0%	FFDEESYSLLR	99.7%	73	25	72.6	7	0	0	1405.66	106	116
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	6	8	23	0.02%	37.0%	FFDEESYSLLRK	99.7%	59.5	25	56.3	2	0	0	1533.76	106	117
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	6	8	23	0.02%	37.0%	NNEDISIIPPLFTVSVDHR	99.7%	53.1	25	53.1	2	2	0	2166.12	121	139
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	6	8	23	0.02%	37.0%	SAHAGTYEVR	99.7%	60	25	53.9	4	0	0	1090.53	96	105
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	6	8	23	0.02%	37.0%	VQNMALYADVGGK	99.7%	82.7	25	75.3	4	0	0	1365.68	61	73
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	6	8	23	0.02%	37.0%	YQVSWSLDHK	99.7%	49.3	25	36.2	2	0	0	1262.62	86	95
Transmembrane 9 superfamily member 3	TM9SF3	TM9S3_HUMAN	67.9	100.0%	2	2	4	0.00%	3.6%	YFSLPFCVGSK	98.4%	32.9	25	24.2	2	0	0	1304.63	60	70
Transmembrane 9 superfamily member 3	TM9SF3	TM9S3_HUMAN	67.9	100.0%	2	2	4	0.00%	3.6%	YLDPSFFQHR	99.7%	44.3	25	35.2	2	0	0	1309.63	211	220
Transmembrane and coiled-coil domain-containing protein 1	TMCO1	TMCO1_HUMAN	21.2	99.8%	2	2	4	0.00%	9.0%	ETITESAGR	98.7%	33.7	25	12.1	2	0	0	963.47	55	63
Transmembrane and coiled-coil domain-containing protein 1	TMCO1	TMCO1_HUMAN	21.2	99.8%	2	2	4	0.00%	9.0%	ILGLAPSR	98.6%	33.6	25	28.4	2	0	0	826.51	161	168
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	6	9	17	0.02%	21.5%	IPDQLVILDMK	99.7%	68.2	25	52.2	6	0	0	1284.72	117	127
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	6	9	17	0.02%	21.5%	ITDSAGHILYSK	99.7%	81.1	25	70.5	2	2	0	1304.68	76	87
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	6	9	17	0.02%	21.5%	ITDSAGHILYSKEDATK	99.7%	75.7	25	68.1	2	2	0	1848.93	76	92
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	6	9	17	0.02%	21.5%	LKPLEVELR	99.7%	40.1	25	36.5	1	0	0	1096.67	144	152
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	6	9	17	0.02%	21.5%	NYEEIAK	94.6%	28	25	17.5	1	0	0	866.43	134	140
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	6	9	17	0.02%	21.5%	NYEEIAKVEK	99.7%	41.5	25	32	1	0	0	1222.63	134	143
Transmembrane emp24 domain-containing protein 2	TMED2	TMED2_HUMAN	22.8	100.0%	2	2	3	0.00%	12.4%	IVMFTIDIGEAPK	99.7%	44.6	25	44.6	1	0	0	1433.77	105	117
Transmembrane emp24 domain-containing protein 2	TMED2	TMED2_HUMAN	22.8	100.0%	2	2	3	0.00%	12.4%	YTFAAHMDGTYK	99.7%	41.3	25	39.2	2	0	0	1420.62	80	91
Transmembrane protein 109	TMEM109	TM109_HUMAN	26.2	99.8%	2	2	3	0.00%	9.1%	EAPVDVLTQIGR	99.7%	59.4	25	51.3	2	0	0	1297.71	48	59
Transmembrane protein 109	TMEM109	TM109_HUMAN	26.2	99.8%	2	2	3	0.00%	9.1%	RDFAPPGQQK	98.7%	33.9	25	21.6	1	0	0	1143.59	37	46
Transmembrane protein 11, mitochondrial	TMEM11	TMM11_HUMAN	21.5	100.0%	4	5	11	0.01%	21.4%	KIYELYAV	96.2%	29.4	25	25.5	1	0	0	998.56	185	192
Transmembrane protein 11, mitochondrial	TMEM11	TMM11_HUMAN	21.5	100.0%	4	5	11	0.01%	21.4%	LPLHTLTSSTPVVLVR	99.7%	59.5	25	59.5	2	2	0	1733.03	146	161
Transmembrane protein 11, mitochondrial	TMEM11	TMM11_HUMAN	21.5	100.0%	4	5	11	0.01%	21.4%	YIVIEPTR	99.7%	53.8	25	43.8	4	0	0	990.56	59	66
Transmembrane protein 11, mitochondrial	TMEM11	TMM11_HUMAN	21.5	100.0%	4	5	11	0.01%	21.4%	YQVEYDAYK	99.4%	37.6	25	37.6	2	0	0	1178.54	134	142
Transmembrane protein 126A	TMEM126A	T126A_HUMAN	21.5	100.0%	5	5	11	0.01%	27.7%	ALQLSEPGKEIH	99.5%	38.3	25	38.3	3	0	0	1321.71	184	195
Transmembrane protein 126A	TMEM126A	T126A_HUMAN	21.5	100.0%	5	5	11	0.01%	27.7%	GNILSYWIR	99.7%	47.5	25	39.1	2	0	0	1121.61	142	150
Transmembrane protein 126A	TMEM126A	T126A_HUMAN	21.5	100.0%	5	5	11	0.01%	27.7%	KINQLPEAER	99.5%	38.8	25	23.7	2	0	0	1197.66	20	29
Transmembrane protein 126A	TMEM126A	T126A_HUMAN	21.5	100.0%	5	5	11	0.01%	27.7%	SNNKENITIVDISR	99.7%	46.2	25	45.8	2	0	0	1602.84	6	19
Transmembrane protein 126A	TMEM126A	T126A_HUMAN	21.5	100.0%	5	5	11	0.01%	27.7%	YQSALLPHK	98.3%	32.6	25	32	2	0	0	1056.58	133	141
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	5	5	10	0.01%	19.4%	ALLANALTSALR	99.7%	95.7	25	92.2	3	0	0	1213.73	58	69
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	5	5	10	0.01%	19.4%	GSNSLPLLR	98.5%	33.2	25	30.7	2	0	0	956.55	135	143
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	5	5	10	0.01%	19.4%	LCLQSIAFISR	99.7%	91.6	25	79	2	0	0	1307.71	231	241
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	5	5	10	0.01%	19.4%	LDTAMWLSR	99.7%	66.9	25	50.6	2	0	0	1092.55	23	31
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	5	5	10	0.01%	19.4%	TLFNELR	97.3%	30.7	25	13.6	1	0	0	892.49	206	212
Transmembrane protein 97	TMEM97	TMM97_HUMAN	20.8	99.8%	2	2	4	0.00%	13.1%	EFKDPLLQEPPAWFK	99.7%	49.8	25	45.8	2	0	0	1844.96	53	67
Transmembrane protein 97	TMEM97	TMM97_HUMAN	20.8	99.8%	2	2	4	0.00%	13.1%	ELYPVEFR	99.7%	46.2	25	34.8	2	0	0	1052.54	37	44
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	11	12	21	0.02%	14.9%	ALVMLLEVR	99.7%	80	25	75.2	4	0	0	1059.62	246	254
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	11	12	21	0.02%	14.9%	ATVGILITTIASK	99.7%	109	25	109	2	0	0	1287.79	116	128
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	11	12	21	0.02%	14.9%	ESQSPDTTIQR	99.7%	52.8	25	42	2	0	0	1261.60	29	39
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	11	12	21	0.02%	14.9%	FSDQFPLPLK	99.7%	60	25	60	2	0	0	1191.64	880	889
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	11	12	21	0.02%	14.9%	GDVEEDETIPDSEQDIRPR	99.7%	37.8	25	37.8	0	1	0	2200.00	328	346
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	11	12	21	0.02%	14.9%	QSSFALLGDLTK	99.7%	75.9	25	62.1	2	0	0	1279.69	693	704
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	11	12	21	0.02%	14.9%	SECLNNIGDSSPLIR	99.7%	65.7	25	65.7	2	0	0	1674.81	101	115
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	11	12	21	0.02%	14.9%	SITCWTLSR	99.0%	34.8	25	16.5	1	0	0	1123.56	464	472
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	11	12	21	0.02%	14.9%	SNILTLMYQCMQDK	99.7%	90.2	25	84.8	1	0	0	1744.81	674	687
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	11	12	21	0.02%	14.9%	TLLENTAITIGR	99.7%	80.2	25	65.4	2	0	0	1301.74	774	785

Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	11	12	21	0.02%	14.9%	YSDIDIILLK	99.7%	49.7	25	49.2	2	0	0	1192.68	318	327
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	11	11	20	0.02%	14.5%	ASFWLGELQR	99.7%	54.6	25	39.4	2	0	0	1206.63	30	39
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	11	11	20	0.02%	14.5%	ETTVGAVTVTHK	99.7%	57.6	25	46.8	2	0	0	1242.67	882	893
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	11	11	20	0.02%	14.5%	GTALVLAR	99.7%	53.1	25	32.9	2	0	0	800.50	564	571
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	11	11	20	0.02%	14.5%	IFTELCETFLEK	99.7%	81.9	25	67.4	2	0	0	1529.76	298	309
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	11	11	20	0.02%	14.5%	IVCTPGQGLGDLR	99.7%	57	25	52.5	2	0	0	1385.72	310	322
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	11	11	20	0.02%	14.5%	LGEHLYK	96.9%	30.2	25	15.8	2	0	0	859.47	349	355
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	11	11	20	0.02%	14.5%	LPETVHTAVR	99.7%	68	25	55.8	1	0	0	1122.63	469	478
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	11	11	20	0.02%	14.5%	SLDSFLLSPEAAVGLLK	99.7%	77.1	25	76.3	2	0	0	1759.98	547	563
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	11	11	20	0.02%	14.5%	SVDPENNPTLVEVLEGVVR	99.7%	79.9	25	79.9	2	0	0	2066.08	450	468
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	11	11	20	0.02%	14.5%	TNDEVIHGIFK	97.6%	31.2	25	6.48	1	0	0	1272.66	356	366
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	11	11	20	0.02%	14.5%	VIQEIWPVLSETLNK	99.7%	46.9	25	46.9	2	0	0	1768.98	637	651
Treacle protein	TCOF1	TCOF_HUMAN	152.1	100.0%	5	5	7	0.01%	3.7%	AGPVAVQVK	99.5%	38.6	25	26.1	1	0	0	868.53	592	600
Treacle protein	TCOF1	TCOF_HUMAN	152.1	100.0%	5	5	7	0.01%	3.7%	GPASVPSVGK	99.7%	43.2	25	40.2	1	0	0	898.50	843	852
Treacle protein	TCOF1	TCOF_HUMAN	152.1	100.0%	5	5	7	0.01%	3.7%	GSLGQGTAPVLPGK	99.7%	47.7	25	37.7	2	0	0	1281.72	733	746
Treacle protein	TCOF1	TCOF_HUMAN	152.1	100.0%	5	5	7	0.01%	3.7%	TNVVTMPTAHPR	98.9%	34.6	25	28.1	1	0	0	1339.68	1019	1030
Treacle protein	TCOF1	TCOF_HUMAN	152.1	100.0%	5	5	7	0.01%	3.7%	VLTELLEQER	99.7%	53.6	25	29.6	2	0	0	1229.67	1318	1327
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	7	9	30	0.03%	22.8%	FFVMTSLR	99.7%	54.5	25	39.9	8	0	0	1016.52	199	206
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	7	9	30	0.03%	22.8%	FIHDQTSPNPK	99.7%	62.9	25	49.1	4	2	0	1283.64	150	160
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	7	9	30	0.03%	22.8%	GLSSLLYGSIPK	99.7%	75.4	25	56.4	2	0	0	1234.70	86	97
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	7	9	30	0.03%	22.8%	GTYQGLTATVLK	99.7%	70.4	25	61.9	4	0	0	1251.69	179	190
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	7	9	30	0.03%	22.8%	NTWDCGLQILK	99.7%	58.7	25	51.7	4	0	0	1347.67	258	268
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	7	9	30	0.03%	22.8%	SHGVLGLYR	99.1%	35.5	25	35.5	2	0	0	1001.55	77	85
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	7	9	30	0.03%	22.8%	TQLQLDER	99.7%	43.8	25	26.5	4	0	0	1002.52	51	58
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	22	29	53	0.05%	39.7%	ADMVIEAVFEDLSLK	99.7%	69.2	25	67.1	1	0	0	1695.85	441	455
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	22	29	53	0.05%	39.7%	ALMGLYHGQVLCK	99.7%	53.2	25	53.2	1	0	0	1489.77	338	350
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	22	29	53	0.05%	39.7%	ALTSFER	99.7%	51.5	25	29.5	2	0	0	823.43	416	422
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	22	29	53	0.05%	39.7%	DATLTALDR	99.7%	72.4	25	33.8	2	0	0	975.51	391	399
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	22	29	53	0.05%	39.7%	DGPGFYTTR	99.7%	63.2	25	54.4	2	0	0	1013.47	541	549
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	22	29	53	0.05%	39.7%	DLNSDMDSILASLK	99.7%	98.3	25	93.7	3	0	0	1521.75	647	660
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	22	29	53	0.05%	39.7%	DSIFSNLTGQLDYQGFEK	99.7%	79	25	79	2	0	0	2061.98	423	440
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	22	29	53	0.05%	39.7%	DTSASAVAVGLK	99.7%	78.8	25	62.1	2	0	0	1118.61	520	531
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	22	29	53	0.05%	39.7%	EVEAVIPDHCIFASNTSALPISEIAAVSK	94.8%	22.8	25	22.8	0	1	0	3068.56	461	489
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	22	29	53	0.05%	39.7%	FGELVMTK	99.7%	46.5	25	28.9	2	0	0	940.48	327	334
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	22	29	53	0.05%	39.7%	FGGGNPELLTQMVSK	99.7%	79	25	71.2	4	0	0	1593.79	611	625
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	22	29	53	0.05%	39.7%	GFYIYQEGVK	99.7%	68.3	25	63.2	2	0	0	1203.60	635	644
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	22	29	53	0.05%	39.7%	ILQEGVDPK	99.7%	45	25	35.8	2	0	0	998.55	561	569
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	22	29	53	0.05%	39.7%	LTAYAMTIPFVR	99.7%	76.6	25	75.8	5	0	0	1382.75	268	279
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	22	29	53	0.05%	39.7%	MGLVDQLVEPLGPGLKPPEER	99.7%	50.5	25	50.3	0	1	0	2290.21	215	235
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	22	29	53	0.05%	39.7%	MQLLEIITTEK	99.7%	83.5	25	72.6	5	0	0	1318.73	506	516
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	22	29	53	0.05%	39.7%	MVGVPAALDMMLTGR	99.7%	49.2	25	47.7	3	0	0	1561.79	191	205
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	22	29	53	0.05%	39.7%	SEVSSDEDIQFR	99.7%	82.5	25	81.7	2	0	0	1411.63	665	676
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	22	29	53	0.05%	39.7%	TGIEQGSDAGYLCESQK	99.7%	102	25	102	2	0	0	1842.82	310	326
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	22	29	53	0.05%	39.7%	TLQEVTQLSQEAQR	99.7%	89.2	25	82	2	1	0	1630.84	112	125
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	22	29	53	0.05%	39.7%	TVLGTPEVLLGALPGAGGTQR	99.7%	83.2	25	83.2	2	2	0	2007.12	167	187
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	22	29	53	0.05%	39.7%	VIGMHYFSPVDK	99.7%	41.9	25	37.4	2	0	0	1392.70	494	505
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	44.3%	AALTGLLHR	99.7%	56.6	25	42.6	2	0	0	951.57	82	90
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	44.3%	ALAMGYKPK	99.7%	42.8	25	39.9	2	0	0	994.54	326	334
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	44.3%	AMDSDWFAENYMGR	99.7%	62.7	25	62.7	1	0	0	1724.67	392	405
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	44.3%	AQDEGLLSDVVPFK	99.7%	60	25	59.3	1	0	0	1517.78	255	268
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	44.3%	DLMPHDLAR	99.6%	39.1	25	32.6	2	0	0	1083.53	73	81

Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	44.3%	DNGIRPSSLEQMAK	99.7%	54.1	25	42.4	4	0	0	1545.77	278	291
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	44.3%	DQLLLGPTYATPK	99.7%	62.3	25	51.9	2	0	0	1416.77	349	361
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	44.3%	EAALGAGFSDK	99.7%	61.7	25	55.4	2	0	0	1065.52	118	128
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	44.3%	EGGQYGLVAACAAGGQGHAMIVEAYPK	99.7%	92.8	25	92.8	0	3	0	2705.28	448	474
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	44.3%	EVVDYIIFGTVIQEVK	99.7%	82.2	25	82.2	3	0	0	1852.01	96	111
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	44.3%	FNNWGGSLSLGHPFGATGCR	99.7%	57.9	25	57.9	0	2	0	2134.99	417	436
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	44.3%	KAQDEGLLSDVVPFK	99.6%	39	25	39	1	0	0	1645.88	254	268
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	44.3%	KLMLDLNK	99.7%	40.3	25	7.34	1	0	0	990.57	181	188
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	44.3%	LAAAFAVSR	99.7%	72.8	25	60.1	2	0	0	905.52	230	238
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	44.3%	LVMAAANR	99.7%	59.6	25.3	47.1	4	0	0	845.47	437	444
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	44.3%	NVVVVDGVR	99.7%	62.3	25	54.2	2	0	0	956.55	53	61
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	44.3%	TPFLLSGTSYK	99.7%	53.8	25	44.8	2	0	0	1213.65	62	72
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	44.3%	TPFLLSGTSYKDLMPHDLAR	99.0%	29.2	25	29.2	0	1	0	2278.15	62	81
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	19	22	38	0.04%	44.3%	VGLPPLEK	99.4%	37.1	25	32.5	1	0	0	852.52	409	416
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	60	0.06%	32.8%	AAGFKDPLLASGTDGVGTK	99.7%	35.9	25	35.9	0	2	0	1804.94	481	499
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	60	0.06%	32.8%	AFAHITGGGLLENIPR	99.7%	68.1	25	64.7	1	2	0	1665.91	677	692
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	60	0.06%	32.8%	AIAFLQQPR	99.7%	40.8	25	26.6	2	0	0	1043.60	425	433
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	60	0.06%	32.8%	AVQEIMQEK	99.2%	36.3	25	28	2	0	0	1091.54	170	178
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	60	0.06%	32.8%	ENLISALEEAKK	99.7%	49.3	25	36.6	3	0	0	1344.74	394	405
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	60	0.06%	32.8%	EQTEQILR	96.7%	29.9	25	18.4	1	0	0	1016.54	744	751
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	60	0.06%	32.8%	ESGVDIAAGNMLVK	99.7%	69.3	25	65.6	3	0	0	1403.72	439	452
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	60	0.06%	32.8%	FGDPECQVILPLLK	99.7%	64	25	62.8	4	0	0	1628.87	293	306
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	60	0.06%	32.8%	GDTVATLSER	99.7%	58.5	25	31	2	0	0	1048.53	966	975
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	60	0.06%	32.8%	HGIPTAQWK	96.3%	29.5	25	28.5	1	0	0	1037.55	117	125
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	60	0.06%	32.8%	IKDTVLQR	99.7%	48.8	25	23.2	2	0	0	972.58	250	257
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	60	0.06%	32.8%	ISNTAISISDHTALAQFCK	99.7%	62.2	25	62.2	0	4	0	2077.04	45	63
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	60	0.06%	32.8%	ITEGDVVVGIASSGLHSNGFSLVR	99.7%	61.8	25	61.8	0	1	0	2414.27	605	628
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	60	0.06%	32.8%	IYSHSLLPVLR	99.7%	57.8	25	49	2	2	0	1297.76	661	671
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	60	0.06%	32.8%	KIEFVVVGPEAPLAAGIVGNLR	99.7%	33.9	25	32.5	0	1	0	2249.30	66	87
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	60	0.06%	32.8%	LDLSVTEAVVAGIAK	99.7%	78.3	25	61.4	2	0	0	1485.85	543	557
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	60	0.06%	32.8%	MLNIHPSLLPSFK	99.7%	46.7	25	40	4	0	0	1496.83	911	923
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	60	0.06%	32.8%	QVLVAPGNAGTACSEK	99.7%	75.9	25	72.8	2	0	0	1601.80	29	44
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	60	0.06%	32.8%	SAGVQCFGPTAEAAQLESSKR	99.7%	39	25	37	0	2	0	2194.06	88	108
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	60	0.06%	32.8%	TFNCGVGAVLVVSK	99.7%	96.6	25	88.4	2	0	0	1450.77	730	743
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	60	0.06%	32.8%	VAVLISGTGSNLQALIDSTR	99.7%	101	25	100	2	0	0	2015.11	810	829
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	60	0.06%	32.8%	VDLGGFAGLFDLK	99.7%	89.3	25	86.1	5	0	0	1351.73	468	480
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	60	0.06%	32.8%	VLAVTAIR	99.7%	59.6	25	27.6	3	0	0	842.55	386	393
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	60	0.06%	32.8%	VLEFNCR	99.6%	39.8	25	35.8	3	0	0	937.46	286	292
Triosephosphate isomerase	TPI1	TPIS_HUMAN	30.8	99.8%	2	2	5	0.00%	9.8%	TATPQQAQEVHEK	99.7%	54.2	25	48.4	4	0	0	1466.72	213	225
Triosephosphate isomerase	TPI1	TPIS_HUMAN	30.8	99.8%	2	2	5	0.00%	9.8%	VVLAYEPVWAIGTGK	99.7%	75.2	25	66.9	1	0	0	1602.89	198	212
TRMT1-like protein	TRMT1L	TRM1L_HUMAN	81.7	100.0%	4	4	5	0.00%	8.2%	NLGIVSVTSTDISSLYAK	99.7%	107	25	107	2	0	0	1868.00	391	408
TRMT1-like protein	TRMT1L	TRM1L_HUMAN	81.7	100.0%	4	4	5	0.00%	8.2%	QLIFCTLAALAEER	99.7%	89.6	25	88.8	1	0	0	1634.86	261	274
TRMT1-like protein	TRMT1L	TRM1L_HUMAN	81.7	100.0%	4	4	5	0.00%	8.2%	SSYIAASTAKPPK	99.7%	49.1	25	49.1	1	0	0	1320.72	214	226
TRMT1-like protein	TRMT1L	TRM1L_HUMAN	81.7	100.0%	4	4	5	0.00%	8.2%	TTDDTTTDNYIAQGK	99.7%	87.2	25	87.2	1	0	0	1643.74	595	609
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	16	18	37	0.04%	25.4%	EDPFVFIPEDDPLFPPIEK	99.7%	66.7	25	65.4	1	0	0	2244.11	517	535
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	16	18	37	0.04%	25.4%	FHQFLVSETESGNISR	99.7%	51.5	25	51.5	0	2	0	1850.90	145	160
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	16	18	37	0.04%	25.4%	FYALDPSFPR	97.5%	31	25	27.2	1	0	0	1212.60	536	545
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	16	18	37	0.04%	25.4%	GAEQLAEGGR	99.7%	83.7	25	74.9	3	0	0	987.49	306	315
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	16	18	37	0.04%	25.4%	IITVSMEDVK	99.7%	52.7	25	44.2	4	0	0	1134.61	619	628
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	16	18	37	0.04%	25.4%	ILCDVPCSGDGTMR	97.2%	30.6	25	30.6	1	0	0	1580.69	265	278
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	16	18	37	0.04%	25.4%	ILDMCAAPGSK	99.7%	44.1	25	44.1	1	0	0	1162.56	180	190

tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	16	18	37	0.04%	25.4%	ILLTQENPFFR	99.7%	84.8	25	81.2	6	0	0	1377.75	629	639
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	16	18	37	0.04%	25.4%	KLSSETYSQAK	99.7%	57.8	25	55.8	2	0	0	1241.64	640	650
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	16	18	37	0.04%	25.4%	LAQEGIYTLYPFINSR	99.7%	94.6	25	94.6	2	1	0	1884.99	603	618
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	16	18	37	0.04%	25.4%	LQIDVDGR	94.9%	28.2	25	26.1	1	0	0	915.49	249	256
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	16	18	37	0.04%	25.4%	LQQQQRPEDAEDGAEGGGK	99.7%	52.3	25	52.3	0	2	0	2012.93	10	28
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	16	18	37	0.04%	25.4%	LSSETYSQAK	99.7%	62.2	25	55.1	2	0	0	1113.54	641	650
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	16	18	37	0.04%	25.4%	MMGLEVLGEK	99.7%	42.6	25	42	2	0	0	1106.56	701	710
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	16	18	37	0.04%	25.4%	NNSGEEFDCAFR	99.7%	71.7	25	71.7	2	0	0	1445.58	591	602
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	16	18	37	0.04%	25.4%	SEGALELADVSNELPGLK	99.7%	131	25	125	4	0	0	1841.95	339	356
tRNA methyltransferase 112 homolog	TRMT112	TR112_HUMAN	14.2	100.0%	2	2	3	0.00%	21.6%	GPVEGYEENEEFLR	99.7%	60.5	25	60.5	2	0	0	1667.75	69	82
tRNA methyltransferase 112 homolog	TRMT112	TR112_HUMAN	14.2	100.0%	2	2	3	0.00%	21.6%	ICPVEFNPNFVAR	99.6%	39.9	25	39.9	1	0	0	1562.78	32	44
tRNA-splicing endonuclease subunit Sen34	TSEN34	SEN34_HUMAN	33.7	99.8%	2	2	3	0.00%	8.7%	FGGDFLVYPGDPLR	98.0%	31.9	25	25.7	1	0	0	1552.78	240	253
tRNA-splicing endonuclease subunit Sen34	TSEN34	SEN34_HUMAN	33.7	99.8%	2	2	3	0.00%	8.7%	LGLPLLLMPEEAR	99.7%	60.5	25	60.5	2	0	0	1451.83	46	58
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	10	12	20	0.02%	24.6%	GGGVGGFLPAMK	99.7%	50.4	25	42.7	2	0	0	1090.57	56	67
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	10	12	20	0.02%	24.6%	GLGHQVATDALVAMEK	99.7%	69.5	25	68.6	2	0	0	1639.85	264	279
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	10	12	20	0.02%	24.6%	GMAAAGNYAWVNR	99.7%	72.8	25	58.6	1	0	0	1380.65	309	321
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	10	12	20	0.02%	24.6%	GQVCVMIHSGSR	99.7%	67.1	25	67.1	1	0	0	1330.64	252	263
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	10	12	20	0.02%	24.6%	LVMEEAPESYK	99.7%	61.7	25	54.2	3	0	0	1311.61	466	476
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	10	12	20	0.02%	24.6%	NVTDVVNTCHDAGISK	99.7%	99.8	25	97.7	2	0	0	1729.82	477	492
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	10	12	20	0.02%	24.6%	QIGNVAALPGIVHR	99.7%	43.6	25	43.6	0	2	0	1444.84	68	81
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	10	12	20	0.02%	24.6%	SSMTFLTR	99.7%	41.2	25	26.9	1	0	0	942.47	322	329
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	10	12	20	0.02%	24.6%	SYNDELQFLEK	99.7%	76	25	40.8	2	0	0	1385.66	4	14
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	10	12	20	0.02%	24.6%	VEQHVVDGKER	99.7%	38.4	25	32.4	2	2	0	1295.67	358	368
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	59.6%	AFVHWYVGEGMEEGEFSEAR	99.7%	34.7	25	34.7	0	3	0	2346.01	403	422
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	59.6%	AVCMLSNTTAIAEAWAR	99.7%	113	25	102	23	12	0	1880.90	374	390
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	59.6%	AVFVDLEPTVIDEVR	99.7%	115	25	114	47	6	0	1701.91	65	79
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	59.6%	AYHEQLSVAEITNACFEPANQMVK	99.7%	72	25	72	0	12	0	2750.29	281	304
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	59.6%	DVNAAIATIK	99.7%	81.6	25	59.7	16	0	0	1015.58	327	336
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	59.6%	EDAANNYAR	99.7%	42.8	25	34.4	1	0	0	1023.45	97	105
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	59.6%	EDMAALEK	99.7%	70	25	45.2	3	0	0	906.42	423	430
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	59.6%	EIIDLVLDR	99.7%	82.2	25	73.9	46	0	0	1085.62	113	121
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	59.6%	FDGALNVDLTEFQTNLVPYPR	99.7%	104	25	104	8	0	0	2409.21	244	264
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	59.6%	FDLMYAK	99.7%	45.9	25	33.9	7	0	0	887.43	395	401
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	59.6%	IHFPLATYAPVISAEK	99.7%	89.1	25	86.5	24	20	0	1756.96	265	280
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	59.6%	LDHKFDLMYAK	99.7%	48.6	25	32.9	8	9	0	1380.70	391	401
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	59.6%	LIGQIVSSITASLR	99.7%	92.1	25	92.1	2	0	0	1457.87	230	243
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	59.6%	LSVDYGKK	99.7%	49.4	25	39.4	12	0	0	909.50	157	164
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	59.6%	NLDIERPTYTNLNR	99.7%	69.2	25	66.1	12	13	0	1718.88	216	229
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	59.6%	QLFHPEQLITGK	99.7%	48.3	25	0	8	5	0	1410.77	85	96
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	59.6%	QLFHPEQLITGKEDAANNYAR	99.7%	79.1	25	79.1	2	14	0	2415.21	85	105
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	59.6%	RNLDIERPTYTNLNR	98.2%	26.7	25	26.7	1	2	0	1874.98	215	229
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	59.6%	TIGGGDDSFNTFFSETGAGK	99.7%	119	25	119	30	0	0	2007.89	41	60
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	59.6%	TIQFVDWCPTGFK	99.7%	88.2	25	83.2	19	0	0	1598.77	340	352
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	59.6%	VGINYQPPTVVPGGDLAK	99.7%	79.9	25	79.9	26	0	0	1824.99	353	370
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	21	0.02%	59.6%	YMACCLLYR	99.7%	53.7	25	53.7	27	0	0	1249.55	312	320
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	38	442	0.43%	59.6%	AFVHWYVGEGMEEGEFSEAR	99.7%	34.7	25	34.7	0	3	0	2346.01	403	422
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	38	442	0.43%	59.6%	AVCMLSNTTAIAEAWAR	99.7%	113	25	102	23	12	0	1880.90	374	390
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	38	442	0.43%	59.6%	AVFVDLEPTVIDEVR	99.7%	115	25	114	47	6	0	1701.91	65	79
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	38	442	0.43%	59.6%	AYHEQLSVAEITNACFEPANQMVK	99.7%	72	25	72	0	12	0	2750.29	281	304
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	38	442	0.43%	59.6%	DVNAAIATIK	99.7%	81.6	25	59.7	16	0	0	1015.58	327	336
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	38	442	0.43%	59.6%	EDAANNYAR	99.7%	42.8	25	34.4	1	0	0	1023.45	97	105

Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	38	442	0.43%	59.6%	EDMAALEK	99.7%	70	25	45.2	3	0	0	906.42	423	430
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	38	442	0.43%	59.6%	EIIDLVLDR	99.7%	82.2	25	73.9	46	0	0	1085.62	113	121
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	38	442	0.43%	59.6%	FDGALNVDLTEFQTNLVPYPR	99.7%	104	25	104	8	0	0	2409.21	244	264
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	38	442	0.43%	59.6%	FDLMYAK	99.7%	45.9	25	33.9	7	0	0	887.43	395	401
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	38	442	0.43%	59.6%	IHFPLATYAPVISAEK	99.7%	89.1	25	86.5	24	20	0	1756.96	265	280
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	38	442	0.43%	59.6%	LDHKFDLMYAK	99.7%	48.6	25	32.9	8	9	0	1380.70	391	401
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	38	442	0.43%	59.6%	LISQIVSSITASLR	99.7%	103	25	103	12	4	0	1487.88	230	243
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	38	442	0.43%	59.6%	LSVDYGKK	99.7%	49.4	25	39.4	12	0	0	909.50	157	164
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	38	442	0.43%	59.6%	NLDIERPTYTNLNR	99.7%	69.2	25	66.1	12	13	0	1718.88	216	229
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	38	442	0.43%	59.6%	QLFHPEQLITGK	99.7%	48.3	25	0	8	5	0	1410.77	85	96
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	38	442	0.43%	59.6%	QLFHPEQLITGKEDAANNYAR	99.7%	79.1	25	79.1	2	14	0	2415.21	85	105
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	38	442	0.43%	59.6%	RNLDIERPTYTNLNR	98.2%	26.7	25	26.7	1	2	0	1874.98	215	229
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	38	442	0.43%	59.6%	SIQFVDWCPTGFK	99.7%	96.8	25	93.9	29	0	0	1584.75	340	352
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	38	442	0.43%	59.6%	TIGGGDDSFNTFFSETGAGK	99.7%	119	25	119	30	0	0	2007.89	41	60
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	38	442	0.43%	59.6%	VGINYQPPTVVPGGDLAK	99.7%	79.9	25	79.9	26	0	0	1824.99	353	370
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	22	38	442	0.43%	59.6%	YMACCLLYR	99.7%	53.7	25	53.7	27	0	0	1249.55	312	320
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	59.9%	AFVHWYVGEGMEEGEFSEAR	99.7%	34.7	25	34.7	0	3	0	2346.01	403	422
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	59.9%	AVCMLSNTTAVAEAWAR	99.7%	72.1	25	66.8	1	2	0	1866.88	374	390
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	59.9%	AVFVDLEPTVIDEVR	99.7%	115	25	114	47	6	0	1701.91	65	79
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	59.9%	AYHEQLTVAEITNACFEPANQMVK	97.9%	26.1	25	17.6	0	4	0	2780.30	281	304
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	59.9%	DVNAAIATIK	99.7%	81.6	25	59.7	16	0	0	1015.58	327	336
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	59.9%	EDAANNYAR	99.7%	42.8	25	34.4	1	0	0	1023.45	97	105
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	59.9%	EDMAALEK	99.7%	70	25	45.2	3	0	0	906.42	423	430
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	59.9%	EIIDLVLDR	99.7%	82.2	25	73.9	46	0	0	1085.62	113	121
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	59.9%	FDGALNVDLTEFQTNLVPYPR	99.7%	104	25	104	8	0	0	2409.21	244	264
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	59.9%	FDLMYAK	99.7%	45.9	25	33.9	7	0	0	887.43	395	401
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	59.9%	IHFPLATYAPVISAEK	99.7%	89.1	25	86.5	24	20	0	1756.96	265	280
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	59.9%	LDHKFDLMYAK	99.7%	48.6	25	32.9	8	9	0	1380.70	391	401
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	59.9%	LISQIVSSITASLR	99.7%	103	25	103	12	4	0	1487.88	230	243
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	59.9%	LSVDYGKK	99.7%	49.4	25	39.4	12	0	0	909.50	157	164
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	59.9%	NLDIERPTYTNLNR	99.7%	69.2	25	66.1	12	13	0	1718.88	216	229
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	59.9%	QLFHPEQLITGK	99.7%	48.3	25	0	8	5	0	1410.77	85	96
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	59.9%	QLFHPEQLITGKEDAANNYAR	99.7%	79.1	25	79.1	2	14	0	2415.21	85	105
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	59.9%	RNLDIERPTYTNLNR	98.2%	26.7	25	26.7	1	2	0	1874.98	215	229
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	59.9%	TIGGGDDSFNTFFSETGAGK	99.7%	119	25	119	30	0	0	2007.89	41	60
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	59.9%	TIQFVDWCPTGFK	99.7%	88.2	25	83.2	19	0	0	1598.77	340	352
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	59.9%	VGINYQPPTVVPGGDLAK	99.7%	79.9	25	79.9	26	0	0	1824.99	353	370
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	4	7	0.01%	59.9%	YMACCLLYR	99.7%	53.7	25	53.7	27	0	0	1249.55	312	320
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	AILVDLEPGTMDSVR	99.7%	110	25	103	42	1	0	1615.84	63	77
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	ALTVPELTQQVFDAK	99.7%	89.3	25	89.3	26	4	0	1659.90	283	297
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	87.8	25	0	0	10	0	3311.53	123	154
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	EIVHIQAGQCGNQIGAK	99.7%	90.9	25	0	4	4	0	1822.92	3	19
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	EVDEQMLNVQNK	99.7%	80.5	25	68.2	22	0	0	1446.69	325	336
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	FPGQLNADLR	99.7%	59.9	25	46.5	17	0	0	1130.60	242	251
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	FPGQLNADLRK	99.7%	45.1	25	33.5	7	6	0	1258.69	242	252
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	FWEVISDEHGIDPTGTYHGDSDLQLDR	99.7%	82.3	25	39.4	0	4	0	3102.41	20	46
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	GHYTEGAELVDSVLDVVR	99.7%	141	25	136	6	17	0	1958.98	104	121
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	GHYTEGAELVDSVLDVVRK	99.7%	61.4	25	60.1	0	4	0	2087.08	104	122
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	IMNTFSVVPSPK	99.7%	97.5	25	87.6	31	0	0	1319.70	163	174
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	IREEYPDR	99.7%	45	25	31.6	7	0	0	1077.53	155	162
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	ISEQFTAMFR	99.7%	86	25	81.7	30	0	0	1229.60	381	390

Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	ISVYYNEATGGK	99.7%	82.6	25	82.6	32	0	0	1301.64	47	58
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	KLAVNMVPFPR	99.7%	64.8	25	64.5	4	2	0	1271.73	252	262
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	LAVNMVPFPR	99.7%	90.9	25	72.4	38	0	0	1143.63	253	262
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	LHFFMPGFAPLTSR	99.7%	58.3	25	44.8	34	28	0	1620.84	263	276
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	LTTPTYGDLNHLVSATMSGVTTCLR	99.7%	100	25	100	6	20	0	2708.34	217	241
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	MAVTFIGNSTAIQELFK	99.7%	153	25	153	20	1	0	1885.97	363	379
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	MAVTFIGNSTAIQELFKR	99.7%	68.4	25	68.4	3	7	0	2042.07	363	380
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	MREIVHIQAGQCGNQIGAK	99.7%	66.7	25	0	0	8	0	2110.06	1	19
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	MSMKEVDEQMLNVQNK	99.7%	60.8	25	2.72	7	17	0	1955.89	321	336
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	NMMAACDPR	99.7%	51.1	25	51.1	21	0	0	1065.43	298	306
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	NSSYFVEWIPNNVK	99.7%	80.5	25	67	20	0	0	1696.83	337	350
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	RISEQFTAMFR	99.7%	53.7	25	45.5	2	1	0	1385.70	380	390
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	SGPFGQIFRPDNFVFGQSGAGNNWAK	99.7%	90.8	25	90.8	2	9	0	2798.34	78	103
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	TAVCDIPPR	99.7%	62.8	25	48.7	32	0	0	1028.52	351	359
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	28	57	570	0.56%	74.3%	YLTVAAVFR	99.7%	88.5	25	84.4	14	0	0	1039.59	310	318
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	30	0.03%	60.9%	AILVDLEPGTMDSVR	99.7%	110	25	103	42	1	0	1615.84	63	77
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	30	0.03%	60.9%	ALTVPELTQQMFDSK	99.7%	108	25	46.1	12	0	0	1707.86	283	297
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	30	0.03%	60.9%	EIVHIQAGQCGNQIGAK	99.7%	90.9	25	0	4	4	0	1822.92	3	19
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	30	0.03%	60.9%	EVDEQMLNVQNK	99.7%	80.5	25	68.2	22	0	0	1446.69	325	336
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	30	0.03%	60.9%	FPGQLNADLR	99.7%	59.9	25	46.5	17	0	0	1130.60	242	251
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	30	0.03%	60.9%	FPGQLNADLRK	99.7%	45.1	25	33.5	7	6	0	1258.69	242	252
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	30	0.03%	60.9%	GHYTEGAELVDSVLDVVR	99.7%	141	25	136	6	17	0	1958.98	104	121
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	30	0.03%	60.9%	GHYTEGAELVDSVLDVVRK	99.7%	61.4	25	60.1	0	4	0	2087.08	104	122
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	30	0.03%	60.9%	IMNTFSVMPSPK	99.7%	85.7	25	79.2	8	0	0	1351.67	163	174
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	30	0.03%	60.9%	INVYYNEATGNK	99.7%	72.8	25	69.7	4	0	0	1385.67	47	58
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	30	0.03%	60.9%	IREEYPDR	99.7%	45	25	31.6	7	0	0	1077.53	155	162
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	30	0.03%	60.9%	ISEQFTAMFR	99.7%	86	25	81.7	30	0	0	1229.60	381	390
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	30	0.03%	60.9%	KLAVNMVPFPR	99.7%	64.8	25	64.5	4	2	0	1271.73	252	262
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	30	0.03%	60.9%	LAVNMVPFPR	99.7%	90.9	25	72.4	38	0	0	1143.63	253	262
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	30	0.03%	60.9%	LHFFMPGFAPLTSR	99.7%	58.3	25	44.8	34	28	0	1620.84	263	276
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	30	0.03%	60.9%	LTTPTYGDLNHLVSATMSGVTTCLR	99.7%	100	25	100	6	20	0	2708.34	217	241
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	30	0.03%	60.9%	MREIVHIQAGQCGNQIGAK	99.7%	66.7	25	0	0	8	0	2110.06	1	19
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	30	0.03%	60.9%	MSATFIGNSTAIQELFK	99.7%	125	25	0	7	0	0	1873.94	363	379
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	30	0.03%	60.9%	MSATFIGNSTAIQELFKR	99.7%	70	25	0	2	4	0	2014.04	363	380
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	30	0.03%	60.9%	MSMKEVDEQMLNVQNK	99.7%	60.8	25	2.72	7	17	0	1955.89	321	336
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	30	0.03%	60.9%	NMMAACDPR	99.7%	51.1	25	51.1	21	0	0	1065.43	298	306
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	30	0.03%	60.9%	NSSYFVEWIPNNVK	99.7%	80.5	25	67	20	0	0	1696.83	337	350
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	30	0.03%	60.9%	RISEQFTAMFR	99.7%	53.7	25	45.5	2	1	0	1385.70	380	390
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	30	0.03%	60.9%	SGPFGQIFRPDNFVFGQSGAGNNWAK	99.7%	90.8	25	90.8	2	9	0	2798.34	78	103
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	30	0.03%	60.9%	TAVCDIPPR	99.7%	62.8	25	48.7	32	0	0	1028.52	351	359
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	4	6	30	0.03%	60.9%	YLTVAAIFR	99.7%	81.9	25	68.2	6	0	0	1053.61	310	318
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	2	2	4	0.00%	36.4%	AILVDLEPGTMDSVR	99.7%	110	25	103	42	1	0	1615.84	63	77
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	2	2	4	0.00%	36.4%	ALTVPELTQQMFDAK	99.7%	102	25	97.2	19	0	0	1691.87	283	297
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	2	2	4	0.00%	36.4%	EIVHIQAGQCGNQIGAK	99.7%	90.9	25	0	4	4	0	1822.92	3	19
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	2	2	4	0.00%	36.4%	EVDEQMLAIQSK	99.7%	80.2	25	66.7	2	0	0	1390.69	325	336
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	2	2	4	0.00%	36.4%	FPGQLNADLR	99.7%	59.9	25	46.5	17	0	0	1130.60	242	251
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	2	2	4	0.00%	36.4%	FPGQLNADLRK	99.7%	45.1	25	33.5	7	6	0	1258.69	242	252
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	2	2	4	0.00%	36.4%	GHYTEGAELVDSVLDVVR	99.7%	141	25	136	6	17	0	1958.98	104	121
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	2	2	4	0.00%	36.4%	GHYTEGAELVDSVLDVVRK	99.7%	61.4	25	60.1	0	4	0	2087.08	104	122
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	2	2	4	0.00%	36.4%	IMNTFSVVPSPK	99.7%	97.5	25	87.6	31	0	0	1319.70	163	174
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	2	2	4	0.00%	36.4%	ISEQFTAMFR	99.7%	86	25	81.7	30	0	0	1229.60	381	390

Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	2	2	4	0.00%	36.4%	KLAVNMVPFPR	99.7%	64.8	25	64.5	4	2	0	1271.73	252	262
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	2	2	4	0.00%	36.4%	LAVNMVPFPR	99.7%	90.9	25	72.4	38	0	0	1143.63	253	262
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	2	2	4	0.00%	36.4%	MREIVHIQAGQCGNQIGAK	99.7%	66.7	25	0	0	8	0	2110.06	1	19
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	2	2	4	0.00%	36.4%	MSSTFIGNSTAIQELFK	99.7%	105	25	0	2	0	0	1873.94	363	379
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	2	2	4	0.00%	36.4%	NMMAACDPR	99.7%	51.1	25	51.1	21	0	0	1065.43	298	306
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	2	2	4	0.00%	36.4%	NSSYFVEWIPNNVK	99.7%	80.5	25	67	20	0	0	1696.83	337	350
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	2	2	4	0.00%	36.4%	RISEQFTAMFR	99.7%	53.7	25	45.5	2	1	0	1385.70	380	390
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	5	17	0.02%	70.0%	ALTVPELTQQMFDAK	99.7%	102	25	97.2	19	0	0	1691.87	283	297
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	5	17	0.02%	70.0%	AVLVDLEPGTMDSVR	99.7%	98.2	25	76.3	19	0	0	1601.82	63	77
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	5	17	0.02%	70.0%	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	87.8	25	0	0	10	0	3311.53	123	154
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	5	17	0.02%	70.0%	EIVHLQAGQCGNQIGAK	99.7%	90.9	25	0	4	4	0	1822.92	3	19
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	5	17	0.02%	70.0%	EVDEQMLSVQSK	99.7%	83.9	25	77.4	2	0	0	1392.67	325	336
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	5	17	0.02%	70.0%	FPGQLNADLR	99.7%	59.9	25	46.5	17	0	0	1130.60	242	251
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	5	17	0.02%	70.0%	FPGQLNADLRK	99.7%	45.1	25	33.5	7	6	0	1258.69	242	252
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	5	17	0.02%	70.0%	FWEVISDEHGIDPTGTYHGDSDLQLER	99.7%	51.1	25	51.1	0	1	0	3116.42	20	46
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	5	17	0.02%	70.0%	IMNTFSVVPSPK	99.7%	97.5	25	87.6	31	0	0	1319.70	163	174
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	5	17	0.02%	70.0%	INVYYNEATGGNYVPR	99.7%	95.7	25	95.7	2	0	0	1829.88	47	62
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	5	17	0.02%	70.0%	IREEFPDR	98.5%	33.3	25	12	1	0	0	1061.54	155	162
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	5	17	0.02%	70.0%	ISEQFTAMFR	99.7%	86	25	81.7	30	0	0	1229.60	381	390
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	5	17	0.02%	70.0%	KLAVNMVPFPR	99.7%	64.8	25	64.5	4	2	0	1271.73	252	262
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	5	17	0.02%	70.0%	LAVNMVPFPR	99.7%	90.9	25	72.4	38	0	0	1143.63	253	262
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	5	17	0.02%	70.0%	LHFFMPGFAPLTSR	99.7%	58.3	25	44.8	34	28	0	1620.84	263	276
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	5	17	0.02%	70.0%	LTTPTYGDLNHLVSATMSGVTTCLR	99.7%	100	25	100	6	20	0	2708.34	217	241
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	5	17	0.02%	70.0%	MAATFIGNSTAIQELFK	99.7%	108	25	7.95	10	0	0	1857.94	363	379
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	5	17	0.02%	70.0%	MAATFIGNSTAIQELFKR	99.7%	70	25	0	2	0	0	2014.04	363	380
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	5	17	0.02%	70.0%	MREIVHLQAGQCGNQIGAK	99.7%	66.7	25	0	0	8	0	2110.06	1	19
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	5	17	0.02%	70.0%	NMMAACDPR	99.7%	51.1	25	51.1	21	0	0	1065.43	298	306
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	5	17	0.02%	70.0%	NSSYFVEWIPNNVK	99.7%	80.5	25	67	20	0	0	1696.83	337	350
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	5	17	0.02%	70.0%	RISEQFTAMFR	99.7%	53.7	25	45.5	2	1	0	1385.70	380	390
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	5	17	0.02%	70.0%	SGPFGQIFRPDNFVFGQSGAGNNWAK	99.7%	90.8	25	90.8	2	9	0	2798.34	78	103
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	5	17	0.02%	70.0%	TAVCDIPPR	99.7%	62.8	25	48.7	32	0	0	1028.52	351	359
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	5	5	17	0.02%	70.0%	YLTVAAVFR	99.7%	88.5	25	84.4	14	0	0	1039.59	310	318
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	ALTVPELTQQMFDAK	99.7%	102	25	97.2	19	0	0	1691.87	283	297
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	AVLVDLEPGTMDSVR	99.7%	98.2	25	76.3	19	0	0	1601.82	63	77
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	87.8	25	0	0	10	0	3311.53	123	154
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	EIVHLQAGQCGNQIGAK	99.7%	90.9	25	0	4	4	0	1822.92	3	19
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	EVDEQMLNVQNK	99.7%	80.5	25	68.2	22	0	0	1446.69	325	336
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	FPGQLNADLR	99.7%	59.9	25	46.5	17	0	0	1130.60	242	251
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	FPGQLNADLRK	99.7%	45.1	25	33.5	7	6	0	1258.69	242	252
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	FWEVISDEHGIDPTGTYHGDSDLQLER	99.7%	51.1	25	51.1	0	1	0	3116.42	20	46
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	GHYTEGAELVDSVLDVVR	99.7%	141	25	136	6	17	0	1958.98	104	121
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	GHYTEGAELVDSVLDVVRK	99.7%	61.4	25	60.1	0	4	0	2087.08	104	122
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	IMNTFSVVPSPK	99.7%	97.5	25	87.6	31	0	0	1319.70	163	174
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	INVYYNEATGGK	99.7%	83.1	25	63.6	10	0	0	1328.65	47	58
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	IREEYPDR	99.7%	45	25	31.6	7	0	0	1077.53	155	162
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	ISEQFTAMFR	99.7%	86	25	81.7	30	0	0	1229.60	381	390
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	KLAVNMVPFPR	99.7%	64.8	25	64.5	4	2	0	1271.73	252	262
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	LAVNMVPFPR	99.7%	90.9	25	72.4	38	0	0	1143.63	253	262
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	LHFFMPGFAPLTSR	99.7%	58.3	25	44.8	34	28	0	1620.84	263	276
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	LTTPTYGDLNHLVSATMSGVTTCLR	99.7%	100	25	100	6	20	0	2708.34	217	241
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	MREIVHLQAGQCGNQIGAK	99.7%	66.7	25	0	0	8	0	2110.06	1	19

Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	MSATFIGNSTAIQELFK	99.7%	125	25	0	7	0	0	1873.94	363	379
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	MSATFIGNSTAIQELFKR	99.7%	70	25	0	2	4	0	2014.04	363	380
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	MSMKEVDEQMLNVQNK	99.7%	60.8	25	2.72	7	17	0	1955.89	321	336
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	NMMAACDPR	99.7%	51.1	25	51.1	21	0	0	1065.43	298	306
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	NSSYFVEWIPNNVK	99.7%	80.5	25	67	20	0	0	1696.83	337	350
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	RISEQFTAMFR	99.7%	53.7	25	45.5	2	1	0	1385.70	380	390
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	SGPFGQIFRPDNFVFGQSGAGNNWAK	99.7%	90.8	25	90.8	2	9	0	2798.34	78	103
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	TAVCDIPPR	99.7%	62.8	25	48.7	32	0	0	1028.52	351	359
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	11	62	0.06%	74.2%	YLTVAAVFR	99.7%	88.5	25	84.4	14	0	0	1039.59	310	318
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	4	6	0.01%	33.2%	AALVDLEPGTMDSVR	99.7%	60.9	25	60.9	1	0	0	1573.79	63	77
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	4	6	0.01%	33.2%	ALTVPELTQQMFDAR	99.7%	55.8	25	55.8	2	0	0	1719.87	283	297
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	4	6	0.01%	33.2%	EVDEQMLAIQSK	99.7%	80.2	25	66.7	2	0	0	1390.69	325	336
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	4	6	0.01%	33.2%	FPGQLNADLR	99.7%	59.9	25	46.5	17	0	0	1130.60	242	251
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	4	6	0.01%	33.2%	FPGQLNADLRK	99.7%	45.1	25	33.5	7	6	0	1258.69	242	252
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	4	6	0.01%	33.2%	IMNTFSVMPSPK	99.7%	85.7	25	79.2	8	0	0	1351.67	163	174
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	4	6	0.01%	33.2%	IREEFPDR	98.5%	33.3	25	12	1	0	0	1061.54	155	162
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	4	6	0.01%	33.2%	ISEQFSAMFR	99.7%	74.8	25	65.4	2	0	0	1231.58	381	390
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	4	6	0.01%	33.2%	KLAVNMVPFPR	99.7%	64.8	25	64.5	4	2	0	1271.73	252	262
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	4	6	0.01%	33.2%	LAVNMVPFPR	99.7%	90.9	25	72.4	38	0	0	1143.63	253	262
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	4	6	0.01%	33.2%	LHFFMPGFAPLTSR	99.7%	58.3	25	44.8	34	28	0	1620.84	263	276
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	4	6	0.01%	33.2%	MASTFIGNSTAIQELFK	99.7%	125	25	0	9	0	0	1873.94	363	379
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	4	6	0.01%	33.2%	MASTFIGNSTAIQELFKR	99.7%	70	25	0	1	0	0	2014.04	363	380
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	4	6	0.01%	33.2%	NMMAACDPR	99.7%	51.1	25	51.1	21	0	0	1065.43	298	306
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	4	4	6	0.01%	33.2%	NSSYFVEWIPNNVK	99.7%	80.5	25	67	20	0	0	1696.83	337	350
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	6	6	11	0.01%	15.7%	AVLLDLEPR	99.7%	42.1	25	36.4	2	0	0	1025.60	64	72
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	6	6	11	0.01%	15.7%	DVFFYQADDEHYIPR	99.7%	62.9	25	62	1	0	0	1914.87	49	63
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	6	6	11	0.01%	15.7%	EAFLEQFR	99.7%	53.7	25	37	2	0	0	1039.52	402	409
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	6	6	11	0.01%	15.7%	KTTVLDVMR	99.7%	53.3	25	44.1	2	0	0	1062.60	287	295
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	6	6	11	0.01%	15.7%	LTQNADCVVVLDNTALNR	99.7%	133	25	133	2	0	0	2016.02	195	212
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	6	6	11	0.01%	15.7%	VIHSILNSPYAK	99.7%	55	25	50.3	2	0	0	1341.75	73	84
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	10	10	17	0.02%	9.6%	AASAAFQENVGR	99.7%	54.8	25	42.2	1	0	0	1220.60	509	520
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	10	10	17	0.02%	9.6%	AVTHTSPEDVSFAESR	99.7%	43.9	25	34	0	2	0	1732.81	800	815
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	10	10	17	0.02%	9.6%	DAAAVLVSR	99.7%	55.1	25	41	2	0	0	901.51	205	213
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	10	10	17	0.02%	9.6%	GACSVGTNVR	99.7%	42	25	21.8	2	0	0	1020.49	455	464
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	10	10	17	0.02%	9.6%	ILQIAESYLIVSDK	99.7%	64.4	25	58.1	1	0	0	1591.89	189	202
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	10	10	17	0.02%	9.6%	ITQLLGLPTYR	99.6%	39.3	25	39.3	2	0	0	1274.75	969	979
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	10	10	17	0.02%	9.6%	LDGNLLTQPGQAR	99.7%	48.2	25	41.8	2	0	0	1382.74	170	182
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	10	10	17	0.02%	9.6%	LPESNQTLLR	99.7%	56.7	25	36.7	1	0	0	1170.65	285	294
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	10	10	17	0.02%	9.6%	LQQVLTGLR	99.7%	69.7	25	44	2	0	0	1027.63	791	799
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	10	10	17	0.02%	9.6%	VIEQLLVGLK	99.7%	67.4	25	67.4	2	0	0	1111.71	361	370
Tyrosine-protein kinase CSK	CSK	CSK_HUMAN	50.7	100.0%	4	4	6	0.01%	10.9%	EASSTQDTGKLPVK	97.8%	31.6	25	17.2	1	0	0	1460.76	338	351
Tyrosine-protein kinase CSK	CSK	CSK_HUMAN	50.7	100.0%	4	4	6	0.01%	10.9%	GDVLTIVAVTK	99.7%	74.7	25	60	2	0	0	1115.67	33	43
Tyrosine-protein kinase CSK	CSK	CSK_HUMAN	50.7	100.0%	4	4	6	0.01%	10.9%	LLYPPETGLFLVR	99.5%	37.9	25	32.4	1	0	0	1517.87	95	107
Tyrosine-protein kinase CSK	CSK	CSK_HUMAN	50.7	100.0%	4	4	6	0.01%	10.9%	NVLVSEDNVAK	99.7%	43.7	25	36.8	2	0	0	1187.63	319	329
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	AFCEPGNVENNGVLSFIK	99.7%	75.2	25	71.5	2	0	0	1994.96	248	265
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	AMLESIGVPLEK	99.7%	70.7	25	56.6	4	0	0	1302.70	103	114
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	APWELLELR	99.7%	54.2	25	37.3	5	0	0	1126.63	85	93
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	DFAAEVVHPGDLK	99.7%	75.9	25	56.8	2	0	0	1397.71	298	310
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	EYTLDVYR	99.7%	53.3	25	46.4	2	0	0	1058.52	128	135
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	GQPDEELKPK	97.7%	31.4	25	28	1	0	0	1140.59	475	484
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	GTDYQLSK	99.2%	36	25	22.5	1	0	0	911.45	120	127

Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	GVESQGMLLCASIEGINR	99.7%	97.6	25	94	2	0	0	1949.94	433	450
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	HPDADSLYVEK	99.7%	54.4	25	45.5	2	0	0	1273.61	381	391
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	HVLFPLK	99.6%	39.7	25	32.9	2	0	0	853.53	266	272
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	IDVGEAEPR	99.7%	72.3	25	57.6	3	0	0	985.50	392	400
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	IITVEKHPDADSLYVEK	99.7%	36.1	25	36.1	0	1	0	1957.03	375	391
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	ISEECIAQWK	99.7%	64.1	25	59.2	2	0	0	1263.60	497	506
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	IYWGTATTGKPHVAYFVPMSK	99.7%	37.1	25	37.1	0	3	0	2354.20	38	58
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	KIFTFAEK	99.6%	38.9	25	24.6	2	0	0	983.56	190	197
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	KLASAAYPDPSK	99.7%	57.1	25	54.8	2	0	0	1247.66	335	346
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	LASAAYPDPSK	99.7%	76.7	25	64.5	2	0	0	1119.57	336	346
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	LLDPIREK	95.1%	28.3	25	10.6	1	0	0	983.59	320	327
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	LSSVVTQHDSK	99.7%	68.6	25	68.6	3	0	0	1200.62	136	146
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	LSSVVTQHDSKK	99.7%	68.2	25	68	2	0	0	1328.72	136	147
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	LVVVLCNLKPQK	99.7%	56	25	56	2	0	0	1410.85	419	430
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	MSSSEEESKIDLLDR	99.7%	66.8	25	66.1	2	1	0	1754.81	223	237
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	NLQEVLGEEK	99.7%	49.1	25	40.7	2	0	0	1158.60	17	26
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	NSEPEEVIPSR	99.7%	62.2	25	51.7	2	0	0	1256.61	357	367
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	NSVEVALNK	99.7%	67.6	25	51.1	2	0	0	973.53	311	319
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	QVEPLDPPAGSAPGEHVFVK	99.7%	41.6	25	41.6	0	2	0	2074.06	451	470
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	RVHLMNPMVPGLTGSK	97.9%	26.2	25	26.1	0	1	0	1768.92	207	222
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	SEFVILR	99.2%	35.8	25	29.7	2	0	0	863.50	273	279
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	SEFVILRDEK	99.7%	43.2	25	30.2	2	0	0	1235.66	273	282
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	TVVSGLVQFVPK	99.7%	80.8	25	65.8	2	0	0	1273.75	401	412
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	TYTAYVDLEK	99.7%	56.5	25	49.2	2	0	0	1202.59	288	297
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	VDAQFGGIDQR	99.7%	77.6	25	68.6	2	0	0	1205.59	179	189
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	VHLMNPMVPGLTGSK	99.7%	63.6	25	32.3	2	0	0	1596.82	208	222
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	VSYYENVIK	99.7%	56.2	25	50.8	4	0	0	1114.58	94	102
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	35	38	76	0.07%	67.0%	YLPALGYSK	98.3%	32.7	25	19	2	0	0	1011.55	198	206
U1 small nuclear ribonucleoprotein 70 kDa	SNRNP70	RU17_HUMAN	51.6	100.0%	2	2	4	0.00%	4.1%	DPIPYLPPLEK	99.7%	44.2	25	20.8	2	0	0	1281.71	17	27
U1 small nuclear ribonucleoprotein 70 kDa	SNRNP70	RU17_HUMAN	51.6	100.0%	2	2	4	0.00%	4.1%	VLVDVER	97.1%	30.4	25	11.2	2	0	0	829.48	174	180
U1 small nuclear ribonucleoprotein A	SNRPA	SNRPA_HUMAN	31.3	100.0%	6	6	9	0.01%	24.5%	AVQGGGATPVVGAVQGPVPGMPPMTQAPR	99.7%	40.2	25	40.2	0	1	0	2759.40	124	152
U1 small nuclear ribonucleoprotein A	SNRPA	SNRPA_HUMAN	31.3	100.0%	6	6	9	0.01%	24.5%	EVSSATNALR	99.7%	62.4	25	40.6	2	0	0	1047.54	61	70
U1 small nuclear ribonucleoprotein A	SNRPA	SNRPA_HUMAN	31.3	100.0%	6	6	9	0.01%	24.5%	GQAFVIFK	99.7%	52.4	25	43.1	2	0	0	909.52	53	60
U1 small nuclear ribonucleoprotein A	SNRPA	SNRPA_HUMAN	31.3	100.0%	6	6	9	0.01%	24.5%	KAVQGGGATPVVGAVQGPVPGMPPMTQAPR	99.7%	44.7	25	44.3	0	2	0	2887.49	123	152
U1 small nuclear ribonucleoprotein A	SNRPA	SNRPA_HUMAN	31.3	100.0%	6	6	9	0.01%	24.5%	SMQGFPFYDKPMR	99.7%	40.7	25	34.9	1	0	0	1603.74	71	83
U1 small nuclear ribonucleoprotein A	SNRPA	SNRPA_HUMAN	31.3	100.0%	6	6	9	0.01%	24.5%	TDSDIIAK	97.0%	30.4	25	18.8	1	0	0	862.45	89	96
U1 small nuclear ribonucleoprotein C	SNRPC	RU1C_HUMAN	17.4	99.8%	2	2	4	0.00%	18.9%	FYCDYCDTYLTHDSPSVR	99.4%	31.4	25	31.4	0	2	0	2298.94	4	21
U1 small nuclear ribonucleoprotein C	SNRPC	RU1C_HUMAN	17.4	99.8%	2	2	4	0.00%	18.9%	WMEEQAQSLIDK	99.7%	71.8	25	68.3	2	0	0	1477.70	41	52
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	7	7	12	0.01%	28.2%	GLLQSGQIPGR	99.7%	79.6	25	36.5	2	0	0	1125.64	222	232
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	7	7	12	0.01%	28.2%	KLDGFPLLR	99.1%	35.6	25	20.8	1	0	0	1058.64	56	64
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	7	7	12	0.01%	28.2%	LDGFPLLR	94.8%	28.1	25	16.4	1	0	0	930.54	57	64
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	7	7	12	0.01%	28.2%	LTAELIEQAAQYTNAVR	99.7%	68.2	25	64.3	2	0	0	1890.99	4	20
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	7	7	12	0.01%	28.2%	NAIANASTLAEVER	99.7%	94.5	25	93.3	2	0	0	1458.75	206	219
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	7	7	12	0.01%	28.2%	SLTYLSILR	99.7%	49.7	25	44.3	2	0	0	1065.63	114	122
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	7	7	12	0.01%	28.2%	TFNPGAGLPTDK	99.7%	58.5	25	53.2	2	0	0	1217.62	180	191
U2 snRNP-associated SURP motif-containing protein	U2SURP	SR140_HUMAN	118.3	99.8%	2	2	3	0.00%	2.5%	LYLVSDVLYNSSAK	99.7%	71.7	25	67	2	0	0	1571.83	595	608
U2 snRNP-associated SURP motif-containing protein	U2SURP	SR140_HUMAN	118.3	99.8%	2	2	3	0.00%	2.5%	LYSILQGDSPTK	99.7%	65.5	25	52.8	1	0	0	1321.70	477	488
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	16	23	53	0.05%	37.1%	ASEVMGPVEAAPEYR	99.7%	98.5	25	95.8	6	0	0	1605.76	77	91
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	16	23	53	0.05%	37.1%	IEEYISK	99.7%	45.3	25	36.1	2	0	0	881.46	67	73
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	16	23	53	0.05%	37.1%	IMGVAGGLTNLSK	99.7%	90	25	73.9	4	0	0	1260.70	231	243
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	16	23	53	0.05%	37.1%	IYEYVESR	99.7%	48.1	25	41	2	0	0	1058.52	204	211

U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	16	23	53	0.05%	37.1%	LEEACDMALELNASK	99.7%	107	25	106	3	0	0	1709.77	187	201
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	16	23	53	0.05%	37.1%	LGLTEIR	99.7%	53.6	25	13.8	2	0	0	801.48	366	372
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	16	23	53	0.05%	37.1%	LGLTEIRK	99.7%	66.5	25	57.1	4	0	0	929.58	366	373
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	16	23	53	0.05%	37.1%	MFAEIMMK	99.3%	36.7	25	33.5	2	0	0	1032.46	59	66
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	16	23	53	0.05%	37.1%	MPACNIMLLGAQR	99.7%	81.4	25	67.3	6	0	0	1490.73	244	256
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	16	23	53	0.05%	37.1%	MSFIAPNLSIIIGASTAAK	99.7%	50.9	25	50.9	2	0	0	1905.05	212	230
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	16	23	53	0.05%	37.1%	QVKPLPAPLDGQR	99.7%	33.8	25	33.8	1	2	0	1418.81	339	351
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	16	23	53	0.05%	37.1%	SSGTASSVAFTPLQGLEIVNPQAAEK	99.7%	72.5	25	72.5	2	2	0	2602.34	445	470
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	16	23	53	0.05%	37.1%	VDSFHESTEGK	99.7%	70.9	25	70.9	5	0	0	1235.55	305	315
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	16	23	53	0.05%	37.1%	VGYELKDEIER	99.7%	64.1	25	50.5	2	2	0	1350.69	316	326
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	16	23	53	0.05%	37.1%	WQEPPPVK	94.5%	28	25	13.6	1	0	0	980.52	331	338
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	16	23	53	0.05%	37.1%	YFSSMAEFLK	99.7%	60.2	25	54.4	3	0	0	1238.58	479	488
U4/U6.U5 tri-snRNP-associated protein 1	SART1	SNUT1_HUMAN	90.3	100.0%	5	5	7	0.01%	9.3%	DLQGLTVEHAIDSFR	99.7%	49.2	25	44	1	0	0	1700.86	253	267
U4/U6.U5 tri-snRNP-associated protein 1	SART1	SNUT1_HUMAN	90.3	100.0%	5	5	7	0.01%	9.3%	EAAGTTAAAGTGGATEQPPR	99.7%	87.4	25	87.4	1	0	0	1813.87	12	31
U4/U6.U5 tri-snRNP-associated protein 1	SART1	SNUT1_HUMAN	90.3	100.0%	5	5	7	0.01%	9.3%	LEQGGTADGLR	99.4%	37	25	29	1	0	0	1116.56	351	361
U4/U6.U5 tri-snRNP-associated protein 1	SART1	SNUT1_HUMAN	90.3	100.0%	5	5	7	0.01%	9.3%	LQAQSLSTVGPR	99.7%	80.6	25	76.3	3	0	0	1256.70	374	385
U4/U6.U5 tri-snRNP-associated protein 1	SART1	SNUT1_HUMAN	90.3	100.0%	5	5	7	0.01%	9.3%	TSSGDASSLSIEETNK	99.7%	71	25	69.5	1	0	0	1625.75	110	125
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	AALETDENLLLCAPTGAGK	99.7%	117	25	102	2	0	0	1943.97	491	509
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	ANSNLVLQADR	99.7%	73.8	25	52.8	2	0	0	1200.63	15	25
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	DEPTGEVLSLVGK	99.7%	88.1	25	76.6	2	0	0	1343.71	34	46
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	DIDAFWLQR	99.7%	64.4	25	51.2	2	0	0	1163.58	262	270
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	DILCGAADEVLAVLK	99.7%	62.8	25	49.7	1	0	0	1586.85	130	144
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	DTLGLFLR	99.7%	48.9	25	28.2	1	0	0	934.54	746	753
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	EEEKLELQK	97.7%	31.3	25	20.5	1	0	0	1145.61	1031	1039
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	EEEVTGPVIAPLFPQK	99.7%	55	25	47.3	2	0	0	1753.94	2044	2059
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	EEGWWVVIGDAK	99.7%	52.3	25	37.3	2	0	0	1388.68	2061	2072
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	EGSASTEVLR	99.7%	51.1	25	38	2	0	0	1048.53	754	763
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	FQIMNEIVYEK	99.7%	72.4	25	58.2	4	0	0	1413.71	701	711
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	FYDDAIVSQK	99.7%	63.6	25	54.3	2	0	0	1185.58	275	284
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	GTQVYSPEK	98.3%	32.7	25	29.4	1	0	0	1008.50	830	838
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	GWAQLTDK	95.4%	28.6	25	23.7	1	0	0	918.47	1103	1110
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	HLILPEK	96.0%	29.2	25	13.9	1	0	0	849.52	1288	1294
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	IIYIAPMR	99.5%	38.5	25	31.2	4	0	0	976.56	538	545
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	IVALSSSLSNAK	99.7%	107	25	100	2	0	0	1189.68	1487	1498
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	KADEVLEILK	99.7%	68.6	25	52.9	2	0	0	1157.68	285	294
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	KPVIVFVPSR	99.7%	56.4	25	54.1	2	0	0	1141.71	1557	1566
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	LIGLSATLPNYEDVATFLR	97.5%	31	25	31	1	0	0	2093.13	648	666
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	LTAIDILTTCAADIQR	99.7%	108	25	105	2	0	0	1774.94	1571	1586
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	LYDLNHNEIGELIR	99.7%	59.2	25	51	1	2	0	1698.88	1153	1166
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	MTQNPNYYNLQGISHR	99.7%	41.6	25	41.6	0	4	0	1951.91	1764	1779
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	NALLQLTDSQIADVAR	99.7%	116	25	112	2	0	0	1727.93	1994	2009
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	NIEMTQEDVR	99.7%	69.2	25	63	3	0	0	1234.57	638	647
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	NQVLVFVHSR	99.7%	67.6	25	63.9	2	0	0	1198.67	719	728
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	SLVQEMVGSFGK	99.7%	89.9	25	85.6	4	0	0	1281.65	546	557
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	SPTLYGISHDDLK	99.7%	53.3	25	48.1	2	0	0	1445.73	932	944
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	TGNFQVTELGR	99.7%	69.5	25	64.4	2	0	0	1221.62	976	986
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	TNLLLQAHLSR	99.7%	62.6	25	56.3	2	0	0	1265.73	1891	1901
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	TYTQLVR	94.6%	28	25	12.5	1	0	0	880.49	604	610
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	VELTITPDFQWDEK	99.7%	60.1	25	52.2	2	0	0	1720.84	1200	1213
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	VFSLSSEFK	98.9%	34.6	25	27	2	0	0	1043.54	1017	1025
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	VPIPVKESIEEPSAK	98.5%	27.4	25	27.1	0	1	0	1622.90	1044	1058

U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	VVLLTGETSTDLK	99.7%	96.3	25	92.2	2	0	0	1375.77	1405	1417
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	WLSCETQLPVSFR	99.7%	71.2	25	63.1	2	0	0	1622.80	1275	1287
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	37	43	75	0.07%	20.4%	YAQAGFEGFK	99.7%	66.1	25	60.6	2	0	0	1117.53	470	479
U5 small nuclear ribonucleoprotein 40 kDa protein	SNRNP40	SNR40_HUMAN	39.3	100.0%	8	8	15	0.01%	23.2%	FVYVWDTTSR	99.7%	68.7	25	62.9	4	0	0	1273.62	308	317
U5 small nuclear ribonucleoprotein 40 kDa protein	SNRNP40	SNR40_HUMAN	39.3	100.0%	8	8	15	0.01%	23.2%	GHTSFVNSCYPAR	99.7%	63.3	25	63.3	1	0	0	1495.67	149	161
U5 small nuclear ribonucleoprotein 40 kDa protein	SNRNP40	SNR40_HUMAN	39.3	100.0%	8	8	15	0.01%	23.2%	GPQLVCTGSDDGTVK	99.7%	60.5	25	60.5	1	0	0	1533.72	163	177
U5 small nuclear ribonucleoprotein 40 kDa protein	SNRNP40	SNR40_HUMAN	39.3	100.0%	8	8	15	0.01%	23.2%	IFQGNVHNFEK	99.7%	66	25	55	3	0	0	1332.67	276	286
U5 small nuclear ribonucleoprotein 40 kDa protein	SNRNP40	SNR40_HUMAN	39.3	100.0%	8	8	15	0.01%	23.2%	KGPELPLVPVK	97.4%	30.9	25	28	1	0	0	1176.74	8	18
U5 small nuclear ribonucleoprotein 40 kDa protein	SNRNP40	SNR40_HUMAN	39.3	100.0%	8	8	15	0.01%	23.2%	RGPQLVCTGSDDGTVK	98.5%	33.2	25	30.2	1	0	0	1689.82	162	177
U5 small nuclear ribonucleoprotein 40 kDa protein	SNRNP40	SNR40_HUMAN	39.3	100.0%	8	8	15	0.01%	23.2%	TVAVWDSETGER	99.7%	52.7	25	50.3	3	0	0	1349.63	132	143
U5 small nuclear ribonucleoprotein 40 kDa protein	SNRNP40	SNR40_HUMAN	39.3	100.0%	8	8	15	0.01%	23.2%	VWDVRPFAPK	97.5%	31	25	24.2	1	0	0	1214.67	261	270
UAP56-interacting factor	FYTTD1	UIF_HUMAN	35.8	100.0%	4	4	6	0.01%	16.7%	GVPLQFDINSVGK	99.7%	48.5	25	46.2	2	0	0	1373.74	273	285
UAP56-interacting factor	FYTTD1	UIF_HUMAN	35.8	100.0%	4	4	6	0.01%	16.7%	LVGATATSSPPPK	97.6%	31.3	25	25.4	1	0	0	1225.68	8	20
UAP56-interacting factor	FYTTD1	UIF_HUMAN	35.8	100.0%	4	4	6	0.01%	16.7%	NIEQYFPVLK	99.6%	38.8	25	32	1	0	0	1250.68	129	138
UAP56-interacting factor	FYTTD1	UIF_HUMAN	35.8	100.0%	4	4	6	0.01%	16.7%	VQAQLNTEQLLDDVVAK	99.7%	107	25	103	2	0	0	1884.01	199	215
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	4	4	6	0.01%	2.1%	LEAASSALGGPTLTHAVTR	99.4%	31.5	25	23.9	0	2	0	1851.99	877	895
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	4	4	6	0.01%	2.1%	SSQLNNPQFVWVVPALR	97.0%	30.3	25	30.3	1	0	0	1955.05	621	637
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	4	4	6	0.01%	2.1%	VAVATILEK	98.7%	33.8	25	32.4	2	0	0	943.58	2236	2244
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	4	4	6	0.01%	2.1%	VLYNLEVLSSK	99.7%	71.8	25	68.7	1	0	0	1264.71	1174	1184
Ubiquitin conjugation factor E4 B	UBE4B	UBE4B_HUMAN	146.2	99.8%	2	2	2	0.00%	1.4%	ELFEEVISK	99.7%	47	25	35.1	1	0	0	1093.58	1181	1189
Ubiquitin conjugation factor E4 B	UBE4B	UBE4B_HUMAN	146.2	99.8%	2	2	2	0.00%	1.4%	ITLPNDETR	98.4%	32.8	25	29.7	1	0	0	1058.55	718	726
Ubiquitin thioesterase OTUB1	OTUB1	OTUB1_HUMAN	31.3	100.0%	5	6	10	0.01%	21.4%	EFCQQEVEPMCK	99.7%	41.9	25	41.9	1	0	0	1584.65	202	213
Ubiquitin thioesterase OTUB1	OTUB1	OTUB1_HUMAN	31.3	100.0%	5	6	10	0.01%	21.4%	EYAEDDNIYQQK	99.7%	62.6	25	62.6	2	0	0	1515.66	60	71
Ubiquitin thioesterase OTUB1	OTUB1	OTUB1_HUMAN	31.3	100.0%	5	6	10	0.01%	21.4%	FFEHFIEGGR	99.7%	62	25	48.1	2	1	0	1238.60	189	198
Ubiquitin thioesterase OTUB1	OTUB1	OTUB1_HUMAN	31.3	100.0%	5	6	10	0.01%	21.4%	IQQEIAVQNPLVSER	99.7%	95.9	25	86.4	2	0	0	1723.93	37	51
Ubiquitin thioesterase OTUB1	OTUB1	OTUB1_HUMAN	31.3	100.0%	5	6	10	0.01%	21.4%	LLTSGYLQR	99.7%	63	25	49	2	0	0	1050.59	177	185
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	9	79	0.08%	56.4%	CCLTYCFNKPEDK	99.7%	59.2	25	59.2	4	0	0	1734.73	144	156
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	9	79	0.08%	56.4%	ECPSDECGAGVFMASHFDR	99.7%	59.1	25	58	8	3	0	2187.85	120	138
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	9	79	0.08%	56.4%	ESTLHLVLR	99.7%	71.1	25	49.8	11	0	0	1067.62	64	72
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	9	79	0.08%	56.4%	IQDKEGIPPDQQR	99.7%	58.1	25	58.1	8	0	0	1523.78	30	42
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	9	79	0.08%	56.4%	TITLEVEPSDTIENVK	99.7%	104	25	99.6	24	0	0	1787.93	12	27
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	9	79	0.08%	56.4%	TLSDYNIQK	99.7%	61.7	25	44.9	17	0	0	1081.55	55	63
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	9	79	0.08%	56.4%	YYKVDENGK	99.6%	39.7	25	30.6	4	0	0	1115.54	105	113
Ubiquitin-conjugating enzyme E2 O	UBE2O	UBE2O_HUMAN	141.3	100.0%	2	2	3	0.00%	1.9%	GLQEGYENSR	99.7%	40.3	25	33.8	2	0	0	1152.53	1089	1098
Ubiquitin-conjugating enzyme E2 O	UBE2O	UBE2O_HUMAN	141.3	100.0%	2	2	3	0.00%	1.9%	LIGTNCIIYPVNSK	98.0%	31.9	25	21.5	1	0	0	1591.85	177	190
Ubiquitin-like modifier-activating enzyme 1	UBA1	UBA1_HUMAN	117.9	100.0%	4	4	5	0.00%	6.2%	AAVATFLQSVQVPEFTPK	97.0%	30.4	25	30.4	1	0	0	1933.04	785	802
Ubiquitin-like modifier-activating enzyme 1	UBA1	UBA1_HUMAN	117.9	100.0%	4	4	5	0.00%	6.2%	LQTSSVLVSGLR	99.4%	37.7	25	36.5	1	0	0	1259.73	70	81
Ubiquitin-like modifier-activating enzyme 1	UBA1	UBA1_HUMAN	117.9	100.0%	4	4	5	0.00%	6.2%	NEEDAAELVALAQAVNAR	99.7%	78.8	25	75.4	1	0	0	1883.95	351	368
Ubiquitin-like modifier-activating enzyme 1	UBA1	UBA1_HUMAN	117.9	100.0%	4	4	5	0.00%	6.2%	SLVASLAEPDFVVTDFAK	99.7%	66.6	25	66.6	2	0	0	1909.00	305	322
Ubiquitin-protein ligase E3A	UBE3A	UBE3A_HUMAN	100.7	100.0%	4	4	6	0.01%	5.5%	EFVNLYSDYILNK	99.7%	74.9	25	65.9	2	0	0	1617.82	712	724
Ubiquitin-protein ligase E3A	UBE3A	UBE3A_HUMAN	100.7	100.0%	4	4	6	0.01%	5.5%	IGDSSQGDNNLQK	99.7%	50.3	25	46.6	1	0	0	1375.65	214	226
Ubiquitin-protein ligase E3A	UBE3A	UBE3A_HUMAN	100.7	100.0%	4	4	6	0.01%	5.5%	VFSSAEALVQSFR	99.7%	63.3	25	56	2	0	0	1440.75	156	168
Ubiquitin-protein ligase E3A	UBE3A	UBE3A_HUMAN	100.7	100.0%	4	4	6	0.01%	5.5%	VYEILELCR	99.7%	47	25	34.7	1	0	0	1194.62	133	141
Ubiquitin-protein ligase E3C	UBE3C	UBE3C_HUMAN	123.9	100.0%	4	4	7	0.01%	3.9%	LPEFYDETLLR	99.7%	44.9	25	41.2	2	0	0	1395.72	1057	1067
Ubiquitin-protein ligase E3C	UBE3C	UBE3C_HUMAN	123.9	100.0%	4	4	7	0.01%	3.9%	NAIIIQSFIR	99.7%	51.4	25	44.8	2	0	0	1174.69	48	57
Ubiquitin-protein ligase E3C	UBE3C	UBE3C_HUMAN	123.9	100.0%	4	4	7	0.01%	3.9%	SGFNPNQGFFK	95.6%	28.8	25	26	1	0	0	1242.59	783	793
Ubiquitin-protein ligase E3C	UBE3C	UBE3C_HUMAN	123.9	100.0%	4	4	7	0.01%	3.9%	VTQLYVPASR	99.7%	53.9	25	53	2	0	0	1133.63	639	648
UDP-glucose 6-dehydrogenase	UGDH	UGDH_HUMAN	55.0	100.0%	3	3	3	0.00%	7.1%	ASVGFGGSCFQK	98.7%	33.7	25	33.6	1	0	0	1244.57	268	279
UDP-glucose 6-dehydrogenase	UGDH	UGDH_HUMAN	55.0	100.0%	3	3	3	0.00%	7.1%	VLIGGDETPEGQR	99.7%	40.5	25	36.7	1	0	0	1370.69	178	190
UDP-glucose 6-dehydrogenase	UGDH	UGDH_HUMAN	55.0	100.0%	3	3	3	0.00%	7.1%	VTVVDVNESR	99.7%	40.6	25	36.9	1	0	0	1117.58	32	41
UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	OGT	OGT1_HUMAN	116.9	99.8%	2	2	2	0.00%	1.8%	AATGEEVPR	99.7%	43.4	25	23.4	1	0	0	929.47	817	825

UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	OGT	OGT1_HUMAN	116.9	99.8%	2	2	2	0.00%	1.8%	EQGNIEEAVR	98.9%	34.6	25	25.5	1	0	0	1144.56	339	348
Uncharacterized protein C11orf84	C11orf84	CK084_HUMAN	41.0	100.0%	3	3	4	0.00%	8.7%	AESPSPAPPPGLR	99.7%	65	25	50.4	1	0	0	1275.67	306	318
Uncharacterized protein C11orf84	C11orf84	CK084_HUMAN	41.0	100.0%	3	3	4	0.00%	8.7%	DREVAEGGLPR	99.6%	39.1	25	30.5	1	0	0	1198.62	295	305
Uncharacterized protein C11orf84	C11orf84	CK084_HUMAN	41.0	100.0%	3	3	4	0.00%	8.7%	GTLDLQVIR	99.1%	35.3	25	29	2	0	0	1014.59	319	327
Uncharacterized protein C2orf47, mitochondrial	C2orf47	CB047_HUMAN	32.5	100.0%	3	3	5	0.00%	12.0%	EFTQGVKPDWTIAR	98.4%	33	25	26.2	1	0	0	1647.85	270	283
Uncharacterized protein C2orf47, mitochondrial	C2orf47	CB047_HUMAN	32.5	100.0%	3	3	5	0.00%	12.0%	FDLLEELVAK	99.7%	57.6	25	48.7	2	0	0	1176.65	164	173
Uncharacterized protein C2orf47, mitochondrial	C2orf47	CB047_HUMAN	32.5	100.0%	3	3	5	0.00%	12.0%	QLLSASYEFQR	99.7%	61.8	25	60.3	2	0	0	1341.68	259	269
Uncharacterized protein C7orf50	C7orf50	CG050_HUMAN	22.1	100.0%	3	3	4	0.00%	23.7%	ASAEGPLLGPEAAPSGEGAGSK	99.7%	55.7	25	55.7	2	0	0	1952.96	22	43
Uncharacterized protein C7orf50	C7orf50	CG050_HUMAN	22.1	100.0%	3	3	4	0.00%	23.7%	EAGLVAQHPPAR	99.3%	36.9	25	31	1	0	0	1245.67	84	95
Uncharacterized protein C7orf50	C7orf50	CG050_HUMAN	22.1	100.0%	3	3	4	0.00%	23.7%	SGAELALDYLCR	99.7%	59.6	25	52.8	1	0	0	1367.66	97	108
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	5	5	9	0.01%	5.8%	EQLLQSNPVLEAFGNAK	99.7%	102	25	99.8	2	0	0	1857.97	140	156
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	5	5	9	0.01%	5.8%	IFLLTNNNLLLADQK	99.7%	73.7	25	73.7	2	0	0	1729.98	1007	1021
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	5	5	9	0.01%	5.8%	IIIAEVVNK	99.7%	51.5	25	38.4	2	0	0	998.62	987	995
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	5	5	9	0.01%	5.8%	SSALVIQSYIR	99.7%	71.6	25	54.2	1	0	0	1236.69	752	762
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	5	5	9	0.01%	5.8%	VSTTLNVAQAYYAR	99.7%	75.1	25	69.3	2	0	0	1556.81	336	349
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	11	11	18	0.02%	13.5%	DGTIDFTPGSELLITK	99.7%	67	25	64.7	2	0	0	1706.89	1032	1047
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	11	11	18	0.02%	13.5%	GEELLSPLNLEQAAYAR	99.7%	86.9	25	77.6	1	0	0	1873.97	362	378
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	11	11	18	0.02%	13.5%	KYEAFLQR	98.4%	33	25	28.9	1	0	0	1054.57	667	674
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	11	11	18	0.02%	13.5%	LGTDEISPR	99.7%	83.2	25	64.7	2	0	0	987.51	901	909
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	11	11	18	0.02%	13.5%	LLQFYAETCPAPER	99.7%	67.7	25	58.9	2	0	0	1694.82	153	166
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	11	11	18	0.02%	13.5%	LLQSNPVLEAFGNAK	99.7%	78.1	25	78.1	2	0	0	1600.87	174	188
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	11	11	18	0.02%	13.5%	NPQSYLYLVK	97.0%	30.3	25	26.7	1	0	0	1224.66	260	269
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	11	11	18	0.02%	13.5%	TSFLLNLR	99.7%	62	25	58.3	2	0	0	963.56	814	821
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	11	11	18	0.02%	13.5%	VLQALGSEPIQYAVPVVK	99.7%	76.8	25	70.7	2	0	0	1911.10	910	927
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	11	11	18	0.02%	13.5%	VNSININQGSITFAGGPGR	99.7%	77.5	25	77.5	1	0	0	1901.98	1013	1031
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	11	11	18	0.02%	13.5%	YLGLLENLR	99.7%	54.2	25	50.7	2	0	0	1090.63	648	656
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	3	3	4	0.00%	3.0%	IGELVGVLVNHFK	99.7%	51.6	25	45.6	2	0	0	1424.83	942	954
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	3	3	4	0.00%	3.0%	NYDTTIHGK	96.2%	29.3	25	24.6	1	0	0	1048.51	367	375
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	3	3	4	0.00%	3.0%	SYIHEVAR	99.1%	35.4	25	28.9	1	0	0	974.51	738	745
Unconventional myosin-IXb	MYO9B	MYO9B_HUMAN	243.4	100.0%	2	2	2	0.00%	1.3%	ELIGMDPVAVFR	95.7%	28.9	25	28.9	1	0	0	1346.71	673	684
Unconventional myosin-IXb	MYO9B	MYO9B_HUMAN	243.4	100.0%	2	2	2	0.00%	1.3%	TILGAGPVLEAFGNAK	96.4%	29.5	25	23.5	1	0	0	1557.86	271	286
Unhealthy ribosome biogenesis protein 2 homolog	URB2	URB2_HUMAN	170.5	100.0%	4	4	5	0.00%	3.2%	ADVQAVVSAVTLLR	99.7%	42.4	25	7.58	1	0	0	1441.84	1262	1275
Unhealthy ribosome biogenesis protein 2 homolog	URB2	URB2_HUMAN	170.5	100.0%	4	4	5	0.00%	3.2%	EGLLDQQQGDVK	99.7%	49.6	25	45.4	1	0	0	1329.66	256	267
Unhealthy ribosome biogenesis protein 2 homolog	URB2	URB2_HUMAN	170.5	100.0%	4	4	5	0.00%	3.2%	GEIAQNLLSLVK	98.2%	32.5	25	24.2	1	0	0	1284.75	868	879
Unhealthy ribosome biogenesis protein 2 homolog	URB2	URB2_HUMAN	170.5	100.0%	4	4	5	0.00%	3.2%	VAEFSLSGSQR	99.7%	70.7	25	64.7	2	0	0	1180.60	107	117
UPF0444 transmembrane protein C12orf23	C12orf23	CL023_HUMAN	11.7	100.0%	2	2	3	0.00%	25.9%	GGVSAVAGGVTAVGSAVVNK	99.7%	83.1	25	83.1	2	0	0	1699.93	85	104
UPF0444 transmembrane protein C12orf23	C12orf23	CL023_HUMAN	11.7	100.0%	2	2	3	0.00%	25.9%	VTGGIFSVTK	98.8%	34.2	25	34.2	1	0	0	1008.57	38	47
UPF0488 protein C8orf33	C8orf33	CH033_HUMAN	25.0	100.0%	4	4	6	0.01%	21.0%	AAAYSAQVQPVDGATR	99.7%	80.6	25	70.4	2	0	0	1604.80	183	198
UPF0488 protein C8orf33	C8orf33	CH033_HUMAN	25.0	100.0%	4	4	6	0.01%	21.0%	AHPLGDEGGTASK	96.5%	29.7	25	29.7	1	0	0	1239.60	57	69
UPF0488 protein C8orf33	C8orf33	CH033_HUMAN	25.0	100.0%	4	4	6	0.01%	21.0%	LPGPVSSAR	99.7%	58	25	30.6	2	0	0	883.50	28	36
UPF0488 protein C8orf33	C8orf33	CH033_HUMAN	25.0	100.0%	4	4	6	0.01%	21.0%	QKEQAIGAIR	95.1%	28.3	25	19.8	1	0	0	1113.64	134	143
UPF0553 protein C9orf64	C9orf64	CI064_HUMAN	39.0	100.0%	3	3	3	0.00%	10.0%	AQILVADTWSVLEGK	97.7%	31.5	25	31.5	1	0	0	1629.88	209	223
UPF0553 protein C9orf64	C9orf64	CI064_HUMAN	39.0	100.0%	3	3	3	0.00%	10.0%	DVFIDSGGVR	96.2%	29.4	25	13.1	1	0	0	1064.54	20	29
UPF0553 protein C9orf64	C9orf64	CI064_HUMAN	39.0	100.0%	3	3	3	0.00%	10.0%	DVTLFEGKR	96.9%	30.2	25	26	1	0	0	1064.57	194	202
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	10	10	16	0.02%	19.8%	AAWEAYLSR	99.7%	48.2	25	24.6	2	0	0	1066.53	469	477
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	10	10	16	0.02%	19.8%	FADIGNTVK	98.1%	32.2	25	20.5	1	0	0	964.51	315	323
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	10	10	16	0.02%	19.8%	FGDFVLK	98.9%	34.5	25	24	2	0	0	825.45	23	29
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	10	10	16	0.02%	19.8%	IASWADLVNAHVVPGSGVVK	99.7%	40.7	25	40.7	0	1	0	2019.10	333	352
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	10	10	16	0.02%	19.8%	KFADIGNTVK	99.7%	50.9	25	45.3	1	0	0	1092.60	314	323
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	10	10	16	0.02%	19.8%	KVDAETVGR	99.7%	65.9	25	53.8	2	0	0	974.53	188	196
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	10	10	16	0.02%	19.8%	LHSVCTLSK	98.2%	32.5	25	25.3	1	0	0	1044.55	170	178

Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	10	10	16	0.02%	19.8%	MLEILEQQK	99.7%	44.3	25	36.3	2	0	0	1131.61	179	187
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	10	10	16	0.02%	19.8%	SGLSSPIYIDLR	99.7%	51.6	25	36	2	0	0	1320.72	30	41
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	10	10	16	0.02%	19.8%	VTDAIVLLDR	99.7%	101	25	72.7	2	0	0	1114.65	146	155
Uridine-cytidine kinase 2	UCK2	UCK2_HUMAN	29.3	99.8%	2	2	4	0.00%	8.4%	TVQIPVYDFVSHSR	99.7%	48.3	25	38.2	2	0	0	1647.85	106	119
Uridine-cytidine kinase 2	UCK2	UCK2_HUMAN	29.3	99.8%	2	2	4	0.00%	8.4%	YADVIIPR	99.6%	39.5	25	39.5	2	0	0	946.54	203	210
Uridine-cytidine kinase-like 1	UCKL1	UCKL1_HUMAN	61.1	100.0%	3	3	3	0.00%	5.8%	EAFAIGLGGGSASGK	99.7%	67.5	25	59	1	0	0	1321.67	97	111
Uridine-cytidine kinase-like 1	UCKL1	UCKL1_HUMAN	61.1	100.0%	3	3	3	0.00%	5.8%	IITTAVDKR	99.0%	35.1	25	33.5	1	0	0	1016.61	503	511
Uridine-cytidine kinase-like 1	UCKL1	UCKL1_HUMAN	61.1	100.0%	3	3	3	0.00%	5.8%	LADIVVPR	98.5%	33.2	25	33.2	1	0	0	882.54	274	281
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	5	6	11	0.01%	21.7%	EITGIGPSTTTETETIAK	99.7%	96.8	25	96.8	2	0	0	1848.94	215	232
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	5	6	11	0.01%	21.7%	ELALPGELTQSR	99.7%	71.1	25	63.8	2	0	0	1313.71	94	105
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	5	6	11	0.01%	21.7%	FESPESQASAEQPEM	99.7%	56.5	25	56.5	1	0	0	1682.69	313	327
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	5	6	11	0.01%	21.7%	HYLFYDGESVSGK	99.7%	60.3	25	56.3	2	0	0	1501.70	39	51
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	5	6	11	0.01%	21.7%	LFLAGYDPTPTMR	99.7%	63.3	25	63.3	4	0	0	1497.74	250	262
Vacuolar protein sorting-associated protein 29	VPS29	VPS29_HUMAN	20.5	99.8%	2	2	4	0.00%	12.6%	GDFDENLNYPEQK	98.7%	33.7	25	33.7	2	0	0	1568.69	61	73
Vacuolar protein sorting-associated protein 29	VPS29	VPS29_HUMAN	20.5	99.8%	2	2	4	0.00%	12.6%	TLAGDVHIVR	99.7%	74.4	25	60.2	2	0	0	1080.62	51	60
Vacuolar protein sorting-associated protein 33B	VPS33B	VP33B_HUMAN	70.6	99.8%	2	2	3	0.00%	3.4%	FIFLTTAVTNSAR	99.7%	53.1	25	42.5	2	0	0	1440.78	595	607
Vacuolar protein sorting-associated protein 33B	VPS33B	VP33B_HUMAN	70.6	99.8%	2	2	3	0.00%	3.4%	IIEQVLER	99.7%	41.3	25	25.6	1	0	0	999.58	524	531
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	9	10	16	0.02%	14.6%	EDGPGIPADIK	98.1%	32.2	25	30.5	1	0	0	1111.56	313	323
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	9	10	16	0.02%	14.6%	ENDAVTIQVLNQLIQK	99.6%	39.6	25	37.9	1	0	0	1826.00	734	749
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	9	10	16	0.02%	14.6%	ILVGTNLVR	99.7%	60.5	25	45.7	2	0	0	984.62	218	226
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	9	10	16	0.02%	14.6%	IPVDTYNNILTVLK	99.7%	82.2	25	78.2	3	0	0	1602.91	404	417
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	9	10	16	0.02%	14.6%	LFDIFSQQVATVIQSR	99.7%	85.2	25	75.8	2	0	0	1852.00	324	339
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	9	10	16	0.02%	14.6%	LLDEAIQAVK	99.7%	50.2	25	33	1	0	0	1099.64	15	24
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	9	10	16	0.02%	14.6%	LNLEHIATSSAVSK	99.7%	73.1	25	71.2	1	1	0	1469.80	383	396
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	9	10	16	0.02%	14.6%	LSQLEGVNVER	99.7%	62.4	25	57.1	2	0	0	1243.66	227	237
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	9	10	16	0.02%	14.6%	SEDPDQQYLILNTAR	99.7%	99.2	25	92.8	2	0	0	1762.86	500	514
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	8	8	13	0.01%	7.4%	ALSPLEEWLR	96.3%	29.5	25	17.9	1	0	0	1213.66	138	147
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	8	8	13	0.01%	7.4%	GALINVPPPFLGLPR	97.2%	30.7	25	30.7	1	0	0	1560.93	619	633
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	8	8	13	0.01%	7.4%	IQQQQPPPGEK	97.3%	30.7	25	26.5	2	0	0	1249.65	253	263
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	8	8	13	0.01%	7.4%	KVDEAIALFQK	99.7%	54.8	25	50.5	2	0	0	1261.72	1252	1262
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	8	8	13	0.01%	7.4%	LHEEGIIYR	97.9%	31.8	25	25.1	1	0	0	1129.60	462	470
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	8	8	13	0.01%	7.4%	LSAAVTEAFVR	99.7%	102	25	95.7	2	0	0	1163.64	451	461
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	8	8	13	0.01%	7.4%	SSAQDPQAVLGALGR	99.7%	87.4	25	76.4	2	0	0	1469.77	123	137
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	8	8	13	0.01%	7.4%	VPLEVQEADEAK	99.7%	85.2	25	85.2	2	0	0	1327.67	1231	1242
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	7	9	15	0.01%	14.6%	FSFTLPYPVK	95.1%	28.4	25	28.3	1	0	0	1198.65	310	319
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	7	9	15	0.01%	14.6%	LESEGSPETLTNLR	99.7%	98.8	25	92.4	2	0	0	1545.78	133	146
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	7	9	15	0.01%	14.6%	LESEGSPETLTNLRK	99.7%	56.7	25	53.5	2	1	0	1673.87	133	147
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	7	9	15	0.01%	14.6%	LRLESEGSPETLTNLR	99.7%	53.1	25	42.8	2	2	0	1814.96	131	146
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	7	9	15	0.01%	14.6%	QVNITVQK	99.7%	48.4	25	34.1	2	0	0	929.54	77	84
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	7	9	15	0.01%	14.6%	RPLFLAPDFDR	96.6%	29.8	25	20.2	1	0	0	1346.72	99	109
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	7	9	15	0.01%	14.6%	VSQWWER	99.7%	49.1	25	35.7	2	0	0	990.48	86	92
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	5	5	19	0.02%	15.3%	FSHGTMPLR	94.9%	28.2	25	23.6	1	0	0	1061.52	151	159
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	5	5	19	0.02%	15.3%	LLETLFVHR	99.7%	63.7	25	38.2	6	0	0	1127.66	142	150
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	5	5	19	0.02%	15.3%	LPVGTTATLYFR	99.7%	78.8	25	78.6	4	0	0	1338.74	68	79
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	5	5	19	0.02%	15.3%	SLKDEDVLQK	99.7%	49.2	25	40.8	4	0	0	1174.63	58	67
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	5	5	19	0.02%	15.3%	YDFTSSR	99.5%	38	25	11.2	4	0	0	875.39	117	123
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	32	0.03%	24.5%	AENSSLNLIGK	99.7%	80.6	25	61.8	2	0	0	1145.62	188	198
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	32	0.03%	24.5%	DFQSGQHVIVR	99.7%	54.6	25	46.7	2	0	0	1285.66	28	38
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	32	0.03%	24.5%	DIEAMDPSILK	99.7%	44.7	25	31.7	2	0	0	1231.62	151	161
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	32	0.03%	24.5%	GILLYGPPGCGK	99.6%	39.3	25	28.3	2	0	0	1231.65	255	266
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	32	0.03%	24.5%	GSMAGSTGVHDTVVNQLLSK	99.7%	49.6	25	47.8	0	2	0	2001.01	338	357

Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	32	0.03%	24.5%	IAEESNFPFIK	99.6%	39.8	25	29	2	0	0	1294.67	556	566
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	32	0.03%	24.5%	KLLIIGTTSR	99.7%	49.4	25	41.4	2	0	0	1101.70	639	648
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	32	0.03%	24.5%	LLDYVPIGPR	99.7%	47.6	25	45.4	2	0	0	1142.66	608	617
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	32	0.03%	24.5%	LLIIGTTSR	99.7%	53	25	50.4	2	0	0	973.60	640	648
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	32	0.03%	24.5%	NFSGAELEGLVR	99.7%	78.7	25	62.6	2	0	0	1291.66	435	446
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	32	0.03%	24.5%	SIDSNPYDTDK	99.7%	42.1	25	41.4	2	0	0	1254.55	106	116
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	32	0.03%	24.5%	SQLSCVVVDDIER	99.7%	105	25	105	2	0	0	1519.74	595	607
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	32	0.03%	24.5%	TPLVSVLLEGPPHSGK	99.7%	55.8	25	55.5	2	0	0	1630.92	534	549
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	32	0.03%	24.5%	VLDDGELLVQQTK	99.7%	84.9	25	84.9	2	0	0	1457.78	517	529
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	32	0.03%	24.5%	VVNGPEILNK	99.7%	46.9	25	44.2	1	0	0	1082.62	284	293
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	32	0.03%	24.5%	YVGESEANIR	99.7%	50	25	44.8	2	0	0	1137.55	294	303
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	32	0.03%	24.5%	YVGESEANIRK	99.7%	54.8	25	50.2	1	0	0	1265.65	294	304
Vesicle-trafficking protein SEC22b	SEC22B	SC22B_HUMAN	24.6	99.8%	2	2	3	0.00%	10.2%	NLGSINTELQDVQR	99.7%	88.3	25	82.7	1	0	0	1586.81	134	147
Vesicle-trafficking protein SEC22b	SEC22B	SC22B_HUMAN	24.6	99.8%	2	2	3	0.00%	10.2%	VLLTMIAR	99.7%	56.6	25	52.5	2	0	0	916.56	2	9
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	DGQVINETSQHHDDLE	99.7%	65.4	25	65.4	4	1	0	1836.80	451	466
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	DNLAEDIMR	99.7%	66.8	25	61	4	0	0	1076.50	176	184
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	EEAENTLQSFR	99.7%	71.5	25	63.7	2	0	0	1323.62	197	207
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	EEAENTLQSFRQDVDNASLAR	99.7%	63.7	25	63.7	0	1	0	2393.13	197	217
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	EKLQEEMLQR	99.7%	52.3	25	36.6	4	0	0	1319.66	187	196
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	EMEENFAVEAANYQDTIGR	99.7%	120	25	120	6	0	0	2186.97	346	364
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	ETNLDSLPLVDTHSK	99.7%	72.7	25	62.5	4	2	0	1668.84	425	439
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	ETNLDSLPLVDTHSKR	99.7%	74.7	25	71.6	2	3	0	1824.95	425	440
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	EYQDLLNVK	99.7%	58.9	25	47.5	6	0	0	1121.58	382	390
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	FADLSEAANR	99.7%	74.6	25	64.3	2	0	0	1093.53	295	304
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	FANYIDK	99.5%	37.9	25	30.4	2	0	0	870.44	114	120
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	FANYIDKVR	99.7%	74.3	25	69.6	4	0	0	1125.61	114	122
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	ILLAELEQLK	99.7%	70.5	25	57.9	8	0	0	1169.71	130	139
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	ILLAELEQLKGQGK	99.7%	71.9	25	71.9	5	3	0	1539.91	130	143
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	ISLPLPNFSSLNLR	99.7%	108	25	89.8	6	0	0	1570.90	411	424
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	KLLEGEESR	99.7%	54	25	36	2	0	0	1060.56	402	410
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	KVESLQEEIAFLK	99.7%	104	25	103	4	2	0	1533.85	223	235
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	LGDLYEEEMR	99.7%	59.2	25	55.5	4	0	0	1254.57	146	155
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	LLEGEESR	99.7%	53.6	25	40.4	4	0	0	932.47	403	410
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	LLQDSVDFSLADAINTEFK	99.7%	124	25	116	7	0	0	2126.07	79	97
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	LQDEIQNMK	99.7%	53	25	48.5	4	0	0	1118.55	365	373
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	LQDEIQNMKEEMAR	99.7%	83.3	25	70.7	7	5	0	1734.82	365	378
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	LQEEMLQR	99.7%	47	25	31.9	4	0	0	1046.53	189	196
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	LQEEMLQREEAENTLQSFR	99.7%	57.3	25	56.6	0	4	0	2351.13	189	207
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	MALDIEIATYR	99.7%	66.3	25	42.3	2	0	0	1311.66	391	401
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	MFGGPGTASRPSSSR	99.4%	31.4	25	29.1	2	2	0	1510.71	14	28
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	NLQEAEEWYK	99.7%	62.9	25	62.9	4	0	0	1309.61	283	292
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	QDVDNASLAR	99.7%	71.2	25	48.4	8	0	0	1088.53	208	217
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	QQYESVAAK	99.7%	54.2	25	39.3	2	0	0	1023.51	274	282
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	QVDQLTNDK	99.7%	60.2	25	38.4	2	0	0	1060.53	160	168
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	QVDQLTNDKAR	99.7%	53.1	25	34.5	3	1	0	1287.67	160	170
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	QVQSLTCEVDALK	99.7%	76.8	25	64	3	0	0	1490.75	322	334
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	QVQSLTCEVDALKGTNESLER	99.7%	64.8	25	64.8	0	2	0	2377.17	322	342
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	RQVDQLTNDK	99.7%	53.6	25	41.8	2	0	0	1216.63	159	168
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	SLYASSPGGVYATR	99.7%	98.4	25	98.4	8	0	0	1428.71	51	64
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	SYVTTSTR	99.7%	47.2	25	37.2	2	0	0	914.46	29	36
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	TNEKVELQELNDR	99.7%	71.6	25	67.5	4	3	0	1587.80	101	113

Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	TYSLGSALRPSTSR	99.7%	41.5	25	41.5	3	2	0	1495.79	37	50
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	VELQELNDR	99.7%	66	25	60.2	4	0	0	1115.57	105	113
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	VESLQEEIAFLK	99.7%	90	25	58.3	2	0	0	1405.76	224	235
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	63	186	0.18%	73.8%	VEVERDNLAEDIMR	99.7%	54.9	25	54.9	4	5	0	1704.82	171	184
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	8	10	17	0.02%	36.7%	GYGFGLIK	99.5%	38.2	25	27.9	1	0	0	854.48	21	28
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	8	10	17	0.02%	36.7%	KLETAVNLAWTAGNSNTR	99.7%	102	25	102	2	2	0	1946.01	201	218
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	8	10	17	0.02%	36.7%	LTFDSSFSPNTGK	99.7%	71.3	25	62.3	2	0	0	1400.67	97	109
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	8	10	17	0.02%	36.7%	LTFDSSFSPNTGKK	99.7%	75.2	25	75.2	2	0	0	1528.76	97	110
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	8	10	17	0.02%	36.7%	LTLSALLDGK	99.7%	84.9	25	0	9	0	0	1030.61	257	266
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	8	10	17	0.02%	36.7%	VNNSSLIGLGYTQTLKPGIK	99.7%	41.8	25	39.4	1	1	0	2103.18	237	256
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	8	10	17	0.02%	36.7%	VTQSNFAVGYK	99.7%	64.3	25	55.2	2	0	0	1213.62	164	174
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	8	10	17	0.02%	36.7%	WTEYGLTFTEK	99.7%	60.9	25	58	2	0	0	1374.66	64	74
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	8	10	17	0.02%	36.7%	YQIDPDACFSAK	99.7%	61.7	25	59.7	2	0	0	1414.63	225	236
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	13	33	0.03%	50.0%	GFGFGLVK	99.2%	36.1	25	28	2	0	0	824.47	32	39
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	13	33	0.03%	50.0%	LTFDTTFSPNTGK	99.7%	91.1	25	76.5	2	0	0	1428.70	108	120
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	13	33	0.03%	50.0%	LTFDTTFSPNTGKK	99.7%	83.3	25	83.3	2	0	0	1556.80	108	121
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	13	33	0.03%	50.0%	LTLSALVDGK	99.7%	84	25	77.1	4	0	0	1016.60	268	277
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	13	33	0.03%	50.0%	NNFAVGYR	99.7%	48.2	25	39.1	4	0	0	940.46	178	185
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	13	33	0.03%	50.0%	SCSGVEFSTSGSSNTDTGK	99.7%	115	25	115	2	0	0	1907.79	46	64
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	13	33	0.03%	50.0%	TGDFQLHTNVNDGTEFGGSIYQK	99.7%	72.2	25	72.2	0	2	0	2528.17	186	208
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	13	33	0.03%	50.0%	VNNSSLIGVGYTQTLRPGVK	99.7%	85.6	25	85.6	2	2	0	2103.16	248	267
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	13	33	0.03%	50.0%	WCEYGLTFTEK	99.7%	58.2	25	56.2	2	0	0	1433.64	75	85
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	13	33	0.03%	50.0%	WNTDNTLGTEIAIEDQICQGLK	99.7%	58.1	25	58.1	2	1	0	2519.21	86	107
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	13	33	0.03%	50.0%	YQLDPTASISAK	99.7%	72.4	25	63.3	6	0	0	1293.67	236	247
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	13	42	0.04%	40.6%	GYGFGMVK	99.6%	39.7	25	34.6	3	0	0	874.41	21	28
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	13	42	0.04%	40.6%	IETSINLAWTAGSNNTR	99.7%	122	25	122	2	0	0	1847.92	202	218
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	13	42	0.04%	40.6%	LSQNNFALGYK	99.7%	65.8	25	58.5	5	0	0	1254.65	164	174
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	13	42	0.04%	40.6%	LTLDTIFVPNTGK	99.7%	109	25	109	4	0	0	1418.79	97	109
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	13	42	0.04%	40.6%	LTLDTIFVPNTGKK	99.7%	47.6	25	47.6	3	3	0	1546.88	97	110
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	13	42	0.04%	40.6%	LTLSALIDGK	99.7%	84.9	25	0	9	0	0	1030.61	257	266
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	13	42	0.04%	40.6%	VCNYGLTFTQK	99.7%	71.9	25	62.9	4	0	0	1330.65	64	74
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	13	42	0.04%	40.6%	VNNASLIGLGYTQTLRPGVK	99.7%	95.9	25	95.9	2	2	0	2101.18	237	256
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	13	42	0.04%	40.6%	WNTDNTLGTEISWENK	99.7%	90.8	25	90.8	2	0	0	1907.88	75	90
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	13	42	0.04%	40.6%	YKVCNYGLTFTQK	99.7%	51.1	25	51.1	1	0	0	1621.80	62	74
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	11	13	42	0.04%	40.6%	YMLDCR	97.9%	31.9	25	29.5	2	0	0	873.36	225	230
V-set and immunoglobulin domain-containing protein 8	VSIG8	VSIG8_HUMAN	43.9	100.0%	3	3	3	0.00%	8.2%	CYASGGSQPLSYK	99.7%	60.6	25	60.6	1	0	0	1417.64	167	179
V-set and immunoglobulin domain-containing protein 8	VSIG8	VSIG8_HUMAN	43.9	100.0%	3	3	3	0.00%	8.2%	INHGSLPHLQQR	99.6%	33.6	25	32.2	0	1	0	1399.76	85	96
V-set and immunoglobulin domain-containing protein 8	VSIG8	VSIG8_HUMAN	43.9	100.0%	3	3	3	0.00%	8.2%	ISGHHYPYR	99.7%	43.6	25	37.5	1	0	0	1129.55	183	191
V-type proton ATPase 116 kDa subunit a isoform 1	ATP6V0A1	VPP1_HUMAN	96.4	100.0%	3	3	4	0.00%	3.8%	DLNPDVNVFQR	96.7%	29.9	25	29.7	1	0	0	1316.66	39	49
V-type proton ATPase 116 kDa subunit a isoform 1	ATP6V0A1	VPP1_HUMAN	96.4	100.0%	3	3	4	0.00%	3.8%	EINTNQEALKR	99.0%	34.8	25	26	1	0	0	1315.70	110	120
V-type proton ATPase 116 kDa subunit a isoform 1	ATP6V0A1	VPP1_HUMAN	96.4	100.0%	3	3	4	0.00%	3.8%	LGFVAGVINR	99.7%	74.3	25	58.9	2	0	0	1045.62	168	177
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	5	6	10	0.01%	9.2%	GVNVSALSR	99.7%	57.3	25	40.1	2	0	0	902.51	121	129
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	5	6	10	0.01%	9.2%	LPANHPLLTGQR	96.9%	24.7	25	24.5	0	1	0	1316.74	221	232
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	5	6	10	0.01%	9.2%	TALVANTSNMPVAAR	99.7%	70.1	25	67.1	2	0	0	1515.79	309	323
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	5	6	10	0.01%	9.2%	TVISQSLSK	98.4%	32.9	25	25.5	1	0	0	962.55	257	265
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	5	6	10	0.01%	9.2%	VGHSELVGEIIR	99.7%	45.6	25	40.5	2	2	0	1308.73	45	56
V-type proton ATPase subunit d 1	ATP6V0D1	VA0D1_HUMAN	40.3	100.0%	4	4	7	0.01%	13.7%	AFIITINSFGTELSK	97.8%	31.6	25	0	1	0	0	1640.89	220	234
V-type proton ATPase subunit d 1	ATP6V0D1	VA0D1_HUMAN	40.3	100.0%	4	4	7	0.01%	13.7%	LYPEGLAQLAR	99.7%	45.5	25	43.8	2	0	0	1230.68	247	257
V-type proton ATPase subunit d 1	ATP6V0D1	VA0D1_HUMAN	40.3	100.0%	4	4	7	0.01%	13.7%	NIVWIAECIAQR	99.7%	74.2	25	65.5	2	0	0	1472.77	328	339
V-type proton ATPase subunit d 1	ATP6V0D1	VA0D1_HUMAN	40.3	100.0%	4	4	7	0.01%	13.7%	NVADYYPEYK	99.7%	54.1	25	52.9	2	0	0	1261.57	266	275
V-type proton ATPase subunit H	ATP6V1H	VATH_HUMAN	55.9	100.0%	6	6	8	0.01%	19.7%	GAVDAAVPTNIIAAK	99.7%	60.3	25	48.6	1	0	0	1410.80	8	22

V-type proton ATPase subunit H	ATP6V1H	VATH_HUMAN	55.9	100.0%	6	6	8	0.01%	19.7%	LGESVQDLSSFDEYSSELK	99.7%	96.2	25	96.2	1	0	0	2132.99	342	360
V-type proton ATPase subunit H	ATP6V1H	VATH_HUMAN	55.9	100.0%	6	6	8	0.01%	19.7%	LLEVSDDPQVLAVAAHDVGEYVR	99.5%	31.8	25	31.8	0	1	0	2495.28	397	419
V-type proton ATPase subunit H	ATP6V1H	VATH_HUMAN	55.9	100.0%	6	6	8	0.01%	19.7%	QLQSEQPQTAAAR	99.7%	60.9	25	58.4	2	0	0	1427.72	470	482
V-type proton ATPase subunit H	ATP6V1H	VATH_HUMAN	55.9	100.0%	6	6	8	0.01%	19.7%	VSIFFDYAR	99.7%	40.7	25	35.4	1	0	0	1117.57	108	116
V-type proton ATPase subunit H	ATP6V1H	VATH_HUMAN	55.9	100.0%	6	6	8	0.01%	19.7%	YNIIPVLSDILQESVK	99.7%	82.1	25	78.3	2	0	0	1831.02	263	278
WASH complex subunit 7	KIAA1033	WASH7_HUMAN	136.4	100.0%	3	3	5	0.00%	3.0%	FLEEYTSQLR	99.7%	57.7	25	54.9	1	0	0	1285.64	34	43
WASH complex subunit 7	KIAA1033	WASH7_HUMAN	136.4	100.0%	3	3	5	0.00%	3.0%	LLPYEQSSLLELIK	99.3%	36.4	25	34	2	0	0	1645.94	68	81
WASH complex subunit 7	KIAA1033	WASH7_HUMAN	136.4	100.0%	3	3	5	0.00%	3.0%	MLVDVFAPEFR	99.7%	46.5	25	39.5	2	0	0	1323.68	993	1003
WASH complex subunit strumpellin	KIAA0196	STRUM_HUMAN	134.3	100.0%	4	4	4	0.00%	4.1%	LASALDLPLLR	99.7%	63.9	25	63.8	1	0	0	1181.73	589	599
WASH complex subunit strumpellin	KIAA0196	STRUM_HUMAN	134.3	100.0%	4	4	4	0.00%	4.1%	LSEFIPAVFR	99.5%	38.4	25	35.4	1	0	0	1178.66	32	41
WASH complex subunit strumpellin	KIAA0196	STRUM_HUMAN	134.3	100.0%	4	4	4	0.00%	4.1%	TALNNTLDLSNVR	99.7%	67.9	25	66.1	1	0	0	1430.76	312	324
WASH complex subunit strumpellin	KIAA0196	STRUM_HUMAN	134.3	100.0%	4	4	4	0.00%	4.1%	VPINESFISMVIGR	99.7%	52.4	25	52.4	1	0	0	1561.84	215	228
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	7	7	12	0.01%	14.0%	DYSGQGVVK	99.1%	35.7	25	23.3	2	0	0	952.47	397	405
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	7	7	12	0.01%	14.0%	IAVVGEGR	99.7%	40	25	24.9	1	0	0	800.46	117	124
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	7	7	12	0.01%	14.0%	LATGSDDNCAAFFEGPPFK	99.7%	90.3	25	77.8	2	0	0	2043.91	162	180
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	7	7	12	0.01%	14.0%	LYSILGTTLKDEGK	99.7%	83.1	25	71.8	2	0	0	1537.85	471	484
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	7	7	12	0.01%	14.0%	VFASLPQVER	99.7%	40.9	25	33.6	2	0	0	1145.63	8	17
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	7	7	12	0.01%	14.0%	YAPSGFYIASGDVSGK	99.7%	125	25	119	2	0	0	1618.77	66	81
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	7	7	12	0.01%	14.0%	YEYQPFAGK	95.5%	28.7	25	25.1	1	0	0	1102.52	96	104
WD repeat-containing protein 5	WDR5	WDR5_HUMAN	36.6	100.0%	3	3	5	0.00%	10.5%	FTLAGHTK	95.8%	28.9	25	18.3	1	0	0	874.48	39	46
WD repeat-containing protein 5	WDR5	WDR5_HUMAN	36.6	100.0%	3	3	5	0.00%	10.5%	IWDTASGQCLK	99.7%	47.4	25	43.4	2	0	0	1278.61	197	207
WD repeat-containing protein 5	WDR5	WDR5_HUMAN	36.6	100.0%	3	3	5	0.00%	10.5%	TLPAHSDPVSAVHFNR	99.7%	41	25	38.6	0	2	0	1747.89	166	181
WD repeat-containing protein 6	WDR6	WDR6_HUMAN	121.7	100.0%	4	4	5	0.00%	5.1%	ATSELILLPVTGLECVGDR	99.7%	74.2	25	71.2	1	0	0	2043.08	12	30
WD repeat-containing protein 6	WDR6	WDR6_HUMAN	121.7	100.0%	4	4	5	0.00%	5.1%	GLGVSALCFK	96.6%	29.8	25	22.6	1	0	0	1051.56	334	343
WD repeat-containing protein 6	WDR6	WDR6_HUMAN	121.7	100.0%	4	4	5	0.00%	5.1%	LFLLQDSGR	99.7%	48.4	25	32.2	1	0	0	1048.58	890	898
WD repeat-containing protein 6	WDR6	WDR6_HUMAN	121.7	100.0%	4	4	5	0.00%	5.1%	VVPINTPTAAVDQTLFPGK	99.7%	43.3	25	43.3	2	0	0	1968.08	419	437
WD repeat-containing protein 82	WDR82	WDR82_HUMAN	35.1	100.0%	4	5	15	0.01%	18.8%	HTGPITCLQFNPK	99.6%	39.4	25	35.8	1	0	0	1512.76	281	293
WD repeat-containing protein 82	WDR82	WDR82_HUMAN	35.1	100.0%	4	5	15	0.01%	18.8%	LILISTNGSFIR	99.7%	80.7	25	73.2	2	0	0	1333.78	208	219
WD repeat-containing protein 82	WDR82	WDR82_HUMAN	35.1	100.0%	4	5	15	0.01%	18.8%	VVALSMSPVDDTFISGSLDK	99.7%	108	25	103	8	0	0	2097.04	110	129
WD repeat-containing protein 82	WDR82	WDR82_HUMAN	35.1	100.0%	4	5	15	0.01%	18.8%	YTHAANTVVYSSNK	99.7%	85.5	25	85	4	0	0	1554.75	71	84
WD40 repeat-containing protein SMU1	SMU1	SMU1_HUMAN	57.5	99.8%	2	2	4	0.00%	3.5%	IQSGQCLR	99.6%	39.8	25	23.4	2	0	0	961.49	293	300
WD40 repeat-containing protein SMU1	SMU1	SMU1_HUMAN	57.5	99.8%	2	2	4	0.00%	3.5%	NPEHFVVCNR	99.7%	43.6	25	41.9	2	0	0	1271.59	409	418
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	39	0.04%	22.5%	AFREEAIK	99.6%	39.2	25	15.7	1	0	0	963.53	641	648
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	39	0.04%	22.5%	ANPQVGVAFPHIK	99.0%	35.1	25	29.2	1	0	0	1377.76	401	413
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	39	0.04%	22.5%	CFSVLGFCK	99.7%	56.6	25	55.8	2	0	0	1117.52	339	347
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	39	0.04%	22.5%	EDGSGDRGDGPFR	99.4%	37.5	25	24.1	1	0	0	1364.58	172	184
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	39	0.04%	22.5%	EEASGSSVTAEEAK	99.7%	111	25	111	3	0	0	1394.63	689	702
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	39	0.04%	22.5%	EEASGSSVTAEEAKK	99.7%	99.2	25	86.2	5	0	0	1522.72	689	703
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	39	0.04%	22.5%	FFMGNQVLK	96.2%	29.3	25	18.5	1	0	0	1099.56	355	363
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	39	0.04%	22.5%	HIEIFTDLSSR	99.7%	54.9	25	45.4	3	0	0	1317.68	131	141
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	39	0.04%	22.5%	LFQCLLHR	99.4%	37.8	25	26.1	2	0	0	1086.59	490	497
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	39	0.04%	22.5%	LGGHGPSFPLK	99.5%	38.5	25	30.5	3	0	0	1109.61	185	195
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	39	0.04%	22.5%	LTIGSNLSIR	99.7%	59.4	25	44.4	2	0	0	1073.63	251	260
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	39	0.04%	22.5%	QYMFSSLK	98.4%	32.9	25	23.5	1	0	0	1003.49	432	439
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	39	0.04%	22.5%	SQLDIIIHSLK	99.7%	60.9	25	54.7	2	0	0	1266.74	145	155
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	39	0.04%	22.5%	TDTLEDLFPTTK	99.7%	78.9	25	70.2	2	0	0	1380.69	470	481
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	39	0.04%	22.5%	TLFPLIEAK	98.9%	34.8	25	16.8	2	0	0	1031.61	535	543
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	39	0.04%	22.5%	VITMFVQR	99.7%	65	25	47	4	0	0	993.56	37	44
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	17	18	39	0.04%	22.5%	YGSDIVPFSK	99.7%	54.9	25	44.5	4	0	0	1112.56	316	325
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	15	17	33	0.03%	34.2%	DSLIFLVDASK	99.7%	92.2	25	81.8	4	0	0	1207.66	36	46
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	15	17	33	0.03%	34.2%	DTGIFLDLMHLK	99.0%	35.1	25	35.1	1	0	0	1402.74	195	206

X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	15	17	33	0.03%	34.2%	FTVPMLK	95.4%	28.6	25	20.1	1	0	0	835.47	576	582
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	15	17	33	0.03%	34.2%	IISSDRDLLAVVFYGTEK	96.2%	23.9	25	23.9	0	1	0	2026.09	75	92
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	15	17	33	0.03%	34.2%	ILELDQFK	99.7%	45.7	25	16.6	2	0	0	1005.56	116	123
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	15	17	33	0.03%	34.2%	IMATPEQVGK	99.7%	57.9	25	44.4	4	0	0	1089.56	452	461
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	15	17	33	0.03%	34.2%	IMLFTNEDNPHGNDSAK	99.7%	105	25	105	2	2	0	1902.87	166	182
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	15	17	33	0.03%	34.2%	IQVTPPGFQLVFLPFADDK	99.7%	46.3	25	39.7	1	0	0	2132.14	425	443
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	15	17	33	0.03%	34.2%	KQELLEALTK	99.7%	50.6	25	35.5	2	0	0	1172.69	596	605
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	15	17	33	0.03%	34.2%	LGSLVDEFK	99.7%	54.8	25	43.3	2	0	0	1007.54	518	526
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	15	17	33	0.03%	34.2%	NIPPYFVALVPQEEELDDQK	99.0%	34.8	25	34.8	2	0	0	2344.17	405	424
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	15	17	33	0.03%	34.2%	NIYVLQELDNPGAK	99.7%	114	25	105	3	0	0	1573.82	101	114
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	15	17	33	0.03%	34.2%	NLEALALDLMEPEQAVDLTLPK	99.7%	71.8	25	71.8	2	0	0	2439.27	489	510
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	15	17	33	0.03%	34.2%	SDSFENPVLQQHFR	99.7%	75.2	25	75.2	2	0	0	1703.81	475	488
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	15	17	33	0.03%	34.2%	TFNTSTGGLLLPSDTKR	99.7%	89.7	25	89.7	2	0	0	1807.96	302	318
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	5	5	11	0.01%	28.0%	AGEAPTENPAPPTQQSSAE	99.7%	49.2	25	49.2	2	0	0	1881.85	354	372
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	5	5	11	0.01%	28.0%	DGVPEGAQLQGPVHR	99.7%	60.3	25	50.1	2	0	0	1559.79	269	283
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	5	5	11	0.01%	28.0%	EDVFVHQTAIK	99.7%	56.7	25	48.8	2	0	0	1286.67	114	124
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	5	5	11	0.01%	28.0%	EDVFVHQTAIKK	99.7%	46.5	25	33.6	1	1	0	1414.77	114	125
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	5	5	11	0.01%	28.0%	GAEAANVTGPDGVPVEGSR	99.7%	69.5	25	69.1	2	0	0	1782.86	151	169
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	5	5	11	0.01%	28.0%	IQAGEIGEMK	99.7%	46.6	25	39.9	3	0	0	1091.54	259	268
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	5	5	11	0.01%	28.0%	IQAGEIGEMKDGVPEGAQLQGPVHR	99.7%	59.2	25	59.2	0	2	0	2632.32	259	283
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	5	5	11	0.01%	28.0%	NDTKEDVFVHQTAIK	99.7%	92.1	25	87.9	3	4	0	1744.89	110	124
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	5	5	11	0.01%	28.0%	NGYGFINR	99.7%	51.5	25	46	5	0	0	940.46	102	109
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	5	5	11	0.01%	28.0%	SVGDGETVEFDVVEGEK	99.7%	116	25	111	7	0	0	1795.82	134	150
YTH domain-containing family protein 2	YTHDF2	YTHD2_HUMAN	62.3	100.0%	3	3	8	0.01%	5.9%	LENNENKPVTNSR	99.7%	42.1	25	38.3	0	2	0	1514.76	515	527
YTH domain-containing family protein 2	YTHDF2	YTHD2_HUMAN	62.3	100.0%	3	3	8	0.01%	5.9%	LGSTEVASNVPK	99.7%	78.5	25	69.5	4	0	0	1201.64	194	205
YTH domain-containing family protein 2	YTHDF2	YTHD2_HUMAN	62.3	100.0%	3	3	8	0.01%	5.9%	SYSEDDIHR	99.7%	51.9	25	51.9	2	0	0	1121.49	417	425
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	12	13	24	0.02%	17.7%	DVFLNGSYNDYVR	99.7%	58.8	25	58.8	2	0	0	1561.73	582	594
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	12	13	24	0.02%	17.7%	GISPIVFDR	99.7%	41.1	25	29.7	2	0	0	1003.56	306	314
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	12	13	24	0.02%	17.7%	GVWSTLPVNEK	99.7%	58.9	25	49.9	2	0	0	1229.65	375	385
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	12	13	24	0.02%	17.7%	IGLEVDR	99.7%	46.1	25	32.7	1	0	0	801.45	155	161
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	12	13	24	0.02%	17.7%	IGLEVDRR	96.8%	30.1	25	19.5	1	0	0	957.55	155	162
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	12	13	24	0.02%	17.7%	QLVSKPLSSSVSNNKR	95.2%	23	25	23	0	1	0	1743.97	68	83
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	12	13	24	0.02%	17.7%	SATEYKNEEYQR	99.7%	63.9	25	55.9	2	0	0	1517.69	91	102
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	12	13	24	0.02%	17.7%	SEASDSGSESVSFTDGSVR	99.7%	112	25	107	1	0	0	1903.82	268	286
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	12	13	24	0.02%	17.7%	SGSSASESYAGSEK	99.7%	80.3	25	80.3	3	0	0	1346.57	315	328
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	12	13	24	0.02%	17.7%	SNNHENVSLAK	99.7%	53.4	25	48.5	3	2	0	1212.60	362	372
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	12	13	24	0.02%	17.7%	SVILIFSVR	99.7%	70	25	66	2	0	0	1033.64	396	404
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	12	13	24	0.02%	17.7%	YVLQDAR	99.7%	42.3	25	26.4	2	0	0	864.46	350	356
Zinc finger CCCH domain-containing protein 11A	ZC3H11A	ZC11A_HUMAN	89.1	100.0%	6	6	7	0.01%	9.9%	KVEAPETNIDK	99.7%	41	25	20.6	1	0	0	1243.65	310	320
Zinc finger CCCH domain-containing protein 11A	ZC3H11A	ZC11A_HUMAN	89.1	100.0%	6	6	7	0.01%	9.9%	LSVQSNPSPQLR	99.7%	73	25	56.2	1	0	0	1325.72	125	136
Zinc finger CCCH domain-containing protein 11A	ZC3H11A	ZC11A_HUMAN	89.1	100.0%	6	6	7	0.01%	9.9%	NLQEGNEVDSQSSIR	99.7%	79.9	25	75.2	1	0	0	1675.79	522	536
Zinc finger CCCH domain-containing protein 11A	ZC3H11A	ZC11A_HUMAN	89.1	100.0%	6	6	7	0.01%	9.9%	TLEEILLER	99.7%	60.3	25	50.1	2	0	0	1115.63	360	368
Zinc finger CCCH domain-containing protein 11A	ZC3H11A	ZC11A_HUMAN	89.1	100.0%	6	6	7	0.01%	9.9%	TVVLPPIVASR	95.1%	28.4	25	28.4	1	0	0	1151.71	443	453
Zinc finger CCCH domain-containing protein 11A	ZC3H11A	ZC11A_HUMAN	89.1	100.0%	6	6	7	0.01%	9.9%	VQQSSESSTSSPSQHEATPGAR	99.7%	40.4	25	40.4	0	1	0	2258.03	485	506
Zinc finger CCCH domain-containing protein 18	ZC3H18	ZCH18_HUMAN	106.4	100.0%	4	4	6	0.01%	5.1%	ASDLEDEESAAR	99.7%	84.5	25	75.5	1	0	0	1292.56	45	56
Zinc finger CCCH domain-containing protein 18	ZC3H18	ZCH18_HUMAN	106.4	100.0%	4	4	6	0.01%	5.1%	GGQYENFR	99.2%	36.3	25	33.6	1	0	0	970.44	382	389
Zinc finger CCCH domain-containing protein 18	ZC3H18	ZCH18_HUMAN	106.4	100.0%	4	4	6	0.01%	5.1%	SSSYSSYSSR	99.7%	56.2	25	55.5	1	0	0	1110.47	576	585
Zinc finger CCCH domain-containing protein 18	ZC3H18	ZCH18_HUMAN	106.4	100.0%	4	4	6	0.01%	5.1%	TLSGSGSGSGSSYSGSSSR	99.7%	96.9	25	96.2	3	0	0	1707.74	683	701
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	100.0%	9	11	21	0.02%	26.0%	AVHNSVAAQLTGVAGH	99.7%	103	25	103	2	2	0	1531.80	389	404
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	100.0%	9	11	21	0.02%	26.0%	DFVVGALILR	99.7%	63.5	25	52.7	2	0	0	1102.66	183	192
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	100.0%	9	11	21	0.02%	26.0%	DPAGEAVDPR	97.1%	30.5	25	30.5	1	0	0	1026.49	103	112

Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	100.0%	9	11	21	0.02%	26.0%	EFDVSFR	96.4%	29.6	25	15.4	1	0	0	899.43	212	218
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	100.0%	9	11	21	0.02%	26.0%	FGIWTGEYK	99.5%	38.7	25	37.7	2	0	0	1100.54	291	299
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	100.0%	9	11	21	0.02%	26.0%	ICFQGDEGACPTR	99.7%	84	25	78.7	2	0	0	1510.64	170	182
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	100.0%	9	11	21	0.02%	26.0%	NETVDVEDIVTWLK	99.7%	83.6	25	63	2	0	0	1660.84	262	275
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	100.0%	9	11	21	0.02%	26.0%	SIGMDPSDIYAVIQIPGSR	99.7%	75	25	71.6	4	0	0	2035.02	193	211
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	100.0%	9	11	21	0.02%	26.0%	TLFILFR	99.7%	43.3	25	43.3	3	0	0	909.56	255	261
Zinc finger HIT domain-containing protein 2	ZNHIT2	ZNHI2_HUMAN	42.9	99.8%	2	2	2	0.00%	5.2%	DASAAEPAAAER	99.7%	43.5	25	43.5	1	0	0	1158.54	168	179
Zinc finger HIT domain-containing protein 2	ZNHIT2	ZNHI2_HUMAN	42.9	99.8%	2	2	2	0.00%	5.2%	IPAIVSLSR	99.1%	35.5	25	1.18	1	0	0	955.59	196	204
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	9	12	24	0.02%	34.0%	EEVEHMIQK	99.7%	44.3	25	28.3	3	0	0	1158.55	57	65
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	9	12	24	0.02%	34.0%	IVLNSIEQYQAHVSGFK	99.7%	86.2	25	86.2	2	2	0	1933.02	246	262
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	9	12	24	0.02%	34.0%	LADPAVTDFPAGK	99.7%	64.6	25	59.9	2	0	0	1301.67	225	237
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	9	12	24	0.02%	34.0%	LWEAVSGAQPVGR	99.7%	71	25	58.9	2	0	0	1369.72	44	56
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	9	12	24	0.02%	34.0%	NQCLFTNTQCK	99.7%	63	25	60.2	2	0	0	1413.63	66	76
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	9	12	24	0.02%	34.0%	RLWEAVSGAQPVGR	99.7%	43.4	25	43.4	0	2	0	1525.82	43	56
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	9	12	24	0.02%	34.0%	TVASSLGQIPMQR	99.7%	83.6	25	71.5	5	0	0	1403.73	270	282
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	9	12	24	0.02%	34.0%	VCCALLISESQK	99.7%	88.2	25	77.1	2	0	0	1407.70	77	88
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	9	12	24	0.02%	34.0%	YLAIHGMETLK	99.7%	47.5	25	42.5	2	0	0	1275.68	104	114
Zinc finger protein 512	ZNF512	ZN512_HUMAN	64.7	99.8%	2	2	4	0.00%	3.9%	AGLAYHLR	99.7%	53.1	25	36.8	3	0	0	900.51	300	307
Zinc finger protein 512	ZNF512	ZN512_HUMAN	64.7	99.8%	2	2	4	0.00%	3.9%	LGAVPATSGPTTFK	98.8%	34.3	25	17.5	1	0	0	1346.73	5	18
Zinc finger protein 768	ZNF768	ZN768_HUMAN	60.2	100.0%	5	5	6	0.01%	10.0%	AFADSSYLLR	99.7%	53.2	25	44.5	1	0	0	1142.58	325	334
Zinc finger protein 768	ZNF768	ZN768_HUMAN	60.2	100.0%	5	5	6	0.01%	10.0%	AFGDSSYLLR	97.5%	31.1	25	20.5	2	0	0	1128.57	353	362
Zinc finger protein 768	ZNF768	ZN768_HUMAN	60.2	100.0%	5	5	6	0.01%	10.0%	AFSQSSDLIR	99.7%	40.8	25	21.8	1	0	0	1123.57	521	530
Zinc finger protein 768	ZNF768	ZN768_HUMAN	60.2	100.0%	5	5	6	0.01%	10.0%	FGQSSVLAIHAR	99.7%	59.7	25	56.8	1	0	0	1285.70	438	449
Zinc finger protein 768	ZNF768	ZN768_HUMAN	60.2	100.0%	5	5	6	0.01%	10.0%	TQSPEFEAQSSK	98.8%	34.1	25	17.4	1	0	0	1338.62	158	169
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	18	18	46	0.05%	20.9%	AGYSQGATQYTQAQQTR	99.7%	119	25	119	1	0	0	1858.87	192	208
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	18	18	46	0.05%	20.9%	AISSASSPQSPGDALR	99.7%	82	25	73	5	0	0	1543.77	954	969
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	18	18	46	0.05%	20.9%	ANGLQSCVIIIR	99.7%	52.8	25	42.9	3	0	0	1343.75	916	927
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	18	18	46	0.05%	20.9%	CLDALAALR	98.0%	32	25	23.7	1	0	0	1002.54	899	907
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	18	18	46	0.05%	20.9%	EDITSSAQFALR	99.7%	98.6	25	91.8	5	0	0	1337.67	1008	1019
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	18	18	46	0.05%	20.9%	GLTTTGNSSLNSTSNTK	99.7%	110	25	110	4	0	0	1682.82	468	484
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	18	18	46	0.05%	20.9%	HATIYPTEEELQAVQK	94.7%	22.7	25	15.3	0	1	0	1856.94	731	746
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	18	18	46	0.05%	20.9%	INFVGGNK	97.0%	30.3	25	17	2	0	0	848.46	502	509
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	18	18	46	0.05%	20.9%	ISCAGPQTYK	99.7%	45.9	25	40.3	3	0	0	1124.54	338	347
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	18	18	46	0.05%	20.9%	IVSITER	95.0%	28.2	25	9.32	1	0	0	817.48	747	753
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	18	18	46	0.05%	20.9%	KVNPDLQVEVKPSIR	99.7%	64	25	63.3	0	3	0	1721.99	613	627
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	18	18	46	0.05%	20.9%	LCECSFNDPNAK	99.7%	55.1	25	50.5	2	0	0	1454.60	586	597
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	18	18	46	0.05%	20.9%	LVSDSLSEHEK	99.7%	51.1	25	47	4	0	0	1243.62	757	767
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	18	18	46	0.05%	20.9%	MQVTITLTSPIIR	99.7%	63.7	25	58.8	1	0	0	1488.85	861	873
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	18	18	46	0.05%	20.9%	NVNLVLLCSEKPSK	99.7%	72.9	25	62.5	3	0	0	1600.87	805	818
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	18	18	46	0.05%	20.9%	STAPAVAYDSK	99.7%	67.9	25	62	2	0	0	1109.55	148	158
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	18	18	46	0.05%	20.9%	STPVTSAVQIPEVK	99.7%	83.7	25	82.1	3	0	0	1455.81	528	541
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	18	18	46	0.05%	20.9%	VSAVPTNMAAK	99.3%	36.5	25	27.5	2	0	0	1104.57	485	495

Table S-1-6. List of proteins identified in immunoprecipitation product of H7N9 NS1 (Replicate 3)

Protein name	Gene name	Accession number	M.W. (kDa)	Protein probability	No. of unique peptide	No. of unique spectra	No. of total spectra	Percentage of total spectra	Sequence coverage	Peptide sequence	Best peptide probability	Mascot			No. of spectra			Calculated +1H peptide mass (AMU)	Peptide index	
												ion score	identity score	delta ion score	+2H	+3H	+4H		start	stop
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	PDK1	PDK1_HUMAN	49.2	99.8%	2	2	4	0.00%	6.0%	AVPLAGFGYGLPISR	99.7%	66	25	61.3	2	0	0	1517.85	349	363
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	PDK1	PDK1_HUMAN	49.2	99.8%	2	2	4	0.00%	6.0%	EISLLPDNLLR	97.5%	30.7	25	25.5	2	0	0	1282.74	93	103
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 3, mitochondrial	PDK3	PDK3_HUMAN	46.9	99.8%	2	2	3	0.00%	7.9%	AAPLAGFGYGLPISR	99.7%	53.9	25	39.9	2	0	0	1489.82	318	332
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 3, mitochondrial	PDK3	PDK3_HUMAN	46.9	99.8%	2	2	3	0.00%	7.9%	SPEDPQVLDNFLQVLIK	99.7%	47.8	25	47.8	1	0	0	1955.05	98	114
10 kDa heat shock protein, mitochondrial	HSPE1	CH10_HUMAN	10.9	100.0%	3	3	5	0.00%	25.5%	GGEIQPVSVK	99.7%	52.1	25	39.8	2	0	0	1013.56	57	66
10 kDa heat shock protein, mitochondrial	HSPE1	CH10_HUMAN	10.9	100.0%	3	3	5	0.00%	25.5%	GKGGEIQPVSVK	98.8%	33.5	25	24.8	1	0	0	1198.68	55	66
10 kDa heat shock protein, mitochondrial	HSPE1	CH10_HUMAN	10.9	100.0%	3	3	5	0.00%	25.5%	VLQATVVAVGSGSK	99.7%	74.7	25	74.7	2	0	0	1315.76	41	54
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	26	29	92	0.09%	32.9%	AFIPAIDSFGFETDLR	99.7%	83.2	25	83.1	4	0	0	1798.90	873	888
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	26	29	92	0.09%	32.9%	DSIVQGFQWGTR	99.7%	81.4	25	75.7	4	0	0	1393.69	764	775
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	26	29	92	0.09%	32.9%	EGPLCDELIR	99.7%	43.2	25	37.6	2	0	0	1201.59	776	785
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	26	29	92	0.09%	32.9%	FFDDPMLLELAK	99.7%	71.8	25	60.9	7	0	0	1438.73	952	963
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	26	29	92	0.09%	32.9%	GGGQIIPTAR	99.7%	40.1	25	34	4	0	0	969.55	804	813
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	26	29	92	0.09%	32.9%	GHVTQDAPIPGSPLYTIK	99.0%	29.1	25	25.4	0	1	0	1894.01	855	872
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	26	29	92	0.09%	32.9%	GLSEDVSISK	99.7%	56.5	25	44.6	4	0	0	1034.54	942	951
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	26	29	92	0.09%	32.9%	GNEEAQIFRPLK	99.7%	55.1	25	44	4	0	0	1401.75	570	581
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	26	29	92	0.09%	32.9%	IAVEPVNPSELPK	99.7%	53.7	25	46.8	3	0	0	1392.77	590	602
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	26	29	92	0.09%	32.9%	ILAQVVGDVDTSLPR	99.7%	86.6	25	79.9	2	0	0	1582.88	380	394
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	26	29	92	0.09%	32.9%	ILDAVVAQEPLHR	99.7%	54.3	25	50.7	4	3	0	1460.82	791	803
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	26	29	92	0.09%	32.9%	ITMIAEPLEK	99.7%	56.2	25	48.8	4	0	0	1144.63	685	694
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	26	29	92	0.09%	32.9%	IYADTFGDINYQEFAK	99.7%	122	25	115	6	0	0	1894.89	326	341
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	26	29	92	0.09%	32.9%	KGLSEDVSISK	99.7%	55.2	25	44.7	1	0	0	1162.63	941	951
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	26	29	92	0.09%	32.9%	LGEFFQTK	99.7%	49.8	25	40.5	4	0	0	969.50	714	721
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	26	29	92	0.09%	32.9%	LWISVAR	95.9%	28.7	25	6.45	1	0	0	844.50	530	536
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	26	29	92	0.09%	32.9%	MYSTDDGVQFHAFGR	99.6%	33.2	25	33.2	0	1	0	1746.75	481	495
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	26	29	92	0.09%	32.9%	SFVEFILEPLYK	99.7%	89.6	25	78.2	6	0	0	1484.80	368	379
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	26	29	92	0.09%	32.9%	STPVTVVLPDTK	99.7%	84.8	25	77.3	6	0	0	1256.71	183	194
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	26	29	92	0.09%	32.9%	TLDELGIHLTK	99.7%	65.4	25	65.4	4	0	0	1239.69	395	405
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	26	29	92	0.09%	32.9%	VADPVVTFCETVVETSSLK	99.7%	80.5	25	80.5	5	0	0	2081.05	655	673
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	26	29	92	0.09%	32.9%	VLGENYTLEDEEDSQICTVGR	99.7%	110	25	110	2	0	0	2427.10	509	529
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	26	29	92	0.09%	32.9%	VLSGTIHAGQPVK	99.7%	89.9	25	82.3	4	0	0	1306.75	496	508
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	26	29	92	0.09%	32.9%	VPAGNWVLIEGVDQPIVK	99.7%	86.1	25	86.1	1	0	0	1934.07	544	561
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	26	29	92	0.09%	32.9%	YDWDLLAAR	99.7%	66.2	25	56.6	4	0	0	1122.56	722	730
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	U5S1_HUMAN	109.4	100.0%	26	29	92	0.09%	32.9%	YHIEVNR	95.1%	28	25	11.9	1	0	0	930.48	537	543
14-3-3 protein beta/alpha	YWHAB	1433B_HUMAN	28.1	99.8%	2	2	3	0.00%	24.4%	AVTEQGHELSNEER	99.7%	57.8	25	51.1	1	0	0	1598.74	30	43
14-3-3 protein beta/alpha	YWHAB	1433B_HUMAN	28.1	99.8%	2	2	3	0.00%	24.4%	DSTLIMQLLR	99.7%	47.7	25	27.5	2	0	0	1205.66	215	224
14-3-3 protein beta/alpha	YWHAB	1433B_HUMAN	28.1	99.8%	2	2	3	0.00%	24.4%	EMQPTHPIR	99.6%	39.1	25	30	2	0	0	1108.56	161	169
14-3-3 protein beta/alpha	YWHAB	1433B_HUMAN	28.1	99.8%	2	2	3	0.00%	24.4%	NLLSVAYK	98.7%	33.3	25	14.2	1	0	0	907.52	44	51
14-3-3 protein beta/alpha	YWHAB	1433B_HUMAN	28.1	99.8%	2	2	3	0.00%	24.4%	VISSIEQK	97.2%	30.2	25	0	1	0	0	903.51	63	70
14-3-3 protein beta/alpha	YWHAB	1433B_HUMAN	28.1	99.8%	2	2	3	0.00%	24.4%	YLSEVASGDNK	99.7%	40.7	25	30.1	2	0	0	1182.56	130	140
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	4	4	8	0.01%	25.9%	DSTLIMQLLR	99.7%	47.7	25	27.5	2	0	0	1205.66	216	225
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	4	4	8	0.01%	25.9%	EAAENSLVAYK	99.7%	48.4	25	43.8	2	0	0	1194.60	143	153
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	4	4	8	0.01%	25.9%	LICCDILDVLDK	99.7%	69.3	25	64	2	0	0	1476.74	95	106
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	4	4	8	0.01%	25.9%	NLLSVAYK	98.7%	33.3	25	14.2	1	0	0	907.52	43	50
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	4	4	8	0.01%	25.9%	VAGMDVELTVEER	99.7%	97.1	25	86.1	2	0	0	1463.70	30	42
14-3-3 protein epsilon	YWHAE	1433E_HUMAN	29.2	100.0%	4	4	8	0.01%	25.9%	YLAEFATGNDRK	99.4%	36.8	25	30.7	2	0	0	1384.69	131	142

14-3-3 protein gamma	YWHAG	1433G_HUMAN	28.3	100.0%	3	3	5	0.00%	24.3%	AYSEAHEISK	99.7%	44	25	32.8	2	0	0	1134.54	153	162
14-3-3 protein gamma	YWHAG	1433G_HUMAN	28.3	100.0%	3	3	5	0.00%	24.3%	DSTLIMQLLR	99.7%	47.7	25	27.5	2	0	0	1205.66	218	227
14-3-3 protein gamma	YWHAG	1433G_HUMAN	28.3	100.0%	3	3	5	0.00%	24.3%	NLLSVAYK	98.7%	33.3	25	14.2	1	0	0	907.52	43	50
14-3-3 protein gamma	YWHAG	1433G_HUMAN	28.3	100.0%	3	3	5	0.00%	24.3%	NVTELNEPLSNEER	99.7%	92.6	25	92.3	2	0	0	1643.79	29	42
14-3-3 protein gamma	YWHAG	1433G_HUMAN	28.3	100.0%	3	3	5	0.00%	24.3%	VISSIEQK	97.2%	30.2	25	0	1	0	0	903.51	62	69
14-3-3 protein gamma	YWHAG	1433G_HUMAN	28.3	100.0%	3	3	5	0.00%	24.3%	YLAEVATGEK	99.1%	34.7	25	29.7	1	0	0	1080.56	133	142
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	4	4	5	0.00%	29.8%	AVTEQGAELSNEER	99.7%	99.9	25	90.8	2	0	0	1532.72	28	41
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	4	4	5	0.00%	29.8%	DSTLIMQLLR	99.7%	47.7	25	27.5	2	0	0	1205.66	213	222
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	4	4	5	0.00%	29.8%	EMQPTHPIR	99.6%	39.1	25	30	2	0	0	1108.56	159	167
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	4	4	5	0.00%	29.8%	NLLSVAYK	98.7%	33.3	25	14.2	1	0	0	907.52	42	49
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	4	4	5	0.00%	29.8%	SICTTVLELLDK	99.7%	40.9	25	34.6	1	0	0	1391.75	92	103
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	4	4	5	0.00%	29.8%	VISSIEQK	97.2%	30.2	25	0	1	0	0	903.51	61	68
14-3-3 protein theta	YWHAQ	1433T_HUMAN	27.8	100.0%	4	4	5	0.00%	29.8%	YLAEVACGDDRK	99.7%	52.6	25	47.4	1	0	0	1396.65	128	139
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	9	10	16	0.02%	44.5%	DICNDVLSLLEK	99.7%	57.9	25	45.4	2	0	0	1418.72	92	103
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	9	10	16	0.02%	44.5%	DSTLIMQLLR	99.7%	47.7	25	27.5	2	0	0	1205.66	213	222
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	9	10	16	0.02%	44.5%	EMQPTHPIR	99.6%	39.1	25	30	2	0	0	1108.56	159	167
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	9	10	16	0.02%	44.5%	FLIPNASQAESK	99.4%	36.8	25	28	2	0	0	1304.68	104	115
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	9	10	16	0.02%	44.5%	GIVDQSQQAYQEAFEISK	99.7%	95.6	25	95.6	2	0	0	2040.99	140	157
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	9	10	16	0.02%	44.5%	NLLSVAYK	98.7%	33.3	25	14.2	1	0	0	907.52	42	49
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	9	10	16	0.02%	44.5%	SVTEQGAELSNEER	99.7%	101	25	89.9	2	0	0	1548.71	28	41
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	9	10	16	0.02%	44.5%	VVSSIEQKTEGAEK	99.7%	47.2	25	42.3	1	0	0	1504.79	61	74
14-3-3 protein zeta/delta	YWHAZ	1433Z_HUMAN	27.7	100.0%	9	10	16	0.02%	44.5%	YLAEVAAGDDKK	99.7%	62.5	25	50.6	2	0	0	1279.65	128	139
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	99.8%	2	2	3	0.00%	4.8%	GEEVGELSR	99.6%	38.8	25	22.5	1	0	0	975.47	361	369
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	CN37_HUMAN	47.6	99.8%	2	2	3	0.00%	4.8%	RPPGVLHCTTK	99.1%	29.2	25	18.6	0	2	0	1265.68	245	255
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	10	12	21	0.02%	33.4%	ALQSVGQIVGEVLK	99.7%	92.1	25	89.9	2	0	0	1440.84	49	62
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	10	12	21	0.02%	33.4%	AVASQLDCNFLK	99.7%	66.5	25	59.7	2	0	0	1365.68	186	197
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	10	12	21	0.02%	33.4%	DHQPCIIFMDEIDAIGGR	98.6%	27.5	25	25.5	0	1	0	2086.97	224	241
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	10	12	21	0.02%	33.4%	EVIELPLTNPELFQR	99.7%	41.1	25	40.1	2	0	0	1797.97	147	161
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	10	12	21	0.02%	33.4%	HGEIDYEAIVK	99.7%	74.5	25	67.1	2	0	0	1273.64	323	333
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	10	12	21	0.02%	33.4%	IHAGPITK	97.9%	31.5	25	29.2	1	0	0	836.50	315	322
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	10	12	21	0.02%	33.4%	KIHIDLPNEQAR	99.7%	47.7	25	40	0	2	0	1433.79	298	309
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	10	12	21	0.02%	33.4%	NVCTEAGMFAIR	99.7%	71.4	25	60.1	4	0	0	1384.63	345	356
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	10	12	21	0.02%	33.4%	VALDMTTLTIMR	99.7%	86.8	25	86	3	0	0	1364.73	98	109
26S protease regulatory subunit 10B	PSMC6	PRS10_HUMAN	44.2	100.0%	10	12	21	0.02%	33.4%	VVSSSIVDKYIGESAR	99.7%	47.9	25	47.9	0	2	0	1709.91	198	213
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	18	23	47	0.04%	55.7%	AICTEAGLMALR	99.7%	74.5	25	65.4	4	0	0	1305.67	397	408
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	18	23	47	0.04%	55.7%	APQETYADIGGLDNQIQEIK	99.7%	101	25	98.6	2	0	0	2203.09	179	198
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	18	23	47	0.04%	55.7%	AVANQTSATFLR	99.7%	88.7	25	78.6	5	0	0	1278.68	238	249
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	18	23	47	0.04%	55.7%	DDLSGADIK	99.5%	38	25	24.5	2	0	0	933.45	388	396
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	18	23	47	0.04%	55.7%	GVILYGPPGTGK	99.7%	42.2	25	0	5	0	0	1158.65	221	232
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	18	23	47	0.04%	55.7%	IETLDPALIRPGR	96.9%	24.6	25	19.9	0	3	0	1450.84	334	346
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	18	23	47	0.04%	55.7%	IFQIHTSR	99.7%	47.2	25	33.2	2	0	0	1001.55	364	371
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	18	23	47	0.04%	55.7%	IKDYLLMEEEFIR	99.7%	37.9	25	36.7	0	2	0	1698.88	68	80
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	18	23	47	0.04%	55.7%	KIEFPLPDEK	99.7%	40.4	25	24	1	0	0	1215.66	350	359
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	18	23	47	0.04%	55.7%	KQEGTPEGLYL	99.7%	48.4	25	41.5	2	0	0	1234.63	430	440
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	18	23	47	0.04%	55.7%	KYEPPVPTR	99.5%	37.5	25	29.7	3	0	0	1086.59	24	32
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	18	23	47	0.04%	55.7%	LPLVTPHTQCR	99.7%	54.8	25	46.6	2	0	0	1321.70	49	59
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	18	23	47	0.04%	55.7%	MTLADDVTLDDLIMAK	99.7%	76.8	25	73.2	3	0	0	1764.88	372	387
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	18	23	47	0.04%	55.7%	NQEQMKPLEEKQEEER	99.7%	43.3	25	43.3	0	2	0	2044.96	81	96
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	18	23	47	0.04%	55.7%	TMLELLNQLDGFDSR	99.7%	109	25	105	5	0	0	1751.86	308	322
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	18	23	47	0.04%	55.7%	VAEEHAPSIVFIDEIDAIGTK	99.7%	71.1	25	71	2	2	0	2254.16	273	293
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	18	23	47	0.04%	55.7%	VAEEHAPSIVFIDEIDAIGTKR	99.7%	64.7	25	64.7	0	2	0	2410.26	273	294

26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	18	23	47	0.04%	55.7%	VHAVIGVLMDDTDPLVTVMK	99.7%	44.9	25	44	0	1	0	2153.13	156	175
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	18	23	47	0.04%	55.7%	VIMATNR	99.2%	35.5	25	29.2	2	0	0	804.44	327	333
26S protease regulatory subunit 4	PSMC1	PRS4_HUMAN	49.2	100.0%	18	23	47	0.04%	55.7%	VVGSELIQK	99.7%	75.9	25	62.9	2	0	0	972.57	250	258
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	17	25	46	0.04%	44.4%	AMEVDERPTEQYSDIGGLDK	99.7%	66.4	25	66.4	0	3	0	2253.03	174	193
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	17	25	46	0.04%	44.4%	APSIIFIDELDAIGTK	99.7%	91.4	25	91.4	2	0	0	1702.93	279	294
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	17	25	46	0.04%	44.4%	AVCVEAGMIALR	99.7%	62.4	25	57.6	3	0	0	1305.67	398	409
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	17	25	46	0.04%	44.4%	DSYLILETLPTEYDSR	99.7%	80.3	25	79.8	2	0	0	1914.93	156	171
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	17	25	46	0.04%	44.4%	EKAPSIIFIDELDAIGTK	99.7%	79.5	25	79.5	2	2	0	1960.06	277	294
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	17	25	46	0.04%	44.4%	EKFENLGIQPPK	99.7%	49.3	25	44.8	2	0	0	1399.76	210	221
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	17	25	46	0.04%	44.4%	FENLGIQPPK	99.7%	44.6	25	21.8	2	0	0	1142.62	212	221
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	17	25	46	0.04%	44.4%	GVLMYGPPGTGK	99.7%	74.1	25	71.5	4	0	0	1176.61	222	233
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	17	25	46	0.04%	44.4%	IMQIHSR	99.2%	35.2	25	19.3	1	0	0	884.48	365	371
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	17	25	46	0.04%	44.4%	KMNVSPDVNYEELAR	99.7%	63.2	25	58.1	0	4	0	1780.85	372	386
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	17	25	46	0.04%	44.4%	LAGPQLVQMFIGDGAK	99.7%	82.9	25	82.9	2	0	0	1644.88	251	266
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	17	25	46	0.04%	44.4%	LLDSEIK	97.6%	30.8	25	11.5	2	0	0	817.47	47	53
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	17	25	46	0.04%	44.4%	MSTEEIIQR	99.7%	64.7	25	45	4	0	0	1106.55	36	44
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	17	25	46	0.04%	44.4%	QTYFLPVIGLVDAEK	99.7%	87.8	25	74.9	2	0	0	1692.92	130	144
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	17	25	46	0.04%	44.4%	TMLELLNQLDGFQPNTQVK	99.7%	82.4	25	82.4	4	0	0	2189.13	309	327
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	17	25	46	0.04%	44.4%	VDILDPALLR	99.7%	51.5	25	37	2	0	0	1124.67	335	344
26S protease regulatory subunit 6A	PSMC3	PRS6A_HUMAN	49.2	100.0%	17	25	46	0.04%	44.4%	VIAATNRVDILDPALLR	99.7%	67.8	25	67.8	1	2	0	1850.09	328	344
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	36	0.03%	42.6%	ADTLDPALLRPGR	95.5%	28.4	25	26	2	0	0	1394.78	314	326
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	36	0.03%	42.6%	AVAHHTTAAFIR	99.7%	63.3	25	59.4	2	2	0	1294.70	218	229
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	36	0.03%	42.6%	EAVELPLTHFELYK	99.7%	61.6	25	58.4	2	0	0	1688.89	179	192
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	36	0.03%	42.6%	EFLHAQEEVKR	99.7%	41.9	25	25.5	2	0	0	1385.72	71	81
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	36	0.03%	42.6%	ELLKPNASVALHK	99.7%	45.1	25	43.8	0	2	0	1419.83	122	134
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	36	0.03%	42.6%	ENAPAIIFIDEIDAIATK	99.7%	80.4	25	80.4	2	1	0	1944.03	256	273
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	36	0.03%	42.6%	FDAQTGADREVQR	99.0%	34.4	25	27.9	2	1	0	1492.71	275	287
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	36	0.03%	42.6%	GVLMYGPPGCGK	99.7%	57.4	25	57.4	4	0	0	1251.59	201	212
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	36	0.03%	42.6%	ILLELLNQMDGFDQNVNVK	99.7%	91.7	25	91.7	3	1	0	2219.14	288	306
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	36	0.03%	42.6%	LIFSTITSK	99.6%	38.8	25	35.3	2	0	0	1009.59	343	351
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	36	0.03%	42.6%	MNLSEEVDLEDYVARPDK	99.7%	90.7	25	90.7	2	0	0	2138.99	352	369
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	36	0.03%	42.6%	QIGIDPPR	99.4%	37.1	25	27.3	1	0	0	895.50	193	200
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	36	0.03%	42.6%	RFDAQTGADR	99.1%	34.8	25	11.6	1	0	0	1136.54	274	283
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	36	0.03%	42.6%	RLIFSTITSK	99.4%	36.5	25	36.5	2	0	0	1165.69	342	351
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	36	0.03%	42.6%	VIMATNR	99.2%	35.5	25	29.2	2	0	0	804.44	307	313
26S protease regulatory subunit 6B	PSMC4	PRS6B_HUMAN	47.4	100.0%	15	21	36	0.03%	42.6%	VVGSEFVQK	99.7%	78.6	25	64.9	2	0	0	992.54	230	238
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	52	0.05%	52.9%	ALDEGDIALLK	99.7%	79.8	25	61.9	2	0	0	1157.64	24	34
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	52	0.05%	52.9%	DIRFELLAR	96.7%	29.5	25	17	1	0	0	1132.65	367	375
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	52	0.05%	52.9%	ELFEMAR	97.8%	31.2	25	25.7	1	0	0	895.43	259	265
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	52	0.05%	52.9%	FDDGAGGDNEVQR	99.7%	85.4	25	85.1	3	0	0	1379.58	285	297
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	52	0.05%	52.9%	FVNLGIEPPK	99.7%	58.4	25	34.8	4	0	0	1113.63	201	210
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	52	0.05%	52.9%	FVNLGIEPPKGVLLFGPPGTGK	99.7%	48.1	25	48.1	0	2	0	2237.27	201	222
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	52	0.05%	52.9%	FVVDLSDQVAPTDIEEGMR	99.7%	96.7	25	88.4	4	0	0	2121.02	121	139
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	52	0.05%	52.9%	GVLLFGPPGTGK	99.7%	75.2	25	72.1	2	0	0	1142.66	211	222
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	52	0.05%	52.9%	IATEKDFLEAVNK	99.7%	73.1	25	64.3	2	1	0	1477.79	403	415
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	52	0.05%	52.9%	IEFSLPDLEGR	99.7%	51.5	25	43.6	2	0	0	1275.66	341	351
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	52	0.05%	52.9%	IINADSEDPK	99.7%	52.1	25	50.4	1	0	0	1101.54	101	110
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	52	0.05%	52.9%	IINADSEDPKYIINVK	99.7%	90.7	25	84.1	2	0	0	1831.98	101	116
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	52	0.05%	52.9%	KIEFSLPDLEGR	99.7%	71.9	25	58.3	2	0	0	1403.75	340	351
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	52	0.05%	52.9%	KINELTGIK	99.7%	47.7	25	34.3	2	0	0	1015.61	58	66
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	52	0.05%	52.9%	LCPNSTGAEIR	99.7%	64.5	25	41.8	2	0	0	1217.59	376	386

26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	52	0.05%	52.9%	LREVVETPLLHPER	99.7%	63.5	25	63.5	1	2	0	1687.95	187	200
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	52	0.05%	52.9%	PDYLGADQRK	99.7%	39.4	25	23.3	2	0	0	1162.59	2	11
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	52	0.05%	52.9%	QVEDDIQQLLK	99.7%	61.9	25	55.2	1	0	0	1328.71	47	57
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	52	0.05%	52.9%	SVCTEAGMFAIR	99.7%	56.7	25	53.2	4	0	0	1357.62	387	398
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	52	0.05%	52.9%	TDACFIR	99.7%	45.5	25	29.7	2	0	0	882.41	233	239
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	52	0.05%	52.9%	TMLELINQLDGFDPR	99.7%	79.5	25	77.9	4	0	0	1777.88	298	312
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	52	0.05%	52.9%	TYGQSTYSR	99.0%	34.7	25	32	1	0	0	1062.49	35	43
26S protease regulatory subunit 7	PSMC2	PRS7_HUMAN	48.6	100.0%	23	28	52	0.05%	52.9%	VIGSELVQK	99.7%	52.4	25	36.9	2	0	0	972.57	240	248
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	27	60	0.06%	55.7%	AVAHHTDCTFIR	99.7%	49.2	25	42.5	2	2	0	1427.68	202	213
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	27	60	0.06%	55.7%	EELQLLQEQGSYVGEVVR	99.7%	88.7	25	85	1	0	0	2076.06	61	78
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	27	60	0.06%	55.7%	EHAPSIIFMDEIDSIGSSR	99.7%	57.5	25	54.6	0	4	0	2104.00	240	258
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	27	60	0.06%	55.7%	ELFVMAR	99.7%	39.4	25	34.3	4	0	0	865.46	233	239
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	27	60	0.06%	55.7%	FVVDVDKNIDINDVTPNCR	99.7%	69.6	25	65.8	0	1	0	2233.09	95	113
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	27	60	0.06%	55.7%	GVCTEAGMYALR	99.7%	74.2	25	67.7	4	0	0	1327.61	361	372
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	27	60	0.06%	55.7%	GVLLYGPPGTGK	99.7%	42.2	25	0	5	0	0	1158.65	185	196
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	27	60	0.06%	55.7%	IAELMPGASGAEVK	99.7%	63.8	25	48.6	4	0	0	1388.71	347	360
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	27	60	0.06%	55.7%	IDILDSALLRPGR	99.7%	48.2	25	41.1	2	2	0	1438.84	298	310
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	27	60	0.06%	55.7%	IEELQLIVNDK	99.7%	96.3	25	89.2	2	0	0	1313.73	28	38
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	27	60	0.06%	55.7%	LEGGSGGDSEVQR	99.7%	87.4	25	82.6	5	0	0	1290.59	259	271
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	27	60	0.06%	55.7%	LLREELQLLQEQGSYVGEVVR	99.7%	44	25	44	0	1	0	2458.33	58	78
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	27	60	0.06%	55.7%	RVHVTQEDFEMAVAK	99.7%	63.5	25	63.5	0	4	0	1759.88	375	389
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	27	60	0.06%	55.7%	TMLELLNQLDGFEATK	99.7%	112	25	109	4	0	0	1838.92	272	287
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	27	60	0.06%	55.7%	VALRNDSYTLHK	99.7%	38.7	25	34.5	0	2	0	1416.76	114	125
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	27	60	0.06%	55.7%	VIMATNR	99.2%	35.5	25	29.2	2	0	0	804.44	291	297
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	27	60	0.06%	55.7%	VPDSTYEMIGGLDK	99.7%	88.3	25	88.3	4	0	0	1524.73	143	156
26S protease regulatory subunit 8	PSMC5	PRS8_HUMAN	45.6	100.0%	18	27	60	0.06%	55.7%	VSGSELVQK	99.7%	65.1	25	34.2	5	0	0	946.52	214	222
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	28	53	0.05%	34.0%	AAVESLGFILFR	99.7%	77.7	25	77.1	5	0	0	1322.75	617	628
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	28	53	0.05%	34.0%	DNLEWLAR	99.7%	45.1	25	36.8	2	0	0	1016.52	388	395
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	28	53	0.05%	34.0%	DTSEDIEELVEPVAAHGPK	99.7%	71	25	70.2	2	2	0	2035.98	916	934
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	28	53	0.05%	34.0%	EAINLLEPMTNDPVNYVR	99.7%	91.6	25	91.6	4	0	0	2088.04	667	684
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	28	53	0.05%	34.0%	EALQLMATYLPK	99.7%	60	25	55	4	0	0	1377.74	418	429
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	28	53	0.05%	34.0%	FTATASLGVIHK	99.7%	34.2	25	33.4	0	2	0	1244.70	402	413
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	28	53	0.05%	34.0%	GLAVGIALVMYGR	99.7%	70.3	25	70.3	2	0	0	1335.75	547	559
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	28	53	0.05%	34.0%	HGGSLGLGLAAMGTAR	99.7%	38.7	25	38.6	0	1	0	1468.77	475	490
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	28	53	0.05%	34.0%	LLHVAVSDVNDDVRR	99.7%	49.3	25	49.3	0	2	0	1707.91	602	616
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	28	53	0.05%	34.0%	MEEADALIESLCR	99.7%	96.6	25	87.2	3	0	0	1552.70	560	572
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	28	53	0.05%	34.0%	NAQAIEDMVGYAQETQHEK	99.7%	46.5	25	46.5	0	2	0	2161.98	525	543
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	28	53	0.05%	34.0%	NNNTDLMILK	99.7%	46.5	25	34.9	3	0	0	1191.60	345	354
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	28	53	0.05%	34.0%	QAIGIALETR	99.7%	58.8	25	45.3	2	0	0	1071.62	149	158
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	28	53	0.05%	34.0%	QDVYDLLK	99.7%	57.9	25	34.4	1	0	0	993.53	491	498
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	28	53	0.05%	34.0%	QFAALVASK	99.7%	54.6	25	35.4	2	0	0	934.54	58	66
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	28	53	0.05%	34.0%	SNCKPSTFAYPAPLEVPK	99.1%	29.4	25	27.8	0	2	0	2006.01	804	821
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	28	53	0.05%	34.0%	TILESNDVPGMLAYSLK	99.7%	100	25	99.1	2	0	0	1850.96	166	182
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	28	53	0.05%	34.0%	TNLYQDDAVTGEAAGLALGLVMLGSK	99.7%	59.3	25	59.3	0	1	0	2607.33	499	524
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	28	53	0.05%	34.0%	TPEQCPSVVSLLSESYNPHVR	99.7%	62.3	25	62.3	0	2	0	2399.17	629	649
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	28	53	0.05%	34.0%	VINDKHDDVMAK	99.7%	72.5	25	65.1	2	0	0	1384.69	716	727
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	28	53	0.05%	34.0%	VLTMPETCR	98.9%	34.2	25	29	1	0	0	1106.53	891	899
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	28	53	0.05%	34.0%	VSTAVLSITAK	99.7%	90.5	25	88.6	2	0	0	1089.65	828	838
26S proteasome non-ATPase regulatory subunit 1	PSMD1	PSMD1_HUMAN	105.8	100.0%	23	28	53	0.05%	34.0%	YQPFKPLSIGGIIILK	99.7%	40.6	25	40.6	2	0	0	1787.08	900	915
26S proteasome non-ATPase regulatory subunit 10	PSMD10	PSD10_HUMAN	24.4	100.0%	2	2	3	0.00%	17.3%	ASTNIQDTEGNTPLHLACDEERVEEAK	99.7%	72.5	25	72.5	0	2	0	3027.40	163	189
26S proteasome non-ATPase regulatory subunit 10	PSMD10	PSD10_HUMAN	24.4	100.0%	2	2	3	0.00%	17.3%	LEELKESILADK	99.7%	56.7	25	44.5	1	0	0	1387.77	19	30

26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	3	3	5	0.00%	8.5%	EQSILELGSLLAK	99.7%	47.7	25	47.7	2	0	0	1400.80	47	59
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	3	3	5	0.00%	8.5%	LYDNLLEQNLIR	99.7%	63.2	25	59	2	0	0	1503.82	326	337
26S proteasome non-ATPase regulatory subunit 11	PSMD11	PSD11_HUMAN	47.5	100.0%	3	3	5	0.00%	8.5%	VQIEHISSLIK	99.5%	37.3	25	35.9	1	0	0	1266.74	345	355
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	3	3	5	0.00%	7.5%	LNIGDLQVTK	99.5%	37.7	25	27.8	2	0	0	1100.63	123	132
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	3	3	5	0.00%	7.5%	SSDEAVILCK	99.7%	51.2	25	29	2	0	0	1121.55	106	115
26S proteasome non-ATPase regulatory subunit 13	PSMD13	PSD13_HUMAN	42.9	100.0%	3	3	5	0.00%	7.5%	VLDLQQIK	97.4%	30.4	25	23	1	0	0	956.58	340	347
26S proteasome non-ATPase regulatory subunit 14	PSMD14	PSDE_HUMAN	34.6	100.0%	4	5	9	0.01%	20.0%	AVAVVVDPIQSVK	99.7%	85.9	25	81.6	2	0	0	1324.78	140	152
26S proteasome non-ATPase regulatory subunit 14	PSMD14	PSDE_HUMAN	34.6	100.0%	4	5	9	0.01%	20.0%	AVEEEDKMTPEQLAIK	99.7%	58.6	25	58.2	3	0	0	1846.91	258	273
26S proteasome non-ATPase regulatory subunit 14	PSMD14	PSDE_HUMAN	34.6	100.0%	4	5	9	0.01%	20.0%	VIDVFAMPQSGTGVSVEAVDPVFQAK	98.4%	27	25	27	0	2	0	2707.37	69	94
26S proteasome non-ATPase regulatory subunit 14	PSMD14	PSDE_HUMAN	34.6	100.0%	4	5	9	0.01%	20.0%	VVIDAFR	99.7%	42.4	25	34.9	2	0	0	819.47	155	161
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	APVQPQQSPAAAPGGTDEKPSGK	99.7%	59.1	25	58.8	0	2	0	2218.11	9	31
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	AVPLALALISVSNPR	99.7%	73.9	25	73.9	4	3	0	1520.92	689	703
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	CALGVFR	99.7%	40.3	25	35	2	0	0	822.43	251	257
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	DIDENAYAK	99.2%	35.5	25	35.5	1	0	0	1038.47	220	228
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	DKAPVQPQQSPAAAPGGTDEKPSGK	99.7%	53.5	25	53.5	0	1	0	2461.23	7	31
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	DPNNLFMVR	99.7%	45.2	25	38.1	4	0	0	1121.54	755	763
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	DTSLYRPALEELRR	99.7%	36	25	35	0	2	0	1718.92	67	80
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	EDVLTLLLPVMGDSK	99.7%	77.7	25	72.4	4	0	0	1629.88	495	509
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	ELDIMEPK	99.6%	38.8	25	18.8	3	0	0	990.48	336	343
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	EPLLTLVK	98.2%	32	25	26.7	1	0	0	912.58	182	189
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	EWQELDDAEK	99.7%	50.1	25	43.8	2	0	0	1262.55	169	178
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	FAADIISVLAMTMSGER	99.7%	94.9	25	34.3	6	0	0	1827.90	121	137
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	FGGSGSQVDSAR	99.7%	100	25	86.1	5	0	0	1167.54	358	369
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	FLRPHYGK	96.9%	29.8	25	17.1	2	0	0	1017.56	98	105
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	GTLTLCPYHSDR	99.7%	56.3	25	56	2	0	0	1419.67	774	785
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	LAQGLTHLGK	99.7%	46.9	25	46.9	2	0	0	1037.61	764	773
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	LGSIFGLGLAYAGSNR	99.7%	116	25	116	2	2	0	1595.85	479	494
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	LLTDDGNKWLYK	99.6%	38.3	25	34.3	1	0	0	1465.77	390	401
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	LNILDTLSK	99.7%	49.3	25	25.6	2	0	0	1016.60	704	712
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	LVGSQEELASWGHEYVR	99.7%	75.3	25	62.9	1	2	0	1959.96	144	160
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	MLVTFDEELRPLPVSVR	99.7%	38	25	34.4	1	2	0	2001.08	829	845
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	MNLASSFVNGFVNAAFGQDK	99.7%	96.8	25	96.8	1	0	0	2133.01	370	389
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	NECDPALALLSDYVLHNSNTMR	99.7%	47.5	25	47.5	0	2	0	2549.18	457	478
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	QMAFMLGR	98.6%	33.2	25	26.3	1	0	0	953.47	293	300
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	SETELKDTYAR	99.7%	52.4	25	52.4	2	1	0	1312.64	546	556
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	SFANTLVDVCAYAGSGNVLK	99.7%	130	25	124	2	0	0	2086.03	589	608
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	SGALLACGIVNSGVR	99.7%	88.7	25	83.6	2	0	0	1473.78	442	456
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	SSTTSMTSVPKPLK	99.7%	76.5	25	76.4	4	0	0	1463.78	84	97
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	TITGFQTHTTPVLLAHGER	99.7%	44.7	25	44.7	0	2	0	2079.10	861	879
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	VGQAVDVVGQAGKPK	99.7%	88.7	25	83.2	4	1	0	1452.82	846	860
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	VQQLLHICSEHFDSK	99.7%	33.6	25	31.8	0	2	0	1840.90	609	623
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	WLPLGLGLNHLGK	99.7%	54.7	25	54.7	2	0	0	1417.83	557	569
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	YGEPTLR	99.1%	34.8	25	33.4	2	0	0	835.43	681	687
26S proteasome non-ATPase regulatory subunit 2	PSMD2	PSMD2_HUMAN	100.2	100.0%	34	45	89	0.08%	48.3%	YLYSSEDYIK	99.7%	56.4	25	48.9	2	0	0	1280.60	432	441
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	AIQLEYSEAR	99.7%	77.9	25	72.2	2	0	0	1179.60	297	306
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	AIQLEYSEARR	96.1%	28.9	25	22.2	1	0	0	1335.70	297	307
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	AIRDGVIEASINHEK	97.8%	25.9	25	25.9	0	2	0	1651.88	441	455
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	ALDLVAAK	99.7%	47.3	25	26.9	2	0	0	800.49	202	209
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	APQHTAVGFK	99.7%	45.5	25	37.6	2	0	0	1055.56	316	325
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	AVQGFFTSNNATR	99.7%	81.5	25	81.5	2	0	0	1412.69	116	128
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	CYYYHAR	95.6%	28.5	25	28.5	1	0	0	1032.44	210	216

26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	DGVIEASINHEK	99.7%	52.2	25	34.9	2	0	0	1311.65	444	455
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	DLESAEERR	99.3%	36.1	25	27.4	2	0	0	1104.53	504	512
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	ELDTVTLEDIKEHVK	99.7%	77.9	25	74.1	2	1	0	1768.93	66	80
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	EMIDIYSTR	99.7%	65.6	25	52	4	0	0	1127.54	462	470
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	EPQLAFHQR	99.7%	54.7	25	42.4	2	0	0	1125.58	471	479
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	EQQDLEFAK	99.6%	38.3	25	34.2	1	0	0	1107.53	515	523
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	EREQQDLEFAK	99.7%	49.7	25	42	2	0	0	1392.68	513	523
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	FNQVLDQFGEK	99.7%	74.5	25	51.2	2	0	0	1324.65	375	385
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	HDADGQATLLNLLLR	99.7%	117	25	117	2	2	0	1649.90	242	256
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	ISDDLMQK	99.7%	55	25	36.7	3	0	0	949.47	187	194
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	ISFCLDIHNMSVK	99.7%	41.1	25	38.8	1	0	0	1563.77	480	492
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	ISLADIAQK	99.7%	70.7	25	31	2	0	0	958.56	417	425
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	LQLDSPEDAEFIVAK	99.7%	101	25	88.3	2	0	0	1674.86	426	440
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	MISLSYSR	99.7%	42.7	25	23	2	0	0	972.48	409	416
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	NYLHYSLYDQAEK	99.7%	78.1	25	65.4	2	2	0	1643.77	257	269
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	RLNHYVLYK	99.2%	30	25	25.1	0	1	0	1205.68	107	115
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	SLMPYFLLTQAVR	99.7%	86.9	25	81.6	6	0	0	1554.84	356	368
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	SVFPEQANNNEWAR	99.7%	78.3	25	77.5	2	0	0	1661.77	274	287
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	VYEFLDKLDVVR	99.7%	74	25	67.2	2	2	0	1495.82	217	228
26S proteasome non-ATPase regulatory subunit 3	PSMD3	PSMD3_HUMAN	61.0	100.0%	27	35	63	0.06%	49.4%	YLYYTGR	99.6%	39.3	25	28.3	2	0	0	935.46	288	294
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	3	3	4	0.00%	13.5%	AAAASAAEAGIATTGTEDSDDALLK	99.7%	53.5	25	53.5	0	1	0	2320.12	238	262
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	3	3	4	0.00%	13.5%	IIAFVGSPVEDNEKDLVK	99.7%	63.5	25	60.9	1	0	0	1973.06	109	126
26S proteasome non-ATPase regulatory subunit 4	PSMD4	PSMD4_HUMAN	40.7	100.0%	3	3	4	0.00%	13.5%	ITFCTGIR	99.7%	43.5	25	34.3	2	0	0	967.50	84	91
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	14	18	32	0.03%	39.1%	DNNMAPYYEALCK	99.7%	59	25	49.4	2	0	0	1604.67	47	59
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	14	18	32	0.03%	39.1%	FLLSLPEHR	99.7%	42	25	35.1	2	0	0	1111.63	24	32
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	14	18	32	0.03%	39.1%	GAEILEVLHSLPAVR	99.7%	88.5	25	88.5	2	0	0	1603.92	243	257
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	14	18	32	0.03%	39.1%	GDAAVRDELMAAVR	99.7%	45	25	41.4	1	3	0	1489.74	33	46
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	14	18	32	0.03%	39.1%	IDKVNEIVETNRPDSK	99.7%	41.4	25	41.4	0	2	0	1856.97	347	362
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	14	18	32	0.03%	39.1%	IGLFYMDNDLITR	99.7%	89.4	25	88.9	4	0	0	1570.79	147	159
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	14	18	32	0.03%	39.1%	IHAYSQLLESYR	99.7%	56.6	25	45.3	2	1	0	1479.76	301	312
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	14	18	32	0.03%	39.1%	KGDLLLNR	99.7%	51.1	25	38.8	2	0	0	928.56	372	379
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	14	18	32	0.03%	39.1%	LDEELEDAEK	99.7%	61.3	25	46.6	2	0	0	1190.54	84	93
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	14	18	32	0.03%	39.1%	LDIVFYLLR	99.7%	64.1	25	47	2	0	0	1151.68	138	146
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	14	18	32	0.03%	39.1%	PLENLEEEGLPK	99.7%	77.5	25	77.5	2	0	0	1367.71	2	13
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	14	18	32	0.03%	39.1%	QYLFSLYECR	99.7%	55.1	25	53.1	1	0	0	1378.65	258	267
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	14	18	32	0.03%	39.1%	VNEIVETNRPDSK	99.7%	56.8	25	41.4	2	0	0	1500.77	350	362
26S proteasome non-ATPase regulatory subunit 6	PSMD6	PSMD6_HUMAN	45.5	100.0%	14	18	32	0.03%	39.1%	VYQGLYCVAIR	99.7%	89.8	25	89.8	2	0	0	1341.70	182	192
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	6	6	8	0.01%	16.3%	DIQTNVYIK	99.4%	37	25	26.5	2	0	0	1093.59	219	227
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	6	6	8	0.01%	16.3%	ILFFNTPK	99.4%	36.5	25	22.2	1	0	0	979.56	290	297
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	6	6	8	0.01%	16.3%	ILFTEATR	99.5%	38.1	25	25.8	1	0	0	950.53	282	289
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	6	6	8	0.01%	16.3%	LVLLELNFLPTTGTK	99.7%	70.6	25	70.6	2	0	0	1658.97	121	135
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	6	6	8	0.01%	16.3%	QVIEYAR	98.5%	32.6	25	15.5	1	0	0	878.47	338	344
26S proteasome non-ATPase regulatory subunit 8	PSMD8	PSMD8_HUMAN	39.6	100.0%	6	6	8	0.01%	16.3%	VAEFHTELER	98.3%	32.2	25	25.8	1	0	0	1230.61	205	214
26S proteasome non-ATPase regulatory subunit 9	PSMD9	PSMD9_HUMAN	24.7	99.8%	2	2	3	0.00%	9.9%	ANYDVLESQK	99.5%	37.2	25	30.3	2	0	0	1166.57	39	48
26S proteasome non-ATPase regulatory subunit 9	PSMD9	PSMD9_HUMAN	24.7	99.8%	2	2	3	0.00%	9.9%	KLGQSESQGPPR	99.7%	54	25	53.4	1	0	0	1283.67	123	134
28S ribosomal protein S10, mitochondrial	MRPS10	RT10_HUMAN	23.0	100.0%	3	4	14	0.01%	18.9%	AVLDSYEYFAVLAAK	99.7%	79.7	25	79.7	4	0	0	1659.86	86	100
28S ribosomal protein S10, mitochondrial	MRPS10	RT10_HUMAN	23.0	100.0%	3	4	14	0.01%	18.9%	FTLLQSVHIYK	99.7%	72.5	25	66.1	4	0	0	1348.76	118	128
28S ribosomal protein S10, mitochondrial	MRPS10	RT10_HUMAN	23.0	100.0%	3	4	14	0.01%	18.9%	NLPEGVAMEVTK	99.7%	44.6	25	33.2	6	0	0	1287.66	163	174
28S ribosomal protein S11, mitochondrial	MRPS11	RT11_HUMAN	20.6	100.0%	3	4	8	0.01%	14.4%	GTGIAAQTAGIAAAAR	99.7%	75.7	25	66.8	2	0	0	1399.77	123	138
28S ribosomal protein S11, mitochondrial	MRPS11	RT11_HUMAN	20.6	100.0%	3	4	8	0.01%	14.4%	KFEEIPIAHIK	99.7%	38.3	25	38.3	0	2	0	1324.76	79	89
28S ribosomal protein S11, mitochondrial	MRPS11	RT11_HUMAN	20.6	100.0%	3	4	8	0.01%	14.4%	KGTGIAAQTAGIAAAAR	99.7%	123	25	116	2	2	0	1527.86	122	138

28S ribosomal protein S12, mitochondrial	MRPS12	RT12_HUMAN	15.2	100.0%	3	3	7	0.01%	15.2%	GVVLCTFTR	99.6%	39.1	25	20.9	4	0	0	1052.56	60	68
28S ribosomal protein S12, mitochondrial	MRPS12	RT12_HUMAN	15.2	100.0%	3	3	7	0.01%	15.2%	KLGPTEGRPQLK	98.4%	27	25	21.1	0	1	0	1323.77	48	59
28S ribosomal protein S12, mitochondrial	MRPS12	RT12_HUMAN	15.2	100.0%	3	3	7	0.01%	15.2%	LGPTEGRPQLK	99.7%	41.5	25	30	2	0	0	1195.68	49	59
28S ribosomal protein S14, mitochondrial	MRPS14	RT14_HUMAN	15.1	100.0%	4	5	8	0.01%	30.5%	HLADHGQLSGIQR	99.7%	39.2	25	31	0	1	0	1431.75	113	125
28S ribosomal protein S14, mitochondrial	MRPS14	RT14_HUMAN	15.1	100.0%	4	5	8	0.01%	30.5%	ILQDVADEEIAALPR	99.7%	73.4	25	65.1	3	0	0	1652.89	66	80
28S ribosomal protein S14, mitochondrial	MRPS14	RT14_HUMAN	15.1	100.0%	4	5	8	0.01%	30.5%	MAYEYADER	99.7%	45.2	25	45.2	3	0	0	1163.47	43	51
28S ribosomal protein S14, mitochondrial	MRPS14	RT14_HUMAN	15.1	100.0%	4	5	8	0.01%	30.5%	MAYEYADERLR	98.4%	32.5	25	32.5	1	0	0	1416.66	43	53
28S ribosomal protein S15, mitochondrial	MRPS15	RT15_HUMAN	29.8	100.0%	3	3	7	0.01%	10.5%	IVANPEDTR	99.7%	45.9	25	36.6	3	0	0	1014.52	115	123
28S ribosomal protein S15, mitochondrial	MRPS15	RT15_HUMAN	29.8	100.0%	3	3	7	0.01%	10.5%	NTNYDVFEK	99.7%	39.4	25	35.1	2	0	0	1129.52	172	180
28S ribosomal protein S15, mitochondrial	MRPS15	RT15_HUMAN	29.8	100.0%	3	3	7	0.01%	10.5%	YLLMSIDQR	99.7%	47.2	25	34.3	2	0	0	1138.59	155	163
28S ribosomal protein S16, mitochondrial	MRPS16	RT16_HUMAN	15.3	100.0%	3	4	8	0.01%	26.3%	AREVLLASQK	99.7%	58.8	25	50.3	2	0	0	1114.66	115	124
28S ribosomal protein S16, mitochondrial	MRPS16	RT16_HUMAN	15.3	100.0%	3	4	8	0.01%	26.3%	FVEQLGSYDPLPNSHGEK	99.7%	64.4	25	64.4	2	2	0	2016.97	47	64
28S ribosomal protein S16, mitochondrial	MRPS16	RT16_HUMAN	15.3	100.0%	3	4	8	0.01%	26.3%	LVALNLDR	99.7%	57.6	25	46.3	2	0	0	913.55	65	72
28S ribosomal protein S17, mitochondrial	MRPS17	RT17_HUMAN	14.5	100.0%	2	2	4	0.00%	15.4%	HELAEIVFK	99.7%	49.1	25	49.1	2	0	0	1085.60	79	87
28S ribosomal protein S17, mitochondrial	MRPS17	RT17_HUMAN	14.5	100.0%	2	2	4	0.00%	15.4%	NLEELNISSAQ	99.7%	81.3	25	61	2	0	0	1217.60	120	130
28S ribosomal protein S18a, mitochondrial	MRPS18A	RT18A_HUMAN	22.2	100.0%	3	4	9	0.01%	16.8%	ESPNPPNPSGQCPICR	99.7%	50.6	25	50.6	4	0	0	1809.80	59	74
28S ribosomal protein S18a, mitochondrial	MRPS18A	RT18A_HUMAN	22.2	100.0%	3	4	9	0.01%	16.8%	LPEGVVPK	97.5%	30.7	25	27.6	1	0	0	838.50	135	142
28S ribosomal protein S18a, mitochondrial	MRPS18A	RT18A_HUMAN	22.2	100.0%	3	4	9	0.01%	16.8%	MPVGSPLLR	99.7%	42.2	25	20.8	4	0	0	969.56	174	182
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	5	6	12	0.01%	30.2%	APSEEDSLSSVPISPYKDEPWK	99.7%	35.5	25	35.5	0	1	0	2461.18	36	57
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	5	6	12	0.01%	30.2%	LYQGHLQEESGPPPESMPK	99.7%	53	25	46.3	0	3	0	2140.00	219	237
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	5	6	12	0.01%	30.2%	TPAEASSTGQTGPQSAL	99.7%	72.1	25	69.6	2	0	0	1602.76	242	258
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	5	6	12	0.01%	30.2%	VVGNPCPICR	99.7%	50.9	25	45.3	2	0	0	1171.57	100	109
28S ribosomal protein S18b, mitochondrial	MRPS18B	RT18B_HUMAN	29.4	100.0%	5	6	12	0.01%	30.2%	YLESEEYQER	99.7%	61.7	25	61.7	4	0	0	1345.59	58	67
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	5	5	10	0.01%	14.2%	FMEPYIFGSR	99.7%	43	25	35.7	2	0	0	1246.59	101	110
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	5	5	10	0.01%	14.2%	GIILFISR	99.7%	57.5	25	47.8	2	0	0	918.58	140	147
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	5	5	10	0.01%	14.2%	HSDFFNVK	99.7%	43.9	25	32.3	2	0	0	993.48	69	76
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	5	5	10	0.01%	14.2%	LFQTAITR	99.7%	65.3	25	47.7	2	0	0	949.55	252	259
28S ribosomal protein S2, mitochondrial	MRPS2	RT02_HUMAN	33.3	100.0%	5	5	10	0.01%	14.2%	LLFGPTVR	96.9%	29.8	25	12.5	2	0	0	902.55	181	188
28S ribosomal protein S21, mitochondrial	MRPS21	RT21_HUMAN	10.7	100.0%	3	6	10	0.01%	39.1%	ILTMDGLIEDIK	99.7%	44.7	25	33.5	2	0	0	1376.73	29	40
28S ribosomal protein S21, mitochondrial	MRPS21	RT21_HUMAN	10.7	100.0%	3	6	10	0.01%	39.1%	IYNMEMAR	99.7%	48.8	25	38.1	2	0	0	1027.47	63	70
28S ribosomal protein S21, mitochondrial	MRPS21	RT21_HUMAN	10.7	100.0%	3	6	10	0.01%	39.1%	TVMVQEGNVESAYR	99.7%	103	25	96.3	6	0	0	1598.75	11	24
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	6	7	14	0.01%	16.9%	DQAAEGINLIK	99.7%	75.4	25	63.7	2	0	0	1171.63	319	329
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	6	7	14	0.01%	16.9%	IDGLLIDQIQR	99.7%	58.2	25	44.1	2	0	0	1283.73	281	291
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	6	7	14	0.01%	16.9%	LMTQAQLEEATR	99.7%	77	25	66.9	6	0	0	1406.69	105	116
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	6	7	14	0.01%	16.9%	MIQVYFPK	98.5%	32.7	25	28	1	0	0	1025.55	192	199
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	6	7	14	0.01%	16.9%	MPPVLEER	94.9%	27.9	25	17	1	0	0	970.50	128	135
28S ribosomal protein S22, mitochondrial	MRPS22	RT22_HUMAN	41.3	100.0%	6	7	14	0.01%	16.9%	VPINDVLAEDK	99.7%	49.8	25	49.8	2	0	0	1212.65	136	146
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	6	7	13	0.01%	30.5%	AFDLFNPNFK	99.7%	56.8	25	56.8	2	0	0	1212.60	84	93
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	6	7	13	0.01%	30.5%	AKFYSVYGSGQR	96.4%	29.2	25	24.6	1	0	0	1362.68	72	83
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	6	7	13	0.01%	30.5%	ALLAEGVILR	99.7%	69.1	25	38	2	0	0	1054.66	124	133
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	6	7	13	0.01%	30.5%	ALLAEGVILRR	99.1%	34.9	25	30	2	0	0	1210.76	124	134
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	6	7	13	0.01%	30.5%	LETVGSIFSR	99.7%	76.2	25	65.4	2	0	0	1108.60	6	15
28S ribosomal protein S23, mitochondrial	MRPS23	RT23_HUMAN	21.8	100.0%	6	7	13	0.01%	30.5%	LGETDEEKLFVETGK	99.7%	60.2	25	60.2	2	2	0	1694.85	109	123
28S ribosomal protein S24, mitochondrial	MRPS24	RT24_HUMAN	19.0	100.0%	5	5	9	0.01%	18.6%	GNQLEICAVVLR	99.7%	70.6	25	58.3	1	0	0	1371.74	114	125
28S ribosomal protein S24, mitochondrial	MRPS24	RT24_HUMAN	19.0	100.0%	5	5	9	0.01%	18.6%	LHLQTVPSK	99.7%	49	25	38.9	2	0	0	1022.60	153	161
28S ribosomal protein S24, mitochondrial	MRPS24	RT24_HUMAN	19.0	100.0%	5	5	9	0.01%	18.6%	RGNQLEICAVVLR	99.7%	49.8	25	45.3	0	2	0	1527.84	113	125
28S ribosomal protein S24, mitochondrial	MRPS24	RT24_HUMAN	19.0	100.0%	5	5	9	0.01%	18.6%	TVEDVFLR	99.7%	55.2	25	46.9	2	0	0	978.53	86	93
28S ribosomal protein S24, mitochondrial	MRPS24	RT24_HUMAN	19.0	100.0%	5	5	9	0.01%	18.6%	TVEDVFLRK	99.4%	37	25	29.6	2	0	0	1106.62	86	94
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	7	11	18	0.02%	49.1%	ECICEVEGQVPCPSLVPLPK	99.7%	50.1	25	50.1	2	0	0	2311.11	138	157
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	7	11	18	0.02%	49.1%	FVFFNIPQIQYK	97.1%	30	25	30	1	0	0	1543.83	47	58
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	7	11	18	0.02%	49.1%	NMTPSPFLR	96.4%	29.2	25	12.9	1	0	0	1078.54	69	77

28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	7	11	18	0.02%	49.1%	NPWVQIMMFK	98.8%	33.6	25	33.6	3	0	0	1325.64	59	68
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	7	11	18	0.02%	49.1%	TLQYLSQGNVVFK	99.7%	78.1	25	64.7	2	0	0	1496.81	12	24
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	7	11	18	0.02%	49.1%	TLQYLSQGNVVFKDSVK	99.7%	73.2	25	73.2	2	1	0	1926.03	12	28
28S ribosomal protein S25, mitochondrial	MRPS25	RT25_HUMAN	20.1	100.0%	7	11	18	0.02%	49.1%	VMTVNYNTHGELGEGAR	99.7%	80.2	25	80.2	3	3	0	1847.87	29	45
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	10	10	17	0.02%	23.9%	EALDVLGAVLK	99.7%	93.8	25	82.9	2	0	0	1127.67	278	288
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	10	10	17	0.02%	23.9%	EEIDHAEYYLYK	99.7%	39.9	25	32.3	1	0	0	1572.72	83	94
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	10	10	17	0.02%	23.9%	IESEGLLSLTTQLVK	99.7%	92.2	25	92.2	2	0	0	1630.93	347	361
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	10	10	17	0.02%	23.9%	KLPVSSLTISR	99.7%	57.7	25	55.2	2	0	0	1200.73	64	74
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	10	10	17	0.02%	23.9%	LIDNISSR	99.7%	41.4	25	13.4	1	0	0	917.51	75	82
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	10	10	17	0.02%	23.9%	LIDNISSREEIDHAEYYLYK	99.7%	34.6	25	34.6	0	1	0	2471.21	75	94
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	10	10	17	0.02%	23.9%	LPQYLER	99.7%	42.9	25	18.5	2	0	0	918.50	327	333
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	10	10	17	0.02%	23.9%	LVEQLDIEETEQSK	99.7%	83.1	25	79	2	0	0	1660.83	313	326
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	10	10	17	0.02%	23.9%	NFGASLLLPGLK	99.7%	71.4	25	64.5	2	0	0	1229.73	203	214
28S ribosomal protein S27, mitochondrial	MRPS27	RT27_HUMAN	47.6	100.0%	10	10	17	0.02%	23.9%	VAASPEDIK	98.1%	31.8	25	26	2	0	0	929.49	266	274
28S ribosomal protein S28, mitochondrial	MRPS28	RT28_HUMAN	20.8	100.0%	3	4	13	0.01%	15.5%	AGGFASALER	99.7%	69.4	25	50.9	4	0	0	978.50	49	58
28S ribosomal protein S28, mitochondrial	MRPS28	RT28_HUMAN	20.8	100.0%	3	4	13	0.01%	15.5%	LLDLELTSR	99.7%	72.4	25	61.5	4	0	0	1059.60	144	152
28S ribosomal protein S28, mitochondrial	MRPS28	RT28_HUMAN	20.8	100.0%	3	4	13	0.01%	15.5%	NVESFASMLR	99.7%	65.1	25	61.3	5	0	0	1169.56	76	85
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	5	5	16	0.02%	15.1%	ELLFLSNANPSLLER	99.7%	61.3	25	47.4	2	0	0	1715.93	379	393
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	5	5	16	0.02%	15.1%	GSPLGEVVEQGITR	99.7%	71.5	25	65.4	6	0	0	1441.76	219	232
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	5	5	16	0.02%	15.1%	NATDAVGIVLK	99.7%	53.5	25	53	2	0	0	1100.63	235	245
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	5	5	16	0.02%	15.1%	NTSFAYPAIR	99.7%	51	25	38	4	0	0	1139.58	114	123
28S ribosomal protein S29, mitochondrial	DAP3	RT29_HUMAN	45.6	100.0%	5	5	16	0.02%	15.1%	TFSEACLMVR	99.6%	38.2	25	37	2	0	0	1213.57	93	102
28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	3	3	5	0.00%	11.1%	EAPETDTSPSLWDVEFAK	99.7%	47.6	25	47.6	2	0	0	2021.93	267	284
28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	3	3	5	0.00%	11.1%	IQFDEGYDNYPGQEK	99.7%	60.1	25	60.1	2	0	0	1802.79	226	240
28S ribosomal protein S31, mitochondrial	MRPS31	RT31_HUMAN	45.3	100.0%	3	3	5	0.00%	11.1%	ISFSNIISDMK	98.1%	31.9	25	21.5	1	0	0	1254.64	199	209
28S ribosomal protein S33, mitochondrial	MRPS33	RT33_HUMAN	12.6	99.8%	2	2	4	0.00%	19.8%	LFGEVTRPTNSK	99.6%	39.3	25	33.3	2	0	0	1348.72	18	29
28S ribosomal protein S33, mitochondrial	MRPS33	RT33_HUMAN	12.6	99.8%	2	2	4	0.00%	19.8%	LFSELPLAK	99.5%	37.7	25	22.3	2	0	0	1017.60	36	44
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	4	5	13	0.01%	17.0%	AWGILTFK	99.7%	44	25	35.8	3	0	0	935.54	114	121
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	4	5	13	0.01%	17.0%	LLQLLGR	99.7%	56.7	25	18.9	4	0	0	812.54	64	70
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	4	5	13	0.01%	17.0%	LPLFGLGR	99.6%	38.2	25	29.7	3	0	0	872.54	71	78
28S ribosomal protein S34, mitochondrial	MRPS34	RT34_HUMAN	25.7	100.0%	4	5	13	0.01%	17.0%	VRPDYTAQNLDHGK	99.7%	42.9	25	40	1	2	0	1613.80	100	113
28S ribosomal protein S35, mitochondrial	MRPS35	RT35_HUMAN	36.8	100.0%	2	2	4	0.00%	7.4%	LSSLNLDDHAK	99.7%	45.2	25	38.6	2	0	0	1212.62	177	187
28S ribosomal protein S35, mitochondrial	MRPS35	RT35_HUMAN	36.8	100.0%	2	2	4	0.00%	7.4%	NEEENENSISQYK	99.7%	62.8	25	62.8	2	0	0	1583.68	301	313
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	4	4	8	0.01%	11.9%	EECGPLPIVVASPR	97.8%	31.1	25	31.1	2	0	0	1523.79	375	388
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	4	4	8	0.01%	11.9%	GALAETGAGAK	98.6%	33.1	25	23.1	2	0	0	945.50	101	111
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	4	4	8	0.01%	11.9%	NGAVQTIAQR	99.7%	53.4	25	44	2	0	0	1057.57	151	160
28S ribosomal protein S5, mitochondrial	MRPS5	RT05_HUMAN	48.0	100.0%	4	4	8	0.01%	11.9%	VSGSINMLSLTQGLFR	99.7%	67.8	25	67.8	2	0	0	1738.92	336	351
28S ribosomal protein S6, mitochondrial	MRPS6	RT06_HUMAN	14.2	99.9%	2	2	3	0.00%	12.8%	DLENLGER	98.9%	34.1	25	17.4	2	0	0	945.46	38	45
28S ribosomal protein S6, mitochondrial	MRPS6	RT06_HUMAN	14.2	99.9%	2	2	3	0.00%	12.8%	TIEALMDR	98.9%	34	25	24.1	1	0	0	964.48	25	32
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	4	4	6	0.01%	15.3%	FYQVPVPLPDR	99.7%	40.7	25	35.4	1	0	0	1330.72	167	177
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	4	4	6	0.01%	15.3%	FYQVPVPLPDRR	98.3%	26.9	25	26.9	0	1	0	1486.82	167	178
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	4	4	6	0.01%	15.3%	LLEAFHNQGPVIK	99.7%	49.6	25	46.5	1	0	0	1465.82	209	221
28S ribosomal protein S7, mitochondrial	MRPS7	RT07_HUMAN	28.1	100.0%	4	4	6	0.01%	15.3%	TSSVFEDPVISK	99.7%	54.8	25	47	3	0	0	1308.67	82	93
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	99.8%	2	2	5	0.00%	7.3%	AIAYLFPSGLFEK	99.7%	53.9	25	45.6	3	0	0	1455.79	107	119
28S ribosomal protein S9, mitochondrial	MRPS9	RT09_HUMAN	45.8	99.8%	2	2	5	0.00%	7.3%	LLTSQCGAAEEEFVQR	99.7%	90.7	25	90.7	2	0	0	1837.88	228	243
2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	GCAT	KBL_HUMAN	45.3	99.8%	2	2	3	0.00%	8.4%	ALGGASGGYTTGPGPLVSLLR	99.7%	75.9	25	75.9	1	0	0	1944.06	266	286
2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	GCAT	KBL_HUMAN	45.3	99.8%	2	2	3	0.00%	8.4%	GIFVIGFSYPVVPK	99.7%	64.2	25	64.2	2	0	0	1522.87	370	383
2'-deoxynucleoside 5'-phosphate N-hydrolase 1	DNPH1	DNPH1_HUMAN	19.1	100.0%	3	4	6	0.01%	22.4%	FGTVLTEHVAAAELGAR	99.7%	68.1	25	68.1	2	2	0	1741.92	49	65
2'-deoxynucleoside 5'-phosphate N-hydrolase 1	DNPH1	DNPH1_HUMAN	19.1	100.0%	3	4	6	0.01%	22.4%	GEPGRPALYFCGSIR	99.6%	32.2	25	31.4	0	1	0	1679.83	16	30
2'-deoxynucleoside 5'-phosphate N-hydrolase 1	DNPH1	DNPH1_HUMAN	19.1	100.0%	3	4	6	0.01%	22.4%	VLSAMIR	95.4%	28.3	25	12.4	1	0	0	805.46	126	132
2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	BCKDHB	ODBB_HUMAN	43.1	100.0%	4	4	6	0.01%	13.5%	LGVSCEVIDLR	99.7%	77.2	25	63.6	2	0	0	1260.66	295	305

2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	BCKDHB	ODBB_HUMAN	43.1	100.0%	4	4	6	0.01%	13.5%	MNLFQSVTSALDNSLAK	99.7%	60.7	25	55.7	1	0	0	1854.93	71	87
2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	BCKDHB	ODBB_HUMAN	43.1	100.0%	4	4	6	0.01%	13.5%	SGDLFNCGSLTIR	99.7%	69.1	25	65.7	2	0	0	1439.69	171	183
2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	BCKDHB	ODBB_HUMAN	43.1	100.0%	4	4	6	0.01%	13.5%	TIIPWDVDTICK	99.7%	40.8	25	32.5	1	0	0	1460.75	306	317
39S ribosomal protein L1, mitochondrial	MRPL1	RM01_HUMAN	36.9	99.8%	2	2	3	0.00%	10.2%	NVEPFTSVLSLPYPFASEINK	98.6%	33.1	25	33.1	1	0	0	2352.21	136	156
39S ribosomal protein L1, mitochondrial	MRPL1	RM01_HUMAN	36.9	99.8%	2	2	3	0.00%	10.2%	VAVFTENASEVK	99.7%	55.5	25	44.8	2	0	0	1293.67	157	168
39S ribosomal protein L10, mitochondrial	MRPL10	RM10_HUMAN	29.3	100.0%	3	3	5	0.00%	14.2%	EIAAVFQDNR	99.7%	56	25	53.5	2	0	0	1162.59	85	94
39S ribosomal protein L10, mitochondrial	MRPL10	RM10_HUMAN	29.3	100.0%	3	3	5	0.00%	14.2%	QGFINYSK	96.2%	29	25	25.4	1	0	0	956.48	189	196
39S ribosomal protein L10, mitochondrial	MRPL10	RM10_HUMAN	29.3	100.0%	3	3	5	0.00%	14.2%	TVPFLPLLGGCIDDTILSR	99.7%	63.7	25	63.7	2	0	0	2087.12	170	188
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	8	9	16	0.02%	47.4%	AGLAMPGPPLGPVLGQR	99.7%	63.7	25	61.7	4	0	0	1630.91	26	42
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	8	9	16	0.02%	47.4%	AQDEAFALQDVPLSSVVR	99.7%	78	25	78	2	0	0	1945.00	125	142
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	8	9	16	0.02%	47.4%	DLSSEELAAFQK	99.7%	84.4	25	72.7	2	0	0	1337.66	158	169
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	8	9	16	0.02%	47.4%	DLSSEELAAFQKER	99.7%	46.5	25	46.5	1	0	0	1622.80	158	171
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	8	9	16	0.02%	47.4%	EADLAAQEEAAKK	99.7%	62.4	25	60.2	2	0	0	1373.69	180	192
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	8	9	16	0.02%	47.4%	GVSINQFCK	99.7%	50	25	44.4	2	0	0	1052.52	43	51
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	8	9	16	0.02%	47.4%	IGQPTVSYFLK	99.7%	70.8	25	67.3	2	0	0	1252.69	82	92
39S ribosomal protein L11, mitochondrial	MRPL11	RM11_HUMAN	20.7	100.0%	8	9	16	0.02%	47.4%	KPEVGGVIR	97.4%	30.5	25	23.9	1	0	0	954.57	13	21
39S ribosomal protein L12, mitochondrial	MRPL12	RM12_HUMAN	21.3	100.0%	3	3	5	0.00%	16.2%	KLVESLPQEIK	99.7%	56.7	25	47	2	0	0	1283.76	163	173
39S ribosomal protein L12, mitochondrial	MRPL12	RM12_HUMAN	21.3	100.0%	3	3	5	0.00%	16.2%	LTEAKPVDK	98.8%	33.6	25	27	1	0	0	1000.57	134	142
39S ribosomal protein L12, mitochondrial	MRPL12	RM12_HUMAN	21.3	100.0%	3	3	5	0.00%	16.2%	NYIQGINLVQAK	99.7%	74.8	25	65.1	2	0	0	1360.76	151	162
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	7	9	15	0.01%	38.2%	APQQWATFAR	99.7%	65.2	25	58.3	2	0	0	1175.60	7	16
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	7	9	15	0.01%	38.2%	IWYLLDGK	98.7%	33.2	25	16.2	1	0	0	1007.56	17	24
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	7	9	15	0.01%	38.2%	LAAMASIR	99.7%	48.3	25	41	2	0	0	848.47	31	38
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	7	9	15	0.01%	38.2%	LAIYGMLPK	99.6%	38.9	25	28.7	3	0	0	1021.58	106	114
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	7	9	15	0.01%	38.2%	LWTPPEDYRL	97.3%	30.4	25	13.2	1	0	0	1289.65	169	178
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	7	9	15	0.01%	38.2%	NLVEELPQPR	99.6%	38.6	25	29.6	2	0	0	1194.65	140	149
39S ribosomal protein L13, mitochondrial	MRPL13	RM13_HUMAN	20.7	100.0%	7	9	15	0.01%	38.2%	VYSSHTGYPGGFR	99.7%	79.4	25	78.4	2	2	0	1427.67	76	88
39S ribosomal protein L14, mitochondrial	MRPL14	RM14_HUMAN	15.9	100.0%	4	5	9	0.01%	37.2%	ALIVGHCMPGPR	96.6%	29.4	25	29.4	1	0	0	1323.67	84	95
39S ribosomal protein L14, mitochondrial	MRPL14	RM14_HUMAN	15.9	100.0%	4	5	9	0.01%	37.2%	FDSNNVVLIEDNGNPVGTR	99.7%	101	25	101	2	0	0	2060.00	100	118
39S ribosomal protein L14, mitochondrial	MRPL14	RM14_HUMAN	15.9	100.0%	4	5	9	0.01%	37.2%	VLAIAQNFV	99.7%	49.6	25	40.7	2	0	0	974.57	137	145
39S ribosomal protein L14, mitochondrial	MRPL14	RM14_HUMAN	15.9	100.0%	4	5	9	0.01%	37.2%	VVDNSALGNSPYHR	99.7%	61.9	25	55.9	2	2	0	1528.75	40	53
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	8	8	14	0.01%	33.1%	GVTIQPLKR	96.6%	29.5	25	20.2	2	0	0	1011.63	126	134
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	8	8	14	0.01%	33.1%	GYLADPAKFPEAR	96.1%	28.9	25	22.1	1	0	0	1434.74	221	233
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	8	8	14	0.01%	33.1%	ILKPTDENLLK	99.7%	44	25	38.8	2	0	0	1283.76	282	292
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	8	8	14	0.01%	33.1%	LGFEGGQTPFYIR	99.7%	62.4	25	55.9	2	0	0	1484.75	65	77
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	8	8	14	0.01%	33.1%	LQYLIDLGR	99.7%	64.1	25	57.9	2	0	0	1090.63	101	109
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	8	8	14	0.01%	33.1%	SLDIVCKPVPFFLR	99.6%	32.5	25	32.5	0	1	0	1690.94	183	196
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	8	8	14	0.01%	33.1%	VDPSQPIDLTQLVNGR	99.7%	59.5	25	59.5	2	0	0	1751.93	110	125
39S ribosomal protein L15, mitochondrial	MRPL15	RM15_HUMAN	33.4	100.0%	8	8	14	0.01%	33.1%	VSLANLKPNPGSK	99.7%	47.1	25	43.5	2	0	0	1324.76	22	34
39S ribosomal protein L16, mitochondrial	MRPL16	RM16_HUMAN	28.5	100.0%	3	3	5	0.00%	12.4%	GAIDHYVTPVK	99.7%	53	25	42.5	2	0	0	1199.64	145	155
39S ribosomal protein L16, mitochondrial	MRPL16	RM16_HUMAN	28.5	100.0%	3	3	5	0.00%	12.4%	IATANMLGIR	99.7%	67.1	25	55.4	2	0	0	1059.60	218	227
39S ribosomal protein L16, mitochondrial	MRPL16	RM16_HUMAN	28.5	100.0%	3	3	5	0.00%	12.4%	VPAPFKPITR	99.7%	44.2	25	27.7	1	0	0	1125.68	124	133
39S ribosomal protein L17, mitochondrial	MRPL17	RM17_HUMAN	20.1	100.0%	2	2	5	0.00%	9.1%	LFQVLAPR	99.7%	65.3	25	48.4	4	0	0	943.57	89	96
39S ribosomal protein L17, mitochondrial	MRPL17	RM17_HUMAN	20.1	100.0%	2	2	5	0.00%	9.1%	MGLGPESR	99.7%	47	25	36.6	1	0	0	846.41	18	25
39S ribosomal protein L18, mitochondrial	MRPL18	RM18_HUMAN	20.6	100.0%	5	5	10	0.01%	24.4%	LQSAMTEGGVVLR	99.7%	91.7	25	85.5	2	0	0	1360.73	161	173
39S ribosomal protein L18, mitochondrial	MRPL18	RM18_HUMAN	20.6	100.0%	5	5	10	0.01%	24.4%	LQSAMTEGGVVLREPQR	99.7%	34.1	25	30.6	0	2	0	1886.98	161	177
39S ribosomal protein L18, mitochondrial	MRPL18	RM18_HUMAN	20.6	100.0%	5	5	10	0.01%	24.4%	NLELLSVAR	99.7%	64.1	25	37.2	2	0	0	1014.59	55	63
39S ribosomal protein L18, mitochondrial	MRPL18	RM18_HUMAN	20.6	100.0%	5	5	10	0.01%	24.4%	NVVACESIGR	99.7%	60	25	51.4	2	0	0	1104.55	121	130
39S ribosomal protein L18, mitochondrial	MRPL18	RM18_HUMAN	20.6	100.0%	5	5	10	0.01%	24.4%	VVVSASTR	99.7%	40.6	25	33.1	2	0	0	818.47	101	108
39S ribosomal protein L19, mitochondrial	MRPL19	RM19_HUMAN	33.5	100.0%	4	4	8	0.01%	13.7%	FLSPEFIPR	99.7%	44	25	39.2	2	0	0	1105.60	75	83
39S ribosomal protein L19, mitochondrial	MRPL19	RM19_HUMAN	33.5	100.0%	4	4	8	0.01%	13.7%	GLGATFILR	99.7%	67.2	25	64.1	2	0	0	947.57	144	152
39S ribosomal protein L19, mitochondrial	MRPL19	RM19_HUMAN	33.5	100.0%	4	4	8	0.01%	13.7%	ISQFLGICIQR	99.7%	64.2	25	59.2	2	0	0	1334.73	130	140

39S ribosomal protein L19, mitochondrial	MRPL19	RM19_HUMAN	33.5	100.0%	4	4	8	0.01%	13.7%	VTTADPYASGK	99.7%	40.4	25	37.7	2	0	0	1109.55	119	129
39S ribosomal protein L2, mitochondrial	MRPL2	RM02_HUMAN	33.3	100.0%	3	3	4	0.00%	11.8%	AAGTCGVLLR	99.7%	48.4	25	28.8	1	0	0	1017.55	209	218
39S ribosomal protein L2, mitochondrial	MRPL2	RM02_HUMAN	33.3	100.0%	3	3	4	0.00%	11.8%	QMQVLETCVATVGR	99.7%	69.8	25	61.5	1	0	0	1591.79	233	246
39S ribosomal protein L2, mitochondrial	MRPL2	RM02_HUMAN	33.3	100.0%	3	3	4	0.00%	11.8%	SADIALVAGGSR	99.7%	61.3	25	49.8	2	0	0	1116.60	136	147
39S ribosomal protein L20, mitochondrial	MRPL20	RM20_HUMAN	17.4	100.0%	3	3	5	0.00%	21.5%	ITAASQEHGLK	99.7%	51.3	25	50.3	2	0	0	1154.62	72	82
39S ribosomal protein L20, mitochondrial	MRPL20	RM20_HUMAN	17.4	100.0%	3	3	5	0.00%	21.5%	VLADLAIYEPK	99.7%	79.1	25	70	2	0	0	1231.69	101	111
39S ribosomal protein L20, mitochondrial	MRPL20	RM20_HUMAN	17.4	100.0%	3	3	5	0.00%	21.5%	YPALIGNLVK	98.6%	33.1	25	29.3	1	0	0	1087.65	83	92
39S ribosomal protein L21, mitochondrial	MRPL21	RM21_HUMAN	22.8	100.0%	3	3	6	0.01%	15.6%	IVTTPQTVLR	99.7%	58.4	25	45.7	2	0	0	1127.68	185	194
39S ribosomal protein L21, mitochondrial	MRPL21	RM21_HUMAN	22.8	100.0%	3	3	6	0.01%	15.6%	LFAVVHFASR	99.7%	63	25	50	2	0	0	1146.64	95	104
39S ribosomal protein L21, mitochondrial	MRPL21	RM21_HUMAN	22.8	100.0%	3	3	6	0.01%	15.6%	VNEMIVTGQYGR	99.7%	64.9	25	44.7	2	0	0	1382.67	83	94
39S ribosomal protein L22, mitochondrial	MRPL22	RM22_HUMAN	23.6	100.0%	5	6	12	0.01%	25.7%	EVLLEAQDMAVR	99.7%	81	25	71.6	4	0	0	1389.70	113	124
39S ribosomal protein L22, mitochondrial	MRPL22	RM22_HUMAN	23.6	100.0%	5	6	12	0.01%	25.7%	EYIQQLR	99.5%	37.7	25	0	2	0	0	949.51	192	198
39S ribosomal protein L22, mitochondrial	MRPL22	RM22_HUMAN	23.6	100.0%	5	6	12	0.01%	25.7%	LVEGPPPPPEPPK	99.7%	64.9	25	59.1	2	0	0	1353.74	172	184
39S ribosomal protein L22, mitochondrial	MRPL22	RM22_HUMAN	23.6	100.0%	5	6	12	0.01%	25.7%	RPAEIYHCR	99.5%	32.1	25	31.2	0	2	0	1201.59	63	71
39S ribosomal protein L22, mitochondrial	MRPL22	RM22_HUMAN	23.6	100.0%	5	6	12	0.01%	25.7%	SNLYIAESTSGR	99.7%	119	25	119	2	0	0	1297.64	132	143
39S ribosomal protein L24, mitochondrial	MRPL24	RM24_HUMAN	24.9	99.9%	2	2	3	0.00%	9.7%	GTMIPSEAPLLHR	96.1%	23.8	25	23.8	0	1	0	1437.75	106	118
39S ribosomal protein L24, mitochondrial	MRPL24	RM24_HUMAN	24.9	99.9%	2	2	3	0.00%	9.7%	KPTEIEWR	97.1%	30.3	25.3	27.2	2	0	0	1058.56	129	136
39S ribosomal protein L27, mitochondrial	MRPL27	RM27_HUMAN	16.1	100.0%	3	3	5	0.00%	24.3%	CLYALEEGIVR	99.7%	73.4	25	58	2	0	0	1322.68	88	98
39S ribosomal protein L27, mitochondrial	MRPL27	RM27_HUMAN	16.1	100.0%	3	3	5	0.00%	24.3%	NTEAVDLITR	99.7%	76.2	25	61.5	2	0	0	1131.60	110	119
39S ribosomal protein L27, mitochondrial	MRPL27	RM27_HUMAN	16.1	100.0%	3	3	5	0.00%	24.3%	TFVHVVPAKPEGTFK	98.9%	28.5	25	28.5	0	1	0	1656.91	129	143
39S ribosomal protein L3, mitochondrial	MRPL3	RM03_HUMAN	38.6	100.0%	2	3	4	0.00%	6.0%	MATLSVGGK	99.4%	37	25	22.8	2	0	0	879.46	142	150
39S ribosomal protein L3, mitochondrial	MRPL3	RM03_HUMAN	38.6	100.0%	2	3	4	0.00%	6.0%	RPGAVATGDIGR	97.5%	30.7	25	20.3	2	0	0	1169.64	239	250
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	5	5	9	0.01%	17.7%	ESLLLQVR	99.7%	55.3	25	37.8	2	0	0	957.57	216	223
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	5	5	9	0.01%	17.7%	ETYCPVIVDNLIQLCK	99.7%	62	25	62	2	0	0	1964.98	174	189
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	5	5	9	0.01%	17.7%	MILFAFGSALAQAR	99.7%	95.1	25	92	2	0	0	1495.81	313	326
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	5	5	9	0.01%	17.7%	NDTGFQEGYPYPYPHTLYLLDK	99.7%	33.5	25	33.5	0	1	0	2631.24	275	296
39S ribosomal protein L37, mitochondrial	MRPL37	RM37_HUMAN	48.1	100.0%	5	5	9	0.01%	17.7%	VYEIPGLEPITFAGK	99.7%	72.5	25	66.8	2	0	0	1633.88	49	63
39S ribosomal protein L39, mitochondrial	MRPL39	RM39_HUMAN	38.7	100.0%	4	5	7	0.01%	13.6%	DAHALIYK	98.9%	34.1	25	24.2	1	0	0	930.50	205	212
39S ribosomal protein L39, mitochondrial	MRPL39	RM39_HUMAN	38.7	100.0%	4	5	7	0.01%	13.6%	DLPFETLEVEAK	99.7%	62.8	25	53.1	2	0	0	1390.71	213	224
39S ribosomal protein L39, mitochondrial	MRPL39	RM39_HUMAN	38.7	100.0%	4	5	7	0.01%	13.6%	IGDFIDVSEGPLIPR	99.7%	44.4	25	41.7	2	0	0	1627.87	257	271
39S ribosomal protein L39, mitochondrial	MRPL39	RM39_HUMAN	38.7	100.0%	4	5	7	0.01%	13.6%	TDPGTVFVMNK	98.5%	32.8	25	30.4	2	0	0	1208.60	73	83
39S ribosomal protein L4, mitochondrial	MRPL4	RM04_HUMAN	34.9	100.0%	4	4	7	0.01%	18.3%	ATENPEQVASEGLPEPVLR	99.7%	84.8	25	80	2	0	0	2036.03	31	49
39S ribosomal protein L4, mitochondrial	MRPL4	RM04_HUMAN	34.9	100.0%	4	4	7	0.01%	18.3%	GPTSYYYMLPMK	99.7%	50.5	25	50.5	3	0	0	1482.66	157	168
39S ribosomal protein L4, mitochondrial	MRPL4	RM04_HUMAN	34.9	100.0%	4	4	7	0.01%	18.3%	KVELPVPTHR	99.1%	35.2	25	30	1	0	0	1175.69	50	59
39S ribosomal protein L4, mitochondrial	MRPL4	RM04_HUMAN	34.9	100.0%	4	4	7	0.01%	18.3%	VGLADLHPDVFATAPR	99.7%	41.2	25	41.2	0	1	0	1678.89	77	92
39S ribosomal protein L40, mitochondrial	MRPL40	RM40_HUMAN	24.5	100.0%	3	3	6	0.01%	16.5%	ATQELIPIEDFITPLK	99.7%	47.5	25	34.9	2	0	0	1828.01	78	93
39S ribosomal protein L40, mitochondrial	MRPL40	RM40_HUMAN	24.5	100.0%	3	3	6	0.01%	16.5%	DPNLFPFEK	99.7%	49.2	25	43.7	2	0	0	1106.55	165	173
39S ribosomal protein L40, mitochondrial	MRPL40	RM40_HUMAN	24.5	100.0%	3	3	6	0.01%	16.5%	VYTQVEFKR	99.7%	66.6	25	60.7	2	0	0	1169.63	198	206
39S ribosomal protein L41, mitochondrial	MRPL41	RM41_HUMAN	15.4	100.0%	4	4	7	0.01%	33.6%	DFKDGTFDPDNLEK	97.6%	30.9	25	28.5	1	0	0	1640.74	103	116
39S ribosomal protein L41, mitochondrial	MRPL41	RM41_HUMAN	15.4	100.0%	4	4	7	0.01%	33.6%	EMVPEFVVPDLTGFK	97.0%	29.9	25	29.9	2	0	0	1723.86	55	69
39S ribosomal protein L41, mitochondrial	MRPL41	RM41_HUMAN	15.4	100.0%	4	4	7	0.01%	33.6%	LFQLYPR	99.7%	44.1	25	34.8	2	0	0	936.53	127	133
39S ribosomal protein L41, mitochondrial	MRPL41	RM41_HUMAN	15.4	100.0%	4	4	7	0.01%	33.6%	YGFEPTQEGK	99.7%	44.6	25	31.6	2	0	0	1155.53	117	126
39S ribosomal protein L43, mitochondrial	MRPL43	RM43_HUMAN	23.4	100.0%	4	4	8	0.01%	19.1%	EVIDFAR	97.7%	31	25	9.95	2	0	0	849.45	50	56
39S ribosomal protein L43, mitochondrial	MRPL43	RM43_HUMAN	23.4	100.0%	4	4	8	0.01%	19.1%	FLASVLHNGLGR	99.7%	63.6	25	55.3	2	0	0	1283.72	10	21
39S ribosomal protein L43, mitochondrial	MRPL43	RM43_HUMAN	23.4	100.0%	4	4	8	0.01%	19.1%	LADQSGLDVIR	99.7%	69.8	25	54.5	2	0	0	1186.64	104	114
39S ribosomal protein L43, mitochondrial	MRPL43	RM43_HUMAN	23.4	100.0%	4	4	8	0.01%	19.1%	SVEEISTLVQK	99.7%	59.9	25	49.2	2	0	0	1232.67	93	103
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	6	6	11	0.01%	22.0%	EAVLLNLK	99.0%	34.5	25	32.1	1	0	0	899.56	113	120
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	6	6	11	0.01%	22.0%	LIAEGPGETVLVAEEEAAR	99.7%	123	25	123	2	0	0	1954.01	280	298
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	6	6	11	0.01%	22.0%	LQENFSLDLLK	99.7%	42.2	25	30.5	2	0	0	1319.72	79	89
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	6	6	11	0.01%	22.0%	LYGFTENR	99.7%	44.5	25	37.3	2	0	0	999.49	304	311
39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	6	6	11	0.01%	22.0%	NLVDFLTGEEVVCHVAR	99.7%	53	25	53	2	0	0	1957.98	155	171

39S ribosomal protein L44, mitochondrial	MRPL44	RM44_HUMAN	37.5	100.0%	6	6	11	0.01%	22.0%	TAFVNSCYIK	99.7%	47.7	25	47.7	2	0	0	1202.59	90	99
39S ribosomal protein L46, mitochondrial	MRPL46	RM46_HUMAN	31.7	100.0%	5	6	11	0.01%	19.0%	ALLLTGDFSQAGNK	99.7%	87.7	25	79.9	2	0	0	1434.76	236	249
39S ribosomal protein L46, mitochondrial	MRPL46	RM46_HUMAN	31.7	100.0%	5	6	11	0.01%	19.0%	DELGDYLKPK	99.0%	34.7	25	33.4	1	0	0	1177.61	258	267
39S ribosomal protein L46, mitochondrial	MRPL46	RM46_HUMAN	31.7	100.0%	5	6	11	0.01%	19.0%	NLVLLVR	99.7%	40.6	25	10.8	2	0	0	826.55	156	162
39S ribosomal protein L46, mitochondrial	MRPL46	RM46_HUMAN	31.7	100.0%	5	6	11	0.01%	19.0%	SLYSDHELR	99.7%	48.3	25	31.4	2	0	0	1119.54	82	90
39S ribosomal protein L46, mitochondrial	MRPL46	RM46_HUMAN	31.7	100.0%	5	6	11	0.01%	19.0%	TLATLSENNMEAK	99.7%	83.4	25	83.4	4	0	0	1437.69	191	203
39S ribosomal protein L47, mitochondrial	MRPL47	RM47_HUMAN	29.5	100.0%	4	5	9	0.01%	13.2%	NMLLTLEQEAK	99.7%	59.7	25	36.7	2	0	0	1289.68	110	120
39S ribosomal protein L47, mitochondrial	MRPL47	RM47_HUMAN	29.5	100.0%	4	5	9	0.01%	13.2%	NMLLTLEQEAKR	99.7%	62.6	25	58	4	0	0	1445.78	110	121
39S ribosomal protein L47, mitochondrial	MRPL47	RM47_HUMAN	29.5	100.0%	4	5	9	0.01%	13.2%	SGAAWTCQQLR	99.7%	54.4	25	48.4	2	0	0	1277.61	81	91
39S ribosomal protein L47, mitochondrial	MRPL47	RM47_HUMAN	29.5	100.0%	4	5	9	0.01%	13.2%	VVQEREDALR	95.4%	28.3	25	5.64	1	0	0	1214.65	145	154
39S ribosomal protein L48, mitochondrial	MRPL48	RM48_HUMAN	23.9	100.0%	4	5	9	0.01%	21.7%	ARPELEELLAK	99.7%	49.8	25	32.7	2	0	0	1268.72	200	210
39S ribosomal protein L48, mitochondrial	MRPL48	RM48_HUMAN	23.9	100.0%	4	5	9	0.01%	21.7%	MLLDSVLTTHER	99.7%	78.2	25	73.6	4	0	0	1414.74	144	155
39S ribosomal protein L48, mitochondrial	MRPL48	RM48_HUMAN	23.9	100.0%	4	5	9	0.01%	21.7%	TIEVLQLQDQGSK	99.7%	101	25	94.5	2	0	0	1458.78	131	143
39S ribosomal protein L48, mitochondrial	MRPL48	RM48_HUMAN	23.9	100.0%	4	5	9	0.01%	21.7%	VEESYAMPTK	99.7%	45.9	25	45.9	1	0	0	1170.53	121	130
39S ribosomal protein L49, mitochondrial	MRPL49	RM49_HUMAN	19.2	100.0%	3	3	5	0.00%	21.1%	FVESVDEYQFVER	99.7%	91.9	25	90.3	2	0	0	1646.77	38	50
39S ribosomal protein L49, mitochondrial	MRPL49	RM49_HUMAN	19.2	100.0%	3	3	5	0.00%	21.1%	GYFDQELK	96.4%	29.2	25	25.9	1	0	0	999.48	151	158
39S ribosomal protein L49, mitochondrial	MRPL49	RM49_HUMAN	19.2	100.0%	3	3	5	0.00%	21.1%	TPVTQVNEVTGTLR	99.7%	96.8	25	95.7	2	0	0	1514.82	135	148
39S ribosomal protein L50, mitochondrial	MRPL50	RM50_HUMAN	18.3	100.0%	2	2	3	0.00%	15.2%	AYTPPEDLQSR	97.8%	31.2	25	30.5	2	0	0	1276.62	59	69
39S ribosomal protein L50, mitochondrial	MRPL50	RM50_HUMAN	18.3	100.0%	2	2	3	0.00%	15.2%	DVLDFYNVPIQDR	99.7%	59.4	25	58.6	1	0	0	1593.79	125	137
39S ribosomal protein L53, mitochondrial	MRPL53	RM53_HUMAN	12.1	99.8%	2	2	4	0.00%	20.5%	STNLNCSVIADVR	99.7%	69.6	25	63.1	2	0	0	1448.72	44	56
39S ribosomal protein L53, mitochondrial	MRPL53	RM53_HUMAN	12.1	99.8%	2	2	4	0.00%	20.5%	TFLQTVSSEK	99.7%	56.7	25	56.7	2	0	0	1139.59	32	41
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	4	4	7	0.01%	19.5%	ENLELILTQSVENVGVR	99.7%	50.3	25	50.3	2	0	0	1913.03	92	108
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	4	4	7	0.01%	19.5%	LLPQGLAVYASPENK	99.7%	42.3	25	42.3	2	0	0	1599.87	123	137
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	4	4	7	0.01%	19.5%	LPEEPITR	99.7%	49.7	25	35.8	2	0	0	954.53	208	215
39S ribosomal protein L9, mitochondrial	MRPL9	RM09_HUMAN	30.2	100.0%	4	4	7	0.01%	19.5%	NLGVVVAPHTLK	99.4%	36.7	25	36.7	1	0	0	1247.75	196	207
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	5	5	9	0.01%	28.7%	GGIVGMTLPIAR	99.7%	56.6	25	45.5	2	0	0	1200.68	173	184
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	5	5	9	0.01%	28.7%	GLVAVITGGASGLGLATAER	99.7%	128	25	128	1	0	0	1813.02	10	29
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	5	5	9	0.01%	28.7%	GQTHTLEDFQR	99.7%	50.2	25	44.7	2	0	0	1331.63	106	116
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	5	5	9	0.01%	28.7%	LVAGEMGQNEPDQGGQR	99.7%	90.9	25	90.9	2	0	0	1785.82	131	147
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	HCD2_HUMAN	26.9	100.0%	5	5	9	0.01%	28.7%	VDVAVNCAGIAVASK	99.7%	99.2	25	98.4	2	0	0	1473.77	85	99
3-ketoacyl-CoA thiolase, mitochondrial	ACAA2	THIM_HUMAN	41.9	99.8%	2	2	3	0.00%	5.5%	DFTATDLSEFAAK	99.7%	92.4	25	87.3	2	0	0	1415.67	26	38
3-ketoacyl-CoA thiolase, mitochondrial	ACAA2	THIM_HUMAN	41.9	99.8%	2	2	3	0.00%	5.5%	ETPALTINR	99.7%	45.3	25	39.7	1	0	0	1014.56	82	90
3-keto-steroid reductase	HSD17B7	DHB7_HUMAN	38.2	99.8%	2	2	3	0.00%	6.2%	ALFFGLFSR	96.0%	28.8	25	21.2	1	0	0	1057.58	103	111
3-keto-steroid reductase	HSD17B7	DHB7_HUMAN	38.2	99.8%	2	2	3	0.00%	6.2%	YATDLLSVALNR	99.7%	50.7	25	50.3	2	0	0	1335.73	198	209
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	7	9	26	0.02%	35.2%	AEAGAGSATEFQFR	99.7%	91.8	25	79	4	0	0	1441.67	140	153
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	7	9	26	0.02%	35.2%	DYLHLPPEIVPATLR	99.2%	30	25	24.7	1	2	0	1733.96	81	95
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	7	9	26	0.02%	35.2%	EQFAWR	97.4%	30.4	25	15.8	1	0	0	836.40	60	65
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	7	9	26	0.02%	35.2%	GLEGERPAR	95.1%	28.1	25	11.1	1	0	0	984.52	108	116
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	7	9	26	0.02%	35.2%	GYVKEQFAWR	99.7%	51.6	25	44.7	2	0	0	1283.65	56	65
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	7	9	26	0.02%	35.2%	IAIYELLFK	99.7%	64.4	25	64.4	7	0	0	1109.66	9	17
40S ribosomal protein S10	RPS10	RS10_HUMAN	18.9	100.0%	7	9	26	0.02%	35.2%	KAEAGAGSATEFQFR	99.7%	124	25	124	4	4	0	1569.77	139	153
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	48	0.04%	53.8%	CPFTGNVSIR	99.7%	67	25	57.6	8	0	0	1150.57	60	69
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	48	0.04%	53.8%	DVQIGDIVTVGECRPLSK	99.7%	91.2	25	84.3	6	2	0	1986.03	119	136
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	48	0.04%	53.8%	DYLHYIR	97.1%	30.1	25	20.9	2	0	0	979.50	91	97
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	48	0.04%	53.8%	EAIEGTYIDK	99.7%	68.4	25	54.9	2	0	0	1138.56	49	58
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	48	0.04%	53.8%	EAIEGTYIDKK	99.7%	51	25	40.3	5	2	0	1266.66	49	59
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	48	0.04%	53.8%	ILSGVVTK	99.7%	44.8	25	14.8	3	0	0	816.52	72	79
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	48	0.04%	53.8%	KCPFTGNVSIR	97.9%	31.3	25	27.7	2	0	0	1278.66	59	69
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	48	0.04%	53.8%	NMSVHLSPCFR	99.7%	48.4	25	47.1	4	3	0	1347.63	108	118
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	48	0.04%	53.8%	QPTIFQNK	98.4%	32.4	25	20.2	3	0	0	975.53	13	20
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	48	0.04%	53.8%	RDYLHYIR	99.7%	47.8	25	20.3	2	0	0	1135.60	90	97

40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	48	0.04%	53.8%	RVLLGETGK	97.9%	31.4	25	16.1	1	0	0	972.58	22	30
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	48	0.04%	53.8%	VLLGETGK	99.4%	37	25	31.3	1	0	0	816.48	23	30
40S ribosomal protein S11	RPS11	RS11_HUMAN	18.4	100.0%	13	18	48	0.04%	53.8%	VLLGETGKEK	99.7%	53.5	25	34.3	2	0	0	1073.62	23	32
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	10	35	0.03%	57.6%	DVIEEYFK	97.8%	31.2	25	31.2	1	0	0	1042.51	122	129
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	10	35	0.03%	57.6%	ESQAKDVIEEYFK	99.7%	52	25	41.6	4	0	0	1585.77	117	129
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	10	35	0.03%	57.6%	KVVGCSCVVVK	99.7%	71.4	25	60.9	4	2	0	1234.66	102	112
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	10	35	0.03%	57.6%	LGEWVGLCK	99.7%	64.5	25	52.9	6	0	0	1061.55	85	93
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	10	35	0.03%	57.6%	LVEALCAEHQINLIK	99.7%	85.2	25	81.9	4	3	0	1750.95	64	78
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	10	35	0.03%	57.6%	QAHLCVLASNCDEPMYVK	99.7%	36.8	25	34.1	0	2	0	2150.97	46	63
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	10	35	0.03%	57.6%	TALIHDGLAR	99.7%	55.5	25	43.7	5	0	0	1066.60	24	33
40S ribosomal protein S12	RPS12	RS12_HUMAN	14.5	100.0%	8	10	35	0.03%	57.6%	VVGCSCVVVK	99.7%	67.8	25	58.3	4	0	0	1106.57	103	112
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	7	9	35	0.03%	43.7%	GLAPDLPEDLYHLIK	99.7%	50.8	25	39.6	4	0	0	1693.92	79	93
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	7	9	35	0.03%	43.7%	GLTPSQIGVILR	99.7%	76.8	25	62.2	4	0	0	1253.76	44	55
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	7	9	35	0.03%	43.7%	KGLTPSQIGVILR	99.7%	79.8	25	75.2	4	2	0	1381.85	43	55
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	7	9	35	0.03%	43.7%	LILIESR	99.7%	54.3	25	30	5	0	0	843.53	115	121
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	7	9	35	0.03%	43.7%	LTSDDVKEQIYK	99.7%	74	25	67	12	1	0	1438.74	28	39
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	7	9	35	0.03%	43.7%	RSVPTWLK	97.2%	30.2	25	7.56	1	0	0	986.58	20	27
40S ribosomal protein S13	RPS13	RS13_HUMAN	17.2	100.0%	7	9	35	0.03%	43.7%	YESSTASALVA	99.7%	45.1	25	45.1	2	0	0	1098.53	141	151
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	59	0.06%	41.7%	ADRDESSPYAAMLAAQDVAQR	99.7%	51.6	25	51.6	0	6	0	2281.05	64	84
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	59	0.06%	41.7%	CKELGITALHIK	99.7%	74.5	25	62.6	4	2	0	1382.78	85	96
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	59	0.06%	41.7%	DESSPYAAMLAAQDVAQR	99.7%	114	25	101	7	0	0	1938.89	67	84
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	59	0.06%	41.7%	ELGITALHIK	99.7%	50.3	25	43.9	4	0	0	1094.66	87	96
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	59	0.06%	41.7%	IEDVTPIPSDSTR	99.7%	65.7	25	61.3	5	0	0	1429.72	129	141
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	59	0.06%	41.7%	IEDVTPIPSDSTRR	99.7%	37.7	25	35.4	2	2	0	1585.82	129	142
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	59	0.06%	41.7%	IGRIEDVTPIPSDSTR	99.7%	52.6	25	51	4	3	0	1755.92	126	141
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	59	0.06%	41.7%	TKTPGPGAQSALR	99.7%	44.8	25	38	3	4	0	1283.71	105	117
40S ribosomal protein S14	RPS14	RS14_HUMAN	16.3	100.0%	9	15	59	0.06%	41.7%	TPGPGAQSALR	99.7%	76	25	72.8	13	0	0	1054.56	107	117
40S ribosomal protein S15	RPS15	RS15_HUMAN	17.0	100.0%	3	7	21	0.02%	22.1%	DMIILPEMVGSMVGVYNGK	99.7%	135	25	132	12	0	0	2101.00	82	100
40S ribosomal protein S15	RPS15	RS15_HUMAN	17.0	100.0%	3	7	21	0.02%	22.1%	EAPPMEKPEVVK	99.7%	51.5	25	44.3	4	0	0	1353.71	66	77
40S ribosomal protein S15	RPS15	RS15_HUMAN	17.0	100.0%	3	7	21	0.02%	22.1%	KEAPPMEKPEVVK	99.7%	39.6	25	37.5	2	3	0	1497.80	65	77
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	9	13	50	0.05%	60.0%	FDVQLKDLEK	99.7%	57.9	25	19.3	7	2	0	1234.67	79	88
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	9	13	50	0.05%	60.0%	FLTVMMK	99.7%	40.4	25	20.3	6	0	0	869.46	37	43
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	9	13	50	0.05%	60.0%	HGYIGEFEIIDDHR	99.7%	83.3	25	75.9	2	6	0	1700.80	44	57
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	9	13	50	0.05%	60.0%	IVVNLTGR	99.7%	49.5	25	30.6	6	0	0	871.54	61	68
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	9	13	50	0.05%	60.0%	LNKCGVISPR	99.7%	53.8	25	35.5	1	0	0	1143.63	69	78
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	9	13	50	0.05%	60.0%	MNVLADALK	99.7%	70.4	25	45.6	13	0	0	990.53	4	12
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	9	13	50	0.05%	60.0%	QVLIRPCSK	97.8%	31.1	25	16.7	3	0	0	1100.62	24	32
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	9	13	50	0.05%	60.0%	VRMNVLADALK	99.7%	37.5	25	26.9	0	2	0	1245.70	2	12
40S ribosomal protein S15a	RPS15A	RS15A_HUMAN	14.8	100.0%	9	13	50	0.05%	60.0%	WQNNLLPSR	99.7%	53	25	43.6	2	0	0	1127.60	89	97
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	18	83	0.08%	54.8%	ALVAYYQK	99.7%	50	25	45.2	7	0	0	955.52	91	98
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	18	83	0.08%	54.8%	DILIQYDR	99.7%	53.6	25	34.4	2	0	0	1035.55	110	117
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	18	83	0.08%	54.8%	EIKDILIQYDR	99.7%	81.2	25	71.7	8	8	0	1405.77	107	117
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	18	83	0.08%	54.8%	GGGHVAQIYAIR	99.7%	52.5	25	51.5	8	2	0	1241.68	74	85
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	18	83	0.08%	54.8%	GPLQSVQVFGR	99.7%	77.1	25	66.6	4	0	0	1187.65	5	15
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	18	83	0.08%	54.8%	LLEPVLLLGK	99.7%	56.3	25	56.3	14	0	0	1094.72	51	60
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	18	83	0.08%	54.8%	LLEPVLLLGKER	99.7%	79.2	25	79.2	2	0	0	1379.86	51	62
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	18	83	0.08%	54.8%	PSKGPLQSVQVFGR	99.7%	47.8	25	44.2	4	4	0	1499.83	2	15
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	18	83	0.08%	54.8%	TLLVADPR	99.7%	45.4	25	19.3	5	0	0	884.52	118	125
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	18	83	0.08%	54.8%	TLLVADPRR	99.7%	40.3	25	28.5	3	0	0	1040.62	118	126
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	18	83	0.08%	54.8%	VKGGGHVAQIYAIR	99.7%	73.8	25	73.8	2	3	0	1468.84	72	85
40S ribosomal protein S16	RPS16	RS16_HUMAN	16.4	100.0%	12	18	83	0.08%	54.8%	VNGRPLEMIEPR	99.7%	37.9	25	36	1	6	0	1410.75	34	45

40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN,RS17_HUMAN	15.6	100.0%	7	12	34	0.03%	40.0%	IAGYVTHLMK	99.7%	63.5	25	57.2	9	0	0	1132.62	50	59
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN,RS17_HUMAN	15.6	100.0%	7	12	34	0.03%	40.0%	LGNDFHTNK	99.6%	39	25	28.2	2	0	0	1045.51	24	32
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN,RS17_HUMAN	15.6	100.0%	7	12	34	0.03%	40.0%	LGNDFHTNKR	99.7%	35.8	25	29.2	2	4	0	1201.61	24	33
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN,RS17_HUMAN	15.6	100.0%	7	12	34	0.03%	40.0%	LLDFGSLSNLQVTQPTVGMNFK	99.7%	68.3	25	68.3	4	2	0	2425.24	108	129
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN,RS17_HUMAN	15.6	100.0%	7	12	34	0.03%	40.0%	RVCEEIAIIPSK	99.7%	43.1	25	28.9	2	1	0	1414.77	33	44
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN,RS17_HUMAN	15.6	100.0%	7	12	34	0.03%	40.0%	VCEEIAIIPSK	99.7%	66.6	25	36.2	4	0	0	1258.67	34	44
40S ribosomal protein S17-like	RPS17L	RS17L_HUMAN,RS17_HUMAN	15.6	100.0%	7	12	34	0.03%	40.0%	VCEEIAIIPSKK	99.7%	59.4	25	46.6	4	0	0	1386.77	34	45
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	68	0.06%	62.5%	ADIDLTKR	99.7%	59.8	25	38.7	2	0	0	931.52	48	55
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	68	0.06%	62.5%	AGELTEDEVER	99.7%	58.7	25	49	6	0	0	1247.58	56	66
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	68	0.06%	62.5%	FQHILR	94.7%	27.8	25	8.14	1	0	0	813.47	9	14
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	68	0.06%	62.5%	HFWGLR	98.9%	33.9	25	25.8	2	0	0	815.43	125	130
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	68	0.06%	62.5%	IAFAITAIK	99.7%	74.8	25	62.8	4	0	0	947.59	26	34
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	68	0.06%	62.5%	IPDWFLNR	99.7%	47.3	25	32.8	13	0	0	1060.56	79	86
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	68	0.06%	62.5%	KADIDLTK	99.7%	51.2	25	39.3	4	0	0	903.51	47	54
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	68	0.06%	62.5%	KIAFAITAIK	99.7%	55.3	25	55.3	2	0	0	1075.69	25	34
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	68	0.06%	62.5%	LREDLER	96.3%	29.1	25	9.34	1	0	0	930.50	107	113
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	68	0.06%	62.5%	RAGELTEDEVER	99.7%	70.1	25	59.4	6	2	0	1403.68	55	66
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	68	0.06%	62.5%	RYAHVVLR	99.1%	35	25	16.9	1	0	0	1013.60	39	46
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	68	0.06%	62.5%	VITIMQNPR	99.7%	60.1	25	50.4	10	0	0	1071.60	67	75
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	68	0.06%	62.5%	VLNTNIDGR	99.7%	49.1	25	41.6	6	0	0	1001.54	15	23
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	68	0.06%	62.5%	YSQVLANGLDNK	99.7%	91.1	25	86.9	5	0	0	1321.67	95	106
40S ribosomal protein S18	RPS18	RS18_HUMAN	17.7	100.0%	15	18	68	0.06%	62.5%	YSQVLANGLDNKLR	99.7%	66.6	25	54.3	2	1	0	1590.86	95	108
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	12	26	0.02%	55.9%	ALAAFLKK	99.7%	40.6	25	30	2	0	0	861.56	17	24
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	12	26	0.02%	55.9%	DLDRIAGQVAAANK	99.4%	37	25	37	1	0	0	1441.78	130	143
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	12	26	0.02%	55.9%	DVNQQEFVR	99.7%	61.2	25	49.9	6	0	0	1134.55	8	16
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	12	26	0.02%	55.9%	ELAPYDENWFYTR	99.7%	73.5	25	73.5	2	0	0	1703.77	44	56
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	12	26	0.02%	55.9%	IAGQVAAANK	99.7%	68	25	53.7	2	0	0	942.54	134	143
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	12	26	0.02%	55.9%	LKVPEWVDTVK	99.7%	51.3	25	41.5	2	2	0	1313.75	28	38
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	12	26	0.02%	55.9%	NGVMPSHFSR	95.4%	28.3	25	19	1	0	0	1147.53	85	94
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	12	26	0.02%	55.9%	PGVTVKDVNQQEFVR	99.7%	56.3	25	56.3	2	2	0	1715.91	2	16
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	12	26	0.02%	55.9%	RVLQALEGLK	99.7%	40.4	25	21.6	2	0	0	1126.69	102	111
40S ribosomal protein S19	RPS19	RS19_HUMAN	16.1	100.0%	10	12	26	0.02%	55.9%	VLQALEGLK	99.7%	63.6	25	50.4	2	0	0	970.59	103	111
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	20	69	0.06%	50.2%	AEDKEWMPVTK	99.7%	55	25	35.1	4	2	0	1333.65	55	65
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	20	69	0.06%	50.2%	AFVAIGDYNGHVGLGVK	99.7%	101	25	97.5	8	0	0	1716.91	126	142
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	20	69	0.06%	50.2%	ATFDAISK	99.7%	54.5	25	35	3	0	0	852.45	239	246
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	20	69	0.06%	50.2%	ESEIIDFFLGASLKDEVLK	99.7%	43.9	25	43.9	1	0	0	2153.14	90	108
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	20	69	0.06%	50.2%	GCTATLGNFAK	99.7%	68.3	25	61.8	3	0	0	1139.55	228	238
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	20	69	0.06%	50.2%	GTGIVSAPVPK	99.7%	60	25	60	6	0	0	1025.60	201	211
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	20	69	0.06%	50.2%	IGKPHTVPCK	99.5%	37.8	25	26.8	2	0	0	1136.62	174	183
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	20	69	0.06%	50.2%	KLLMMAGIDDCYTSAR	99.7%	94	25	94	4	8	0	1844.87	212	227
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	20	69	0.06%	50.2%	LLMMAGIDDCYTSAR	99.7%	73.9	25	12.5	7	0	0	1732.77	213	227
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	20	69	0.06%	50.2%	LSIVPVRR	99.7%	48.8	25	34.1	5	0	0	939.61	160	167
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	20	69	0.06%	50.2%	SLEEIYLFSLPIK	99.7%	82.2	25	82.2	6	0	0	1551.87	77	89
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	20	69	0.06%	50.2%	SPYQEFTDHLVK	99.7%	64.8	25	62.2	4	2	0	1463.72	264	275
40S ribosomal protein S2	RPS2	RS2_HUMAN	31.3	100.0%	13	20	69	0.06%	50.2%	TYSYLTPDLWK	99.7%	63.3	25	63.3	4	0	0	1386.69	247	257
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	5	9	19	0.02%	29.4%	DTGKTPVEPEVAIHR	99.7%	48.3	25	48.3	2	2	0	1648.87	5	19
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	5	9	19	0.02%	29.4%	LIDLHSPSEIVK	99.7%	53	25	42.1	4	2	0	1350.76	88	99
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	5	9	19	0.02%	29.4%	RLIDLHSPSEIVK	99.7%	41.8	25	33.5	1	1	0	1506.86	87	99
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	5	9	19	0.02%	29.4%	TPVEPEVAIHR	99.7%	66.3	25	59.4	2	3	0	1247.67	9	19
40S ribosomal protein S20	RPS20	RS20_HUMAN	13.4	100.0%	5	9	19	0.02%	29.4%	VCADLIR	99.3%	36.4	25	25.5	2	0	0	846.45	35	41
40S ribosomal protein S21	RPS21	RS21_HUMAN	9.1	99.8%	2	2	5	0.00%	22.9%	MGESDDSILR	99.7%	69.3	25	61.8	2	0	0	1138.50	62	71

40S ribosomal protein S21	RPS21	RS21_HUMAN	9.1	99.8%	2	2	5	0.00%	22.9%	TYAICGAIR	99.7%	44.8	25	39.6	3	0	0	1024.52	52	60
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	5	6	17	0.02%	29.4%	AHLGTALK	99.6%	38.4	25	17.7	2	0	0	810.48	30	37
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	5	6	17	0.02%	29.4%	ANPFGGASHAK	99.7%	45.6	25	43.5	6	0	0	1056.52	38	48
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	5	6	17	0.02%	29.4%	GHAVGDIPGVR	99.7%	39.6	25	32.4	2	0	0	1077.58	109	119
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	5	6	17	0.02%	29.4%	KGHAVGDIPGVR	99.7%	60.6	25	60.6	2	2	0	1205.68	108	119
40S ribosomal protein S23	RPS23	RS23_HUMAN	15.8	100.0%	5	6	17	0.02%	29.4%	VANVSLLALYK	99.7%	86.5	25	86.5	3	0	0	1190.71	125	135
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	11	55	0.05%	30.1%	KQMVIDVLHPGK	99.7%	43.5	25	37.8	2	4	0	1380.77	21	32
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	11	55	0.05%	30.1%	QMVIDVLHPGK	99.7%	62.1	25	51.7	6	4	0	1236.68	22	32
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	11	55	0.05%	30.1%	TTGFGMIYDSLDYAK	99.7%	80.6	25	80.6	23	0	0	1697.77	69	83
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	11	55	0.05%	30.1%	TTGFGMIYDSLDYAKK	99.7%	58.3	25	58.3	2	0	0	1809.87	69	84
40S ribosomal protein S24	RPS24	RS24_HUMAN	15.4	100.0%	5	11	55	0.05%	30.1%	TTPDVIFVFGFR	99.7%	75.3	25	73.9	14	0	0	1398.74	50	61
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	6	7	36	0.03%	36.0%	AALQELLSK	99.7%	68.4	25	46.8	11	0	0	972.57	86	94
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	6	7	36	0.03%	36.0%	AQVIYTR	99.7%	51.3	25	42.8	4	0	0	850.48	105	111
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	6	7	36	0.03%	36.0%	ATYDKLCK	99.1%	35	25	26.6	2	0	0	998.50	53	60
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	6	7	36	0.03%	36.0%	DKLNNLVLFDK	99.7%	66.5	25	65.4	7	1	0	1318.74	42	52
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	6	7	36	0.03%	36.0%	LITPAVVSER	99.7%	71.6	25	60.5	9	0	0	1084.64	67	76
40S ribosomal protein S25	RPS25	RS25_HUMAN	13.7	100.0%	6	7	36	0.03%	36.0%	LNNLVLFDK	99.7%	59	25	52.6	2	0	0	1075.61	44	52
40S ribosomal protein S26	RPS26	RS26_HUMAN	13.0	100.0%	4	5	28	0.03%	44.3%	DISEASVFDAYVLPK	99.7%	91.6	25	71.3	12	0	0	1653.84	52	66
40S ribosomal protein S26	RPS26	RS26_HUMAN	13.0	100.0%	4	5	28	0.03%	44.3%	FRPAGAAPRPPPKPM	99.7%	35	25	31.7	0	1	0	1589.87	101	115
40S ribosomal protein S26	RPS26	RS26_HUMAN	13.0	100.0%	4	5	28	0.03%	44.3%	LHYCVSCAIHSK	99.7%	71.9	25	67.9	2	4	0	1474.69	71	82
40S ribosomal protein S26	RPS26	RS26_HUMAN	13.0	100.0%	4	5	28	0.03%	44.3%	NIVEAAAVR	99.7%	73.6	25	66.1	9	0	0	942.54	43	51
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	4	6	26	0.02%	39.3%	DLLHPSPEEEK	99.3%	36.4	25	23.1	2	1	0	1293.63	6	16
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	4	6	26	0.02%	39.3%	DLLHPSPEEEKR	99.7%	40.2	25	39.2	0	2	0	1449.73	6	17
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	4	6	26	0.02%	39.3%	LTEGCSFR	99.7%	49.1	25	47.5	9	0	0	969.45	73	80
40S ribosomal protein S27	RPS27	RS27_HUMAN	9.5	100.0%	4	6	26	0.02%	39.3%	LVQSPNSYFMDVK	99.7%	79.7	25	77.2	12	0	0	1543.75	24	36
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	28	122	0.11%	76.1%	ACYGVLR	99.7%	39.4	25	27.8	2	0	0	838.42	118	124
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	28	122	0.11%	76.1%	AELNEFLTR	99.7%	62.1	25	46.9	12	0	0	1092.57	19	27
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	28	122	0.11%	76.1%	DEILPTTPISEQK	99.7%	82.1	25	67	4	0	0	1470.77	215	227
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	28	122	0.11%	76.1%	ELAEDGYSGVEVR	99.7%	86.7	25	78.7	10	0	0	1423.67	28	40
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	28	122	0.11%	76.1%	ELTAVVQK	99.7%	44.5	25	25.4	2	0	0	887.52	68	75
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	28	122	0.11%	76.1%	FGFPEGSVELYAEK	99.7%	91.7	25	81.4	11	0	0	1572.76	77	90
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	28	122	0.11%	76.1%	FIMESGAK	99.7%	53.7	25	30.7	6	0	0	898.43	125	132
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	28	122	0.11%	76.1%	FVADGIFK	99.7%	46.4	25	37.5	3	0	0	896.49	11	18
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	28	122	0.11%	76.1%	FVDGLMIHSGDPVNYYVDTAVR	99.7%	75.3	25	75.3	4	4	0	2484.19	152	173
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	28	122	0.11%	76.1%	GCEVVVSGK	99.7%	59.5	25	53.5	4	0	0	934.47	133	141
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	28	122	0.11%	76.1%	GCEVVVSGKLR	98.9%	34	25	28.9	1	0	0	1203.65	133	143
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	28	122	0.11%	76.1%	GGKPEPPAMPQPVPTA	99.7%	61.7	25	53.9	9	0	0	1573.80	228	243
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	28	122	0.11%	76.1%	GLCAIAQAESLR	99.7%	81.9	25	71	12	0	0	1288.67	95	106
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	28	122	0.11%	76.1%	IMLPWDPTGK	99.7%	40.3	25	34.6	4	0	0	1173.60	188	197
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	28	122	0.11%	76.1%	IRELTAVVQK	99.7%	43.4	25	32.5	4	0	0	1156.70	66	75
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	28	122	0.11%	76.1%	KFVADGIFK	99.7%	50.8	25	35.8	4	0	0	1024.58	10	18
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	28	122	0.11%	76.1%	KPLPDHVSIVEPK	99.7%	50.3	25	40.8	2	1	0	1458.83	202	214
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	28	122	0.11%	76.1%	RFGFPEGSVELYAEK	99.7%	56.3	25	52	1	1	0	1728.86	76	90
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	28	122	0.11%	76.1%	TEIIILATR	99.7%	75.5	25	70.9	19	0	0	1029.63	46	54
40S ribosomal protein S3	RPS3	RS3_HUMAN	26.7	100.0%	20	28	122	0.11%	76.1%	TQNVLGEK	99.5%	37.3	25	23.8	2	0	0	888.48	55	62
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	31	115	0.11%	63.6%	ACQSIYPLHDVFVR	99.7%	70.6	25	64	4	4	0	1704.85	200	213
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	31	115	0.11%	63.6%	ACQSIYPLHDVFVRK	96.0%	23.7	25	23.7	0	1	0	1832.95	200	214
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	31	115	0.11%	63.6%	ADGYEPPVQESV	99.7%	58.7	25	58.7	4	0	0	1290.58	253	264
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	31	115	0.11%	63.6%	APAMFNIR	99.7%	57.1	25	45.7	7	0	0	935.48	35	42
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	31	115	0.11%	63.6%	ATGDETGAKVER	99.7%	62	25	49.7	2	0	0	1233.61	241	252
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	31	115	0.11%	63.6%	EVQTNDLKEVVNK	99.7%	73.2	25	65.4	7	1	0	1515.80	175	187

40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	31	115	0.11%	63.6%	KMMEIMTR	99.6%	38.6	25	31.4	2	0	0	1039.51	167	174
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	31	115	0.11%	63.6%	KTSYAQHQQVR	99.7%	51.9	25	44	1	3	0	1345.70	152	162
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	31	115	0.11%	63.6%	LFCVGFTK	99.7%	54.4	25	40.8	9	0	0	971.50	137	144
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	31	115	0.11%	63.6%	LIPDSIGKDIEK	99.7%	61.3	25	53.4	5	0	0	1327.75	188	199
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	31	115	0.11%	63.6%	LITEDVQGK	99.7%	61.5	25	44.2	6	0	0	1002.55	86	94
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	31	115	0.11%	63.6%	LMELHGEGSSSGK	99.7%	76.5	25	68.6	11	4	0	1347.62	228	240
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	31	115	0.11%	63.6%	MMEIMTR	99.7%	42.9	25	34.8	6	0	0	911.41	168	174
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	31	115	0.11%	63.6%	NCLTNFHGMDLTR	99.7%	85.6	25	78.3	6	6	0	1578.72	95	107
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	31	115	0.11%	63.6%	TSYAQHQQVR	99.7%	78.8	25	71.3	4	0	0	1217.60	153	162
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	31	115	0.11%	63.6%	TTDGYLLR	99.7%	68.7	25	51.6	10	0	0	938.49	129	136
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	31	115	0.11%	63.6%	VERADGYEPPVQESV	99.7%	53	25	53	1	0	0	1674.80	250	264
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	31	115	0.11%	63.6%	VFEVSLADLQNDEVAFR	99.7%	89.1	25	89.1	6	0	0	1951.98	66	82
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	31	115	0.11%	63.6%	VFEVSLADLQNDEVAFRK	99.7%	108	25	106	2	2	0	2080.07	66	83
40S ribosomal protein S3a	RPS3A	RS3A_HUMAN	29.9	100.0%	20	31	115	0.11%	63.6%	VVDPFSKK	97.9%	31.3	25	21.3	1	0	0	919.52	21	28
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	19	28	128	0.12%	64.3%	DANGNSFATR	99.7%	69.4	25	58.1	4	0	0	1052.48	212	221
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	19	28	128	0.12%	64.3%	ECLPLIIFLR	99.7%	58.1	25	52	6	0	0	1273.73	40	49
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	19	28	128	0.12%	64.3%	ERHPGSFDVVHVK	99.7%	51.9	25	51.9	2	4	0	1506.78	199	211
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	19	28	128	0.12%	64.3%	FDTGNLCMVTGGANLGR	99.7%	131	25	124	9	2	0	1798.82	175	191
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	19	28	128	0.12%	64.3%	GIPHLVTHDAR	99.7%	59.3	25	52.1	4	2	0	1215.66	135	145
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	19	28	128	0.12%	64.3%	GNKPWISLPR	99.7%	40.4	25	36.7	5	0	0	1167.66	231	240
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	19	28	128	0.12%	64.3%	HPGSFDVVHVK	99.7%	58.9	25	57.9	4	3	0	1221.64	201	211
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	19	28	128	0.12%	64.3%	ITPEEAKYK	96.4%	29.2	25	17.2	1	0	0	1078.58	114	122
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	19	28	128	0.12%	64.3%	LRECLPLIIFLR	99.7%	56.5	25	56.5	4	4	0	1542.92	38	49
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	19	28	128	0.12%	64.3%	LSNIFVIGK	99.7%	64.1	25	64.1	13	0	0	990.60	222	230
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	19	28	128	0.12%	64.3%	LTGVFAPRPSTGPHK	99.7%	47.5	25	40.7	3	0	0	1564.86	23	37
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	19	28	128	0.12%	64.3%	LTIAEER	99.6%	38.2	25	13.5	7	0	0	831.46	246	252
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	19	28	128	0.12%	64.3%	TDITYPAGFMDVISIDK	99.7%	80.9	25	80.9	15	0	0	1885.93	78	94
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	19	28	128	0.12%	64.3%	TIRYPDPLIK	99.7%	40.5	25	30.1	2	4	0	1215.71	146	155
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	19	28	128	0.12%	64.3%	VNDTIQIDLETGK	99.7%	104	25	104	11	0	0	1445.75	156	168
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	19	28	128	0.12%	64.3%	VNDTIQIDLETGKITDFIK	99.7%	49.9	25	49.9	0	2	0	2163.15	156	174
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	19	28	128	0.12%	64.3%	YALTGDEVK	99.7%	57.1	25	44.2	7	0	0	995.50	54	62
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	19	28	128	0.12%	64.3%	YALTGDEVKK	99.7%	60.5	25	47.5	6	0	0	1123.60	54	63
40S ribosomal protein S4, X isoform	RPS4X	RS4X_HUMAN	29.6	100.0%	19	28	128	0.12%	64.3%	YPDPLIK	99.5%	37.2	25	12.1	4	0	0	845.48	149	155
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	7	7	23	0.02%	37.3%	AQCPIVER	97.9%	31.5	25	20.5	2	0	0	972.49	64	71
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	7	7	23	0.02%	37.3%	KAQCPIVER	98.8%	33.7	25	30.2	2	0	0	1100.59	63	71
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	7	7	23	0.02%	37.3%	LTNSMMMHGR	99.7%	44.2	25	33.9	2	0	0	1177.53	72	81
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	7	7	23	0.02%	37.3%	QAVDVSPLR	99.7%	69.1	25	59.2	2	0	0	984.55	137	145
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	7	7	23	0.02%	37.3%	TIAECLADELINAAK	99.7%	107	25	105	11	0	0	1631.83	168	182
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	7	7	23	0.02%	37.3%	VNQAIWLLCTGAR	99.7%	91.5	25	86.4	2	0	0	1501.79	147	159
40S ribosomal protein S5	RPS5	RS5_HUMAN	22.9	100.0%	7	7	23	0.02%	37.3%	WSTDDVQINDISLQDYIAVK	99.7%	86.1	25	86.1	2	0	0	2323.15	23	42
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	11	16	53	0.05%	37.8%	DIPGLTDTTVPR	99.7%	73.6	25	60.2	10	0	0	1284.68	120	131
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	11	16	53	0.05%	37.8%	GCIVDANLSVLNLVIVK	99.7%	133	25	119	10	0	0	1827.04	99	115
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	11	16	53	0.05%	37.8%	KLFNLSK	99.7%	41.6	25	29.5	2	0	0	849.52	143	149
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	11	16	53	0.05%	37.8%	LFNLSKEDDVR	99.7%	52.7	25	39	3	2	0	1335.69	144	154
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	11	16	53	0.05%	37.8%	LIEVDDER	99.7%	53.6	25	48	5	0	0	988.49	15	22
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	11	16	53	0.05%	37.8%	LIEVDDERK	99.7%	47.8	25	38.1	2	0	0	1116.59	15	23
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	11	16	53	0.05%	37.8%	LNISFPATGCQK	99.7%	59.8	25	58.4	2	0	0	1335.67	3	14
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	11	16	53	0.05%	37.8%	MATEVAADALGEEWK	99.7%	126	25	126	8	0	0	1636.75	32	46
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	11	16	53	0.05%	37.8%	MATEVAADALGEEWKGYVVR	99.7%	93.7	25	91.1	2	3	0	2211.08	32	51
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	11	16	53	0.05%	37.8%	MKLNISFPATGCQK	99.7%	74.2	25	63.4	2	1	0	1610.80	1	14
40S ribosomal protein S6	RPS6	RS6_HUMAN	28.7	100.0%	11	16	53	0.05%	37.8%	NKEEAAEYAK	98.8%	33.8	25	23	1	0	0	1152.55	202	211

40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	12	14	47	0.04%	48.5%	AIIIFVPVPQLK	99.7%	63	25	63	10	0	0	1337.86	59	70
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	12	14	47	0.04%	48.5%	AQQNNVEHKVETFSGVYK	99.7%	81.1	25	81.1	2	2	0	2078.03	161	178
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	12	14	47	0.04%	48.5%	DVNFEFPEFQL	99.7%	74.3	25	70	7	0	0	1384.64	184	194
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	12	14	47	0.04%	48.5%	EIEVGGGR	96.1%	28.9	25	22.5	2	0	0	816.42	50	57
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	12	14	47	0.04%	48.5%	ELNITAAK	99.7%	52.6	25	39	3	0	0	859.49	42	49
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	12	14	47	0.04%	48.5%	HVVFIAQR	94.5%	27.6	25	27.6	1	0	0	969.56	91	98
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	12	14	47	0.04%	48.5%	KAIIIFVPVPQLK	99.7%	68.4	25	68.4	5	0	0	1465.95	58	70
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	12	14	47	0.04%	48.5%	LTGKDVNFEFPEFQL	99.7%	58.2	25	57.8	5	0	0	1783.89	180	194
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	12	14	47	0.04%	48.5%	TLTAVHDAILEDLVFPSEIVGK	99.7%	69.6	25	69.6	1	3	0	2367.28	121	142
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	12	14	47	0.04%	48.5%	TLTAVHDAILEDLVFPSEIVGKR	99.7%	82.8	25	82.8	0	2	0	2523.38	121	143
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	12	14	47	0.04%	48.5%	VETFSGVYK	99.7%	42.7	25	19.7	2	0	0	1029.53	170	178
40S ribosomal protein S7	RPS7	RS7_HUMAN	22.1	100.0%	12	14	47	0.04%	48.5%	VETFSGVYKK	98.9%	34.1	25	28.6	2	0	0	1157.62	170	179
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	18	60	0.06%	59.1%	ADGYVLEGK	99.7%	71.7	25	68.5	2	0	0	951.48	185	193
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	18	60	0.06%	59.1%	ADGYVLEGKELEFYLR	99.7%	51.5	25	50.6	2	2	0	1901.96	185	200
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	18	60	0.06%	59.1%	ELEFYLR	99.7%	42.6	25	30.5	2	0	0	969.50	194	200
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	18	60	0.06%	59.1%	ELEFYLRK	98.0%	31.6	25	23	2	0	0	1097.60	194	201
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	18	60	0.06%	59.1%	IIDVVYNASNNELVR	99.7%	107	25	101	12	2	0	1718.91	78	92
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	18	60	0.06%	59.1%	ISSLLEEQFQQGK	99.7%	89.5	25	73.7	9	0	0	1506.78	158	170
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	18	60	0.06%	59.1%	KYELGRPAANTK	99.7%	67.8	25	60.6	2	0	0	1347.74	26	37
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	18	60	0.06%	59.1%	LDVGNFSWGSECCTR	99.7%	92.5	25	92.5	3	0	0	1787.75	60	74
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	18	60	0.06%	59.1%	LDVGNFSWGSECCTRK	98.1%	26.5	25	26.5	0	1	0	1915.84	60	75
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	18	60	0.06%	59.1%	LLACIASRPGQCGR	99.7%	43.8	25	40.9	1	2	0	1558.79	171	184
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	18	60	0.06%	59.1%	LTPEEEEILNK	99.7%	68.2	25	58.7	5	0	0	1314.68	129	139
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	18	60	0.06%	59.1%	NCIVLIDSTPYR	99.7%	85.4	25	67.8	8	0	0	1450.74	99	110
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	18	60	0.06%	59.1%	QWYESHYALPLGR	99.7%	45.4	25	42	2	1	0	1619.80	111	123
40S ribosomal protein S8	RPS8	RS8_HUMAN	24.2	100.0%	14	18	60	0.06%	59.1%	YELGRPAANTK	99.7%	56.9	25	46.6	2	0	0	1219.64	27	37
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	21	24	67	0.06%	55.2%	ELLTLDEK	99.0%	34.5	25	23.3	2	0	0	960.53	59	66
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	21	24	67	0.06%	55.2%	ELLTLDEKDPR	97.4%	30.5	25	30.4	2	0	0	1328.71	59	69
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	21	24	67	0.06%	55.2%	HIDFSLR	99.7%	43.3	25	17.9	2	0	0	887.47	156	162
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	21	24	67	0.06%	55.2%	IEDFLER	99.7%	52.9	25	44.8	2	0	0	921.47	102	108
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	21	24	67	0.06%	55.2%	IEDFLERR	94.9%	27.9	25	11.9	1	0	0	1077.57	102	109
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	21	24	67	0.06%	55.2%	IGVLDEGK	99.7%	55.9	25	29.1	4	0	0	830.46	84	91
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	21	24	67	0.06%	55.2%	IGVLDEGKMK	99.7%	51.3	25	43.1	4	0	0	1089.60	84	93
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	21	24	67	0.06%	55.2%	KQVVNIPSFIVR	99.7%	48.9	25	48.9	2	2	0	1399.84	139	150
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	21	24	67	0.06%	55.2%	LDYILGLK	99.2%	35.4	25	32.6	1	0	0	934.56	94	101
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	21	24	67	0.06%	55.2%	LDYILGLKIEDFLER	99.2%	35.7	25	34.7	1	0	0	1837.01	94	108
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	21	24	67	0.06%	55.2%	LFEGNALLR	99.7%	65.9	25	48.8	11	0	0	1032.58	71	79
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	21	24	67	0.06%	55.2%	LFEGNALLRR	98.6%	33.2	25	22.6	1	0	0	1188.68	71	80
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	21	24	67	0.06%	55.2%	LIGEYGLR	99.7%	57.3	25	45	2	0	0	920.52	31	38
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	21	24	67	0.06%	55.2%	LQTQVFK	95.1%	28	25	9.46	1	0	0	863.50	110	116
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	21	24	67	0.06%	55.2%	MKLDYILGLK	99.7%	45.8	25	32	6	0	0	1209.69	92	101
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	21	24	67	0.06%	55.2%	QVVNIPSFIVR	99.7%	54.5	25	45.1	10	0	0	1271.75	140	150
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	21	24	67	0.06%	55.2%	RLFEGNALLR	99.7%	66.6	25	40.9	2	0	0	1188.68	70	79
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	21	24	67	0.06%	55.2%	RLQTQVFK	98.8%	33.8	25	24.6	2	0	0	1019.60	109	116
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	21	24	67	0.06%	55.2%	SPYGGGRPGR	97.8%	31.2	25	21	4	0	0	1003.51	163	172
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	21	24	67	0.06%	55.2%	SRLDQELK	99.0%	34.7	25	11.4	4	0	0	988.54	23	30
40S ribosomal protein S9	RPS9	RS9_HUMAN	22.6	100.0%	21	24	67	0.06%	55.2%	VKFTLAK	95.5%	28.3	25	23.9	1	0	0	806.51	46	52
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	4	4	14	0.01%	16.3%	AIVAIENPADVSVISSR	99.7%	78.1	25	78.1	5	0	0	1740.95	64	80
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	4	4	14	0.01%	16.3%	FAAATGATPIAGR	99.7%	94.2	25	83.2	5	0	0	1203.65	90	102
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	4	4	14	0.01%	16.3%	LLVVTDPR	99.7%	57.5	25	45	2	0	0	912.55	121	128
40S ribosomal protein SA	RPSA	RSSA_HUMAN	32.9	100.0%	4	4	14	0.01%	16.3%	SDGIYIINLK	99.7%	53.2	25	37.5	2	0	0	1135.64	43	52

4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	18	0.02%	16.8%	ADLLLSTQPGREEGSPLELER	99.7%	60.6	25	60.6	0	2	0	2310.19	593	613
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	18	0.02%	16.8%	FTGLSKEELLK	99.7%	50.4	25	44.5	1	0	0	1264.71	161	171
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	18	0.02%	16.8%	GENSWFSTQVDTVATK	99.7%	105	25	102	2	0	0	1769.83	314	329
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	18	0.02%	16.8%	GLVLGPIHK	99.7%	42.5	25	42.4	2	0	0	933.59	258	266
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	18	0.02%	16.8%	GQSEDPGSLLSLFR	99.7%	65.7	25	53.5	2	0	0	1505.76	511	524
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	18	0.02%	16.8%	LLTSFLPAQLLR	99.7%	50.2	25	44.6	3	0	0	1371.84	440	451
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	18	0.02%	16.8%	VAEDEAEAAAAAK	99.7%	95.9	25	90	2	0	0	1245.60	148	160
4F2 cell-surface antigen heavy chain	SLC3A2	4F2_HUMAN	68.0	100.0%	8	8	18	0.02%	16.8%	VILDLTPNYR	99.7%	59.9	25	47.2	4	0	0	1203.67	304	313
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	6	7	14	0.01%	9.0%	AALEEVYPDLTPEETRR	94.5%	22.6	25	22.6	0	1	0	1988.99	660	676
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	6	7	14	0.01%	9.0%	ELTMASLPFTFDVER	99.7%	55.1	25	55.1	3	0	0	1755.86	316	330
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	6	7	14	0.01%	9.0%	NSLGGDVLFVGK	99.7%	63.8	25	63.8	3	0	0	1205.65	677	688
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	6	7	14	0.01%	9.0%	NSPGSQVASNPR	99.7%	90.5	25	86.7	5	0	0	1213.59	447	458
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	6	7	14	0.01%	9.0%	VVQSYVEGLCWVLR	99.7%	59.6	25	53.8	1	0	0	1707.89	538	551
5'-3' exoribonuclease 2	XRN2	XRN2_HUMAN	108.6	100.0%	6	7	14	0.01%	9.0%	YAWQGVALLPFVDER	99.7%	63.5	25	59.6	1	0	0	1763.91	642	656
5'-AMP-activated protein kinase catalytic subunit alpha-2	PRKAA2	AAPK2_HUMAN	62.3	100.0%	7	8	12	0.01%	15.0%	DLKPENVLLDAHMNAK	99.7%	37	25	37	0	1	0	1807.94	139	154
5'-AMP-activated protein kinase catalytic subunit alpha-2	PRKAA2	AAPK2_HUMAN	62.3	100.0%	7	8	12	0.01%	15.0%	GGVFYIPEYLNR	99.7%	47.2	25	40.9	2	0	0	1427.73	228	239
5'-AMP-activated protein kinase catalytic subunit alpha-2	PRKAA2	AAPK2_HUMAN	62.3	100.0%	7	8	12	0.01%	15.0%	IADFGLSNMMSDGEFLR	99.7%	58.6	25	58.6	3	0	0	1934.86	155	171
5'-AMP-activated protein kinase catalytic subunit alpha-2	PRKAA2	AAPK2_HUMAN	62.3	100.0%	7	8	12	0.01%	15.0%	IGEHQLTGHK	95.8%	28.6	25	25.9	1	0	0	1119.59	32	41
5'-AMP-activated protein kinase catalytic subunit alpha-2	PRKAA2	AAPK2_HUMAN	62.3	100.0%	7	8	12	0.01%	15.0%	MPPLIADSPK	99.7%	49.4	25	41.7	2	0	0	1084.57	370	379
5'-AMP-activated protein kinase catalytic subunit alpha-2	PRKAA2	AAPK2_HUMAN	62.3	100.0%	7	8	12	0.01%	15.0%	SIDDEVVEQR	99.7%	46.7	25	33.1	1	0	0	1189.57	471	480
5'-AMP-activated protein kinase catalytic subunit alpha-2	PRKAA2	AAPK2_HUMAN	62.3	100.0%	7	8	12	0.01%	15.0%	VVNAYHLR	99.7%	54.9	25	42.4	2	0	0	971.54	432	439
5'-nucleotidase domain-containing protein 2	NT5DC2	NT5D2_HUMAN	60.7	100.0%	2	2	3	0.00%	5.2%	QGNLFDFLR	99.7%	61.6	25	47.5	2	0	0	1109.57	336	344
5'-nucleotidase domain-containing protein 2	NT5DC2	NT5D2_HUMAN	60.7	100.0%	2	2	3	0.00%	5.2%	VLYFGDHLYSDLADLMLR	95.3%	23.2	25	22.4	0	1	0	2157.07	353	370
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	21	30	60	0.06%	42.8%	AAVEEGIVLGGGCALLR	99.7%	113	25	106	2	2	0	1684.91	430	446
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	21	30	60	0.06%	42.8%	ALMLQGVDLLADAVAVTMGPK	99.7%	49.8	25	49.8	0	5	0	2129.13	38	58
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	21	30	60	0.06%	42.8%	CEFQDAYVLLSEK	99.7%	83.5	25	72.1	2	0	0	1601.75	237	249
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	21	30	60	0.06%	42.8%	CIPALDSLTPANEDQK	99.7%	80.4	25	78.8	2	0	0	1771.85	447	462
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	21	30	60	0.06%	42.8%	GANPVEIR	99.7%	50.4	25	15.7	2	0	0	855.47	134	141
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	21	30	60	0.06%	42.8%	GANPVEIRR	99.1%	34.9	25	25.3	1	0	0	1011.57	134	142
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	21	30	60	0.06%	42.8%	GVMLAVDAVIAELKK	99.7%	65.7	25	64.1	4	0	0	1556.91	143	157
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	21	30	60	0.06%	42.8%	GYISPYFINTSK	99.7%	75.3	25	68.8	2	0	0	1389.70	222	233
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	21	30	60	0.06%	42.8%	IGIEIIKR	99.7%	61	25	31.1	2	0	0	941.61	463	470
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	21	30	60	0.06%	42.8%	IPAMTIAK	98.9%	34.2	25	26.4	1	0	0	860.49	474	481
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	21	30	60	0.06%	42.8%	ISSIQSIVPALEIANAHR	99.7%	82.3	25	82.3	2	2	0	1919.07	251	268
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	21	30	60	0.06%	42.8%	LVQDVANNTNEEAGDGTTTATVLAR	99.7%	175	25	175	2	2	0	2560.25	97	121
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	21	30	60	0.06%	42.8%	NAGVEGSLIVEK	99.7%	77.8	25	60.5	2	0	0	1215.66	482	493
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	21	30	60	0.06%	42.8%	TLNDELEIIEGMK	99.7%	98.4	25	90.5	2	0	0	1504.76	206	218
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	21	30	60	0.06%	42.8%	TVIIEQSWGSPK	99.7%	87	25	74.2	2	0	0	1344.72	61	72
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	21	30	60	0.06%	42.8%	VGEVIVTK	99.7%	70.3	25	49	2	0	0	844.51	345	352
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	21	30	60	0.06%	42.8%	VGEVIVTKDDAMLLK	99.7%	65.6	25	60.8	4	4	0	1630.91	345	359
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	21	30	60	0.06%	42.8%	VGGTSDVEVNEK	99.7%	85.2	25	80	3	0	0	1233.60	406	417
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	21	30	60	0.06%	42.8%	VGGTSDVEVNEKK	99.7%	74.3	25	58.7	2	2	0	1361.69	406	418
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	21	30	60	0.06%	42.8%	VGLQVVAVK	99.7%	78.2	25	68.9	2	0	0	912.59	293	301
60 kDa heat shock protein, mitochondrial	HSPD1	CH60_HUMAN	61.1	100.0%	21	30	60	0.06%	42.8%	VTDALNATR	99.7%	76.3	25	60.4	2	0	0	960.51	421	429
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	13	16	27	0.03%	31.0%	AIADWYNEK	99.2%	35.4	25	32.5	2	0	0	1109.53	151	159
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	13	16	27	0.03%	31.0%	ALDAAFYK	99.3%	35.8	25	34.6	2	0	0	898.47	352	359
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	13	16	27	0.03%	31.0%	ALLQEMPLTALLR	99.7%	94	25	82.8	3	0	0	1468.86	271	283
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	13	16	27	0.03%	31.0%	EHLLTNHLK	96.5%	29.4	25	0	1	0	0	1104.62	256	264
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	13	16	27	0.03%	31.0%	FLCFGSEGGTYYIK	99.7%	92.1	25	88.7	2	0	0	1641.76	36	49
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	13	16	27	0.03%	31.0%	GGMALALAVTK	99.7%	75.9	25	67.3	3	0	0	1047.59	160	170
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	13	16	27	0.03%	31.0%	GMLDMCGFDTGALDVIR	99.7%	91.5	25	91.5	2	0	0	1870.85	515	531

60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	13	16	27	0.03%	31.0%	IPTHLFTFIQFK	99.7%	44.2	25	35.9	1	2	0	1491.84	121	132
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	13	16	27	0.03%	31.0%	LGLENAEALIR	99.7%	82.9	25	73.6	2	0	0	1198.68	53	63
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	13	16	27	0.03%	31.0%	LSHLKPSSEGLAIVTK	99.7%	45.7	25	45.5	0	2	0	1679.97	185	200
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	13	16	27	0.03%	31.0%	MTANSVLEPGNSEVSLVCEK	99.7%	72.1	25	72.1	2	0	0	2180.02	288	307
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	13	16	27	0.03%	31.0%	QIANSQDGYVWQVTDMNR	99.7%	86	25	86	1	0	0	2124.98	15	32
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	RO60_HUMAN	60.7	100.0%	13	16	27	0.03%	31.0%	WRPDEEILK	99.7%	51.7	25	43.3	2	0	0	1185.63	343	351
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	14	20	75	0.07%	55.8%	AFLADPSAFVAAAPVAAATTAAPAAAAAPAK	99.7%	105	25	105	2	6	0	2752.47	267	297
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	14	20	75	0.07%	55.8%	AGAIAPCEVTVPAQNTGLGPEK	99.7%	70.2	25	70.2	2	2	0	2180.10	113	134
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	14	20	75	0.07%	55.8%	CFIVGADNVGSK	99.7%	52.4	25	45.8	1	0	0	1266.61	27	38
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	14	20	75	0.07%	55.8%	DMLLANK	99.1%	34.8	25	27.4	2	0	0	804.43	100	106
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	14	20	75	0.07%	55.8%	DMLLANKVPAAAR	99.7%	61.6	25	51.8	2	0	0	1369.76	100	112
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	14	20	75	0.07%	55.8%	EDLTEIR	99.6%	39.2	25	17.6	2	0	0	875.45	93	99
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	14	20	75	0.07%	55.8%	EDLTEIRDMLLANK	99.7%	44.8	25	41.9	4	1	0	1660.86	93	106
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	14	20	75	0.07%	55.8%	GHLENNPALEK	99.7%	65.5	25	49	2	2	0	1221.62	67	77
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	14	20	75	0.07%	55.8%	GNVGFVFTK	99.7%	69	25	50.1	7	0	0	968.52	84	92
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	14	20	75	0.07%	55.8%	GTIEILSDVQLIK	99.7%	77.8	25	66.4	10	0	0	1428.83	150	162
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	14	20	75	0.07%	55.8%	IIQLLDDYPK	99.7%	80.2	25	67.1	4	0	0	1217.68	17	26
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	14	20	75	0.07%	55.8%	TSFFQALGITTK	99.7%	108	25	102	16	0	0	1313.71	135	146
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	14	20	75	0.07%	55.8%	VEAKEESEESDEDMGFGLFD	99.7%	73.6	25	73.6	3	0	0	2278.92	298	317
60S acidic ribosomal protein P0	RPLP0	RLA0_HUMAN	34.3	100.0%	14	20	75	0.07%	55.8%	VLALSVETDYTFPLAEK	99.7%	90.5	25	90.5	7	0	0	1896.00	248	264
60S acidic ribosomal protein P2	RPLP2	RLA2_HUMAN	11.7	100.0%	4	6	12	0.01%	69.6%	ILDSVGIEADDDRLNK	99.7%	96.3	25	93.8	2	2	0	1772.90	26	41
60S acidic ribosomal protein P2	RPLP2	RLA2_HUMAN	11.7	100.0%	4	6	12	0.01%	69.6%	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	99.7%	57.1	25	57.1	0	2	0	2774.43	62	94
60S acidic ribosomal protein P2	RPLP2	RLA2_HUMAN	11.7	100.0%	4	6	12	0.01%	69.6%	NIEDVIAQGIGK	99.7%	102	25	88.5	2	0	0	1256.68	50	61
60S acidic ribosomal protein P2	RPLP2	RLA2_HUMAN	11.7	100.0%	4	6	12	0.01%	69.6%	YVASYLLAALGGNSSPSAK	99.7%	76.3	25	73.6	2	2	0	1868.98	3	21
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	22	43	0.04%	61.2%	AKVDEFPLCGHMVSDEYEQLSSEALEAAR	99.7%	89.8	25	89.8	0	2	0	3297.50	41	69
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	22	43	0.04%	61.2%	EHVIEALR	97.1%	30	25	27.2	1	0	0	966.54	146	153
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	22	43	0.04%	61.2%	EHVIEALRR	94.8%	27.8	25	3.09	1	0	0	1122.64	146	154
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	22	43	0.04%	61.2%	FNADEFEDMVAEK	99.7%	77.5	25	76.9	3	0	0	1560.65	176	188
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	22	43	0.04%	61.2%	FNADEFEDMVAEKR	99.7%	81.5	25	77.9	2	3	0	1700.76	176	189
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	22	43	0.04%	61.2%	GAFGKPQGTVAR	99.7%	58.4	25	45.8	4	0	0	1188.65	117	128
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	22	43	0.04%	61.2%	GPLDKWR	98.9%	34.2	25	27.3	1	0	0	871.48	204	210
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	22	43	0.04%	61.2%	ICANKYMVK	97.2%	30.2	25	27.5	1	0	0	1142.57	70	78
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	22	43	0.04%	61.2%	IRIFDLGR	98.3%	32.3	25	20.4	1	0	0	989.59	31	38
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	22	43	0.04%	61.2%	LQNKEHVIEALR	99.7%	43.2	25	41.6	0	1	0	1449.82	142	153
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	22	43	0.04%	61.2%	MLSCAGADR	99.7%	53	25	43.4	5	0	0	980.43	102	110
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	22	43	0.04%	61.2%	RLIPDGCGVK	99.7%	45	25	32.6	2	0	0	1114.60	189	198
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	22	43	0.04%	61.2%	VDEFPLCGHMVSDEYEQLSSEALEAAR	99.7%	63.2	25	63.2	0	3	0	3098.37	43	69
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	22	43	0.04%	61.2%	VHIGQVIMSIR	99.7%	52.3	25	51.2	8	4	0	1252.72	129	139
60S ribosomal protein L10	RPL10	RL10_HUMAN	24.6	100.0%	15	22	43	0.04%	61.2%	VRLHPFHVIR	99.5%	32.1	25	26.9	0	1	0	1273.76	89	98
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	11	23	43	0.04%	43.8%	AGKFPSLLTHNENMVAK	99.4%	31	25	28.9	0	4	0	1856.97	131	147
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	11	23	43	0.04%	43.8%	AVDIPHMDIEALK	99.7%	52.7	25	50.3	4	1	0	1467.75	79	91
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	11	23	43	0.04%	43.8%	AVDIPHMDIEALKK	99.7%	74.1	25	69.2	4	3	0	1579.85	79	92
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	11	23	43	0.04%	43.8%	DTLYEAVR	99.7%	52	25	30.2	3	0	0	966.49	8	15
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	11	23	43	0.04%	43.8%	FPSLLTHNENMVAK	99.7%	63	25	52.8	4	4	0	1600.82	134	147
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	11	23	43	0.04%	43.8%	FSVCVLGDQQHCDEAK	99.7%	78.2	25	78.2	2	2	0	1892.83	63	78
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	11	23	43	0.04%	43.8%	ILGPGLNK	99.4%	36.6	25	20.8	2	0	0	811.50	123	130
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	11	23	43	0.04%	43.8%	KNWQNVR	97.1%	30	25	21.3	1	0	0	944.51	196	202
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	11	23	43	0.04%	43.8%	KYDAFLASESLIK	99.7%	83.3	25	83.3	2	2	0	1484.80	106	118
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	11	23	43	0.04%	43.8%	VLCLAVAVGHVK	99.7%	85	25	85	2	2	0	1265.74	162	173
60S ribosomal protein L10a	RPL10A	RL10A_HUMAN	24.8	100.0%	11	23	43	0.04%	43.8%	YDAFLASESLIK	99.7%	46	25	40.7	1	0	0	1356.70	107	118
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	11	39	0.04%	39.3%	AEEILEK	98.6%	33.1	25	13.1	2	0	0	831.45	79	85

60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	11	39	0.04%	39.3%	AEEILEKGLK	99.7%	41.5	25	34.3	1	0	0	1129.65	79	88
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	11	39	0.04%	39.3%	IAVHCTVR	99.7%	52.6	25	45.8	3	0	0	955.51	68	75
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	11	39	0.04%	39.3%	ISKEEAMR	99.7%	51	25	31.1	2	0	0	963.49	157	164
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	11	39	0.04%	39.3%	KLCLNICVGESGDR	99.7%	53.1	25	53.1	2	0	0	1620.78	19	32
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	11	39	0.04%	39.3%	LCLNICVGESGDR	99.7%	67.3	25	67.3	2	0	0	1492.69	20	32
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	11	39	0.04%	39.3%	VLEQLTGQTPVFSK	99.7%	98.3	25	89.8	13	0	0	1546.85	39	52
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	11	39	0.04%	39.3%	VLEQLTGQTPVFSKAR	99.7%	45.1	25	45.1	2	0	0	1773.99	39	54
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	11	39	0.04%	39.3%	WFQQKYDGIILPGK	99.7%	51.1	25	51.1	1	2	0	1692.91	165	178
60S ribosomal protein L11	RPL11	RL11_HUMAN	20.3	100.0%	10	11	39	0.04%	39.3%	YDGIILPGK	99.7%	70.1	25	67.9	9	0	0	975.55	170	178
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	6	8	28	0.03%	54.5%	CTGGEVGATSALAPK	99.7%	96.8	25	76.6	4	0	0	1418.69	17	31
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	6	8	28	0.03%	54.5%	EILGTAQSVGCNVDGR	99.7%	108	25	108	3	0	0	1675.81	131	146
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	6	8	28	0.03%	54.5%	HPHDIIDDINSGAVECPAS	99.7%	55.1	25	55	1	0	0	2046.92	147	165
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	6	8	28	0.03%	54.5%	HSGNITFDEIVNIAR	99.7%	104	25	104	2	3	0	1685.86	100	114
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	6	8	28	0.03%	54.5%	IGPLGLSPK	99.7%	51.7	25	35.4	7	0	0	881.55	32	40
60S ribosomal protein L12	RPL12	RL12_HUMAN	17.8	100.0%	6	8	28	0.03%	54.5%	QAQIEVVPSASALIIK	99.7%	87.2	25	87.2	6	2	0	1666.97	68	83
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	13	66	0.06%	34.6%	GFSLEELR	99.7%	52.4	25	36.9	13	0	0	950.49	75	82
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	13	66	0.06%	34.6%	LATQLTGPVMPVR	99.7%	65.2	25	64.1	10	0	0	1382.78	146	158
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	13	66	0.06%	34.6%	NKSTESLQANVQR	99.7%	60.4	25	56.2	1	0	0	1474.76	104	116
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	13	66	0.06%	34.6%	RVATWFNQPAR	99.7%	53.3	25	45	2	2	0	1345.71	21	31
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	13	66	0.06%	34.6%	SKLILFPR	99.5%	37.5	25	37.5	2	0	0	973.62	122	129
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	13	66	0.06%	34.6%	STESLQANVQR	99.7%	92.3	25	80.6	13	0	0	1232.62	106	116
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	13	66	0.06%	34.6%	TIGISVDPR	99.7%	71	25	53.1	9	0	0	957.54	93	101
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	13	66	0.06%	34.6%	VATWFNQPAR	99.7%	77.9	25	64.4	4	0	0	1189.61	22	31
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	13	66	0.06%	34.6%	VATWFNQPARK	99.7%	44.9	25	44	2	0	0	1317.71	22	32
60S ribosomal protein L13	RPL13	RL13_HUMAN	24.3	100.0%	10	13	66	0.06%	34.6%	VITEEEKNFK	99.7%	53.9	25	43.5	6	2	0	1236.65	168	177
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	10	11	27	0.03%	37.9%	CEGINISGNFYR	99.7%	71.7	25	65	2	0	0	1429.65	38	49
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	10	11	27	0.03%	37.9%	IDKYTEVLK	99.7%	42.4	25	28.2	1	0	0	1108.63	189	197
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	10	11	27	0.03%	37.9%	KFAYLGR	99.7%	41	25	29.6	2	0	0	854.49	134	140
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	10	11	27	0.03%	37.9%	LAHEVGWK	99.7%	45.6	25	30.2	2	0	0	939.50	141	148
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	10	11	27	0.03%	37.9%	LAHEVGWKYQAVTATLEEK	99.7%	43	25	43	0	2	0	2173.13	141	159
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	10	11	27	0.03%	37.9%	LKYLAFLR	99.7%	46.2	25	37.7	1	0	0	1023.64	52	59
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	10	11	27	0.03%	37.9%	RMVVPAALK	99.5%	37.6	25	22.3	1	0	0	984.60	117	125
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	10	11	27	0.03%	37.9%	VFDGIPPPYDKK	99.7%	41.6	25	32.5	4	2	0	1375.73	104	115
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	10	11	27	0.03%	37.9%	YQAVTATLEEK	99.7%	81.6	25	71.3	9	0	0	1252.64	149	159
60S ribosomal protein L13a	RPL13A	RL13A_HUMAN	23.6	100.0%	10	11	27	0.03%	37.9%	YQAVTATLEEKR	99.7%	48.8	25	48.8	1	0	0	1408.74	149	160
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	9	77	0.07%	27.9%	ALVDGPCTQVR	99.7%	82	25	76.8	5	0	0	1215.62	36	46
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	9	77	0.07%	27.9%	CMQLTDFILK	99.7%	53.7	25	39.3	11	0	0	1284.63	54	63
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	9	77	0.07%	27.9%	LVAIVDVIDQNR	99.7%	93.6	25	93.6	32	0	0	1354.77	24	35
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	9	77	0.07%	27.9%	MTDFDRFK	99.7%	42.9	25	42.9	8	0	0	1059.49	104	111
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	9	77	0.07%	27.9%	RFVEVGR	99.7%	42.9	25	32.1	3	0	0	862.49	5	11
60S ribosomal protein L14	RPL14	RL14_HUMAN	23.4	100.0%	6	9	77	0.07%	27.9%	VAYVSFGPHAGK	99.7%	56.5	25	55.1	16	2	0	1232.64	12	23
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	7	9	16	0.02%	32.8%	GATYGKPVHHGVNQLK	99.7%	49.9	25	40.3	2	2	0	1705.91	78	93
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	7	9	16	0.02%	32.8%	NPDTQWITKPVHK	99.7%	39.4	25	39.3	1	1	0	1563.83	145	157
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	7	9	16	0.02%	32.8%	NTLQLHR	99.7%	47.2	25	34.8	3	0	0	881.50	196	202
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	7	9	16	0.02%	32.8%	RNPDTQWITKPVHK	99.7%	34.9	25	27.8	0	2	0	1719.93	144	157
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	7	9	16	0.02%	32.8%	SLQSVAEER	99.7%	45	25	36.6	3	0	0	1018.52	97	105
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	7	9	16	0.02%	32.8%	VLNSYWVGEDSTYK	99.5%	38	25	38	1	0	0	1660.79	115	128
60S ribosomal protein L15	RPL15	RL15_HUMAN	24.1	100.0%	7	9	16	0.02%	32.8%	YIQELWR	99.7%	47.9	25	25.1	1	0	0	1007.53	6	12
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	15	50	0.05%	45.1%	EQIVPKPEEEVAQK	99.7%	61	25	52.4	2	0	0	1623.86	154	167
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	15	50	0.05%	45.1%	EQIVPKPEEEVAQKK	99.7%	38	25	35.1	2	2	0	1751.95	154	168
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	15	50	0.05%	45.1%	GLDVDSLVIEHIQVNK	99.7%	96.2	25	84.3	11	2	0	1778.96	106	121

60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	15	50	0.05%	45.1%	KSAEFLLHMLK	99.7%	52.9	25	46	4	0	0	1316.74	86	96
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	15	50	0.05%	45.1%	NAESNAELK	98.9%	34.2	25	27.4	1	0	0	975.47	97	105
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	15	50	0.05%	45.1%	QWGWTQGR	99.7%	47.4	25	33.6	3	0	0	1018.49	75	82
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	15	50	0.05%	45.1%	QWGWTQGRWPK	94.6%	27.6	25	21.3	1	0	0	1429.71	75	85
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	15	50	0.05%	45.1%	SAEFLLHMLK	99.7%	63.3	25	55.5	7	0	0	1188.64	87	96
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	15	50	0.05%	45.1%	VRYSLDPENPTK	99.6%	38.8	25	35.8	2	0	0	1418.73	2	13
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	15	50	0.05%	45.1%	YLKDVTLQK	99.7%	48.2	25	39.9	4	0	0	1107.64	47	55
60S ribosomal protein L17	RPL17	RL17_HUMAN	21.4	100.0%	11	15	50	0.05%	45.1%	YSLDPENPTK	99.7%	61.4	25	56.4	9	0	0	1163.56	4	13
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	11	14	57	0.05%	50.0%	APGTPHSHTKPYVR	99.7%	47	25	45.8	1	2	0	1547.81	155	168
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	11	14	57	0.05%	50.0%	GCGTVLLSGPR	99.7%	84.4	25	64.5	6	0	0	1116.58	133	143
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	11	14	57	0.05%	50.0%	ILTFDQLALDSPK	99.7%	118	25	112	16	0	0	1460.80	120	132
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	11	14	57	0.05%	50.0%	LKVCALR	95.2%	28.1	25	26.5	1	0	0	859.52	98	104
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	11	14	57	0.05%	50.0%	RTNSTFNQVVLK	99.6%	38.4	25	3.11	2	0	0	1406.78	38	49
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	11	14	57	0.05%	50.0%	SQDIYLR	99.2%	35.3	25	15.8	2	0	0	894.47	20	26
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	11	14	57	0.05%	50.0%	TAVVVGTITDDVR	99.7%	120	25	112	8	0	0	1345.73	79	91
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	11	14	57	0.05%	50.0%	TAVVVGTITDDVRVQEVPK	99.7%	49.6	25	49.6	2	2	0	2026.12	79	97
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	11	14	57	0.05%	50.0%	TNRPPLSLSR	99.0%	34.4	25	31.1	6	0	0	1140.65	56	65
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	11	14	57	0.05%	50.0%	TNSTFNQVVLK	99.7%	69.5	25	56.7	5	0	0	1250.67	39	49
60S ribosomal protein L18	RPL18	RL18_HUMAN	21.6	100.0%	11	14	57	0.05%	50.0%	TNSTFNQVVLKR	99.7%	45.5	25	45.5	3	1	0	1406.78	39	50
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	13	16	51	0.05%	47.7%	AHSIQIMK	98.4%	32.6	25	23.1	3	0	0	943.50	121	128
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	13	16	51	0.05%	47.7%	AHSIQIMKVEEIAASK	97.0%	24.8	25	24.8	0	1	0	1770.94	121	136
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	13	16	51	0.05%	47.7%	DLTTAGAVTQCYR	99.7%	70.7	25	63.8	5	0	0	1455.69	99	111
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	13	16	51	0.05%	47.7%	EYRDLTTAGAVTQCYR	99.7%	63.2	25	56.7	4	4	0	1903.90	96	111
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	13	16	51	0.05%	47.7%	FWYFVSQLK	99.7%	52.6	25	50.7	2	0	0	1217.64	44	52
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	13	16	51	0.05%	47.7%	FWYFVSQLKK	99.7%	36.4	25	28.6	2	2	0	1345.73	44	53
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	13	16	51	0.05%	47.7%	IFAPNHVVAK	99.7%	44.2	25	37	4	0	0	1095.63	32	41
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	13	16	51	0.05%	47.7%	IKFPLPHR	96.3%	29.1	25	22.2	1	0	0	1007.62	150	157
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	13	16	51	0.05%	47.7%	KSSGEIVYCGQVFEK	99.7%	71.3	25	67.7	2	2	0	1730.84	56	70
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	13	16	51	0.05%	47.7%	NFGIWLR	99.7%	40.4	25	24.7	4	0	0	905.50	77	83
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	13	16	51	0.05%	47.7%	SSGEIVYCGQVFEK	99.7%	100	25	98.1	10	0	0	1602.75	57	70
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	13	16	51	0.05%	47.7%	VEEIAASK	99.7%	53.1	25	40	2	0	0	846.46	129	136
60S ribosomal protein L18a	RPL18A	RL18A_HUMAN	20.8	100.0%	13	16	51	0.05%	47.7%	VKNFGIWLR	99.7%	44.3	25	40.8	3	0	0	1132.66	75	83
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	8	8	24	0.02%	27.6%	HMYHSLYLK	96.9%	29.8	25	23.7	1	0	0	1207.59	118	126
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	8	8	24	0.02%	27.6%	ILMEHIHK	99.7%	45.5	25	36.5	3	0	0	1020.57	137	144
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	8	8	24	0.02%	27.6%	KLLADQAEAR	99.7%	68.6	25	63.7	3	0	0	1114.62	153	162
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	8	8	24	0.02%	27.6%	KVWLDPNETNEIANANSR	99.7%	54.4	25	54.2	0	2	0	2071.02	21	38
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	8	8	24	0.02%	27.6%	LLADQAEAR	99.7%	73.7	25	60.3	6	0	0	986.53	154	162
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	8	8	24	0.02%	27.6%	LLADQAEARR	98.0%	31.6	25	14	3	0	0	1142.63	154	163
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	8	8	24	0.02%	27.6%	RLASSVLR	97.6%	30.9	25	20.2	2	0	0	901.56	9	16
60S ribosomal protein L19	RPL19	RL19_HUMAN	23.5	100.0%	8	8	24	0.02%	27.6%	VWLDPNETNEIANANSR	99.7%	138	25	138	4	0	0	1942.93	22	38
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	7	11	35	0.03%	42.5%	EKGTWVQLK	99.2%	35.3	25	22.4	2	0	0	1088.61	121	129
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	7	11	35	0.03%	42.5%	GDIVDIKGMGTVQK	99.7%	50.5	25	40.1	2	0	0	1476.77	37	50
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	7	11	35	0.03%	42.5%	GTWVQLK	99.1%	34.8	25	20	2	0	0	831.47	123	129
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	7	11	35	0.03%	42.5%	GTWVQLKR	99.7%	42.6	25	24.9	4	0	0	987.57	123	130
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	7	11	35	0.03%	42.5%	HGVVPLATYMR	99.7%	61.9	25	57.1	5	1	0	1243.66	22	32
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	7	11	35	0.03%	42.5%	TNGKEPELLEPIPYEFMA	99.7%	78	25	78	4	0	0	2094.01	143	160
60S ribosomal protein L21	RPL21	RL21_HUMAN	18.6	100.0%	7	11	35	0.03%	42.5%	VYNVTQHAVGIVVNK	99.7%	116	25	109	9	6	0	1640.91	64	78
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	30	0.03%	36.7%	AGNLGGGVVTIER	99.7%	94.4	25	85.6	8	0	0	1242.68	53	65
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	30	0.03%	36.7%	ITVTSEVPFSK	99.7%	74.2	25	69.7	6	0	0	1207.66	70	80
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	30	0.03%	36.7%	ITVTSEVPFSKR	99.7%	51.5	25	46.3	3	2	0	1363.76	70	81
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	30	0.03%	36.7%	NNLRDWLR	99.3%	36.1	25	13.2	2	0	0	1086.58	94	101

60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	30	0.03%	36.7%	SKITVTSEVPFSK	99.7%	92.9	25	90.3	5	2	0	1422.78	68	80
60S ribosomal protein L22	RPL22	RL22_HUMAN	14.8	100.0%	6	8	30	0.03%	36.7%	VVANSKESYELR	99.7%	47.5	25	44.3	2	0	0	1394.73	102	113
60S ribosomal protein L22-like 1	RPL22L1	RL22L_HUMAN	14.6	99.8%	2	3	6	0.01%	26.2%	NNLRDWLR	99.3%	36.1	25	13.2	2	0	0	1086.58	88	95
60S ribosomal protein L22-like 1	RPL22L1	RL22L_HUMAN	14.6	99.8%	2	3	6	0.01%	26.2%	TGNLGNVVHIER	99.7%	53.8	25	43.1	2	0	0	1308.70	48	59
60S ribosomal protein L22-like 1	RPL22L1	RL22L_HUMAN	14.6	99.8%	2	3	6	0.01%	26.2%	VVASDKETYELR	99.7%	83.6	25	83.6	2	2	0	1409.73	96	107
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	9	18	82	0.08%	52.9%	ECADLWPR	99.7%	48.9	25	34.9	4	0	0	1046.47	124	131
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	9	18	82	0.08%	52.9%	GSAITGPVAK	99.7%	56.6	25	45.6	5	0	0	900.52	114	123
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	9	18	82	0.08%	52.9%	ISLGLPVGAVINCADNTGAK	99.7%	109	25	97	13	3	0	1970.04	16	35
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	9	18	82	0.08%	52.9%	KVHPAVVIR	97.0%	30	25	30	2	0	0	1018.65	75	83
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	9	18	82	0.08%	52.9%	LNRLPAAGVGDMVMATVK	99.7%	69.6	25	69.6	5	9	0	1874.98	49	66
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	9	18	82	0.08%	52.9%	LPAAGVGDMVMATVK	99.7%	96	25	90	26	2	0	1459.76	52	66
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	9	18	82	0.08%	52.9%	LPAAGVGDMVMATVKK	99.7%	60.5	25	60.5	4	4	0	1587.86	52	67
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	9	18	82	0.08%	52.9%	NLYIISVK	99.7%	40.3	25	34.8	4	0	0	949.57	36	43
60S ribosomal protein L23	RPL23	RL23_HUMAN	14.9	100.0%	9	18	82	0.08%	52.9%	VHPAVVIR	96.8%	29.7	25	26.1	1	0	0	890.56	76	83
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	13	19	85	0.08%	53.8%	EAPAPPKAEAK	99.7%	50.2	25	49.5	3	0	0	1108.60	8	18
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	13	19	85	0.08%	53.8%	FPLTTESAMK	99.7%	49.3	25	32.8	9	0	0	1140.56	79	88
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	13	19	85	0.08%	53.8%	FPLTTESAMKK	99.7%	41.8	25	35.8	3	1	0	1268.66	79	89
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	13	19	85	0.08%	53.8%	IEDNNTLVFIVDVK	99.7%	94.2	25	85.1	8	0	0	1618.87	90	103
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	13	19	85	0.08%	53.8%	KIEDNNTLVFIVDVK	99.7%	53.8	25	50.3	2	5	0	1746.96	89	103
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	13	19	85	0.08%	53.8%	KLYDIDVAK	99.7%	55.5	25	49.5	3	0	0	1064.60	115	123
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	13	19	85	0.08%	53.8%	LAPDYDALDVANK	99.7%	89.3	25	81.8	18	0	0	1404.70	140	152
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	13	19	85	0.08%	53.8%	LAPDYDALDVANKIGII	99.2%	35.3	25	35.3	1	0	0	1800.97	140	156
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	13	19	85	0.08%	53.8%	LDHYAIIK	99.7%	52.8	25	17.5	5	0	0	972.55	71	78
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	13	19	85	0.08%	53.8%	LYDIDVAK	99.7%	58.6	25	49.2	4	0	0	936.50	116	123
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	13	19	85	0.08%	53.8%	NKLDHYAIIK	99.7%	46.9	25	14.9	2	1	0	1214.69	69	78
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	13	19	85	0.08%	53.8%	VNTLIRPDGEK	99.7%	54	25	43.6	13	1	0	1241.69	124	134
60S ribosomal protein L23a	RPL23A	RL23A_HUMAN	17.7	100.0%	13	19	85	0.08%	53.8%	VNTLIRPDGEKK	99.7%	41.1	25	40.3	2	4	0	1369.78	124	135
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	14	79	0.07%	35.7%	AITGASLADIMAK	99.7%	110	25	99.5	33	0	0	1261.68	81	93
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	14	79	0.07%	35.7%	AITGASLADIMAKR	99.7%	46.8	25	46.8	3	0	0	1433.78	81	94
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	14	79	0.07%	35.7%	CESAFLSK	99.7%	47.6	25	43.7	8	0	0	941.44	36	43
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	14	79	0.07%	35.7%	CESAFLSKR	99.7%	60.4	25	44	2	0	0	1097.54	36	44
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	14	79	0.07%	35.7%	MKVELCSFSGYK	99.7%	72.6	25	66.8	9	3	0	1448.69	1	12
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	14	79	0.07%	35.7%	QINWTVLYR	99.7%	49.9	25	45.2	4	0	0	1192.65	48	56
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	14	79	0.07%	35.7%	TDGKVFQFLNAK	99.7%	36.9	25	35.1	0	2	0	1367.73	24	35
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	14	79	0.07%	35.7%	VELCSFSGYK	99.7%	57.5	25	48.1	2	0	0	1189.56	3	12
60S ribosomal protein L24	RPL24	RL24_HUMAN	17.8	100.0%	9	14	79	0.07%	35.7%	VFQFLNAK	99.7%	52.8	25	46.1	13	0	0	966.54	28	35
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	10	14	40	0.04%	46.9%	ANGTTVHVGIHPSK	99.7%	59.2	25	52.5	2	1	0	1417.75	90	103
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	10	14	40	0.04%	46.9%	DDEVQVVR	99.7%	54.5	25	30.1	6	0	0	959.48	52	59
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	10	14	40	0.04%	46.9%	FNPFVTSDR	99.7%	52.4	25	39.2	7	0	0	1082.53	3	11
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	10	14	40	0.04%	46.9%	HFNAPSHIR	98.6%	33.1	25	29.8	2	0	0	1078.55	18	26
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	10	14	40	0.04%	46.9%	KDDEVQVVR	99.7%	59.5	25	40.7	5	0	0	1087.57	51	59
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	10	14	40	0.04%	46.9%	KIMSSPLSK	99.4%	36.8	25	25.7	2	0	0	990.57	28	36
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	10	14	40	0.04%	46.9%	KYVIYIER	99.7%	52.6	25	52.6	2	0	0	1083.62	77	84
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	10	14	40	0.04%	46.9%	MKFNPFVTSDR	99.7%	66.1	25	60.4	5	1	0	1357.66	1	11
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	10	14	40	0.04%	46.9%	YKEETIEK	99.7%	41.4	25	30.4	2	0	0	1039.53	135	142
60S ribosomal protein L26	RPL26	RL26_HUMAN	17.3	100.0%	10	14	40	0.04%	46.9%	YVIYIER	99.7%	42	25	39.8	5	0	0	955.52	78	84
60S ribosomal protein L26-like 1	RPL26L1	RL26L_HUMAN	17.3	99.8%	2	2	6	0.01%	46.9%	ANGTTVHVGIHPSK	99.7%	59.2	25	52.5	2	1	0	1417.75	90	103
60S ribosomal protein L26-like 1	RPL26L1	RL26L_HUMAN	17.3	99.8%	2	2	6	0.01%	46.9%	DDEVQVVR	99.7%	54.5	25	30.1	6	0	0	959.48	52	59
60S ribosomal protein L26-like 1	RPL26L1	RL26L_HUMAN	17.3	99.8%	2	2	6	0.01%	46.9%	FNPFVTSDR	99.7%	52.4	25	39.2	7	0	0	1082.53	3	11
60S ribosomal protein L26-like 1	RPL26L1	RL26L_HUMAN	17.3	99.8%	2	2	6	0.01%	46.9%	HFNAPSHVR	98.7%	33.5	25	24	2	0	0	1064.54	18	26
60S ribosomal protein L26-like 1	RPL26L1	RL26L_HUMAN	17.3	99.8%	2	2	6	0.01%	46.9%	KDDEVQVVR	99.7%	59.5	25	40.7	5	0	0	1087.57	51	59

60S ribosomal protein L26-like 1	RPL26L1	RL26L_HUMAN	17.3	99.8%	2	2	6	0.01%	46.9%	KIMSSPLSK	99.4%	36.8	25	25.7	2	0	0	990.57	28	36
60S ribosomal protein L26-like 1	RPL26L1	RL26L_HUMAN	17.3	99.8%	2	2	6	0.01%	46.9%	KYVIYIER	99.7%	52.6	25	52.6	2	0	0	1083.62	77	84
60S ribosomal protein L26-like 1	RPL26L1	RL26L_HUMAN	17.3	99.8%	2	2	6	0.01%	46.9%	MKFNPFVTSDR	99.7%	66.1	25	60.4	5	1	0	1357.66	1	11
60S ribosomal protein L26-like 1	RPL26L1	RL26L_HUMAN	17.3	99.8%	2	2	6	0.01%	46.9%	YKEELIEK	99.7%	41.3	25	23.4	4	0	0	1051.57	135	142
60S ribosomal protein L26-like 1	RPL26L1	RL26L_HUMAN	17.3	99.8%	2	2	6	0.01%	46.9%	YVIYIER	99.7%	42	25	39.8	5	0	0	955.52	78	84
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	9	14	47	0.04%	55.9%	DVFRDPALK	97.1%	30.1	25	12.7	2	0	0	1060.58	99	107
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	9	14	47	0.04%	55.9%	NIDDGTSDRPYSHALVAGIDR	99.7%	60.3	25	60.3	2	2	0	2272.10	28	48
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	9	14	47	0.04%	55.9%	NKWFFQK	99.7%	41.9	25	20.1	2	0	0	997.53	127	133
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	9	14	47	0.04%	55.9%	TVVNKDVFR	99.7%	43.8	25	34.9	2	0	0	1077.61	94	102
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	9	14	47	0.04%	55.9%	VKFEER	97.1%	30	25	19.7	1	0	0	807.44	116	121
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	9	14	47	0.04%	55.9%	VVLVLAGR	99.7%	48.4	25	48.3	9	0	0	826.55	10	17
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	9	14	47	0.04%	55.9%	VYNYNHLMPTR	99.7%	44	25	37.5	8	6	0	1423.68	74	84
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	9	14	47	0.04%	55.9%	YSVDIPLDK	99.7%	51.7	25	43.8	10	0	0	1049.55	85	93
60S ribosomal protein L27	RPL27	RL27_HUMAN	15.8	100.0%	9	14	47	0.04%	55.9%	YSVDIPLDKTVVNK	99.7%	61.1	25	61.1	2	1	0	1590.87	85	98
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	7	8	31	0.03%	46.6%	IKSVGGACVLVA	99.5%	37.8	25	37.8	1	0	0	1173.67	137	148
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	7	8	31	0.03%	46.6%	INFDKYHPGYFGK	99.7%	66.8	25	56.2	2	2	0	1585.78	43	55
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	7	8	31	0.03%	46.6%	LWTLVSEQTR	99.7%	57.2	25	46.3	4	0	0	1232.66	78	87
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	7	8	31	0.03%	46.6%	NKTGAAPIIDVVR	99.2%	29.8	25	25.3	0	1	0	1353.79	93	105
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	7	8	31	0.03%	46.6%	NQSFCPTVNLDK	99.7%	58.1	25	48.7	3	0	0	1422.67	66	77
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	7	8	31	0.03%	46.6%	SGYYKVLGK	95.2%	28.1	25	25.5	1	0	0	1014.56	106	114
60S ribosomal protein L27a	RPL27A	RL27A_HUMAN	16.6	100.0%	7	8	31	0.03%	46.6%	TGAAPIIDVVR	99.7%	71.4	25	71.4	17	0	0	1111.65	95	105
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	10	12	36	0.03%	41.6%	GVVVVIKR	99.7%	48.7	25	42.7	2	0	0	869.59	59	66
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	10	12	36	0.03%	41.6%	KPATSYVR	99.7%	41.1	25	26	2	0	0	921.52	72	79
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	10	12	36	0.03%	41.6%	KTVGVEPAADGK	99.7%	41.2	25	32.4	4	0	0	1171.63	47	58
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	10	12	36	0.03%	41.6%	NCSSFLIK	99.4%	36.5	25	23.7	4	0	0	968.49	12	19
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	10	12	36	0.03%	41.6%	NCSSFLIKR	99.7%	44.1	25	41.2	2	0	0	1124.59	12	20
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	10	12	36	0.03%	41.6%	NKQTYSTEPNNLK	99.7%	58.3	25	45	2	2	0	1536.77	21	33
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	10	12	36	0.03%	41.6%	QTYSTEPNNLK	99.7%	52.2	25	42.7	6	0	0	1294.63	23	33
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	10	12	36	0.03%	41.6%	TVGVEPAADGK	99.7%	56.9	25	53.7	4	0	0	1043.54	48	58
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	10	12	36	0.03%	41.6%	TVGVEPAADGKGVVVVIK	99.7%	52.3	25	36.2	4	2	0	1738.01	48	65
60S ribosomal protein L28	RPL28	RL28_HUMAN	15.7	100.0%	10	12	36	0.03%	41.6%	YNGLIHR	99.7%	41.2	25	26.5	2	0	0	872.47	40	46
60S ribosomal protein L29	RPL29	RL29_HUMAN	17.8	100.0%	3	3	22	0.02%	15.1%	AQAAAPASVPAQAPK	99.7%	84.7	25	83.6	18	0	0	1377.75	135	149
60S ribosomal protein L29	RPL29	RL29_HUMAN	17.8	100.0%	3	3	22	0.02%	15.1%	AQAAAPASVPAQAPKR	99.7%	43.8	25	43.8	0	1	0	1533.85	135	150
60S ribosomal protein L29	RPL29	RL29_HUMAN	17.8	100.0%	3	3	22	0.02%	15.1%	LAYIAHPK	98.9%	34.2	25	26.3	3	0	0	912.53	96	103
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	21	28	92	0.09%	46.4%	AFMGPLKK	97.8%	31.2	25	24.7	4	0	0	891.51	387	394
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	21	28	92	0.09%	46.4%	AGMTHIVR	99.7%	49.9	25	35.1	2	0	0	884.48	51	58
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	21	28	92	0.09%	46.4%	AHLMEIQVNGGTVAEK	99.7%	109	25	108	1	1	0	1696.87	178	193
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	21	28	92	0.09%	46.4%	DDPSKPVHLTAFLGYK	99.7%	50.3	25	48.5	3	4	0	1787.93	35	50
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	21	28	92	0.09%	46.4%	ERLEQQVPVNQVFGQDEMIDVIGVTK	99.7%	78.3	25	78.3	0	4	0	2971.52	199	224
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	21	28	92	0.09%	46.4%	FQTMEEK	97.0%	29.9	25	23.4	1	0	0	912.41	379	385
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	21	28	92	0.09%	46.4%	FQTMEEKK	95.5%	28.4	25	17.8	1	0	0	1040.51	379	386
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	21	28	92	0.09%	46.4%	HGSLGFLPR	99.7%	61	25	54.4	9	0	0	983.54	11	19
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	21	28	92	0.09%	46.4%	IGQGYLIK	99.7%	55.9	25	29.5	7	0	0	891.53	287	294
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	21	28	92	0.09%	46.4%	IGQGYLIKDGK	99.7%	58.1	25	54	2	0	0	1191.67	287	297
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	21	28	92	0.09%	46.4%	KSLLVQTK	97.7%	31.1	25	21.6	1	0	0	916.58	349	356
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	21	28	92	0.09%	46.4%	KVACIGAWHPAR	99.7%	43.5	25	43.5	0	3	0	1365.72	250	261
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	21	28	92	0.09%	46.4%	LEQQVPVNQVFGQDEMIDVIGVTK	99.7%	51	25	47.7	0	4	0	2686.38	201	224
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	21	28	92	0.09%	46.4%	NNASTDYDLSDK	99.7%	73.6	25	73.4	12	0	0	1342.58	301	312
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	21	28	92	0.09%	46.4%	SFPKDDPSKPVHLTAFLGYK	99.7%	35.2	25	34.6	0	2	0	2247.18	31	50
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	21	28	92	0.09%	46.4%	SINPLGGFVHYGEVTNDFVMLK	99.7%	48.9	25	48.9	0	4	0	2437.22	313	334
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	21	28	92	0.09%	46.4%	TVFAEHISDECK	99.7%	77.4	25	75.8	5	0	0	1435.65	104	115

60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	21	28	92	0.09%	46.4%	TVFAEHISDECKR	99.7%	63.6	25	63.4	4	4	0	1591.75	104	116
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	21	28	92	0.09%	46.4%	VACIGAWHPAR	99.7%	69.1	25	65.6	4	3	0	1237.63	251	261
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	21	28	92	0.09%	46.4%	VIAHTQMR	99.7%	47.8	25	36.2	3	0	0	955.51	162	169
60S ribosomal protein L3	RPL3	RL3_HUMAN	46.1	100.0%	21	28	92	0.09%	46.4%	YCQVIR	99.2%	35.5	25	22.1	4	0	0	838.42	156	161
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	15	52	0.05%	59.1%	KSEIEYYAMLAK	99.7%	69.3	25	60.9	8	6	0	1445.73	57	68
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	15	52	0.05%	59.1%	KSLESINSR	99.7%	57.4	25	45.6	2	0	0	1033.56	9	17
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	15	52	0.05%	59.1%	LVILANNCPALR	99.7%	68.5	25	53.5	6	0	0	1353.77	45	56
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	15	52	0.05%	59.1%	LVILANNCPALRK	99.7%	44.4	25	34.7	2	1	0	1481.86	45	57
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	15	52	0.05%	59.1%	SEIEYYAMLAK	99.7%	90.5	25	77.9	8	0	0	1333.63	58	68
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	15	52	0.05%	59.1%	SLESINSR	99.7%	39.5	25	30.6	4	0	0	905.47	10	17
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	15	52	0.05%	59.1%	TGVHHYSGNNIELGTACGK	99.7%	80	25	80	3	4	0	2014.94	69	87
60S ribosomal protein L30	RPL30	RL30_HUMAN	12.8	100.0%	8	15	52	0.05%	59.1%	VCTLAIIDPGDSDIIR	99.7%	95	25	87.5	7	1	0	1757.91	91	106
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	10	50	0.05%	50.4%	EMGTPDVR	99.7%	51.5	25	44.4	5	0	0	920.41	56	63
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	10	50	0.05%	50.4%	EYTINIHK	95.1%	28	25	15.8	1	0	0	1017.54	24	31
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	10	50	0.05%	50.4%	EYTINIHKR	99.7%	56.4	25	42	4	0	0	1173.64	24	32
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	10	50	0.05%	50.4%	FAMKEMGTPDVR	99.6%	33.2	25	23	2	1	0	1413.65	52	63
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	10	50	0.05%	50.4%	LYTLVTYVPVTTFK	99.7%	80.3	25	80.3	13	0	0	1644.92	102	115
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	10	50	0.05%	50.4%	NEDEDSPNKLYTLVTYVPVTTFK	99.7%	41	25	38.3	0	3	0	2673.33	93	115
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	10	50	0.05%	50.4%	NLQTVNVDEN	99.7%	63.3	25	61.4	4	0	0	1145.54	116	125
60S ribosomal protein L31	RPL31	RL31_HUMAN	14.5	100.0%	8	10	50	0.05%	50.4%	SAINEVVTR	99.7%	78.9	25	60.4	17	0	0	988.54	15	23
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	6	14	43	0.04%	35.6%	ELEVLLMCNK	99.7%	65.2	25	53	9	0	0	1264.63	84	93
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	6	14	43	0.04%	35.6%	FKGQILMPNIGYGSNK	99.7%	60.7	25	60.7	4	3	0	1782.92	49	64
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	6	14	43	0.04%	35.6%	GQILMPNIGYGSNK	99.7%	64.1	25	58.6	8	0	0	1507.76	51	64
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	6	14	43	0.04%	35.6%	GQILMPNIGYGSNKK	99.7%	56.6	25	52.9	4	2	0	1619.86	51	65
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	6	14	43	0.04%	35.6%	HMLPSGFR	95.0%	28	25	27.3	1	0	0	944.48	68	75
60S ribosomal protein L32	RPL32	RL32_HUMAN	15.9	100.0%	6	14	43	0.04%	35.6%	SYCAEIAHNVSSK	99.7%	90.9	25	89.4	11	1	0	1465.67	94	106
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	8	8	18	0.02%	41.0%	AFLIEEQK	99.7%	57.8	25	39.6	4	0	0	977.53	94	101
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	8	8	18	0.02%	41.0%	AFLIEEQKIVVK	99.7%	62.3	25	61.2	2	0	0	1416.85	94	105
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	8	8	18	0.02%	41.0%	AYGGSMCAK	95.2%	28.1	25	28.1	1	0	0	944.40	77	85
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	8	8	18	0.02%	41.0%	IVYLYTK	99.7%	43.7	25	31.1	3	0	0	899.52	30	36
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	8	8	18	0.02%	41.0%	IVYLYTKK	99.7%	45.3	25	35.5	2	0	0	1027.62	30	37
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	8	8	18	0.02%	41.0%	LSYNTASNK	99.7%	75.1	25	53.8	4	0	0	997.49	11	19
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	8	8	18	0.02%	41.0%	RAFLIEEQK	98.2%	31.9	25	19.9	1	0	0	1133.63	93	101
60S ribosomal protein L34	RPL34	RL34_HUMAN	13.3	100.0%	8	8	18	0.02%	41.0%	SACGVCPGR	99.7%	42.7	25	39.4	1	0	0	963.41	44	52
60S ribosomal protein L35	RPL35	RL35_HUMAN	14.6	100.0%	5	7	25	0.02%	35.0%	ERLYPLR	94.7%	27.7	25	12.9	1	0	0	946.55	111	117
60S ribosomal protein L35	RPL35	RL35_HUMAN	14.6	100.0%	5	7	25	0.02%	35.0%	QLDDLKVELSQLR	99.7%	87.8	25	75.4	5	2	0	1556.86	20	32
60S ribosomal protein L35	RPL35	RL35_HUMAN	14.6	100.0%	5	7	25	0.02%	35.0%	VLTVINQTQK	99.7%	73.5	25	70.1	12	0	0	1143.67	57	66
60S ribosomal protein L35	RPL35	RL35_HUMAN	14.6	100.0%	5	7	25	0.02%	35.0%	VLTVINQTQKENLR	99.7%	98.9	25	98.9	2	2	0	1655.94	57	70
60S ribosomal protein L35	RPL35	RL35_HUMAN	14.6	100.0%	5	7	25	0.02%	35.0%	YKPLDLRPK	97.9%	31.3	25	31.3	1	0	0	1129.67	78	86
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	35	0.03%	40.9%	AIFAGYKR	99.7%	45.1	25	37.4	4	0	0	925.53	9	16
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	35	0.03%	40.9%	DETEFYLGK	99.7%	60.5	25	57.2	4	0	0	1101.51	37	45
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	35	0.03%	40.9%	DETEFYLGKR	99.7%	43.1	25	37.3	4	0	0	1257.61	37	46
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	35	0.03%	40.9%	IEGVYAR	99.7%	45.2	25	30.8	3	0	0	807.44	30	36
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	35	0.03%	40.9%	IEGVYARDETEFYLGK	99.7%	52.9	25	52.9	2	0	0	1889.93	30	45
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	35	0.03%	40.9%	NNTVTPGGKPNK	99.7%	42.6	25	35.5	4	0	0	1226.65	55	66
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	35	0.03%	40.9%	VMLYPSR	97.7%	31	25	20.4	4	0	0	881.46	103	109
60S ribosomal protein L35a	RPL35A	RL35A_HUMAN	12.5	100.0%	8	9	35	0.03%	40.9%	VMLYPSRI	99.6%	38.2	25	32.2	10	0	0	978.54	103	110
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	5	10	27	0.03%	32.4%	ALRYPMAVGLNK	99.7%	44.7	25	38.3	1	2	0	1348.74	2	13
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	5	10	27	0.03%	32.4%	EELSNVLAAMR	99.7%	104	25	96.3	7	0	0	1232.63	88	98
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	5	10	27	0.03%	32.4%	EVCGFAPYER	99.7%	60.4	25	60.4	6	0	0	1227.55	46	55
60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	5	10	27	0.03%	32.4%	REELSNVLAAMR	99.7%	67.6	25	61.7	3	2	0	1388.73	87	98

60S ribosomal protein L36	RPL36	RL36_HUMAN	12.3	100.0%	5	10	27	0.03%	32.4%	YPMAVGLNK	99.7%	54	25	41.1	6	0	0	1008.52	5	13
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	4	4	14	0.01%	24.5%	DSLYAQGR	99.3%	36	25	34.9	2	0	0	909.44	31	38
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	4	4	14	0.01%	24.5%	GKDSLYAQGR	99.7%	60.4	25	54.4	4	0	0	1094.56	29	38
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	4	4	14	0.01%	24.5%	KGQVIQF	98.8%	33.7	25	33.7	2	0	0	819.47	100	106
60S ribosomal protein L36a-like	RPL36AL	RL36L_HUMAN	12.5	100.0%	4	4	14	0.01%	24.5%	LECVEPNCR	99.7%	44.4	25	43.9	6	0	0	1176.51	70	78
60S ribosomal protein L37a	RPL37A	RL37A_HUMAN	10.3	100.0%	4	4	13	0.01%	51.1%	AVGIWHCGSCMK	98.7%	33.4	25	33.4	1	0	0	1421.61	51	62
60S ribosomal protein L37a	RPL37A	RL37A_HUMAN	10.3	100.0%	4	4	13	0.01%	51.1%	KIEISQHAK	99.7%	62.5	25	53.1	4	0	0	1053.61	28	36
60S ribosomal protein L37a	RPL37A	RL37A_HUMAN	10.3	100.0%	4	4	13	0.01%	51.1%	TVAGGAWTYNTTSAVTVK	99.7%	91.9	25	83.8	5	0	0	1826.93	63	80
60S ribosomal protein L37a	RPL37A	RL37A_HUMAN	10.3	100.0%	4	4	13	0.01%	51.1%	YTCSFCGK	96.4%	29.2	25	29.2	3	0	0	1022.41	37	44
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	3	3	14	0.01%	34.3%	LKQSLPPGLAVK	98.9%	34.3	25	34.3	2	0	0	1250.78	56	67
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	3	3	14	0.01%	34.3%	QSLPPGLAVK	99.7%	72.8	25	68.1	8	0	0	1009.60	58	67
60S ribosomal protein L38	RPL38	RL38_HUMAN	8.2	100.0%	3	3	14	0.01%	34.3%	YLYTLVITDKEK	99.7%	59.9	25	54.2	4	0	0	1485.82	41	52
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	127	0.12%	47.8%	AAAAAAAALQAK	99.7%	92.8	25	87.1	14	0	0	956.55	354	364
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	127	0.12%	47.8%	APIRPDIVNFVHTNLR	99.7%	53.5	25	53.5	2	4	0	1862.04	30	45
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	127	0.12%	47.8%	AWNDIKK	99.4%	37	25	24	1	0	0	874.48	176	182
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	127	0.12%	47.8%	FCIWTESAFR	99.7%	51.1	25	44.7	10	0	0	1316.61	249	258
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	127	0.12%	47.8%	GPCIIYNEDNGIIK	99.7%	73.6	25	73.6	2	0	0	1605.79	206	219
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	127	0.12%	47.8%	IEEVPELPLVVEDK	99.7%	52.4	25	52.4	2	0	0	1608.87	144	157
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	127	0.12%	47.8%	IEEVPELPLVVEDKVEGYK	99.7%	92.5	25	92.5	2	0	0	2185.16	144	162
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	127	0.12%	47.8%	KLDELYGTWR	99.7%	55.7	25	53.5	2	2	0	1280.66	259	268
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	127	0.12%	47.8%	LAPGGHVGR	99.7%	54.9	25	45.5	4	0	0	863.48	240	248
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	127	0.12%	47.8%	LDELYGTWR	99.7%	75.3	25	70.1	2	0	0	1152.57	260	268
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	127	0.12%	47.8%	MINTDLSR	99.7%	57.6	25	45.6	11	0	0	949.48	284	291
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	127	0.12%	47.8%	NIPGITLLNVSK	99.7%	79.8	25	75.5	13	0	0	1268.76	223	234
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	127	0.12%	47.8%	NIPGITLLNVSKLNILK	99.7%	85.1	25	85.1	2	0	0	1850.15	223	239
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	127	0.12%	47.8%	NVTLPAVFK	99.7%	40.8	25	27.2	5	0	0	988.58	21	29
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	127	0.12%	47.8%	QPYAVSELAGHQTSAESWGTGR	99.7%	106	25	105	2	3	0	2332.10	50	71
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	127	0.12%	47.8%	RGPCIIYNEDNGIIK	99.7%	80.4	25	60.6	2	4	0	1761.90	205	219
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	127	0.12%	47.8%	SGQGAFGNMCR	99.7%	55	25	53.8	8	0	0	1184.49	87	97
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	127	0.12%	47.8%	SNYNLPMHK	99.7%	43.8	25	43.8	9	0	0	1119.53	275	283
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	127	0.12%	47.8%	TKEAVLLLK	99.7%	55	25	50.7	4	0	0	1014.66	164	172
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	127	0.12%	47.8%	VDKAAAAAAALQAK	99.7%	62	25	40.9	1	0	0	1298.74	351	364
60S ribosomal protein L4	RPL4	RL4_HUMAN	47.7	100.0%	21	31	127	0.12%	47.8%	YAICSALAASALPALVMSK	99.7%	100	25	100	10	6	0	1937.02	122	140
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	14	30	80	0.07%	40.4%	DIICQIAYAR	99.7%	62.3	25	47.2	2	0	0	1222.63	59	68
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	14	30	80	0.07%	40.4%	EFNAEVHR	99.7%	51.3	25	40.1	2	0	0	1001.48	189	196
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	14	30	80	0.07%	40.4%	EFNAEVHRK	99.7%	42.3	25	32.1	2	0	0	1129.57	189	197
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	14	30	80	0.07%	40.4%	FPGYDSESK	99.7%	55.5	25	49.7	2	0	0	1029.45	180	188
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	14	30	80	0.07%	40.4%	GAVDGGLSIPHSTK	99.7%	80.7	25	76.5	5	2	0	1338.70	165	178
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	14	30	80	0.07%	40.4%	GAVDGGLSIPHSTKR	99.7%	70.2	25	63.9	2	0	0	1494.80	165	179
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	14	30	80	0.07%	40.4%	HIMGQNVADYMR	99.7%	51.4	25	42.8	8	4	0	1450.66	198	209
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	14	30	80	0.07%	40.4%	IEGDMIVCAAYAHELPK	99.7%	88.1	25	88.1	4	8	0	1916.92	69	85
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	14	30	80	0.07%	40.4%	NSVTPDMMEEMYK	99.7%	59.5	25	59.5	5	0	0	1574.65	229	241
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	14	30	80	0.07%	40.4%	NSVTPDMMEEMYKK	99.7%	80.8	25	80.8	8	2	0	1702.75	229	242
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	14	30	80	0.07%	40.4%	RFPGYDSESK	99.7%	41	25	27.4	2	0	0	1185.55	179	188
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	14	30	80	0.07%	40.4%	VGLTNYAAAYCTGLLLAR	99.7%	99.7	25	99.7	8	2	0	1927.01	90	107
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	14	30	80	0.07%	40.4%	VTNRDIICQIAYAR	99.7%	48.5	25	40.5	2	2	0	1692.89	55	68
60S ribosomal protein L5	RPL5	RL5_HUMAN	34.4	100.0%	14	30	80	0.07%	40.4%	YLMEEDEDAYKK	99.7%	71.5	25	64.7	4	4	0	1533.68	210	221
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	19	60	0.06%	45.8%	AIPQLQGYLR	99.7%	69.2	25	64.2	4	0	0	1158.66	263	272
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	19	60	0.06%	45.8%	ASITPGTILIILTGR	99.7%	116	25	116	13	2	0	1525.93	142	156
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	19	60	0.06%	45.8%	AVDSQILPK	99.7%	68.1	25	38.3	4	0	0	970.56	252	260
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	19	60	0.06%	45.8%	EKYEITEQR	99.7%	40.5	25	32.5	2	0	0	1195.60	238	246

60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	19	60	0.06%	45.8%	FVIATSTK	99.7%	44.8	25	34.7	2	0	0	866.50	193	200
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	19	60	0.06%	45.8%	HLTDAYFKK	99.4%	36.8	25	26.9	2	0	0	1122.59	211	219
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	19	60	0.06%	45.8%	HQEGEIFDTEK	99.7%	61.8	25	61.8	2	0	0	1332.61	227	237
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	19	60	0.06%	45.8%	HQEGEIFDTEKEK	99.7%	51.7	25	49.7	0	2	0	1589.74	227	239
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	19	60	0.06%	45.8%	KPFSQHVR	99.7%	39.6	25	26.1	2	0	0	998.55	131	138
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	19	60	0.06%	45.8%	QLASGLLLVTGPLVLNR	99.7%	92.1	25	92.1	6	2	0	1764.07	167	183
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	19	60	0.06%	45.8%	SVFALTNGIYPHK	99.7%	45.1	25	40.1	2	0	0	1446.77	273	285
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	19	60	0.06%	45.8%	VLATVTKPVGGDK	99.7%	69.9	25	68	6	2	0	1284.75	88	100
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	19	60	0.06%	45.8%	YEITEQR	99.7%	41.4	25	30	2	0	0	938.46	240	246
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	19	60	0.06%	45.8%	YYPTEDVPR	99.7%	66.8	25	65	2	0	0	1139.54	115	123
60S ribosomal protein L6	RPL6	RL6_HUMAN	32.7	100.0%	15	19	60	0.06%	45.8%	YYPTEDVPRK	99.7%	34.8	25	22.1	2	1	0	1267.63	115	124
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	21	50	0.05%	53.2%	AGNFYVPAEPK	99.7%	45.3	25	41.4	3	0	0	1192.60	78	88
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	21	50	0.05%	53.2%	ASINMLR	99.7%	68.8	25	51.4	6	0	0	804.44	128	134
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	21	50	0.05%	53.2%	EANNFLWPFK	99.7%	46.5	25	39	3	0	0	1265.63	203	212
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	21	50	0.05%	53.2%	EVPAVPETLKK	99.3%	35.8	25	23.7	3	0	0	1210.70	10	20
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	21	50	0.05%	53.2%	FKEANNFLWPFK	99.7%	64.2	25	55.2	3	1	0	1540.79	201	212
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	21	50	0.05%	53.2%	IALTDNALIAR	99.7%	93.4	25	80.4	5	0	0	1170.68	167	177
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	21	50	0.05%	53.2%	IVEPYIAWGYPNLK	99.7%	58.9	25	31.2	4	0	0	1662.89	135	148
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	21	50	0.05%	53.2%	KAGNFYVPAEPK	99.7%	55.5	25	52.4	4	1	0	1320.69	77	88
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	21	50	0.05%	53.2%	KVLQLLR	99.7%	44.5	25	27.3	2	0	0	869.59	107	113
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	21	50	0.05%	53.2%	LRQIFNGTFVK	99.7%	35.1	25	34.2	0	1	0	1322.76	114	124
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	21	50	0.05%	53.2%	QIFNGTFVK	97.8%	31.1	25	28.3	1	0	0	1053.57	116	124
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	21	50	0.05%	53.2%	RIALTDNALIAR	99.7%	71.6	25	53.2	2	1	0	1326.79	166	177
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	21	50	0.05%	53.2%	SVNELIYK	99.7%	52.6	25	41.7	2	0	0	965.53	149	156
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	21	50	0.05%	53.2%	SVNELIYKR	99.7%	51.1	25	37.2	4	0	0	1121.63	149	157
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	21	50	0.05%	53.2%	TTHFVEGGDAGNREDQINR	99.7%	55.1	25	55.1	2	0	0	2115.98	224	242
60S ribosomal protein L7	RPL7	RL7_HUMAN	29.2	100.0%	16	21	50	0.05%	53.2%	YGIICMEDLIHEIYTVGK	99.7%	48.1	25	48.1	1	1	0	2170.06	182	199
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	56	0.05%	45.5%	AGVNTVTTLVENK	99.7%	87.6	25	82.3	8	0	0	1345.73	138	150
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	56	0.05%	45.5%	AGVNTVTTLVENKK	99.7%	85.2	25	85.2	2	2	0	1473.83	138	151
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	56	0.05%	45.5%	HWGGNVLGPK	99.3%	36.2	25	35.8	1	0	0	1064.56	236	245
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	56	0.05%	45.5%	KMGVPYCIIK	99.7%	52.9	25	47	3	4	0	1208.65	176	185
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	56	0.05%	45.5%	KTCTTVAFTQVNSEDK	99.7%	98.4	25	98.4	1	0	0	1828.87	197	212
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	56	0.05%	45.5%	KVAPAPAVVK	99.7%	39.9	25	38.6	2	0	0	979.63	11	20
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	56	0.05%	45.5%	KVVNPLFEK	99.7%	41.2	25	25.3	2	0	0	1073.64	26	34
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	56	0.05%	45.5%	LKVPPAINQFTQALDR	99.7%	55.5	25	55.5	4	3	0	1811.02	74	89
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	56	0.05%	45.5%	MGVPYCIIK	99.0%	34.7	25	24.2	2	0	0	1080.56	177	185
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	56	0.05%	45.5%	NFGIGQDIQPK	99.7%	60.7	25	50.9	3	0	0	1216.63	38	48
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	56	0.05%	45.5%	QTATQLLK	99.7%	45.1	25	26	3	0	0	902.53	90	97
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	56	0.05%	45.5%	TCTTVAFTQVNSEDK	99.7%	101	25	96.4	2	0	0	1700.78	198	212
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	56	0.05%	45.5%	TCTTVAFTQVNSEDKGALAK	99.7%	118	25	118	2	2	0	2141.05	198	217
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	56	0.05%	45.5%	TNYNDRYDEIR	99.5%	38	25	24.9	1	1	0	1458.66	224	234
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	56	0.05%	45.5%	VAPAPAVVKK	94.6%	27.7	25	27.7	1	0	0	979.63	12	21
60S ribosomal protein L7a	RPL7A	RL7A_HUMAN	30.0	100.0%	16	24	56	0.05%	45.5%	VPPAINQFTQALDR	99.7%	99.8	25	96.6	5	2	0	1569.84	76	89
60S ribosomal protein L7-like 1	RPL7L1	RL7L_HUMAN	28.7	100.0%	4	4	7	0.01%	20.7%	IDGVSLLVQR	99.7%	73	25	54	2	0	0	1099.65	96	105
60S ribosomal protein L7-like 1	RPL7L1	RL7L_HUMAN	28.7	100.0%	4	4	7	0.01%	20.7%	IVEPYVTWGFPNLK	99.7%	40.4	25	29.6	2	0	0	1662.89	133	146
60S ribosomal protein L7-like 1	RPL7L1	RL7L_HUMAN	28.7	100.0%	4	4	7	0.01%	20.7%	KIPLVPENLLK	98.8%	33.7	25	33.7	2	0	0	1263.80	8	18
60S ribosomal protein L7-like 1	RPL7L1	RL7L_HUMAN	28.7	100.0%	4	4	7	0.01%	20.7%	TIPLTDNTVIEEHLGK	99.1%	34.9	25	34.9	1	0	0	1779.95	164	179
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	9	12	34	0.03%	31.9%	ASGNYATVISHNPETK	99.7%	81.1	25	74.1	6	2	0	1688.82	129	144
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	9	12	34	0.03%	31.9%	ASGNYATVISHNPETKK	99.7%	64.1	25	58.7	2	2	0	1816.92	129	145
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	9	12	34	0.03%	31.9%	AVDFAER	99.7%	51.5	25	43.4	2	0	0	807.40	31	37
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	9	12	34	0.03%	31.9%	AVVGVVAGGGR	99.7%	95.4	25	81.3	8	0	0	941.55	164	174

60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	9	12	34	0.03%	31.9%	DIIHDPGR	98.8%	33.7	25	22	2	0	0	922.47	47	54
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	9	12	34	0.03%	31.9%	GIVKDIIHDPGR	99.7%	52.1	25	50.3	2	2	0	1319.74	43	54
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	9	12	34	0.03%	31.9%	IDKPILK	96.3%	29.1	25	3.98	2	0	0	826.54	175	181
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	9	12	34	0.03%	31.9%	KVGLIAAR	99.7%	47.6	25	33.4	2	0	0	827.55	234	241
60S ribosomal protein L8	RPL8	RL8_HUMAN	28.0	100.0%	9	12	34	0.03%	31.9%	TELFIAAEGIHTGQFVYCGK	99.7%	41.8	25	41.8	0	2	0	2241.10	73	92
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	12	18	48	0.04%	71.4%	DELILEGNDIELVSNSAALIQQATTVK	99.7%	64.9	25	64.9	0	1	0	2884.52	142	168
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	12	18	48	0.04%	71.4%	DFNHINVELSLLGK	99.7%	68	25	68	6	2	0	1598.85	37	50
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	12	18	48	0.04%	71.4%	DFNHINVELSLLGKK	99.7%	63.4	25	60.3	2	2	0	1726.95	37	51
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	12	18	48	0.04%	71.4%	FLDGIYVSEK	99.7%	77.7	25	66.4	11	0	0	1170.60	175	184
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	12	18	48	0.04%	71.4%	FLDGIYVSEKGTVQQADE	99.7%	61.6	25	53.7	2	0	0	1998.97	175	192
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	12	18	48	0.04%	71.4%	KFLDGIYVSEK	99.7%	88	25	77.6	3	0	0	1298.70	174	184
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	12	18	48	0.04%	71.4%	MKTILSNQTVDIPENVDITLK	98.6%	27.5	25	27.5	0	2	0	2388.27	1	21
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	12	18	48	0.04%	71.4%	MRPGVACSVSQAQK	99.7%	56.4	25	55.7	0	4	0	1518.75	128	141
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	12	18	48	0.04%	71.4%	SVYAHFPINVVIQENGSLVEIR	99.7%	56.6	25	53.5	0	2	0	2484.32	94	115
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	12	18	48	0.04%	71.4%	TICSHVQNMIK	99.7%	67.3	25	62.4	4	3	0	1330.66	72	82
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	12	18	48	0.04%	71.4%	TILSNQTVDIPENVDITLK	99.7%	90.9	25	90.9	2	0	0	2113.14	3	21
60S ribosomal protein L9	RPL9	RL9_HUMAN	21.9	100.0%	12	18	48	0.04%	71.4%	TVIVKGPR	99.3%	35.9	25	35.9	2	0	0	869.56	24	31
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	10	11	15	0.01%	17.0%	AIGVLTSGGDAQGMNAAVR	99.7%	140	25	140	4	0	0	1787.91	26	44
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	10	11	15	0.01%	17.0%	FTTDDSICVLGISK	99.7%	84.8	25	84.8	1	0	0	1555.77	711	724
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	10	11	15	0.01%	17.0%	GGTPSAFDR	98.8%	33.8	25	22.1	2	0	0	907.43	311	319
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	10	11	15	0.01%	17.0%	IIEVVDAIMTTAQSHQR	99.7%	109	25	109	1	1	0	1912.00	194	210
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	10	11	15	0.01%	17.0%	LAIKLPDDQIPK	96.2%	23.9	25	21.6	0	1	0	1350.80	397	408
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	10	11	15	0.01%	17.0%	NGQIDKEAVQK	99.7%	54.3	25	39.7	2	0	0	1229.65	151	161
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	10	11	15	0.01%	17.0%	NVIFQPVAELK	98.8%	33.8	25	26.3	1	0	0	1257.72	726	736
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	10	11	15	0.01%	17.0%	NVIFQPVAELKK	99.4%	36.5	25	30.7	2	0	0	1385.82	726	737
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	10	11	15	0.01%	17.0%	SFAGNLNTYK	99.7%	47.7	25	42.9	2	0	0	1114.55	386	395
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	10	11	15	0.01%	17.0%	SFAGNLNTYKR	99.1%	35.2	25	34.6	1	0	0	1270.65	386	396
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	10	11	15	0.01%	17.0%	TFVLEVMGR	99.7%	63.2	25	55.6	2	0	0	1051.56	211	219
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	10	11	15	0.01%	17.0%	VTILGHVQR	98.3%	32.2	25	22.5	1	0	0	1022.61	302	310
6-phosphofructokinase type C	PFKP	K6PP_HUMAN	85.6	100.0%	10	11	15	0.01%	17.0%	YLEEIATQMR	99.7%	68.3	25	56.7	2	0	0	1253.62	487	496
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	38	0.04%	25.9%	AIGVLTSGGDAQGMNAAVR	99.7%	140	25	140	4	0	0	1787.91	17	35
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	38	0.04%	25.9%	AMLWLSEK	99.7%	44	25	33.9	2	0	0	977.51	682	689
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	38	0.04%	25.9%	AVAFSPVTELKK	99.7%	43.3	25	43.3	2	0	0	1289.75	716	727
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	38	0.04%	25.9%	EQWWLSLR	99.7%	40.6	25	23.9	2	0	0	1117.58	738	745
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	38	0.04%	25.9%	GGTPSAFDR	98.8%	33.8	25	22.1	2	0	0	907.43	302	310
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	38	0.04%	25.9%	GQLESIVENIR	99.7%	65.7	25	57.1	2	0	0	1257.68	475	485
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	38	0.04%	25.9%	GQVQEVGWHDVAGWLGR	99.7%	44.3	25	44.3	0	2	0	1893.94	445	461
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	38	0.04%	25.9%	IMEVIDAITTTAQSHQR	99.7%	51	25	14.6	0	2	0	1913.98	185	201
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	38	0.04%	25.9%	LLAHQKPPK	96.8%	29.7	25	29.7	1	0	0	1031.64	387	395
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	38	0.04%	25.9%	SNFSLAILNVGAPAAGMNAAVR	99.7%	99.9	25	99.9	3	2	0	2144.13	398	419
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	38	0.04%	25.9%	TFVLEVMGR	99.7%	63.2	25	55.6	2	0	0	1051.56	202	210
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	38	0.04%	25.9%	TNVLGHLQQGGAPTPFDR	99.7%	66.9	25	64.1	1	4	0	1907.97	655	672
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	38	0.04%	25.9%	VFANAPDSACVIGLK	99.7%	79.6	25	71.8	2	0	0	1561.80	699	713
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	38	0.04%	25.9%	VFLIYEGYEGLVEGGENIK	99.7%	65	25	55	2	1	0	2129.08	48	66
6-phosphofructokinase, liver type	PFKL	K6PL_HUMAN	85.0	100.0%	15	20	38	0.04%	25.9%	VTVLGHVQR	99.7%	65.6	25	65.6	2	0	0	1008.59	293	301
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	15	0.01%	21.9%	AIAVLTSGGDAQGMNAAVR	99.7%	104	25	104	1	0	0	1801.92	17	35
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	15	0.01%	21.9%	ALVFQPVAELK	99.7%	51.8	25	46.2	1	0	0	1214.71	717	727
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	15	0.01%	21.9%	ALVFQPVAELKDQTDFEHR	99.4%	31	25	31	0	1	0	2243.15	717	735
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	15	0.01%	21.9%	DLQANVEHLVQK	99.7%	56.7	25	47.8	2	0	0	1393.74	604	615
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	15	0.01%	21.9%	GGTPSAFDR	98.8%	33.8	25	22.1	2	0	0	907.43	302	310
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	15	0.01%	21.9%	GITNLCVIGGDGSLTGADTFR	99.7%	127	25	126	2	0	0	2124.04	109	129

6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	15	0.01%	21.9%	IGLIQGNR	99.6%	38.5	25	37.1	2	0	0	870.52	425	432
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	15	0.01%	21.9%	IMEIVDAITTTAQSHQR	99.7%	52.3	25	4.51	0	1	0	1929.97	185	201
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	15	0.01%	21.9%	SEWSDLLSDLQK	99.7%	90.1	25	82.6	2	0	0	1420.70	130	141
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	15	0.01%	21.9%	SGSHTVAVMNVGAPAAGMNAAVR	98.0%	26.3	25	26.3	0	1	0	2168.07	398	420
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	15	0.01%	21.9%	TFVLEVMGR	99.7%	63.2	25	55.6	2	0	0	1051.56	202	210
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	15	0.01%	21.9%	VLVVHDGFEGLAK	99.7%	53.5	25	53.5	2	0	0	1383.76	433	445
6-phosphofructokinase, muscle type	PFKM	K6PF_HUMAN	85.2	100.0%	10	10	15	0.01%	21.9%	VTVLGHVQR	99.7%	65.6	25	65.6	2	0	0	1008.59	293	301
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	7	8	13	0.01%	18.8%	FQFDGDKK	98.7%	33.4	25	18.9	1	0	0	984.48	310	317
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	7	8	13	0.01%	18.8%	GILFVGSGVSGGEEGAR	99.7%	90.5	25	84.1	2	0	0	1591.81	120	136
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	7	8	13	0.01%	18.8%	IISYAQGFMLLR	99.7%	69.1	25	62.3	4	0	0	1427.77	332	343
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	7	8	13	0.01%	18.8%	LVPLLDTGDIIIDGGNSEYR	99.7%	109	25	109	2	0	0	2160.12	88	107
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	7	8	13	0.01%	18.8%	TIFQGIAAK	99.6%	39.1	25	29.4	1	0	0	948.55	155	163
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	7	8	13	0.01%	18.8%	TVSKVDDFLANEAK	96.6%	29.4	25	29.4	1	0	0	1536.79	35	48
6-phosphogluconate dehydrogenase, decarboxylating	PGD	6PGD_HUMAN	53.1	100.0%	7	8	13	0.01%	18.8%	YGPSLMPGGNK	99.7%	46.7	25	37.3	2	0	0	1136.54	137	147
6-phosphogluconolactonase	PGLS	6PGL_HUMAN	27.5	99.8%	2	2	3	0.00%	8.9%	TVIFVATGEGK	99.7%	63.5	25	58	2	0	0	1121.62	198	208
6-phosphogluconolactonase	PGLS	6PGL_HUMAN	27.5	99.8%	2	2	3	0.00%	8.9%	VTLTLPVLNAAR	99.2%	35.3	25	35.3	1	0	0	1267.77	186	197
6-pyruvoyl tetrahydrobiopterin synthase	PTS	PTPS_HUMAN	16.4	100.0%	2	2	4	0.00%	18.6%	FLSDEENLKLFGK	99.7%	39.7	25	39.7	2	0	0	1539.81	30	42
6-pyruvoyl tetrahydrobiopterin synthase	PTS	PTPS_HUMAN	16.4	100.0%	2	2	4	0.00%	18.6%	VYETDNNIVVYKGE	99.7%	61.6	25	61.4	2	0	0	1642.80	132	145
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	37	0.03%	37.6%	DAGTIAGLNVMR	99.7%	64.5	25	57	4	0	0	1233.63	186	197
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	37	0.03%	37.6%	ELEEIVQPIISK	99.7%	55.5	25	49	2	0	0	1397.79	622	633
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	37	0.03%	37.6%	IDTRNELESYAYSLK	98.4%	27.2	25	25.5	0	1	0	1801.90	559	573
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	37	0.03%	37.6%	IEWLESHQDADIEDFKAK	99.7%	35.5	25	35.3	0	1	0	2174.04	602	619
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	37	0.03%	37.6%	IINEPTAAAIAYGLDK	99.7%	129	25	127	2	0	0	1659.90	198	213
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	37	0.03%	37.6%	IINEPTAAAIAYGLDKR	99.7%	83.8	25	83.8	2	2	0	1816.00	198	214
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	37	0.03%	37.6%	ITITNDQNR	98.8%	33.8	25	20.4	2	0	0	1074.55	524	532
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	37	0.03%	37.6%	ITPSYVAFTPEGER	97.4%	30.5	25	28.4	1	0	0	1566.78	61	74
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	37	0.03%	37.6%	LTPEEIER	97.7%	30.9	25	0	1	0	0	986.52	533	540
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	37	0.03%	37.6%	NQLTSNPENTVFDAK	99.7%	99.7	25	92.8	2	0	0	1677.81	82	96
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	37	0.03%	37.6%	SDIDEIVLVGGSTR	99.7%	57.3	25	57.3	2	0	0	1460.76	354	367
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	37	0.03%	37.6%	SQIFSTASDNQPTVTIK	99.7%	109	25	95	2	0	0	1836.93	448	464
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	37	0.03%	37.6%	TFAPEEISAMVLTK	99.7%	93.8	25	85.4	2	0	0	1536.80	139	152
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	37	0.03%	37.6%	TKPYIQVDIGGGQTK	99.7%	58.4	25	52.7	2	0	0	1604.86	124	138
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	37	0.03%	37.6%	TWNDPSVQQDIK	99.7%	68.7	25	61.2	2	0	0	1430.69	102	113
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	37	0.03%	37.6%	VEIIANDQGNR	99.7%	72.3	25	0	2	0	0	1228.63	50	60
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	37	0.03%	37.6%	VLEDSDLKK	99.7%	39.8	25	26	2	0	0	1046.57	345	353
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	37	0.03%	37.6%	VMEHFIK	97.4%	30.5	25	20.3	2	0	0	903.48	262	268
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	37	0.03%	37.6%	VTHAVVTVPAYFNDAQR	99.7%	53.8	25	52.8	1	2	0	1887.97	165	181
78 kDa glucose-regulated protein	HSPA5	GRP78_HUMAN	72.3	100.0%	18	21	37	0.03%	37.6%	VYEGERPLTK	99.7%	48.2	25	44.5	2	0	0	1191.64	465	474
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	4	5	17	0.02%	11.6%	FLPGYVGGIQEGAVTPAGVVNK	99.7%	108	25	108	4	2	0	2173.17	121	142
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	4	5	17	0.02%	11.6%	LLVSGFWGVAR	99.7%	83.7	25	83.1	5	0	0	1204.68	394	404
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	4	5	17	0.02%	11.6%	SLDGVTNDR	99.6%	38.6	25	27.4	2	0	0	976.47	14	22
7-dehydrocholesterol reductase	DHCR7	DHCR7_HUMAN	54.5	100.0%	4	5	17	0.02%	11.6%	VIECSYTSADGQR	99.7%	104	25	104	4	0	0	1485.66	377	389
Acetolactate synthase-like protein	ILVBL	ILVBL_HUMAN	67.9	99.8%	2	2	3	0.00%	6.3%	AAVETLGVPCFLGGMAR	98.7%	33.5	25	32.7	2	0	0	1748.88	306	322
Acetolactate synthase-like protein	ILVBL	ILVBL_HUMAN	67.9	99.8%	2	2	3	0.00%	6.3%	NAQMAQSPILLLGGAASTLLQNR	99.7%	57.6	25	51.8	0	1	0	2367.28	135	157
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	12	13	35	0.03%	31.6%	DGLTDVYNK	99.6%	38.9	25	34.5	2	0	0	1024.49	182	190
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	12	13	35	0.03%	31.6%	EAYMGNVLQGGEGQAPTR	99.7%	96.5	25	96.5	6	0	0	1877.88	88	105
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	12	13	35	0.03%	31.6%	EVVIVSATR	99.7%	69.3	25	68.5	4	0	0	973.57	41	49
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	12	13	35	0.03%	31.6%	IHMGSCAENTAK	98.7%	33.3	25	30.1	1	0	0	1318.59	191	202
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	12	13	35	0.03%	31.6%	IVGHLTHALK	96.9%	29.8	25	17.5	1	0	0	1088.66	394	403
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	12	13	35	0.03%	31.6%	LEDLIVK	99.1%	35.2	25	25.8	2	0	0	829.50	175	181
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	12	13	35	0.03%	31.6%	LGSIAIQGAIEK	99.7%	44.4	25	44	5	0	0	1199.70	67	78

Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	12	13	35	0.03%	31.6%	LNVTPLAR	99.7%	44.2	25	38.5	4	0	0	883.54	304	311
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	12	13	35	0.03%	31.6%	NEQDAYAINSYTR	99.7%	106	25	106	5	0	0	1544.70	209	221
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	12	13	35	0.03%	31.6%	QAVLGAGLPISTPCTTINK	99.7%	55.7	25	55.7	2	0	0	1941.05	106	124
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	12	13	35	0.03%	31.6%	RLNVTPLAR	98.6%	33.1	25	31.9	1	0	0	1039.64	303	311
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	THIL_HUMAN	45.2	100.0%	12	13	35	0.03%	31.6%	TPIGSFLGSLSLLPATK	99.7%	108	25	108	2	0	0	1701.98	50	66
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	14	14	20	0.02%	7.7%	AIGIGAYLVR	99.7%	58.9	25	41.6	2	0	0	1032.62	1824	1833
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	14	14	20	0.02%	7.7%	DEPIHILNVAIK	99.7%	48.2	25	48.2	2	0	0	1361.78	1283	1294
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	14	14	20	0.02%	7.7%	DFTVASPAEFVTR	96.9%	29.8	25	29.2	1	0	0	1439.72	99	111
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	14	14	20	0.02%	7.7%	DIIVIGNDITYR	99.7%	57.5	25	43.3	2	0	0	1391.75	1676	1687
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	14	14	20	0.02%	7.7%	EGLPLMVFANWR	99.5%	37.8	25	37.5	1	0	0	1448.74	2036	2047
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	14	14	20	0.02%	7.7%	GVISDILDWK	99.7%	47.9	25	47.9	2	0	0	1145.62	2200	2209
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	14	14	20	0.02%	7.7%	IGLAEEIR	99.5%	37.5	25	23.7	1	0	0	900.52	1724	1731
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	14	14	20	0.02%	7.7%	IGSFGPQEDLLFLR	99.7%	54.1	25	45.1	2	0	0	1591.85	1688	1701
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	14	14	20	0.02%	7.7%	ITDIIGKEEGIGPENLR	99.7%	40.1	25	40.1	0	1	0	1854.00	1782	1798
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	14	14	20	0.02%	7.7%	ITSENPDEGFKPSSGTVQELNFR	99.7%	43.3	25	43.3	0	1	0	2552.23	510	532
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	14	14	20	0.02%	7.7%	LPELLLK	98.9%	34.2	25	12.9	1	0	0	825.54	218	224
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	14	14	20	0.02%	7.7%	TIQVENSHLILTGAGALNK	99.7%	39.4	25	39.4	0	1	0	1979.09	1838	1856
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	14	14	20	0.02%	7.7%	VEVGTEVTDYR	99.7%	56.3	25	55	2	0	0	1267.62	1410	1420
Acetyl-CoA carboxylase 1	ACACA	ACACA_HUMAN	265.6	100.0%	14	14	20	0.02%	7.7%	VQQAELHTGSLPR	99.7%	61.8	25	54.2	1	0	0	1435.77	826	838
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN,ACTG_HUMAN	41.7	100.0%	23	41	241	0.23%	70.1%	AGFAGDDAPR	99.7%	75.6	25	64.6	23	0	0	976.45	19	28
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN,ACTG_HUMAN	41.7	100.0%	23	41	241	0.23%	70.1%	AVFPSIVGRPR	99.7%	55.5	25	48.8	3	0	0	1198.71	29	39
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN,ACTG_HUMAN	41.7	100.0%	23	41	241	0.23%	70.1%	CDVDIRK	99.0%	34.5	25	17	3	0	0	905.45	285	291
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN,ACTG_HUMAN	41.7	100.0%	23	41	241	0.23%	70.1%	CPEALFQPSFLGMESCGIHETTFNSIMK	99.7%	36.7	25	18.4	0	3	0	3247.46	257	284
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN,ACTG_HUMAN	41.7	100.0%	23	41	241	0.23%	70.1%	DLTDYLMK	99.7%	52.5	25	38.6	7	0	0	998.49	184	191
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN,ACTG_HUMAN	41.7	100.0%	23	41	241	0.23%	70.1%	DLYANTVLSGGTTMYPGIADR	99.7%	115	25	115	16	3	0	2231.07	292	312
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN,ACTG_HUMAN	41.7	100.0%	23	41	241	0.23%	70.1%	DSYVGDEAQSK	99.7%	82.8	25	76.2	12	0	0	1198.52	51	61
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN,ACTG_HUMAN	41.7	100.0%	23	41	241	0.23%	70.1%	DSYVGDEAQSKR	99.7%	69.2	25	69.2	10	0	0	1354.62	51	62
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN,ACTG_HUMAN	41.7	100.0%	23	41	241	0.23%	70.1%	EITALAPSTMK	99.7%	64.6	25	60.4	36	0	0	1177.61	316	326
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN,ACTG_HUMAN	41.7	100.0%	23	41	241	0.23%	70.1%	EKLCYVALDFEQEMATAASSSSLEK	96.7%	24.4	25	24.4	0	1	0	2823.31	214	238
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN,ACTG_HUMAN	41.7	100.0%	23	41	241	0.23%	70.1%	GYSFTTTAER	99.7%	82.6	25	71.1	29	0	0	1132.53	197	206
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN,ACTG_HUMAN	41.7	100.0%	23	41	241	0.23%	70.1%	HQGVMVGMGQK	99.7%	57	25	30	9	3	0	1187.57	40	50
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN,ACTG_HUMAN	41.7	100.0%	23	41	241	0.23%	70.1%	IIAPPERK	99.2%	35.8	25	27.1	2	0	0	923.57	329	336
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN,ACTG_HUMAN	41.7	100.0%	23	41	241	0.23%	70.1%	IWHHTFYNELR	99.7%	51.3	25	49.1	2	2	0	1515.75	85	95
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN,ACTG_HUMAN	41.7	100.0%	23	41	241	0.23%	70.1%	KDLYANTVLSGGTTMYPGIADR	99.7%	115	25	115	1	2	0	2343.17	291	312
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN,ACTG_HUMAN	41.7	100.0%	23	41	241	0.23%	70.1%	LCYVALDFEQEMATAASSSSLEK	99.7%	136	25	136	11	11	0	2550.17	216	238
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN,ACTG_HUMAN	41.7	100.0%	23	41	241	0.23%	70.1%	LDLAGRDLTDYLMK	99.7%	51.2	25	45.2	4	2	0	1623.84	178	191
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN,ACTG_HUMAN	41.7	100.0%	23	41	241	0.23%	70.1%	QEYDESGPSIVHR	99.7%	64.6	25	55.8	2	4	0	1516.70	360	372
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN,ACTG_HUMAN	41.7	100.0%	23	41	241	0.23%	70.1%	QEYDESGPSIVHRK	96.4%	24	25	17.5	0	1	0	1644.80	360	373
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN,ACTG_HUMAN	41.7	100.0%	23	41	241	0.23%	70.1%	RGILTLK	94.5%	27.6	25	12	1	0	0	800.54	62	68
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN,ACTG_HUMAN	41.7	100.0%	23	41	241	0.23%	70.1%	SYELPDGQVITIGNER	99.7%	111	25	95.8	11	0	0	1790.89	239	254
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN,ACTG_HUMAN	41.7	100.0%	23	41	241	0.23%	70.1%	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	99.7%	63.7	25	63.7	0	4	0	3183.61	148	177
Actin, cytoplasmic 1	ACTB	ACTB_HUMAN,ACTG_HUMAN	41.7	100.0%	23	41	241	0.23%	70.1%	VAPEEHPVLLTEAPLNPK	99.7%	70.6	25	42.7	12	11	0	1954.06	96	113
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	3	3	4	0.00%	9.4%	DLMVGDEASELR	99.7%	42.8	25	37.3	1	0	0	1350.62	54	65
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	3	3	4	0.00%	9.4%	ILLTEPPMNPTK	99.7%	41.9	25	34.7	2	0	0	1353.74	107	118
Actin-related protein 2	ACTR2	ARP2_HUMAN	44.8	100.0%	3	3	4	0.00%	9.4%	LCYVGYNIEQEQK	99.7%	60.7	25	60.7	1	0	0	1643.77	220	232
Actin-related protein 2/3 complex subunit 2	ARPC2	ARPC2_HUMAN	34.3	99.9%	2	2	2	0.00%	6.0%	MILLEVNNR	99.7%	42.9	25	41.3	1	0	0	1101.61	1	9
Actin-related protein 2/3 complex subunit 2	ARPC2	ARPC2_HUMAN	34.3	99.9%	2	2	2	0.00%	6.0%	NCFASVFEK	95.9%	28.7	25	27.2	1	0	0	1101.50	119	127
Actin-related protein 2/3 complex subunit 3	ARPC3	ARPC3_HUMAN	20.5	100.0%	3	4	6	0.01%	19.7%	DTDIVDEAIYYFK	99.7%	82.9	25	77.9	2	0	0	1591.75	38	50
Actin-related protein 2/3 complex subunit 3	ARPC3	ARPC3_HUMAN	20.5	100.0%	3	4	6	0.01%	19.7%	LIGNMALLPIR	99.7%	57.7	25	52.1	2	0	0	1210.73	15	25
Actin-related protein 2/3 complex subunit 3	ARPC3	ARPC3_HUMAN	20.5	100.0%	3	4	6	0.01%	19.7%	VFDPQNDKPSK	99.7%	50.4	25	41.1	2	0	0	1274.64	148	158
Actin-related protein 2/3 complex subunit 4	ARPC4	ARPC4_HUMAN	19.7	99.9%	2	2	5	0.00%	11.3%	AENFFILR	99.7%	46.3	25	26.4	2	0	0	1009.55	98	105

Actin-related protein 2/3 complex subunit 4	ARPC4	ARPC4_HUMAN	19.7	99.9%	2	2	5	0.00%	11.3%	ELLLQPVTISR	99.7%	57.7	25	57.7	3	0	0	1268.76	45	55
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	8	9	14	0.01%	27.0%	AEPEDHYFLLTEPPLNTPENR	97.5%	25.4	25	23.7	0	1	0	2482.19	103	123
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	8	9	14	0.01%	27.0%	DITYFIQQLLR	99.7%	77	25	62.1	2	0	0	1409.78	199	209
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	8	9	14	0.01%	27.0%	FMEQVIFK	97.7%	31.1	25	29.6	2	0	0	1041.54	92	99
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	8	9	14	0.01%	27.0%	GVDDLDFFIGDEAIEKPTYATK	99.7%	43.6	25	43.6	0	2	0	2444.19	54	75
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	8	9	14	0.01%	27.0%	LGYAGNTEPQFIIPSCIAIK	99.7%	41.6	25	41.6	1	0	0	2192.14	19	38
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	8	9	14	0.01%	27.0%	LSEELSGGR	99.4%	36.8	25	28.7	1	0	0	947.48	349	357
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	8	9	14	0.01%	27.0%	NIVLSGGSTMFR	99.7%	69.2	25	69.2	4	0	0	1281.66	318	329
Actin-related protein 3	ACTR3	ARP3_HUMAN	47.4	100.0%	8	9	14	0.01%	27.0%	YSYVCPDLVK	99.5%	38.1	25	35.8	1	0	0	1243.60	231	240
Activated RNA polymerase II transcriptional coactivator p15	SUB1	TCP4_HUMAN	14.4	100.0%	4	4	6	0.01%	40.9%	DDNMFQIGK	99.7%	47	25	46.8	2	0	0	1083.48	60	68
Activated RNA polymerase II transcriptional coactivator p15	SUB1	TCP4_HUMAN	14.4	100.0%	4	4	6	0.01%	40.9%	ELVSSSSSGSDSDSEVDKK	99.7%	42.7	25	42.7	2	0	0	1942.87	6	24
Activated RNA polymerase II transcriptional coactivator p15	SUB1	TCP4_HUMAN	14.4	100.0%	4	4	6	0.01%	40.9%	EQISDIDDAVR	97.7%	31	25	31	1	0	0	1260.61	115	125
Activated RNA polymerase II transcriptional coactivator p15	SUB1	TCP4_HUMAN	14.4	100.0%	4	4	6	0.01%	40.9%	GISLNPEQWSQLK	99.1%	34.9	25	34.9	1	0	0	1499.79	102	114
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	7	7	11	0.01%	3.1%	ALFEIALR	98.3%	32.2	25	12	1	0	0	932.56	1092	1099
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	7	7	11	0.01%	3.1%	DLADWLNIK	99.7%	48.6	25	36.1	2	0	0	1087.58	1498	1506
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	7	7	11	0.01%	3.1%	LWGWASPLR	99.7%	40	25	19.2	2	0	0	1085.59	1120	1128
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	7	7	11	0.01%	3.1%	RLEPLGIIVK	99.2%	35.7	25	28.7	1	0	0	1137.74	553	562
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	7	7	11	0.01%	3.1%	SVGDVALSQIVR	98.4%	32.5	25	23.6	1	0	0	1243.70	595	606
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	7	7	11	0.01%	3.1%	TGYFSSTDLGR	99.7%	62.6	25	53.8	2	0	0	1203.56	973	983
Activating signal cointegrator 1 complex subunit 3	ASCC3	ASCC3_HUMAN	251.5	100.0%	7	7	11	0.01%	3.1%	TVAAELAIFR	99.7%	87.1	25	83.7	2	0	0	1090.63	1356	1365
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	99.8%	2	2	5	0.00%	6.5%	ETFLTSPEELYR	99.7%	47.2	25	42.4	3	0	0	1484.73	213	224
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	AHSA1_HUMAN	38.3	99.8%	2	2	5	0.00%	6.5%	LDGEASINNR	99.7%	54.3	25	44.8	2	0	0	1088.53	64	73
Acyl-CoA dehydrogenase family member 10	ACAD10	ACD10_HUMAN	118.8	100.0%	3	3	3	0.00%	4.6%	AVIFDMGGVLIPSPGR	99.1%	34.8	25	33.8	1	0	0	1628.88	44	59
Acyl-CoA dehydrogenase family member 10	ACAD10	ACD10_HUMAN	118.8	100.0%	3	3	3	0.00%	4.6%	GLQTAVLSNNFYLPNQK	98.2%	32	25	32	1	0	0	1907.00	149	165
Acyl-CoA dehydrogenase family member 10	ACAD10	ACD10_HUMAN	118.8	100.0%	3	3	3	0.00%	4.6%	TSVPVDSFFSLLTSER	99.7%	58.6	25	56.5	1	0	0	1784.91	115	130
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	22	26	48	0.04%	39.0%	DFGGVTNGKPEDK	99.7%	58.2	25	54.3	1	0	0	1363.65	250	262
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	22	26	48	0.04%	39.0%	FFTEEVDSR	99.7%	59.1	25	52	2	0	0	1129.52	77	85
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	22	26	48	0.04%	39.0%	FSMGSVVAGLLK	99.7%	93.7	25	85.8	4	0	0	1224.67	305	316
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	22	26	48	0.04%	39.0%	GIILAGTEEQK	99.7%	47.9	25	37.3	2	0	0	1158.64	152	162
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	22	26	48	0.04%	39.0%	GSNTCEVHFENTK	99.7%	50.4	25	50.4	2	0	0	1522.66	267	279
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	22	26	48	0.04%	39.0%	ILLIFEGTNEILR	99.7%	91.7	25	79	2	0	0	1530.89	421	433
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	22	26	48	0.04%	39.0%	IPVENILGEVGDGFK	99.7%	97.7	25	97.7	2	0	0	1586.84	280	294
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	22	26	48	0.04%	39.0%	ITAFIVER	99.7%	52	25	41.2	2	0	0	948.55	242	249
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	22	26	48	0.04%	39.0%	LASGEHIAAFCLTEPASGSDAASIR	99.7%	51.9	25	48.8	0	2	0	2531.22	169	193
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	22	26	48	0.04%	39.0%	LIEMTAEYACTR	99.7%	98.1	25	91.9	4	0	0	1457.68	318	329
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	22	26	48	0.04%	39.0%	LSEFGLIQEK	99.7%	70.4	25	54	2	0	0	1163.63	336	345
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	22	26	48	0.04%	39.0%	MYIALTGLQHAGR	99.7%	64.8	25	63.7	2	1	0	1430.76	434	446
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	22	26	48	0.04%	39.0%	TEVVDSDGSVK	99.2%	35.4	25	30.6	2	0	0	1135.55	229	239
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	22	26	48	0.04%	39.0%	TEVVDSDGSVKDK	99.7%	54.2	25	50.6	2	0	0	1378.67	229	241
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	22	26	48	0.04%	39.0%	TIMEEQLVLK	99.7%	48.1	25	28.5	2	0	0	1203.67	522	531
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	22	26	48	0.04%	39.0%	TVETLLLR	99.7%	62.3	25	36.7	2	0	0	944.58	511	518
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	22	26	48	0.04%	39.0%	VAMNILNSGR	99.7%	87.3	25	77.1	2	0	0	1090.57	295	304
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	22	26	48	0.04%	39.0%	VSQQILEK	99.7%	57.1	25	37.2	2	0	0	944.54	601	608
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	22	26	48	0.04%	39.0%	VSTVMDTVGR	99.7%	80.4	25	71	4	0	0	1064.54	460	469
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	22	26	48	0.04%	39.0%	VWITNGGLANIFTVFAK	99.7%	60.3	25	60.3	1	0	0	1851.02	212	228
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	22	26	48	0.04%	39.0%	YAPENLDEQIK	99.7%	49.8	25	40.1	1	0	0	1319.65	589	599
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	ACAD9_HUMAN	68.8	100.0%	22	26	48	0.04%	39.0%	YAPENLDEQIKK	99.7%	44.7	25	35	2	0	0	1447.74	589	600
Acyl-coenzyme A thioesterase 1	ACOT1	ACOT1_HUMAN	46.3	99.8%	2	2	3	0.00%	4.8%	GALFQAHAR	99.7%	49.2	25	26	1	0	0	970.52	43	51
Acyl-coenzyme A thioesterase 1	ACOT1	ACOT1_HUMAN	46.3	99.8%	2	2	3	0.00%	4.8%	GLAPEQPVTLR	99.4%	36.7	25	34.4	2	0	0	1180.67	25	35
Acyl-coenzyme A thioesterase 13	ACOT13	ACO13_HUMAN	15.0	100.0%	4	4	12	0.01%	37.9%	GAPGVSVDMNITYMSPAK	99.7%	60.8	25	60.8	2	0	0	1869.87	78	95
Acyl-coenzyme A thioesterase 13	ACOT13	ACO13_HUMAN	15.0	100.0%	4	4	12	0.01%	37.9%	ITLVSAAPGK	99.7%	50.2	25	34.1	4	0	0	956.58	28	37

Acyl-coenzyme A thioesterase 13	ACOT13	ACO13_HUMAN	15.0	100.0%	4	4	12	0.01%	37.9%	LGEDIVITAHVLK	99.7%	57.1	25	47.8	2	0	0	1407.82	96	108
Acyl-coenzyme A thioesterase 13	ACOT13	ACO13_HUMAN	15.0	100.0%	4	4	12	0.01%	37.9%	TLAFTSVDLTNK	99.7%	93.3	25	84.8	4	0	0	1309.70	112	123
Acyl-coenzyme A thioesterase 8	ACOT8	ACOT8_HUMAN	35.9	99.8%	2	2	4	0.00%	7.8%	LFGGQIVGQALVAAAK	99.7%	61.1	25	55.5	2	0	0	1542.90	54	69
Acyl-coenzyme A thioesterase 8	ACOT8	ACOT8_HUMAN	35.9	99.8%	2	2	4	0.00%	7.8%	LPVLYQVER	99.7%	56.8	25	52.7	2	0	0	1116.64	92	100
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	ACOT9_HUMAN	49.9	100.0%	3	3	4	0.00%	6.6%	IFGGFLMR	99.7%	63.3	25	53.4	2	0	0	940.51	310	317
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	ACOT9_HUMAN	49.9	100.0%	3	3	4	0.00%	6.6%	SLEICHPQER	99.7%	41.3	25	41.3	1	0	0	1268.61	295	304
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	ACOT9_HUMAN	49.9	100.0%	3	3	4	0.00%	6.6%	VHSEVASLQEK	99.2%	35.3	25	25.8	1	0	0	1226.64	373	383
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	5	5	9	0.01%	16.1%	ATVFLNPAACK	99.7%	55.5	25	49	2	0	0	1191.62	63	73
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	5	5	9	0.01%	16.1%	EQPVFAMTGLR	99.7%	62.4	25	56.6	2	0	0	1264.64	200	210
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	5	5	9	0.01%	16.1%	GDFITIGSR	99.7%	68	25	53.3	2	0	0	965.51	343	351
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	5	5	9	0.01%	16.1%	GETVPLDVLQIK	99.7%	43.9	25	42.3	2	0	0	1311.75	185	196
Acylglycerol kinase, mitochondrial	AGK	AGK_HUMAN	47.1	100.0%	5	5	9	0.01%	16.1%	IPIGFIPLGETSSLSHTLFAESGNK	99.7%	49.8	25	49.8	0	1	0	2615.37	147	171
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	8	12	28	0.03%	59.4%	AELEIQKDALEPGQR	99.7%	69.1	25	67.6	2	2	0	1696.89	108	122
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	8	12	28	0.03%	59.4%	DISPVLKDPASFR	99.7%	41.9	25	41	1	1	0	1444.78	28	40
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	8	12	28	0.03%	59.4%	EKLAPVPFFSLLQYE	99.3%	36	25	36	2	0	0	1780.95	166	180
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	8	12	28	0.03%	59.4%	IDYIAGLDSR	99.7%	64.2	25	61.8	5	0	0	1122.58	58	67
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	8	12	28	0.03%	59.4%	LAPVPFFSLLQYE	99.7%	60.9	25	60.9	2	0	0	1523.81	168	180
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	8	12	28	0.03%	59.4%	LQAEVLECVSLVELTSLK	99.7%	127	25	126	4	0	0	2031.10	146	163
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	8	12	28	0.03%	59.4%	SFPDFPTPGVVFR	99.7%	42.4	25	33.4	4	0	0	1465.75	15	27
Adenine phosphoribosyltransferase	APRT	APT_HUMAN	19.6	100.0%	8	12	28	0.03%	59.4%	VVVVDDLLATGGTMNAACELLGR	99.7%	119	25	109	4	1	0	2374.21	123	145
Adenylate kinase 2, mitochondrial	AK2	KAD2_HUMAN	26.5	99.8%	2	2	4	0.00%	8.8%	AVLLGPPGAGK	98.9%	34	25	34	2	0	0	979.59	18	28
Adenylate kinase 2, mitochondrial	AK2	KAD2_HUMAN	26.5	99.8%	2	2	4	0.00%	8.8%	NGFLLDGFPR	99.7%	43.3	25	38	2	0	0	1135.59	94	103
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	6	8	15	0.01%	30.0%	AVILGPPGSGK	99.7%	44.5	25	25.9	2	0	0	995.59	8	18
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	6	8	15	0.01%	30.0%	DVAKPVIELYK	99.7%	41.2	25	32.7	2	0	0	1274.74	176	186
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	6	8	15	0.01%	30.0%	GVLHQFSGTETNK	99.7%	62.7	25	62.7	2	2	0	1417.71	189	201
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	6	8	15	0.01%	30.0%	IWPYVYTLFSNK	99.7%	46.5	25	43.3	2	0	0	1530.80	202	213
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	6	8	15	0.01%	30.0%	LMMSELENR	99.7%	59.4	25	56.8	3	0	0	1122.53	72	80
Adenylate kinase 4, mitochondrial	AK4	KAD4_HUMAN	25.3	100.0%	6	8	15	0.01%	30.0%	SLLVPDHVITR	99.6%	38.6	25	37.2	2	0	0	1249.73	61	71
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	8	8	14	0.01%	23.6%	FLEEEVYPLLKPYESVMK	99.7%	34.9	25	33.5	0	2	0	2214.14	460	477
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	8	8	14	0.01%	23.6%	IQVDAYFSPIHSQLDHLLDPSSFTGR	99.7%	33.5	25	33.5	0	2	0	2943.46	427	452
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	8	8	14	0.01%	23.6%	NALDLLLPK	99.7%	53.7	25	37.2	2	0	0	996.61	126	134
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	8	8	14	0.01%	23.6%	QEGGDNDLIER	99.5%	37.4	25	21	2	0	0	1245.57	416	426
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	8	8	14	0.01%	23.6%	QELPFMATENIIMAMVK	99.7%	67.3	25	58.8	1	0	0	1965.98	375	391
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	8	8	14	0.01%	23.6%	SNLENIDFK	99.7%	55.5	25	49.7	1	0	0	1079.54	67	75
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	8	8	14	0.01%	23.6%	VLSQQAASVVK	99.7%	77.4	25	61.3	2	0	0	1129.66	405	415
Adenylosuccinate lyase	ADSL	PUR8_HUMAN	54.9	100.0%	8	8	14	0.01%	23.6%	YASPEMCFVFSDR	99.7%	54.6	25	54.6	2	0	0	1608.68	21	33
Adenylosuccinate synthetase isozyme 2	ADSS	PURA2_HUMAN	50.1	100.0%	5	5	7	0.01%	15.8%	DGVYFLYEALHGPPK	99.7%	42.7	25	42.7	1	0	0	1705.86	233	247
Adenylosuccinate synthetase isozyme 2	ADSS	PURA2_HUMAN	50.1	100.0%	5	5	7	0.01%	15.8%	FIEDELQIPVK	99.7%	40.3	25	29.6	2	0	0	1330.73	431	441
Adenylosuccinate synthetase isozyme 2	ADSS	PURA2_HUMAN	50.1	100.0%	5	5	7	0.01%	15.8%	LDILDMFTEIK	99.6%	38.9	25	35.3	1	0	0	1337.70	363	373
Adenylosuccinate synthetase isozyme 2	ADSS	PURA2_HUMAN	50.1	100.0%	5	5	7	0.01%	15.8%	VGIGAFPTEQDNEIGELLQTR	99.7%	48.2	25	48.2	1	0	0	2287.16	304	324
Adenylosuccinate synthetase isozyme 2	ADSS	PURA2_HUMAN	50.1	100.0%	5	5	7	0.01%	15.8%	VVDLLAQDADIVCR	99.7%	81	25	79.8	2	0	0	1586.82	46	59
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	5	11	0.01%	47.0%	AAYFGVYDTAK	99.7%	88.5	25	88.5	8	0	0	1205.58	189	199
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	5	11	0.01%	47.0%	DFLAGGVAAAVSK	99.7%	101	25	95.4	2	0	0	1205.65	11	23
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	5	11	0.01%	47.0%	EFHGLGDCIIK	99.7%	55.5	25	43.1	2	1	0	1288.64	153	163
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	5	11	0.01%	47.0%	EQGFLSFWR	99.7%	44.2	25	41.6	4	0	0	1169.57	64	72
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	5	11	0.01%	47.0%	GADIMYTGTVDCWR	99.7%	79.5	25	72.7	5	0	0	1644.71	246	259
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	5	11	0.01%	47.0%	GAWSNVLR	99.7%	72.1	25	55.7	4	0	0	902.48	273	280
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	5	11	0.01%	47.0%	GMGGAFVLVLYDEIK	99.7%	77.6	25	0	2	0	0	1627.84	281	295
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	5	11	0.01%	47.0%	GMGGAFVLVLYDEIKK	99.7%	41.2	25	0	2	0	0	1755.94	281	296
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	5	11	0.01%	47.0%	GNLANVIR	99.3%	36	25	15.5	1	0	0	856.50	73	80
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	5	11	0.01%	47.0%	KGADIMYTGTVDCWR	99.7%	49.4	25	49.4	2	2	0	1772.81	245	259

ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	5	11	0.01%	47.0%	LLLQVQHASK	99.7%	48.4	25	32.1	16	0	0	1136.68	34	43
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	5	11	0.01%	47.0%	QLFLGGVDR	99.7%	57.9	25	32.7	2	0	0	1004.55	97	105
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	5	11	0.01%	47.0%	RMMMQSGR	99.7%	52	25	46	2	0	0	996.45	237	244
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	5	11	0.01%	47.0%	TAVAPIER	99.7%	42.1	25	29.4	3	0	0	856.49	24	31
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	5	11	0.01%	47.0%	YFPTQALNFAFK	99.7%	91.1	25	76.7	32	0	0	1446.74	81	92
ADP/ATP translocase 1	SLC25A4	ADT1_HUMAN	33.1	100.0%	4	5	11	0.01%	47.0%	YFPTQALNFAFKDK	99.7%	81.3	25	79.7	3	0	0	1689.86	81	94
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	20	26	124	0.12%	50.7%	AAYFGIYDTAK	99.7%	63.2	25	45.2	4	0	0	1219.60	189	199
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	20	26	124	0.12%	50.7%	DFLAGGVAAAISK	99.7%	104	25	95.6	9	0	0	1219.67	11	23
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	20	26	124	0.12%	50.7%	DFLAGGVAAAISKTAVAPIER	99.7%	55.3	25	55.3	1	0	0	2057.14	11	31
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	20	26	124	0.12%	50.7%	EQGVLSFWR	99.7%	68.2	25	68.2	16	0	0	1121.57	64	72
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	20	26	124	0.12%	50.7%	GAWSNVLR	99.7%	72.1	25	55.7	4	0	0	902.48	273	280
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	20	26	124	0.12%	50.7%	GLGDCLVK	98.3%	32.3	25	18.5	2	0	0	861.45	156	163
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	20	26	124	0.12%	50.7%	GMGGAFVLVLYDEIK	99.7%	77.6	25	0	2	0	0	1627.84	281	295
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	20	26	124	0.12%	50.7%	GMGGAFVLVLYDEIKK	99.7%	41.2	25	0	2	0	0	1755.94	281	296
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	20	26	124	0.12%	50.7%	GNLANVIR	99.3%	36	25	15.5	1	0	0	856.50	73	80
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	20	26	124	0.12%	50.7%	GTDIMYTGTLDCWR	99.7%	93.7	25	88.8	5	0	0	1704.74	246	259
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	20	26	124	0.12%	50.7%	GTDIMYTGTLDCWRK	99.7%	55.8	25	55.8	2	0	0	1816.84	246	260
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	20	26	124	0.12%	50.7%	KGTDIMYTGTLDCWR	99.7%	85.4	25	85.4	4	4	0	1816.84	245	259
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	20	26	124	0.12%	50.7%	LAADVGKAGAER	99.7%	60.5	25	50.1	1	0	0	1157.63	141	152
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	20	26	124	0.12%	50.7%	LLLQVQHASK	99.7%	48.4	25	32.1	16	0	0	1136.68	34	43
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	20	26	124	0.12%	50.7%	QIFLGGVDK	99.7%	61.9	25	37.2	4	0	0	976.55	97	105
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	20	26	124	0.12%	50.7%	QIFLGGVDKR	99.7%	51.3	25	40	7	0	0	1132.65	97	106
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	20	26	124	0.12%	50.7%	RMMMQSGR	99.7%	52	25	46	2	0	0	996.45	237	244
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	20	26	124	0.12%	50.7%	TAVAPIER	99.7%	42.1	25	29.4	3	0	0	856.49	24	31
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	20	26	124	0.12%	50.7%	YFPTQALNFAFK	99.7%	91.1	25	76.7	32	0	0	1446.74	81	92
ADP/ATP translocase 2	SLC25A5	ADT2_HUMAN	32.9	100.0%	20	26	124	0.12%	50.7%	YFPTQALNFAFKDK	99.7%	81.3	25	79.7	3	0	0	1689.86	81	94
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	8	39	0.04%	46.0%	AAYFGVYDTAK	99.7%	88.5	25	88.5	8	0	0	1205.58	189	199
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	8	39	0.04%	46.0%	DFLAGGIAAAISK	99.7%	104	25	100	22	0	0	1233.68	11	23
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	8	39	0.04%	46.0%	EQGVLSFWR	99.7%	68.2	25	68.2	16	0	0	1121.57	64	72
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	8	39	0.04%	46.0%	GADIMYTGTVDCWR	99.7%	79.5	25	72.7	5	0	0	1644.71	246	259
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	8	39	0.04%	46.0%	GAWSNVLR	99.7%	72.1	25	55.7	4	0	0	902.48	273	280
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	8	39	0.04%	46.0%	GLGDCLVK	98.3%	32.3	25	18.5	2	0	0	861.45	156	163
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	8	39	0.04%	46.0%	GMGGAFVLVLYDELK	99.7%	77.6	25	0	2	0	0	1627.84	281	295
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	8	39	0.04%	46.0%	GMGGAFVLVLYDELKK	99.7%	41.2	25	0	2	0	0	1755.94	281	296
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	8	39	0.04%	46.0%	GNLANVIR	99.3%	36	25	15.5	1	0	0	856.50	73	80
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	8	39	0.04%	46.0%	KGADIMYTGTVDCWR	99.7%	49.4	25	49.4	2	2	0	1772.81	245	259
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	8	39	0.04%	46.0%	LLLQVQHASK	99.7%	48.4	25	32.1	16	0	0	1136.68	34	43
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	8	39	0.04%	46.0%	QIFLGGVDK	99.7%	61.9	25	37.2	4	0	0	976.55	97	105
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	8	39	0.04%	46.0%	RMMMQSGR	99.7%	52	25	46	2	0	0	996.45	237	244
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	8	39	0.04%	46.0%	TAVAPIER	99.7%	42.1	25	29.4	3	0	0	856.49	24	31
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	8	39	0.04%	46.0%	YFPTQALNFAFK	99.7%	91.1	25	76.7	32	0	0	1446.74	81	92
ADP/ATP translocase 3	SLC25A6	ADT3_HUMAN	32.9	100.0%	4	8	39	0.04%	46.0%	YFPTQALNFAFKDK	99.7%	81.3	25	79.7	3	0	0	1689.86	81	94
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN,ARF3_HUMAN	20.7	100.0%	2	3	9	0.01%	39.2%	DAVLLVFANK	99.7%	93.4	25	88.7	4	0	0	1089.63	118	127
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN,ARF3_HUMAN	20.7	100.0%	2	3	9	0.01%	39.2%	ILMVGLDAAGK	99.7%	79.8	25	62.1	10	0	0	1087.62	20	30
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN,ARF3_HUMAN	20.7	100.0%	2	3	9	0.01%	39.2%	LGEIVTTIPTIGFNVETVEYK	99.7%	48.4	25	48.4	3	0	0	2323.24	39	59
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN,ARF3_HUMAN	20.7	100.0%	2	3	9	0.01%	39.2%	NISFTVWDVGGQDK	99.7%	110	25	98.3	4	0	0	1565.76	60	73
ADP-ribosylation factor 1	ARF1	ARF1_HUMAN,ARF3_HUMAN	20.7	100.0%	2	3	9	0.01%	39.2%	QDLPNAMNAAEITDK	99.7%	83.5	25	79.3	5	0	0	1646.77	128	142
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	7	10	28	0.03%	49.4%	DAVLLLFANK	99.7%	53	25	40.7	2	0	0	1103.65	118	127
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	7	10	28	0.03%	49.4%	ILMVGLDAAGK	99.7%	79.8	25	62.1	10	0	0	1087.62	20	30
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	7	10	28	0.03%	49.4%	IQEVADELQK	99.7%	58.4	25	41	2	0	0	1172.62	100	109
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	7	10	28	0.03%	49.4%	LGEIVTTIPTIGFNVETVEYK	99.7%	48.4	25	48.4	3	0	0	2323.24	39	59

ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	7	10	28	0.03%	49.4%	MLLVDELR	99.7%	48.3	25	19.9	4	0	0	988.55	110	117
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	7	10	28	0.03%	49.4%	NICFTVWDVGGQDR	99.7%	108	25	102	2	0	0	1666.76	60	73
ADP-ribosylation factor 4	ARF4	ARF4_HUMAN	20.5	100.0%	7	10	28	0.03%	49.4%	QDLPNAMAISEMTDK	99.7%	79.2	25	77.9	5	0	0	1695.76	128	142
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	100.0%	4	4	9	0.01%	45.0%	DAVLLVFANK	99.7%	93.4	25	88.7	4	0	0	1089.63	118	127
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	100.0%	4	4	9	0.01%	45.0%	ILMVGLDAAGK	99.7%	79.8	25	62.1	10	0	0	1087.62	20	30
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	100.0%	4	4	9	0.01%	45.0%	LGEIVTTIPTIGFNVETVEYK	99.7%	48.4	25	48.4	3	0	0	2323.24	39	59
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	100.0%	4	4	9	0.01%	45.0%	NICFTVWDVGGQDK	99.7%	106	25	103	2	0	0	1638.76	60	73
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	100.0%	4	4	9	0.01%	45.0%	QDMPNAMPVSELTDK	99.7%	53.2	25	53.2	1	0	0	1707.76	128	142
ADP-ribosylation factor 5	ARF5	ARF5_HUMAN	20.5	100.0%	4	4	9	0.01%	45.0%	VQESADELQK	99.7%	65.9	25	59.1	2	0	0	1146.56	100	109
ADP-ribosylation factor 6	ARF6	ARF6_HUMAN	20.1	100.0%	4	6	12	0.01%	30.3%	DAIILIFANK	99.7%	63	25	0	2	0	0	1117.66	114	123
ADP-ribosylation factor 6	ARF6	ARF6_HUMAN	20.1	100.0%	4	6	12	0.01%	30.3%	FNVWDVGGQDK	99.7%	71.9	25	57.9	2	0	0	1264.60	59	69
ADP-ribosylation factor 6	ARF6	ARF6_HUMAN	20.1	100.0%	4	6	12	0.01%	30.3%	ILMLGLDAAGK	99.7%	85.5	25	63.9	4	0	0	1117.63	16	26
ADP-ribosylation factor 6	ARF6	ARF6_HUMAN	20.1	100.0%	4	6	12	0.01%	30.3%	LGQSVTTIPTVGFNVETVTYK	99.7%	56.7	25	56.7	2	2	0	2254.20	35	55
ADP-ribosylation factor-like protein 1	ARL1	ARL1_HUMAN	20.4	100.0%	5	6	9	0.01%	34.8%	AILVVFANK	99.7%	70.9	25	70.9	2	0	0	974.60	119	127
ADP-ribosylation factor-like protein 1	ARL1	ARL1_HUMAN	20.4	100.0%	5	6	9	0.01%	34.8%	ILILGLDGAGK	99.7%	78	25	77.9	1	0	0	1069.66	20	30
ADP-ribosylation factor-like protein 1	ARL1	ARL1_HUMAN	20.4	100.0%	5	6	9	0.01%	34.8%	KWQIFK	97.3%	30.4	25	13.6	2	0	0	849.50	152	157
ADP-ribosylation factor-like protein 1	ARL1	ARL1_HUMAN	20.4	100.0%	5	6	9	0.01%	34.8%	LQVGEVVTTIPTIGFNVETVTYK	98.8%	28.2	25	28.2	0	1	0	2508.36	37	59
ADP-ribosylation factor-like protein 1	ARL1	ARL1_HUMAN	20.4	100.0%	5	6	9	0.01%	34.8%	SELVAMLEEEELRK	99.7%	56.6	25	55.2	3	0	0	1691.85	105	118
ADP-ribosylation factor-like protein 2	ARL2	ARL2_HUMAN	20.9	100.0%	6	7	14	0.01%	40.2%	ELQSLLVEER	99.7%	76.4	25	64.1	2	0	0	1215.66	105	114
ADP-ribosylation factor-like protein 2	ARL2	ARL2_HUMAN	20.9	100.0%	6	7	14	0.01%	40.2%	FNGEDIDTISPTLGFNIK	99.5%	38.1	25	38.1	1	0	0	1980.99	36	53
ADP-ribosylation factor-like protein 2	ARL2	ARL2_HUMAN	20.9	100.0%	6	7	14	0.01%	40.2%	LAGATLLIFANK	99.7%	95.2	25	95.2	3	0	0	1231.74	115	126
ADP-ribosylation factor-like protein 2	ARL2	ARL2_HUMAN	20.9	100.0%	6	7	14	0.01%	40.2%	LLMLGLDNAGK	99.7%	72.8	25	58.2	4	0	0	1144.64	19	29
ADP-ribosylation factor-like protein 2	ARL2	ARL2_HUMAN	20.9	100.0%	6	7	14	0.01%	40.2%	LNIWDVGGQK	99.7%	60.9	25	55.9	2	0	0	1129.60	62	71
ADP-ribosylation factor-like protein 2	ARL2	ARL2_HUMAN	20.9	100.0%	6	7	14	0.01%	40.2%	QDLPGALSSNAIR	99.7%	82.3	25	70.5	2	0	0	1341.71	127	139
ADP-ribosylation factor-like protein 6	ARL6	ARL6_HUMAN	21.1	100.0%	5	5	7	0.01%	32.3%	GEGLQEGVDWLQDQIQTVK	99.7%	43.9	25	43.9	2	0	0	2143.07	167	185
ADP-ribosylation factor-like protein 6	ARL6	ARL6_HUMAN	21.1	100.0%	5	5	7	0.01%	32.3%	IPILFFANK	99.1%	34.9	25	19.4	2	0	0	1062.63	123	131
ADP-ribosylation factor-like protein 6	ARL6	ARL6_HUMAN	21.1	100.0%	5	5	7	0.01%	32.3%	LSVLLGLK	99.5%	37.7	25	32.9	1	0	0	842.57	7	14
ADP-ribosylation factor-like protein 6	ARL6	ARL6_HUMAN	21.1	100.0%	5	5	7	0.01%	32.3%	NLWEHYYK	96.8%	29.7	25	22.6	1	0	0	1152.55	78	85
ADP-ribosylation factor-like protein 6	ARL6	ARL6_HUMAN	21.1	100.0%	5	5	7	0.01%	32.3%	SSSLSFTVFDMSGQGR	99.7%	57	25	57	1	0	0	1705.79	60	75
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	10	10	14	0.01%	14.1%	EITWKDFVNNYLSK	97.7%	31	25	30.9	1	0	0	1756.89	169	182
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	10	10	14	0.01%	14.1%	GAILTGPPGTGK	99.3%	35.9	25	35.9	1	0	0	1068.61	343	354
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	10	10	14	0.01%	14.1%	GLGYAQYLPK	96.4%	29.2	25	23.1	1	0	0	1109.60	602	611
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	10	10	14	0.01%	14.1%	GMGGLFSVGETTAK	98.4%	32.5	25	24.8	1	0	0	1354.67	284	297
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	10	10	14	0.01%	14.1%	ILINDAYKR	99.7%	49.5	25	38.5	2	0	0	1105.64	703	711
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	10	10	14	0.01%	14.1%	NLETLQQELGIEGENR	99.7%	106	25	98.2	1	0	0	1842.92	225	240
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	10	10	14	0.01%	14.1%	QIFIGPPDIK	97.0%	30	25	10.8	1	0	0	1127.65	472	481
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	10	10	14	0.01%	14.1%	VALLLLEK	99.7%	56.2	25	56.2	2	0	0	898.60	726	733
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	10	10	14	0.01%	14.1%	VGQISFDLPR	99.7%	87.4	25	65	2	0	0	1131.62	670	679
AFG3-like protein 2	AFG3L2	AFG32_HUMAN	88.6	100.0%	10	10	14	0.01%	14.1%	VSEEIFFGR	99.7%	66.2	25	48	2	0	0	1083.55	633	641
A-kinase anchor protein 8-like	AKAP8L	AKP8L_HUMAN	71.6	99.8%	2	2	2	0.00%	3.4%	IQFVCSLCK	99.7%	42.7	25	24.6	1	0	0	1154.57	387	395
A-kinase anchor protein 8-like	AKAP8L	AKP8L_HUMAN	71.6	99.8%	2	2	2	0.00%	3.4%	QTADFLQEYVTNK	99.7%	81.5	25	74.3	1	0	0	1556.76	427	439
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	7	7	13	0.01%	15.9%	FAVALLDDSVR	99.7%	79.5	25	59.1	2	0	0	1205.65	166	176
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	7	7	13	0.01%	15.9%	GALLSVGWSTGR	99.7%	58.5	25	55	2	0	0	1203.65	467	478
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	7	7	13	0.01%	15.9%	GQWINLPVLQLTK	99.7%	67.9	25	53.7	2	0	0	1509.88	40	52
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	7	7	13	0.01%	15.9%	ILATTPSAVFR	99.7%	64.5	25	57.8	2	0	0	1175.68	302	312
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	7	7	13	0.01%	15.9%	LLSASPVDAAIR	99.7%	61.8	25	55.5	2	0	0	1212.69	259	270
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	7	7	13	0.01%	15.9%	VQDGKPVILLFR	99.7%	49.5	25	49.5	2	0	0	1384.83	421	432
Aladin	AAAS	AAAS_HUMAN	59.6	100.0%	7	7	13	0.01%	15.9%	VWDVSTETCVPLPWFR	99.7%	40.5	25	38.2	1	0	0	1991.97	271	286
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	21	0.02%	16.5%	AAFLNFFR	99.7%	54.8	25	46.3	2	0	0	985.53	44	51
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	21	0.02%	16.5%	AGLDPDLETR	99.7%	42	25	37.4	2	0	0	1086.54	178	187
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	21	0.02%	16.5%	AGQEDVLFPVAR	97.4%	30.5	25	26	1	0	0	1301.68	581	592

Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	21	0.02%	16.5%	DIWLSLGVPASR	99.7%	47.6	25	39.5	2	0	0	1313.72	188	199
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	21	0.02%	16.5%	EADGSLQPLPQR	99.4%	36.9	25	26.9	1	0	0	1310.67	251	262
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	21	0.02%	16.5%	ELGQSLAQEVK	99.7%	69.5	25	61.4	2	0	0	1201.64	791	801
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	21	0.02%	16.5%	GVQLDSAGLER	99.7%	76.8	25	65.7	2	0	0	1144.60	461	471
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	21	0.02%	16.5%	LDVTTQTPLTPEQLR	99.7%	79.7	25	74.5	2	0	0	1711.92	664	678
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	21	0.02%	16.5%	LLAVTGEQAQQAR	99.7%	83.7	25	72.6	2	0	0	1384.75	778	790
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	21	0.02%	16.5%	LVPSASVRPR	99.7%	42.8	25	39.3	1	0	0	1081.65	58	67
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	21	0.02%	16.5%	LWISYFDGDPK	99.7%	43.8	25	39.2	1	0	0	1340.65	167	177
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	21	0.02%	16.5%	SLDEVYPDPVR	99.6%	38.5	25	32.1	1	0	0	1289.64	712	722
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	21	0.02%	16.5%	TGAVGDLVIIGDR	99.7%	69	25	62.2	1	0	0	1285.71	757	769
Alanine--tRNA ligase, mitochondrial	AARS2	SYAM_HUMAN	107.3	100.0%	14	14	21	0.02%	16.5%	TNFYAEQGGQASDR	99.7%	94.4	25	94.4	1	0	0	1543.68	562	575
Aldehyde dehydrogenase family 16 member A1	ALDH16A1	A16A1_HUMAN	85.1	99.8%	2	2	3	0.00%	2.9%	AAEAEVELSAR	99.7%	55	25	44.7	1	0	0	1145.58	619	629
Aldehyde dehydrogenase family 16 member A1	ALDH16A1	A16A1_HUMAN	85.1	99.8%	2	2	3	0.00%	2.9%	LLWTLESLVTGR	99.7%	63.7	25	58.7	2	0	0	1387.79	118	129
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	8	9	19	0.02%	20.5%	KIEEVVER	99.7%	62.6	25	46	2	0	0	1001.56	429	436
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	8	9	19	0.02%	20.5%	LAPALATGNTVVMK	99.7%	94.5	25	87.7	4	0	0	1385.78	196	209
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	8	9	19	0.02%	20.5%	LLNLLADLVER	99.7%	75.3	25	67.1	2	0	0	1268.76	104	114
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	8	9	19	0.02%	20.5%	TFVEESIYNEFLER	99.7%	81.6	25	73.6	2	0	0	1775.85	325	338
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	8	9	19	0.02%	20.5%	VAEQTPLSALYLASLIK	99.7%	107	25	107	3	0	0	1817.04	210	226
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	8	9	19	0.02%	20.5%	VGNPFELDTQQGPQVDKEQFER	99.7%	47.8	25	47.8	0	2	0	2561.23	348	369
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	8	9	19	0.02%	20.5%	VLGYIQLGQK	99.7%	67.3	25	57.1	2	0	0	1118.66	370	379
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	AL1B1_HUMAN	57.2	100.0%	8	9	19	0.02%	20.5%	YGLAAAVFTR	99.7%	104	25	99.6	2	0	0	1068.58	442	451
Aldehyde dehydrogenase, mitochondrial	ALDH2	ALDH2_HUMAN	56.4	100.0%	5	5	6	0.01%	11.8%	EEIFGPVMQILK	98.3%	32.2	25	14.1	2	0	0	1403.76	415	426
Aldehyde dehydrogenase, mitochondrial	ALDH2	ALDH2_HUMAN	56.4	100.0%	5	5	6	0.01%	11.8%	LLCGGGIAADR	99.7%	71.4	25	58.9	1	0	0	1102.57	384	394
Aldehyde dehydrogenase, mitochondrial	ALDH2	ALDH2_HUMAN	56.4	100.0%	5	5	6	0.01%	11.8%	TIEEVVGR	94.6%	27.6	25	22.5	1	0	0	902.49	429	436
Aldehyde dehydrogenase, mitochondrial	ALDH2	ALDH2_HUMAN	56.4	100.0%	5	5	6	0.01%	11.8%	VAEQTPLTALYVANLIK	99.7%	69.3	25	69.3	1	0	0	1844.05	210	226
Aldehyde dehydrogenase, mitochondrial	ALDH2	ALDH2_HUMAN	56.4	100.0%	5	5	6	0.01%	11.8%	VIQVAAGSSNLKR	99.6%	39.2	25	39.2	1	0	0	1342.78	269	281
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	6	6	9	0.01%	12.8%	FGGLAAGEDNGQR	99.6%	39.1	25	35.1	1	0	0	1291.60	491	503
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	6	6	9	0.01%	12.8%	GISDPLTVFEQTEAAAR	99.7%	85.8	25	77.9	2	0	0	1804.91	587	603
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	6	6	9	0.01%	12.8%	GVQFAPFSTCR	99.7%	42	25	36.2	1	0	0	1269.60	556	566
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	6	6	9	0.01%	12.8%	NIYGNIEDLVVHIK	99.7%	65.9	25	63.9	2	0	0	1626.89	324	337
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	6	6	9	0.01%	12.8%	TIISLDTSQMNR	99.7%	40.3	25	40.3	1	0	0	1378.70	254	265
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	ADAS_HUMAN	72.9	100.0%	6	6	9	0.01%	12.8%	YGSVAFPNFEQGVACLR	99.7%	91.8	25	91.8	2	0	0	1914.92	390	406
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	5	5	7	0.01%	12.6%	GAPTTSLISVAVTK	99.7%	95.8	25	82.6	1	0	0	1344.77	219	232
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	5	5	7	0.01%	12.6%	IQVLGSLVSLEMGK	99.7%	79.7	25	74.9	2	0	0	1473.83	125	138
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	5	5	7	0.01%	12.6%	IWADIPAPK	95.7%	28.6	25	18.1	1	0	0	1010.57	101	109
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	5	5	7	0.01%	12.6%	VGNPWDPNVLYGPLHTK	99.2%	30	25	30	0	1	0	1906.98	359	375
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	AL7A1_HUMAN	58.5	100.0%	5	5	7	0.01%	12.6%	VNLLSFTGSTQVGK	99.7%	92.4	25	92.4	2	0	0	1450.79	267	280
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	13	15	27	0.03%	51.9%	ACYLSINPQKDETLETEK	99.7%	67.8	25	67.8	2	2	0	2139.03	221	238
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	13	15	27	0.03%	51.9%	AGFAGDQIPK	99.7%	63.2	25	47.3	2	0	0	1003.52	23	32
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	13	15	27	0.03%	51.9%	AQYYLPDGSTIEIGPSR	99.7%	118	25	117	2	0	0	1866.92	239	255
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	13	15	27	0.03%	51.9%	DQLQTFSEEHPVLLTEAPLNPR	99.7%	58.4	25	52.4	0	2	0	2534.29	97	118
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	13	15	27	0.03%	51.9%	EGYDFHSSSEFEIVK	99.7%	64.6	25	55.9	2	0	0	1773.80	201	215
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	13	15	27	0.03%	51.9%	ISAPQER	94.6%	27.6	25	10.7	1	0	0	800.43	330	336
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	13	15	27	0.03%	51.9%	IWQYVYSK	99.6%	38.5	25	27.2	2	0	0	1086.56	89	96
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	13	15	27	0.03%	51.9%	LLSEVKK	99.3%	36.4	25	15.9	1	0	0	816.52	314	320
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	13	15	27	0.03%	51.9%	LYSTWIGGSILASLDTFKK	99.7%	53.5	25	53.5	1	0	0	2100.14	337	355
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	13	15	27	0.03%	51.9%	TLFSNIVLSGGSTLFK	99.7%	131	25	131	2	0	0	1683.93	293	308
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	13	15	27	0.03%	51.9%	TTGVVLDSGDGVTHAVPIYEGFAMPHSIMR	99.7%	54.6	25	54.6	0	2	0	3189.53	153	182
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	13	15	27	0.03%	51.9%	VMAGALEGDIFIGPK	99.7%	98.6	25	0	4	0	0	1533.80	47	61
Alpha-centractin	ACTR1A	ACTZ_HUMAN	42.6	100.0%	13	15	27	0.03%	51.9%	YCFPNYVGRPK	99.7%	53.5	25	53.5	2	0	0	1400.68	33	43
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	10	12	24	0.02%	32.7%	AAVPSGASTGIYEALELR	99.7%	113	25	112	2	0	0	1804.94	33	50

Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	10	12	24	0.02%	32.7%	DATNVGDEGGFAPNILENKEGLELLK	99.7%	79.2	25	79.2	0	2	0	2743.38	203	228
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	10	12	24	0.02%	32.7%	GNPTVEVDLFTSK	99.7%	59.2	25	17.4	1	0	0	1406.72	16	28
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	10	12	24	0.02%	32.7%	IGAEVYHNLK	99.7%	60.6	25	48.8	3	0	0	1143.62	184	193
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	10	12	24	0.02%	32.7%	KLNVTEQEK	99.7%	49.3	25	25.2	1	0	0	1088.59	81	89
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	10	12	24	0.02%	32.7%	LAMQEFMILPVGAANFR	99.7%	85.3	25	85.3	4	1	0	1939.98	163	179
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	10	12	24	0.02%	32.7%	SCNCLLLK	97.1%	30.1	25	22.8	1	0	0	1007.50	336	343
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	10	12	24	0.02%	32.7%	VNQIGSVTESLQACK	99.7%	116	25	0	4	0	0	1633.82	344	358
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	10	12	24	0.02%	32.7%	VVIGMDVAASEFFR	99.7%	55.2	25	55.2	1	0	0	1556.78	240	253
Alpha-enolase	ENO1	ENOA_HUMAN	47.2	100.0%	10	12	24	0.02%	32.7%	YISPDQLADLYK	99.7%	78.6	25	69.9	4	0	0	1425.73	270	281
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	14	14	24	0.02%	29.3%	ALEAELAALR	99.7%	67.7	25	51.2	2	0	0	1056.60	121	130
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	14	14	24	0.02%	29.3%	DGLAEEVQR	99.7%	42.2	25	30	1	0	0	1016.50	169	177
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	14	14	24	0.02%	29.3%	DVDGATLAR	99.5%	37.4	25	27.8	2	0	0	917.47	202	210
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	14	14	24	0.02%	29.3%	EYQDLLNVK	99.7%	55.2	25	43.9	6	0	0	1121.58	378	386
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	14	14	24	0.02%	29.3%	FANLNEQAAR	99.7%	74.3	25	32.3	2	0	0	1133.57	291	300
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	14	14	24	0.02%	29.3%	KVESLLDELAFVR	99.7%	42.2	25	39.2	0	1	0	1518.85	216	228
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	14	14	24	0.02%	29.3%	LSGAGGAGGFR	99.7%	58	25	41.7	2	0	0	949.49	29	39
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	14	14	24	0.02%	29.3%	NLQSAEEWYK	99.7%	43.1	25	30.1	1	0	0	1267.60	279	288
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	14	14	24	0.02%	29.3%	QILELEER	99.7%	43.7	25	11.8	2	0	0	1029.56	339	346
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	14	14	24	0.02%	29.3%	RPPASDGLDLSQAAAR	99.7%	34.4	25	24.4	0	1	0	1624.84	68	83
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	14	14	24	0.02%	29.3%	SNIEETTISSQK	99.7%	69.4	25	58	2	0	0	1336.66	487	498
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	14	14	24	0.02%	29.3%	SNIEETTISSQKI	99.7%	55.5	25	55.5	2	0	0	1449.74	487	499
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	14	14	24	0.02%	29.3%	TIEIEGLR	99.7%	41.7	25	31.2	2	0	0	930.53	323	330
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	14	14	24	0.02%	29.3%	TNEKEQLQGLNDR	99.7%	59.2	25	51.7	2	0	0	1544.77	92	104
Alpha-internexin	INA	AINX_HUMAN	55.4	100.0%	14	14	24	0.02%	29.3%	VGELFQR	99.7%	67.7	25	42.3	2	0	0	848.46	139	145
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	8	11	22	0.02%	36.5%	GAEADQIIEYLK	99.7%	73	25	59	4	0	0	1349.69	15	26
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	8	11	22	0.02%	36.5%	IEILAPPNGSVPGDR	99.7%	42.4	25	38.4	2	0	0	1534.82	236	250
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	8	11	22	0.02%	36.5%	IGCIITAR	99.7%	71.2	25	54.1	2	0	0	903.51	159	166
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	8	11	22	0.02%	36.5%	ITFDAFPGEPDKELNPK	99.7%	44.9	25	44.9	2	2	0	1917.96	251	267
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	8	11	22	0.02%	36.5%	IWEQIQPDLHTNDECVATYK	98.8%	28.2	25	28.2	0	1	0	2460.15	270	289
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	8	11	22	0.02%	36.5%	QQSIAGSADSKPIDVSR	99.7%	71.7	25	69.6	2	2	0	1758.90	138	154
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	8	11	22	0.02%	36.5%	QQVSLLK	99.3%	36	25	14.6	1	0	0	815.50	27	33
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	AIMP1_HUMAN	34.4	100.0%	8	11	22	0.02%	36.5%	TVVSGLVNHVPLEQMQNR	99.7%	41.8	25	41.8	0	4	0	2037.05	188	205
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	4	4	9	0.01%	15.9%	FLFSLFGQK	99.1%	35	25	28.4	2	0	0	1086.60	216	224
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	4	4	9	0.01%	15.9%	FSIQTMCPIEGEGNIAR	99.7%	77.8	25	76.7	3	0	0	1938.91	199	215
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	4	4	9	0.01%	15.9%	SCENLAPFNTALK	99.7%	62.5	25	51.3	2	0	0	1464.72	305	317
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	AIMP2_HUMAN	35.3	100.0%	4	4	9	0.01%	15.9%	VLSTVHTHSSVK	99.7%	47.2	25	35.3	2	0	0	1294.71	148	159
Anaphase-promoting complex subunit 1	ANAPC1	APC1_HUMAN	216.5	100.0%	6	6	7	0.01%	4.0%	CLILWDDILPNSK	99.7%	44.3	25	32.5	1	0	0	1586.83	1412	1424
Anaphase-promoting complex subunit 1	ANAPC1	APC1_HUMAN	216.5	100.0%	6	6	7	0.01%	4.0%	DLETLPFGIALPIR	99.7%	46.6	25	44.1	1	0	0	1554.89	943	956
Anaphase-promoting complex subunit 1	ANAPC1	APC1_HUMAN	216.5	100.0%	6	6	7	0.01%	4.0%	FSEQGGTPQNVATSSSLTAHLR	99.7%	39.2	25	39.2	0	1	0	2288.13	285	306
Anaphase-promoting complex subunit 1	ANAPC1	APC1_HUMAN	216.5	100.0%	6	6	7	0.01%	4.0%	LQVEQEENR	98.9%	34.1	25	34.1	1	0	0	1144.56	906	914
Anaphase-promoting complex subunit 1	ANAPC1	APC1_HUMAN	216.5	100.0%	6	6	7	0.01%	4.0%	LVLEFFSSR	99.7%	57.8	25	50	2	0	0	1097.60	1816	1824
Anaphase-promoting complex subunit 1	ANAPC1	APC1_HUMAN	216.5	100.0%	6	6	7	0.01%	4.0%	WVDSNVPQIIR	99.5%	37.5	25	31.4	1	0	0	1326.72	1425	1435
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	18	22	37	0.03%	34.4%	AGQERPSVTSYK	99.7%	53.2	25	41.7	2	0	0	1322.67	182	193
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	18	22	37	0.03%	34.4%	AIQLNSNSVQALLLK	99.7%	106	25	96.7	2	0	0	1611.94	365	379
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	18	22	37	0.03%	34.4%	AISTICSLEK	99.7%	55.9	25	48.1	2	0	0	1121.59	254	263
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	18	22	37	0.03%	34.4%	ALTQRPDYIK	97.9%	31.3	25	16.2	1	0	0	1204.67	468	477
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	18	22	37	0.03%	34.4%	AYAFVHTGDNSR	99.7%	56.7	25	56.7	2	0	0	1337.62	242	253
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	18	22	37	0.03%	34.4%	DMAAAGLHSNVR	99.7%	61	25	56.8	4	0	0	1241.61	43	54
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	18	22	37	0.03%	34.4%	DNVDLLGSLADLYFR	99.7%	75.5	25	75.5	2	0	0	1710.87	269	283
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	18	22	37	0.03%	34.4%	EAMVMANNVYK	99.7%	42.4	25	32.4	1	0	0	1269.60	425	435
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	18	22	37	0.03%	34.4%	EQKYEDGIALLR	99.5%	31.5	25	21.2	1	1	0	1434.76	489	500

Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	18	22	37	0.03%	34.4%	FEQAQMLDPYLIK	99.7%	95.7	25	85.3	2	0	0	1595.81	294	306
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	18	22	37	0.03%	34.4%	GMDVYGYLLAR	99.7%	72.2	25	71.5	4	0	0	1257.63	307	317
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	18	22	37	0.03%	34.4%	LEDVENLGCR	99.7%	69.9	25	64.2	2	0	0	1204.56	321	330
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	18	22	37	0.03%	34.4%	MAECYTMLK	99.7%	46.9	25	46.9	1	0	0	1146.50	142	150
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	18	22	37	0.03%	34.4%	NALANQSDCVLHR	99.7%	68.5	25	63.3	2	0	0	1497.72	501	513
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	18	22	37	0.03%	34.4%	VQEAIIHFR	99.7%	52.6	25	45	2	0	0	1112.62	389	397
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	18	22	37	0.03%	34.4%	VRPSTGNSASTPQSQCLPSEIEVK	99.7%	45.8	25	45.8	0	2	0	2572.27	116	139
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	18	22	37	0.03%	34.4%	YEDGIALLR	99.7%	53	25	42.1	2	0	0	1049.56	492	500
Anaphase-promoting complex subunit 7	ANAPC7	APC7_HUMAN	66.9	100.0%	18	22	37	0.03%	34.4%	YTMALQQK	99.7%	47.5	25	35.2	2	0	0	982.50	100	107
Angio-associated migratory cell protein	AAMP	AAMP_HUMAN	46.7	99.8%	2	2	4	0.00%	5.5%	AVVGYEDGTIR	99.7%	54.3	25	51.3	2	0	0	1179.60	230	240
Angio-associated migratory cell protein	AAMP	AAMP_HUMAN	46.7	99.8%	2	2	4	0.00%	5.5%	DASLVVTTSGDHK	99.7%	58.6	25	48.7	2	0	0	1329.66	411	423
Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	ANFY1_HUMAN	128.4	100.0%	3	3	3	0.00%	2.7%	FQLQLLR	98.7%	33.2	25	11.5	1	0	0	917.56	145	151
Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	ANFY1_HUMAN	128.4	100.0%	3	3	3	0.00%	2.7%	GDLFAATFLIK	99.7%	44.4	25	36.7	1	0	0	1195.67	300	310
Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	ANFY1_HUMAN	128.4	100.0%	3	3	3	0.00%	2.7%	TQDGETALQLAIR	99.7%	69.1	25	59.7	1	0	0	1415.75	652	664
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	18	21	32	0.03%	22.1%	AAMIWIVGEYAER	99.7%	91.6	25	90	2	0	0	1508.76	446	458
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	18	21	32	0.03%	22.1%	CVSTLLDLIQTK	99.7%	82.3	25	60.3	2	0	0	1390.76	391	402
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	18	21	32	0.03%	22.1%	DCEDPNPLIR	99.4%	36.9	25	32.6	1	0	0	1228.56	94	103
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	18	21	32	0.03%	22.1%	DCPLNAEAASSK	99.7%	61.8	25	51.8	1	0	0	1262.57	865	876
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	18	21	32	0.03%	22.1%	DLDYYGTLLK	99.7%	69.1	25	61	2	0	0	1200.61	273	282
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	18	21	32	0.03%	22.1%	EYATEVDVDFVR	99.7%	83.8	25	83.8	1	0	0	1442.68	360	371
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	18	21	32	0.03%	22.1%	GLEISGTFTR	99.7%	68.5	25	63.2	2	0	0	1080.57	731	740
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	18	21	32	0.03%	22.1%	ITEYLCEPLRK	99.7%	44.7	25	35.9	2	0	0	1421.75	118	128
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	18	21	32	0.03%	22.1%	KGEIFELK	99.7%	43.4	25	24.4	2	0	0	963.55	12	19
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	18	21	32	0.03%	22.1%	LAPPLVTLLSAEPELQYVALR	99.7%	46.1	25	46.1	1	1	0	2293.32	284	304
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	18	21	32	0.03%	22.1%	LASQANIAQVLAELK	99.7%	99.3	25	93	2	0	0	1568.90	345	359
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	18	21	32	0.03%	22.1%	LLSTDPVAAK	99.7%	39.3	25	20.6	1	0	0	1014.58	529	538
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	18	21	32	0.03%	22.1%	LQSSNIFTVAK	99.7%	64.9	25	53.5	2	0	0	1207.67	877	887
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	18	21	32	0.03%	22.1%	LSHANSAVVLSAVK	99.7%	63.8	25	63.8	1	2	0	1395.80	248	261
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	18	21	32	0.03%	22.1%	MEPLNNLQVAVK	99.7%	64.9	25	53.6	2	0	0	1355.74	806	817
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	18	21	32	0.03%	22.1%	NINLIVQK	99.7%	41.8	25	37.6	2	0	0	941.58	305	312
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	18	21	32	0.03%	22.1%	VNYVVQEAIVVIK	99.7%	48.9	25	38.2	1	0	0	1473.87	403	415
AP-1 complex subunit beta-1	AP1B1	AP1B1_HUMAN	104.6	100.0%	18	21	32	0.03%	22.1%	YNDPIYVK	99.7%	41.6	25	29.5	2	0	0	1011.51	328	335
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	13	13	23	0.02%	16.1%	AALCAVHVIR	99.7%	76.1	25	75	2	0	0	1109.62	157	166
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	13	13	23	0.02%	16.1%	ADCASGIFLAAEK	99.7%	74.1	25	69.2	2	0	0	1352.65	398	410
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	13	13	23	0.02%	16.1%	AVEYNALFK	99.7%	51.2	25	45.6	2	0	0	1054.56	563	571
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	13	13	23	0.02%	16.1%	ELLYFLDSCEPEFK	99.7%	69.4	25	60.1	2	0	0	1789.84	384	397
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	13	13	23	0.02%	16.1%	FTCTVNR	99.6%	38.2	25	26.7	2	0	0	897.42	537	543
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	13	13	23	0.02%	16.1%	GYALTAIMK	99.1%	35	25	0	1	0	0	983.52	524	532
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	13	13	23	0.02%	16.1%	IEFTFER	99.5%	37.9	25	29.3	1	0	0	941.47	717	723
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	13	13	23	0.02%	16.1%	IGYLGAMLLLDER	99.7%	75.1	25	73.5	1	0	0	1463.79	84	96
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	13	13	23	0.02%	16.1%	SSFREEDNTYR	99.7%	38.5	25	32.5	0	1	0	1403.62	36	46
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	13	13	23	0.02%	16.1%	TVQTDHNAVQR	99.7%	61.2	25	48.7	3	0	0	1268.63	335	345
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	13	13	23	0.02%	16.1%	VLAINILGR	99.7%	65.9	25	54.3	2	0	0	968.63	307	315
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	13	13	23	0.02%	16.1%	VLTTAGSYVR	99.7%	78.2	25	70.7	2	0	0	1066.59	425	434
AP-1 complex subunit gamma-1	AP1G1	AP1G1_HUMAN	91.4	100.0%	13	13	23	0.02%	16.1%	YVALTSLLK	99.7%	45.5	25	45.5	2	0	0	1007.61	326	334
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	7	8	14	0.01%	21.0%	FEIPYFTTSGIQVR	99.7%	83	25	80.6	2	0	0	1657.86	380	393
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	7	8	14	0.01%	21.0%	HNNLYLVATSK	99.7%	68.7	25	59.8	2	0	0	1259.67	62	72
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	7	8	14	0.01%	21.0%	ILQEYITQEGHK	99.7%	74.8	25	55.8	2	0	0	1458.76	130	141
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	7	8	14	0.01%	21.0%	SVELEDVKFHQCVR	98.0%	26.3	25	12	0	1	0	1745.86	230	243
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	7	8	14	0.01%	21.0%	TISFIPPDGEFELMSYR	95.6%	28.5	25	27.2	1	0	0	2017.96	252	268
AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	7	8	14	0.01%	21.0%	VFLSGMPELR	99.7%	61.8	25	58.5	4	0	0	1148.61	202	211

AP-1 complex subunit mu-1	AP1M1	AP1M1_HUMAN	48.6	100.0%	7	8	14	0.01%	21.0%	YITQNGDYQLR	99.7%	40.7	25	40.7	2	0	0	1370.67	411	421
AP-1 complex subunit sigma-1A	AP1S1	AP1S1_HUMAN	18.7	100.0%	4	5	14	0.01%	25.3%	AIEQADLLQEEDESPR	99.7%	106	25	106	4	0	0	1842.87	134	149
AP-1 complex subunit sigma-1A	AP1S1	AP1S1_HUMAN	18.7	100.0%	4	5	14	0.01%	25.3%	ELMQVVLAR	99.7%	70.6	25	59.2	4	0	0	1058.60	34	42
AP-1 complex subunit sigma-1A	AP1S1	AP1S1_HUMAN	18.7	100.0%	4	5	14	0.01%	25.3%	FMLLFSR	98.8%	33.6	25	25.6	1	0	0	913.50	4	10
AP-1 complex subunit sigma-1A	AP1S1	AP1S1_HUMAN	18.7	100.0%	4	5	14	0.01%	25.3%	MCSFLEWR	99.7%	42.1	25	42.1	5	0	0	1128.50	46	53
AP-1 complex subunit sigma-2	AP1S2	AP1S2_HUMAN	18.6	100.0%	3	3	7	0.01%	26.8%	AIEQADLLQEEAETPR	99.7%	92.7	25	90.1	2	0	0	1812.90	133	148
AP-1 complex subunit sigma-2	AP1S2	AP1S2_HUMAN	18.6	100.0%	3	3	7	0.01%	26.8%	ELVQTVLAR	99.7%	64.2	25	43	4	0	0	1028.61	33	41
AP-1 complex subunit sigma-2	AP1S2	AP1S2_HUMAN	18.6	100.0%	3	3	7	0.01%	26.8%	MCSFLEWR	99.7%	42.1	25	42.1	5	0	0	1128.50	45	52
AP-1 complex subunit sigma-2	AP1S2	AP1S2_HUMAN	18.6	100.0%	3	3	7	0.01%	26.8%	MQFMLLFSR	98.0%	31.5	25	26.5	1	0	0	1172.60	1	9
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	27	0.03%	19.1%	ACNQLGQFLQHR	99.7%	44.5	25	32.3	0	2	0	1471.72	330	341
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	27	0.03%	19.1%	ALLLSTYIK	99.7%	56.1	25	56.1	2	0	0	1021.63	539	547
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	27	0.03%	19.1%	EMGEAFAADIPR	99.7%	54.6	25	49.4	2	0	0	1306.61	142	153
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	27	0.03%	19.1%	FFQPTEMAAQDFFQR	99.7%	85.7	25	85.7	3	0	0	1862.85	864	878
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	27	0.03%	19.1%	FINLFPETK	99.7%	44	25	32.8	2	0	0	1108.60	548	556
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	27	0.03%	19.1%	GLAVFISDIR	99.7%	80.9	25	62.1	2	0	0	1090.63	12	21
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	27	0.03%	19.1%	IAGDYVSEEVWYR	99.7%	84.9	25	84.9	2	0	0	1586.75	452	464
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	27	0.03%	19.1%	ILVAGDSMDSVK	99.7%	62.3	25	48.3	2	0	0	1234.63	154	165
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	27	0.03%	19.1%	QSAALCLLR	99.7%	48	25	29.5	2	0	0	1031.57	166	174
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	27	0.03%	19.1%	TCVSLAVSR	99.7%	43	25	24.1	1	0	0	992.52	224	232
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	27	0.03%	19.1%	THIDTVINALK	98.6%	33.1	25	27.5	2	0	0	1224.69	368	378
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	27	0.03%	19.1%	TSVQFQNFSPTVVHPGDLQTQLAVQTK	99.7%	47.3	25	47.3	0	1	0	2970.53	784	810
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	27	0.03%	19.1%	VGGYILGEFGNLIAGDPR	99.7%	90.6	25	87.9	2	0	0	1847.97	499	516
AP-2 complex subunit alpha-1	AP2A1	AP2A1_HUMAN	107.5	100.0%	14	15	27	0.03%	19.1%	YLALESMCTLASSEFSHEAVK	98.5%	27.3	25	27.3	0	2	0	2373.11	347	367
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	10	14	0.01%	23.3%	ACNQLGQFLQHR	99.7%	44.5	25	32.3	0	2	0	1471.72	329	340
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	10	14	0.01%	23.3%	ALLLSTYIK	99.7%	56.1	25	56.1	2	0	0	1021.63	538	546
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	10	14	0.01%	23.3%	EMAEAFAGEIPK	99.7%	65.3	25	54.1	1	0	0	1292.62	142	153
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	10	14	0.01%	23.3%	FFQPTEMASQDFFQR	99.7%	75.7	25	19.8	2	0	0	1878.85	826	840
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	10	14	0.01%	23.3%	FVNLFPEVKPTIQDVLR	97.8%	25.9	25	25.9	0	1	0	2015.13	547	563
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	10	14	0.01%	23.3%	GLAVFISDIR	99.7%	80.9	25	62.1	2	0	0	1090.63	12	21
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	10	14	0.01%	23.3%	IAGDYVSEEVWYR	99.7%	84.9	25	84.9	2	0	0	1586.75	451	463
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	10	14	0.01%	23.3%	NNGVLFENQLLQIGLK	99.7%	60.8	25	60.8	1	0	0	1800.00	713	728
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	10	14	0.01%	23.3%	QSAALCLLR	99.7%	48	25	29.5	2	0	0	1031.57	166	174
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	10	14	0.01%	23.3%	THIETVINALK	99.7%	41.8	25	41.2	1	0	0	1238.71	367	377
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	10	14	0.01%	23.3%	TTQIGCLLR	99.7%	49.5	25	32	2	0	0	1061.58	898	906
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	10	14	0.01%	23.3%	TVFEALQAPACHENLVK	99.7%	48.7	25	48.7	1	0	0	1926.97	481	497
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	10	14	0.01%	23.3%	VGGYILGEFGNLIAGDPR	99.7%	90.6	25	87.9	2	0	0	1847.97	498	515
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	10	14	0.01%	23.3%	VLVAGDTMDSVK	99.7%	42.2	25	22.2	3	0	0	1234.63	154	165
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	10	14	0.01%	23.3%	YGGTFQNVSVQLPITLNK	99.7%	96.6	25	96.6	2	0	0	1979.06	808	825
AP-2 complex subunit alpha-2	AP2A2	AP2A2_HUMAN	104.0	100.0%	9	10	14	0.01%	23.3%	YLALESMCTLASSEFSHEAVK	98.5%	27.3	25	27.3	0	2	0	2373.11	346	366
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	10	11	17	0.02%	25.7%	LNYSDHDVIK	99.7%	47	25	38.1	1	0	0	1203.60	411	420
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	10	11	17	0.02%	25.7%	MCDVMAAYFGK	99.7%	67.6	25	67.6	2	0	0	1292.55	85	95
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	10	11	17	0.02%	25.7%	QNVNAAMVFEFLYK	99.7%	41	25	40.6	1	0	0	1689.83	71	84
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	10	11	17	0.02%	25.7%	SGIYETR	98.8%	33.8	25	26.8	1	0	0	825.41	428	434
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	10	11	17	0.02%	25.7%	SISFIPPDGEFELMR	99.0%	34.3	25	27.4	2	0	0	1737.85	262	276
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	10	11	17	0.02%	25.7%	SNFKPSLLAQK	99.7%	54.7	25	50	2	0	0	1232.70	309	319
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	10	11	17	0.02%	25.7%	SPVTNIAR	99.1%	34.9	25	23.4	2	0	0	857.48	45	52
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	10	11	17	0.02%	25.7%	TFITQQGIK	99.6%	38.6	25	30.2	2	0	0	1035.58	131	139
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	10	11	17	0.02%	25.7%	VNVIHAR	99.0%	34.6	25	28.8	2	0	0	808.48	34	40
AP-2 complex subunit mu	AP2M1	AP2M1_HUMAN	49.7	100.0%	10	11	17	0.02%	25.7%	WARPPISMNFEVPFAPSGLK	98.5%	27.5	25	27.5	0	2	0	2244.16	381	400
AP-2 complex subunit sigma	AP2S1	AP2S1_HUMAN	17.0	100.0%	3	3	6	0.01%	21.1%	FILIQNR	99.3%	35.8	25	6.78	1	0	0	903.54	4	10
AP-2 complex subunit sigma	AP2S1	AP2S1_HUMAN	17.0	100.0%	3	3	6	0.01%	21.1%	HTNFVEFR	99.1%	35.2	25	24.5	3	0	0	1049.52	46	53

AP-2 complex subunit sigma	AP2S1	AP2S1_HUMAN	17.0	100.0%	3	3	6	0.01%	21.1%	VYTVVDEMFLAGEIR	99.7%	51.6	25	36.3	2	0	0	1741.88	110	124
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	11	11	22	0.02%	11.2%	ASILWLIGENCER	99.7%	42.7	25	42.7	2	0	0	1560.78	497	509
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	11	11	22	0.02%	11.2%	EGSTAQLIINTEK	99.7%	67.6	25	62.8	2	0	0	1403.74	1064	1076
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	11	11	22	0.02%	11.2%	LLDSITVPVAR	99.7%	56.2	25	50.5	1	0	0	1183.70	486	496
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	11	11	22	0.02%	11.2%	LLTQYILNLGK	99.7%	73.5	25	68.7	5	0	0	1275.77	553	563
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	11	11	22	0.02%	11.2%	LQILNLGAK	99.7%	57.5	25	41.8	2	0	0	969.61	534	542
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	11	11	22	0.02%	11.2%	LYSLDPEQK	98.0%	31.6	25	25.9	1	0	0	1092.56	177	185
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	11	11	22	0.02%	11.2%	NASELFPAVVK	99.7%	65.4	25	50.7	2	0	0	1174.65	75	85
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	11	11	22	0.02%	11.2%	NVEVIELAK	99.4%	36.5	25	34.7	2	0	0	1014.58	650	658
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	11	11	22	0.02%	11.2%	TVIGSVLLR	99.7%	58.3	25	51.9	2	0	0	957.61	1077	1085
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	11	11	22	0.02%	11.2%	VVNVANVGAVPSGQDNIHR	99.7%	38	25	38	0	1	0	1946.02	1026	1044
AP-3 complex subunit beta-1	AP3B1	AP3B1_HUMAN	121.3	100.0%	11	11	22	0.02%	11.2%	YDQNYDIR	99.7%	59.7	25	49.2	2	0	0	1086.49	564	571
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	7	7	13	0.01%	7.3%	ALDLLYGMVSK	99.7%	51.7	25	51.7	2	0	0	1209.65	360	370
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	7	7	13	0.01%	7.3%	AVFHEEEQR	97.4%	30.5	25	27.3	1	0	0	1144.54	643	651
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	7	7	13	0.01%	7.3%	DVPVAEEVSALFAGELNPVAPK	99.7%	51.4	25	51.4	1	0	0	2252.18	589	610
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	7	7	13	0.01%	7.3%	ILIEDSDQNLK	99.7%	56.3	25	56	2	0	0	1287.68	310	320
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	7	7	13	0.01%	7.3%	LFGALTPLEPR	99.7%	39.8	25	31.6	2	0	0	1213.69	244	254
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	7	7	13	0.01%	7.3%	MSFQNLLAK	99.7%	48.5	25	40.4	2	0	0	1051.56	1079	1087
AP-3 complex subunit delta-1	AP3D1	AP3D1_HUMAN	130.2	100.0%	7	7	13	0.01%	7.3%	NYLSLAPLFFK	99.7%	54.7	25	52.4	3	0	0	1312.73	217	227
AP-3 complex subunit mu-1	AP3M1	AP3M1_HUMAN	46.9	100.0%	2	2	2	0.00%	8.4%	GLVNLQSGAPKPEENPSLNIQFK	99.7%	34	25	34	0	1	0	2480.31	356	378
AP-3 complex subunit mu-1	AP3M1	AP3M1_HUMAN	46.9	100.0%	2	2	2	0.00%	8.4%	LLDDVSFHPCIR	98.4%	27.1	25	23.6	0	1	0	1471.74	227	238
AP-3 complex subunit sigma-1	AP3S1	AP3S1_HUMAN	21.7	100.0%	4	4	9	0.01%	23.3%	FYQPYSEDTQQQIIR	99.7%	75.8	25	65	2	0	0	1915.92	19	33
AP-3 complex subunit sigma-1	AP3S1	AP3S1_HUMAN	21.7	100.0%	4	4	9	0.01%	23.3%	NINIGDISIK	99.7%	44.9	25	31.4	2	0	0	1086.62	176	185
AP-3 complex subunit sigma-1	AP3S1	AP3S1_HUMAN	21.7	100.0%	4	4	9	0.01%	23.3%	NMNLPEIPR	98.7%	33.3	25	23	2	0	0	1099.56	167	175
AP-3 complex subunit sigma-1	AP3S1	AP3S1_HUMAN	21.7	100.0%	4	4	9	0.01%	23.3%	SEAGLAGAPAR	99.7%	69.5	25	60.3	3	0	0	999.52	150	160
AP-3 complex subunit sigma-2	AP3S2	AP3S2_HUMAN	22.0	99.8%	2	2	5	0.00%	10.4%	NINLPEIPR	97.2%	30.2	25	30.2	2	0	0	1065.61	167	175
AP-3 complex subunit sigma-2	AP3S2	AP3S2_HUMAN	22.0	99.8%	2	2	5	0.00%	10.4%	SEGGLSAAPAR	99.6%	38.6	25	23.1	3	0	0	1015.52	150	160
Apolipoprotein O-like	APOOL	APOOL_HUMAN	29.2	99.8%	2	2	3	0.00%	11.2%	HSVPLPTELSSEAK	97.8%	31.1	25	27.8	1	0	0	1494.78	219	232
Apolipoprotein O-like	APOOL	APOOL_HUMAN	29.2	99.8%	2	2	3	0.00%	11.2%	MGVITVSGLAGLVSAR	99.7%	75.9	25	73.2	2	0	0	1530.87	115	130
Apoptosis regulator BAX	BAX	BAX_HUMAN	21.2	99.8%	2	2	3	0.00%	10.4%	KLSECLK	99.1%	34.9	25	6.44	1	0	0	877.48	58	64
Apoptosis regulator BAX	BAX	BAX_HUMAN	21.2	99.8%	2	2	3	0.00%	10.4%	TGALLLQGFIQDR	99.7%	57.8	25	57.8	2	0	0	1431.80	22	34
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	19	22	48	0.04%	38.7%	AALSASEGEEVPQDK	99.7%	64.9	25	59.9	2	0	0	1530.73	113	127
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	19	22	48	0.04%	38.7%	ALGTEVIQLFPEK	99.7%	94	25	87.6	4	0	0	1444.80	325	337
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	19	22	48	0.04%	38.7%	CLIATGGTPR	99.7%	47.4	25	37.9	2	0	0	1045.55	256	265
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	19	22	48	0.04%	38.7%	DGEQHEDLNEVAK	99.7%	71.7	25	64.9	2	1	0	1483.67	594	606
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	19	22	48	0.04%	38.7%	ELWFSDDPNVTK	99.7%	43.4	25	41.1	2	0	0	1450.69	178	189
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	19	22	48	0.04%	38.7%	ILPEYLSNWTMEK	99.7%	76.4	25	69.1	4	0	0	1623.81	343	355
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	19	22	48	0.04%	38.7%	ISGLGLTPEQK	99.7%	50.5	25	44.8	4	0	0	1142.64	99	109
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	19	22	48	0.04%	38.7%	KVVQLDVR	99.7%	41.6	25	25	2	0	0	956.59	232	239
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	19	22	48	0.04%	38.7%	LFNIHED	96.2%	29	25	25.6	2	0	0	887.43	607	613
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	19	22	48	0.04%	38.7%	LNDGSQITYEK	99.7%	74.9	25	68.2	3	0	0	1267.62	245	255
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	19	22	48	0.04%	38.7%	SATEQSGTGIR	99.7%	65.5	25	40.3	2	0	0	1106.54	519	529
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	19	22	48	0.04%	38.7%	SITIIGGGFLGSELACALGR	99.7%	117	25	117	1	0	0	1992.06	302	321
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	19	22	48	0.04%	38.7%	SNIWVAGDAACFYDIK	99.7%	116	25	116	4	0	0	1829.85	431	446
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	19	22	48	0.04%	38.7%	TGGLEIDSDFGGFR	99.7%	78.5	25	78	2	0	0	1470.69	409	422
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	19	22	48	0.04%	38.7%	VETDHIVAAVGLEPNVELAK	99.7%	39.2	25	39.2	0	2	0	2104.13	389	408
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	19	22	48	0.04%	38.7%	VLIVSEDPELPYMRPPLSK	99.7%	59.3	25	58	0	2	0	2183.18	159	177
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	19	22	48	0.04%	38.7%	VMPNAIVQSVGVSSGK	99.7%	102	25	98.8	4	0	0	1572.84	363	378
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	19	22	48	0.04%	38.7%	VNAELQAR	99.7%	52.7	25	29.4	1	0	0	900.49	423	430
Apoptosis-inducing factor 1, mitochondrial	AIFM1	AIFM1_HUMAN	66.9	100.0%	19	22	48	0.04%	38.7%	VVQLDVR	99.7%	49	25	39.3	2	0	0	828.49	233	239
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	9	9	25	0.02%	8.2%	AAPCIYWLPLTDSQIVQK	99.7%	75	25	69.5	3	0	0	2103.09	1220	1237

Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	9	9	25	0.02%	8.2%	GLLVDRPSETK	99.2%	35.8	25	22.1	2	0	0	1214.67	1097	1107
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	9	9	25	0.02%	8.2%	GVPAGNSDTEGGQPGR	99.7%	81.4	25	75.6	4	0	0	1498.69	832	847
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	9	9	25	0.02%	8.2%	KPSISITTESLK	99.7%	53.1	25	50.7	4	0	0	1303.75	861	872
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	9	9	25	0.02%	8.2%	RLSQPESAEK	99.1%	35.1	25	28.1	1	0	0	1144.60	708	717
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	9	9	25	0.02%	8.2%	SGVSITIDDPVR	99.7%	59.4	25	47.1	3	0	0	1258.66	987	998
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	9	9	25	0.02%	8.2%	SQEQEVLER	99.7%	41.8	25	28.7	2	0	0	1117.55	328	336
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	9	9	25	0.02%	8.2%	TGTLVEEAFWIDK	99.7%	71.2	25	60.8	2	0	0	1508.76	1035	1047
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	ACINU_HUMAN	151.9	100.0%	9	9	25	0.02%	8.2%	VTLGDTLTR	99.7%	55.9	25	43.7	4	0	0	975.55	971	979
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	75	0.07%	40.0%	AAYPDLENPPLLVTPSQQAK	99.7%	93.4	25	93.4	4	0	0	2152.13	90	109
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	75	0.07%	40.0%	AYQCVVLLQGK	99.7%	71.4	25	52.8	2	0	0	1278.69	290	300
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	75	0.07%	40.0%	FPEILQK	99.7%	44.1	25	14.2	3	0	0	874.50	581	587
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	75	0.07%	40.0%	GESFYQDR	97.3%	30.3	25	30.3	1	0	0	1001.43	334	341
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	75	0.07%	40.0%	GFDILGIKPVQR	99.7%	46.1	25	39.8	3	2	0	1342.78	648	659
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	75	0.07%	40.0%	GFVQVDDGRK	99.7%	44.5	25	34.5	3	0	0	1120.57	353	362
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	75	0.07%	40.0%	GNTAAYLLYAFTR	99.7%	61	25	57.9	4	0	0	1460.75	528	540
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	75	0.07%	40.0%	IVFVPGCSIPLTIVK	99.7%	72.5	25	60.3	5	0	0	1642.96	363	377
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	75	0.07%	40.0%	LANIDEEMLQK	99.7%	63.2	25	58.6	3	0	0	1303.66	547	557
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	75	0.07%	40.0%	LFEFAGYDVLR	99.7%	75.2	25	64.1	5	0	0	1329.68	224	234
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	75	0.07%	40.0%	LICDVSR	96.2%	29	25	24.7	1	0	0	862.45	310	316
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	75	0.07%	40.0%	LLQQEEEIK	99.7%	42.8	25	27.7	2	0	0	1129.61	12	20
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	75	0.07%	40.0%	LMDLLGEGLKR	99.7%	49	25	43.9	2	1	0	1244.70	462	472
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	75	0.07%	40.0%	LNDYIFSFDK	99.7%	74.6	25	74.6	4	0	0	1261.61	513	522
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	75	0.07%	40.0%	MLLCEAVAAVMAK	99.7%	81.8	25	81.8	6	0	0	1406.72	635	647
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	75	0.07%	40.0%	NMINIISR	99.7%	45.2	25	25.9	4	0	0	960.53	72	79
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	75	0.07%	40.0%	SDGGYTYDTSDLAAIK	99.7%	108	25	97	4	0	0	1676.77	378	393
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	75	0.07%	40.0%	SLTAEIDR	99.7%	41.7	25	27.4	2	0	0	904.47	21	28
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	75	0.07%	40.0%	STIIGESISR	99.7%	68.6	25	58.1	4	0	0	1062.58	214	223
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	75	0.07%	40.0%	VEIAGPGFINVHLR	99.7%	70.3	25	70.3	2	2	0	1521.85	154	167
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	75	0.07%	40.0%	VIVDFSSPNIAK	99.6%	38.2	25	28	1	0	0	1289.71	194	205
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	75	0.07%	40.0%	VLTAEELNAAQTSVAYGCIK	99.7%	92.3	25	88	1	0	0	2138.08	485	504
Arginine--tRNA ligase, cytoplasmic	RARS	SYRC_HUMAN	75.4	100.0%	23	29	75	0.07%	40.0%	YADLSHNR	99.7%	46	25	32.9	4	0	0	975.46	505	512
Argininosuccinate synthase	ASS1	ASSY_HUMAN	46.5	100.0%	4	4	6	0.01%	8.7%	FELSCYSLAPQIK	99.7%	59.7	25	54.7	1	0	0	1555.78	128	140
Argininosuccinate synthase	ASS1	ASSY_HUMAN	46.5	100.0%	4	4	6	0.01%	8.7%	GQVYILGR	99.7%	41.9	25	34.7	2	0	0	905.52	356	363
Argininosuccinate synthase	ASS1	ASSY_HUMAN	46.5	100.0%	4	4	6	0.01%	8.7%	MPEFYNR	97.4%	30.5	25	27.6	1	0	0	956.43	147	153
Argininosuccinate synthase	ASS1	ASSY_HUMAN	46.5	100.0%	4	4	6	0.01%	8.7%	VFIEDVSR	99.7%	50.9	25	37.8	2	0	0	964.51	59	66
Armadillo repeat-containing protein 6	ARMC6	ARMC6_HUMAN	54.1	100.0%	3	3	3	0.00%	7.4%	DQSGVQELVK	97.2%	30.1	25	11.9	1	0	0	1102.57	336	345
Armadillo repeat-containing protein 6	ARMC6	ARMC6_HUMAN	54.1	100.0%	3	3	3	0.00%	7.4%	GAYPIIFTAWK	99.7%	43.6	25	39.5	1	0	0	1266.69	135	145
Armadillo repeat-containing protein 6	ARMC6	ARMC6_HUMAN	54.1	100.0%	3	3	3	0.00%	7.4%	IIVEGGGAVAALQAMK	99.7%	56.2	25	56.2	1	0	0	1527.86	407	422
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	20	37	0.03%	38.3%	ADWLSHYWMPK	99.7%	50.3	25	39.3	2	0	0	1433.67	530	540
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	20	37	0.03%	38.3%	AMTEDGFLAVCSEAK	99.7%	112	25	112	4	0	0	1628.73	148	162
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	20	37	0.03%	38.3%	APSPEKAEEESER	99.7%	74.1	25	74.1	2	0	0	1458.67	380	392
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	20	37	0.03%	38.3%	ASVGMYLISK	97.0%	30	25	23.4	2	0	0	1084.57	341	350
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	20	37	0.03%	38.3%	DVPLHALYDNVEK	99.7%	62.9	25	61.7	2	0	0	1512.77	209	221
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	20	37	0.03%	38.3%	EAFSDGITSVK	99.7%	68.3	25	67.6	2	0	0	1153.57	468	478
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	20	37	0.03%	38.3%	ELYLFDVLR	99.7%	64.3	25	52.7	2	0	0	1167.64	396	404
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	20	37	0.03%	38.3%	ETFEDSNLIPK	99.7%	47.4	25	35.8	2	0	0	1292.64	450	460
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	20	37	0.03%	38.3%	FSSYYLSLPPEMR	99.5%	37.5	25	37.5	2	0	0	1589.77	425	437
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	20	37	0.03%	38.3%	IGCLLSGGLDSSLVAATLLK	99.7%	93.9	25	93.9	1	0	0	1988.11	253	272
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	20	37	0.03%	38.3%	ILFNNAVK	98.6%	32.9	25	5.68	2	0	0	918.54	237	244
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	20	37	0.03%	38.3%	ILQEYVEHQVDDAMMANAAQK	99.7%	70.9	25	70.7	0	2	0	2436.12	484	504
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	20	37	0.03%	38.3%	LAVVDPLFGMQPIR	99.7%	75.2	25	74.7	4	0	0	1555.87	50	63

Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	20	37	0.03%	38.3%	LFPGFEIETVK	99.6%	38.6	25	22.6	1	0	0	1279.69	222	232
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	20	37	0.03%	38.3%	TTAAHGLELR	99.7%	65.9	25	51.8	2	0	0	1068.58	408	417
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	20	37	0.03%	38.3%	VASVEMVK	95.1%	28	25	17.2	2	0	0	862.47	196	203
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	20	37	0.03%	38.3%	VPFLDHR	99.7%	39.5	25	33.5	2	0	0	883.48	418	424
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	ASNS_HUMAN	64.4	100.0%	18	20	37	0.03%	38.3%	WINATDPSAR	99.5%	37.8	25	33.1	1	0	0	1130.56	541	550
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	99.9%	2	2	4	0.00%	6.1%	FVTVQTISGTGALR	99.7%	66.6	25	61	2	0	0	1449.81	126	139
Aspartate aminotransferase, mitochondrial	GOT2	AATM_HUMAN	47.5	99.9%	2	2	4	0.00%	6.1%	IAAAILNTPDLR	99.7%	51.4	25	38.9	2	0	0	1267.74	326	337
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	23	29	52	0.05%	51.3%	ADEVVWVR	99.7%	60	25	50.7	2	0	0	973.51	56	63
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	23	29	52	0.05%	51.3%	ALHHGIDLEK	99.4%	37.1	25	26.8	1	0	0	1132.61	442	451
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	23	29	52	0.05%	51.3%	EIMDAAEDYAK	99.7%	45.2	25	45.2	4	0	0	1255.55	16	26
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	23	29	52	0.05%	51.3%	ESIVDVEGVVR	99.7%	86.2	25	78.7	2	0	0	1201.64	111	121
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	23	29	52	0.05%	51.3%	FGAPPHAGGGIGLER	99.7%	67.7	25	53.5	2	2	0	1435.74	461	475
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	23	29	52	0.05%	51.3%	FLEPTLR	98.8%	33.6	25	19.9	2	0	0	875.50	339	345
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	23	29	52	0.05%	51.3%	FQTEIQTVNK	99.7%	60.2	25	31.1	2	0	0	1207.63	321	330
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	23	29	52	0.05%	51.3%	GFVEIQTPK	99.7%	59.3	25	39.1	2	0	0	1018.56	214	222
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	23	29	52	0.05%	51.3%	IGSCTQQDVELHVQK	99.7%	85.2	25	85.2	2	0	0	1741.85	127	141
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	23	29	52	0.05%	51.3%	IHDPQLLTER	99.7%	34.5	25	26.1	0	2	0	1221.66	432	441
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	23	29	52	0.05%	51.3%	IYVISLAEPR	99.7%	63.2	25	56.4	2	0	0	1160.67	142	151
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	23	29	52	0.05%	51.3%	LEYCEALAMLR	99.7%	66.3	25	63	2	0	0	1368.67	346	356
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	23	29	52	0.05%	51.3%	LPLQLDDAVRPEAEGEEEGR	99.7%	57.2	25	57.2	1	2	0	2223.09	152	171
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	23	29	52	0.05%	51.3%	LQSGICHLFR	99.7%	51.5	25	41.5	2	2	0	1230.64	198	207
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	23	29	52	0.05%	51.3%	NNAYLAQSPQLYK	99.7%	88.7	25	80.5	2	0	0	1509.77	242	254
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	23	29	52	0.05%	51.3%	QCFLVLR	99.7%	51.8	25	17.3	2	0	0	935.51	75	81
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	23	29	52	0.05%	51.3%	QQQFNVQALVAVGDHASK	99.7%	40.7	25	40.7	0	2	0	1940.00	82	99
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	23	29	52	0.05%	51.3%	QSNSYDMFMR	99.7%	57.2	25	56.3	2	0	0	1278.52	412	421
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	23	29	52	0.05%	51.3%	QTSMFPR	95.2%	28.1	25	20.1	1	0	0	882.41	488	494
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	23	29	52	0.05%	51.3%	TSTSQAVFR	99.7%	73.8	25	68.1	2	0	0	996.51	189	197
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	23	29	52	0.05%	51.3%	VFSIGPVFR	99.7%	58	25	56.9	1	0	0	1021.58	265	273
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	23	29	52	0.05%	51.3%	VTMLFLGLHNVR	99.7%	66.3	25	62.6	2	2	0	1399.79	476	487
Aspartate--tRNA ligase, cytoplasmic	DARS	SYDC_HUMAN	57.1	100.0%	23	29	52	0.05%	51.3%	YGISSMIQSQEKPDR	99.7%	49.6	25	48.6	1	1	0	1754.84	29	43
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	8	9	13	0.01%	21.9%	ETTNIFSNCGCVR	99.7%	47.6	25	47.6	1	0	0	1557.68	346	358
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	8	9	13	0.01%	21.9%	ITSDEPLTKDDIPVFLR	99.7%	37.4	25	30.7	0	2	0	1959.04	254	270
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	8	9	13	0.01%	21.9%	LASEEPPDDEEALATIR	99.7%	75.5	25	67.5	1	0	0	1855.89	289	305
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	8	9	13	0.01%	21.9%	LIGNLCYK	99.5%	37.6	25	29.7	1	0	0	980.52	377	384
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	8	9	13	0.01%	21.9%	LSGVMVPAPIQDLEALR	99.7%	53.9	25	49.7	2	0	0	1824.99	11	27
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	8	9	13	0.01%	21.9%	SPELVQAMFPK	99.7%	66.7	25	62.5	1	0	0	1262.65	227	237
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	8	9	13	0.01%	21.9%	VEQESLLTAFR	99.7%	72.3	25	64.8	1	0	0	1292.68	123	133
Ataxin-10	ATXN10	ATX10_HUMAN	53.5	100.0%	8	9	13	0.01%	21.9%	VTLLDLMIAK	99.7%	70.1	25	59.1	4	0	0	1116.67	244	253
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	7	10	17	0.02%	40.2%	HVVQSISTQQEKETIAK	99.7%	33.9	25	33	0	2	0	1926.03	222	238
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	7	10	17	0.02%	40.2%	HYLFDVQR	98.3%	32.2	25	26.4	1	0	0	1077.55	164	171
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	7	10	17	0.02%	40.2%	NNIAMALEVTYR	99.7%	85.6	25	85	1	0	0	1394.71	172	183
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	7	10	17	0.02%	40.2%	QASIQHIQNAIDTEK	99.7%	67.5	25	64.5	2	1	0	1695.87	140	154
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	7	10	17	0.02%	40.2%	TGVTGPYVLGTGLILYALSK	99.7%	77.5	25	77.5	2	1	0	2023.15	71	90
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	7	10	17	0.02%	40.2%	YGLIPEEFFQFLYPK	99.7%	41.9	25	41.9	3	0	0	1890.97	56	70
ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	AT5F1_HUMAN	28.9	100.0%	7	10	17	0.02%	40.2%	YGPFVADFADKLNEQK	99.7%	74.5	25	70.4	2	2	0	1841.91	116	131
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	AVDSLVPIGR	99.7%	87.9	25	85.8	7	0	0	1026.59	195	204
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	EAYPGDVFYLHSR	99.7%	79.8	25	72.9	6	3	0	1553.74	335	347
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	EIVTNFLAGFEA	99.7%	94.1	25	94.1	4	0	0	1310.66	542	553
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	ELIIGDR	99.4%	37.1	25	28.3	4	0	0	815.46	208	214
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	EPMQTGIK	99.7%	45	25	36.2	2	0	0	903.46	187	194
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	EVAAFAQFGSDLDAATQQLLSR	99.7%	134	25	134	3	3	0	2338.17	442	463

ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	FENAFLSHVVSQHQALLGTIR	99.7%	74.9	25	74.9	0	2	0	2367.26	507	527
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	GIRPAINVGLSVSR	99.7%	57.7	25	57.7	4	4	0	1438.85	403	416
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	GMSLNLEPDNVGVVVFGNDK	99.7%	102	25	94.8	4	0	0	2104.04	104	123
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	GYLDKLEPSK	99.7%	40.3	25	35	6	0	0	1149.62	494	503
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	HALIIYDDLSK	99.7%	71.9	25	70.7	4	0	0	1287.69	306	316
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	ILGADTSVDLEETGR	99.7%	139	25	137	11	0	0	1575.79	59	73
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	ISVREPMQTGIK	99.7%	53.4	25	40.9	2	1	0	1358.75	183	194
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	LELAQYR	99.7%	39.7	25	21.2	2	0	0	892.49	435	441
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	LKEIVTNFLAGFEA	99.7%	81.3	25	81.3	12	0	0	1551.84	540	553
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	LYCIYVAIGQK	99.7%	74.9	25	69.8	3	0	0	1327.71	242	252
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	NVQAEEMVEFSSGLK	99.7%	121	25	117	5	0	0	1683.79	89	103
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	QGQYSPMAIEEQVAVIYAGVR	99.7%	104	25	97.1	3	3	0	2309.16	473	493
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	QMSLLLR	99.7%	46.2	25	24.9	4	0	0	860.50	323	329
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	RLTDADAMK	98.3%	32.3	25	18.1	1	0	0	1020.51	262	270
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	RSTVAQLVK	97.9%	31.4	25	14.4	1	0	0	1001.61	253	261
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	STVAQLVK	99.7%	60.2	25	38.5	4	0	0	845.51	254	261
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	TGAIVDVPVGEELLGR	99.7%	88.2	25	85.9	9	0	0	1624.89	134	149
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	TGTAEMSSILEER	99.7%	105	25	93.9	4	0	0	1423.67	46	58
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	TSIAIDTIINQK	99.7%	96.3	25	82.2	10	0	0	1316.74	219	230
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	VLSIGDGIAR	99.7%	70.2	25	55.6	14	0	0	1000.58	74	83
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	VVDALGNAIDGK	99.7%	78.4	25	68.6	2	0	0	1171.63	150	161
ATP synthase subunit alpha, mitochondrial	ATP5A1	ATPA_HUMAN	59.8	100.0%	28	39	156	0.15%	57.3%	VVDALGNAIDGKGPIGSK	99.7%	83.7	25	83.7	5	4	0	1710.94	150	167
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	48	210	0.20%	71.8%	AHGGYSVFAGVGER	99.7%	82.7	25	77.8	4	4	0	1406.68	226	239
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	48	210	0.20%	71.8%	AIAELGIYPAVDPLDSTSR	99.7%	96.9	25	96.6	8	0	0	1988.03	388	406
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	48	210	0.20%	71.8%	DQEGQDVLLFIDNIFR	99.7%	123	25	123	3	0	0	1921.97	295	310
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	48	210	0.20%	71.8%	EGNDLYHEMIESGVINLK	99.7%	74.8	25	65.8	2	2	0	2061.00	242	259
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	48	210	0.20%	71.8%	FLSQPFQVAEVFTGHMGK	99.7%	69.3	25	68.5	4	6	0	2023.01	463	480
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	48	210	0.20%	71.8%	FTQAGSEVSALLGR	99.7%	103	25	90.8	13	0	0	1435.75	311	324
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	48	210	0.20%	71.8%	GFQQILAGEYDHLPEQAFYMVGPIEEAVAK	99.7%	90	25	90	0	4	0	3366.64	490	519
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	48	210	0.20%	71.8%	GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	99.7%	92.7	25	92.7	0	2	0	3714.89	352	387
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	48	210	0.20%	71.8%	IGLFGGAGVGK	99.7%	50.2	25	43.4	9	0	0	975.56	202	212
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	48	210	0.20%	71.8%	IMDPNIVGSEHYDVAR	99.7%	81.8	25	81.2	9	7	0	1831.86	407	422
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	48	210	0.20%	71.8%	IMNVIGEPIDER	99.7%	70	25	60.2	12	0	0	1385.71	144	155
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	48	210	0.20%	71.8%	IMNVIGEPIDERGPIK	99.7%	68.8	25	68.8	4	2	0	1780.96	144	159
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	48	210	0.20%	71.8%	IPSAVGYQPTLATDMGTMQER	99.7%	104	25	28.6	11	1	0	2282.08	325	345
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	48	210	0.20%	71.8%	IPVGPETLGR	99.7%	57.7	25	52.1	5	0	0	1038.59	134	143
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	48	210	0.20%	71.8%	KGSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	99.7%	102	25	102	0	2	0	3842.98	351	387
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	48	210	0.20%	71.8%	LVLEVAQHLGESTVR	99.7%	101	25	101	8	4	0	1650.92	95	109
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	48	210	0.20%	71.8%	QFAPIHAEAPEFMEMSVEQEILVTGIK	99.7%	50.9	25	38.1	0	3	0	3044.51	162	188
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	48	210	0.20%	71.8%	SLQDIIAILGMDELSEEDKLTVSR	99.7%	72.6	25	72.6	0	2	0	2675.38	433	456
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	48	210	0.20%	71.8%	TIAMDGTEGLVR	99.7%	82.2	25	69.1	15	0	0	1262.64	110	121
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	48	210	0.20%	71.8%	TREGNDLYHEMIESGVINLK	99.7%	53.1	25	47	0	3	0	2318.14	240	259
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	48	210	0.20%	71.8%	TVLIMELINNVAK	99.7%	92.1	25	79.7	19	0	0	1457.84	213	225
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	48	210	0.20%	71.8%	VALTGLTVAEYFR	99.7%	111	25	99.4	6	0	0	1439.79	282	294
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	48	210	0.20%	71.8%	VALVYGQMNEPPGAR	99.7%	106	25	88.7	16	0	0	1601.81	265	279
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	48	210	0.20%	71.8%	VLDSGAPIK	99.7%	61.4	25	45.7	6	0	0	899.52	125	133
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	48	210	0.20%	71.8%	VLDSGAPIKIPVGPETLGR	99.7%	75.8	25	75.8	4	6	0	1919.10	125	143
ATP synthase subunit beta, mitochondrial	ATP5B	ATPB_HUMAN	56.6	100.0%	26	48	210	0.20%	71.8%	VVDLLAPYAK	99.7%	51.1	25	50.2	4	0	0	1088.64	189	198
ATP synthase subunit d, mitochondrial	ATP5H	ATP5H_HUMAN	18.5	100.0%	2	2	4	0.00%	11.8%	SCAEWVSLSK	99.7%	47	25	47	2	0	0	1166.55	100	109
ATP synthase subunit d, mitochondrial	ATP5H	ATP5H_HUMAN	18.5	100.0%	2	2	4	0.00%	11.8%	SWNETLTSR	99.7%	43.9	25	33.1	2	0	0	1093.53	33	41
ATP synthase subunit e, mitochondrial	ATP5I	ATP5I_HUMAN	7.9	99.8%	2	2	3	0.00%	24.6%	ELAEDDSILK	99.1%	34.8	25	26	1	0	0	1132.57	60	69

ATP synthase subunit e, mitochondrial	ATP5I	ATP5I_HUMAN	7.9	99.8%	2	2	3	0.00%	24.6%	YNYLKPR	99.7%	46.2	25	40.1	2	0	0	953.52	30	36
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	25	0.02%	47.6%	IVNSAQTGSFK	99.7%	82.2	25	64.6	6	0	0	1151.61	56	66
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	25	0.02%	47.6%	KIVNSAQTGSFK	99.7%	66.8	25	64.4	4	0	0	1279.70	55	66
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	25	0.02%	47.6%	LATFWYYAK	99.3%	36.1	25	35	1	0	0	1162.59	27	35
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	25	0.02%	47.6%	TPALVNAAVTYSKPR	99.7%	95	25	94.3	4	4	0	1587.89	12	26
ATP synthase subunit g, mitochondrial	ATP5L	ATP5L_HUMAN	11.4	100.0%	5	6	25	0.02%	47.6%	VELVPPTPAEIPR	99.7%	67.6	25	58.2	6	0	0	1417.81	36	48
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	15	34	0.03%	32.2%	ELIEIISGAAALD	99.7%	85.3	25	82.8	3	0	0	1314.72	286	298
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	15	34	0.03%	32.2%	EVMLVGIGDK	99.7%	50.5	25	49.4	4	0	0	1076.57	127	136
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	15	34	0.03%	32.2%	EVMLVGIGDKIR	99.7%	80.2	25	59.8	4	0	0	1329.76	127	138
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	15	34	0.03%	32.2%	GLCGAIHSSIAK	99.7%	67	25	58.9	2	0	0	1213.64	101	112
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	15	34	0.03%	32.2%	HLLIGVSSDR	99.7%	61.2	25	43.5	2	0	0	1096.61	91	100
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	15	34	0.03%	32.2%	IYGLGSLALYEK	99.7%	89.6	25	83.5	4	0	0	1326.73	68	79
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	15	34	0.03%	32.2%	NASEMIDKLTLTFNR	99.7%	91.7	25	87.9	4	4	0	1752.90	263	277
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	15	34	0.03%	32.2%	SEVATLTAAGK	99.7%	77.5	25	59.5	2	0	0	1047.57	116	126
ATP synthase subunit gamma, mitochondrial	ATP5C1	ATPG_HUMAN	33.0	100.0%	9	15	34	0.03%	32.2%	THSDQFLVAFK	99.7%	72.3	25	62.9	3	2	0	1292.66	144	154
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	7	8	26	0.02%	35.7%	LVRPPVQVYGIEGR	99.7%	46.2	25	46.2	0	4	0	1582.91	27	40
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	7	8	26	0.02%	35.7%	QNKLEQVEK	97.7%	30.9	25	14.1	1	0	0	1115.61	52	60
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	7	8	26	0.02%	35.7%	SFLSQGQVLK	99.7%	59.8	25	50.9	3	0	0	1106.62	163	172
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	7	8	26	0.02%	35.7%	TDPSILGGMIVR	99.7%	60.9	25	53.6	6	0	0	1274.68	177	188
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	7	8	26	0.02%	35.7%	VAASVLNPYVK	99.7%	63.8	25	59.8	4	0	0	1160.67	74	84
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	7	8	26	0.02%	35.7%	VAQILKEPK	99.5%	37.4	25	23.9	4	0	0	1025.64	65	73
ATP synthase subunit O, mitochondrial	ATP5O	ATPO_HUMAN	23.3	100.0%	7	8	26	0.02%	35.7%	YATALYSAASK	99.7%	92.4	25	82.4	4	0	0	1145.58	41	51
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	25	29	62	0.06%	41.8%	AEGPGRGDEPSPS	99.7%	48.8	25	48.8	3	0	0	1255.56	622	634
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	25	29	62	0.06%	41.8%	AERENADIIR	98.5%	32.7	25	12.3	1	0	0	1186.62	247	256
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	25	29	62	0.06%	41.8%	ATLNAFLYR	99.7%	71.1	25	61.6	2	0	0	1068.58	479	487
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	25	29	62	0.06%	41.8%	DALNLAQMQEQTLQLEQQSK	99.7%	120	25	119	2	1	0	2316.15	73	92
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	25	29	62	0.06%	41.8%	DKWSNFDPTGLER	99.2%	29.8	25	28.9	1	2	0	1564.74	45	57
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	25	29	62	0.06%	41.8%	GEGAGPPPPLPPAQPGAEGGGDR	99.7%	102	25	96.5	2	0	0	2081.01	13	35
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	25	29	62	0.06%	41.8%	GLGDRPAPK	99.7%	46.1	25	38.9	4	0	0	910.51	36	44
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	25	29	62	0.06%	41.8%	GLLLFVDEADAFLR	99.7%	100	25	96.1	3	0	0	1578.85	453	466
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	25	29	62	0.06%	41.8%	INEMVHFDLPGQEER	99.7%	47.9	25	47.9	0	1	0	1813.85	515	529
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	25	29	62	0.06%	41.8%	INEMVHFDLPGQEERER	99.7%	41.4	25	41.4	0	3	0	2114.99	515	531
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	25	29	62	0.06%	41.8%	ITVLEALR	99.7%	54.6	25	37.4	4	0	0	914.57	339	346
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	25	29	62	0.06%	41.8%	LAQFDYGR	99.7%	48.4	25	23.9	3	0	0	969.48	554	561
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	25	29	62	0.06%	41.8%	LAQFDYGRK	99.7%	43.4	25	43.4	2	0	0	1097.57	554	562
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	25	29	62	0.06%	41.8%	LFDWANTSR	99.7%	61.9	25	49.1	2	0	0	1109.54	443	451
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	25	29	62	0.06%	41.8%	LGKPSLVR	99.7%	41.2	25	26.1	2	0	0	869.56	327	334
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	25	29	62	0.06%	41.8%	LLSRPQDALEGVVLSPSLEAR	99.7%	60.8	25	60.1	0	2	0	2250.25	355	375
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	25	29	62	0.06%	41.8%	LTEGMSGR	99.7%	50.5	25	46	2	0	0	850.41	569	576
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	25	29	62	0.06%	41.8%	MYFDKYVLKPATEGK	95.2%	23.1	25	23.1	0	1	0	1789.92	535	549
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	25	29	62	0.06%	41.8%	NILMYGPPGTGK	99.7%	68.9	25	58.3	4	0	0	1263.64	395	406
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	25	29	62	0.06%	41.8%	QQQLLNEENLR	99.7%	61.4	25	50.3	4	0	0	1384.72	195	205
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	25	29	62	0.06%	41.8%	QRYEDQLK	99.1%	35.2	25	22.6	1	0	0	1079.55	187	194
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	25	29	62	0.06%	41.8%	QTVLESIR	99.7%	42	25	23	3	0	0	945.54	268	275
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	25	29	62	0.06%	41.8%	TAGTLFGEGFR	99.7%	72.6	25	68.4	4	0	0	1155.58	276	286
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	25	29	62	0.06%	41.8%	VRDIAIATR	99.5%	37.2	25	33.2	2	0	0	1014.61	376	384
ATPase family AAA domain-containing protein 3A	ATAD3A	ATD3A_HUMAN	71.4	100.0%	25	29	62	0.06%	41.8%	YVLKPATEGK	95.6%	28.4	25	18.1	1	0	0	1105.63	540	549
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	6	12	0.01%	34.4%	AERENADIIR	98.5%	32.7	25	12.3	1	0	0	1186.62	199	208
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	6	12	0.01%	34.4%	DKWSNFDPTGLER	99.2%	29.8	25	28.9	1	2	0	1564.74	45	57
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	6	12	0.01%	34.4%	EALNLAQMQEQTLQLEQQSK	99.7%	113	25	109	2	0	0	2330.17	73	92
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	6	12	0.01%	34.4%	EYEAAVEQLK	99.0%	34.5	25	15.8	1	0	0	1179.59	95	104

ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	6	12	0.01%	34.4%	GEGAGPPPPLPPAQPGAEGGGDR	99.7%	102	25	96.5	2	0	0	2081.01	13	35
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	6	12	0.01%	34.4%	GLGDRPAPK	99.7%	46.1	25	38.9	4	0	0	910.51	36	44
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	6	12	0.01%	34.4%	GLLLFMDEADAFLR	99.7%	81	25	76.2	2	0	0	1610.82	405	418
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	6	12	0.01%	34.4%	HILLYGPPGTGK	99.7%	46.4	25	35.6	2	0	0	1252.71	347	358
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	6	12	0.01%	34.4%	ITVLEALR	99.7%	54.6	25	37.4	4	0	0	914.57	291	298
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	6	12	0.01%	34.4%	LAQFDYGR	99.7%	48.4	25	23.9	3	0	0	969.48	506	513
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	6	12	0.01%	34.4%	LAQFDYGRK	99.7%	43.4	25	43.4	2	0	0	1097.57	506	514
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	6	12	0.01%	34.4%	LFDWANTSR	99.7%	61.9	25	49.1	2	0	0	1109.54	395	403
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	6	12	0.01%	34.4%	LGKPSLVR	99.7%	41.2	25	26.1	2	0	0	869.56	279	286
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	6	12	0.01%	34.4%	LKEYEAAVEQLK	99.7%	72.9	25	71.2	4	0	0	1420.77	93	104
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	6	12	0.01%	34.4%	LLSRPQDVLEGVVLSPSLEAR	95.5%	23.2	25	23.2	0	1	0	2278.28	307	327
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	6	12	0.01%	34.4%	LTEGMSGR	99.7%	50.5	25	46	2	0	0	850.41	521	528
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	6	12	0.01%	34.4%	QQQLLNEENLR	99.7%	61.4	25	50.3	4	0	0	1384.72	147	157
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	6	12	0.01%	34.4%	QRYEDQLK	99.1%	35.2	25	22.6	1	0	0	1079.55	139	146
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	6	12	0.01%	34.4%	QTVLESIR	99.7%	42	25	23	3	0	0	945.54	220	227
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	6	12	0.01%	34.4%	TAGTLFGEGFR	99.7%	72.6	25	68.4	4	0	0	1155.58	228	238
ATPase family AAA domain-containing protein 3B	ATAD3B	ATD3B_HUMAN	72.6	100.0%	6	6	12	0.01%	34.4%	VRDIAIATR	99.5%	37.2	25	33.2	2	0	0	1014.61	328	336
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	6	6	9	0.01%	8.3%	LSSDTALLGR	99.7%	39.7	25	34.5	1	0	0	1032.57	275	284
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	6	6	9	0.01%	8.3%	SFQGALEFK	97.2%	30.2	25	22	1	0	0	1026.53	487	495
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	6	6	9	0.01%	8.3%	STVLSLLLR	99.7%	80.1	25	49.1	2	0	0	1001.64	534	542
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	6	6	9	0.01%	8.3%	TSLFSSILR	99.7%	62	25	41.6	2	0	0	1023.58	249	257
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	6	6	9	0.01%	8.3%	TVLVIAHR	99.7%	42.1	25	36.6	2	0	0	908.57	684	691
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	ABCBA_HUMAN	79.2	100.0%	6	6	9	0.01%	8.3%	VTQDSLAQATQLAEER	99.7%	103	25	92.5	1	0	0	1759.88	342	357
ATP-binding cassette sub-family B member 7, mitochondrial	ABCB7	ABCB7_HUMAN	82.6	100.0%	4	4	6	0.01%	6.3%	AGAAFFNEVR	99.7%	46.2	25	34.7	2	0	0	1081.54	201	210
ATP-binding cassette sub-family B member 7, mitochondrial	ABCB7	ABCB7_HUMAN	82.6	100.0%	4	4	6	0.01%	6.3%	AMNIVVPFMFK	99.7%	50.4	25	42.8	1	0	0	1296.68	152	162
ATP-binding cassette sub-family B member 7, mitochondrial	ABCB7	ABCB7_HUMAN	82.6	100.0%	4	4	6	0.01%	6.3%	QALIDMNTLFTLLK	99.3%	36.1	25	36.1	1	0	0	1620.90	436	449
ATP-binding cassette sub-family B member 7, mitochondrial	ABCB7	ABCB7_HUMAN	82.6	100.0%	4	4	6	0.01%	6.3%	VAISLGFLGGAK	99.7%	81.2	25	66.8	2	0	0	1132.67	140	151
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	7	7	13	0.01%	13.5%	AVVDKVFFSR	99.7%	49.9	25	49.9	1	0	0	1167.65	57	66
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	7	7	13	0.01%	13.5%	DQVIYPDGREDQK	99.7%	75	25	61.5	2	0	0	1562.74	521	533
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	7	7	13	0.01%	13.5%	EYLDNVQLGHILER	99.7%	59.6	25	55.4	2	0	0	1698.88	544	557
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	7	7	13	0.01%	13.5%	FSMGFIDSIIAK	99.7%	68.1	25	60.6	1	0	0	1344.69	311	322
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	7	7	13	0.01%	13.5%	IANPDQLLTQDVEK	99.7%	96.1	25	92.1	2	0	0	1583.83	182	195
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	7	7	13	0.01%	13.5%	VLGELWPLFGGR	99.7%	70.6	25	61.5	4	0	0	1343.75	485	496
ATP-binding cassette sub-family D member 3	ABCD3	ABCD3_HUMAN	75.5	100.0%	7	7	13	0.01%	13.5%	YLYEEYLQAFTYYK	99.7%	76.4	25	76.4	1	0	0	1893.89	161	174
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	6	10	0.01%	13.4%	ADIFMFDEPSSYLDVK	99.7%	65.6	25	65.3	2	0	0	1876.87	235	250
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	6	10	0.01%	13.4%	AIIKPQYVDQIPK	97.6%	25.6	25	21	0	1	0	1512.88	166	178
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	6	10	0.01%	13.4%	CPFGALSIVNLPSNLEK	99.7%	52.2	25	52.2	1	0	0	1858.97	65	81
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	6	10	0.01%	13.4%	GSELQNYFTK	99.7%	51.5	25	43.4	1	0	0	1186.57	149	158
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	6	10	0.01%	13.4%	NVEDLSGGELQR	99.7%	53.7	25	45.8	2	0	0	1316.64	213	224
ATP-binding cassette sub-family E member 1	ABCE1	ABCE1_HUMAN	67.3	100.0%	6	6	10	0.01%	13.4%	VAETANEEEVKK	99.7%	62.5	25	56.7	3	0	0	1346.68	333	344
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	7	7	17	0.02%	9.0%	ADDPYAHLSK	99.5%	37.8	25	30.1	1	0	0	1116.53	246	255
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	7	7	17	0.02%	9.0%	AVSEEQQPALK	99.7%	64.6	25	55	3	0	0	1199.63	164	174
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	7	7	17	0.02%	9.0%	GAVIVVSHDAR	99.7%	58.5	25	46.1	2	0	0	1123.62	790	800
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	7	7	17	0.02%	9.0%	GFNLPYQDAR	99.7%	45.2	25	30.8	4	0	0	1180.57	714	723
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	7	7	17	0.02%	9.0%	LQGQLEQGDDTAAER	99.7%	95.8	25	91.8	2	0	0	1630.77	397	411
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	7	7	17	0.02%	9.0%	STLLLLLTGK	99.7%	54.8	25	54.8	2	0	0	1058.68	665	674
ATP-binding cassette sub-family F member 1	ABCF1	ABCF1_HUMAN	95.9	100.0%	7	7	17	0.02%	9.0%	VVFAELACR	99.7%	52.8	25	46.5	3	0	0	1064.56	751	759
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	11	13	23	0.02%	21.0%	ETTEVDLLTK	99.4%	37	25	27	1	0	0	1148.60	49	58
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	11	13	23	0.02%	21.0%	EVPIPEHIDIYHLTR	99.3%	30.3	25	26.2	0	2	0	1831.97	135	149
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	11	13	23	0.02%	21.0%	ILHGLGFTPAMQR	97.8%	25.9	25	23.5	0	2	0	1440.78	211	223
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	11	13	23	0.02%	21.0%	IPPPVIMVQNVSFK	99.7%	76.5	25	76.5	2	2	0	1568.89	391	404

ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	11	13	23	0.02%	21.0%	LEELDADKAEMR	99.7%	56.3	25	52.8	1	0	0	1435.67	196	207
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	11	13	23	0.02%	21.0%	LIQQVAQEIWVCEK	99.7%	76.2	25	66.2	2	0	0	1743.91	575	588
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	11	13	23	0.02%	21.0%	LLTGELLPTDGMIR	99.7%	92	25	89.5	4	0	0	1528.84	442	455
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	11	13	23	0.02%	21.0%	LVDEEPQLTK	99.7%	45.2	25	27.4	2	0	0	1171.62	609	618
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	11	13	23	0.02%	21.0%	MMASGLTER	99.6%	38.9	25	28	1	0	0	1027.45	366	374
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	11	13	23	0.02%	21.0%	SMLLSAIGK	99.7%	43.3	25	26.8	2	0	0	935.52	125	133
ATP-binding cassette sub-family F member 2	ABCF2	ABCF2_HUMAN	71.3	100.0%	11	13	23	0.02%	21.0%	YYTGNYDQYVK	99.7%	70.7	25	63.5	2	0	0	1413.63	305	315
ATP-binding cassette sub-family F member 3	ABCF3	ABCF3_HUMAN	79.7	100.0%	4	4	5	0.00%	6.2%	ASVILAGLGFTPK	99.6%	39.2	25	39.2	1	0	0	1273.75	307	319
ATP-binding cassette sub-family F member 3	ABCF3	ABCF3_HUMAN	79.7	100.0%	4	4	5	0.00%	6.2%	GGVILVSHDER	99.7%	47	25	42.9	1	0	0	1181.63	658	668
ATP-binding cassette sub-family F member 3	ABCF3	ABCF3_HUMAN	79.7	100.0%	4	4	5	0.00%	6.2%	LLLGDLAPVR	99.7%	46	25	29.5	2	0	0	1066.66	537	546
ATP-binding cassette sub-family F member 3	ABCF3	ABCF3_HUMAN	79.7	100.0%	4	4	5	0.00%	6.2%	LSVSADLESR	99.7%	45	25	29.8	1	0	0	1076.56	511	520
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	AFDSGIIPMEFVNK	99.7%	97.2	25	89.8	8	0	0	1583.78	949	962
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	AIVWGMQTR	99.7%	46	25	36.8	3	0	0	1061.56	499	507
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	AKPAMPQDSVPSPR	99.7%	49.5	25	49.5	3	0	0	1480.76	470	483
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	AVQGMLDFDYVCSR	99.7%	104	25	104	4	0	0	1660.75	508	521
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	DEPSVAAMVYPFTGDHK	99.7%	74.3	25	74.3	4	0	0	1879.85	522	538
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	DGVYVLDLAAK	99.7%	71.4	25	64.7	7	0	0	1163.63	210	220
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	DLVSSLTSGLLTIGDR	99.7%	114	25	112	7	0	0	1646.90	919	934
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	DYQGPLKEHEVTIFVR	98.0%	26.2	25	26.2	0	1	0	1931.00	363	378
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	EAYPEEAYIADLDAK	99.7%	88.3	25	87.1	3	0	0	1697.79	245	259
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	FGGALDAAAK	99.7%	74.3	25	56.5	2	0	0	920.48	935	944
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	FICTTSAIQNR	99.7%	58.3	25	53.8	3	0	0	1310.65	18	28
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	GQELIYAGMPITEVFK	99.7%	66	25	66	2	0	0	1811.93	849	864
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	GVTIIGPATVGGIKPGCFK	99.7%	53.6	25	50.4	2	0	0	1872.04	617	635
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	IGNTGGMLDNILASK	99.7%	93.7	25	85.2	9	0	0	1503.78	636	650
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	KPASFMTSICDER	99.7%	64.4	25	54.1	1	2	0	1541.71	836	848
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	LGLVGVNLTLDGVK	99.7%	83.6	25	80.9	4	0	0	1397.84	69	82
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	LGQEATVGK	99.7%	66.9	25	49.3	4	0	0	902.49	89	97
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	LLVGVDEK	99.7%	50.2	25	28.5	2	0	0	872.51	152	159
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	LNPEDIKK	97.0%	29.9	25	6.36	1	0	0	956.54	160	167
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	LYRPGSVAYVSR	99.7%	53.2	25	48.9	3	4	0	1367.74	651	662
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	MIVVLGEIGGTEEYK	99.7%	112	25	109	4	0	0	1637.85	712	726
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	RGGPNYQEGLR	99.7%	43	25	33.7	2	0	0	1246.63	379	389
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	SAYDSTMETMNYAQIR	99.7%	111	25	111	6	0	0	1880.82	577	592
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	SGGMSNELNNIISR	99.7%	84.2	25	72.2	5	0	0	1491.72	663	676
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	SINNPDMR	99.2%	35.3	25	21.4	3	0	0	962.44	979	986
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	SMGFIGHYLDQK	99.7%	47.8	25	41.5	3	0	0	1395.67	1066	1077
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	STTLFSR	98.5%	32.7	25	21.4	1	0	0	811.43	489	495
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	TIAIIAEGIPEALTR	99.7%	109	25	98.6	9	1	0	1567.91	593	607
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	TILSLMTR	99.7%	49.3	25	35.7	4	0	0	934.54	322	329
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	TTDGVYEGVAIGGDR	99.7%	110	25	97.1	2	0	0	1509.72	677	691
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	VDATADYICK	99.7%	58.1	25	58.1	3	0	0	1155.54	221	230
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	VTPDTDWAR	99.5%	37.5	25	33.8	1	0	0	1060.51	34	42
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	WGDIEFPPPFGR	99.7%	50	25	50	2	0	0	1417.69	233	244
ATP-citrate synthase	ACLY	ACLY_HUMAN	120.8	100.0%	34	47	126	0.12%	38.2%	YQDTPGVK	97.6%	30.9	25	21	1	0	0	907.45	704	711
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	9	10	17	0.02%	17.2%	AAAAADLANR	99.7%	87.4	25	77.1	2	0	0	943.50	453	462
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	9	10	17	0.02%	17.2%	DLIEFGMIPEFVGR	99.7%	54.8	25	47.4	3	0	0	1638.82	486	499
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	9	10	17	0.02%	17.2%	DVGGEGVQQGLLK	99.7%	88	25	79.7	2	0	0	1299.69	374	386
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	9	10	17	0.02%	17.2%	LLEGTIVNVPEK	99.7%	58.7	25	58.7	1	0	0	1311.75	387	398
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	9	10	17	0.02%	17.2%	LLQDANYNVEK	99.7%	73.4	25	60.2	2	0	0	1306.66	339	349
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	9	10	17	0.02%	17.2%	SGESNTHQDIEEKDR	99.7%	49.5	25	49.5	0	2	0	1744.77	463	477

ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	9	10	17	0.02%	17.2%	SNILLLGPTGSGK	99.7%	94	25	92.3	1	0	0	1256.72	287	299
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	9	10	17	0.02%	17.2%	TLLAQTLAK	99.7%	45.8	25	35.8	2	0	0	958.59	300	308
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	CLPX_HUMAN	69.2	100.0%	9	10	17	0.02%	17.2%	YLGFGTPSNLGK	99.7%	55.2	25	46.7	2	0	0	1253.65	438	449
ATP-dependent DNA helicase Q1	RECQL	RECQ1_HUMAN	73.5	99.8%	2	2	3	0.00%	3.9%	ISSMVVMENVGQQK	99.7%	67.6	25	60.2	1	0	0	1549.77	426	439
ATP-dependent DNA helicase Q1	RECQL	RECQ1_HUMAN	73.5	99.8%	2	2	3	0.00%	3.9%	VAGVVAPTLPR	99.7%	45.8	25	45.8	2	0	0	1079.66	529	539
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	AAECNIVVTQPR	99.7%	71.9	25	63.1	7	0	0	1357.69	435	446
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	AAMEALVVEVTK	99.7%	87.1	25	81.2	15	0	0	1276.68	1105	1116
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	AENNSEVGASGYGVPGPTWDR	99.7%	96.8	25	96.8	5	0	0	2162.97	121	141
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	AIEPPPLDAVIEAEHTLR	99.7%	53.4	25	53.4	3	2	0	1971.05	820	837
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	DFVNYLVR	99.7%	56.4	25	43.4	9	0	0	1025.54	64	71
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	DINTDFLLVVLR	99.7%	96.3	25	87.6	8	0	0	1417.81	517	528
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	DVVQAYPEVR	99.7%	67.4	25	56.3	8	0	0	1175.61	529	538
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	ELDALDANDELTPLGR	99.7%	124	25	114	8	0	0	1741.86	838	853
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	ETPFELIEALLK	99.7%	49.1	25	46.1	1	0	0	1402.78	631	642
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	GANLKDYYSR	99.7%	65.5	25	58.9	5	0	0	1186.59	142	151
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	GISHVIVDEIHER	99.7%	55.1	25	55.1	0	8	0	1503.79	504	516
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	GMTLVTPLQLLLFASK	99.7%	94.5	25	94.5	20	0	0	1748.00	1058	1073
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	ISAVSVAER	99.7%	77.8	25	60.3	5	0	0	931.52	448	456
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	KEGETVEPYK	97.9%	31.3	25	21.2	1	0	0	1179.59	266	275
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	KMTPSYEIR	99.7%	44.6	25	32.4	4	0	0	1124.58	16	24
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	KVFDPVPVGVTK	99.7%	61.3	25	58.9	5	0	0	1285.75	697	708
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	LAAQSCALSLVR	99.7%	79.2	25	72.5	8	0	0	1288.70	237	248
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	LAQFEPSQR	99.7%	55.6	25	45.9	7	0	0	1075.55	315	323
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	LETHMTPEMFR	99.7%	33.8	25	30.9	6	3	0	1391.64	785	795
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	LFTAHNNMTNYATVWASK	99.7%	39	25	37.8	0	2	0	2084.99	738	755
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	LGGIGQFLAK	99.7%	78.9	25	73.8	11	0	0	1003.59	810	819
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	LNMATLR	99.7%	56.5	25	39.1	5	0	0	818.46	945	951
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	LNQYFQK	99.7%	47.8	25	38.2	8	0	0	940.49	185	191
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	LQISHEAAACITGLR	99.7%	82.9	25	82.9	2	5	0	1639.86	1090	1104
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	LSMSQLNEK	99.7%	62.6	25	54.3	8	0	0	1049.53	622	630
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	MGGEEAEIR	99.7%	82.8	25	60	15	0	0	991.45	930	938
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	MTPSYEIR	99.7%	40.4	25	36.4	3	0	0	996.48	17	24
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	NFLYAWCGK	99.7%	43.5	25	16.8	4	0	0	1158.54	6	14
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	QPAIISQLDPVNER	99.7%	84.7	25	83.8	6	0	0	1579.84	1117	1130
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	RISAVSVAER	99.7%	51.1	25	40	8	0	0	1087.62	447	456
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	RLNMATLR	99.6%	38.9	25	20.1	1	0	0	974.56	944	951
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	SFIAEMTIYIK	99.7%	78.8	25	70.5	2	0	0	1331.69	210	220
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	SSVNCPFSSQDMK	99.7%	61.1	25	61.1	5	0	0	1502.63	1025	1037
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	TPLHEIALSIK	99.7%	69.3	25	65.1	4	7	0	1221.72	796	806
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	TTQVPQFILDDFIQNDR	99.7%	80.1	25	67.7	8	0	0	2050.02	418	434
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	VFDPVPVGVTK	99.7%	54.2	25	53.6	8	0	0	1157.66	698	708
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	VQSDGQIVLVDDWIK	99.7%	94.2	25	83.5	3	0	0	1714.90	1075	1089
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	VRPGFCFHLCSR	99.7%	69.2	25	69.2	0	2	0	1535.74	768	779
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	YGDGPRPPK	99.7%	43.1	25	42.4	8	0	0	986.51	1155	1163
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	YPSPFFVFGEK	99.7%	47.7	25	43.2	11	0	0	1317.65	1038	1048
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	YQILPLHSQIPR	99.7%	50.6	25	37	6	5	0	1464.83	681	692
ATP-dependent RNA helicase A	DHX9	DHX9_HUMAN	141.0	100.0%	42	55	294	0.28%	35.7%	YTQVGPDHNR	99.7%	44.9	25	32.7	9	0	0	1186.56	200	209
ATP-dependent RNA helicase DDX1	DDX1	DDX1_HUMAN	82.4	100.0%	4	4	6	0.01%	6.2%	EAQTSFLHLGYLPNQLFR	95.6%	23.4	25	18.8	0	1	0	2134.11	721	738
ATP-dependent RNA helicase DDX1	DDX1	DDX1_HUMAN	82.4	100.0%	4	4	6	0.01%	6.2%	ELLIIGGVAAR	99.7%	69.4	25	67.7	2	0	0	1111.68	320	330
ATP-dependent RNA helicase DDX1	DDX1	DDX1_HUMAN	82.4	100.0%	4	4	6	0.01%	6.2%	FLICTDVAAR	99.7%	59.4	25	54.5	2	0	0	1165.60	568	577
ATP-dependent RNA helicase DDX1	DDX1	DDX1_HUMAN	82.4	100.0%	4	4	6	0.01%	6.2%	LNLSQVR	99.7%	41.1	25	13.4	1	0	0	829.49	359	365

ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	7	8	18	0.02%	12.1%	ELAMQTFGVLK	99.7%	64.3	25	58.3	4	0	0	1236.67	262	272
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	7	8	18	0.02%	12.1%	ISDIQSQLEK	99.7%	47.6	25	8.45	1	0	0	1160.62	558	567
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	7	8	18	0.02%	12.1%	LGNGINIIVATPGR	99.7%	68.5	25	68.5	2	0	0	1394.81	298	311
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	7	8	18	0.02%	12.1%	QTMLFSATQTR	99.7%	64.5	25	43.6	2	0	0	1283.64	359	369
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	7	8	18	0.02%	12.1%	SIRPLLEGR	98.6%	32.9	25	23.9	3	0	0	1040.62	209	217
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	7	8	18	0.02%	12.1%	TLAFLIPAVELIVK	99.7%	67.2	25	67.2	4	0	0	1526.96	230	243
ATP-dependent RNA helicase DDX18	DDX18	DDX18_HUMAN	75.4	100.0%	7	8	18	0.02%	12.1%	VPLSEFDFSWSK	99.7%	71.2	25	71.2	2	0	0	1441.70	546	557
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	14	17	37	0.03%	36.8%	AAQSLLNK	98.7%	33.2	25	12.6	1	0	0	844.49	56	63
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	14	17	37	0.03%	36.8%	DPNSPLYSVK	99.7%	44.5	25	22.2	2	0	0	1119.57	82	91
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	14	17	37	0.03%	36.8%	GLAVNMVDSK	99.7%	61.2	25	55.1	4	0	0	1033.53	436	445
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	14	17	37	0.03%	36.8%	HSMNILNR	99.7%	55.4	25	41.4	2	0	0	984.50	446	453
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	14	17	37	0.03%	36.8%	IQEHFNK	99.0%	34.7	25	23.3	2	0	0	915.47	454	460
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	14	17	37	0.03%	36.8%	ISEQIVIGTPGTVLDWCSK	99.7%	80.9	25	78.9	2	0	0	2103.08	208	226
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	14	17	37	0.03%	36.8%	LDTDDLDEIEK	99.7%	62.2	25	51.5	2	0	0	1305.61	465	475
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	14	17	37	0.03%	36.8%	QYYVLCSSR	99.7%	54.8	25	52	2	0	0	1175.55	308	316
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	14	17	37	0.03%	36.8%	SNLVDNTNQVEVLQR	99.7%	94.1	25	81.4	4	0	0	1728.89	67	81
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	14	17	37	0.03%	36.8%	TAAFVLAMLSR	99.7%	81.6	25	72.7	6	0	0	1179.66	144	154
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	14	17	37	0.03%	36.8%	TASWLAAELSK	99.7%	88.8	25	77.2	1	0	0	1176.63	344	354
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	14	17	37	0.03%	36.8%	VEPSDRYPQCLCLSPTYELALQTGK	99.7%	67.3	25	67.3	0	2	0	2925.41	155	179
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	14	17	37	0.03%	36.8%	VFVLDEADVMIATQGHQDQSIR	99.7%	74.5	25	73.1	0	3	0	2472.22	237	258
ATP-dependent RNA helicase DDX19A	DDX19A	DD19A_HUMAN	54.0	100.0%	14	17	37	0.03%	36.8%	VLVTTNVCAR	99.7%	57.6	25	49.7	4	0	0	1132.61	385	394
ATP-dependent RNA helicase DDX24	DDX24	DDX24_HUMAN	96.3	100.0%	4	4	5	0.00%	5.2%	DKLDILGAAETGSGK	99.7%	61.7	25	61.7	1	0	0	1474.78	229	243
ATP-dependent RNA helicase DDX24	DDX24	DDX24_HUMAN	96.3	100.0%	4	4	5	0.00%	5.2%	NLEQFAR	98.6%	33.1	25	19.9	1	0	0	877.45	629	635
ATP-dependent RNA helicase DDX24	DDX24	DDX24_HUMAN	96.3	100.0%	4	4	5	0.00%	5.2%	RPEIVVATPGR	99.7%	42.8	25	35.2	2	0	0	1194.70	437	447
ATP-dependent RNA helicase DDX24	DDX24	DDX24_HUMAN	96.3	100.0%	4	4	5	0.00%	5.2%	SLVFANSISCIK	98.2%	32.1	25	2.14	1	0	0	1338.71	590	601
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	27	0.03%	30.7%	CMALAQLLVEQNFPAIAIHR	99.7%	73.1	25	73.1	0	3	0	2295.21	299	318
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	27	0.03%	30.7%	DFLLKPELLR	98.8%	33.9	25	21.9	2	0	0	1243.74	48	57
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	27	0.03%	30.7%	DVQEIFR	99.1%	34.8	25	13	2	0	0	906.47	209	215
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	27	0.03%	30.7%	ELAFQISK	99.7%	39.7	25	30	2	0	0	935.52	123	130
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	27	0.03%	30.7%	GLAITFVSDENDAK	99.7%	76	25	70.8	2	0	0	1479.73	384	397
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	27	0.03%	30.7%	GSYVSIHSSGFR	99.7%	59.2	25	52.7	2	0	0	1296.63	36	47
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	27	0.03%	30.7%	ILNDVQDR	99.7%	57	25	45.3	2	0	0	972.51	398	405
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	27	0.03%	30.7%	ILVATNLFGR	99.7%	69.4	25	52.7	4	0	0	1103.66	339	348
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	27	0.03%	30.7%	NCPHVVVGTPGR	99.7%	70.9	25	58	2	2	0	1292.65	163	174
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	27	0.03%	30.7%	VNIVFNYDMPEDSDTYLHR	99.7%	63.8	25	63.8	1	0	0	2328.06	355	373
ATP-dependent RNA helicase DDX39A	DDX39A	DX39A_HUMAN	49.1	100.0%	11	13	27	0.03%	30.7%	VSVFFGGLSIK	99.7%	58.9	25	54.7	3	0	0	1153.66	144	154
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	18	34	0.03%	29.5%	DKDAYSSFGSR	99.7%	60.6	25	58.8	2	0	0	1232.55	65	75
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	18	34	0.03%	29.5%	DLLDLLVEAK	99.7%	71.3	25	62.9	4	0	0	1128.65	555	564
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	18	34	0.03%	29.5%	DLMACAQTGSGK	99.7%	56.2	25	49.5	2	0	0	1238.55	219	230
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	18	34	0.03%	29.5%	DREEALHQFR	98.5%	27.3	25	24.7	1	1	0	1300.64	479	488
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	18	34	0.03%	29.5%	ELAVQIYEEAR	99.7%	48.2	25	40.2	2	0	0	1320.68	277	287
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	18	34	0.03%	29.5%	ELAVQIYEEARK	99.7%	75	25	65.9	1	0	0	1448.77	277	288
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	18	34	0.03%	29.5%	GLDISNVK	99.3%	36.1	25	18.1	1	0	0	845.47	504	511
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	18	34	0.03%	29.5%	IGLDFCK	99.7%	42.3	25	38.4	2	0	0	852.43	336	342
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	18	34	0.03%	29.5%	IVEQDTMPPK	99.4%	36.8	25	29.4	2	0	0	1173.58	364	373
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	18	34	0.03%	29.5%	LEQELFSGGNTGINFEK	99.7%	122	25	110	2	0	0	1882.92	146	162
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	18	34	0.03%	29.5%	MLDMGFEPQIR	99.7%	72.5	25	66.6	7	0	0	1336.64	352	362
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	18	34	0.03%	29.5%	QSSGASSSSFSSSR	99.7%	97.8	25	86.2	2	0	0	1361.59	604	617
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	18	34	0.03%	29.5%	QYPISLVLAPTR	99.7%	46	25	36.3	2	0	0	1357.78	265	276
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	18	34	0.03%	29.5%	SFLLDLLNATGK	99.7%	109	25	95.2	2	0	0	1291.73	429	440
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	18	34	0.03%	29.5%	SPILVATAVAAR	99.7%	113	25	104	2	0	0	1168.70	492	503

ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	18	34	0.03%	29.5%	VGSTSENITQK	99.7%	63.9	25	51.9	2	0	0	1163.59	408	418
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	18	34	0.03%	29.5%	VRPCVVYGGADIGQQIR	99.7%	61.3	25	49.8	0	2	0	1887.99	295	311
ATP-dependent RNA helicase DDX3X	DDX3X	DDX3X_HUMAN	73.2	100.0%	17	18	34	0.03%	29.5%	YLVLDEADR	99.7%	60.2	25	42.1	2	0	0	1093.55	343	351
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	6	6	11	0.01%	13.0%	EGAFSNFPISEETIK	99.7%	71.2	25	70.4	6	0	0	1668.81	136	150
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	6	6	11	0.01%	13.0%	GVTYLFPIQVK	99.7%	79.1	25	57.9	2	0	0	1264.73	156	166
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	6	6	11	0.01%	13.0%	NGIDILVGTPGR	99.7%	82.9	25	74	3	0	0	1211.67	258	269
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	6	6	11	0.01%	13.0%	QNAQCLHGDIAQSQR	97.4%	25.2	25	25.2	0	1	0	1725.81	413	427
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	6	6	11	0.01%	13.0%	SRYEQVDLVGK	99.5%	38.1	25	8.03	1	0	0	1293.68	343	353
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	6	6	11	0.01%	13.0%	TFSFAIPLIER	99.7%	74.9	25	74.2	4	0	0	1293.72	188	198
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	6	6	11	0.01%	13.0%	VGVPSTMDLVK	98.1%	31.7	25	30.1	1	0	0	1145.62	514	524
ATP-dependent RNA helicase DDX50	DDX50	DDX50_HUMAN	82.6	100.0%	6	6	11	0.01%	13.0%	VLVATNVAAR	99.7%	77.9	25	72.9	2	0	0	1013.61	441	450
ATP-dependent RNA helicase DDX54	DDX54	DDX54_HUMAN	98.6	100.0%	5	5	6	0.01%	6.8%	FEEEELQR	95.5%	28.3	25	18.8	1	0	0	1079.50	552	559
ATP-dependent RNA helicase DDX54	DDX54	DDX54_HUMAN	98.6	100.0%	5	5	6	0.01%	6.8%	GLDIPLLDNVINYSFPAK	96.7%	29.5	25	29.5	1	0	0	1989.07	401	418
ATP-dependent RNA helicase DDX54	DDX54	DDX54_HUMAN	98.6	100.0%	5	5	6	0.01%	6.8%	SRPAPSPESIKR	99.7%	35	25	35	0	1	0	1324.73	522	533
ATP-dependent RNA helicase DDX54	DDX54	DDX54_HUMAN	98.6	100.0%	5	5	6	0.01%	6.8%	TACFLLPMFER	99.0%	34.6	25	33.4	2	0	0	1384.68	147	157
ATP-dependent RNA helicase DDX54	DDX54	DDX54_HUMAN	98.6	100.0%	5	5	6	0.01%	6.8%	VADNAQQQYVR	99.7%	45.3	25	36.4	1	0	0	1291.64	511	521
ATP-dependent RNA helicase DDX55	DDX55	DDX55_HUMAN	68.5	99.8%	2	2	2	0.00%	5.2%	NKDVAAEAVTGSGK	99.7%	58.9	25	46.6	1	0	0	1346.69	46	59
ATP-dependent RNA helicase DDX55	DDX55	DDX55_HUMAN	68.5	99.8%	2	2	2	0.00%	5.2%	TGLFSATQTQEVENLVR	99.7%	67.6	25	67.6	1	0	0	1892.97	198	214
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	6	6	11	0.01%	5.8%	FEDCTSPETVIK	99.7%	48.5	25	42.4	2	0	0	1425.66	648	659
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	6	6	11	0.01%	5.8%	IFDPAPPGSR	99.7%	45	25	43.7	2	0	0	1056.55	824	833
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	6	6	11	0.01%	5.8%	LIVTSATLDAVK	99.7%	84.2	25	84.2	2	0	0	1230.73	713	724
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	6	6	11	0.01%	5.8%	NPDGSLSQAAMMQSALAK	99.7%	81	25	81	1	0	0	1819.87	467	484
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	6	6	11	0.01%	5.8%	TQMSILEQR	99.7%	57	25	38	2	0	0	1105.57	554	562
ATP-dependent RNA helicase DHX8	DHX8	DHX8_HUMAN	139.3	100.0%	6	6	11	0.01%	5.8%	VANVADVVSK	99.7%	65.3	25	59.8	2	0	0	1001.56	306	315
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L1_HUMAN	86.5	100.0%	8	8	12	0.01%	14.6%	ANAPCVIFIDELDSVGGK	98.3%	32.3	25	30.8	1	0	0	1904.94	429	446
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L1_HUMAN	86.5	100.0%	8	8	12	0.01%	14.6%	EIQIVLEGK	99.7%	43.7	25	31.6	1	0	0	1028.60	760	768
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L1_HUMAN	86.5	100.0%	8	8	12	0.01%	14.6%	GTVGFSGAELENLVNQAALK	99.7%	64.3	25	64.3	2	0	0	2018.06	537	556
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L1_HUMAN	86.5	100.0%	8	8	12	0.01%	14.6%	LAETQNIAPSFVK	99.7%	95.8	25	95	2	0	0	1417.77	225	237
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L1_HUMAN	86.5	100.0%	8	8	12	0.01%	14.6%	LSPETQSAIEQEIR	99.7%	72.6	25	62.5	2	0	0	1600.82	709	722
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L1_HUMAN	86.5	100.0%	8	8	12	0.01%	14.6%	NLAEALLTYETLDAK	99.7%	54.4	25	53	2	0	0	1664.87	745	759
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L1_HUMAN	86.5	100.0%	8	8	12	0.01%	14.6%	TGFAEGFLK	99.3%	36.3	25	33.9	1	0	0	969.50	270	278
ATP-dependent zinc metalloprotease YME1L1	YME1L1	YME1L1_HUMAN	86.5	100.0%	8	8	12	0.01%	14.6%	TTTGLDSAVDPVQMK	99.7%	64.9	25	64.9	1	0	0	1578.77	320	334
Autophagy protein 5	ATG5	ATG5_HUMAN	32.4	99.8%	2	2	3	0.00%	8.4%	IYQTTTERPFIQK	99.7%	49	25	47.5	2	0	0	1624.87	189	201
Autophagy protein 5	ATG5	ATG5_HUMAN	32.4	99.8%	2	2	3	0.00%	8.4%	VSYLTLVTDK	99.7%	63.9	25	57.5	1	0	0	1138.64	42	51
BAG family molecular chaperone regulator 2	BAG2	BAG2_HUMAN	23.8	99.8%	2	2	3	0.00%	13.3%	IIDEVVNKFLDDLGNAK	99.7%	49.7	25	49.7	2	0	0	1903.02	116	132
BAG family molecular chaperone regulator 2	BAG2	BAG2_HUMAN	23.8	99.8%	2	2	3	0.00%	13.3%	TLQQNAESRFN	99.7%	58	25	50.1	1	0	0	1307.63	201	211
Basic leucine zipper and W2 domain-containing protein 1	BZW1	BZW1_HUMAN	48.0	99.9%	2	2	4	0.00%	6.4%	AEVLSEEPILK	99.7%	69.1	25	57.4	2	0	0	1227.68	369	379
Basic leucine zipper and W2 domain-containing protein 1	BZW1	BZW1_HUMAN	48.0	99.9%	2	2	4	0.00%	6.4%	IVVLFYK	97.6%	30.8	25	30.8	1	0	0	881.55	362	368
Basic leucine zipper and W2 domain-containing protein 1	BZW1	BZW1_HUMAN	48.0	99.9%	2	2	4	0.00%	6.4%	LMELFPANK	99.7%	52.3	25	42.6	2	0	0	1062.57	215	223
Basic leucine zipper and W2 domain-containing protein 2	BZW2	BZW2_HUMAN	48.2	100.0%	3	3	5	0.00%	7.4%	IVVLFYK	97.6%	30.8	25	30.8	1	0	0	881.55	363	369
Basic leucine zipper and W2 domain-containing protein 2	BZW2	BZW2_HUMAN	48.2	100.0%	3	3	5	0.00%	7.4%	LLELFPVNR	99.7%	39.4	25	30.6	2	0	0	1100.65	216	224
Basic leucine zipper and W2 domain-containing protein 2	BZW2	BZW2_HUMAN	48.2	100.0%	3	3	5	0.00%	7.4%	YFTDAGLKELSDFLR	99.7%	54.4	25	53.3	2	0	0	1774.90	233	247
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	6	6	16	0.02%	8.0%	ETGYVVERPSTTK	99.5%	37.9	25	33.1	1	0	0	1466.75	463	475
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	6	6	16	0.02%	8.0%	LLASTLVHSVK	99.7%	61.5	25	56.7	4	0	0	1167.71	570	580
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	6	6	16	0.02%	8.0%	MAPVPLDDSNRPASLTK	98.5%	32.7	25	32.7	1	0	0	1827.93	551	567
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	6	6	16	0.02%	8.0%	NTEEEGLKYK	99.7%	39.4	25	23.6	4	0	0	1210.60	430	439
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	6	6	16	0.02%	8.0%	SSFYPDGGDQETAK	99.7%	62	25	48	3	0	0	1501.64	319	332
Bcl-2-associated transcription factor 1	BCLAF1	BCLF1_HUMAN	106.1	100.0%	6	6	16	0.02%	8.0%	TIAPQNAPR	99.7%	43	25	31.8	3	0	0	967.53	304	312
Beta-casein	CSN2	CASB_HUMAN	25.4	99.8%	2	3	6	0.01%	11.9%	SPTIPFFDPQIPK	99.7%	45	25	43.2	2	0	0	1486.79	120	132
Beta-casein	CSN2	CASB_HUMAN	25.4	99.8%	2	3	6	0.01%	11.9%	VLPIPQQVVPYPQR	99.7%	63.3	25	62	2	2	0	1633.94	176	189
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	11	12	21	0.02%	21.1%	AGATLDLLVENMGR	99.7%	88.3	25	76	3	0	0	1459.76	469	482

Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	11	12	21	0.02%	21.1%	AYVAVDGIPQGVLER	99.7%	60.1	25	55.9	2	0	0	1586.85	443	457
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	11	12	21	0.02%	21.1%	MFEIDYSR	99.7%	47.9	25	47.3	2	0	0	1060.48	31	38
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	11	12	21	0.02%	21.1%	QHYGFVLYR	99.7%	40.5	25	34.8	1	0	0	1182.61	411	419
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	11	12	21	0.02%	21.1%	SLYPLTFIQVK	99.7%	77.4	25	77.4	2	0	0	1308.76	400	410
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	11	12	21	0.02%	21.1%	SSDPDYLAAVDK	99.7%	66.4	25	46.9	2	0	0	1280.60	149	160
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	11	12	21	0.02%	21.1%	TEAVASSLYDILAR	99.7%	98	25	82.8	2	0	0	1508.80	286	299
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	11	12	21	0.02%	21.1%	TTLPQDCSNPAPLSSPLNGVHDR	99.2%	29.8	25	29.8	0	1	0	2476.19	420	442
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	11	12	21	0.02%	21.1%	TVGAALDILCPSGPIK	99.7%	103	25	98.2	2	0	0	1611.88	384	399
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	11	12	21	0.02%	21.1%	VNYGAYINDFK	99.7%	68.7	25	59.1	2	0	0	1303.63	483	493
Beta-galactosidase	GLB1	BGAL_HUMAN	76.1	100.0%	11	12	21	0.02%	21.1%	YISGSIHYSR	99.7%	68.2	25	66.2	2	0	0	1182.59	50	59
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	8	8	12	0.01%	23.8%	AVAQAGTVGTLLIVK	99.7%	103	25	97.6	2	0	0	1440.88	95	109
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	8	8	12	0.01%	23.8%	EGPPPASPAQLLSK	99.7%	71.1	25	69.8	1	0	0	1391.75	421	434
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	8	8	12	0.01%	23.8%	LEQPDPGAVAAAAILR	99.7%	87.8	25	82.8	2	0	0	1591.88	552	567
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	8	8	12	0.01%	23.8%	MGGSSGALYGLFLTAAAQPLK	99.7%	50	25	50	1	0	0	2069.07	443	463
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	8	8	12	0.01%	23.8%	SPGADLLQVLTK	99.7%	92.6	25	84.4	2	0	0	1241.71	511	522
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	8	8	12	0.01%	23.8%	VAGALAEAGVGLEEIAK	99.7%	102	25	90.2	2	0	0	1597.88	163	179
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	8	8	12	0.01%	23.8%	VALLSGGGSGHEPAHAGFIGK	99.7%	41.6	25	31.5	0	1	0	1962.02	49	69
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DAK	DHAK_HUMAN	58.9	100.0%	8	8	12	0.01%	23.8%	VAPAEPQEAPDSTAAGGSASK	99.7%	102	25	102	1	0	0	1940.92	352	372
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	AALLNQHYQVNFK	99.7%	52.1	25	50.7	2	0	0	1545.82	217	229
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	AIQGGTSHHLGQNFSK	99.7%	68.7	25	64.5	1	1	0	1681.84	1235	1250
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	AYVDDTPAEQMK	99.7%	72.8	25	67.8	4	0	0	1383.61	289	300
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	DQDLEPGAPSMGAK	99.7%	64.3	25	42.9	4	0	0	1431.64	1464	1477
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	DQVDIAVQELLQLK	99.7%	102	25	81.5	4	0	0	1611.90	926	939
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	ERPTPSLNNNCTTSEDSLVLYNR	99.7%	70.8	25	70.8	0	1	0	2680.26	734	756
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	EYIPGQPPLSQSSDSSPTR	99.7%	73.9	25	70.2	2	0	0	2045.98	871	889
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	FAGGDYTTTIEAFISASGR	99.3%	36.4	25	36.4	1	0	0	1963.94	1216	1234
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	FNHWELK	94.9%	27.9	25	13.6	1	0	0	973.49	1355	1361
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	FVELPGAEMGK	99.7%	48.5	25	39.7	2	0	0	1177.59	187	197
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	GDIIQLQR	99.7%	48.6	25	26.1	2	0	0	942.54	667	674
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	GFFICDQPYEPVSPYSCK	99.7%	56	25	56	1	0	0	2193.96	676	693
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	GNAAWQEQLK	99.7%	58.9	25	42.5	2	0	0	1144.57	130	139
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	GSQFGQSCCLR	99.7%	52	25	52	2	0	0	1299.56	329	339
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	INEAVECLLSLK	99.7%	82	25	72.1	6	0	0	1388.75	850	861
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	KPYIWEYSR	99.6%	38.8	25	27.7	2	0	0	1241.63	417	425
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	KVIDPVAPR	99.7%	45.5	25	41.4	2	0	0	994.60	498	506
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	LGVENCYFPMFVSQSALEK	99.7%	59.9	25	59.9	4	0	0	2219.05	1071	1089
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	LLSVNIR	99.7%	43.9	25	25.6	2	0	0	814.51	1334	1340
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	LNLNNTVLSK	99.7%	63.3	25	50.3	4	0	0	1115.64	426	435
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	LNQWCNVVR	99.7%	67.7	25	55.4	2	0	0	1188.59	1144	1152
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	LTVAENEAETK	99.7%	81.6	25	80.6	7	0	0	1204.61	1390	1400
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	NPEVGLKPVWYSPK	99.7%	63.6	25	58.1	2	0	0	1613.87	536	549
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	NQGGGLSSSGAGEGQGPK	99.7%	95.7	25	95.7	5	0	0	1587.74	992	1009
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	NSEPAGLETPEAK	99.7%	60.8	25	49.3	3	0	0	1342.65	890	902
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	QFAYQNSWGLTTR	99.7%	70	25	57.6	2	0	0	1571.76	1266	1278
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	SCQFVAVR	99.7%	46.8	25	22.9	5	0	0	966.48	1376	1383
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	SLCIPFKPLCELQPGAK	98.7%	27.9	25	23.9	0	1	0	1958.02	1478	1494
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	SLIGVEYKPVSATGAEDKDK	99.1%	29.6	25	29.6	0	1	0	2107.09	944	963
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	SLYDEVAAQGEVVR	99.7%	111	25	108	4	0	0	1535.77	825	838
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	SLYDEVAAQGEVVRK	99.7%	70.8	25	70.8	1	0	0	1663.87	825	839
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	TELAEPIAIRPTSETVMYPAYAK	95.4%	23.2	25	23.2	0	1	0	2567.31	1110	1132
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	TGQEYKPGNPPAEIGQNISSNSSASILESK	99.7%	69.9	25	69.9	0	2	0	3103.52	795	824

Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	THVADFAPEVAWVTR	99.7%	59	25	58	1	1	0	1698.86	1092	1106
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	VASQGEVVR	99.7%	55.5	25	45.1	4	0	0	944.52	908	916
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	VAVQGDVVR	99.7%	58.5	25	32	4	0	0	942.54	757	765
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	VIDPVAPR	99.7%	45.1	25	45.1	1	0	0	866.51	499	506
Bifunctional glutamate/proline--tRNA ligase	EPRS	SYEP_HUMAN	170.6	100.0%	38	43	98	0.09%	33.2%	WFGFLEAQQAFQSVGTK	99.7%	70.1	25	65.8	1	0	0	1943.97	150	166
Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	MTHFD2	MTDC_HUMAN	37.9	100.0%	3	3	6	0.01%	12.6%	AGYITPVPGGVGPMTVAMLMK	99.7%	45.7	25	42.5	2	0	0	2090.09	302	322
Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	MTHFD2	MTDC_HUMAN	37.9	100.0%	3	3	6	0.01%	12.6%	EGAAVIDVGINR	99.7%	74.8	25	62	2	0	0	1213.65	267	278
Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	MTHFD2	MTDC_HUMAN	37.9	100.0%	3	3	6	0.01%	12.6%	LVGDVDFEGVR	99.7%	58.1	25	47.2	2	0	0	1205.62	289	299
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	10	10	17	0.02%	12.1%	ANSSVVSVNCK	99.7%	52.7	25	52.3	2	0	0	1164.57	587	597
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	10	10	17	0.02%	12.1%	EIPVESIEEVSK	99.7%	51.6	25	42.9	2	0	0	1358.71	258	269
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	10	10	17	0.02%	12.1%	ESQATLEER	99.3%	35.9	25	25.8	2	0	0	1062.51	5	13
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	10	10	17	0.02%	12.1%	ILEFYSK	97.7%	31	25	17.5	1	0	0	899.49	887	893
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	10	10	17	0.02%	12.1%	LGCFEIAK	99.7%	45	25	36.5	2	0	0	937.48	894	901
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	10	10	17	0.02%	12.1%	LLPGIEVLWTGPK	98.9%	34	25	34	2	0	0	1422.84	241	253
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	10	10	17	0.02%	12.1%	LLPIDGANDLFFQPPPLTPTSK	99.7%	44.6	25	44.6	1	0	0	2381.28	692	713
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	10	10	17	0.02%	12.1%	SMMACLLSSLK	99.7%	42.4	25	23.7	2	0	0	1240.61	859	869
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	10	10	17	0.02%	12.1%	STELIPR	96.1%	28.9	25	18.1	1	0	0	815.46	300	306
Bifunctional protein NCOAT	MGEA5	NCOAT_HUMAN	102.9	100.0%	10	10	17	0.02%	12.1%	WELNTYLYAPK	99.7%	48.7	25	48.7	2	0	0	1397.71	88	98
Bifunctional purine biosynthesis protein PURH	ATIC	PUR9_HUMAN	64.6	100.0%	5	5	6	0.01%	10.1%	ALFEEVPELLTEAEK	94.7%	27.8	25	25.2	1	0	0	1717.89	510	524
Bifunctional purine biosynthesis protein PURH	ATIC	PUR9_HUMAN	64.6	100.0%	5	5	6	0.01%	10.1%	DVSELTGFPEMLGGR	98.6%	33.2	25	33.2	1	0	0	1607.77	50	64
Bifunctional purine biosynthesis protein PURH	ATIC	PUR9_HUMAN	64.6	100.0%	5	5	6	0.01%	10.1%	SLFSNVVTK	99.7%	41.9	25	38.4	2	0	0	994.56	398	406
Bifunctional purine biosynthesis protein PURH	ATIC	PUR9_HUMAN	64.6	100.0%	5	5	6	0.01%	10.1%	TLFGLHLSQK	97.3%	30.4	25	28	1	0	0	1143.65	380	389
Bifunctional purine biosynthesis protein PURH	ATIC	PUR9_HUMAN	64.6	100.0%	5	5	6	0.01%	10.1%	TLTPISAAYAR	97.9%	31.3	25	29.2	1	0	0	1163.64	295	305
Bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase	GNE	GLCNE_HUMAN	79.3	99.8%	2	2	3	0.00%	3.9%	EVGAFGTPVINLGTR	99.7%	63	25	57.5	2	0	0	1530.83	307	321
Bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase	GNE	GLCNE_HUMAN	79.3	99.8%	2	2	3	0.00%	3.9%	TLVLFPNIDAGSK	98.7%	33.4	25	26.1	1	0	0	1374.76	247	259
BolA-like protein 2	BOLA2	BOLA2_HUMAN	10.1	99.8%	2	3	6	0.01%	29.1%	DLEAEHVEVEDTTLNR	99.7%	79.9	25	79.9	2	2	0	1869.88	15	30
BolA-like protein 2	BOLA2	BOLA2_HUMAN	10.1	99.8%	2	3	6	0.01%	29.1%	FEGKPLLQR	99.3%	36.4	25	31.8	2	0	0	1087.63	44	52
BRCA1-A complex subunit BRE	BRE	BRE_HUMAN	43.6	99.8%	2	2	3	0.00%	7.3%	ISPMLSPFISSVVR	97.9%	31.4	25	30.1	1	0	0	1532.85	10	23
BRCA1-A complex subunit BRE	BRE	BRE_HUMAN	43.6	99.8%	2	2	3	0.00%	7.3%	LPVDFSNIPTYLLK	99.7%	68.1	25	68.1	2	0	0	1619.90	177	190
BRCA1-associated ATM activator 1	BRAT1	BRAT1_HUMAN	88.1	99.8%	2	2	3	0.00%	2.8%	SCDLLLFLR	99.7%	74.5	25	53.7	2	0	0	1136.61	719	727
BRCA1-associated ATM activator 1	BRAT1	BRAT1_HUMAN	88.1	99.8%	2	2	3	0.00%	2.8%	VTQALNVLTTTFGR	99.7%	59.2	25	59.2	1	0	0	1520.84	214	227
BRCA2 and CDKN1A-interacting protein	BCCIP	BCCIP_HUMAN	36.0	100.0%	3	3	4	0.00%	14.6%	APVNTAELTDLLIQQNHIGSVIK	99.7%	34.9	25	34.9	0	1	0	2474.36	85	107
BRCA2 and CDKN1A-interacting protein	BCCIP	BCCIP_HUMAN	36.0	100.0%	3	3	4	0.00%	14.6%	KGTQCVEQIQELVLR	97.5%	25.4	25	17.1	0	1	0	1800.96	137	151
BRCA2 and CDKN1A-interacting protein	BCCIP	BCCIP_HUMAN	36.0	100.0%	3	3	4	0.00%	14.6%	LLQQLFLK	99.7%	54.8	25	40.9	2	0	0	1002.63	77	84
Bromodomain adjacent to zinc finger domain protein 1A	BAZ1A	BAZ1A_HUMAN	178.7	100.0%	3	3	4	0.00%	2.6%	DFIEDYVDILR	99.7%	54.6	25	50.8	2	0	0	1397.69	632	642
Bromodomain adjacent to zinc finger domain protein 1A	BAZ1A	BAZ1A_HUMAN	178.7	100.0%	3	3	4	0.00%	2.6%	IQSAIACTNIFPLGR	97.8%	31.2	25	31.2	1	0	0	1660.88	793	807
Bromodomain adjacent to zinc finger domain protein 1A	BAZ1A	BAZ1A_HUMAN	178.7	100.0%	3	3	4	0.00%	2.6%	SLDLDSCTLSEILR	99.5%	38.1	25	38.1	1	0	0	1621.81	541	554
Bystin	BYSL	BYST_HUMAN	49.6	100.0%	3	3	3	0.00%	6.9%	ELQSAVPR	98.1%	31.9	25	24.5	1	0	0	899.49	420	427
Bystin	BYSL	BYST_HUMAN	49.6	100.0%	3	3	3	0.00%	6.9%	FYNLVLLPR	99.7%	67.2	25	50.4	1	0	0	1134.67	249	257
Bystin	BYSL	BYST_HUMAN	49.6	100.0%	3	3	3	0.00%	6.9%	GTGEAEEEYVGPR	99.7%	71.1	25	57.8	1	0	0	1393.62	41	53
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	AAEEIGIK	99.7%	62.3	25	37	2	0	0	830.46	59	66
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	AAQAPSSFQLLYDLK	99.7%	110	25	108	2	0	0	1651.87	805	819
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	AYIQENLELVEK	99.7%	68.4	25	64.3	2	0	0	1448.76	722	733
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	DDSNLYINVK	99.7%	76.6	25	64.1	2	0	0	1180.58	47	56
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	DVDGLTSINAGR	99.7%	59	25	50	2	0	0	1217.61	123	134
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	EIGLLSEEVELYGETK	99.7%	112	25	112	2	0	0	1808.92	337	352
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	EISAQIR	99.7%	43.9	25	13.7	2	0	0	816.46	11	17
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	FSDIQIR	99.7%	46.7	25	14.8	2	0	0	878.47	489	495
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	GALALAQAVQR	99.7%	90	25	83.2	4	0	0	1097.64	794	804
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	GCLELIK	96.4%	29.2	25	10.5	1	0	0	832.46	151	157
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	GDLNDCFIPCTPK	99.7%	50.4	25	50.4	2	0	0	1536.68	138	150

C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	GVPTGFILPIR	99.7%	65.9	25	58.5	4	0	0	1169.70	879	889
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	IFHELTQTDK	99.7%	52.5	25	37.3	2	2	0	1231.63	464	473
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	ITIGQAPTEK	99.7%	44	25	42.5	2	0	0	1057.59	544	553
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	IYGADDIELLPEAQHK	99.7%	85.1	25	77.7	2	2	0	1811.92	833	848
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	KGEPVSAEDLGVSGALTVLMK	99.7%	34.4	25	33.7	0	1	0	2117.12	596	616
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	KITIGQAPTEK	99.7%	61.9	25	35.1	2	0	0	1185.68	543	553
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	KVVGDVAYDEAK	99.7%	75.1	25	70.8	2	0	0	1293.67	251	262
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	LAILQVGNR	99.7%	76.1	25	66.1	2	0	0	983.60	38	46
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	LDIDPETITWQR	99.7%	91.7	25	84.5	3	0	0	1486.75	521	532
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	LVGPEGFVVTEAGFGADIGMEK	99.7%	87.7	25	87.7	2	2	0	2239.10	658	679
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	MFGIPVVVAVNAFK	99.7%	85.7	25	79.9	6	0	0	1491.84	747	760
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	QGFGNLPICMAK	99.2%	35.7	25	31	1	0	0	1335.66	855	866
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	QPSQGPTFGIK	98.9%	34.3	25	23.6	2	0	0	1159.61	411	421
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	TDPTTLTDEEINR	99.7%	73.7	25	59.8	3	0	0	1504.71	505	517
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	TDTESELDLISR	99.7%	90.8	25	83.8	2	0	0	1378.67	761	772
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	THLSLSHNPEQK	99.7%	68.9	25	66.3	2	0	0	1390.71	867	878
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	TPVPSDIDISR	99.7%	60.7	25	59.3	2	0	0	1199.63	314	324
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	VLLSALER	99.7%	59.5	25	42.4	5	0	0	900.55	355	362
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	VVGDVAYDEAK	99.7%	70.5	25	68.4	2	0	0	1165.57	252	262
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	VVGDVAYDEAKER	99.7%	82	25	75.3	1	0	0	1450.72	252	264
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	WMIQYNNLNLK	99.7%	52.7	25	40.2	2	0	0	1436.74	303	313
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	YSGLCPHVVVLVATVR	99.7%	61	25	60.7	0	2	0	1769.97	687	702
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	C1TC_HUMAN	101.6	100.0%	34	38	83	0.08%	40.6%	YVVVTGITPTPLGEGK	99.7%	96.7	25	93.5	2	0	0	1630.91	371	386
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	AAFALGGLGSGFASNR	99.7%	98.3	25	89.6	2	0	0	1495.77	556	571
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	ASDPGLPAEEPK	99.7%	45.4	25	45.4	2	0	0	1210.60	1858	1869
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	ATGYPLAYVAAK	99.7%	48.7	25	48.7	2	0	0	1224.66	697	708
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	EATAGNPGGQTVR	99.7%	57.5	25	54.5	2	0	0	1257.62	359	371
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	EIEYEVVR	95.9%	28.7	25	10	1	0	0	1036.53	599	606
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	ELSDLESAR	99.7%	62.1	25	55	2	0	0	1019.50	1067	1075
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	FLSSAAAVSK	99.7%	48.3	25	43.4	2	0	0	980.54	1110	1119
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	GESLADSVQTMSCYADVVVLR	97.3%	30.3	25	30.3	1	0	0	2300.09	2004	2024
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	GEVAYIDGQVLVPPGYGQDVR	99.4%	36.8	25	32.4	2	0	0	2232.13	1790	1810
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	GHNQPCLLVGSGR	99.7%	43.6	25	43.6	1	0	0	1394.70	275	287
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	HPQPGAVELAAK	96.9%	29.8	25	19.7	1	0	0	1217.66	2025	2036
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	ILALDCGLK	99.7%	39.5	25	21.1	2	0	0	1002.57	178	186
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	KEEILLIK	94.5%	27.6	25	11.4	1	0	0	985.63	1618	1625
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	LALGIPLPELR	99.7%	71.9	25	71.9	2	0	0	1191.75	709	719
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	LFVEALGQIGPAPPLK	99.7%	92.7	25	92.7	2	0	0	1649.96	1435	1450
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	LGGAVLSFSEATSSVQK	99.7%	136	25	134	2	0	0	1680.88	1987	2003
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	LGYPVLVR	98.6%	33	25	26.8	2	0	0	916.56	548	555
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	LLDTIGISQPQWR	99.7%	81.7	25	81.7	2	0	0	1526.83	1054	1066
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	LYLNETFSELR	99.7%	52.9	25	44.2	2	0	0	1384.71	1557	1567
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	MAEIGEHVAPSEAANSLEQAQAAAER	99.7%	86.4	25	84.5	0	2	0	2680.26	522	547
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	MALLATVLGR	99.7%	95.7	25	81.5	4	0	0	1044.62	2215	2224
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	MALLATVLGRF	99.7%	68.1	25	65.7	2	0	0	1207.69	2215	2225
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	NILLTIGSYK	99.6%	38.6	25	32.7	2	0	0	1121.66	1314	1323
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	NKSELLPTVR	99.7%	43.7	25	37.9	1	0	0	1156.67	1324	1333
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	NSVTGGTAAFEPSVDYCVVK	99.7%	98.4	25	98.4	2	0	0	2100.99	720	739
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	QELGICPAVK	96.7%	29.5	25	13.1	1	0	0	1114.59	892	901
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	SELLPTVR	96.2%	29	25	21.4	1	0	0	914.53	1326	1333
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	SFEEAFQK	98.1%	31.8	25	25.5	2	0	0	985.46	771	778

CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	SILEQLAEK	99.7%	53.7	25	41.1	2	0	0	1030.58	1379	1387
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	SVGEVMGIGR	99.7%	49.1	25	39.2	4	0	0	1020.51	761	770
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	SVHICHVAR	98.7%	33.4	25	31.7	2	0	0	1078.56	1609	1617
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	TLGVDLVALATR	99.7%	86	25	75.2	2	0	0	1228.73	1229	1240
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	TPHVLVLGSGVYR	99.7%	65.8	25	65.8	2	2	0	1397.79	932	944
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	TSSSFAAAMAR	99.7%	98.2	25	86.2	4	0	0	1099.52	1976	1986
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	VFNTGGAPR	99.7%	51.2	25	40.2	2	0	0	918.48	169	177
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	VHVDCMTSQK	96.5%	29.4	25	23.4	1	0	0	1204.55	1451	1460
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	VIMGEEVEPVGLMTGSGVVGVK	99.7%	77.7	25	76.4	3	0	0	2187.14	1241	1262
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	VLGTSPEAIDSAENR	99.7%	125	25	124	2	0	0	1558.77	1034	1048
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	VNEISVEVDSDPR	99.7%	85.7	25	73.7	2	0	0	1458.71	2188	2200
CAD protein	CAD	PYR1_HUMAN	243.0	100.0%	40	45	80	0.07%	21.4%	VPQFSFSR	99.7%	48	25	39.8	2	0	0	967.50	1263	1270
Calcium uniporter protein, mitochondrial	MCU	MCU_HUMAN	39.9	100.0%	3	3	4	0.00%	10.0%	LEDLKEQLAPLEK	99.7%	67.2	25	57.2	2	0	0	1525.85	207	219
Calcium uniporter protein, mitochondrial	MCU	MCU_HUMAN	39.9	100.0%	3	3	4	0.00%	10.0%	LRDPLQVHLPLR	99.5%	32.1	25	32.1	0	1	0	1456.87	334	345
Calcium uniporter protein, mitochondrial	MCU	MCU_HUMAN	39.9	100.0%	3	3	4	0.00%	10.0%	VAIYSPDGVR	96.9%	29.8	25	24.2	1	0	0	1076.57	125	134
Calcium/calmodulin-dependent protein kinase type II subunit gamma	CAMK2G	KCC2G_HUMAN	62.6	100.0%	3	3	3	0.00%	6.1%	DLKPENLLLASK	98.4%	32.5	25	18.9	1	0	0	1340.78	136	147
Calcium/calmodulin-dependent protein kinase type II subunit gamma	CAMK2G	KCC2G_HUMAN	62.6	100.0%	3	3	3	0.00%	6.1%	FYFENLLSK	99.5%	37.2	25	28.8	1	0	0	1160.60	477	485
Calcium/calmodulin-dependent protein kinase type II subunit gamma	CAMK2G	KCC2G_HUMAN	62.6	100.0%	3	3	3	0.00%	6.1%	NLINQMLTINPAK	99.7%	47	25	47	1	0	0	1469.81	247	259
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	10	0.01%	19.2%	AGQTTYSGVIDCFR	99.7%	76.1	25	76.1	2	0	0	1574.73	552	565
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	10	0.01%	19.2%	AGQTTYSGVIDCFRK	99.7%	71.5	25	71.5	1	0	0	1702.82	552	566
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	10	0.01%	19.2%	DIPFSAIYFPVYAHCK	99.7%	74	25	33.2	2	0	0	1927.94	491	506
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	10	0.01%	19.2%	DLGIFGLYK	98.8%	33.8	25	33.8	1	0	0	1025.57	474	482
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	10	0.01%	19.2%	GLIPQLIGVAPEK	99.7%	60.9	25	0	4	0	0	1334.80	391	403
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	10	0.01%	19.2%	IVQLLAGVADQTK	99.7%	78.6	25	78.6	2	0	0	1355.79	56	68
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	10	0.01%	19.2%	LATATFAGIENK	99.7%	82.1	25	72.2	2	0	0	1235.66	641	652
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	10	0.01%	19.2%	LQVAGEITTGPR	99.7%	69.8	25	51.4	2	0	0	1241.69	454	465
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	10	0.01%	19.2%	LTVNDFVR	99.7%	55.7	25	48.4	2	0	0	963.53	407	414
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	10	0.01%	19.2%	NIFLQYASTEVDGER	99.7%	87.9	25	87.9	1	0	0	1741.84	18	32
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	10	0.01%	19.2%	VSALNVLR	99.7%	64.2	25	44.6	2	0	0	871.54	466	473
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	CMC1_HUMAN	74.8	100.0%	6	6	10	0.01%	19.2%	YEGFFGLYR	99.7%	47.1	25	47	2	0	0	1151.55	382	390
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	26	50	0.05%	39.1%	AGQTTYSGVIDCFR	99.7%	76.1	25	76.1	2	0	0	1574.73	554	567
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	26	50	0.05%	39.1%	AGQTTYSGVIDCFRK	99.7%	71.5	25	71.5	1	0	0	1702.82	554	568
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	26	50	0.05%	39.1%	ASGDSARPVLLQVAESAYR	99.7%	52.1	25	52.1	2	2	0	1990.04	313	331
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	26	50	0.05%	39.1%	DIPFSAIYFPCYAHVK	99.7%	61.1	25	25.6	2	0	0	1927.94	493	508
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	26	50	0.05%	39.1%	DLGFFGIYK	99.7%	56.5	25	48.7	2	0	0	1059.55	476	484
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	26	50	0.05%	39.1%	FGLGSVAGAVGATAVYPIDLVK	99.7%	87.3	25	87.3	2	1	0	2105.16	332	353
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	26	50	0.05%	39.1%	FGLYLPLFKPSVSTSK	99.6%	38.5	25	38.5	2	2	0	1784.00	654	669
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	26	50	0.05%	39.1%	GLLPQLLGVAPEK	99.7%	60.9	25	0	4	0	0	1334.80	393	405
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	26	50	0.05%	39.1%	IAPLEEGTLPFNLAEAQR	99.7%	91.5	25	91.3	2	2	0	1969.04	293	310
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	26	50	0.05%	39.1%	ILREEGPK	99.1%	35.2	25	30.6	1	0	0	941.54	569	576
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	26	50	0.05%	39.1%	INLPAPNPDHVGGYK	99.7%	67.1	25	64.3	2	0	0	1591.82	627	641
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	26	50	0.05%	39.1%	LAVATFAGIENK	99.7%	78.4	25	67.9	2	0	0	1233.68	642	653
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	26	50	0.05%	39.1%	LQVAGEITTGPR	99.7%	69.8	25	51.4	2	0	0	1241.69	456	467
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	26	50	0.05%	39.1%	LTVNDFVR	99.7%	55.7	25	48.4	2	0	0	963.53	409	416
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	26	50	0.05%	39.1%	MTLADIER	99.7%	50.9	25	44.3	2	0	0	948.48	285	292
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	26	50	0.05%	39.1%	NGEFFMSPNDFVTR	99.7%	77	25	73.2	3	0	0	1660.74	30	43
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	26	50	0.05%	39.1%	SSPQFGVTLLTYELLQR	99.7%	97.7	25	96.2	2	0	0	1952.05	589	605
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	26	50	0.05%	39.1%	STGSFVGELMYK	99.7%	52.2	25	45.4	2	0	0	1318.63	361	372
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	26	50	0.05%	39.1%	TVELLSGVVDQTK	99.7%	94	25	86.6	2	0	0	1388.76	57	69
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	26	50	0.05%	39.1%	VSALSVVR	99.7%	52.4	25	41.2	2	0	0	830.51	468	475
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	CMC2_HUMAN	74.2	100.0%	21	26	50	0.05%	39.1%	YEGFFGLYR	99.7%	47.1	25	47	2	0	0	1151.55	384	392

Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	11	12	22	0.02%	31.4%	EGIPGLYR	98.4%	32.4	25	17.1	1	0	0	904.49	438	445
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	11	12	22	0.02%	31.4%	FISGSMAGATAQTFIYPMEVMK	99.7%	68.1	25	68.1	2	0	0	2380.14	292	313
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	11	12	22	0.02%	31.4%	HEGLGAFYK	99.7%	52.2	25	49.9	2	0	0	1021.51	337	345
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	11	12	22	0.02%	31.4%	HSTGIDIGDSLTIPDEFTEDEKK	99.7%	54.5	25	54.5	0	2	0	2547.21	168	190
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	11	12	22	0.02%	31.4%	MNIFGGFR	99.7%	46.5	25	38.7	2	0	0	941.47	232	239
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	11	12	22	0.02%	31.4%	NGDGVVDIGELQEGLR	99.7%	81.2	25	81.2	2	0	0	1670.83	34	49
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	11	12	22	0.02%	31.4%	NLGIPLGQDAEEK	99.7%	64.3	25	63.1	2	0	0	1383.71	50	62
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	11	12	22	0.02%	31.4%	QLLAGGIAGAVSR	99.7%	102	25	94.8	2	0	0	1212.71	197	209
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	11	12	22	0.02%	31.4%	TGQYSGIYDCAK	99.7%	73.3	25	73.3	2	0	0	1362.60	321	332
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	11	12	22	0.02%	31.4%	VLPAVGISYVVYENMK	99.7%	74.4	25	74.4	4	0	0	1797.95	454	469
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	SCMC1_HUMAN	53.4	100.0%	11	12	22	0.02%	31.4%	YETLFQALDR	99.6%	38.8	25	37.8	1	0	0	1255.63	24	33
Calmodulin	CALM1	CALM_HUMAN	16.8	99.8%	2	2	2	0.00%	22.1%	EAFSLFDKDGDGTITTK	99.7%	47	25	47	1	0	0	1844.89	15	31
Calmodulin	CALM1	CALM_HUMAN	16.8	99.8%	2	2	2	0.00%	22.1%	VFDKDGNGYISAAELR	99.1%	29.5	25	29.5	0	1	0	1754.87	92	107
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	3	3	5	0.00%	2.8%	APAEEEVGPR	99.7%	68.7	25	66.7	2	0	0	1054.52	964	973
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	3	3	5	0.00%	2.8%	AVASSPAATNSEVK	99.7%	51.4	25	43.5	2	0	0	1331.68	550	563
Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	CAMP3_HUMAN	134.8	100.0%	3	3	5	0.00%	2.8%	DLPDGHAASPR	99.4%	36.5	25	27.5	1	0	0	1135.55	326	336
Calpain-2 catalytic subunit	CAPN2	CAN2_HUMAN	80.0	100.0%	5	5	7	0.01%	9.4%	FADDQLIIDFDNFVR	99.7%	45	25	41.1	1	0	0	1827.89	650	664
Calpain-2 catalytic subunit	CAPN2	CAN2_HUMAN	80.0	100.0%	5	5	7	0.01%	9.4%	NYPNTFWMNPQYLIK	99.7%	72	25	70.5	2	0	0	1928.94	376	390
Calpain-2 catalytic subunit	CAPN2	CAN2_HUMAN	80.0	100.0%	5	5	7	0.01%	9.4%	RPTEICADPQFIIGGATR	99.5%	32.2	25	31.6	0	1	0	2002.02	77	94
Calpain-2 catalytic subunit	CAPN2	CAN2_HUMAN	80.0	100.0%	5	5	7	0.01%	9.4%	SDGFSIETCK	99.7%	40.1	25	40.1	1	0	0	1143.50	569	578
Calpain-2 catalytic subunit	CAPN2	CAN2_HUMAN	80.0	100.0%	5	5	7	0.01%	9.4%	SDTFINLR	99.7%	68.8	25	34.7	2	0	0	965.51	462	469
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	9	11	17	0.02%	60.0%	GKPLALVEEIR	99.7%	54	25	48.4	2	2	0	1224.73	149	159
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	9	11	17	0.02%	60.0%	IGFDVVTLSGTR	99.7%	73.8	25	69.3	2	0	0	1264.69	48	59
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	9	11	17	0.02%	60.0%	MELFSQLFIQAVR	99.7%	56.6	25	48.1	2	0	0	1581.85	118	130
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	9	11	17	0.02%	60.0%	NHLLPDIVTCVQSSR	99.7%	41.2	25	41.2	1	0	0	1738.89	175	189
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	9	11	17	0.02%	60.0%	QTLSTPGTIILGTIPVPK	99.7%	81.5	25	81.5	2	0	0	1836.08	131	148
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	9	11	17	0.02%	60.0%	RIGFDVVTLSGTR	98.8%	33.8	25	33.8	1	0	0	1420.79	47	59
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	9	11	17	0.02%	60.0%	SSGVPVDGFYTEEVR	99.7%	78.1	25	67.5	2	0	0	1641.78	28	42
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	9	11	17	0.02%	60.0%	VCVIDEIGK	99.7%	40.4	25	27.6	2	0	0	1032.54	109	117
Cancer-related nucleoside-triphosphatase	NTPCR	NTPCR_HUMAN	20.7	100.0%	9	11	17	0.02%	60.0%	VGQYVVDLTSFEQLALPVLR	99.7%	49.2	25	40.4	1	0	0	2247.24	78	97
Carbonic anhydrase 2	CA2	CAH2_HUMAN	29.2	99.8%	2	2	3	0.00%	10.0%	AVQQPDGLAVLGIFLK	99.1%	35	25	35	1	0	0	1668.97	133	148
Carbonic anhydrase 2	CA2	CAH2_HUMAN	29.2	99.8%	2	2	3	0.00%	10.0%	SADFTNFDPR	99.7%	40.4	25	31.6	2	0	0	1169.52	172	181
Carbonyl reductase [NADPH] 1	CBR1	CBR1_HUMAN	30.4	99.8%	2	2	3	0.00%	11.9%	EYGGLDVLVNNAGIAFK	99.7%	86.3	25	85.3	2	0	0	1779.93	80	96
Carbonyl reductase [NADPH] 1	CBR1	CBR1_HUMAN	30.4	99.8%	2	2	3	0.00%	11.9%	GQAAVQQLQAEGLSPR	99.7%	91.5	25	77.8	1	0	0	1652.87	43	58
Cartilage-associated protein	CRTAP	CRTAP_HUMAN	46.6	100.0%	2	3	5	0.00%	5.7%	FLQFAYFK	99.3%	36.4	25	18.6	2	0	0	1063.56	150	157
Cartilage-associated protein	CRTAP	CRTAP_HUMAN	46.6	100.0%	2	3	5	0.00%	5.7%	TSITDMELALPDFFK	99.7%	44.9	25	44.9	3	0	0	1727.86	224	238
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	3	3	4	0.00%	8.8%	LVNSQGQLR	98.7%	33.3	25	22.3	2	0	0	1014.57	74	82
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	3	3	4	0.00%	8.8%	MLVSGQGPVMENAQGLGFR	99.7%	65	25	65	1	0	0	2022.97	134	152
Cat eye syndrome critical region protein 5	CECR5	CECR5_HUMAN	46.3	100.0%	3	3	4	0.00%	8.8%	NVVTVDELR	98.9%	34.1	25	14.9	1	0	0	1044.57	153	161
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	9	17	0.02%	12.5%	AAALVLQTIWGYK	99.7%	71.1	25	69.6	2	0	0	1433.82	821	833
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	9	17	0.02%	12.5%	ALSAIADLLTNEHER	99.7%	94.8	25	89.8	2	0	0	1652.86	711	725
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	9	17	0.02%	12.5%	GIPVLVGLLDHPK	99.7%	64.6	25	64.6	2	0	0	1357.82	409	421
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	9	17	0.02%	12.5%	GYELLFQPEVVR	99.7%	56.8	25	44.2	3	0	0	1449.77	655	666
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	9	17	0.02%	12.5%	QDVYGPQPQVR	99.7%	53.5	25	43.8	2	0	0	1286.65	254	264
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	9	17	0.02%	12.5%	SDFQVNLNNASR	99.7%	78.2	25	64.9	1	0	0	1364.66	847	858
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	9	17	0.02%	12.5%	SLDNNYSTPNER	99.7%	48.2	25	48.2	2	0	0	1409.63	899	910
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	9	17	0.02%	12.5%	VGGSSVDLHR	99.7%	69.1	25	49.1	2	0	0	1026.53	265	274
Catenin delta-1	CTNND1	CTND1_HUMAN	108.2	100.0%	9	9	17	0.02%	12.5%	YQEAAPNVANNTGPHAASCFGAK	99.0%	29.1	25	28.3	0	1	0	2375.08	600	622
CCAAT/enhancer-binding protein zeta	CEBPZ	CEBPZ_HUMAN	121.0	99.9%	2	2	3	0.00%	1.9%	ALLVQVVNK	99.7%	48.6	25	44.8	2	0	0	983.62	382	390
CCAAT/enhancer-binding protein zeta	CEBPZ	CEBPZ_HUMAN	121.0	99.9%	2	2	3	0.00%	1.9%	MLSALLTGVNR	99.7%	55.9	25	46.7	1	0	0	1174.66	482	492
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	15	15	26	0.02%	6.8%	EVTAAQVAR	99.7%	43.3	25	33.7	2	0	0	944.52	284	292

CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	15	15	26	0.02%	6.8%	GAFGVGQEQIDAFLK	99.7%	78.8	25	73.3	2	0	0	1579.81	194	208
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	15	15	26	0.02%	6.8%	GNAPEGLPQLMEVVR	99.7%	45.2	25	38.4	2	0	0	1609.84	1800	1814
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	15	15	26	0.02%	6.8%	GQQELLYVVPFVAK	99.7%	96.7	25	92.7	2	0	0	1590.89	1228	1241
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	15	15	26	0.02%	6.8%	IVEPPENIQEK	99.7%	41.7	25	38.9	2	0	0	1295.68	1088	1098
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	15	15	26	0.02%	6.8%	LATEFELRK	99.1%	35.2	25	31.8	1	0	0	1106.62	1523	1531
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	15	15	26	0.02%	6.8%	MVLNETYR	99.7%	49.5	25	46.2	1	0	0	1025.51	1164	1171
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	15	15	26	0.02%	6.8%	MYYFGIAALDR	96.8%	29.7	25	26.2	1	0	0	1319.65	950	960
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	15	15	26	0.02%	6.8%	NLDEQLSAPK	99.7%	46.2	25	35.4	2	0	0	1114.57	1311	1320
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	15	15	26	0.02%	6.8%	NLILSAFPR	99.7%	51.5	25	41.5	2	0	0	1030.60	2130	2138
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	15	15	26	0.02%	6.8%	SLDLIESLLR	99.7%	74.2	25	55.3	2	0	0	1158.67	450	459
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	15	15	26	0.02%	6.8%	SLLEVVVLSR	99.7%	63.4	25	31.6	2	0	0	1114.68	1641	1650
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	15	15	26	0.02%	6.8%	SNYEAMIDR	99.6%	38.8	25	36.7	1	0	0	1114.48	1815	1823
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	15	15	26	0.02%	6.8%	SPVTFLSDLR	99.7%	65.3	25	51.8	2	0	0	1134.62	2188	2197
CCR4-NOT transcription complex subunit 1	CNOT1	CNOT1_HUMAN	266.9	100.0%	15	15	26	0.02%	6.8%	YLFLNAIANQLR	99.7%	63.2	25	59.5	2	0	0	1435.81	2264	2275
CCR4-NOT transcription complex subunit 2	CNOT2	CNOT2_HUMAN	59.7	99.8%	2	2	4	0.00%	5.6%	EGSGNPTPLINPLAGR	99.7%	75.3	25	75.3	2	0	0	1592.84	240	255
CCR4-NOT transcription complex subunit 2	CNOT2	CNOT2_HUMAN	59.7	99.8%	2	2	4	0.00%	5.6%	TNSMSSSGLGSPNR	99.7%	49.5	25	49.5	2	0	0	1410.63	155	168
CDK5 regulatory subunit-associated protein 1	CDK5RAP1	CK5P1_HUMAN	67.7	99.8%	2	2	2	0.00%	3.8%	DFPDEVLQLIHER	98.8%	33.8	25	33.8	1	0	0	1610.82	379	391
CDK5 regulatory subunit-associated protein 1	CDK5RAP1	CK5P1_HUMAN	67.7	99.8%	2	2	2	0.00%	3.8%	ITSASSQTLR	99.7%	54.3	25	51.2	1	0	0	1063.57	576	585
CDP-diacylglycerol--inositol 3-phosphatidyltransferase	CDIPT	CDIPT_HUMAN	23.5	100.0%	5	8	22	0.02%	27.2%	FGAMLDMLTDR	99.7%	47.4	25	37.7	1	0	0	1269.60	63	73
CDP-diacylglycerol--inositol 3-phosphatidyltransferase	CDIPT	CDIPT_HUMAN	23.5	100.0%	5	8	22	0.02%	27.2%	MGLWVTAPIALLK	99.7%	59.7	25	36.1	7	0	0	1412.83	174	186
CDP-diacylglycerol--inositol 3-phosphatidyltransferase	CDIPT	CDIPT_HUMAN	23.5	100.0%	5	8	22	0.02%	27.2%	MIDLSGNPVLR	99.7%	73.8	25	70	9	0	0	1214.66	122	132
CDP-diacylglycerol--inositol 3-phosphatidyltransferase	CDIPT	CDIPT_HUMAN	23.5	100.0%	5	8	22	0.02%	27.2%	NMAALDAADR	99.7%	47.9	25	42.3	3	0	0	1063.48	200	209
CDP-diacylglycerol--inositol 3-phosphatidyltransferase	CDIPT	CDIPT_HUMAN	23.5	100.0%	5	8	22	0.02%	27.2%	SLISVIHLITAAR	99.7%	67.6	25	67.6	2	0	0	1393.85	187	199
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	4	4	6	0.01%	4.6%	FAEFQYLQPGPPR	99.7%	53.1	25	53.1	2	0	0	1549.78	405	417
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	4	4	6	0.01%	4.6%	LAEAEETAR	99.7%	50.7	25	48	2	0	0	989.49	868	876
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	4	4	6	0.01%	4.6%	LTPLQLEIQR	98.9%	34	25	24.1	1	0	0	1210.72	896	905
Cell cycle and apoptosis regulator protein 2	CCAR2	CCAR2_HUMAN	102.9	100.0%	4	4	6	0.01%	4.6%	VVTQNICQYR	99.7%	54.9	25	54.9	1	0	0	1280.64	748	757
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	4	4	8	0.01%	16.4%	ILLDDTGLAYICQTYER	99.7%	52	25	52	1	0	0	2044.01	189	205
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	4	4	8	0.01%	16.4%	LTSLGVIGALVK	99.7%	89.4	25	80.6	3	0	0	1170.75	137	148
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	4	4	8	0.01%	16.4%	NLQEGQVTDPR	99.7%	53.3	25	48.2	2	0	0	1256.62	282	292
Cell differentiation protein RCD1 homolog	RQCD1	RCD1_HUMAN	33.6	100.0%	4	4	8	0.01%	16.4%	TVATFILQK	99.7%	61.9	25	45.4	2	0	0	1020.61	180	188
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	6	7	12	0.01%	12.2%	DGSGTDHFIQALDSLSR	99.7%	47	25	43.3	0	2	0	1818.86	390	406
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	6	7	12	0.01%	12.2%	EFYEVVQSQR	99.7%	54.1	25	46.5	2	0	0	1284.62	9	18
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	6	7	12	0.01%	12.2%	ISFEYDLR	99.7%	46.7	25	34.8	2	0	0	1042.52	270	277
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	6	7	12	0.01%	12.2%	LQEFLADMGLPLK	99.7%	50.9	25	40.4	3	0	0	1474.80	311	323
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	6	7	12	0.01%	12.2%	VQTFSIHFGFK	99.3%	36.1	25	29.2	1	0	0	1310.69	358	368
Cell division control protein 45 homolog	CDC45	CDC45_HUMAN	65.6	100.0%	6	7	12	0.01%	12.2%	YVTDVGVLQR	99.7%	72.8	25	55.7	2	0	0	1149.63	238	247
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	16	18	34	0.03%	28.8%	AAGIEIQK	96.7%	29.6	25	18	2	0	0	829.48	193	200
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	16	18	34	0.03%	28.8%	AQDVLVQEMEVVK	99.7%	70.8	25	57.9	1	0	0	1487.78	632	644
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	16	18	34	0.03%	28.8%	ESDLPSAILQTSGVSEFTK	99.7%	106	25	106	2	0	0	2009.01	272	290
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	16	18	34	0.03%	28.8%	GGLNTPLHESDFSGVTPQR	99.7%	53	25	53	1	1	0	2011.98	381	399
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	16	18	34	0.03%	28.8%	GVDYNAEIPFEK	99.7%	50.7	25	50.7	2	0	0	1381.66	207	218
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	16	18	34	0.03%	28.8%	ILLGGYQSR	99.7%	60.3	25	42.1	4	0	0	1006.57	719	727
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	16	18	34	0.03%	28.8%	ILQEAQNLMALTNVDTPLK	99.7%	101	25	101	2	2	0	2112.14	362	380
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	16	18	34	0.03%	28.8%	LGLLGLPAPK	99.7%	70.7	25	70.7	4	0	0	978.63	478	487
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	16	18	34	0.03%	28.8%	LVLPAPQISDAELQEVVK	99.7%	90	25	89.2	2	0	0	1949.10	295	312
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	16	18	34	0.03%	28.8%	QTAEESGITNSASSTLLSEYNVTNNSVALR	97.9%	26	25	26	0	1	0	3156.53	322	351
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	16	18	34	0.03%	28.8%	QVVQTPNTVLSTPFR	99.7%	75.1	25	70.2	2	0	0	1686.92	400	414
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	16	18	34	0.03%	28.8%	TIAPIIGR	99.3%	36	25	36	1	0	0	840.53	84	91
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	16	18	34	0.03%	28.8%	TPSNGAEGLTPR	99.7%	89.5	25	78.8	2	0	0	1199.60	415	426
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	16	18	34	0.03%	28.8%	TVGFGTNNSEHITYLEHNPYEK	99.7%	49.7	25	49.7	0	2	0	2550.19	602	623

Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	16	18	34	0.03%	28.8%	VGQASEIAR	99.7%	72.8	25	55.1	2	0	0	930.50	313	321
Cell division cycle 5-like protein	CDC5L	CDC5L_HUMAN	92.3	100.0%	16	18	34	0.03%	28.8%	YADLLLEK	99.7%	46.1	25	43.1	1	0	0	964.54	788	795
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	8	8	13	0.01%	15.4%	AWYGLGQTYEILK	99.7%	84.6	25	79.4	2	0	0	1541.80	401	413
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	8	8	13	0.01%	15.4%	AYAVGDVEK	99.5%	37.5	25	29.2	2	0	0	951.48	459	467
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	8	8	13	0.01%	15.4%	IENMDTFSNLLYVR	99.7%	64.5	25	57.1	2	0	0	1714.85	297	310
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	8	8	13	0.01%	15.4%	MLVALGECYEK	99.7%	43.1	25	43.1	1	0	0	1312.63	435	445
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	8	8	13	0.01%	15.4%	MPFYCLYYYR	99.5%	37.8	25	35	2	0	0	1475.65	414	423
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	8	8	13	0.01%	15.4%	QLLLIAGLTR	99.7%	77.6	25	68.5	1	0	0	1097.70	35	44
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	8	8	13	0.01%	15.4%	VETCCVIGNYYSLR	99.7%	44.9	25	44.9	1	0	0	1733.80	331	344
Cell division cycle protein 23 homolog	CDC23	CDC23_HUMAN	68.8	100.0%	8	8	13	0.01%	15.4%	YQNLIDVGFSK	99.7%	53.9	25	49.4	2	0	0	1283.66	251	261
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	4	4	5	0.00%	16.1%	ELKLENHQENSR	98.2%	26.6	25	22	0	1	0	1496.75	205	216
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	4	4	5	0.00%	16.1%	EQDQRPLHPVANPHAEISTK	99.7%	38.1	25	38.1	0	1	0	2267.15	149	168
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	4	4	5	0.00%	16.1%	VFFTCNACGESVK	99.7%	50.3	25	50.3	1	0	0	1518.67	2	14
Cell growth-regulating nucleolar protein	LYAR	LYAR_HUMAN	43.6	100.0%	4	4	5	0.00%	16.1%	VRELLEQISAFDNVPR	99.7%	52.2	25	48.7	0	2	0	1886.01	94	109
Cellular nucleic acid-binding protein	CNBP	CNBP_HUMAN	19.5	99.8%	2	2	3	0.00%	12.4%	DCDLQEDACYNCGR	99.7%	57.9	25	57.9	1	0	0	1775.64	66	79
Cellular nucleic acid-binding protein	CNBP	CNBP_HUMAN	19.5	99.8%	2	2	3	0.00%	12.4%	TSEVNCYR	99.7%	40.4	25	40.4	2	0	0	1028.45	153	160
Cellular tumor antigen p53	TP53	P53_HUMAN	43.7	100.0%	3	3	6	0.01%	8.7%	ALPNNTSSSPQPK	99.7%	47.3	25	40.8	2	0	0	1340.68	307	319
Cellular tumor antigen p53	TP53	P53_HUMAN	43.7	100.0%	3	3	6	0.01%	8.7%	SVTCTYSPALNK	99.7%	54.6	25	47.1	3	0	0	1340.65	121	132
Cellular tumor antigen p53	TP53	P53_HUMAN	43.7	100.0%	3	3	6	0.01%	8.7%	TYQGSYGFR	98.0%	31.6	25	31.6	1	0	0	1078.50	102	110
Centrin-2	CETN2	CETN2_HUMAN	19.7	100.0%	3	4	6	0.01%	24.4%	EAFDLFDADGTGTIDVK	99.6%	38.7	25	38.7	1	0	0	1813.85	35	51
Centrin-2	CETN2	CETN2_HUMAN	19.7	100.0%	3	4	6	0.01%	24.4%	MISEIDKEGTGK	99.7%	40.6	25	37.6	3	0	0	1323.65	72	83
Centrin-2	CETN2	CETN2_HUMAN	19.7	100.0%	3	4	6	0.01%	24.4%	MNFGDFLTVMTQK	99.7%	64.6	25	56.4	2	0	0	1547.72	84	96
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	7	10	20	0.02%	38.9%	CGVQSFYTPR	99.7%	70.8	25	70.8	1	0	0	1214.56	219	228
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	7	10	20	0.02%	38.9%	GAEHITTYTFNTHK	99.7%	54.2	25	54.2	1	2	0	1619.78	197	210
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	7	10	20	0.02%	38.9%	LLLDTFEYQGLVK	99.7%	94.7	25	81.2	4	0	0	1538.85	135	147
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	7	10	20	0.02%	38.9%	SGASGASAAPAASAAAALAPSATR	99.7%	91.9	25	91.1	2	0	0	1985.00	18	41
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	7	10	20	0.02%	38.9%	SMVTEEFNGSDWEK	99.7%	73.3	25	73.3	4	0	0	1674.70	248	261
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	7	10	20	0.02%	38.9%	SNPGGFGIAPHCLDEGTVR	99.7%	48.3	25	47.5	2	2	0	1983.93	229	247
Centromere protein V	CENPV	CENPV_HUMAN	29.9	100.0%	7	10	20	0.02%	38.9%	SQAVEKPPSEKPR	99.3%	30.6	25	29.2	0	2	0	1452.78	53	65
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	4	4	6	0.01%	7.6%	AMGTLLNTAISEVIGK	99.7%	60.7	25	60.7	2	0	0	1633.88	652	667
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	4	4	6	0.01%	7.6%	LGIVWQDVLPVNIYCK	99.7%	64.5	25	58.1	1	0	0	1917.03	636	651
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	4	4	6	0.01%	7.6%	NLMTSEIHNTVK	99.7%	59.7	25	53.2	1	0	0	1386.70	413	424
Centromere/kinetochore protein zw10 homolog	ZW10	ZW10_HUMAN	88.8	100.0%	4	4	6	0.01%	7.6%	QLLDLPLDTDLENEK	99.7%	62.6	25	54.3	2	0	0	1755.90	306	320
Chaperone activity of bc1 complex-like, mitochondrial	ADCK3	ADCK3_HUMAN	72.0	100.0%	3	3	4	0.00%	8.5%	DKLEYFEERPFAAASIGQVHLAR	99.7%	64.3	25	64.3	0	1	0	2647.36	326	348
Chaperone activity of bc1 complex-like, mitochondrial	ADCK3	ADCK3_HUMAN	72.0	100.0%	3	3	4	0.00%	8.5%	LANFGGLAVGLGFGALAEVAKK	99.7%	38.1	25	35.5	0	2	0	2103.20	214	235
Chaperone activity of bc1 complex-like, mitochondrial	ADCK3	ADCK3_HUMAN	72.0	100.0%	3	3	4	0.00%	8.5%	VALLDFGATR	99.7%	82.4	25	72.9	1	0	0	1062.59	503	512
Chitobiosyldiphosphodolichol beta-mannosyltransferase	ALG1	ALG1_HUMAN	52.5	99.8%	2	2	3	0.00%	5.6%	ETPLDLQHR	95.1%	28	25	23.2	1	0	0	1108.57	224	232
Chitobiosyldiphosphodolichol beta-mannosyltransferase	ALG1	ALG1_HUMAN	52.5	99.8%	2	2	3	0.00%	5.6%	IQIVGLTELQSLAVGPR	99.7%	48.6	25	48.6	2	0	0	1794.05	83	99
Chromatin target of PRMT1 protein	CHTOP	CHTOP_HUMAN	26.4	100.0%	5	9	26	0.02%	29.0%	ASMQQQQQLASAR	99.7%	84.3	25	74.1	14	0	0	1462.71	39	51
Chromatin target of PRMT1 protein	CHTOP	CHTOP_HUMAN	26.4	100.0%	5	9	26	0.02%	29.0%	EQLDNQLDAYMSK	99.7%	100	25	100	4	0	0	1570.71	214	226
Chromatin target of PRMT1 protein	CHTOP	CHTOP_HUMAN	26.4	100.0%	5	9	26	0.02%	29.0%	GHLDAELDAYMAQTDPETND	99.7%	92.4	25	92.4	1	0	0	2221.92	229	248
Chromatin target of PRMT1 protein	CHTOP	CHTOP_HUMAN	26.4	100.0%	5	9	26	0.02%	29.0%	LAQQMENRPSVQAALK	99.7%	55.6	25	50.2	4	2	0	1799.94	55	70
Chromatin target of PRMT1 protein	CHTOP	CHTOP_HUMAN	26.4	100.0%	5	9	26	0.02%	29.0%	NKQPTPVNIR	95.3%	28.2	25	16.2	1	0	0	1166.66	29	38
Chromobox protein homolog 3	CBX3	CBX3_HUMAN	20.8	100.0%	3	4	5	0.00%	23.5%	IIGATDSSGELMFLMK	99.7%	77.8	25	26	2	0	0	1728.86	126	141
Chromobox protein homolog 3	CBX3	CBX3_HUMAN	20.8	100.0%	3	4	5	0.00%	23.5%	KVEEAEPEEFVVEK	99.7%	69.9	25	67.1	2	0	0	1661.83	21	34
Chromobox protein homolog 3	CBX3	CBX3_HUMAN	20.8	100.0%	3	4	5	0.00%	23.5%	WKDSDEADLVLAK	99.7%	53.2	25	41	1	0	0	1489.75	142	154
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	7	7	8	0.01%	8.4%	GGQAPGFLLR	99.5%	37.3	25	19.6	1	0	0	1015.57	10	19
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	7	7	8	0.01%	8.4%	GIPTYIYYFPR	99.7%	58.2	25	55.8	1	0	0	1389.72	867	877
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	7	7	8	0.01%	8.4%	GSVLIPGLVEGSTK	99.6%	39.3	25	30.6	1	0	0	1356.77	617	630
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	7	7	8	0.01%	8.4%	LLQPFLLR	99.4%	36.6	25	27.5	2	0	0	999.64	253	260
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	7	7	8	0.01%	8.4%	LQNILSQLR	99.7%	47.4	25	30.1	1	0	0	1084.65	311	319

Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	7	7	8	0.01%	8.4%	SFEQLVNLQK	99.7%	45.8	25	37.8	1	0	0	1205.65	591	600
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	CHD1L_HUMAN	101.0	100.0%	7	7	8	0.01%	8.4%	SYQLEGVNWLAQR	97.9%	31.4	25	29.4	1	0	0	1563.79	48	60
Chromodomain-helicase-DNA-binding protein 4	CHD4	CHD4_HUMAN	218.0	100.0%	8	8	10	0.01%	4.5%	APEPTPQQVAQQQ	99.7%	44.2	25	28.7	2	0	0	1421.70	1900	1912
Chromodomain-helicase-DNA-binding protein 4	CHD4	CHD4_HUMAN	218.0	100.0%	8	8	10	0.01%	4.5%	AYVSLFMR	99.7%	40.7	25	30.3	1	0	0	986.51	1458	1465
Chromodomain-helicase-DNA-binding protein 4	CHD4	CHD4_HUMAN	218.0	100.0%	8	8	10	0.01%	4.5%	ENEFSFEDNAIR	99.7%	47.7	25	47.7	1	0	0	1470.65	818	829
Chromodomain-helicase-DNA-binding protein 4	CHD4	CHD4_HUMAN	218.0	100.0%	8	8	10	0.01%	4.5%	GAADVEKVEEK	99.7%	42.5	25	25.4	2	0	0	1174.60	1637	1647
Chromodomain-helicase-DNA-binding protein 4	CHD4	CHD4_HUMAN	218.0	100.0%	8	8	10	0.01%	4.5%	HHYEQQQEDLAR	96.7%	29.5	25	29.5	1	0	0	1553.71	1320	1331
Chromodomain-helicase-DNA-binding protein 4	CHD4	CHD4_HUMAN	218.0	100.0%	8	8	10	0.01%	4.5%	IGVMSLIR	99.5%	37.5	25	20.8	1	0	0	904.53	1496	1503
Chromodomain-helicase-DNA-binding protein 4	CHD4	CHD4_HUMAN	218.0	100.0%	8	8	10	0.01%	4.5%	NFEALNAR	99.0%	34.4	25	22.3	1	0	0	934.47	993	1000
Chromodomain-helicase-DNA-binding protein 4	CHD4	CHD4_HUMAN	218.0	100.0%	8	8	10	0.01%	4.5%	TVQTAVFLYSLYK	99.7%	62.8	25	62.8	1	0	0	1532.84	758	770
Chromosome transmission fidelity protein 18 homolog	CHTF18	CTF18_HUMAN	107.4	99.8%	2	2	3	0.00%	2.7%	NLIQTLVSGIAPATR	99.6%	38.2	25	38.2	1	0	0	1553.90	735	749
Chromosome transmission fidelity protein 18 homolog	CHTF18	CTF18_HUMAN	107.4	99.8%	2	2	3	0.00%	2.7%	VVQGLFDNFLR	96.6%	29.5	25	28	2	0	0	1307.71	648	658
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	ALEHFTDLYDIKR	99.7%	50.6	25	43	0	2	0	1620.84	626	638
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	CNEPAVWSQLAK	96.9%	29.9	25	21	1	0	0	1402.68	1102	1113
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	ENPYYDSR	95.4%	28.2	25	20.4	1	0	0	1043.44	896	903
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	ESYVETELIFALAK	99.7%	67.4	25	64	2	0	0	1612.85	1166	1179
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	EVCFACVDGK	99.7%	50.2	25	50.2	3	0	0	1184.51	1255	1264
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	GQCDLELINVCNENSLFK	99.7%	61.3	25	61.3	2	0	0	2153.00	924	941
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	HELIEFR	95.9%	28.7	25	28.3	1	0	0	943.50	1502	1508
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	IAAYLFK	97.8%	31.1	25	24.2	2	0	0	825.49	1510	1516
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	IHEGCEEPATHNALAK	99.7%	34.9	25	34.9	0	2	0	1776.83	866	881
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	ISGETIFVTAPHEATAGIIGVNR	99.7%	70.3	25	70.3	0	2	0	2353.25	298	320
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	IVLDNSVFSEHR	99.7%	71.9	25	71.9	3	2	0	1415.73	1011	1022
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	IYIDSNNNPER	99.7%	65.3	25	55.2	4	0	0	1334.63	882	892
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	KFNALFAQGNYSEAAK	97.7%	25.7	25	25.7	0	1	0	1758.88	367	382
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	LAELEEFINGPNNAHIQQVGDR	99.7%	44.8	25	40.8	0	1	0	2464.22	1183	1204
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	LHIIEVGTPPTGNQPFPK	99.7%	38.8	25	38.8	0	2	0	1945.05	228	245
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	LLLPWLEAR	99.7%	46.6	25	29.5	3	0	0	1110.67	857	865
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	LLYNNVSNFGR	99.7%	62	25	62	4	0	0	1296.67	1216	1226
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	LPVVIGGLLDVDCSEDVIK	99.7%	73.5	25	73.5	3	0	0	2041.09	812	830
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	LTDQLPLIIVCDR	97.0%	29.9	25	29.9	1	0	0	1555.85	768	780
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	NLQNLLILTAIK	99.7%	84.3	25	83.9	5	0	0	1353.85	1023	1034
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	NNLAGAEELFAR	99.7%	99.8	25	96.8	4	0	0	1304.66	355	366
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	SVDPTLALSVYLR	99.7%	60.7	25	58.3	4	0	0	1433.80	469	481
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	TLQIFNIEMK	99.7%	61.8	25	48.5	2	0	0	1252.66	87	96
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	VANVELYYR	99.7%	75.3	25	72.4	4	0	0	1126.59	1398	1406
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	VDKLDASESLR	98.3%	32.3	25	27.7	1	0	0	1232.65	1610	1620
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	VGYTPDWIFLLR	99.7%	84.9	25	79.5	3	0	0	1479.80	508	519
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	VIQCFAETGQVQK	99.7%	94.5	25	77.2	4	0	0	1507.76	488	500
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	VVGAMQLYSVDR	99.7%	66.4	25	60	3	0	0	1337.69	177	188
Clathrin heavy chain 1	CLTC	CLH1_HUMAN	191.6	100.0%	29	30	75	0.07%	22.4%	WLLLTGISAQQNR	99.7%	77.3	25	64	3	0	0	1499.83	164	176
Clathrin light chain A	CLTA	CLCA_HUMAN	27.1	100.0%	2	2	3	0.00%	7.3%	LEALDANSR	99.6%	38.6	25	34.6	1	0	0	988.51	121	129
Clathrin light chain A	CLTA	CLCA_HUMAN	27.1	100.0%	2	2	3	0.00%	7.3%	LQSEPESIR	98.9%	34	25	23.2	2	0	0	1058.55	103	111
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	17	17	29	0.03%	12.8%	DLSGMFTTESR	99.7%	65.1	25	51.5	2	0	0	1243.56	703	713
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	17	17	29	0.03%	12.8%	EVLLVALGSR	99.7%	81.7	25	66.6	2	0	0	1056.64	848	857
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	17	17	29	0.03%	12.8%	GFLYFNR	95.0%	27.9	25	23	1	0	0	916.47	986	992
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	17	17	29	0.03%	12.8%	HGFLILSR	99.4%	36.7	25	30.8	1	0	0	942.55	572	579
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	17	17	29	0.03%	12.8%	IFLWSLR	99.7%	48.5	25	0	2	0	0	934.55	1190	1196
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	17	17	29	0.03%	12.8%	ISVLPAYLSYDAPWPVR	99.7%	76	25	76	1	0	0	1947.04	998	1014
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	17	17	29	0.03%	12.8%	LGNSLLLK	98.9%	34	25	16.8	2	0	0	857.55	388	395
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	17	17	29	0.03%	12.8%	LSVVEYDPGTHDLK	99.7%	56.4	25	48.3	2	0	0	1572.79	103	116

Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	17	17	29	0.03%	12.8%	NGALSVLQK	99.7%	42.5	25	28.8	1	0	0	929.54	509	517
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	17	17	29	0.03%	12.8%	NVLDGELLNR	99.7%	77	25	61.3	2	0	0	1142.62	1397	1406
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	17	17	29	0.03%	12.8%	QGELPLVK	99.6%	38.2	25	30.7	2	0	0	883.52	840	847
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	17	17	29	0.03%	12.8%	SSFLPSYIIDVR	99.7%	81.3	25	66.8	2	0	0	1396.75	183	194
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	17	17	29	0.03%	12.8%	TLSLHYFEEPELR	99.7%	36.5	25	36.5	0	1	0	1633.82	117	129
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	17	17	29	0.03%	12.8%	VLVDSSFGQPTTQGEAR	99.7%	94.8	25	93	2	0	0	1791.89	817	833
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	17	17	29	0.03%	12.8%	VYAVATSTNTPCAR	99.7%	98.6	25	88.9	2	0	0	1510.73	1033	1046
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	17	17	29	0.03%	12.8%	YIVQVSPLGIR	99.7%	60.4	25	40.1	2	0	0	1244.74	617	627
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	CPSF1_HUMAN	160.9	100.0%	17	17	29	0.03%	12.8%	YLYLSTMER	99.7%	49.5	25	39.7	2	0	0	1175.58	1407	1415
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	12	12	20	0.02%	18.5%	DEQLLTNVLETLR	99.7%	41.3	25	38.9	1	0	0	1543.83	216	228
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	12	12	20	0.02%	18.5%	DLFIQWCQDPK	99.7%	68.3	25	64.5	2	0	0	1449.68	340	350
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	12	12	20	0.02%	18.5%	ELEEYLEKEK	99.1%	35.1	25	24.9	1	0	0	1309.65	391	400
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	12	12	20	0.02%	18.5%	FLIDNPSEK	99.3%	36.4	25	7.14	2	0	0	1062.55	367	375
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	12	12	20	0.02%	18.5%	FSQIVNLK	99.4%	36.8	25	23.3	2	0	0	948.55	131	138
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	12	12	20	0.02%	18.5%	GDGNVLIAVDTAGR	99.7%	42.3	25	42.3	1	0	0	1357.71	229	242
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	12	12	20	0.02%	18.5%	IRDLLYEQYAIV	99.7%	50.8	25	50.8	2	0	0	1495.82	771	782
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	12	12	20	0.02%	18.5%	LGLNCAIYATIPVYK	99.7%	74.9	25	73.6	1	0	0	1695.91	78	92
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	12	12	20	0.02%	18.5%	LHETVDATSETHIYQVR	99.7%	56.5	25	56.5	0	2	0	1998.99	593	609
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	12	12	20	0.02%	18.5%	NSIILTYR	99.7%	47.5	25	34.1	2	0	0	979.56	351	358
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	12	12	20	0.02%	18.5%	VLELAQLLDQIWR	99.7%	53.5	25	53.5	2	0	0	1596.91	243	255
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	CPSF2_HUMAN	88.5	100.0%	12	12	20	0.02%	18.5%	VVLASQPDLECGFSR	99.7%	76.9	25	75.6	2	0	0	1677.83	325	339
Cleavage and polyadenylation specificity factor subunit 4	CPSF4	CPSF4_HUMAN	30.3	99.8%	2	2	3	0.00%	10.8%	SGAAVCEFFLK	99.7%	50.7	25	50.7	2	0	0	1228.60	36	46
Cleavage and polyadenylation specificity factor subunit 4	CPSF4	CPSF4_HUMAN	30.3	99.8%	2	2	3	0.00%	10.8%	TPQVIGVMQSQNSSAGNR	99.7%	111	25	109	1	0	0	1873.92	218	235
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	5	6	10	0.01%	24.2%	GVTQFGNK	99.7%	40.6	25	22.6	2	0	0	850.44	16	23
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	5	6	10	0.01%	24.2%	LFLVQLQEK	99.7%	63.4	25	44.8	2	0	0	1117.66	174	182
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	5	6	10	0.01%	24.2%	LMTEILGR	99.7%	42.9	25	33.4	2	0	0	932.52	124	131
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	5	6	10	0.01%	24.2%	LPGGELNPGEDEVEGLKR	99.7%	78.6	25	77.8	1	2	0	1908.97	106	123
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	CPSF5_HUMAN	26.2	100.0%	5	6	10	0.01%	24.2%	YIQQTKPLTLER	99.7%	48.2	25	28.8	1	0	0	1489.84	24	35
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	8	11	22	0.02%	20.0%	AISSSAISR	99.5%	37.4	25	22.9	2	0	0	891.49	423	431
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	8	11	22	0.02%	20.0%	AVSDASAGDYGSAIETLVTAISLIK	99.7%	88.3	25	88.3	2	0	0	2452.28	432	456
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	8	11	22	0.02%	20.0%	GAAPNVVYTYTGK	99.7%	87	25	83.7	2	0	0	1340.68	67	79
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	8	11	22	0.02%	20.0%	GDYGPPGR	96.9%	29.8	25	29.8	1	0	0	818.38	393	400
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	8	11	22	0.02%	20.0%	GFALVGVGSEASSK	99.7%	114	25	106	3	0	0	1308.68	125	138
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	8	11	22	0.02%	20.0%	QFLSQFEMQSR	99.7%	61.3	25	54.4	4	0	0	1400.66	162	172
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	8	11	22	0.02%	20.0%	TPLSEAEFEEIMNR	99.7%	129	25	125	4	0	0	1665.78	407	420
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	CPSF6_HUMAN	59.2	100.0%	8	11	22	0.02%	20.0%	VLISSLQDCLHGIESK	99.7%	71.7	25	71.7	2	2	0	1798.94	468	483
Cleavage and polyadenylation specificity factor subunit 7	CPSF7	CPSF7_HUMAN	52.1	100.0%	4	4	8	0.01%	12.7%	AVSGASAGDYSDAIETLLTAIAVIK	99.7%	57	25	52.6	0	1	0	2436.29	355	379
Cleavage and polyadenylation specificity factor subunit 7	CPSF7	CPSF7_HUMAN	52.1	100.0%	4	4	8	0.01%	12.7%	QNLSQFEAQAR	99.7%	83.1	25	73.1	3	0	0	1291.64	163	173
Cleavage and polyadenylation specificity factor subunit 7	CPSF7	CPSF7_HUMAN	52.1	100.0%	4	4	8	0.01%	12.7%	SYSVGASGSSSR	99.7%	64	25	59	2	0	0	1144.52	407	418
Cleavage and polyadenylation specificity factor subunit 7	CPSF7	CPSF7_HUMAN	52.1	100.0%	4	4	8	0.01%	12.7%	TPAILYTYSGLR	99.7%	62.4	25	57.9	2	0	0	1354.74	67	78
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	21	22	63	0.06%	19.4%	ASNLENSTYDLYTIPK	99.7%	99.2	25	93.8	4	0	0	1828.90	383	398
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	21	22	63	0.06%	19.4%	DADSITLFDVQQK	99.7%	73.3	25	63.4	2	0	0	1479.73	468	480
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	21	22	63	0.06%	19.4%	DADSQNPDAPEGK	99.7%	50	25	50	1	0	0	1343.57	399	411
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	21	22	63	0.06%	19.4%	DVAVMQLR	99.7%	45.6	25	32.1	7	0	0	931.50	351	358
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	21	22	63	0.06%	19.4%	GFFEGTIASK	99.7%	56.7	25	56.7	4	0	0	1056.54	816	825
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	21	22	63	0.06%	19.4%	GITGVDLFGTTDAVVK	99.7%	79.7	25	75.2	3	0	0	1592.85	183	198
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	21	22	63	0.06%	19.4%	LLELGPKPEVAQQTR	99.7%	45.2	25	43.8	0	3	0	1678.95	1128	1142
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	21	22	63	0.06%	19.4%	LNDLIQR	99.7%	52.7	25	37.6	4	0	0	871.50	1003	1009
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	21	22	63	0.06%	19.4%	LVGQSIIAYLQK	99.7%	99.4	25	99.4	6	0	0	1332.79	620	631
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	21	22	63	0.06%	19.4%	NLSPGAVESDVR	99.7%	69.4	25	56.8	3	0	0	1243.63	171	182
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	21	22	63	0.06%	19.4%	QELILSNSEDK	97.1%	30	25	25.3	1	0	0	1275.64	261	271

Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	21	22	63	0.06%	19.4%	QLFLQTYAR	99.7%	52.2	25	39.1	3	0	0	1139.62	957	965
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	21	22	63	0.06%	19.4%	SILLSVPLLVVDNK	99.7%	75.9	25	75.9	5	0	0	1509.93	1031	1044
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	21	22	63	0.06%	19.4%	SSGLTAVWVAR	99.7%	70.5	25	47.3	2	0	0	1146.63	413	423
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	21	22	63	0.06%	19.4%	TALNLFFK	99.7%	51.7	25	47.4	3	0	0	953.55	1107	1114
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	21	22	63	0.06%	19.4%	TGVQTFR	95.9%	28.8	25	21.4	2	0	0	808.43	282	288
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	21	22	63	0.06%	19.4%	TLDLPIYVTR	99.7%	62.8	25	58.4	4	0	0	1190.68	563	572
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	21	22	63	0.06%	19.4%	VLTIDPTEFK	97.2%	30.2	25	25.9	1	0	0	1162.64	589	598
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	21	22	63	0.06%	19.4%	VTTVTEIGKDVIGLR	99.7%	49.5	25	49.5	1	0	0	1600.93	1203	1217
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	21	22	63	0.06%	19.4%	VWDISGLR	99.7%	49	25	33.5	2	0	0	945.52	161	168
Coatomer subunit alpha	COPA	COPA_HUMAN	138.3	100.0%	21	22	63	0.06%	19.4%	YAVTTGDHGIIR	99.7%	46.2	25	40.6	2	0	0	1302.68	551	562
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	AAAQCYIDLIIK	99.7%	63.2	25	53.8	3	0	0	1378.74	280	291
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	ALSGYCGFMAANLYAR	99.7%	96.6	25	96.6	2	0	0	1764.82	883	898
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	CIYNLLQSSSPAVK	99.7%	90.3	25	90.3	2	0	0	1579.81	248	261
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	DLQHPNEFIR	99.7%	42.3	25	29	2	0	0	1268.64	108	117
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	EAELLEPLMPAIR	99.7%	50.2	25	38.3	2	0	0	1481.80	129	141
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	EAGELKPEEEITVGPVQK	99.7%	70.9	25	66.8	1	2	0	1953.02	496	513
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	EDIQSVMTEIR	99.7%	70.5	25	68.6	2	0	0	1320.65	470	480
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	FVLPLQDHTIK	98.7%	33.5	25	14.2	1	0	0	1310.75	65	75
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	GALWILGEYCSTK	99.7%	81.8	25	80.3	4	0	0	1497.74	457	469
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	KEEDRPPLR	96.2%	29	25	26.6	1	0	0	1139.62	535	543
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	KPITDDDVDR	99.7%	65.8	25	50.1	2	0	0	1173.57	603	612
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	LKEAELLEPLMPAIR	99.7%	49	25	46	0	1	0	1738.98	127	141
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	LLLVFWEIVPK	99.7%	67.6	25	64.8	4	0	0	1356.83	77	87
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	LPGLLMTIIR	99.7%	61.3	25	56.4	4	0	0	1126.70	55	64
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	LVEKPSPLTLAPHDFANIK	99.7%	54.7	25	54.7	0	2	0	2090.16	768	786
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	LVTEMGTYATQSALSSSRPTK	99.7%	40.9	25	40.9	0	4	0	2228.12	514	534
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	MLEVFHAIK	99.7%	50.4	25	39.1	2	0	0	1087.60	442	450
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	NAVLAIYTIYR	99.7%	81.2	25	81.2	3	0	0	1296.73	154	164
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	NVEELVIVLK	99.7%	44.1	25	37.8	2	0	0	1155.70	352	361
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	NVEELVIVLKK	98.4%	32.4	25	32.4	1	0	0	1283.79	352	362
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	NVTVQPDDPISFMQLTAK	99.7%	94.5	25	92.4	2	0	0	2004.01	662	679
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	SLGEIPIVESEIKK	99.7%	59.5	25	57.9	2	0	0	1541.88	482	495
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	SQGMALSLGDK	99.7%	52.8	25	43.8	3	0	0	1106.55	933	943
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	TLQLALDLVSSR	99.7%	88.8	25	88.8	2	0	0	1315.76	340	351
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	TNNVSEHEDTDKYR	99.7%	55.1	25	55.1	0	4	0	1707.76	367	380
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	VASTENGIIFGNIVYDVSGAASDR	99.7%	34.3	25	33.4	0	1	0	2455.21	791	814
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	VIIMILNGEK	99.7%	48.8	25	41.2	2	0	0	1129.67	45	54
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	VLQDLVMDILR	99.7%	74.8	25	70.7	8	0	0	1314.75	317	327
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	VLSECSPLMNDIFNK	99.7%	87.2	25	87.2	2	0	0	1766.85	619	633
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	VLSTPDLEVR	99.2%	35.2	25	24	2	0	0	1128.63	328	337
Coatomer subunit beta	COPB1	COPB_HUMAN	107.1	100.0%	31	36	77	0.07%	39.7%	YVALVQEK	99.6%	38.6	25	27	2	0	0	949.54	568	575
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	5	5	12	0.01%	6.3%	AAESLADPTEYENLFPGLK	99.7%	69	25	68	4	0	0	2065.01	784	802
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	5	5	12	0.01%	6.3%	HSEVQQANLK	99.7%	55.2	25	47.2	4	0	0	1153.60	319	328
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	5	5	12	0.01%	6.3%	LPEAAFLAR	99.7%	59.5	25	48.2	2	0	0	987.56	751	759
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	5	5	12	0.01%	6.3%	TMYLLGYIPK	99.7%	54.7	25	54	1	0	0	1198.65	560	569
Coatomer subunit beta'	COPB2	COPB2_HUMAN	102.5	100.0%	5	5	12	0.01%	6.3%	VFNYNTLER	99.7%	41.1	25	32.2	1	0	0	1155.58	83	91
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	20	22	42	0.04%	38.9%	ENVNLAQIR	99.7%	69.1	25	52.6	3	0	0	1056.58	123	131
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	20	22	42	0.04%	38.9%	FSTETTFLVDKYEIL	98.5%	32.7	25	32.7	1	0	0	1805.92	497	511
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	20	22	42	0.04%	38.9%	GKEVDNFVDK	99.7%	48	25	41.2	2	0	0	1150.57	232	241
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	20	22	42	0.04%	38.9%	GVQLQTHPNVDKK	99.7%	44	25	40.3	1	1	0	1463.80	324	336
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	20	22	42	0.04%	38.9%	IEGLLAAFPK	99.7%	55.1	25	44.5	2	0	0	1058.62	29	38

Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	20	22	42	0.04%	38.9%	KNYCNIQVTK	99.7%	56.5	25	53.8	2	0	0	1267.65	476	485
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	20	22	42	0.04%	38.9%	LFTAESLIGLK	99.7%	89.4	25	77.7	2	0	0	1191.70	337	347
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	20	22	42	0.04%	38.9%	LFTAESLIGLKNPEK	99.7%	58	25	48.3	1	0	0	1659.93	337	351
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	20	22	42	0.04%	38.9%	LYMVLITTK	99.7%	66.4	25	66.4	2	0	0	1081.63	64	72
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	20	22	42	0.04%	38.9%	NSNILEDLETLR	99.7%	83.9	25	76.5	4	0	0	1416.73	73	84
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	20	22	42	0.04%	38.9%	NTLEWCLPVIDAK	99.7%	71.1	25	58.9	2	0	0	1558.79	436	448
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	20	22	42	0.04%	38.9%	NYCNIQVTK	99.7%	40.2	25	29.1	2	0	0	1139.55	477	485
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	20	22	42	0.04%	38.9%	QHTFVETESVR	99.7%	63.7	25	63.7	2	0	0	1332.65	45	55
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	20	22	42	0.04%	38.9%	SEGETIMSSSMGK	99.7%	45.3	25	36.7	2	0	0	1375.57	244	256
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	20	22	42	0.04%	38.9%	SFPVNSDVGVLK	99.7%	59	25	54.7	2	0	0	1261.68	352	363
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	20	22	42	0.04%	38.9%	TFTEMDSHEEK	99.7%	55.1	25	48.4	2	0	0	1353.56	132	142
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	20	22	42	0.04%	38.9%	TRIEGLLAAFPK	99.7%	34.6	25	26.2	2	2	0	1315.77	27	38
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	20	22	42	0.04%	38.9%	VAPAPARPSGPSK	99.7%	54.6	25	29.8	1	0	0	1234.69	212	224
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	20	22	42	0.04%	38.9%	VLLAAAVCTK	99.7%	58	25	54	2	0	0	1045.61	2	11
Coatomer subunit delta	ARCN1	COPD_HUMAN	57.2	100.0%	20	22	42	0.04%	38.9%	VTQVDGNSPVR	99.7%	59.4	25	43.7	2	0	0	1171.61	486	496
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	8	9	16	0.02%	35.7%	APPAPGPASGGSGEVDELFDVK	99.7%	116	25	116	2	0	0	2097.01	2	23
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	8	9	16	0.02%	35.7%	DSIVAELDREMSR	99.7%	48.8	25	46.1	2	0	0	1536.73	98	110
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	8	9	16	0.02%	35.7%	DVERDVFLYR	99.6%	39.2	25	29.5	2	0	0	1311.67	49	58
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	8	9	16	0.02%	35.7%	ENDFDRLVLQYAPSA	99.5%	37.5	25	25.3	2	0	0	1737.84	294	308
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	8	9	16	0.02%	35.7%	LDRLDLAR	97.6%	30.9	25	29.3	1	0	0	971.56	159	166
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	8	9	16	0.02%	35.7%	LQDAYYIFQEMADK	99.7%	79.3	25	58.2	4	0	0	1734.80	198	211
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	8	9	16	0.02%	35.7%	MFADYLAHESR	99.3%	36.2	25	36.2	1	0	0	1355.60	86	96
Coatomer subunit epsilon	COPE	COPE_HUMAN	34.5	100.0%	8	9	16	0.02%	35.7%	NAFYIGSYQQCINEAQR	99.7%	101	25	101	2	0	0	2061.94	24	40
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	50	0.05%	34.1%	AIVDCIISIIEENSESK	99.7%	51.3	25	51.3	1	0	0	1919.96	416	432
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	50	0.05%	34.1%	ALCQITDSTMLQAIER	99.7%	93	25	93	2	0	0	1849.91	127	142
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	50	0.05%	34.1%	ALQQYTLEPSEKPFDLK	98.3%	26.9	25	23	0	1	0	2007.04	561	577
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	50	0.05%	34.1%	ATFYLNVLEQK	99.7%	69.2	25	60.4	2	0	0	1325.71	528	538
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	50	0.05%	34.1%	DSPLFDFIESCLR	99.7%	62	25	57.2	1	0	0	1598.75	248	260
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	50	0.05%	34.1%	ELAPAVSVLQLFCSSPK	99.7%	110	25	110	5	1	0	1845.98	284	300
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	50	0.05%	34.1%	EMSCIAEDVIIVTSSLTK	99.7%	53.4	25	51	1	0	0	1996.00	94	111
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	50	0.05%	34.1%	FGAQNEEMLPSILVLLK	99.7%	70.3	25	62	1	0	0	1902.04	498	514
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	50	0.05%	34.1%	GGHDILVR	98.8%	33.8	25	10.4	1	0	0	866.48	836	843
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	50	0.05%	34.1%	ILHLLGQEGPK	99.7%	59.6	25	59.1	2	2	0	1204.71	455	465
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	50	0.05%	34.1%	LFQSNDPTLR	99.7%	64.2	25	47.4	2	0	0	1190.62	76	85
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	50	0.05%	34.1%	LLLLDTVTMQVTAR	99.7%	77.9	25	77.3	2	0	0	1589.89	846	859
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	50	0.05%	34.1%	QEIFQEQLAAVPEFR	99.7%	73.8	25	66.8	2	0	0	1804.92	610	624
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	50	0.05%	34.1%	SAVLQEAR	99.7%	44.8	25	13.3	3	0	0	873.48	25	32
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	50	0.05%	34.1%	SIATLAITTLLK	99.7%	97.9	25	97.9	6	0	0	1244.78	339	350
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	50	0.05%	34.1%	SLEELPVDIILASVG	99.1%	35	25	34.5	2	0	0	1554.86	860	874
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	50	0.05%	34.1%	SLPYNQPGTCYTLVALPK	99.7%	68.8	25	68	2	0	0	2022.04	697	714
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	50	0.05%	34.1%	SSPEPVALTESETEYVIR	99.7%	113	25	110	2	0	0	2006.99	632	649
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	50	0.05%	34.1%	TLEEAVGNIVK	99.0%	34.6	25	27.6	1	0	0	1172.65	796	806
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	50	0.05%	34.1%	VFNETPINPR	99.7%	43.9	25	37.8	2	0	0	1186.62	33	42
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	50	0.05%	34.1%	VVLEHEEVR	99.7%	59.1	25	47.2	4	0	0	1109.59	480	488
Coatomer subunit gamma-1	COPG1	COPG1_HUMAN	97.7	100.0%	22	24	50	0.05%	34.1%	VVVVQAISALCQK	99.7%	77	25	77	2	0	0	1414.81	377	389
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	6	6	16	0.02%	11.7%	AIVDCIISIVEENPESK	99.7%	76.2	25	74.4	4	0	0	1915.97	416	432
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	6	6	16	0.02%	11.7%	ATFYLNVLQQR	99.7%	59.7	25	54.8	2	0	0	1352.73	528	538
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	6	6	16	0.02%	11.7%	IFNETPINPR	99.7%	54.8	25	47.9	4	0	0	1200.64	33	42
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	6	6	16	0.02%	11.7%	ITDGTMLQAIER	99.7%	83.8	25	61.2	2	0	0	1347.69	131	142
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	6	6	16	0.02%	11.7%	LFQSNDQTLR	99.7%	50.7	25	34.7	1	0	0	1221.62	76	85
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	6	6	16	0.02%	11.7%	SAVLQEAR	99.7%	44.8	25	13.3	3	0	0	873.48	25	32

Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	6	6	16	0.02%	11.7%	SIATLAITTLLK	99.7%	97.9	25	97.9	6	0	0	1244.78	339	350
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	6	6	16	0.02%	11.7%	VVLENEAVR	99.7%	49.8	25	45.6	3	0	0	1028.57	480	488
Coatomer subunit gamma-2	COPG2	COPG2_HUMAN	97.6	100.0%	6	6	16	0.02%	11.7%	VVVVQAISALCQK	99.7%	77	25	77	2	0	0	1414.81	377	389
COBW domain-containing protein 1	CBWD1	————————	44.1	99.8%	2	2	3	0.00%	5.6%	IPVTIITGYLGAGK	99.7%	82.6	25	82.6	2	0	0	1402.83	42	55
COBW domain-containing protein 1	CBWD1	————————	44.1	99.8%	2	2	3	0.00%	5.6%	NLDKDILK	99.4%	36.8	25	23.9	1	0	0	958.56	363	370
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	5	5	17	0.02%	42.2%	AVLFCLSEDKK	99.7%	57.6	25	53.7	2	0	0	1309.68	35	45
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	5	5	17	0.02%	42.2%	EILVGDVGQTVDDPYATFVK	99.7%	96	25	96	2	0	0	2166.10	54	73
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	5	5	17	0.02%	42.2%	HELQANCYEEVKDR	99.7%	37.8	25	37.8	0	2	0	1790.81	133	146
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	5	5	17	0.02%	42.2%	LGGSAVISLEGKPL	99.7%	75.1	25	70.9	5	0	0	1340.78	153	166
Cofilin-1	CFL1	COF1_HUMAN	18.5	100.0%	5	5	17	0.02%	42.2%	YALYDATYETK	99.7%	66.2	25	54.3	6	0	0	1337.63	82	92
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	3	3	5	0.00%	2.7%	FALTFGLDQLK	99.7%	43.3	25	0	2	0	0	1252.69	955	965
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	3	3	5	0.00%	2.7%	HTDTDVLEACSK	99.7%	53.2	25	50.6	1	0	0	1375.62	623	634
Cohesin subunit SA-2	STAG2	STAG2_HUMAN	141.3	100.0%	3	3	5	0.00%	2.7%	YYNDYGDIIK	99.7%	50.4	25	44.5	2	0	0	1263.59	892	901
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	13	17	28	0.03%	29.8%	ARVEENFLK	99.7%	56.8	25	43.6	2	0	0	1105.60	411	419
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	13	17	28	0.03%	29.8%	ELLESNFTLVGDDGTNK	99.7%	92.5	25	87.2	2	0	0	1851.90	173	189
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	13	17	28	0.03%	29.8%	ELLESNFTLVGDDGTNKEATSTGK	99.7%	50.6	25	50.6	0	2	0	2526.22	173	196
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	13	17	28	0.03%	29.8%	EMQDLSEFCSDKPK	99.7%	56.6	25	48.6	1	0	0	1713.75	275	288
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	13	17	28	0.03%	29.8%	IMNEEDPEKQR	99.7%	49.5	25	49.5	4	1	0	1388.65	444	454
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	13	17	28	0.03%	29.8%	IMQEEGQPLK	99.6%	39	25	32.3	2	0	0	1172.60	342	351
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	13	17	28	0.03%	29.8%	LAQAWFNTHR	99.7%	34.6	25	28.9	0	2	0	1243.63	163	172
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	13	17	28	0.03%	29.8%	LNQENEHIYNLWCSGR	99.7%	40	25	40	0	2	0	2032.93	197	212
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	13	17	28	0.03%	29.8%	MMRPVSDQVQIK	99.6%	32.3	25	26.1	0	2	0	1431.74	237	248
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	13	17	28	0.03%	29.8%	QDLLNVLAR	99.7%	70	25	57.1	2	0	0	1041.61	228	236
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	13	17	28	0.03%	29.8%	RQDLLNVLAR	99.7%	44	25	41.7	2	0	0	1197.71	227	236
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	13	17	28	0.03%	29.8%	TLLFTFNVPGSGNTYPK	99.7%	68.9	25	67.2	2	0	0	1855.96	358	374
Coiled-coil domain-containing protein 47	CCDC47	CCD47_HUMAN	55.9	100.0%	13	17	28	0.03%	29.8%	VCCEGMLIQLR	99.7%	73.9	25	73.8	2	0	0	1378.66	213	223
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	6	6	11	0.01%	26.0%	AAANEQLTR	99.7%	61.3	25	48.3	2	0	0	973.51	96	104
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	6	6	11	0.01%	26.0%	LSENVIDR	99.7%	55.4	25	48.9	2	0	0	945.50	28	35
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	6	6	11	0.01%	26.0%	RVAEELALEQAK	98.9%	34	25	30.8	1	0	0	1356.75	65	76
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	6	6	11	0.01%	26.0%	VAEELALEQAK	99.7%	87.6	25	78.6	2	0	0	1200.65	66	76
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	6	6	11	0.01%	26.0%	VTFEADENENITVVK	99.7%	44	25	43.3	2	0	0	1707.84	10	24
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCHD3	CHCH3_HUMAN	26.2	100.0%	6	6	11	0.01%	26.0%	YSGAYGASVSDEELK	99.7%	111	25	111	2	0	0	1575.72	49	63
Coiled-coil-helix-coiled-coil-helix domain-containing protein 6, mitochondrial	CHCHD6	CHCH6_HUMAN	26.5	99.8%	2	2	3	0.00%	10.2%	ASLPTGEGSISHEEQK	99.7%	49.9	25	46.2	1	0	0	1669.80	118	133
Coiled-coil-helix-coiled-coil-helix domain-containing protein 6, mitochondrial	CHCHD6	CHCH6_HUMAN	26.5	99.8%	2	2	3	0.00%	10.2%	LSENVVNR	99.6%	38.5	25	35.4	2	0	0	930.50	30	37
Cold-inducible RNA-binding protein	CIRBP	CIRBP_HUMAN	18.6	99.8%	2	2	4	0.00%	14.0%	DSYDSYATHNE	99.7%	75	25	75	2	0	0	1301.49	162	172
Cold-inducible RNA-binding protein	CIRBP	CIRBP_HUMAN	18.6	99.8%	2	2	4	0.00%	14.0%	YGQISEVVVVKDR	99.7%	96.4	25	91.4	2	0	0	1491.82	29	41
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	C1QBP_HUMAN	31.4	100.0%	5	7	11	0.01%	31.6%	AFVDFLSDEIKEER	99.7%	92.5	25	88.7	2	2	0	1697.84	81	94
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	C1QBP_HUMAN	31.4	100.0%	5	7	11	0.01%	31.6%	ALVLDCHYPEDEVGQEDEAESDIFSIR	99.7%	66.3	25	66.3	0	1	0	3136.41	181	207
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	C1QBP_HUMAN	31.4	100.0%	5	7	11	0.01%	31.6%	EVSFQSTGESEWK	99.7%	69.3	25	66.9	2	0	0	1513.68	208	220
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	C1QBP_HUMAN	31.4	100.0%	5	7	11	0.01%	31.6%	MSGGWELELNGTEAK	99.7%	74.7	25	74.7	1	0	0	1621.75	105	119
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	C1QBP_HUMAN	31.4	100.0%	5	7	11	0.01%	31.6%	VEEQEPELTSTPNFVVEVIK	99.7%	83.5	25	83.5	2	1	0	2287.17	155	174
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	11	11	21	0.02%	9.4%	AIIDEFEQK	96.4%	29.3	25	23.8	1	0	0	1092.56	1280	1288
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	11	11	21	0.02%	9.4%	DLAYCVSQLPLTER	99.7%	59.4	25	59.4	2	0	0	1664.83	1225	1238
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	11	11	21	0.02%	9.4%	EAVLNAYR	99.7%	57.8	25	42.6	2	0	0	935.49	691	698
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	11	11	21	0.02%	9.4%	ELEIGQAGSQR	99.7%	56.7	25	43.6	2	0	0	1187.60	1302	1312
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	11	11	21	0.02%	9.4%	GNAIYNLLPDIISR	99.7%	73.2	25	70.6	3	0	0	1558.86	1160	1173
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	11	11	21	0.02%	9.4%	IYQLLAK	97.5%	30.6	25	20.3	1	0	0	848.52	520	526
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	11	11	21	0.02%	9.4%	KITEAIGIISK	99.7%	46.3	25	36.9	2	0	0	1172.73	633	643
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	11	11	21	0.02%	9.4%	LLENPTINHQK	99.7%	39.8	25	24.4	1	0	0	1306.71	205	215
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	11	11	21	0.02%	9.4%	LSDADLAGPLQK	99.7%	55.4	25	43	2	0	0	1227.66	441	452
Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	11	11	21	0.02%	9.4%	SGGVNQYVVQEVLSIK	99.7%	63.8	25	58.2	4	0	0	1719.93	20	35

Condensin complex subunit 1	NCAPD2	CND1_HUMAN	157.2	100.0%	11	11	21	0.02%	9.4%	YQPLASTASDNDFVTPEPR	99.7%	71	25	71	1	0	0	2107.99	1325	1343
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	5	5	8	0.01%	7.6%	APLQQCAEDR	99.7%	65	25	60.1	2	0	0	1187.55	304	313
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	5	5	8	0.01%	7.6%	QSMWSLLTALSGK	99.7%	43.8	25	43.8	1	0	0	1421.75	649	661
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	5	5	8	0.01%	7.6%	VAAGTLDASTK	99.7%	43.9	25	43.9	2	0	0	1033.55	153	163
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	5	5	8	0.01%	7.6%	VDAVHADVYR	97.5%	30.7	25	23	1	0	0	1144.57	169	178
Condensin complex subunit 2	NCAPH	CND2_HUMAN	82.6	100.0%	5	5	8	0.01%	7.6%	VFDLQFSTDSPR	99.7%	85.9	25	81.9	2	0	0	1411.69	72	83
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	6	6	16	0.02%	7.0%	APIVTVGVNNDPADVR	99.7%	90.3	25	90.3	2	0	0	1636.87	471	486
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	6	6	16	0.02%	7.0%	ASELKEEIK	97.4%	30.5	25	15.1	1	0	0	1046.57	518	526
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	6	6	16	0.02%	7.0%	IQAVLALSR	99.3%	36.4	25	27.6	2	0	0	970.60	160	168
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	6	6	16	0.02%	7.0%	LLSDFLDSEVSELR	99.7%	94.2	25	91.3	4	0	0	1622.83	695	708
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	6	6	16	0.02%	7.0%	LMFSGLLVSSR	99.7%	50	25	50	3	0	0	1209.67	718	728
Condensin complex subunit 3	NCAPG	CND3_HUMAN	114.3	100.0%	6	6	16	0.02%	7.0%	TQIVTEIISEIR	99.7%	64.3	25	61	4	0	0	1401.79	459	470
Condensin-2 complex subunit D3	NCAPD3	CNDD3_HUMAN	168.9	100.0%	4	4	8	0.01%	3.3%	FLVQEIMFDR	99.7%	44.5	25	41.1	2	0	0	1297.66	443	452
Condensin-2 complex subunit D3	NCAPD3	CNDD3_HUMAN	168.9	100.0%	4	4	8	0.01%	3.3%	SALQVLVSILK	99.7%	57.8	25	52.5	2	0	0	1170.75	560	570
Condensin-2 complex subunit D3	NCAPD3	CNDD3_HUMAN	168.9	100.0%	4	4	8	0.01%	3.3%	TFAAQSLVQLLSK	99.7%	86.6	25	83.7	2	0	0	1405.81	372	384
Condensin-2 complex subunit D3	NCAPD3	CNDD3_HUMAN	168.9	100.0%	4	4	8	0.01%	3.3%	YIFTLGDIAQLCPAR	99.5%	37.5	25	37.5	2	0	0	1737.90	856	870
Conserved oligomeric Golgi complex subunit 1	COG1	COG1_HUMAN	109.0	100.0%	5	5	8	0.01%	7.1%	ALQLLYDLR	99.7%	52.6	25	43.8	2	0	0	1104.64	806	814
Conserved oligomeric Golgi complex subunit 1	COG1	COG1_HUMAN	109.0	100.0%	5	5	8	0.01%	7.1%	ELLVSALQELESSTSNSPSNK	99.7%	70.4	25	68	1	0	0	2233.12	443	463
Conserved oligomeric Golgi complex subunit 1	COG1	COG1_HUMAN	109.0	100.0%	5	5	8	0.01%	7.1%	FGLLPLSMTSTR	99.2%	35.3	25	29.2	2	0	0	1322.71	911	922
Conserved oligomeric Golgi complex subunit 1	COG1	COG1_HUMAN	109.0	100.0%	5	5	8	0.01%	7.1%	QALTDFLLAR	99.7%	66.4	25	60.2	2	0	0	1147.65	225	234
Conserved oligomeric Golgi complex subunit 1	COG1	COG1_HUMAN	109.0	100.0%	5	5	8	0.01%	7.1%	TSVLFGLVTGTENQLAPR	99.7%	66.4	25	66.4	1	0	0	1903.03	872	889
Conserved oligomeric Golgi complex subunit 4	COG4	COG4_HUMAN	89.1	99.7%	2	2	2	0.00%	3.3%	LLQEAEQR	94.5%	27.6	25	19.6	1	0	0	986.53	187	194
Conserved oligomeric Golgi complex subunit 4	COG4	COG4_HUMAN	89.1	99.7%	2	2	2	0.00%	3.3%	VTEILDYWGPNSGPLTWR	99.7%	62.6	25	62.6	1	0	0	2104.05	742	759
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	8	8	13	0.01%	10.1%	AEGSSTASSGSQLAEGK	99.7%	75.8	25	75.8	2	0	0	1566.72	503	519
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	8	8	13	0.01%	10.1%	GVISTPVIR	99.6%	38.9	25	28.5	2	0	0	941.58	987	995
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	8	8	13	0.01%	10.1%	GVQGFQDYIEK	99.7%	39.6	25	30.7	1	0	0	1283.63	2	12
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	8	8	13	0.01%	10.1%	LYEPDQLQELK	99.7%	52.8	25	38.7	2	0	0	1375.71	748	758
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	8	8	13	0.01%	10.1%	NIQDTSDLDAIAK	99.7%	69.2	25	60.2	2	0	0	1403.70	292	304
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	8	8	13	0.01%	10.1%	NQAAIQGRPPYAASAEEVAK	98.5%	27.4	25	27.4	0	1	0	2071.06	1010	1029
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	8	8	13	0.01%	10.1%	SPQTPELVEALAFR	99.7%	46.4	25	46.4	2	0	0	1557.83	652	665
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	F120A_HUMAN	121.9	100.0%	8	8	13	0.01%	10.1%	VAAASGHCGAFSGSDSSR	99.7%	34.3	25	34.3	0	1	0	1723.75	912	929
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	6	6	12	0.01%	13.8%	AESTPEIAEQR	99.7%	55.9	25	43.1	3	0	0	1230.60	225	235
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	6	6	12	0.01%	13.8%	DSQTQAILTK	99.7%	46.8	25	35.6	1	0	0	1104.59	239	248
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	6	6	12	0.01%	13.8%	EGSQGELTPANSQSR	99.7%	61.5	25	54.8	3	0	0	1560.72	472	486
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	6	6	12	0.01%	13.8%	MALSFVQR	99.5%	37.3	25	26.7	2	0	0	951.51	77	84
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	6	6	12	0.01%	13.8%	TLYTQIR	99.5%	38	25	36.9	1	0	0	894.50	364	370
COP9 signalosome complex subunit 1	GPS1	CSN1_HUMAN	55.5	100.0%	6	6	12	0.01%	13.8%	VSVYLQNWSHVLSYVSK	99.5%	32.1	25	32.1	0	2	0	2009.05	208	224
COP9 signalosome complex subunit 7a	COPS7A	CSN7A_HUMAN	30.3	99.8%	2	2	3	0.00%	7.6%	ELAESDFASTFR	99.7%	51.3	25	47.8	2	0	0	1372.64	54	65
COP9 signalosome complex subunit 7a	COPS7A	CSN7A_HUMAN	30.3	99.8%	2	2	3	0.00%	7.6%	LEVDYSIGR	99.7%	48.1	25	35.3	1	0	0	1051.54	152	160
COP9 signalosome complex subunit 8	COPS8	CSN8_HUMAN	23.2	100.0%	3	3	4	0.00%	23.0%	FIPLSEPAPVPPIPNEQQLAR	98.4%	32.4	25	32.4	1	0	0	2313.26	179	199
COP9 signalosome complex subunit 8	COPS8	CSN8_HUMAN	23.2	100.0%	3	3	4	0.00%	23.0%	GILEQGWQADSTTR	99.7%	49.2	25	39.9	2	0	0	1561.76	147	160
COP9 signalosome complex subunit 8	COPS8	CSN8_HUMAN	23.2	100.0%	3	3	4	0.00%	23.0%	KPVAGALDVSFNK	99.7%	40.9	25	34.4	1	0	0	1345.75	166	178
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	5	5	8	0.01%	16.8%	FCTGLTQIETLFK	99.7%	76.8	25	73	2	0	0	1557.80	253	265
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	5	5	8	0.01%	16.8%	FSEVLKR	99.7%	42.4	25	22.8	2	0	0	878.51	308	314
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	5	5	8	0.01%	16.8%	LAVEALSSLDGDLAGR	99.7%	99.8	25	99.8	1	0	0	1586.84	157	172
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	5	5	8	0.01%	16.8%	LGFSEVELVQMVVDGVK	99.7%	46.4	25	46.4	1	0	0	1864.97	342	358
Creatine kinase B-type	CKB	KCRB_HUMAN	42.6	100.0%	5	5	8	0.01%	16.8%	VLTPELYAELR	99.7%	57.1	25	41.2	2	0	0	1303.73	33	43
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	15	16	27	0.03%	20.8%	AIANVPPIQEK	99.7%	52.3	25	50	2	0	0	1179.67	517	527
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	15	16	27	0.03%	20.8%	AIYELAISQPR	99.5%	37.3	25	29.5	2	0	0	1260.69	661	671
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	15	16	27	0.03%	20.8%	APAEVQITAEQLLR	99.7%	83.5	25	71.1	2	0	0	1538.85	183	196
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	15	16	27	0.03%	20.8%	FAELETILGDIDR	99.7%	94.2	25	86.7	2	0	0	1491.77	646	658

Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	15	16	27	0.03%	20.8%	FEENQKEFER	99.7%	41.4	25	27	1	0	0	1355.62	422	431
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	15	16	27	0.03%	20.8%	FLEFGPENCTSWIK	99.7%	62.4	25	55.8	2	0	0	1727.81	632	645
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	15	16	27	0.03%	20.8%	FVLVHPDVK	99.7%	45.4	25	32.7	2	0	0	1053.61	369	377
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	15	16	27	0.03%	20.8%	GIEDIIVSK	99.7%	55.6	25	48.1	1	0	0	973.56	467	475
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	15	16	27	0.03%	20.8%	ITDEEELNDYKLR	95.5%	23.3	25	23.1	0	1	0	1637.80	214	226
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	15	16	27	0.03%	20.8%	LDMPEVLWK	99.7%	44.7	25	39.9	2	0	0	1130.59	672	680
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	15	16	27	0.03%	20.8%	LMLLESWR	99.7%	47.2	25	42.8	4	0	0	1047.57	752	759
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	15	16	27	0.03%	20.8%	LVESDAEAEAVR	99.7%	85.3	25	76.9	2	0	0	1288.64	500	511
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	15	16	27	0.03%	20.8%	SFEEEFGTASDKER	99.7%	85.5	25	85.5	2	0	0	1631.72	760	773
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	15	16	27	0.03%	20.8%	VWISFAQFELSSGK	99.7%	72.4	25	65.4	1	0	0	1598.82	711	724
Crooked neck-like protein 1	CRNKL1	CRNL1_HUMAN	100.5	100.0%	15	16	27	0.03%	20.8%	YTYMEEMLGNVAGAR	99.7%	67.9	25	67.9	1	0	0	1704.77	316	330
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	4	4	6	0.01%	13.4%	DVATVAFCDAQSTQEIHEK	96.5%	24.2	25	24.2	0	1	0	2148.99	47	65
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	4	4	6	0.01%	13.4%	IGSGFDNIDIK	99.7%	61.2	25	43.2	2	0	0	1178.61	98	108
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	4	4	6	0.01%	13.4%	IRGETLGIIGLGR	99.7%	35.9	25	33.7	0	1	0	1354.82	172	184
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	4	4	6	0.01%	13.4%	VGQAVALR	99.7%	70	25	54.4	2	0	0	813.49	185	192
C-terminal-binding protein 1	CTBP1	CTBP1_HUMAN	47.5	100.0%	4	4	6	0.01%	13.4%	VQSVEQIR	99.7%	40.5	25	23.2	2	0	0	958.53	156	163
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	3	3	6	0.01%	8.8%	GAALDVHESEPFSFAQGPLK	99.7%	46.6	25	46.6	0	2	0	2100.04	292	311
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	3	3	6	0.01%	8.8%	IGSGYDNVDIK	99.7%	47.4	25	39.3	2	0	0	1180.58	104	114
C-terminal-binding protein 2	CTBP2	CTBP2_HUMAN	48.9	100.0%	3	3	6	0.01%	8.8%	VQSVEQIR	99.7%	40.5	25	23.2	2	0	0	958.53	162	169
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	48	0.04%	40.1%	ALEHSALAINHK	99.7%	52	25	51.3	2	2	0	1303.71	320	331
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	48	0.04%	40.1%	CSNPLDTSVK	99.1%	34.8	25	31.5	2	0	0	1120.53	218	227
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	48	0.04%	40.1%	ENFCNIHVSLVPQPSSTGEQK	99.7%	34.3	25	32.7	0	2	0	2371.13	173	193
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	48	0.04%	40.1%	FSDSYASVIK	99.7%	67.4	25	45.2	2	0	0	1116.56	310	319
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	48	0.04%	40.1%	FVGQDVEGER	99.7%	68.7	25	53.1	2	0	0	1135.54	499	508
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	48	0.04%	40.1%	GIIASSVGTILK	99.7%	70.4	25	66.8	2	0	0	1158.71	17	28
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	48	0.04%	40.1%	GLGLSPDLVVCR	99.7%	45.4	25	37.2	2	0	0	1285.69	206	217
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	48	0.04%	40.1%	HRFEVNPVWK	99.7%	56.2	25	51.6	0	2	0	1311.70	480	489
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	48	0.04%	40.1%	IQAIAWAR	99.7%	64	25	46.9	2	0	0	928.54	382	389
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	48	0.04%	40.1%	IYQYVINK	99.7%	43	25	31.4	2	0	0	1040.58	93	100
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	48	0.04%	40.1%	KLYGDADYLEER	99.7%	71.6	25	68.5	2	2	0	1471.71	466	477
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	48	0.04%	40.1%	LCSAHGVLVPGGFGVR	99.7%	71.5	25	62.4	2	2	0	1625.86	361	376
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	48	0.04%	40.1%	LLETCSIALVGK	99.7%	78.5	25	70.8	1	0	0	1303.73	295	306
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	48	0.04%	40.1%	LYGDADYLEER	99.7%	73.6	25	65.2	2	0	0	1343.61	467	477
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	48	0.04%	40.1%	RLDLPIER	99.7%	47.7	25	30.4	2	0	0	1011.59	269	276
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	48	0.04%	40.1%	SCGLHVTSIK	99.7%	45.1	25	37	2	0	0	1101.57	29	38
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	48	0.04%	40.1%	TVQVVPHITDAIQEWVMR	99.7%	54.6	25	54.6	0	4	0	2122.11	110	127
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	48	0.04%	40.1%	VPLLLEEQGVVDYFLR	99.7%	99.8	25	99.8	2	1	0	1890.04	253	268
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	48	0.04%	40.1%	YIDSADLEPITSQEEPVR	99.7%	97	25	91.1	2	0	0	2062.00	336	353
CTP synthase 1	CTPS1	PYRG1_HUMAN	66.7	100.0%	20	25	48	0.04%	40.1%	YILVTGGVISGIGK	99.7%	117	25	113	2	0	0	1376.82	3	16
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	5	5	9	0.01%	14.5%	ALEHSALAINHK	99.7%	52	25	51.3	2	2	0	1303.71	320	331
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	5	5	9	0.01%	14.5%	GIIASSIGTILK	99.7%	77.6	25	54.4	2	0	0	1172.73	17	28
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	5	5	9	0.01%	14.5%	GLGLSPDLIVCR	99.7%	43.3	25	30.4	2	0	0	1299.71	206	217
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	5	5	9	0.01%	14.5%	LHLPIGDSASNLLFK	98.3%	26.9	25	25.7	0	1	0	1624.91	270	284
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	5	5	9	0.01%	14.5%	LQAISWAR	99.7%	45	25	35.7	2	0	0	944.53	382	389
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	5	5	9	0.01%	14.5%	VPVLLEEQSIVK	99.7%	62.3	25	62.3	2	0	0	1353.80	253	264
CTP synthase 2	CTPS2	PYRG2_HUMAN	65.7	100.0%	5	5	9	0.01%	14.5%	YILVTGGVISGIGK	99.7%	117	25	113	2	0	0	1376.82	3	16
Cullin-1	CUL1	CUL1_HUMAN	89.7	99.8%	2	2	3	0.00%	2.7%	LLIQAAIVR	99.7%	63.5	25	54.6	2	0	0	996.66	709	717
Cullin-1	CUL1	CUL1_HUMAN	89.7	99.8%	2	2	3	0.00%	2.7%	QIGLDQIWDDLR	99.7%	59.6	25	49.6	1	0	0	1471.75	14	25
Cullin-4B	CUL4B	CUL4B_HUMAN	104.0	100.0%	4	4	5	0.00%	4.5%	ETVEEQASTTER	99.7%	73.8	25	70.2	1	0	0	1379.63	830	841
Cullin-4B	CUL4B	CUL4B_HUMAN	104.0	100.0%	4	4	5	0.00%	4.5%	QYQIDAAIVR	99.7%	58.5	25	45.2	1	0	0	1176.64	847	856
Cullin-4B	CUL4B	CUL4B_HUMAN	104.0	100.0%	4	4	5	0.00%	4.5%	SIFLFLDR	99.7%	48.8	25	43	1	0	0	1010.57	305	312

Cullin-4B	CUL4B	CUL4B_HUMAN	104.0	100.0%	4	4	5	0.00%	4.5%	TIDGILLLIER	99.7%	82.3	25	76.1	2	0	0	1255.76	346	356
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	AADIDQEVK	99.7%	41.3	25	24.5	2	0	0	988.49	578	586
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	AADIDQEVKER	99.7%	68.1	25	61.3	3	0	0	1273.64	578	588
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	ADVFHAYLSLLK	99.7%	50	25	37.3	2	0	0	1376.76	392	403
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	ALTLIAGSPLK	99.7%	90.1	25	82.7	6	0	0	1083.68	631	641
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	AVAALLTIPEAEK	99.7%	63.3	25	46.2	3	0	0	1325.77	1179	1191
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	DLLDTVLPHLYNETK	98.1%	31.9	25	31.9	1	0	0	1770.93	1043	1057
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	DSIKLDDDSER	99.4%	36.4	25	25	1	0	0	1292.60	37	47
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	EGPAVVGQFIQDVK	99.7%	60.9	25	50.9	4	0	0	1486.79	813	826
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	EVEMGPFK	97.2%	30.2	25	21.5	1	0	0	936.45	1065	1072
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	FMATNDLMTELQK	99.7%	89.5	25	82.6	5	0	0	1541.73	24	36
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	FTISDHPQPIDPLLK	99.7%	50	25	37.8	2	2	0	1720.93	991	1005
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	GYLISGSSYAR	99.7%	51.3	25	39	3	0	0	1173.59	972	982
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	HTVDDGLDIR	99.7%	54.3	25	40	2	0	0	1140.56	1073	1082
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	HTVDDGLDIRK	99.7%	41.6	25	35.8	1	0	0	1268.66	1073	1083
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	IGEYLEK	99.7%	53	25	39.3	2	0	0	851.45	249	255
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	ISGSILNELIGLVR	99.7%	83	25	76.6	3	0	0	1483.88	730	743
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	ITSEALLVTQQLVK	99.7%	75.8	25	61.5	4	1	0	1542.91	535	548
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	LGTLSALDILIK	99.7%	82.4	25	71.5	6	0	0	1256.78	668	679
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	LLEDKNGEVQNLAVK	99.7%	42.7	25	28.5	0	1	0	1669.91	56	70
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	LSTLCPSAVLQR	99.7%	53	25	47.4	2	0	0	1344.73	1130	1141
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	LTLIDPETLLPR	99.7%	73.5	25	73.5	10	0	0	1380.81	958	969
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	MLTFLMLVR	99.7%	48.3	25	31.6	4	0	0	1139.63	1121	1129
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	MLTGPVYSQSTALTHK	99.7%	95.9	25	93.6	4	4	0	1733.89	778	793
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	MTSSDKDFR	99.7%	42.6	25	30.5	2	0	0	1086.49	15	23
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	NCIGDFLK	98.9%	34.1	25	24.8	1	0	0	966.47	1006	1013
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	NVVAECLGK	99.4%	36.8	25	30.9	4	0	0	989.51	949	957
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	SVILEAFSSPSEEVK	99.7%	100	25	95.8	6	0	0	1621.83	859	873
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	TLEDPDLNVR	99.7%	59.4	25	49	2	0	0	1171.60	1014	1023
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	TVIGELPPASSGSALAANVCK	99.7%	109	25	109	2	0	0	2042.06	112	132
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	TVSPALISR	99.3%	36.3	25	24.1	1	0	0	943.56	374	382
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	TYIQCIAAISR	99.7%	97.8	25	89.4	2	0	0	1295.68	233	243
Cullin-associated NEDD8-dissociated protein 1	CAND1	CAND1_HUMAN	136.4	100.0%	32	39	103	0.10%	29.8%	VIRPLDQPSSFDATPYIK	99.7%	48.3	25	48.3	0	4	0	2047.09	549	566
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	19	45	0.04%	54.2%	ALGTPNNEVWPEVESLQDYK	99.7%	47.1	25	47.1	2	0	0	2289.10	219	238
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	19	45	0.04%	54.2%	DLKPQNLLIDDKGTIK	99.7%	67.4	25	67.4	2	4	0	1811.03	128	143
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	19	45	0.04%	54.2%	IGEGTYGVVYK	99.7%	91.6	25	44.4	4	0	0	1185.62	10	20
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	19	45	0.04%	54.2%	IRLESEEEGVPSTAIR	99.7%	87.5	25	87.5	2	1	0	1785.93	35	50
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	19	45	0.04%	54.2%	KPLFHGDSEIDQLFR	99.7%	77.9	25	77.9	0	2	0	1801.92	201	215
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	19	45	0.04%	54.2%	LADFGLAR	99.7%	58.9	25	0	5	0	0	862.48	144	151
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	19	45	0.04%	54.2%	LESEEEGVPSTAIR	99.7%	53.4	25	41.3	2	0	0	1516.75	37	50
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	19	45	0.04%	54.2%	MALNHPYFNDLDNQIK	99.7%	62.4	25	62.4	4	0	0	1948.92	280	295
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	19	45	0.04%	54.2%	MLIYDPAK	99.0%	34.6	25	31.8	1	0	0	950.50	267	274
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	19	45	0.04%	54.2%	MLIYDPAKR	99.7%	49.7	25	42.6	4	0	0	1122.60	267	275
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	19	45	0.04%	54.2%	NLDENGLDLLSK	99.7%	82.1	25	62.5	3	0	0	1330.69	255	266
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	19	45	0.04%	54.2%	SPEVLLGSAR	99.7%	83.9	25	73.1	4	0	0	1028.57	171	180
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	19	45	0.04%	54.2%	WKPGSLASHVK	99.7%	34	25	30.3	0	2	0	1209.67	244	254
Cyclin-dependent kinase 1	CDK1	CDK1_HUMAN	34.1	100.0%	14	19	45	0.04%	54.2%	YLDSIPPGQYMDSSLVK	99.7%	42.6	25	33.6	3	0	0	1912.94	90	106
Cyclin-dependent kinase 11B	CDK11B	CD11B_HUMAN	92.7	100.0%	4	4	6	0.01%	4.9%	APELLLGAK	99.7%	49.4	25	40.2	2	0	0	911.56	605	613
Cyclin-dependent kinase 11B	CDK11B	CD11B_HUMAN	92.7	100.0%	4	4	6	0.01%	4.9%	AQHPNIVTVR	96.9%	29.8	25	24.1	1	0	0	1134.64	492	501
Cyclin-dependent kinase 11B	CDK11B	CD11B_HUMAN	92.7	100.0%	4	4	6	0.01%	4.9%	EGFPITSLR	99.5%	38.1	25	21.8	1	0	0	1019.55	476	484
Cyclin-dependent kinase 11B	CDK11B	CD11B_HUMAN	92.7	100.0%	4	4	6	0.01%	4.9%	IEEGTYGVVYR	99.7%	76.6	25	76.4	2	0	0	1285.64	444	454

Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	9	16	0.02%	35.9%	ALFPGDSEIDQLFR	99.7%	68.6	25	64.3	2	0	0	1607.81	201	214
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	9	16	0.02%	35.9%	APEILLGCK	99.7%	58.2	25	55.9	2	0	0	1000.55	170	178
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	9	16	0.02%	35.9%	DLKPQNLLINTEGAIK	99.7%	67.4	25	67.4	2	2	0	1767.00	127	142
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	9	16	0.02%	35.9%	ELNHPNIVK	96.4%	29.2	25	16.6	1	0	0	1063.59	57	65
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	9	16	0.02%	35.9%	FMDASALTGIPLPLIK	99.7%	63.8	25	63.8	4	0	0	1686.95	90	105
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	9	16	0.02%	35.9%	IGEGTYGVVYK	99.7%	91.6	25	44.4	4	0	0	1185.62	10	20
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	9	16	0.02%	35.9%	LADFGLAR	99.7%	58.9	25	0	5	0	0	862.48	143	150
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	9	16	0.02%	35.9%	LTGEVVALKK	99.7%	44	25	35	2	0	0	1057.66	25	34
Cyclin-dependent kinase 2	CDK2	CDK2_HUMAN	33.9	100.0%	7	9	16	0.02%	35.9%	SLLSQMLHYDPNKR	98.2%	26.6	25	23.1	0	1	0	1701.87	261	274
Cyclin-dependent kinase 5	CDK5	CDK5_HUMAN	33.3	99.8%	2	2	2	0.00%	9.3%	DLKPQNLLINR	99.6%	39.2	25	35.8	1	0	0	1323.77	126	136
Cyclin-dependent kinase 5	CDK5	CDK5_HUMAN	33.3	99.8%	2	2	2	0.00%	9.3%	DLLQNLLK	99.5%	37.8	25	24.1	1	0	0	956.58	261	268
Cyclin-dependent kinase 5	CDK5	CDK5_HUMAN	33.3	99.8%	2	2	2	0.00%	9.3%	LADFGLAR	99.7%	58.9	25	0	5	0	0	862.48	142	149
Cyclin-dependent kinase 9	CDK9	CDK9_HUMAN	42.8	100.0%	3	3	6	0.01%	11.3%	GSQITQQSTNQSR	99.7%	71.2	25	61.5	2	0	0	1434.69	346	358
Cyclin-dependent kinase 9	CDK9	CDK9_HUMAN	42.8	100.0%	3	3	6	0.01%	11.3%	LADFGLAR	99.7%	58.9	25	0	5	0	0	862.48	165	172
Cyclin-dependent kinase 9	CDK9	CDK9_HUMAN	42.8	100.0%	3	3	6	0.01%	11.3%	LLVLDPAQR	99.5%	38	25	30.7	2	0	0	1024.62	295	303
Cyclin-dependent kinase 9	CDK9	CDK9_HUMAN	42.8	100.0%	3	3	6	0.01%	11.3%	NPATTNQTEFER	99.7%	72.2	25	72.2	2	0	0	1407.65	359	370
Cyclin-dependent kinase inhibitor 2A, isoforms 1/2/3	CDKN2A	CD2A1_HUMAN	16.5	99.8%	2	2	4	0.00%	18.6%	ALLEAGALPNAPNSYGR	99.7%	51.3	25	50.3	2	0	0	1713.89	30	46
Cyclin-dependent kinase inhibitor 2A, isoforms 1/2/3	CDKN2A	CD2A1_HUMAN	16.5	99.8%	2	2	4	0.00%	18.6%	EGFLDTLVVLHR	99.1%	34.9	25	34.9	2	0	0	1398.77	88	99
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	6	7	12	0.01%	13.8%	AAQELQEGQR	99.7%	72.8	25	57.1	2	0	0	1129.56	360	369
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	6	7	12	0.01%	13.8%	CVVILPDSVR	95.5%	28.4	25	22	1	0	0	1157.63	370	379
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	6	7	12	0.01%	13.8%	FDSPESHVGVAWR	99.7%	56.1	25	46.2	1	2	0	1486.71	197	209
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	6	7	12	0.01%	13.8%	LKNEIPNSHILDQYR	99.0%	28.9	25	28.9	0	2	0	1839.97	210	224
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	6	7	12	0.01%	13.8%	PSETPQAEVGPTGCPHR	99.7%	61.3	25	61.3	0	2	0	1819.84	2	18
Cystathionine beta-synthase	CBS	CBS_HUMAN	60.6	100.0%	6	7	12	0.01%	13.8%	SNDEEAFTFAR	99.7%	74.4	25	74.4	2	0	0	1286.56	326	336
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	5	5	8	0.01%	10.2%	ADLTEYLSTHYK	97.2%	25	25	24.1	0	1	0	1440.70	214	225
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	5	5	8	0.01%	10.2%	EHTAYYIK	99.7%	46.8	25	38.1	1	0	0	1024.51	127	134
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	5	5	8	0.01%	10.2%	FTGSEIR	99.3%	35.8	25	30.5	2	0	0	809.42	270	276
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	5	5	8	0.01%	10.2%	IAEVDASVVR	99.7%	79.9	25	52	2	0	0	1058.58	433	442
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	QCR1_HUMAN	52.6	100.0%	5	5	8	0.01%	10.2%	LCTSATESEVAR	99.7%	67.7	25	58.6	2	0	0	1323.62	379	390
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	41	0.04%	45.0%	ATAAPAGAPPQPQDLEFTK	99.7%	73.1	25	68.7	2	0	0	1909.97	24	42
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	41	0.04%	45.0%	AVAFQNPQTHVIENLHAAAYR	99.7%	60.1	25	60.1	0	2	0	2350.21	163	183
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	41	0.04%	45.0%	ENMAYTVECLR	99.7%	64.6	25	55.1	3	0	0	1401.61	117	127
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	41	0.04%	45.0%	GSNTTSHLHQAVAK	99.7%	67.3	25	58.2	2	0	0	1450.74	302	315
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	41	0.04%	45.0%	LPNGLVIASLENYSPVSR	99.7%	97	25	97	2	2	0	1929.04	43	60
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	41	0.04%	45.0%	LTSSLTTK	96.6%	29.5	25	29.5	1	0	0	850.49	85	92
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	41	0.04%	45.0%	MALIGLGVSHPVLK	99.7%	81.2	25	79.1	3	3	0	1450.85	218	231
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	41	0.04%	45.0%	NALANPLYCPDYR	99.7%	60.3	25	50.7	2	0	0	1566.74	184	196
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	41	0.04%	45.0%	QVAEQFLNMR	99.7%	67	25	59.4	4	0	0	1235.62	232	241
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	41	0.04%	45.0%	SMAASGNLGHTPFVDEL	99.7%	69.5	25	66.2	4	0	0	1745.82	437	453
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	41	0.04%	45.0%	TIAQGNLSNTDVQAAK	99.7%	95.2	25	85.3	3	0	0	1630.84	360	375
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	41	0.04%	45.0%	VTSEELHYFVQNHFTSAR	99.7%	53	25	53	0	2	0	2165.04	200	217
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	41	0.04%	45.0%	WEVADLQPQLK	99.7%	57.1	25	47.9	2	0	0	1326.71	149	159
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	QCR2_HUMAN	48.4	100.0%	14	22	41	0.04%	45.0%	YEDFSNLGTTHLLR	99.7%	83.1	25	82.1	2	2	0	1665.82	71	84
Cytochrome b-c1 complex subunit 8	UQCRQ	QCR8_HUMAN	9.9	100.0%	4	4	7	0.01%	31.7%	GREFGNLTR	98.2%	32	25	16.2	2	0	0	1049.55	2	10
Cytochrome b-c1 complex subunit 8	UQCRQ	QCR8_HUMAN	9.9	100.0%	4	4	7	0.01%	31.7%	IRESFFR	99.6%	38.3	25	25.5	2	0	0	954.52	42	48
Cytochrome b-c1 complex subunit 8	UQCRQ	QCR8_HUMAN	9.9	100.0%	4	4	7	0.01%	31.7%	KNPAAYENDK	99.1%	35.2	25	30.2	2	0	0	1149.55	73	82
Cytochrome b-c1 complex subunit 8	UQCRQ	QCR8_HUMAN	9.9	100.0%	4	4	7	0.01%	31.7%	NPAAYENDK	98.1%	31.8	25	31.8	1	0	0	1021.46	74	82
Cytochrome b-c1 complex subunit 9	UQCR10	QCR9_HUMAN	7.3	99.8%	2	3	6	0.01%	38.1%	AFDQGADAIYDHINEGK	99.7%	62.4	25	62.4	2	2	0	1863.85	35	51
Cytochrome b-c1 complex subunit 9	UQCR10	QCR9_HUMAN	7.3	99.8%	2	3	6	0.01%	38.1%	LYSLLFR	99.7%	49.1	25	32.8	2	0	0	911.53	10	16
Cytochrome b-c1 complex subunit Rieske, mitochondrial	UQCRFS1	UCRI_HUMAN	29.7	100.0%	2	3	6	0.01%	10.9%	NAVTQFVSSMSASADVLALAK	99.7%	96.7	25	89.9	3	0	0	2110.08	131	151
Cytochrome b-c1 complex subunit Rieske, mitochondrial	UQCRFS1	UCRI_HUMAN	29.7	100.0%	2	3	6	0.01%	10.9%	RLEVLDSTK	99.7%	40.8	25	30.7	3	0	0	1060.60	93	101

Cytochrome c	CYCS	CYC_HUMAN	11.7	99.8%	2	2	3	0.00%	23.8%	TGPNLHGLFGR	99.1%	35.2	25	32.2	1	0	0	1168.62	29	39
Cytochrome c	CYCS	CYC_HUMAN	11.7	99.8%	2	2	3	0.00%	23.8%	TGQAPGYSYTAANK	99.7%	48.2	25	48.2	2	0	0	1428.68	41	54
Cytochrome c oxidase assembly protein COX11, mitochondrial	COX11	COX11_HUMAN	31.4	100.0%	3	3	5	0.00%	15.9%	IQCFCFEEQR	99.3%	35.8	25	35.8	2	0	0	1416.60	215	224
Cytochrome c oxidase assembly protein COX11, mitochondrial	COX11	COX11_HUMAN	31.4	100.0%	3	3	5	0.00%	15.9%	LYCQTTGLGGSAVAGHASDK	99.3%	30.4	25	30.4	0	1	0	1992.94	119	138
Cytochrome c oxidase assembly protein COX11, mitochondrial	COX11	COX11_HUMAN	31.4	100.0%	3	3	5	0.00%	15.9%	VDLITLSYTFFEAK	99.7%	102	25	102	2	0	0	1646.87	252	265
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	5	9	26	0.02%	23.3%	ILYMTDEVNDPSLTIK	99.7%	104	25	102	8	0	0	1867.94	83	98
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	5	9	26	0.02%	23.3%	LLDVDNR	99.7%	44.8	25	21.5	2	0	0	844.45	135	141
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	5	9	26	0.02%	23.3%	LLDVDNRVVLPIEAPIR	99.7%	56.1	25	47.4	2	3	0	1932.13	135	151
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	5	9	26	0.02%	23.3%	MMITSQDVLHSWAVPTLGLK	99.7%	51.9	25	7.84	1	6	0	2243.16	152	171
Cytochrome c oxidase subunit 2	MT-CO2	COX2_HUMAN	25.6	100.0%	5	9	26	0.02%	23.3%	VVLPIEAPIR	99.7%	44.2	25	44.2	4	0	0	1106.69	142	151
Cytochrome c oxidase subunit 7A2, mitochondrial	COX7A2	CX7A2_HUMAN	9.4	100.0%	3	3	5	0.00%	30.1%	GGVADALLYR	99.7%	88.5	25	65.7	2	0	0	1034.56	47	56
Cytochrome c oxidase subunit 7A2, mitochondrial	COX7A2	CX7A2_HUMAN	9.4	100.0%	3	3	5	0.00%	30.1%	LFQEDDEIPLYLK	99.7%	93.2	25	78.1	2	0	0	1622.83	34	46
Cytochrome c oxidase subunit 7A2, mitochondrial	COX7A2	CX7A2_HUMAN	9.4	100.0%	3	3	5	0.00%	30.1%	QKLFQEDDEIPLYLK	99.7%	53.2	25	52.7	1	0	0	1878.99	32	46
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	8	8	12	0.01%	12.6%	ANYLASPPLVIAYAIAGTIR	99.7%	56	25	56	1	0	0	2074.17	548	567
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	8	8	12	0.01%	12.6%	FVEFFGPGVAQLSIADR	99.7%	84.8	25	84.4	2	0	0	1852.96	277	293
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	8	8	12	0.01%	12.6%	GPFLLGIK	99.7%	44	25	38	2	0	0	844.53	786	793
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	8	8	12	0.01%	12.6%	NIEVPFKPAR	98.6%	33.2	25	21.4	1	0	0	1170.66	73	82
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	8	8	12	0.01%	12.6%	SPPFFENLTLDLQPPK	99.7%	74.8	25	71.2	2	0	0	1842.96	645	660
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	8	8	12	0.01%	12.6%	VILQDFTGVPAVVDFAAMR	99.5%	37.7	25	36.8	1	0	0	2049.08	83	101
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	8	8	12	0.01%	12.6%	VLLEAAIR	99.7%	54.1	25	47.3	1	0	0	884.56	41	48
Cytoplasmic aconitate hydratase	ACO1	ACOC_HUMAN	98.4	100.0%	8	8	12	0.01%	12.6%	YQQAGLPLIVLAGK	99.7%	79	25	79	2	0	0	1470.87	759	772
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	AATSPALFNR	99.7%	68.7	25	51.3	2	0	0	1047.56	3079	3088
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	ADLAAVEAK	99.7%	55.9	25	42.2	2	0	0	887.48	3463	3471
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	AERPDVDEKR	99.7%	33.8	25	28.8	1	2	0	1214.61	3719	3728
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	AISKDHLYGTLDPNTR	98.1%	26.5	25	26.5	0	2	0	1800.92	2258	2273
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	AKEALELTDTGLLSGSEER	97.7%	25.8	25	25.8	0	1	0	2019.02	1300	1318
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	ALGEYLER	99.7%	52.4	25	47.5	2	0	0	950.49	1614	1621
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	ALGHQLGR	99.2%	35.7	25	25.8	2	0	0	851.48	1918	1925
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	ANEVEQMIR	99.7%	47.4	25	38.3	2	0	0	1089.54	3430	3438
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	ASLACGPMVK	99.7%	40.8	25	31.7	2	0	0	1033.52	3385	3394
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	ASVVTLPVYLNFTR	99.7%	60.7	25	59.9	4	0	0	1579.88	4602	4615
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	CYLTMTQALEAR	99.7%	77.6	25	76.3	2	0	0	1456.69	1888	1899
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	DLFQVAFNR	99.7%	59.6	25	59.6	4	0	0	1109.57	3862	3870
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	DLPPVSGSIIWAK	99.7%	59.5	25	56.8	2	0	0	1382.77	640	652
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	DSAIQQQVANLQMK	99.7%	91.6	25	79.9	3	0	0	1573.80	1229	1242
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	DYIPVDQEELRDYVK	99.7%	55.1	25	55.1	2	0	0	1881.92	2880	2894
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	EAIVNSCVFVHQTLHQANAR	99.7%	33.4	25	33.4	0	1	0	2294.15	3141	3160
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	EALELTDTGLLSGSEER	99.7%	123	25	116	2	0	0	1819.89	1302	1318
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	EFGPVVIDYGK	99.6%	39.2	25	39.2	2	0	0	1223.63	1101	1111
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	EGLMLDSHEELYK	99.7%	52	25	50	3	0	0	1563.74	3040	3052
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	EHINSVSAMK	99.0%	34.5	25	26.1	2	0	0	1115.55	1499	1508
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	EQPWVSVQPR	97.7%	30.9	25	28.5	1	0	0	1225.63	1348	1357
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	ESPEVLLTLDILK	99.7%	82.8	25	76.9	2	0	0	1469.85	293	305
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	EVWNTYELDLVNYQNK	99.7%	76.4	25	76.4	2	0	0	2027.97	1468	1483
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	EWTDGLFTHVLR	99.7%	81.6	25	68.3	2	0	0	1473.75	2274	2285
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	EYQTQLIQR	98.9%	34.1	25	22.3	1	0	0	1178.62	603	611
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	FGQMLGSNMTEFHSQISK	99.4%	31.3	25	31.3	0	1	0	2041.95	1131	1148
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	FLSDPQVHTVLVER	99.7%	90.2	25	90.2	2	0	0	1639.88	68	81
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	FNALFVRPHIR	99.7%	34.4	25	28.9	0	2	0	1369.79	588	598
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	FNYGFEYLGVQDK	99.7%	106	25	106	2	0	0	1579.74	1866	1878
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	FQSISTEFLALMK	99.7%	85.1	25	81.1	3	0	0	1530.79	1568	1580

Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	FTQDTQPHYIYSPR	99.7%	67.6	25	67.6	2	0	0	1752.83	2784	2797
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	FVAWMNGLSVYQIK	99.7%	61.7	25	61.7	2	0	0	1655.86	2949	2962
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	GTVGEPTYDAEFQHFLR	96.8%	24.6	25	20.7	0	1	0	1966.93	3894	3910
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	GWDDLFNK	99.4%	37	25	20.6	2	0	0	994.46	1489	1496
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	GWENHVEGQK	99.7%	41.4	25	31.2	2	0	0	1183.55	672	681
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	IAFIMDESNVLDSGFLER	99.7%	74.4	25	66.7	2	0	0	2072.00	2990	3007
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	IFTIESTR	99.7%	57.3	25	43.5	2	0	0	966.53	717	724
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	IFVFEPPPGVK	99.3%	35.9	25	30	1	0	0	1229.69	4144	4154
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	IMFEVQDLK	99.7%	58.1	25	49.1	3	0	0	1138.58	2341	2349
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	INEWLTLVEK	99.7%	67.5	25	55.3	2	0	0	1244.69	1698	1707
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	INMLVIELK	99.7%	71.1	25	59.1	2	0	0	1088.64	1396	1404
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	IQFVGACNPPTDPGR	99.7%	103	25	96.2	2	0	0	1628.79	2706	2720
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	IQGLTVEQAEAVVR	99.7%	98.3	25	87.8	4	0	0	1512.84	3924	3937
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	ITNQVIYLNPPIEECR	99.7%	54.6	25	54.6	2	0	0	1959.00	964	979
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	IWAHEALR	99.7%	45.6	25	20.8	2	0	0	995.54	2824	2831
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	KFLSDPQVHTVLVER	99.7%	38.8	25	38.8	0	1	0	1767.98	67	81
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	KIIDSVR	95.0%	28	25	3.63	1	0	0	830.51	2286	2292
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	KYEFGESDLR	99.7%	51.2	25	41.3	2	0	0	1243.60	4204	4213
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	LAETVFNFQEK	99.7%	48.4	25	42.6	2	0	0	1325.67	836	846
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	LCDEQLSSQSHYDFGLR	99.3%	30.5	25	29.1	0	1	0	2054.92	2075	2091
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	LEGVEGVAHIIDPK	99.7%	57	25	54.7	2	1	0	1476.81	2244	2257
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	LFLTMEINPK	99.7%	49.8	25	37.5	2	0	0	1205.66	4124	4133
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	LGGSPFGPAGTGK	99.7%	67.8	25	64.4	2	0	0	1145.60	1900	1912
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	LKQDGDSFR	99.7%	55.4	25	52.6	2	0	0	1065.53	682	690
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	LLNTFLER	99.7%	57.1	25	44	2	0	0	1005.57	4264	4271
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	LNTQEIFDDWAR	99.7%	88.3	25	80.6	2	0	0	1507.72	693	704
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	LQGEFQLR	99.7%	47.9	25	32.3	2	0	0	990.54	3734	3741
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	LRDQLGTAK	99.7%	52	25	39.6	2	0	0	1001.57	568	576
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	LSLSNAISTALPLTQLR	99.7%	71.2	25	64.5	2	0	0	1798.04	4575	4591
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	LVQTPLTDR	99.7%	45.6	25	34.1	2	0	0	1042.59	1879	1887
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	MLSAVSQQVQCIQEALR	99.7%	93.8	25	88.7	3	0	0	1960.99	1967	1983
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	MVVLSLPR	99.7%	45.8	25	45.8	4	0	0	914.55	991	998
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	NTISLLVAGLK	99.7%	57.6	25	41.2	2	0	0	1128.70	799	809
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	NVVHELR	99.6%	39	25	32.4	1	0	0	866.48	957	963
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	NYMSNPSYNYEIVNR	99.7%	98.2	25	95.6	4	0	0	1879.83	3370	3384
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	QLIAQVMLYSQGFR	99.7%	49.8	25	47.7	2	0	0	1653.88	2047	2060
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	QLQNISLAAASGGAK	99.7%	63.8	25	57.3	1	0	0	1428.78	4488	4502
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	QNLDALLNQLK	99.7%	70.2	25	57.7	2	0	0	1269.72	1361	1371
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	QPQGHLLLIGVSGAGK	99.4%	31.3	25	21.2	0	1	0	1574.90	2928	2943
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	QTDVLQQLSIQMANAK	99.7%	97.5	25	97.5	2	0	0	1787.93	1850	1865
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	QYASYEFVQR	99.7%	57.6	25	48.8	2	0	0	1290.61	1379	1388
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	SFEWLSQMR	99.7%	64.3	25	56.2	2	0	0	1183.56	1835	1843
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	SIPLDEGEDEAQR	99.7%	41.2	25	41.2	1	0	0	1458.67	2384	2396
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	SIPLDEGEDEAQRR	99.1%	35.1	25	31.7	1	0	0	1614.77	2384	2397
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	SLETCMYDHK	99.7%	54	25	54	2	0	0	1283.54	863	872
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	SLLQALNEVK	99.7%	70.7	25	66.2	4	0	0	1114.65	3748	3757
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	SMANPPAAVK	99.1%	35.2	25	28.5	2	0	0	985.51	3309	3318
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	SNSLAFIK	98.4%	32.5	25	21.2	2	0	0	879.49	113	120
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	SPLVMDVLNIQGVQR	99.7%	111	25	103	4	1	0	1684.91	1585	1599
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	SSLQSQCLNEVLK	99.7%	68.3	25	58.5	2	0	0	1505.76	3706	3718
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	SVLVSAGNVK	99.1%	34.7	25	25.5	2	0	0	973.57	2095	2104

Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	SVLVSAGNVKR	99.7%	52.5	25	44.7	2	0	0	1129.67	2095	2105
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	TEYLSNADER	99.7%	41.5	25	38.4	2	0	0	1197.54	3550	3559
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	TFDHYCEYRR	95.6%	23.3	25	17.4	0	1	0	1446.62	2634	2643
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	TFSEILNR	99.7%	53.6	25	40.9	2	0	0	979.52	873	880
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	TFSSIPVSR	99.5%	38	25	29.8	5	0	0	993.54	4160	4168
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	TLINELVK	98.9%	34	25	11.4	2	0	0	929.57	4450	4457
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	TLMAQSIYGGR	99.7%	83.3	25	78.6	2	0	0	1196.61	4245	4255
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	TMTLFSALR	99.7%	60.3	25	51.7	4	0	0	1055.56	2602	2610
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	TPNGVVLAPVQLGK	99.7%	62.3	25	62.3	2	0	0	1392.82	2644	2657
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	TPVIDADKPVSSQLR	99.7%	70.6	25	70.3	2	2	0	1625.89	122	136
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	TPVSITEHPK	99.7%	50	25	44.8	2	0	0	1108.60	1688	1697
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	TSAPITCELLNK	99.7%	61.7	25	53.1	2	0	0	1346.70	1993	2004
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	TSFLDDAFRK	99.7%	63.7	25	55.4	2	0	0	1199.61	3612	3621
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	TTDLLTDWEK	99.2%	35.3	25	35.3	1	0	0	1221.60	1254	1263
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	TVENIKDPLFR	99.4%	36.6	25	32.7	2	0	0	1331.73	4401	4411
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	VAAPDVVVPTLDTVR	99.7%	58.8	25	58.8	2	0	0	1551.87	2562	2576
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	VDNEFDQR	99.7%	53	25	43.9	2	0	0	1022.45	4256	4263
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	VEPLRNELQK	98.6%	33.1	25	16.8	2	0	0	1225.69	3409	3418
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	VLLTTQGVDMISK	99.7%	99.4	25	93.7	5	0	0	1404.78	4330	4342
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	VLRPQVTAVAQQNQGEVPEPQDMK	99.7%	79.2	25	74.9	0	4	0	2662.36	483	506
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	VMSQEIQEQLHK	99.7%	56.5	25	47.9	2	0	0	1469.74	3255	3266
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	VNFLPEIITLSK	99.7%	68.3	25	62.8	2	0	0	1373.80	737	748
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	VPQIEVETHK	99.7%	49	25	35.8	2	0	0	1179.64	2552	2561
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	VPVNLLR	99.6%	39.2	25	25.7	2	0	0	810.52	4134	4140
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	VQVALEELQDLK	99.7%	55	25	47.9	2	0	0	1384.77	1319	1330
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	VQYPQSQACK	99.4%	37	25	22.3	1	0	0	1208.57	625	634
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	VTDFGDKVEDPTFLNQLQSGVNR	99.7%	68.7	25	68.7	0	2	0	2579.27	229	251
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	VTFVNFTVTR	99.7%	82.1	25	74.9	2	0	0	1183.65	3696	3705
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	WAIAQLNYADMLK	99.7%	62.5	25	62.2	1	0	0	1536.79	3395	3407
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	DYHC1_HUMAN	532.4	100.0%	111	127	237	0.22%	27.3%	YATLATVSR	99.7%	57.7	25	45.7	2	0	0	981.54	2350	2358
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	8	8	12	0.01%	21.6%	AEDNFEDIITKPPVR	97.1%	24.9	25	24.9	0	1	0	1743.89	345	359
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	8	8	12	0.01%	21.6%	AGATSEGVLANFFNSLLSK	99.7%	114	25	112	2	0	0	1926.00	436	454
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	8	8	12	0.01%	21.6%	FCLQYGAALIYTSVK	99.7%	74.7	25	74.7	1	0	0	1733.89	274	288
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	8	8	12	0.01%	21.6%	IGILHENFQTLK	95.6%	23.4	25	18.9	0	1	0	1412.79	333	344
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	8	8	12	0.01%	21.6%	IPAVVVEK	99.7%	42.8	25	33.8	2	0	0	854.53	311	318
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	8	8	12	0.01%	21.6%	NVLLLGEDGAGK	99.7%	74	25	69.1	1	0	0	1185.65	69	80
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	8	8	12	0.01%	21.6%	SGQKPVLDVHAELDR	99.7%	34.5	25	34.2	0	2	0	1663.88	487	501
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	DC1L1_HUMAN	56.6	100.0%	8	8	12	0.01%	21.6%	SVSSNVASVSPIPAGSK	99.7%	83.3	25	79.4	2	0	0	1586.84	412	428
Cytoplasmic dynein 2 heavy chain 1	DYNC2H1	DYHC2_HUMAN	492.6	100.0%	4	4	5	0.00%	1.2%	IAEALLSDLPGFR	99.5%	38	25	37.3	1	0	0	1401.77	502	514
Cytoplasmic dynein 2 heavy chain 1	DYNC2H1	DYHC2_HUMAN	492.6	100.0%	4	4	5	0.00%	1.2%	TVAGGGLETISNLK	99.7%	73.3	25	55	1	0	0	1359.75	999	1012
Cytoplasmic dynein 2 heavy chain 1	DYNC2H1	DYHC2_HUMAN	492.6	100.0%	4	4	5	0.00%	1.2%	VLSFPGGSLLLAGR	99.7%	72.2	25	72.2	2	0	0	1386.81	2643	2656
Cytoplasmic dynein 2 heavy chain 1	DYNC2H1	DYHC2_HUMAN	492.6	100.0%	4	4	5	0.00%	1.2%	VTTLTTHAGIR	99.7%	47.9	25	39.2	1	0	0	1169.66	1388	1398
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	10	11	21	0.02%	9.8%	ALNLAYSSIYGSYR	99.7%	49.3	25	3.17	2	0	0	1577.80	893	906
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	10	11	21	0.02%	9.8%	AVGPSSTQLYMVR	99.7%	70.1	25	56	2	0	0	1424.72	551	563
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	10	11	21	0.02%	9.8%	DFVSEAYLITLGK	99.7%	55.2	25	0	4	0	0	1455.77	151	163
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	10	11	21	0.02%	9.8%	EANHNVSAPYGR	99.6%	39.3	25	36.3	1	1	0	1314.62	827	838
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	10	11	21	0.02%	9.8%	LGTPQQIAIAR	99.7%	59.9	25	51.9	2	0	0	1167.68	1066	1076
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	10	11	21	0.02%	9.8%	NVIQSVLQAIR	99.5%	37.4	25	23	2	0	0	1240.74	505	515
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	10	11	21	0.02%	9.8%	SGDGEGTPVEHVR	99.7%	41.3	25	38.5	1	0	0	1339.62	1228	1240
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	10	11	21	0.02%	9.8%	SSLEGPTILDIEK	99.7%	86.6	25	72.3	2	0	0	1401.75	582	594
Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	10	11	21	0.02%	9.8%	TVEVLEPEVTK	99.7%	57	25	44.8	2	0	0	1243.68	111	121

Cytoplasmic FMR1-interacting protein 1	CYFIP1	CYFP1_HUMAN	145.2	100.0%	10	11	21	0.02%	9.8%	YSNSEVVTGSGR	99.7%	95.4	25	93.8	2	0	0	1255.59	366	377
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	5	5	7	0.01%	3.1%	EGLDEVAGIINDAK	99.7%	53.5	25	48.3	1	0	0	1443.73	879	892
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	5	5	7	0.01%	3.1%	LDDIFEPVLIPEPK	99.7%	43.5	25	41	2	0	0	1624.88	1510	1523
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	5	5	7	0.01%	3.1%	MQGQSPPAPTR	99.5%	37.7	25	28.2	1	0	0	1169.57	812	822
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	5	5	7	0.01%	3.1%	TTGEVVSGVVSK	99.7%	43.7	25	33	2	0	0	1162.63	85	96
Cytoskeleton-associated protein 5	CKAP5	CKAP5_HUMAN	225.5	100.0%	5	5	7	0.01%	3.1%	VNDFLAEIFKK	99.0%	34.5	25	34.5	1	0	0	1323.73	1829	1839
Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	NUBP2_HUMAN	28.8	100.0%	3	3	5	0.00%	13.3%	GWAPVFLDR	97.1%	30.1	25	12.2	1	0	0	1060.56	75	83
Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	NUBP2_HUMAN	28.8	100.0%	3	3	5	0.00%	13.3%	STISTELALALR	99.7%	66.3	25	62.3	2	0	0	1274.73	29	40
Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	NUBP2_HUMAN	28.8	100.0%	3	3	5	0.00%	13.3%	VGILDVDLCGPSIPR	99.7%	71.3	25	62.8	2	0	0	1610.86	46	60
Cytosolic non-specific dipeptidase	CNDP2	CNDP2_HUMAN	52.9	99.8%	2	2	3	0.00%	4.4%	TGQEIPVNVR	99.3%	35.9	25	26.5	2	0	0	1112.61	150	159
Cytosolic non-specific dipeptidase	CNDP2	CNDP2_HUMAN	52.9	99.8%	2	2	3	0.00%	4.4%	TVFGVEPDLTR	97.3%	30.4	25	19.9	1	0	0	1233.65	403	413
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	25	37	121	0.11%	53.8%	AGTGVDNVDLEAATR	99.7%	107	25	95.7	8	0	0	1488.73	76	90
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	25	37	121	0.11%	53.8%	AGTGVDNVDLEAATRK	99.7%	67.9	25	64.1	2	1	0	1616.82	76	91
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	25	37	121	0.11%	53.8%	ALQSGQCAGAALDVFTEEPPRDR	99.7%	61.8	25	61.8	0	2	0	2488.19	248	270
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	25	37	121	0.11%	53.8%	ALVDHENVISCPHLGASTK	99.7%	76.2	25	76.2	1	2	0	2048.02	271	289
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	25	37	121	0.11%	53.8%	CGEEIAVQFVDMVK	99.7%	114	25	110	4	0	0	1624.77	295	308
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	25	37	121	0.11%	53.8%	DLPLLLFR	99.7%	57.4	25	48.3	15	0	0	986.60	462	469
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	25	37	121	0.11%	53.8%	EELIAELQDCEGLIVR	99.7%	77	25	77	2	1	0	1886.95	39	54
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	25	37	121	0.11%	53.8%	FMGTELNGK	99.7%	48.1	25	40.7	4	0	0	996.48	138	146
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	25	37	121	0.11%	53.8%	GGIVDEGALLR	99.7%	81.5	25	52.9	4	0	0	1099.61	237	247
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	25	37	121	0.11%	53.8%	GTIQVITQGTSLK	99.7%	84.1	25	84	10	0	0	1345.77	352	364
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	25	37	121	0.11%	53.8%	ILQDGGLQVVEK	99.7%	80.4	25	75.3	6	0	0	1298.73	22	33
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	25	37	121	0.11%	53.8%	KILQDGGLQVVEK	99.7%	73.7	25	66.7	2	2	0	1426.83	21	33
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	25	37	121	0.11%	53.8%	KVLISDSLDPCCR	98.8%	28.4	25	24	0	1	0	1562.77	8	20
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	25	37	121	0.11%	53.8%	LLSYQTSLVSDGETWHVMGISSLLPSLEAWK	99.7%	81.9	25	81.9	0	3	0	3447.75	492	522
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	25	37	121	0.11%	53.8%	MQSFGMK	99.7%	40.4	25	29.9	1	0	0	828.37	164	170
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	25	37	121	0.11%	53.8%	NAGNCLSPAVIVGLLK	99.7%	87.2	25	87.2	5	1	0	1625.90	365	380
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	25	37	121	0.11%	53.8%	QADVNLVNAK	99.7%	54.8	25	50.7	2	0	0	1071.58	385	394
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	25	37	121	0.11%	53.8%	QHVTEAFQFHF	99.7%	71.4	25	67.4	2	0	0	1390.65	523	533
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	25	37	121	0.11%	53.8%	QIPQATASMK	99.7%	49	25	39.1	3	0	0	1090.56	120	129
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	25	37	121	0.11%	53.8%	QNLSKEELIAELQDCEGLIVR	99.4%	31.1	25	28.6	0	1	0	2457.27	34	54
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	25	37	121	0.11%	53.8%	TLGILGLGR	99.7%	62.3	25	56	9	0	0	899.57	147	155
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	25	37	121	0.11%	53.8%	TQTSDPAMLPTMIGLLAEAGVR	99.7%	124	25	123	6	6	0	2272.17	470	491
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	25	37	121	0.11%	53.8%	VLISDSLDPCCR	99.7%	69.5	25	69.5	3	0	0	1434.67	9	20
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	25	37	121	0.11%	53.8%	VLISDSLDPCCRK	99.2%	35.3	25	30.8	2	0	0	1562.77	9	21
D-3-phosphoglycerate dehydrogenase	PHGDH	SERA_HUMAN	56.7	100.0%	25	37	121	0.11%	53.8%	VTADVINAAEK	99.7%	95.4	25	82.8	10	0	0	1130.61	59	69
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	7	8	16	0.02%	13.2%	ESVLTATSILNNPIVK	99.7%	90.2	25	87.8	2	0	0	1698.96	444	459
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	7	8	16	0.02%	13.2%	FGGSYGGR	99.7%	48.4	25	39.7	2	0	0	800.37	103	110
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	7	8	16	0.02%	13.2%	FGPYESYDSR	99.7%	52.1	25	52.1	2	0	0	1220.52	71	80
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	7	8	16	0.02%	13.2%	MAFTCSFCK	99.7%	43.3	25	42.2	4	0	0	1151.47	310	318
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	7	8	16	0.02%	13.2%	NQGGSSWEAPYSR	99.7%	52.2	25	52.2	2	0	0	1438.63	126	138
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	7	8	16	0.02%	13.2%	NSLDSFGGR	99.7%	55.4	25	44.3	2	0	0	952.45	117	125
DBIRD complex subunit ZNF326	ZNF326	ZN326_HUMAN	65.7	100.0%	7	8	16	0.02%	13.2%	SGYGFNEPEQSR	99.7%	51.1	25	50.6	2	0	0	1370.60	91	102
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	6	6	9	0.01%	3.9%	ESFCITSFLCSTK	99.7%	44.5	25	44.5	1	0	0	1579.71	565	577
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	6	6	9	0.01%	3.9%	ESGVSLIATVTR	99.7%	69.3	25	54.9	2	0	0	1232.68	1146	1157
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	6	6	9	0.01%	3.9%	IGCTVSLLNFYK	99.7%	55.3	25	52.4	1	0	0	1414.74	1179	1190
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	6	6	9	0.01%	3.9%	ILSNVFCLIK	99.7%	41.8	25	37.8	2	0	0	1206.69	854	863
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	6	6	9	0.01%	3.9%	LDWGNEQLGLDLVPR	99.7%	46.6	25	46.6	2	0	0	1724.90	150	164
Dedicator of cytokinesis protein 4	DOCK4	DOCK4_HUMAN	225.2	100.0%	6	6	9	0.01%	3.9%	TSLYLVQSLPGISR	99.7%	54.1	25	54.1	1	0	0	1533.86	1441	1454
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	8	11	20	0.02%	30.2%	DVILADLLPSLAVYLR	99.3%	36.3	25	36.3	1	0	0	1771.04	286	301
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	8	11	20	0.02%	30.2%	HATQAFFDCLR	99.7%	56.3	25	55	1	0	0	1365.64	212	222

Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	8	11	20	0.02%	30.2%	NAVVVITGATSGLGK	99.7%	108	25	100	2	0	0	1386.80	52	66
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	8	11	20	0.02%	30.2%	SPVEVAQDVLAAVGK	99.7%	99.8	25	94.5	2	0	0	1482.82	268	282
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	8	11	20	0.02%	30.2%	SPVEVAQDVLAAVGKK	99.7%	73	25	73	2	0	0	1610.91	268	283
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	8	11	20	0.02%	30.2%	TLAPGLFFSLMASR	99.7%	73.5	25	73.1	4	0	0	1510.81	302	315
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	8	11	20	0.02%	30.2%	VMETNYFGPVALTK	99.7%	88.6	25	69.8	4	0	0	1585.79	162	175
Dehydrogenase/reductase SDR family member 7B	DHRS7B	DRS7B_HUMAN	35.1	100.0%	8	11	20	0.02%	30.2%	YGVMDTTTAQGR	99.7%	80.3	25	80.3	4	0	0	1315.59	256	267
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	6	6	11	0.01%	14.7%	ASGTNDKPGGPHYILR	98.6%	27.6	25	27.6	0	1	0	1682.86	525	540
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	6	6	11	0.01%	14.7%	NAAGNFYINDK	99.7%	50.8	25	45.3	2	0	0	1226.58	499	509
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	6	6	11	0.01%	14.7%	SADVESVVSGTLR	99.7%	101	25	94.5	2	0	0	1319.68	326	338
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	6	6	11	0.01%	14.7%	SSPSLTILAGGK	99.7%	50.3	25	41.8	2	0	0	1130.64	409	420
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	6	6	11	0.01%	14.7%	STGSIVGQQPFGGAR	99.7%	65.2	25	59.5	2	0	0	1461.74	510	524
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	AL4A1_HUMAN	61.7	100.0%	6	6	11	0.01%	14.7%	VANEPVLAFTQGSPER	99.7%	94.3	25	94.3	2	0	0	1714.88	32	47
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	CEYPAACNALETLLIHR	99.7%	50.1	25	49.5	0	2	0	2030.98	606	622
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	EAVQLVNTR	99.7%	61.4	25	44.4	2	0	0	1029.57	531	539
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	EAVQLVNTREEVEDLCR	99.7%	49.2	25	47.4	0	2	0	2060.01	531	547
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	EMAIPVLEAR	98.4%	32.5	25	18.8	1	0	0	1144.60	150	159
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	EMMLVTSGAVAFGK	99.7%	88.8	25	77.1	4	0	0	1440.72	111	124
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	FASYLTFSPSEVK	99.7%	72.9	25	72.2	3	0	0	1475.74	650	662
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	FGLGAEVGISTSR	99.7%	77.2	25	71.5	2	0	0	1293.68	733	745
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	GDECGLALGR	99.7%	53	25	44.8	2	0	0	1047.49	85	94
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	GKDHVVSDFSEHGSLK	99.7%	60.7	25	60.7	0	2	0	1741.85	766	781
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	GPVGLEGLLTTK	99.7%	73.6	25	73.6	2	0	0	1184.69	750	761
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	HEILLSQSVR	99.7%	56.2	25	47.3	2	0	0	1181.66	129	138
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	ILHLLTQEALSIHGVK	99.6%	32.3	25	32.3	0	2	0	1772.04	515	530
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	LAAPLLKR	99.7%	43.6	25	43.6	2	0	0	881.59	418	425
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	LASIVEQVSVLQNQGR	99.7%	88.8	25	76.2	2	0	0	1740.96	95	110
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	LGSAVVTR	99.7%	75.4	25	54.7	4	0	0	802.48	77	84
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	LIDIFYPGDQQSVTFGTK	99.7%	97.6	25	97.6	4	0	0	2029.03	283	300
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	LNSLAIGLR	99.7%	88.3	25	73.8	2	0	0	956.59	433	441
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	LRHEILLSQSVR	98.7%	33.3	25	33.3	1	2	0	1450.85	127	138
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	MIDLIIPR	99.7%	61.6	25	49.8	5	0	0	970.58	551	558
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	MLATLEPEQR	99.7%	61.5	25	48.9	5	0	0	1187.61	376	385
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	NLNGTLHELLR	99.7%	52.3	25	44.4	2	0	0	1279.71	202	212
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	QALHSGQNQLK	99.7%	50.8	25	43.6	2	2	0	1223.65	139	149
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	QIAASSQDSVGR	99.7%	86.6	25	80.1	2	0	0	1218.61	442	453
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	SWSNIPFITVPLSR	99.7%	76.3	25	68	2	0	0	1616.88	42	55
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	TPLFDQIIDMLR	99.7%	90.6	25	87.2	5	0	0	1461.78	627	638
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	VGMGGMEAK	99.7%	43.6	25	37.4	2	0	0	879.41	303	311
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	VGTFFSEVKPAGPTVEQQGEMAR	99.7%	95.2	25	95.2	0	4	0	2481.21	349	371
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	VSGHVITDIVEGK	99.7%	61.1	25	58.8	2	2	0	1353.74	335	347
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	VSGHVITDIVEGKK	99.7%	57.4	25	57.4	0	2	0	1481.83	335	348
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P5CS_HUMAN	87.3	100.0%	30	38	82	0.08%	43.3%	YLHENLPIPQR	99.0%	28.8	25	28.3	0	2	0	1379.74	782	792
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	12	19	0.02%	23.6%	DKEVGNLYDMFHTR	99.7%	44.9	25	44.9	0	1	0	1724.81	353	366
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	12	19	0.02%	23.6%	EQIVGPLESPVEDSLWPYK	99.7%	85.6	25	85.6	2	0	0	2186.10	270	288
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	12	19	0.02%	23.6%	FAEQLIR	99.7%	48.1	25	26.2	2	0	0	876.49	545	551
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	12	19	0.02%	23.6%	FENLGVSSLGER	99.7%	58.2	25	55.2	2	0	0	1307.66	86	97
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	12	19	0.02%	23.6%	FIPLARPEVK	98.3%	32.3	25	16	1	0	0	1169.70	221	230
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	12	19	0.02%	23.6%	IIDTPQFQR	99.7%	53.9	25	37.7	2	0	0	1117.60	135	143
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	12	19	0.02%	23.6%	ISTAIDDMEAYTK	99.7%	75.2	25	71.9	1	0	0	1457.68	409	421
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	12	19	0.02%	23.6%	NQVSQLLPEK	99.2%	35.5	25	25.7	2	0	0	1155.64	535	544
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	12	19	0.02%	23.6%	QLGGGYYVFPGASHNR	95.6%	23.4	25	18.6	0	1	0	1722.83	149	164

Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	12	19	0.02%	23.6%	SFLYEIVSNKR	99.7%	61.2	25	61.2	2	0	0	1355.73	295	305
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	12	19	0.02%	23.6%	VGNIIDTMITDAFLK	99.7%	83.2	25	83.2	1	0	0	1650.88	378	392
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	SAMH1_HUMAN	72.2	100.0%	12	12	19	0.02%	23.6%	YVGETQPTGQIK	99.7%	56.9	25	49.5	2	0	0	1320.68	456	467
Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial	DUT	DUT_HUMAN	26.6	99.7%	2	2	3	0.00%	7.1%	IAQLICER	99.4%	36.6	25	33	2	0	0	1002.54	217	224
Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial	DUT	DUT_HUMAN	26.6	99.7%	2	2	3	0.00%	7.1%	LSEHATAPTR	94.6%	27.7	25	19.2	1	0	0	1082.56	119	128
Dephospho-CoA kinase domain-containing protein	DCAKD	DCAKD_HUMAN	26.6	100.0%	4	4	7	0.01%	20.8%	INAQLPLTDK	99.7%	62.3	25	61.2	2	0	0	1112.63	159	168
Dephospho-CoA kinase domain-containing protein	DCAKD	DCAKD_HUMAN	26.6	100.0%	4	4	7	0.01%	20.8%	MFLVGLTGGIASGK	99.7%	115	25	115	2	0	0	1350.75	1	14
Dephospho-CoA kinase domain-containing protein	DCAKD	DCAKD_HUMAN	26.6	100.0%	4	4	7	0.01%	20.8%	QVILLHTELER	95.5%	28.4	25	11.8	1	0	0	1350.77	188	198
Dephospho-CoA kinase domain-containing protein	DCAKD	DCAKD_HUMAN	26.6	100.0%	4	4	7	0.01%	20.8%	YVILDIPLLFETK	99.7%	101	25	101	2	0	0	1563.90	109	121
Derlin-1	DERL1	DERL1_HUMAN	28.8	99.8%	2	2	7	0.01%	10.0%	NFLSTPQFLYR	99.7%	45.9	25	33.2	4	0	0	1385.72	198	208
Derlin-1	DERL1	DERL1_HUMAN	28.8	99.8%	2	2	7	0.01%	10.0%	YWFAATVAVPLVGK	99.7%	45.6	25	45.6	3	0	0	1521.85	17	30
Dermcidin	DCD	DCD_HUMAN	11.3	100.0%	4	5	56	0.05%	35.5%	DAVEDLESVGK	99.7%	68.7	25	46.6	16	0	0	1161.56	86	96
Dermcidin	DCD	DCD_HUMAN	11.3	100.0%	4	5	56	0.05%	35.5%	ENAGEDPGLAR	99.7%	82.5	25	82.4	32	0	0	1128.53	43	53
Dermcidin	DCD	DCD_HUMAN	11.3	100.0%	4	5	56	0.05%	35.5%	GAVHDVKDVLDSVL	98.7%	33.2	25	33.2	1	0	0	1466.79	97	110
Dermcidin	DCD	DCD_HUMAN	11.3	100.0%	4	5	56	0.05%	35.5%	LGKDAVEDLESVGK	99.7%	81.5	25	74.4	5	2	0	1459.76	83	96
Desmoglein-1	DSG1	DSG1_HUMAN	113.7	100.0%	5	5	7	0.01%	7.2%	ALNSMGQDLERPLELR	99.3%	30.4	25	30.2	0	1	0	1857.95	129	144
Desmoglein-1	DSG1	DSG1_HUMAN	113.7	100.0%	5	5	7	0.01%	7.2%	ESSNVVVTER	99.7%	47.5	25	37.8	2	0	0	1119.56	916	925
Desmoglein-1	DSG1	DSG1_HUMAN	113.7	100.0%	5	5	7	0.01%	7.2%	ISGVGIDQPPYGIFVINQK	99.7%	64.7	25	64.2	2	0	0	2045.11	87	105
Desmoglein-1	DSG1	DSG1_HUMAN	113.7	100.0%	5	5	7	0.01%	7.2%	YQGTILSIDDNLQR	99.7%	54.6	25	54.6	1	0	0	1635.83	460	473
Desmoglein-1	DSG1	DSG1_HUMAN	113.7	100.0%	5	5	7	0.01%	7.2%	YVMGNNPADLLAVDSR	99.7%	57	25	54.8	1	0	0	1734.85	423	438
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	14	15	30	0.03%	4.8%	AELIVQPELK	99.7%	44.3	25	35.1	4	0	0	1139.67	85	94
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	14	15	30	0.03%	4.8%	ALLQAILQTEDMLK	99.7%	77.4	25	77.4	7	0	0	1602.88	772	785
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	14	15	30	0.03%	4.8%	FLSEMLK	95.9%	28.7	25	8.86	1	0	0	867.46	1016	1022
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	14	15	30	0.03%	4.8%	IEVLEEELR	99.7%	50.5	25	38.2	2	0	0	1129.61	1034	1042
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	14	15	30	0.03%	4.8%	IVQLKPR	95.1%	28	25	18.2	1	0	0	853.56	445	451
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	14	15	30	0.03%	4.8%	LASLEELKR	99.5%	37.9	25	25.4	2	0	0	1058.62	1076	1084
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	14	15	30	0.03%	4.8%	LLEAQIATGGIIDPK	99.1%	35.2	25	29.9	1	0	0	1538.88	2367	2381
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	14	15	30	0.03%	4.8%	QLQNIIQATSR	99.7%	56.1	25	56	3	0	0	1271.71	271	281
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	14	15	30	0.03%	4.8%	RVEEDIQQQK	99.7%	46.4	25	36.3	1	0	0	1272.65	1425	1434
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	14	15	30	0.03%	4.8%	SLSEEIKR	99.1%	35.2	25	14.2	1	0	0	961.53	1404	1411
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	14	15	30	0.03%	4.8%	SQLQISNNR	97.7%	31	25	17.8	2	0	0	1059.55	1754	1762
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	14	15	30	0.03%	4.8%	SVEEVASEIQPFLR	99.7%	41.6	25	29.5	2	0	0	1603.83	2000	2013
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	14	15	30	0.03%	4.8%	YGDGIQLTR	99.7%	41	25	32	1	0	0	1022.53	95	103
Desmoplakin	DSP	DESP_HUMAN	331.8	100.0%	14	15	30	0.03%	4.8%	YIELLTR	99.5%	37.8	25	34.6	2	0	0	907.52	1003	1009
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	5	6	10	0.01%	32.1%	IMQDFESDTFFPEIDLEK	99.7%	51.2	25	51.2	3	0	0	2220.01	139	156
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	5	6	10	0.01%	32.1%	INLVLSR	99.7%	51.1	25	32.7	2	0	0	814.51	72	78
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	5	6	10	0.01%	32.1%	KTWFSIPEK	96.8%	29.7	25	17.7	1	0	0	1135.61	56	64
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	5	6	10	0.01%	32.1%	LLPEYPGVLSDVQEEK	99.7%	102	25	98.9	2	0	0	1815.94	159	174
Dihydrofolate reductase	DHFR	DYR_HUMAN	21.5	100.0%	5	6	10	0.01%	32.1%	NGDLPWPPLR	99.7%	44.3	25	43.4	2	0	0	1164.62	20	29
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	17	30	0.03%	39.3%	ADGGTQVIDTK	99.7%	73.2	25	65.6	2	0	0	1104.55	167	177
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	17	30	0.03%	39.3%	ALTGGIAHLFK	99.7%	68.2	25	60.5	2	0	0	1127.66	133	143
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	17	30	0.03%	39.3%	EANLAASFGK	99.7%	77.6	25	70.6	2	0	0	1007.52	496	505
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	17	30	0.03%	39.3%	FPFAANSR	99.7%	42.4	25	32.8	2	0	0	909.46	421	428
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	17	30	0.03%	39.3%	GIEMSEVR	97.5%	30.7	25	30.3	2	0	0	936.45	110	117
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	17	30	0.03%	39.3%	GRIPVNTR	97.9%	31.4	25	17.8	1	0	0	912.54	335	342
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	17	30	0.03%	39.3%	IPNIYAIGDVVAGPMLAHK	99.7%	80.9	25	80.9	2	3	0	1979.08	347	365
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	17	30	0.03%	39.3%	LGADVTAVEFLGHVGGVGIDMEISK	99.7%	64	25	64	0	2	0	2530.29	235	259
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	17	30	0.03%	39.3%	NETLGGTCLNVGCIPSK	99.7%	95.9	25	92.4	2	0	0	1819.87	73	89
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	17	30	0.03%	39.3%	NLGLEELGIELDPR	99.7%	83.1	25	73.3	2	0	0	1567.83	321	334
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	17	30	0.03%	39.3%	SEEQLKEEGIEYK	99.7%	72.8	25	72.8	2	2	0	1581.76	405	417
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	17	30	0.03%	39.3%	TNADTDGMVK	99.7%	54.8	25	53	1	0	0	1051.47	431	440

Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	17	30	0.03%	39.3%	VCHAHPTLSEAFR	99.7%	43.4	25	38.5	0	2	0	1524.74	483	495
Dihydrolipoyl dehydrogenase, mitochondrial	DLD	DLDH_HUMAN	54.2	100.0%	14	17	30	0.03%	39.3%	VLGAHILGPGAGEMVNEAALALEYGASCEDIAR	99.7%	71.4	25	68.1	0	1	0	3354.65	450	482
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	5	6	9	0.01%	9.9%	DVPLGTPLCIIVEK	99.7%	83.7	25	83.7	2	0	0	1553.86	283	296
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	5	6	9	0.01%	9.9%	GVETIANDVVSLATK	99.7%	89.7	25	84.2	2	0	0	1516.82	533	547
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	5	6	9	0.01%	9.9%	ILVAEGTR	97.9%	31.5	25	24.1	1	0	0	858.50	148	155
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	5	6	9	0.01%	9.9%	VPLPSLSPTMQAGTIAR	99.7%	62.5	25	62.5	3	0	0	1738.95	94	110
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	ODP2_HUMAN	69.0	100.0%	5	6	9	0.01%	9.9%	YLEKPITMLL	97.1%	30.1	25	26.7	1	0	0	1236.69	638	647
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	9	10	17	0.02%	19.8%	GMYDGPVYEVPATPK	99.7%	76.2	25	73.9	2	0	0	1623.77	497	511
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	9	10	17	0.02%	19.8%	INCPVYITK	99.7%	51.7	25	43.6	1	0	0	1107.59	246	254
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	9	10	17	0.02%	19.8%	IVFEDGNINVNK	99.7%	57.7	25	54.1	2	0	0	1361.71	452	463
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	9	10	17	0.02%	19.8%	MDENQFVAVTSTNAAK	99.7%	75.6	25	75.2	3	0	0	1725.81	375	390
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	9	10	17	0.02%	19.8%	NLHQSNFSLSGAQIDDNNPR	99.7%	56.9	25	56.9	0	1	0	2227.05	533	552
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	9	10	17	0.02%	19.8%	QIGENLIVPGGVK	99.7%	58.1	25	58	2	0	0	1323.76	44	56
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	9	10	17	0.02%	19.8%	SAADIIALAR	99.7%	75.9	25	64.9	2	0	0	1000.58	259	268
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	9	10	17	0.02%	19.8%	SIPHITSDR	95.8%	28.7	25	23.5	2	0	0	1025.54	8	16
Dihydropyrimidinase-related protein 1	CRMP1	DPYL1_HUMAN	62.2	100.0%	9	10	17	0.02%	19.8%	VFGLQGVSR	99.7%	52.8	25	41.6	2	0	0	962.54	488	496
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	10	10	19	0.02%	21.9%	GAPAVVISQGR	99.7%	65.3	25	62.2	2	0	0	1054.60	441	451
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	10	10	19	0.02%	21.9%	GVNSFLVFMAYK	99.7%	51.6	25	44.5	2	0	0	1375.71	160	171
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	10	10	19	0.02%	21.9%	IFNFYPR	99.1%	35.2	25	7.09	2	0	0	956.50	391	397
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	10	10	19	0.02%	21.9%	LAEIHGVPR	99.7%	63.9	25	53.6	2	0	0	991.57	488	496
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	10	10	19	0.02%	21.9%	MFVTPGAGR	97.7%	31	25	30.2	2	0	0	935.48	459	467
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	10	10	19	0.02%	21.9%	NLHQSGFSLSGSQADDHIAR	99.7%	68.5	25	68.5	0	2	0	2140.02	533	552
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	10	10	19	0.02%	21.9%	QANCPLYVTK	99.0%	34.6	25	29.6	2	0	0	1193.60	245	254
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	10	10	19	0.02%	21.9%	QIGENLIVPGGIK	99.7%	43.2	25	43.2	2	0	0	1337.78	44	56
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	10	10	19	0.02%	21.9%	TIDAHGLMVLPGGVDVHTR	99.7%	39.1	25	36.9	0	1	0	1988.04	57	75
Dihydropyrimidinase-related protein 4	DPYSL4	DPYL4_HUMAN	61.9	100.0%	10	10	19	0.02%	21.9%	VAVGSDADLVIWNPK	99.7%	87.1	25	80	2	0	0	1583.84	401	415
Dihydropyrimidinase-related protein 5	DPYSL5	DPYL5_HUMAN	61.4	100.0%	5	5	6	0.01%	12.4%	FVAVTSSNAAK	99.7%	57.3	25	47.9	2	0	0	1094.58	373	383
Dihydropyrimidinase-related protein 5	DPYSL5	DPYL5_HUMAN	61.4	100.0%	5	5	6	0.01%	12.4%	IIPGADADVVVWDPEATK	99.7%	64.4	25	62.3	1	0	0	1895.98	394	411
Dihydropyrimidinase-related protein 5	DPYSL5	DPYL5_HUMAN	61.4	100.0%	5	5	6	0.01%	12.4%	IPHGVSGVQDR	95.6%	28.4	25	18.4	1	0	0	1164.61	344	354
Dihydropyrimidinase-related protein 5	DPYSL5	DPYL5_HUMAN	61.4	100.0%	5	5	6	0.01%	12.4%	TPYLGDVAVVVHPGKK	99.7%	39.2	25	39.2	0	1	0	1679.95	490	505
Dihydropyrimidinase-related protein 5	DPYSL5	DPYL5_HUMAN	61.4	100.0%	5	5	6	0.01%	12.4%	VHAENGELVAEGAK	99.7%	53.7	25	53.7	1	0	0	1423.72	190	203
Diphosphoinositol polyphosphate phosphohydrolase 3-beta	NUDT11	NUD11_HUMAN	18.6	100.0%	2	2	2	0.00%	12.8%	EVYEEAGVK	99.7%	40.6	25	25	1	0	0	1023.50	65	73
Diphosphoinositol polyphosphate phosphohydrolase 3-beta	NUDT11	NUD11_HUMAN	18.6	100.0%	2	2	2	0.00%	12.8%	LLGVFEQNQDRK	94.9%	27.9	25	22.4	1	0	0	1446.77	79	90
DNA dC->dU-editing enzyme APOBEC-3C	APOBEC3C	ABC3C_HUMAN	22.8	100.0%	2	3	3	0.00%	14.7%	AMYPGTFYFQFK	97.4%	30.5	25	30.5	2	0	0	1499.70	11	22
DNA dC->dU-editing enzyme APOBEC-3C	APOBEC3C	ABC3C_HUMAN	22.8	100.0%	2	3	3	0.00%	14.7%	CFLSWFCDDILSPNTK	99.7%	44.4	25	39.3	1	0	0	2002.90	70	85
DNA ligase 3	LIG3	DNLI3_HUMAN	112.9	100.0%	3	3	6	0.01%	3.4%	SEAHTADGISIR	95.5%	28.3	25	22.1	1	0	0	1256.62	792	803
DNA ligase 3	LIG3	DNLI3_HUMAN	112.9	100.0%	3	3	6	0.01%	3.4%	VIQEGLEGLVLK	99.7%	91.5	25	83.8	2	0	0	1297.77	649	660
DNA ligase 3	LIG3	DNLI3_HUMAN	112.9	100.0%	3	3	6	0.01%	3.4%	VLLDIFTGVR	99.7%	75.7	25	74.8	3	0	0	1132.67	933	942
DNA methyltransferase 1-associated protein 1	DMAP1	DMAP1_HUMAN	53.0	100.0%	5	5	7	0.01%	13.7%	DAPPLLPSDTGQGYR	99.7%	43.7	25	40.4	2	0	0	1586.78	67	81
DNA methyltransferase 1-associated protein 1	DMAP1	DMAP1_HUMAN	53.0	100.0%	5	5	7	0.01%	13.7%	DTIIDVVGAPLTPNSR	98.5%	32.7	25	30.2	1	0	0	1667.90	434	449
DNA methyltransferase 1-associated protein 1	DMAP1	DMAP1_HUMAN	53.0	100.0%	5	5	7	0.01%	13.7%	EVYALLYSDKK	99.7%	51.6	25	45.7	1	0	0	1328.71	56	66
DNA methyltransferase 1-associated protein 1	DMAP1	DMAP1_HUMAN	53.0	100.0%	5	5	7	0.01%	13.7%	LITAADTTAEQR	99.7%	75.2	25	59.5	2	0	0	1289.67	271	282
DNA methyltransferase 1-associated protein 1	DMAP1	DMAP1_HUMAN	53.0	100.0%	5	5	7	0.01%	13.7%	SDLVLLYELK	99.7%	50.4	25	41.8	1	0	0	1192.68	369	378
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	15	15	27	0.03%	20.3%	ALNLFQGSVEDTTGSQSLAALLNK	99.7%	107	25	107	2	0	0	2477.29	309	332
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	15	15	27	0.03%	20.3%	DIYQDLNR	96.9%	29.9	25	10.8	1	0	0	1036.51	236	243
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	15	15	27	0.03%	20.3%	DSLIIIDELGR	99.7%	79.9	25	67.3	2	0	0	1243.69	742	752
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	15	15	27	0.03%	20.3%	GVSTFMAEMLETASILR	97.9%	31.3	25	22.4	1	0	0	1855.93	721	737
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	15	15	27	0.03%	20.3%	LDSSAQFGYYFR	99.7%	87.2	25	87.2	2	0	0	1453.67	513	524
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	15	15	27	0.03%	20.3%	LLLAVFVTPLTDLR	99.7%	89.6	25	89.6	3	0	0	1570.96	431	444
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	15	15	27	0.03%	20.3%	LNLVEAFVEDAELR	99.7%	110	25	109	2	0	0	1617.85	360	373
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	15	15	27	0.03%	20.3%	LTSLNEEYTK	99.7%	71	25	62.5	2	0	0	1197.60	556	565

DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	15	15	27	0.03%	20.3%	LYQGINQLPNVIQALEK	99.7%	79.6	25	79.6	2	0	0	1941.08	407	423
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	15	15	27	0.03%	20.3%	NLQSVVLSK	99.7%	50.7	25	28.7	2	0	0	987.58	74	82
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	15	15	27	0.03%	20.3%	NNSFVNEIISR	99.7%	62.4	25	44.2	2	0	0	1292.66	919	929
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	15	15	27	0.03%	20.3%	QAANLQDCYR	99.7%	49.3	25	43.5	1	0	0	1238.56	397	406
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	15	15	27	0.03%	20.3%	QTLQEDLLR	99.7%	50.8	25	40.6	2	0	0	1115.61	374	382
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	15	15	27	0.03%	20.3%	QVGVGYVDSIQR	99.7%	66.7	25	62.8	2	0	0	1320.69	160	171
DNA mismatch repair protein Msh2	MSH2	MSH2_HUMAN	104.7	100.0%	15	15	27	0.03%	20.3%	TEYEEAQDAIVK	99.7%	54.4	25	47.1	1	0	0	1395.66	568	579
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	17	18	32	0.03%	14.0%	AYGVCFVDTSLGK	99.7%	70.3	25	65	2	0	0	1416.68	555	567
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	17	18	32	0.03%	14.0%	EVCLASER	98.0%	31.5	25	28.2	1	0	0	963.46	1335	1342
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	17	18	32	0.03%	14.0%	GTATFDGTAIANAVVK	99.7%	102	25	94.5	2	0	0	1535.81	1218	1233
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	17	18	32	0.03%	14.0%	IIDFLSALEGFK	99.7%	83.6	25	68.9	3	0	0	1352.75	855	866
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	17	18	32	0.03%	14.0%	IIGIMEEVADGFK	99.7%	46.8	25	46.8	2	0	0	1421.73	871	883
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	17	18	32	0.03%	14.0%	KLPDLER	96.7%	29.6	25	0	1	0	0	870.50	814	820
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	17	18	32	0.03%	14.0%	LANLINAEER	99.4%	36.5	25	28.1	1	0	0	1142.62	1015	1024
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	17	18	32	0.03%	14.0%	LANLPEEVIQK	99.7%	56	25	40.3	2	0	0	1253.71	1305	1315
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	17	18	32	0.03%	14.0%	LSDGIGVMLPQVLK	99.7%	56.2	25	54	4	0	0	1485.83	647	660
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	17	18	32	0.03%	14.0%	QVISLQTK	95.8%	28.6	25	19.7	1	0	0	916.55	889	896
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	17	18	32	0.03%	14.0%	SELALSALGGCVFYLK	99.7%	41.5	25	41.5	2	0	0	1727.90	677	692
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	17	18	32	0.03%	14.0%	STVDAEAVHK	99.7%	44.3	25	35.1	2	0	0	1056.53	1343	1352
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	17	18	32	0.03%	14.0%	TIVYWGIGR	99.7%	46.7	25	38.1	2	0	0	1064.59	966	974
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	17	18	32	0.03%	14.0%	TLLEEEYFR	99.7%	44.5	25	32.4	2	0	0	1199.59	636	644
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	17	18	32	0.03%	14.0%	VDTCHTPFGK	98.6%	32.9	25	32.9	1	0	0	1161.54	762	771
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	17	18	32	0.03%	14.0%	VHVQFFDDSPTR	99.7%	52.3	25	52.3	2	0	0	1447.70	129	140
DNA mismatch repair protein Msh6	MSH6	MSH6_HUMAN	152.8	100.0%	17	18	32	0.03%	14.0%	YQLEIPENFTTR	99.7%	50.2	25	44.7	2	0	0	1510.75	977	988
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	17	30	0.03%	17.7%	DLEDQEQLLR	99.7%	65.6	25	45.5	2	0	0	1258.63	1088	1097
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	17	30	0.03%	17.7%	DNCPLVANLVTASLR	99.7%	75.6	25	75.6	2	0	0	1642.86	835	849
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	17	30	0.03%	17.7%	ELNLAISR	99.7%	45.6	25	27	2	0	0	915.53	167	174
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	17	30	0.03%	17.7%	EVSHLNALEER	99.6%	38.8	25	29.8	1	0	0	1296.65	1040	1050
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	17	30	0.03%	17.7%	FGVSSVAEAMALGR	99.7%	92.4	25	91	3	0	0	1394.71	763	776
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	17	30	0.03%	17.7%	IDISQLVITK	99.7%	85.5	25	61.1	2	0	0	1129.68	876	885
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	17	30	0.03%	17.7%	IFEPILGEGR	99.7%	68.2	25	61.6	2	0	0	1130.62	969	978
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	17	30	0.03%	17.7%	LLEQGIR	99.2%	35.3	25	0	3	0	0	828.49	226	232
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	17	30	0.03%	17.7%	LPCLEISQSVTGFGR	99.7%	70.5	25	70.5	2	0	0	1663.85	711	725
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	17	30	0.03%	17.7%	SEGGEDYTGATVIEPLK	99.7%	108	25	108	2	0	0	1765.85	575	591
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	17	30	0.03%	17.7%	VGGLLAFAK	99.7%	40.6	25	40.6	2	0	0	875.54	999	1007
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	17	30	0.03%	17.7%	VLSFDIECAGR	99.7%	39.9	25	35.8	2	0	0	1266.61	312	322
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	17	30	0.03%	17.7%	VPYVIISAAK	99.7%	51.5	25	51.5	2	0	0	1060.64	922	931
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	17	30	0.03%	17.7%	VQMDMLQVLLR	99.7%	45.3	25	30.4	2	0	0	1345.73	455	465
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	17	30	0.03%	17.7%	VSANSVYGFTGAQVGK	99.7%	82.3	25	75	2	0	0	1584.80	695	710
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	17	30	0.03%	17.7%	VTGVPLSYLLSR	98.3%	32.3	25	4.26	1	0	0	1304.76	538	549
DNA polymerase delta catalytic subunit	POLD1	DPOD1_HUMAN	123.6	100.0%	16	17	30	0.03%	17.7%	VYFPYLLISK	99.2%	35.4	25	35.1	1	0	0	1242.71	797	806
DNA polymerase delta subunit 2	POLD2	DPOD2_HUMAN	51.3	99.8%	2	2	2	0.00%	6.0%	FLGTSGQNVSDIFR	99.7%	74.5	25	65.5	1	0	0	1540.78	341	354
DNA polymerase delta subunit 2	POLD2	DPOD2_HUMAN	51.3	99.8%	2	2	2	0.00%	6.0%	LVTGTVLAVFGSVR	99.7%	50.8	25	41.7	1	0	0	1418.84	153	166
DNA polymerase delta subunit 3	POLD3	DPOD3_HUMAN	51.4	99.8%	2	2	2	0.00%	5.4%	FSAIQCAAAVPR	99.7%	58.4	25	43.7	1	0	0	1290.66	132	143
DNA polymerase delta subunit 3	POLD3	DPOD3_HUMAN	51.4	99.8%	2	2	2	0.00%	5.4%	IVEQPTVSVTEPK	99.7%	43.8	25	43.8	1	0	0	1426.78	262	274
DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	7	7	12	0.01%	3.7%	AIPLAIFQAEPTVR	99.7%	42.8	25	42.8	2	0	0	1525.87	1093	1106
DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	7	7	12	0.01%	3.7%	ALFGIFIPSQR	99.4%	37.1	25	32.1	2	0	0	1248.71	1498	1508
DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	7	7	12	0.01%	3.7%	ASVFVLDTVR	99.7%	47.5	25	43.2	1	0	0	1106.62	1510	1519
DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	7	7	12	0.01%	3.7%	GSTLEEVYGSVAK	96.1%	29	25	23.1	1	0	0	1339.67	996	1008
DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	7	7	12	0.01%	3.7%	IFQSSVFEAFLK	99.7%	64.1	25	53.4	2	0	0	1415.76	984	995
DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	7	7	12	0.01%	3.7%	IITIPAALQQVK	98.4%	32.6	25	30.6	2	0	0	1294.81	1144	1155

DNA polymerase epsilon catalytic subunit A	POLE	DPOE1_HUMAN	261.5	100.0%	7	7	12	0.01%	3.7%	VADYWLDVLYSK	99.7%	89.7	25	86.7	2	0	0	1471.75	1009	1020
DNA primase large subunit	PRIM2	PRI2_HUMAN	58.8	100.0%	3	3	5	0.00%	6.9%	IPFADALDLFR	99.7%	76.3	25	68.1	2	0	0	1277.69	186	196
DNA primase large subunit	PRIM2	PRI2_HUMAN	58.8	100.0%	3	3	5	0.00%	6.9%	ISPGGISQILDLVK	99.7%	78.5	25	76.1	2	0	0	1439.85	403	416
DNA primase large subunit	PRIM2	PRI2_HUMAN	58.8	100.0%	3	3	5	0.00%	6.9%	SLPAVQSDER	99.7%	41	25	34	1	0	0	1101.55	236	245
DNA primase small subunit	PRIM1	PRI1_HUMAN	49.9	100.0%	5	5	8	0.01%	13.6%	ALKEDFGFK	99.7%	47.5	25	46.9	1	0	0	1054.56	145	153
DNA primase small subunit	PRIM1	PRI1_HUMAN	49.9	100.0%	5	5	8	0.01%	13.6%	LGAFQAQEK	99.7%	43.1	25	31.2	2	0	0	991.52	96	104
DNA primase small subunit	PRIM1	PRI1_HUMAN	49.9	100.0%	5	5	8	0.01%	13.6%	SGIVEYLSLVK	99.7%	55.2	25	53	2	0	0	1207.69	183	193
DNA primase small subunit	PRIM1	PRI1_HUMAN	49.9	100.0%	5	5	8	0.01%	13.6%	VDQFDPFTVPTISFICR	99.7%	62.5	25	62.5	1	0	0	2042.01	339	355
DNA primase small subunit	PRIM1	PRI1_HUMAN	49.9	100.0%	5	5	8	0.01%	13.6%	VFEHFLENLDK	99.7%	51.1	25	45.1	2	0	0	1390.70	394	404
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	15	15	27	0.03%	11.4%	DVNGELIAVQR	99.7%	62.3	25	43.9	2	0	0	1213.65	88	98
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	15	15	27	0.03%	11.4%	EQVSPLETTLEK	99.7%	52.2	25	40.1	2	0	0	1373.72	910	921
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	15	15	27	0.03%	11.4%	GQDIEYIEIR	99.7%	75.7	25	68.8	2	0	0	1235.63	1157	1166
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	15	15	27	0.03%	11.4%	LEENIDNIKR	99.7%	43.2	25	37.7	1	0	0	1243.66	1060	1069
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	15	15	27	0.03%	11.4%	LKEIEHNLSK	98.6%	33.1	25	28.5	1	0	0	1210.68	255	264
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	15	15	27	0.03%	11.4%	LQGIDLDR	99.7%	59.5	25	48.2	2	0	0	929.51	816	823
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	15	15	27	0.03%	11.4%	MEVISLQNEK	99.6%	39.3	25	13.7	2	0	0	1190.61	502	511
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	15	15	27	0.03%	11.4%	NIDQCSEIVK	99.7%	49.3	25	40.2	2	0	0	1205.58	1292	1301
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	15	15	27	0.03%	11.4%	SELLVEQGR	99.7%	62.3	25	44.7	2	0	0	1030.55	344	352
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	15	15	27	0.03%	11.4%	SYENELDPLK	99.0%	34.4	25	28.3	2	0	0	1207.58	243	252
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	15	15	27	0.03%	11.4%	VCLTDVTIMER	99.7%	78.8	25	67.2	2	0	0	1336.66	787	797
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	15	15	27	0.03%	11.4%	VIAQLSECEK	99.7%	52.3	25	45.5	2	0	0	1176.59	983	992
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	15	15	27	0.03%	11.4%	VLASLIIR	99.7%	66.6	25	48.6	1	0	0	884.59	1207	1214
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	15	15	27	0.03%	11.4%	WLQDNLTLR	99.7%	44.1	25	29	2	0	0	1158.63	1017	1025
DNA repair protein RAD50	RAD50	RAD50_HUMAN	153.9	100.0%	15	15	27	0.03%	11.4%	YELQQLEGSSDR	99.7%	78.8	25	72.9	2	0	0	1424.67	462	473
DNA replication licensing factor MCM2	MCM2	MCM2_HUMAN	101.9	99.8%	2	2	3	0.00%	2.5%	GLALALFGGEPK	99.7%	70	25	54.4	2	0	0	1172.67	494	505
DNA replication licensing factor MCM2	MCM2	MCM2_HUMAN	101.9	99.8%	2	2	3	0.00%	2.5%	VMLESFIDTQK	96.1%	28.9	25	2.48	1	0	0	1310.67	797	807
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	25	26	54	0.05%	35.5%	AILCLLLGGVER	99.7%	73.6	25	61.7	7	0	0	1313.76	316	327
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	25	26	54	0.05%	35.5%	ALKDFVASIDATYAK	99.7%	79.5	25	73.4	1	0	0	1612.86	79	93
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	25	26	54	0.05%	35.5%	APAGQLPR	99.7%	45.6	25	30.5	2	0	0	809.46	208	215
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	25	26	54	0.05%	35.5%	DAQPSFSAEDIAK	99.7%	69.6	25	65.9	2	0	0	1378.65	271	283
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	25	26	54	0.05%	35.5%	DLENGSHIR	99.7%	39.8	25	31.1	2	0	0	1040.51	328	336
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	25	26	54	0.05%	35.5%	DSEEPFSSVEIQAALSK	99.7%	116	25	102	2	0	0	1836.89	775	791
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	25	26	54	0.05%	35.5%	DYLDFLDDEEDQGIYQSK	99.7%	72.8	25	72.8	1	0	0	2192.95	18	35
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	25	26	54	0.05%	35.5%	EAHAQSIGMNR	99.7%	75.7	25	73.7	2	0	0	1213.57	757	767
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	25	26	54	0.05%	35.5%	ELISDNQYR	99.7%	66.3	25	57.2	2	0	0	1137.55	38	46
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	25	26	54	0.05%	35.5%	ESQKVELSESR	97.4%	30.4	25	20.2	1	0	0	1291.65	733	743
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	25	26	54	0.05%	35.5%	GDINILLIGDPSVAK	99.7%	58.2	25	58.2	2	0	0	1524.86	337	351
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	25	26	54	0.05%	35.5%	GGYTSGTFR	99.7%	43.5	25	38.1	2	0	0	945.44	249	257
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	25	26	54	0.05%	35.5%	GSSGVGLTAAVTTDQETGER	99.7%	122	25	122	2	0	0	1935.93	372	391
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	25	26	54	0.05%	35.5%	LIVNVNDLR	99.7%	45.8	25	36.7	2	0	0	1055.62	47	55
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	25	26	54	0.05%	35.5%	LLNNAFEELVAFQR	99.7%	81.1	25	80.4	5	0	0	1663.88	65	78
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	25	26	54	0.05%	35.5%	LTESINR	98.2%	32	25	15.6	1	0	0	832.45	768	774
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	25	26	54	0.05%	35.5%	SKDIFDQLAK	99.7%	50.7	25	44.1	2	0	0	1164.63	292	301
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	25	26	54	0.05%	35.5%	SVDVILDDDLVDK	99.7%	74.3	25	65.4	2	0	0	1445.74	216	228
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	25	26	54	0.05%	35.5%	SVHYCPATK	99.5%	38	25	28.2	2	0	0	1062.50	144	152
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	25	26	54	0.05%	35.5%	TAIHEVMEQGR	99.7%	43.9	25	39.2	1	0	0	1286.62	420	430
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	25	26	54	0.05%	35.5%	TLETLIR	99.4%	36.6	25	9.26	2	0	0	845.51	617	623
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	25	26	54	0.05%	35.5%	TPMENIGLQDSLLSR	99.7%	87.6	25	87.6	3	0	0	1689.85	464	478
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	25	26	54	0.05%	35.5%	TVLIACNVK	99.6%	38.8	25	16	2	0	0	1017.58	258	266
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	25	26	54	0.05%	35.5%	VALLDVFR	99.7%	54.9	25	34.2	2	0	0	932.56	749	756
DNA replication licensing factor MCM3	MCM3	MCM3_HUMAN	91.0	100.0%	25	26	54	0.05%	35.5%	YVLCTAPR	99.7%	47.6	25	37.3	2	0	0	979.50	357	364

DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	12	13	28	0.03%	16.6%	ALADDDFLTVTGK	99.7%	101	25	94.5	2	0	0	1365.69	846	858
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	12	13	28	0.03%	16.6%	DMFEEALR	96.3%	29.1	25	21.4	1	0	0	1010.46	838	845
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	12	13	28	0.03%	16.6%	GILLQLFGGTR	99.7%	93.5	25	86.3	6	0	0	1174.69	479	489
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	12	13	28	0.03%	16.6%	IAEPSVCGR	99.7%	46.3	25	27.4	2	0	0	988.49	322	330
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	12	13	28	0.03%	16.6%	LASALAPSIYEHEDIKK	99.7%	37.9	25	37.6	0	2	0	1885.01	462	478
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	12	13	28	0.03%	16.6%	LHGLDEEAEQK	99.7%	41.4	25	38.8	2	0	0	1268.61	429	439
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	12	13	28	0.03%	16.6%	LVIWGTDVNVAACK	99.7%	94.9	25	94.9	2	0	0	1545.81	150	163
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	12	13	28	0.03%	16.6%	RLHGLDEEAEQK	97.8%	31.1	25	23.4	1	0	0	1424.71	428	439
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	12	13	28	0.03%	16.6%	TGIVDISILTTGMSATSR	99.7%	82.5	25	81.9	2	0	0	1822.96	778	795
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	12	13	28	0.03%	16.6%	TSVLAAANPIESQWNPK	99.7%	81.8	25	77.7	2	0	0	1825.94	611	627
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	12	13	28	0.03%	16.6%	TTIENIQLPHTLLSR	99.7%	73.9	25	61.6	2	2	0	1735.97	629	643
DNA replication licensing factor MCM4	MCM4	MCM4_HUMAN	96.6	100.0%	12	13	28	0.03%	16.6%	YQQLFEDIR	99.7%	59	25	39.2	2	0	0	1211.61	820	828
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	18	19	34	0.03%	28.1%	AGITTTLNSR	99.7%	87.5	25	62.3	2	0	0	1033.56	472	481
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	18	19	34	0.03%	28.1%	AIACLLFGGSR	99.7%	76.9	25	76.9	2	0	0	1164.62	352	362
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	18	19	34	0.03%	28.1%	CSVLAAANSVFGR	99.7%	69.1	25	65.8	2	0	0	1351.68	482	494
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	18	19	34	0.03%	28.1%	FAIGSQVSEHSIIK	99.7%	71.6	25	59.8	2	0	0	1515.82	683	696
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	18	19	34	0.03%	28.1%	GSSAAGLTASVMR	99.7%	89.7	25	80.5	2	0	0	1207.61	408	420
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	18	19	34	0.03%	28.1%	HMQLYCDR	99.5%	37.2	25	32.2	3	0	0	1122.48	244	251
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	18	19	34	0.03%	28.1%	IPGIIIAASAVR	99.7%	89.7	25	89.7	2	0	0	1180.74	151	162
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	18	19	34	0.03%	28.1%	LAALPNVYEVISK	99.7%	60.7	25	60.7	3	0	0	1416.81	325	337
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	18	19	34	0.03%	28.1%	LQPFATEADVEEALR	99.7%	100	25	96	2	0	0	1688.85	628	642
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	18	19	34	0.03%	28.1%	QLEAIVR	98.7%	33.5	25	19.1	1	0	0	828.49	612	618
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	18	19	34	0.03%	28.1%	QPAEHLQLLEEAAK	99.7%	33.4	25	31.9	0	2	0	1576.83	91	104
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	18	19	34	0.03%	28.1%	SFAGAVSPQEEEEFRR	98.1%	31.7	25	31.7	1	0	0	1838.87	309	324
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	18	19	34	0.03%	28.1%	SIAPSIFGGTDMK	99.7%	53.4	25	51.9	2	0	0	1323.66	338	350
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	18	19	34	0.03%	28.1%	SIAPSIFGGTDMKK	99.7%	41.4	25	41.4	1	0	0	1467.75	338	351
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	18	19	34	0.03%	28.1%	VAIHEAMEQQTISIAK	94.8%	22.8	25	22.8	0	1	0	1784.92	456	471
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	18	19	34	0.03%	28.1%	VLGIQVDTDGSGR	99.7%	71.3	25	71.3	2	0	0	1316.68	296	308
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	18	19	34	0.03%	28.1%	VLQLMLR	99.7%	44.5	25	29.9	2	0	0	872.54	711	717
DNA replication licensing factor MCM5	MCM5	MCM5_HUMAN	82.3	100.0%	18	19	34	0.03%	28.1%	VTIMGIYSIK	99.7%	55.4	25	40.7	2	0	0	1124.64	263	272
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	19	35	0.03%	24.5%	DFYVAFQDLPTR	99.7%	78	25	66.4	2	0	0	1471.72	109	120
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	19	35	0.03%	24.5%	EIESEIDSEEELINK	99.7%	96	25	86.3	2	0	0	1776.84	755	769
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	19	35	0.03%	24.5%	ELRDEEQTAESIK	99.7%	53.6	25	45.5	2	0	0	1547.75	314	326
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	19	35	0.03%	24.5%	ESEDFIVEQYK	99.7%	51.5	25	48.5	2	0	0	1386.64	589	599
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	19	35	0.03%	24.5%	GDINVCIVGDPSTAK	99.7%	55.6	25	45.2	2	0	0	1545.76	388	402
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	19	35	0.03%	24.5%	GVLLMLFGGVPK	99.7%	71	25	58.1	2	0	0	1230.73	367	378
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	19	35	0.03%	24.5%	HVEEFSPR	94.7%	27.7	25	27.7	1	0	0	1000.48	408	415
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	19	35	0.03%	24.5%	IQETQAELPR	99.7%	81.1	25	63.8	2	0	0	1184.63	208	217
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	19	35	0.03%	24.5%	ISNLIVLHLR	99.7%	55.5	25	40.7	2	0	0	1177.74	723	732
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	19	35	0.03%	24.5%	LGFSEYCR	99.7%	47.8	25	47.8	2	0	0	1031.46	715	722
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	19	35	0.03%	24.5%	LVFLACCVAPTNPR	99.7%	71.4	25	71.4	2	0	0	1617.82	296	309
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	19	35	0.03%	24.5%	MHCCDEVQPK	99.3%	36	25	36	1	0	0	1303.52	634	643
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	19	35	0.03%	24.5%	QNINLSAPIMSR	99.5%	37.8	25	29.6	1	0	0	1343.71	518	529
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	19	35	0.03%	24.5%	SELVNWYLK	99.7%	40.5	25	33.8	2	0	0	1151.61	746	754
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	19	35	0.03%	24.5%	TSILAAANPISGHYDR	99.7%	87.6	25	83.8	2	2	0	1685.86	497	512
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	19	35	0.03%	24.5%	VSGVDGYETEGIR	99.7%	86.8	25	76	2	0	0	1381.66	270	282
DNA replication licensing factor MCM6	MCM6	MCM6_HUMAN	92.9	100.0%	17	19	35	0.03%	24.5%	YLQLAEELIRPER	99.6%	33.2	25	25.1	2	2	0	1629.90	46	58
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	22	26	54	0.05%	39.5%	AGILTTLNAR	99.7%	43.8	25	29.1	2	0	0	1029.61	472	481
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	22	26	54	0.05%	39.5%	ALLLLLVGGVDQSPR	99.7%	83.1	25	83.1	4	0	0	1550.93	353	367
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	22	26	54	0.05%	39.5%	CSILAAANPAYGR	99.7%	80.2	25	66.3	2	0	0	1363.68	482	494
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	22	26	54	0.05%	39.5%	DSLLGDKGQTAR	99.7%	69.1	25	63.1	2	1	0	1260.65	642	653

DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	22	26	54	0.05%	39.5%	FLQEFYQDDELGKK	99.7%	56.8	25	45.3	1	0	0	1759.85	16	29
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	22	26	54	0.05%	39.5%	GNINICLMGDPGVAK	99.7%	51.3	25	51.3	1	0	0	1558.77	373	387
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	22	26	54	0.05%	39.5%	GSSGVGLTAAVLR	99.7%	94.6	25	82.4	2	0	0	1187.67	408	420
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	22	26	54	0.05%	39.5%	IAQPGDHVSVTGIFLPILR	99.7%	86.2	25	86.2	2	4	0	2033.15	264	282
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	22	26	54	0.05%	39.5%	LAASIAPEIYGHEDVKK	96.8%	24.5	25	22.4	0	1	0	1840.98	336	352
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	22	26	54	0.05%	39.5%	LAQHITYVHQHSR	99.7%	43.4	25	43.1	0	2	0	1589.83	533	545
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	22	26	54	0.05%	39.5%	LFADAVQELLPQYK	99.7%	69.8	25	51.5	4	0	0	1634.88	76	89
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	22	26	54	0.05%	39.5%	QIAEEDFYEK	99.7%	45.3	25	43.5	2	0	0	1271.58	326	335
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	22	26	54	0.05%	39.5%	QVVQGLLSETYLEAHR	99.7%	79.6	25	79.6	0	2	0	1842.97	287	302
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	22	26	54	0.05%	39.5%	RFELYFQGPSSNKPR	99.7%	43.2	25	43.2	0	2	0	1825.93	133	147
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	22	26	54	0.05%	39.5%	SEDDESGAGELTR	99.7%	60.7	25	60.7	1	0	0	1365.58	309	321
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	22	26	54	0.05%	39.5%	SITVLVEGENTR	99.7%	79	25	69	2	0	0	1317.70	252	263
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	22	26	54	0.05%	39.5%	SLEQNIQLPAALLSR	99.7%	89.3	25	89.3	3	0	0	1652.93	500	514
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	22	26	54	0.05%	39.5%	SPQNQYPAELMR	99.7%	46	25	46	2	0	0	1449.68	121	132
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	22	26	54	0.05%	39.5%	SQLLSYIDR	99.7%	56.4	25	33.1	2	0	0	1094.58	388	396
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	22	26	54	0.05%	39.5%	TLLAILR	99.4%	36.6	25	5.73	2	0	0	799.54	605	611
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	22	26	54	0.05%	39.5%	TQRPADVIFATVR	99.7%	42.8	25	37.2	2	2	0	1473.82	654	666
DNA replication licensing factor MCM7	MCM7	MCM7_HUMAN	81.3	100.0%	22	26	54	0.05%	39.5%	YGNQLVR	99.7%	55.7	25	37.7	4	0	0	849.46	33	39
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	22.9%	AEEVATFFAK	99.7%	76.2	25	59.7	4	0	0	1112.56	253	262
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	22.9%	AVAILCNHQR	99.7%	57.9	25	49.8	2	0	0	1181.62	625	634
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	22.9%	AVALYFIDK	99.7%	51	25	34.8	3	0	0	1039.58	476	484
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	22.9%	CDFTQMSQYFK	99.7%	65.2	25	60.6	2	0	0	1454.61	300	310
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	22.9%	ELTAPDENIPAK	99.7%	47.7	25	45.1	3	0	0	1297.66	604	615
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	22.9%	EYGFCIMDNHK	94.7%	27.8	25	25.9	1	0	0	1413.59	337	347
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	22.9%	GPVFAPPYEPLPENVK	99.7%	65.2	25	63	4	0	0	1753.92	224	239
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	22.9%	HLQDLMEGLTAK	99.7%	70.1	25	32.5	4	0	0	1355.70	576	587
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	22.9%	ITVAWCK	99.7%	43.6	25	18.6	2	0	0	877.46	728	734
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	22.9%	LEVQATDREENK	99.7%	55.3	25	48.1	3	0	0	1431.71	701	712
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	22.9%	LNTGILNK	99.7%	60.7	25	35.6	2	0	0	872.52	568	575
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	22.9%	MLDHEYTTK	99.7%	53.5	25	46.4	4	0	0	1137.52	263	271
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	22.9%	NIITNLSK	96.0%	28.8	25	23.1	1	0	0	902.53	292	299
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	22.9%	NLQLFMENK	99.7%	48	25	44.3	2	0	0	1136.58	550	558
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	22.9%	TYNASITLQQQLK	99.7%	88.6	25	76.6	2	0	0	1507.81	591	603
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	22.9%	VPSPPPGHK	99.0%	34.7	25	19.4	1	0	0	915.50	392	400
DNA topoisomerase 1	TOP1	TOP1_HUMAN	90.7	100.0%	17	20	44	0.04%	22.9%	YIMLNPSSR	99.7%	43.7	25	36.1	4	0	0	1096.55	426	434
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	46	0.04%	18.7%	DKYGVFPLR	98.7%	33.5	25	29.8	1	0	0	1094.60	479	487
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	46	0.04%	18.7%	DPALNSGVSQKPDPAK	99.7%	69	25	64.9	1	0	0	1623.83	1444	1459
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	46	0.04%	18.7%	EKQDEQVGLPGK	99.7%	57.4	25	44.8	2	0	0	1327.69	1185	1196
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	46	0.04%	18.7%	ELILFSNSDNER	99.7%	77	25	70.4	3	0	0	1436.70	702	713
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	46	0.04%	18.7%	EVTFVPGLYK	98.7%	33.3	25	30.4	1	0	0	1152.63	74	83
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	46	0.04%	18.7%	EWLLGMLGAESAK	99.7%	71.9	25	69.4	2	0	0	1404.72	1035	1047
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	46	0.04%	18.7%	FLEEFITPIVK	99.7%	53.5	25	48.3	2	0	0	1335.76	569	579
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	46	0.04%	18.7%	FTVETASR	99.7%	52.8	25	39.3	2	0	0	910.46	177	184
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	46	0.04%	18.7%	GFQQISFVNSIATSK	99.7%	81.3	25	76.6	2	0	0	1626.85	307	321
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	46	0.04%	18.7%	GIPVVEHKVEK	99.5%	37.6	25	32.2	1	0	0	1234.72	124	134
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	46	0.04%	18.7%	HVDYVADQIVTK	99.7%	76.2	25	74.5	2	0	0	1387.72	325	336
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	46	0.04%	18.7%	IFDEILVNAADNK	99.7%	103	25	99.6	4	0	0	1461.76	84	96
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	46	0.04%	18.7%	IIIENKPK	99.1%	35.1	25	23.1	2	0	0	954.60	1063	1070
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	46	0.04%	18.7%	KYDTVLDILR	99.7%	61.9	25	52.9	2	0	0	1235.70	1011	1020
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	46	0.04%	18.7%	LCNIFSTK	99.6%	38.6	25	35.4	2	0	0	982.50	169	176
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	46	0.04%	18.7%	LMDGEEPLPMLPSYK	95.1%	28.1	25	10.3	1	0	0	1719.83	879	893

DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	46	0.04%	18.7%	NSTECTLILTEGDSAK	99.7%	110	25	87.2	2	0	0	1738.82	451	466
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	46	0.04%	18.7%	QIMENAEINNIIK	99.7%	88.4	25	78.3	1	0	0	1529.80	500	512
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	46	0.04%	18.7%	SFGSTCQLSEK	99.7%	59	25	52.7	2	0	0	1243.56	387	397
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	46	0.04%	18.7%	SVVSDLEADDVK	99.7%	54.8	25	40.6	1	0	0	1276.63	1374	1385
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	46	0.04%	18.7%	TLAVSGLGVVGR	99.7%	87.7	25	78.1	3	0	0	1128.67	467	478
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	46	0.04%	18.7%	TQMAEVLPSPR	99.6%	38.5	25	34.3	1	0	0	1228.64	1205	1215
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	46	0.04%	18.7%	VTIDPENNLISIWNNGK	99.7%	51	25	51	2	0	0	1926.99	107	123
DNA topoisomerase 2-alpha	TOP2A	TOP2A_HUMAN	174.4	100.0%	24	25	46	0.04%	18.7%	YIFTMLSSLAR	99.7%	73.3	25	70.8	4	0	0	1301.69	805	815
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	20	0.02%	11.0%	DKLDETGVALK	99.7%	48.1	25	36.5	1	0	0	1188.65	298	308
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	20	0.02%	11.0%	DLIQMLVQR	99.7%	61.9	25	46.2	2	0	0	1115.62	1093	1101
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	20	0.02%	11.0%	ELILFSNSDNER	99.7%	77	25	70.4	3	0	0	1436.70	723	734
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	20	0.02%	11.0%	EVTFVPGLYK	98.7%	33.3	25	30.4	1	0	0	1152.63	95	104
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	20	0.02%	11.0%	GFQQISFVNSIATTK	99.7%	76.2	25	58.1	2	0	0	1640.86	328	342
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	20	0.02%	11.0%	GIPVVEHKVEK	99.5%	37.6	25	32.2	1	0	0	1234.72	145	155
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	20	0.02%	11.0%	IFDEILVNAADNK	99.7%	103	25	99.6	4	0	0	1461.76	105	117
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	20	0.02%	11.0%	LAQAEAAGLHK	99.7%	55.7	25	42.8	3	0	0	1108.61	998	1008
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	20	0.02%	11.0%	LCNIFSTK	99.6%	38.6	25	35.4	2	0	0	982.50	190	197
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	20	0.02%	11.0%	LLFPAVDDNLLK	99.7%	63.5	25	57.5	4	0	0	1357.77	837	848
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	20	0.02%	11.0%	NTVEITELPVR	99.7%	44.7	25	41.3	4	0	0	1270.70	940	950
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	20	0.02%	11.0%	QIMENAEINNIIK	99.7%	88.4	25	78.3	1	0	0	1529.80	521	533
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	20	0.02%	11.0%	SQDFGNLFSFPSYSQK	99.7%	83.7	25	83.5	1	0	0	1851.85	1441	1456
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	20	0.02%	11.0%	YAGPEDDAAITLAFSK	99.7%	79.7	25	79.7	2	0	0	1668.81	661	676
DNA topoisomerase 2-beta	TOP2B	TOP2B_HUMAN	183.3	100.0%	9	9	20	0.02%	11.0%	YIFTMLSTLAR	99.6%	38.3	25	30.2	1	0	0	1315.71	826	836
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	AALSALESFLK	99.7%	87.3	25	61.8	8	0	0	1149.65	311	321
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	AAYLSDPR	94.5%	27.6	25	16.9	1	0	0	892.45	3826	3833
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	AIRPQIDLKR	99.7%	39.8	25	35.6	0	1	0	1209.74	255	264
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	APPCEYKDWLTK	99.7%	49.1	25	47.1	2	0	0	1507.73	3834	3845
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	AQEPESGLSEETQVK	99.7%	80.2	25	69.7	2	0	0	1631.78	4091	4105
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	ATQMPEGGQGAPPMYQLYK	99.7%	53.5	25	49.3	2	0	0	2082.96	945	963
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	ATQQQHDFTLTQTADGR	99.7%	90.4	25	84	2	2	0	1917.91	2637	2653
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	AYVPALQMAFK	99.7%	45.4	25	24.8	5	0	0	1254.66	747	757
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	CFFLSK	98.5%	32.9	25	24.3	2	0	0	801.40	3187	3192
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	CFGTGAAGNR	99.7%	65.3	25	54	2	0	0	1010.45	1312	1321
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	CGAALAGHQLIR	99.7%	63.9	25	62	2	1	0	1266.67	25	36
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	CLMDQATDPNILGR	99.7%	110	25	110	2	0	0	1603.76	4106	4119
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	DCLSIPYR	97.4%	30.5	25	25.3	1	0	0	1023.49	2247	2254
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	DFGLLVFVR	99.7%	63.5	25	48.5	2	0	0	1065.61	62	70
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	DILETHLR	99.7%	41.6	25	32.3	2	0	0	996.55	1413	1420
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	DILPCLDGYLK	99.7%	42.1	25	29.1	2	0	0	1306.67	791	801
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	DLCNTHLMR	99.4%	37.1	25	32.8	2	0	0	1175.53	1362	1370
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	DLLLNTMSQEEK	99.7%	65.9	25	56.9	2	0	0	1436.69	3814	3825
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	DQNILLGTTYR	99.7%	87.8	25	80.9	4	0	0	1293.68	3325	3335
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	DVDFMYVELIQR	99.7%	92.8	25	83.8	4	0	0	1543.75	380	391
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	EIFNFVLK	99.1%	34.9	25	17.1	2	0	0	1009.57	247	254
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	ELLNPVVEFVSHPSTTCR	99.7%	99.7	25	93.5	2	2	0	2085.04	2453	2470
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	ELSIAIR	97.5%	30.7	25	18.2	2	0	0	801.48	358	364
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	EMKPVIFLDVFLPR	99.7%	39.3	25	39.3	0	1	0	1719.95	900	913
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	EQQHVMEELFQSSFR	99.7%	68.2	25	64.4	1	4	0	1910.87	1769	1783
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	ETGLMYSIMVHALR	99.7%	65.5	25	65.5	2	0	0	1620.82	3976	3989
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	FMNAVFFLLPK	99.7%	98	25	81.6	4	0	0	1326.73	2378	2388
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	FNNYVDCMK	99.7%	41	25	33.1	2	0	0	1190.50	1736	1744

DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	FNNYVDCMKK	98.5%	32.8	25	19.9	1	0	0	1318.59	1736	1745
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	FVPLLPGNR	96.2%	29	25	29	1	0	0	1012.59	1194	1202
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	FYGELALK	98.4%	32.4	25	28.5	1	0	0	940.51	156	163
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	FYGELALKK	99.7%	44	25	39.4	2	0	0	1068.61	156	164
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	FYQGFLFSEKPEK	99.7%	54.3	25	49.3	2	0	0	1619.81	1961	1973
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	GGSWIQEINVAEK	99.7%	80.5	25	66.4	2	0	0	1430.73	4024	4036
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	GIFTSEIGTK	99.7%	62.2	25	53.7	3	0	0	1052.56	2941	2950
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	GLSSLLCNFTK	99.7%	75.2	25	62.7	2	0	0	1239.64	226	236
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	GPESESEDHRASGEVR	99.7%	34.1	25	34.1	0	1	0	1741.77	500	515
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	GYGLFAGPCK	99.6%	39	25	33.7	2	0	0	1069.51	365	374
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	HDVGAYMLMYK	99.7%	49.4	25	42	2	0	0	1327.62	3850	3860
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	HGDLPDIQIK	99.7%	60.2	25	48.7	4	0	0	1135.61	2777	2786
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	HNLEIIK	99.7%	43.2	25	17.5	2	0	0	866.51	2233	2239
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	HSSLITPLQAVAQR	99.7%	76.1	25	75.4	2	2	0	1520.85	2787	2800
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	IAGFDER	96.8%	29.7	25	10.8	1	0	0	807.40	3719	3725
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	IAPYSVEIK	99.7%	42.7	25	26.2	2	0	0	1019.58	100	108
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	ICSKPVVLPK	99.1%	35.1	25	22.7	2	0	0	1140.68	490	499
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	IIANALSSEPACLAEIEEDKAR	99.7%	44.6	25	44.6	0	1	0	2400.21	3336	3357
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	ILDVMYSR	99.7%	55.9	25	50.6	4	0	0	996.52	1876	1883
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	ILELSGSSSEDSEK	99.7%	90.3	25	90.3	2	0	0	1480.70	3359	3372
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	IMEFTTTLLNTSPEGWK	99.7%	110	25	104	4	0	0	1983.97	1341	1357
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	INQVFHGSCITEGNELTK	99.7%	60.4	25	60.4	0	2	0	2046.99	1896	1913
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	IPALDLLIK	99.7%	46.8	25	38.2	2	0	0	995.65	125	133
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	KGGSWIQEINVAEK	99.7%	54.9	25	48.2	1	0	0	1558.82	4023	4036
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	KNILEESLCELVAK	99.7%	88.2	25	88.2	2	2	0	1645.88	2334	2347
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	KQNNFSLAMK	99.7%	63.7	25	54.7	2	0	0	1180.61	3248	3257
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LAAVVSACK	99.7%	56	25	45	2	0	0	918.51	1448	1456
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LACDVDQVTR	99.7%	63.6	25	45.5	2	0	0	1176.57	972	981
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LAGANPAVITCDELLLGHEK	99.7%	46.9	25	46	0	2	0	2121.10	4051	4070
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LATTILQHWK	99.7%	62.1	25	53.5	2	0	0	1210.69	1618	1627
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LCYDAFTENMAGENQLLER	99.7%	98.1	25	98.1	3	0	0	2290.01	1918	1936
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LGASLAFNNIYR	99.7%	69.9	25	40.5	3	0	0	1338.72	1076	1087
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LGLPGDEVDNK	97.7%	31.1	25	29	2	0	0	1156.58	2705	2715
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LGLPGDEVDNKVK	99.7%	54	25	51.9	2	0	0	1383.75	2705	2717
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LGNPIVPLNIR	99.7%	47.5	25	47.5	3	0	0	1205.74	2133	2143
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LLEEALLR	99.7%	57.6	25	52.8	4	0	0	956.58	2892	2899
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LLLQGEADQSLLTFIDK	99.7%	97	25	96.9	3	0	0	1904.04	3051	3067
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LLNFLMK	99.7%	40.8	25	30.9	2	0	0	878.52	2215	2221
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LLNTWTNR	99.7%	58	25	45.4	2	0	0	1017.55	3160	3167
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LLNTWTNRYPDAK	99.0%	34.4	25	26.9	1	1	0	1591.82	3160	3172
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LLPAELPAKR	99.7%	45	25	45	1	0	0	1107.69	2900	2909
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LLQDFNR	99.7%	39.4	25	16.5	1	0	0	905.48	2836	2842
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LLQIIER	99.7%	45.3	25	31.2	4	0	0	884.56	3468	3474
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LLQIIERYPEETLSLMTK	97.6%	25.6	25	25.6	0	1	0	2177.19	3468	3485
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LLSITVR	99.4%	36.7	25	14.1	2	0	0	801.52	669	675
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LNESTFDTQITK	99.7%	83.3	25	73.2	2	0	0	1396.70	1858	1869
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LNESTFDTQITKK	99.7%	62.8	25	62.8	2	0	0	1524.79	1858	1870
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LPPDVLR	96.0%	28.8	25	28.8	1	0	0	809.49	2916	2922
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LPVLAGCLK	99.7%	52.6	25	48	2	0	0	970.58	217	225
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LQETLSAADR	99.7%	87	25	62.4	4	0	0	1103.57	15	24
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LQYFMEQFYGIIR	99.7%	60.9	25	60.9	2	0	0	1723.85	338	350

DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LSDFNDITNMLLLK	99.7%	88.6	25	84	5	0	0	1636.86	3656	3669
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LSFAVPFR	99.7%	55.3	25	45.6	4	0	0	936.53	892	899
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LSLMYAR	99.7%	47.2	25	28.3	3	0	0	869.46	2739	2745
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LVINTEEVFRPYAK	99.7%	63	25	53.6	2	1	0	1678.92	2149	2162
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LYSLALHPNAFK	98.9%	34	25	27.5	2	2	0	1373.76	1063	1074
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	LYSLALHPNAFKR	99.4%	30.8	25	29.4	0	1	0	1529.86	1063	1075
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	MAVLALLAK	99.7%	61.9	25	52.6	4	0	0	929.59	1643	1651
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	MDPMNIWDDIITNR	99.7%	79.7	25	79.7	4	0	0	1765.79	3173	3186
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	MEVQEQEEDISSLIR	99.7%	81.7	25	71.3	2	0	0	1805.86	3218	3232
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	MKQDAQVVLYR	99.7%	75.9	25	68	2	2	0	1350.72	2763	2773
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	MQLVCCR	94.5%	27.6	25	19.6	1	0	0	966.43	453	459
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	MSPYKDILETHLR	99.7%	51.5	25	51.5	0	2	0	1618.83	1408	1420
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	MSTSPEAFLALR	99.7%	87	25	71.7	8	0	0	1322.68	3890	3901
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	MVSAVLNGMLDQSFR	99.7%	72.7	25	72.7	1	0	0	1667.82	1592	1606
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	MYAALGDPK	99.7%	55.9	25	54	4	0	0	965.48	3613	3621
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	NCISTVVHQGLIR	99.7%	71	25	63	2	2	0	1496.80	477	489
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	NFWSHETR	98.7%	33.5	25	27.2	1	0	0	1076.49	2523	2530
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	NILEESLCELVAK	99.7%	88.7	25	81.3	2	0	0	1517.79	2335	2347
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	NLDLAVLELMQSSVDNTK	99.7%	114	25	114	3	0	0	2006.01	1574	1591
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	NLLIFENLIDLK	99.7%	85.5	25	73.3	2	0	0	1444.84	1974	1985
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	NLLIFENLIDLKR	99.7%	70.2	25	68.3	2	0	0	1600.94	1974	1986
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	NLLTVTSSDEMMK	99.7%	93.3	25	90.3	6	0	0	1500.69	869	881
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	NLSSNEAISLEEIR	99.7%	103	25	85.4	2	0	0	1574.80	839	852
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	NNWEVSALSR	99.7%	63.6	25	56.7	2	0	0	1175.58	811	820
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	NVDSNNKELSIAIR	99.7%	89.1	25	84.6	2	1	0	1572.83	351	364
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	QCLPSLDLSCK	99.7%	57.9	25	45.2	2	0	0	1320.63	1498	1508
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	QDAQVVLYR	99.7%	54.4	25	39.2	2	0	0	1091.58	2765	2773
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	QFINLMLPMK	99.4%	36.8	25	22	4	0	0	1234.67	3966	3975
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	QGNLSSQVPLK	99.7%	53.9	25	43.6	1	0	0	1170.65	3148	3158
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	QGNLSSQVPLKR	99.7%	42	25	38.5	1	1	0	1326.75	3148	3159
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	QITPQQQEK	95.0%	28	25	25.2	1	0	0	1099.57	1043	1051
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	QITQSALLAEAR	99.7%	88	25	65.9	2	0	0	1300.72	2951	2962
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	QLFSSLFSGILK	99.7%	77.8	25	67.4	2	0	0	1339.76	2807	2818
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	QMFLTQTDTGDDR	99.7%	71.5	25	68.8	2	0	0	1527.67	394	406
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	RLSFAVPFR	99.7%	45.1	25	34.5	2	0	0	1092.63	891	899
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	RYNFPVEVEVPMER	99.4%	31.3	25	27.8	0	1	0	1764.87	1987	2000
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	SDPGLLTNTMDVFVK	99.7%	99.8	25	95	6	0	0	1636.83	3993	4007
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	SIELFYK	95.7%	28.5	25	10.9	1	0	0	899.49	1187	1193
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	SIGEYDVLR	99.7%	57.9	25	47.7	2	0	0	1051.54	2932	2940
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	SKDFVQVMR	99.7%	54.6	25	43.5	2	0	0	1109.58	2417	2425
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	SLEYCSTASIDSENPPDLNK	99.7%	90.6	25	90.6	2	0	0	2240.00	3010	3029
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	SLGPPQGEEDSVPR	99.7%	77.1	25	75.7	2	0	0	1467.71	2107	2120
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	SLGTIQQCCDAIDHLCR	99.7%	50.7	25	50	0	2	0	2046.92	1120	1136
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	SLNSIEFR	99.7%	42.5	25	28.2	3	0	0	965.51	72	79
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	SMEEDPQTSR	99.7%	39.4	25	30.8	3	0	0	1179.49	237	246
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	SPNLWLK	99.2%	35.7	25	23.2	2	0	0	857.49	1203	1209
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	SQGCSEQVLTVLK	99.7%	78.2	25	69.1	4	0	0	1448.74	3290	3302
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	STVLTPMFVETQASQGTLQTR	99.7%	104	25	104	4	1	0	2295.17	2599	2619
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	TETVTSFR	99.7%	52.2	25	40.2	3	0	0	940.47	3865	3872
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	TSALSDETKNNWEVSALSR	99.7%	49.3	25	49.3	0	2	0	2108.03	802	820
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	TVGALQVLGTEAQSSLLK	99.7%	147	25	143	4	0	0	1815.02	1275	1292

DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	TVSLLDENNVSSYLSK	99.7%	115	25	109	4	0	0	1768.90	3303	3318
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	TYSVVPMTSR	99.6%	38.5	25	28.2	1	0	0	1140.57	3790	3799
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	VCLDIIYK	99.7%	44.8	25	25	2	0	0	1023.55	2434	2441
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	VEGMTELYFQLK	99.7%	64.6	25	60.2	2	0	0	1457.73	2405	2416
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	VFLALAAK	99.3%	36.3	25	14.6	2	0	0	832.53	464	471
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	VIAGLYQR	99.7%	41.1	25	32.4	1	0	0	919.54	3373	3380
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	VLEQLIVAHFPMQSR	99.7%	52.1	25	50.8	2	3	0	1783.95	1713	1727
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	VTELALTASDR	99.7%	106	25	89.1	2	0	0	1175.63	914	924
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	VTVMASLR	99.7%	52.8	25	36.5	2	0	0	876.50	3726	3733
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	VVQMLGSLGGQINK	99.7%	97.4	25	78	4	0	0	1459.79	855	868
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	YAVPSAGLR	97.1%	30	25	26.1	2	0	0	933.52	265	273
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	YFEGVSPK	99.5%	37.4	25	30.7	1	0	0	926.46	682	689
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	YNFPVEVEVPMER	99.7%	65.9	25	57.9	4	0	0	1608.77	1988	2000
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	YPEETLSLMTK	99.7%	58.5	25	49.6	4	0	0	1311.65	3475	3485
DNA-dependent protein kinase catalytic subunit	PRKDC	PRKDC_HUMAN	469.1	100.0%	145	184	366	0.34%	36.4%	YSCFALFVK	99.7%	39.5	25	32.7	2	0	0	1134.57	701	709
DNA-directed RNA polymerase I subunit RPA49	POLR1E	RPA49_HUMAN	54.0	100.0%	2	2	2	0.00%	5.8%	LSYVGNNFGTGALK	98.9%	33.9	25	26.9	1	0	0	1440.75	129	142
DNA-directed RNA polymerase I subunit RPA49	POLR1E	RPA49_HUMAN	54.0	100.0%	2	2	2	0.00%	5.8%	SALGPGVPHIINTK	99.1%	34.8	25	33.2	1	0	0	1403.80	358	371
DNA-directed RNA polymerase II subunit RPB1	POLR2A	RPB1_HUMAN	217.2	100.0%	3	3	4	0.00%	2.3%	TPSLTVFLLGQSAR	99.7%	78.1	25	73.2	2	0	0	1489.84	1136	1149
DNA-directed RNA polymerase II subunit RPB1	POLR2A	RPB1_HUMAN	217.2	100.0%	3	3	4	0.00%	2.3%	TVITPDPNLSIDQVGVPR	99.4%	37.1	25	37.1	1	0	0	1921.04	365	382
DNA-directed RNA polymerase II subunit RPB1	POLR2A	RPB1_HUMAN	217.2	100.0%	3	3	4	0.00%	2.3%	YSPTSPTYSPTSPK	99.4%	37	25	36.8	1	0	0	1512.72	1909	1922
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	4	4	7	0.01%	3.8%	EGEEQLQTQHQK	98.6%	32.9	25	30.1	2	0	0	1454.69	135	146
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	4	4	7	0.01%	3.8%	GPIQILNR	99.7%	54	25	44.6	2	0	0	910.55	1065	1072
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	4	4	7	0.01%	3.8%	NLTYSAPLYVDITK	99.7%	50.5	25	43.6	2	0	0	1597.85	117	130
DNA-directed RNA polymerase II subunit RPB2	POLR2B	RPB2_HUMAN	133.9	100.0%	4	4	7	0.01%	3.8%	VSGDDVIIGK	98.5%	32.6	25	21.3	1	0	0	1002.55	860	869
DNA-directed RNA polymerase II subunit RPB3	POLR2C	RPB3_HUMAN	31.4	100.0%	4	4	6	0.01%	17.5%	FIIENTDLAVANSIR	99.7%	84	25	79.8	2	0	0	1675.90	21	35
DNA-directed RNA polymerase II subunit RPB3	POLR2C	RPB3_HUMAN	31.4	100.0%	4	4	6	0.01%	17.5%	ITELTDENVK	98.5%	32.8	25	22.6	1	0	0	1161.60	11	20
DNA-directed RNA polymerase II subunit RPB3	POLR2C	RPB3_HUMAN	31.4	100.0%	4	4	6	0.01%	17.5%	LGLIPLISDDIVDK	99.1%	35	25	28.6	1	0	0	1510.87	68	81
DNA-directed RNA polymerase II subunit RPB3	POLR2C	RPB3_HUMAN	31.4	100.0%	4	4	6	0.01%	17.5%	PYANQPTVR	99.1%	35	25	33.8	2	0	0	1045.54	2	10
DNA-directed RNA polymerase II subunit RPB7	POLR2G	RPB7_HUMAN	19.3	100.0%	4	4	6	0.01%	30.2%	GEVVDAVVTQVNK	99.7%	72.8	25	64.4	2	0	0	1357.73	82	94
DNA-directed RNA polymerase II subunit RPB7	POLR2G	RPB7_HUMAN	19.3	100.0%	4	4	6	0.01%	30.2%	LFTEVEGTCTGK	98.5%	32.8	25	32.8	1	0	0	1341.64	30	41
DNA-directed RNA polymerase II subunit RPB7	POLR2G	RPB7_HUMAN	19.3	100.0%	4	4	6	0.01%	30.2%	VGLFTEIGPMSCFISR	99.7%	42.9	25	40.5	1	0	0	1829.89	95	110
DNA-directed RNA polymerase II subunit RPB7	POLR2G	RPB7_HUMAN	19.3	100.0%	4	4	6	0.01%	30.2%	YFGPNLLNTVK	99.7%	47.7	25	47.7	2	0	0	1265.69	17	27
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	7	7	12	0.01%	5.1%	IDEVAVPVHVAK	99.7%	59.6	25	45.4	2	0	0	1276.73	377	388
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	7	7	12	0.01%	5.1%	LAPVYLSNR	99.6%	39	25	35.3	2	0	0	1032.58	686	694
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	7	7	12	0.01%	5.1%	LEVNAETVR	99.1%	34.8	25	21.4	1	0	0	1030.55	1142	1150
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	7	7	12	0.01%	5.1%	LLVEGDNLR	99.6%	38.7	25	29.8	2	0	0	1028.57	1225	1233
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	7	7	12	0.01%	5.1%	NELILTTESIMK	99.7%	67.1	25	53.4	2	0	0	1391.75	943	954
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	7	7	12	0.01%	5.1%	TAETGYMQR	99.7%	51.6	25	40.2	1	0	0	1056.48	865	873
DNA-directed RNA polymerase III subunit RPC1	POLR3A	RPC1_HUMAN	155.6	100.0%	7	7	12	0.01%	5.1%	VVVQGIPEVSR	99.7%	55.4	25	55.3	2	0	0	1182.68	1199	1209
DNA-directed RNA polymerase III subunit RPC2	POLR3B	RPC2_HUMAN	127.8	100.0%	2	2	4	0.00%	2.1%	GAVGASVTSSTHEK	99.7%	60.7	25	58.1	2	0	0	1330.66	197	210
DNA-directed RNA polymerase III subunit RPC2	POLR3B	RPC2_HUMAN	127.8	100.0%	2	2	4	0.00%	2.1%	VILIQEQLSK	99.7%	55.6	25	43.3	2	0	0	1170.71	177	186
DNA-directed RNA polymerase III subunit RPC3	POLR3C	RPC3_HUMAN	60.6	99.8%	2	2	3	0.00%	4.7%	ALASLATATLESVVQER	99.7%	60.5	25	58.7	2	0	0	1758.96	341	357
DNA-directed RNA polymerase III subunit RPC3	POLR3C	RPC3_HUMAN	60.6	99.8%	2	2	3	0.00%	4.7%	SIANLIER	99.5%	37.3	25	28.6	1	0	0	915.53	442	449
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	5	5	6	0.01%	5.3%	LLQEAPGK	98.8%	33.7	25	12.4	1	0	0	855.49	194	201
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	5	5	6	0.01%	5.3%	LSLAQHLR	99.7%	59	25	48.8	1	0	0	937.56	783	790
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	5	5	6	0.01%	5.3%	LSLDVEQAPSGQHSQAQLSGQQQR	99.7%	36.2	25	36.2	0	1	0	2592.28	202	225
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	5	5	6	0.01%	5.3%	VAQVLEGFITR	99.7%	78.4	25	68.2	2	0	0	1232.70	977	987
DNA-directed RNA polymerase, mitochondrial	POLRMT	RPOM_HUMAN	138.6	100.0%	5	5	6	0.01%	5.3%	VCVVSVEKPTLPSK	99.2%	29.6	25	24	0	1	0	1542.86	412	425
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	5	7	11	0.01%	37.3%	ADQFEYVMYGK	99.7%	64.9	25	64.9	2	0	0	1350.60	85	95
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	5	7	11	0.01%	37.3%	IEGDETSTEAATR	99.7%	61.5	25	57.9	2	0	0	1379.63	99	111
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	5	7	11	0.01%	37.3%	LQGDANNLHGFEVDSR	99.7%	68.8	25	63.2	1	1	0	1771.84	125	140

DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	5	7	11	0.01%	37.3%	LSAYVSYGGLLMR	99.7%	91	25	82.7	4	0	0	1445.75	112	124
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	RPAB3_HUMAN	17.1	100.0%	5	7	11	0.01%	37.3%	VYRIEGDETSTEAATR	99.7%	39.8	25	39.5	1	0	0	1797.86	96	111
DNA-directed RNA polymerases I, II, and III subunit RPABC5	POLR2L	RPAB5_HUMAN	7.6	99.8%	2	3	5	0.00%	29.9%	LLNYAPLEK	99.2%	35.3	25	23.6	1	0	0	1060.60	59	67
DNA-directed RNA polymerases I, II, and III subunit RPABC5	POLR2L	RPAB5_HUMAN	7.6	99.8%	2	3	5	0.00%	29.9%	MLLAHVDLIEK	99.7%	59.4	25	52.9	4	0	0	1281.72	48	58
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	3	3	5	0.00%	9.3%	ELYDKGGEQAIK	99.7%	45.6	25	30.1	2	0	0	1350.69	62	73
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	3	3	5	0.00%	9.3%	TIVITSHPGQIVK	99.7%	62.7	25	62.7	2	0	0	1392.82	284	296
DnaJ homolog subfamily A member 1	DNAJA1	DNJA1_HUMAN	44.9	100.0%	3	3	5	0.00%	9.3%	YHPDKNPNEGEK	95.1%	23	25	23	0	1	0	1427.66	33	44
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	9	9	16	0.02%	25.2%	DGNDLHMTYK	99.7%	46.7	25	45.1	2	0	0	1193.53	263	272
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	9	9	16	0.02%	25.2%	EISFAYEVLSNPEKR	99.7%	65.9	25	64.7	2	0	0	1781.91	49	63
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	9	9	16	0.02%	25.2%	IGLVEALCGFQFTFK	99.7%	87.3	25	79	1	0	0	1729.90	273	287
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	9	9	16	0.02%	25.2%	ILEVHVDK	99.7%	50.5	25	31.3	2	0	0	952.55	216	223
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	9	9	16	0.02%	25.2%	LYDILGVPPGASENELKK	99.7%	43.1	25	36.8	0	2	0	1943.05	9	26
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	9	9	16	0.02%	25.2%	NVLCSACSGQGGK	99.7%	66.2	25	66.2	2	0	0	1337.59	140	152
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	9	9	16	0.02%	25.2%	VIEPGCVR	97.1%	30.1	25	26.9	1	0	0	929.49	303	310
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	9	9	16	0.02%	25.2%	VSLEDLYNGK	99.7%	64.2	25	52.9	2	0	0	1137.58	122	131
DnaJ homolog subfamily A member 2	DNAJA2	DNJA2_HUMAN	45.7	100.0%	9	9	16	0.02%	25.2%	YGEQGLR	99.7%	52.6	25	33.2	2	0	0	822.41	69	75
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	4	5	12	0.01%	10.8%	EFTVNIMDTCER	99.7%	44.2	25	44.2	1	0	0	1530.66	227	238
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	4	5	12	0.01%	10.8%	GGPTVDPEELFR	99.7%	54.7	25	54.7	2	0	0	1316.65	176	187
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	4	5	12	0.01%	10.8%	GSIIISPCVVCR	99.7%	50	25	37.6	3	0	0	1360.71	282	293
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	DNJA3_HUMAN	52.5	100.0%	4	5	12	0.01%	10.8%	VMIPVPAGVEDGQTVR	99.7%	71.2	25	62.9	6	0	0	1683.87	304	319
DnaJ homolog subfamily B member 12	DNAJB12	DJB12_HUMAN	41.8	99.8%	2	2	4	0.00%	6.7%	AIGTAYAVLSNPEK	99.7%	61.1	25	55.4	2	0	0	1433.76	153	166
DnaJ homolog subfamily B member 12	DNAJB12	DJB12_HUMAN	41.8	99.8%	2	2	4	0.00%	6.7%	NVEDDYIANLR	99.7%	55.6	25	52	2	0	0	1321.64	316	326
DnaJ homolog subfamily B member 6	DNAJB6	DNJB6_HUMAN	36.1	99.8%	2	2	6	0.01%	7.4%	QVAEAYEVLSDAK	99.7%	87.7	25	81.6	4	0	0	1422.71	48	60
DnaJ homolog subfamily B member 6	DNAJB6	DNJB6_HUMAN	36.1	99.8%	2	2	6	0.01%	7.4%	VDYYEVLGVQR	99.7%	65.2	25	36.4	2	0	0	1340.68	2	12
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	6	6	13	0.01%	9.0%	ASNLLYGQLK	99.7%	67.1	25	63.4	2	0	0	1106.62	493	502
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	6	6	13	0.01%	9.0%	GVNSYPSLFIFR	99.7%	40.8	25	40.4	2	0	0	1399.74	197	208
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	6	6	13	0.01%	9.0%	ILYDILAFAK	99.7%	54.9	25	54.2	4	0	0	1166.68	439	448
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	6	6	13	0.01%	9.0%	NFQEEQINTR	99.7%	68.1	25	42.8	2	0	0	1278.61	757	766
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	6	6	13	0.01%	9.0%	NSILFLNSLDAK	99.7%	62.5	25	56.7	2	0	0	1334.73	326	337
DnaJ homolog subfamily C member 10	DNAJC10	DJC10_HUMAN	91.1	100.0%	6	6	13	0.01%	9.0%	YDFGIYDDDPEIITLER	99.7%	51.9	25	51.9	1	0	0	2073.97	120	136
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	4	4	7	0.01%	8.4%	AGFFGTVVEYGAER	99.7%	90.1	25	81.5	2	0	0	1502.73	328	341
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	4	4	7	0.01%	8.4%	GLEMEGWEVVER	99.7%	76.6	25	61.6	1	0	0	1433.67	85	96
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	4	4	7	0.01%	8.4%	LIIKPYLR	99.0%	34.3	25	17.5	2	0	0	1015.67	406	413
DnaJ homolog subfamily C member 11	DNAJC11	DJC11_HUMAN	63.3	100.0%	4	4	7	0.01%	8.4%	VIDVTVPLQCLVK	99.7%	73	25	68	2	0	0	1483.86	485	497
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	8	8	12	0.01%	4.3%	AGFLAFTQLPK	99.7%	40.4	25	26.5	1	0	0	1192.67	440	450
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	8	8	12	0.01%	4.3%	DSLLASLLDGVR	99.7%	71.7	25	63.2	1	0	0	1258.70	312	323
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	8	8	12	0.01%	4.3%	ELIVGEIFVR	99.7%	56.7	25	55.5	1	0	0	1174.68	1685	1694
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	8	8	12	0.01%	4.3%	ENGLEVLQEAFSR	99.7%	72	25	57.4	2	0	0	1491.74	1443	1455
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	8	8	12	0.01%	4.3%	IFIAQPAWVLR	99.7%	58.7	25	42.6	2	0	0	1313.77	1987	1997
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	8	8	12	0.01%	4.3%	IVDGPDPENIILILK	99.7%	55.5	25	49.1	2	0	0	1648.95	1360	1374
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	8	8	12	0.01%	4.3%	QLVLETLYALTSSTK	99.7%	53.6	25	52.4	1	0	0	1666.93	1831	1845
DnaJ homolog subfamily C member 13	DNAJC13	DJC13_HUMAN	254.4	100.0%	8	8	12	0.01%	4.3%	TELLTEALR	99.6%	38.2	25	22.1	2	0	0	1045.59	91	99
DnaJ homolog subfamily C member 7	DNAJC7	DNJC7_HUMAN	56.4	99.8%	2	2	4	0.00%	4.3%	AVQFFVQALR	99.7%	50	25	43	2	0	0	1178.67	229	238
DnaJ homolog subfamily C member 7	DNAJC7	DNJC7_HUMAN	56.4	99.8%	2	2	4	0.00%	4.3%	EALGDAQQSVR	99.7%	74.4	25	71.1	2	0	0	1173.59	80	90
DnaJ homolog subfamily C member 9	DNAJC9	DNJC9_HUMAN	29.9	99.8%	2	2	3	0.00%	8.1%	ELGLDEGVDSLK	99.7%	52.4	25	50.2	1	0	0	1274.65	206	217
DnaJ homolog subfamily C member 9	DNAJC9	DNJC9_HUMAN	29.9	99.8%	2	2	3	0.00%	8.1%	VSLQVHPDR	99.6%	38.8	25	25.1	2	0	0	1050.57	38	46
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	9	16	0.02%	33.1%	EGNFDIVSGTR	99.7%	63.7	25	62.8	1	0	0	1194.58	137	147
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	9	16	0.02%	33.1%	ENLPLIVWLLVK	99.7%	65.5	25	65.5	2	0	0	1436.89	38	49
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	9	16	0.02%	33.1%	GYVFQMEMIVR	99.7%	61.4	25	61.4	2	0	0	1404.67	206	216
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	9	16	0.02%	33.1%	LGGNEIVSFLK	99.7%	63.4	25	62.1	2	0	0	1176.66	241	251
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	9	16	0.02%	33.1%	LGLGTAYIHGMK	99.7%	71.2	25	70.3	4	0	0	1260.68	96	107

Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	9	16	0.02%	33.1%	QKEGNFDIVSGTR	98.0%	31.6	25	29.1	1	0	0	1450.73	135	147
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	9	16	0.02%	33.1%	QLNYTIGEVPISFVDR	99.7%	72.1	25	68.2	2	0	0	1850.96	219	234
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	DPM1_HUMAN	29.6	100.0%	8	9	16	0.02%	33.1%	YSVLLPTYNER	99.7%	42.6	25	42.6	2	0	0	1354.70	27	37
Dolichol-phosphate mannosyltransferase subunit 3	DPM3	DPM3_HUMAN	10.1	99.8%	2	2	6	0.01%	23.9%	ELQSQIQEAR	99.7%	70.2	25	54.5	4	0	0	1201.62	73	82
Dolichol-phosphate mannosyltransferase subunit 3	DPM3	DPM3_HUMAN	10.1	99.8%	2	2	6	0.01%	23.9%	VATFHDCEDAAR	99.7%	40.7	25	40.7	2	0	0	1391.60	61	72
Dolichyldiphosphatase 1	DOLPP1	DOPP1_HUMAN	27.0	100.0%	3	3	7	0.01%	15.5%	DTSLIPNVLWFEYTVTR	99.7%	59.8	25	54.8	1	0	0	2054.06	207	223
Dolichyldiphosphatase 1	DOLPP1	DOPP1_HUMAN	27.0	100.0%	3	3	7	0.01%	15.5%	FLDLLWR	99.5%	37.2	25	12.6	2	0	0	962.55	130	136
Dolichyldiphosphatase 1	DOLPP1	DOPP1_HUMAN	27.0	100.0%	3	3	7	0.01%	15.5%	IAAWPVSEFFLIR	99.7%	73	25	63.5	4	0	0	1548.86	194	206
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	8	9	16	0.02%	20.2%	ELGSECGIEFDEEK	99.7%	79.3	25	77.7	1	0	0	1641.70	140	153
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	8	9	16	0.02%	20.2%	LPDVYGVFQFK	99.7%	58.8	25	51.3	2	0	0	1312.69	381	391
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	8	9	16	0.02%	20.2%	NTLLIAGLQAR	99.7%	96.1	25	73.7	2	0	0	1169.70	240	250
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	8	9	16	0.02%	20.2%	SSLNPILFR	99.7%	56	25	39.6	2	0	0	1046.60	190	198
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	8	9	16	0.02%	20.2%	TADDPSLSLIK	96.8%	29.7	25	20	2	0	0	1159.62	78	88
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	8	9	16	0.02%	20.2%	TLVLLDNLNVR	99.7%	75.2	25	60.8	2	0	0	1269.75	47	57
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	8	9	16	0.02%	20.2%	WVFKEEGVLR	99.7%	48.7	25	38	2	1	0	1262.69	298	307
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	OST48_HUMAN	50.8	100.0%	8	9	16	0.02%	20.2%	YSQTGNYELAVALSR	99.7%	112	25	105	2	0	0	1671.83	283	297
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	19	24	45	0.04%	37.9%	ALTSEIALLQSR	99.7%	94.1	25	82.3	3	0	0	1301.74	525	536
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	19	24	45	0.04%	37.9%	ATSFLLALEPELEAR	99.7%	72.8	25	72.8	4	0	0	1659.90	66	80
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	19	24	45	0.04%	37.9%	DVPAYSQDTFK	99.7%	53.4	25	43.1	2	0	0	1270.60	205	215
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	19	24	45	0.04%	37.9%	FPLFGGWK	98.3%	32.2	25	19.4	2	0	0	951.51	320	327
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	19	24	45	0.04%	37.9%	FVDHVFDEQVIDSLTVK	99.7%	92	25	92	2	2	0	1991.01	355	371
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	19	24	45	0.04%	37.9%	GEDEEENNLEVR	99.7%	60.4	25	50.7	1	0	0	1432.62	90	101
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	19	24	45	0.04%	37.9%	HFDETVNR	95.6%	28.5	25	15	1	0	0	1017.47	495	502
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	19	24	45	0.04%	37.9%	IDHILDAL	99.6%	38.8	25	31	2	0	0	909.50	600	607
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	19	24	45	0.04%	37.9%	LKTEGSDLCDR	99.6%	38.7	25	25.9	2	1	0	1293.61	537	547
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	19	24	45	0.04%	37.9%	LPVALDPGAK	99.0%	34.6	25	34.6	2	0	0	980.58	117	126
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	19	24	45	0.04%	37.9%	NIEIDSPYEISR	99.7%	61.5	25	48.4	1	0	0	1435.71	380	391
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	19	24	45	0.04%	37.9%	NLVEQHIQDIVVHYTFNK	99.7%	60	25	60	0	2	0	2197.14	415	432
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	19	24	45	0.04%	37.9%	QFVVFEGNHYFYSPYPTK	99.6%	33.3	25	33.3	0	2	0	2223.05	152	169
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	19	24	45	0.04%	37.9%	QPDSGISSIR	98.1%	31.8	25	17.9	2	0	0	1059.54	269	278
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	19	24	45	0.04%	37.9%	SEDLLDYGPFR	99.7%	73.1	25	72.2	2	0	0	1311.62	194	204
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	19	24	45	0.04%	37.9%	VACITEQVLTLVNK	99.7%	72.9	25	70.3	1	0	0	1587.88	475	488
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	19	24	45	0.04%	37.9%	VACITEQVLTLVNKR	99.7%	85.5	25	76.5	2	2	0	1743.98	475	489
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	19	24	45	0.04%	37.9%	VHYENNSPFLTITSMTR	99.7%	48.4	25	48.4	0	3	0	2009.97	216	232
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	RPN1_HUMAN	68.6	100.0%	19	24	45	0.04%	37.9%	VTAEVVLAHLGGGSTSR	99.7%	101	25	100	2	2	0	1653.89	49	65
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	12	14	30	0.03%	28.4%	EDQVIQLMNAIFSK	94.9%	27.9	25	21.2	1	0	0	1635.84	230	243
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	12	14	30	0.03%	28.4%	FELDTSER	99.7%	46.5	25	29.4	2	0	0	996.46	461	468
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	12	14	30	0.03%	28.4%	FPEEEAPSTVLSQNLFTPK	99.7%	63.7	25	63.7	2	0	0	2134.07	505	523
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	12	14	30	0.03%	28.4%	FSSGYYDFLVEVEGDNR	99.2%	35.6	25	35.6	1	0	0	1996.89	341	357
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	12	14	30	0.03%	28.4%	ISTEVGITNVDLSTVDKDQSIAPK	99.7%	51.4	25	51.4	0	3	0	2530.33	369	392
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	12	14	30	0.03%	28.4%	LQVTNVLSQPLTQATVK	99.7%	129	25	119	5	1	0	1840.05	290	306
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	12	14	30	0.03%	28.4%	SIVEEIEDLVAR	99.7%	65.7	25	47.4	2	0	0	1372.73	179	190
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	12	14	30	0.03%	28.4%	TGQEVVFVAEPDNK	99.7%	84.5	25	74.9	2	0	0	1532.76	443	456
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	12	14	30	0.03%	28.4%	TGQEVVFVAEPDNKNVYK	99.7%	49.5	25	49.5	1	0	0	2037.03	443	460
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	12	14	30	0.03%	28.4%	TSFTPVGDVFELNFMNVK	99.7%	72.3	25	72.3	6	0	0	2061.00	323	340
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	12	14	30	0.03%	28.4%	YHVPVVVVPEGSASDTHEQAILR	99.7%	50.6	25	50.6	0	2	0	2503.29	267	289
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	RPN2_HUMAN	69.3	100.0%	12	14	30	0.03%	28.4%	YIANTVELR	99.7%	44.5	25	38.5	2	0	0	1078.59	358	366
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	DAD1	DAD1_HUMAN	12.5	99.8%	2	2	5	0.00%	17.7%	ADFQGISPER	99.7%	64.4	25	59.3	4	0	0	1119.54	83	92
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	DAD1	DAD1_HUMAN	12.5	99.8%	2	2	5	0.00%	17.7%	SASVVSVISR	99.7%	42.7	25	35.5	1	0	0	1004.57	2	11
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	7	7	12	0.01%	10.2%	EGSPVLLNCLMYK	96.3%	29.1	25	24.9	1	0	0	1523.76	629	641
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	7	7	12	0.01%	10.2%	FGQVYTEAK	99.7%	55.7	25	50.2	2	0	0	1042.52	647	655

Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	7	7	12	0.01%	10.2%	FHNWFDDR	99.7%	43.9	25	41.1	2	0	0	1136.49	68	75
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	7	7	12	0.01%	10.2%	FLAEEGFYK	99.7%	44.6	25	28.4	2	0	0	1103.54	59	67
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	7	7	12	0.01%	10.2%	FYSLLDPSYAK	99.7%	45.1	25	40.1	2	0	0	1303.66	330	340
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	7	7	12	0.01%	10.2%	LNPQQFEVLFR	94.7%	27.8	25	22.6	1	0	0	1390.75	290	300
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	STT3A_HUMAN	80.5	100.0%	7	7	12	0.01%	10.2%	VGQAMASTEEK	99.3%	36.2	25	28.9	2	0	0	1150.54	555	565
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	STT3B	STT3B_HUMAN	93.7	100.0%	3	4	6	0.01%	5.0%	ESDYFTPQGEFR	98.3%	32.1	25	32.1	1	0	0	1475.64	692	703
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	STT3B	STT3B_HUMAN	93.7	100.0%	3	4	6	0.01%	5.0%	FYSLWDTGYAK	99.7%	60	25	56.4	2	0	0	1350.64	384	394
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	STT3B	STT3B_HUMAN	93.7	100.0%	3	4	6	0.01%	5.0%	SSLNSSPWSGLMALGNSR	99.7%	65.6	25	63	3	0	0	1879.90	13	30
Dolichyl-phosphate beta-glucosyltransferase	ALG5	ALG5_HUMAN	36.9	100.0%	2	2	3	0.00%	7.7%	ETLPSIWDSPTK	99.7%	45.7	25	33.8	2	0	0	1373.69	54	65
Dolichyl-phosphate beta-glucosyltransferase	ALG5	ALG5_HUMAN	36.9	100.0%	2	2	3	0.00%	7.7%	QLSVVVPSYNEEK	99.7%	42.9	25	35.1	1	0	0	1491.77	66	78
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	10	10	29	0.03%	21.0%	ATVTAMIAR	99.7%	67.2	25	57.1	2	0	0	933.52	449	457
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	10	10	29	0.03%	21.0%	EFVMQVK	99.6%	39	25	24.9	1	0	0	880.46	318	324
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	10	10	29	0.03%	21.0%	ELLYGGTSPTAETILK	99.7%	104	25	99.8	4	0	0	1692.91	458	473
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	10	10	29	0.03%	21.0%	LAQIQQAK	99.7%	48.9	25	36.7	4	0	0	899.53	291	298
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	10	10	29	0.03%	21.0%	LPPLPAVER	99.7%	46.3	25	45.7	2	0	0	991.59	252	260
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	10	10	29	0.03%	21.0%	NAAENMLEILGFK	99.7%	98.2	25	98.2	5	0	0	1449.74	343	355
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	10	10	29	0.03%	21.0%	NAAIAVLEELKK	99.7%	45.4	25	26.8	2	0	0	1298.77	240	251
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	10	10	29	0.03%	21.0%	TKPIVKPQTSPEYGQGINPISR	99.7%	41.2	25	41.2	0	1	0	2410.31	269	290
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	10	10	29	0.03%	21.0%	VPQAQPTKPALK	99.7%	63.8	25	63.5	4	0	0	1277.76	356	367
Double-stranded RNA-binding protein Staufen homolog 1	STAU1	STAU1_HUMAN	63.2	100.0%	10	10	29	0.03%	21.0%	VSVGEFVGEGEGK	99.7%	96.2	25	90.1	4	0	0	1293.63	220	232
Double-stranded RNA-binding protein Staufen homolog 2	STAU2	STAU2_HUMAN	62.6	100.0%	6	6	13	0.01%	16.3%	ALQALQNEPIPER	99.7%	53.3	25	45.3	2	0	0	1478.80	175	187
Double-stranded RNA-binding protein Staufen homolog 2	STAU2	STAU2_HUMAN	62.6	100.0%	6	6	13	0.01%	16.3%	ASTNLQDQLEK	99.7%	42.2	25	24.4	3	0	0	1246.63	377	387
Double-stranded RNA-binding protein Staufen homolog 2	STAU2	STAU2_HUMAN	62.6	100.0%	6	6	13	0.01%	16.3%	EFVMQVK	99.6%	39	25	24.9	1	0	0	880.46	339	345
Double-stranded RNA-binding protein Staufen homolog 2	STAU2	STAU2_HUMAN	62.6	100.0%	6	6	13	0.01%	16.3%	IQGFQAALSALK	99.7%	53.8	25	45.3	1	0	0	1246.72	506	517
Double-stranded RNA-binding protein Staufen homolog 2	STAU2	STAU2_HUMAN	62.6	100.0%	6	6	13	0.01%	16.3%	LAQIQQAK	99.7%	48.9	25	36.7	4	0	0	899.53	312	319
Double-stranded RNA-binding protein Staufen homolog 2	STAU2	STAU2_HUMAN	62.6	100.0%	6	6	13	0.01%	16.3%	VGNEVATGTGPNKK	99.6%	33.3	25	32.8	0	3	0	1371.72	346	359
Double-stranded RNA-binding protein Staufen homolog 2	STAU2	STAU2_HUMAN	62.6	100.0%	6	6	13	0.01%	16.3%	VISGTTLGYLSPK	99.7%	66.3	25	65.3	3	0	0	1335.75	430	442
Double-stranded RNA-binding protein Staufen homolog 2	STAU2	STAU2_HUMAN	62.6	100.0%	6	6	13	0.01%	16.3%	VSVGEFSAEGEGNSK	99.7%	61.5	25	54.3	1	0	0	1496.69	243	257
Double-stranded RNA-specific adenosine deaminase	ADAR	DSRAD_HUMAN	136.1	100.0%	6	7	10	0.01%	6.6%	AMTILLEEAK	99.7%	70.4	25	60	2	0	0	1118.61	565	574
Double-stranded RNA-specific adenosine deaminase	ADAR	DSRAD_HUMAN	136.1	100.0%	6	7	10	0.01%	6.6%	DINAVLIDMER	99.7%	61.1	25	56.3	1	0	0	1288.66	329	339
Double-stranded RNA-specific adenosine deaminase	ADAR	DSRAD_HUMAN	136.1	100.0%	6	7	10	0.01%	6.6%	LVDQSGPPHEPK	99.7%	45.4	25	37.6	2	0	0	1303.66	746	757
Double-stranded RNA-specific adenosine deaminase	ADAR	DSRAD_HUMAN	136.1	100.0%	6	7	10	0.01%	6.6%	SVTLGYLFSQGHLTR	99.7%	94.2	25	94.2	1	0	0	1678.89	1064	1078
Double-stranded RNA-specific adenosine deaminase	ADAR	DSRAD_HUMAN	136.1	100.0%	6	7	10	0.01%	6.6%	TAESQTPTPSATSFFSGK	99.7%	89	25	89	2	0	0	1843.87	596	613
Double-stranded RNA-specific adenosine deaminase	ADAR	DSRAD_HUMAN	136.1	100.0%	6	7	10	0.01%	6.6%	YLNTNPVGGLLEYAR	99.7%	95.7	25	91.4	2	0	0	1679.88	722	736
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	17	0.02%	25.2%	DVKPSNILVNSR	99.7%	49.2	25	47.4	2	0	0	1341.75	194	205
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	17	0.02%	25.2%	ISELGAGNGGVVTK	99.7%	80.9	25	75.2	2	0	0	1301.71	75	88
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	17	0.02%	25.2%	LNQPGTPTR	99.7%	48	25	48	2	0	0	983.53	389	397
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	17	0.02%	25.2%	LPNGVFTPDFQEFVNK	99.7%	53	25	52	1	0	0	1851.93	333	348
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	17	0.02%	25.2%	RIPEEILGK	99.4%	36.8	25	30.4	2	0	0	1054.63	164	172
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	17	0.02%	25.2%	RLEAFLTQK	99.5%	37.6	25	24	2	0	0	1105.64	53	61
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	17	0.02%	25.2%	VGELKDDDFER	99.7%	54.4	25	48.1	2	2	0	1322.62	64	74
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	17	0.02%	25.2%	VQHRPSGLIMAR	99.6%	32.3	25	32.3	0	1	0	1364.76	89	100
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	MP2K2_HUMAN	44.4	100.0%	9	10	17	0.02%	25.2%	YPIPPPDAK	99.6%	39	25	19.6	1	0	0	997.54	265	273
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	22	26	43	0.04%	20.0%	AEITDAEGLGLK	99.7%	82	25	70.9	2	0	0	1216.64	933	944
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	22	26	43	0.04%	20.0%	AFLQGGQEATDIALLLR	99.7%	66.2	25	62.5	1	0	0	1816.00	769	785
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	22	26	43	0.04%	20.0%	ASEQIYGTPSSSPYECLR	99.7%	82.4	25	74.7	2	0	0	2044.93	873	890
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	22	26	43	0.04%	20.0%	DLEEKLETLR	99.7%	57.5	25	40.1	2	0	0	1245.67	226	235
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	22	26	43	0.04%	20.0%	DLETSCSDIR	99.7%	67.2	25	56.5	2	0	0	1195.53	786	795
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	22	26	43	0.04%	20.0%	DSPLLLQQISAMR	99.7%	75.9	25	75.9	2	0	0	1471.79	1089	1101
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	22	26	43	0.04%	20.0%	ELTNQQEASVER	99.7%	76.9	25	68.4	2	0	0	1403.68	533	544
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	22	26	43	0.04%	20.0%	EQLDMAGAR	99.7%	40.2	25	38	1	0	0	990.47	487	495

Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	22	26	43	0.04%	20.0%	FTQSALDCMSVEVGR	99.7%	73.7	25	73.7	3	0	0	1699.78	752	766
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	22	26	43	0.04%	20.0%	GSDGAASSYQLK	99.7%	67.6	25	57.5	2	0	0	1183.56	350	361
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	22	26	43	0.04%	20.0%	GTVAYVGATLFATGK	99.7%	42.3	25	42.3	1	0	0	1455.78	42	56
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	22	26	43	0.04%	20.0%	IKGEELSEANVR	99.7%	71.2	25	65.8	2	1	0	1344.71	961	972
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	22	26	43	0.04%	20.0%	KNQELEVVR	99.7%	44.3	25	26.3	1	0	0	1114.62	398	406
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	22	26	43	0.04%	20.0%	LEETQALLR	99.7%	39.5	25	18.7	1	0	0	1072.60	998	1006
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	22	26	43	0.04%	20.0%	LKDALVR	97.6%	30.9	25	11.6	1	0	0	814.51	370	376
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	22	26	43	0.04%	20.0%	LSHEGPGSELPAGALYR	98.6%	27.5	25	26.4	0	2	0	1753.89	1134	1150
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	22	26	43	0.04%	20.0%	MQEQQADLQR	99.7%	58.3	25	44.5	4	0	0	1262.58	265	274
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	22	26	43	0.04%	20.0%	NQELEVVR	99.7%	49	25	31.5	2	0	0	986.53	399	406
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	22	26	43	0.04%	20.0%	SPSAQLMEQVAQLK	99.7%	82.9	25	73.3	3	0	0	1529.80	1180	1193
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	22	26	43	0.04%	20.0%	VDELTTDLEILK	99.7%	86.9	25	61.5	2	0	0	1388.75	332	343
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	22	26	43	0.04%	20.0%	VTFSCAAGFGQR	99.7%	86.7	25	81.6	2	0	0	1300.61	1248	1259
Dynactin subunit 1	DCTN1	DCTN1_HUMAN	141.7	100.0%	22	26	43	0.04%	20.0%	WVGVILDEAK	99.7%	50.1	25	36.8	2	0	0	1129.63	57	66
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	9	10	16	0.02%	15.9%	FATEYCNTIEGTAK	99.7%	67	25	54.1	1	0	0	1604.73	340	353
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	9	10	16	0.02%	15.9%	GVSPEPIHLK	98.7%	33.5	25	22.9	2	0	0	1076.61	124	133
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	9	10	16	0.02%	15.9%	IFSPNVVNLTLVDLPGMTK	99.7%	108	25	101	3	0	0	2058.13	134	152
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	9	10	16	0.02%	15.9%	LGIIGVVNR	99.7%	77.7	25	58.1	2	0	0	940.59	239	247
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	9	10	16	0.02%	15.9%	RLEEPSLR	99.7%	50.6	25	38.3	2	0	0	999.56	423	430
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	9	10	16	0.02%	15.9%	SSLLDDLLTESEDMAQR	99.5%	37.3	25	37.3	1	0	0	1922.90	693	709
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	9	10	16	0.02%	15.9%	SYFLIVR	99.7%	48.2	25	39.3	2	0	0	897.52	653	659
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	9	10	16	0.02%	15.9%	TLESVDPLGGLNTIDILTAIR	99.7%	90.7	25	90.7	1	0	0	2211.22	377	397
Dynamin-1-like protein	DNM1L	DNM1L_HUMAN	81.9	100.0%	9	10	16	0.02%	15.9%	YIETSELCGGAR	99.7%	61	25	44.5	2	0	0	1355.63	354	365
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	17	19	31	0.03%	24.4%	AIPNQGEILVIR	98.9%	34.3	25	34.3	1	0	0	1322.78	511	522
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	17	19	31	0.03%	24.4%	ALLQMVQQFGVDFEK	99.7%	69.1	25	69.1	2	0	0	1752.90	328	342
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	17	19	31	0.03%	24.4%	DMILQFISR	99.7%	54.2	25	28	2	0	0	1122.60	158	166
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	17	19	31	0.03%	24.4%	ESSLILAVTPANMDLANSDALK	99.7%	91.2	25	91.2	3	0	0	2289.16	167	188
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	17	19	31	0.03%	24.4%	EVDPQGLR	99.7%	49.6	25	37	2	0	0	913.47	192	199
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	17	19	31	0.03%	24.4%	FPFELVK	99.7%	49.4	25	0	2	0	0	879.50	370	376
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	17	19	31	0.03%	24.4%	GMEELIPLVNK	99.7%	40.7	25	33.2	1	0	0	1242.68	5	15
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	17	19	31	0.03%	24.4%	GYIGVVNR	99.7%	43.3	25	34.8	2	0	0	877.49	230	237
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	17	19	31	0.03%	24.4%	IEGSGDQVDTLELSGGAR	99.7%	88.5	25	86.2	1	0	0	1803.87	344	361
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	17	19	31	0.03%	24.4%	LQSQLLSLEK	99.7%	63.5	25	0	2	0	0	1158.67	300	309
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	17	19	31	0.03%	24.4%	NLVDSYVAIINK	99.7%	71.9	25	61.2	2	0	0	1348.75	658	669
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	17	19	31	0.03%	24.4%	SSVLENFVGR	99.7%	57.6	25	41.1	2	0	0	1107.58	45	54
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	17	19	31	0.03%	24.4%	TEHAEFLHCK	99.7%	40.5	25	35.2	1	0	0	1271.58	78	87
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	17	19	31	0.03%	24.4%	TGLFTPDLAFEAIVK	99.7%	80.9	25	72.2	2	0	0	1621.88	400	414
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	17	19	31	0.03%	24.4%	TLNQQLTNHIR	99.7%	58.9	25	52	2	0	0	1337.73	280	290
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	17	19	31	0.03%	24.4%	VPVGDQPPDIEYQIK	99.7%	78.9	25	68.2	2	0	0	1697.87	143	157
Dynamin-2	DNM2	DYN2_HUMAN	98.1	100.0%	17	19	31	0.03%	24.4%	VYSPHVLNLTLIDLPGITK	99.7%	39	25	39	0	2	0	2093.20	124	142
Dynein light chain 1, cytoplasmic	DYNLL1	DYL1_HUMAN	10.4	100.0%	2	3	10	0.01%	37.1%	NADMSEEMQQDSVECATQALEK	99.7%	62.3	25	58.5	2	4	0	2546.03	10	31
Dynein light chain 1, cytoplasmic	DYNLL1	DYL1_HUMAN	10.4	100.0%	2	3	10	0.01%	37.1%	NFGSYVTHETK	99.7%	55.6	25	46.2	4	0	0	1282.61	61	71
Dynein light chain Tctex-type 1	DYNLT1	DYLT1_HUMAN	12.5	99.8%	2	3	4	0.00%	23.0%	EAIESAIGGNAYQHSK	99.7%	65.2	25	64.8	2	0	0	1674.81	23	38
Dynein light chain Tctex-type 1	DYNLT1	DYLT1_HUMAN	12.5	99.8%	2	3	4	0.00%	23.0%	YIVTCVIMQK	98.4%	32.5	25	24.8	2	0	0	1270.65	63	72
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	8	8	17	0.02%	3.0%	EGQWDCSVCLVR	99.7%	61.4	25	55.4	2	0	0	1508.66	1607	1618
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	8	8	17	0.02%	3.0%	ELLQSFDSALQSVK	99.7%	91.3	25	88.8	4	0	0	1564.82	257	270
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	8	8	17	0.02%	3.0%	ELVGPPLAETVFTPK	99.7%	84.8	25	84.4	3	0	0	1597.88	1384	1398
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	8	8	17	0.02%	3.0%	FGISEPGNQEK	99.6%	38.4	25	29.7	1	0	0	1205.58	1900	1910
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	8	8	17	0.02%	3.0%	IAVAVLEETTR	99.7%	111	25	100	2	0	0	1201.68	2467	2477
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	8	8	17	0.02%	3.0%	IIDDSDSNLSVVK	99.7%	96.5	25	0	2	0	0	1404.72	721	733
E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	8	8	17	0.02%	3.0%	SGFEGMFTK	99.5%	38	25	33.7	1	0	0	1003.46	1597	1605

E3 SUMO-protein ligase RanBP2	RANBP2	RBP2_HUMAN	358.2	100.0%	8	8	17	0.02%	3.0%	SGSSFVHQASFK	99.7%	62	25	53.6	2	0	0	1281.62	1447	1458
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	AALPLTTSDTK	99.7%	49.2	25	40.8	2	0	0	1117.61	1498	1508
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	ADGTATAPPPR	99.6%	38.3	25	33.7	2	0	0	1053.53	707	717
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	AGSSTPGDAPPAVAEVQGR	99.7%	64.2	25	64.2	2	0	0	1766.87	2885	2903
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	AIQDPAFSDGIR	99.7%	71.9	25	63.4	2	0	0	1289.65	518	529
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	ALAELFGLLVK	99.7%	84.2	25	72.6	2	0	0	1173.72	1062	1072
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	DGGSGNSTIIVSR	99.7%	57.7	25	49.6	2	0	0	1262.63	2359	2371
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	DSAVAISGADSR	99.7%	73.5	25	61.5	1	0	0	1148.55	2930	2941
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	EMFNPMYALFR	99.7%	44.1	25	44.1	1	0	0	1418.66	4072	4082
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	EVLGSLPNVFSALCLNAR	99.7%	44.8	25	44.8	1	0	0	1960.03	599	616
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	EVLQNQLGIRPPTR	98.5%	27.4	25	23.5	0	1	0	1620.92	2983	2996
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	EYNLEQQR	99.7%	51.2	25	27.4	1	0	0	1079.51	3647	3654
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	FLQFVTGTSK	99.7%	65.4	25	56	2	0	0	1127.61	4296	4305
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	GLQSFVQCQPFER	99.7%	59	25	52	2	0	0	1595.76	617	629
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	HADHSSLTLGSGSSTTR	99.7%	37.7	25	36	0	1	0	1713.82	2522	2538
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	LGSSGLGSASSIQAAVR	99.7%	99.1	25	93	2	0	0	1560.83	3750	3766
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	LLECYFTR	99.7%	41.3	25	25.8	2	0	0	1101.54	4123	4130
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	LLSLISIALPENK	99.7%	57.5	25	56.6	2	0	0	1410.86	3456	3468
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	LPGGVQNFPQFSALR	99.7%	62	25	62	2	0	0	1630.87	1226	1240
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	NLCYHAQTR	98.4%	32.4	25	26.7	2	0	0	1162.54	3211	3219
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	NPDIFTEVANCCIR	99.7%	78.7	25	78.1	2	0	0	1708.78	1881	1894
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	QIGTLLAELR	99.7%	42.9	25	33.5	2	0	0	1113.66	3637	3646
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	QVVNQVWEAADVLIK	99.7%	51.9	25	46.5	2	0	0	1711.94	1483	1497
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	SILTLSHEPK	99.3%	36.2	25	36.2	2	0	0	1124.63	830	839
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	SLLSILQR	99.7%	45.7	25	25.6	2	0	0	929.58	3225	3232
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	TLTSIVHLER	99.7%	49.7	25	41.2	2	0	0	1168.67	330	339
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	VLLSPDYLPAMR	99.7%	39.5	25	39.5	2	0	0	1374.75	633	644
E3 ubiquitin-protein ligase HUWE1	HUWE1	HUWE1_HUMAN	481.9	100.0%	27	27	48	0.04%	7.6%	VSDGGSSSTDFK	99.7%	61.8	25	61.8	2	0	0	1186.52	3559	3570
E3 ubiquitin-protein ligase MYCBP2	MYCBP2	MYCB2_HUMAN	510.1	100.0%	3	3	4	0.00%	0.7%	ALSVVSTVVR	99.7%	39.4	25	27.2	1	0	0	1030.63	1871	1880
E3 ubiquitin-protein ligase MYCBP2	MYCBP2	MYCB2_HUMAN	510.1	100.0%	3	3	4	0.00%	0.7%	MLVIVVLPVR	95.7%	28.5	25	28.5	1	0	0	1138.74	1627	1636
E3 ubiquitin-protein ligase MYCBP2	MYCBP2	MYCB2_HUMAN	510.1	100.0%	3	3	4	0.00%	0.7%	NAIAETIIALTK	99.7%	45.7	25	45.7	2	0	0	1257.74	4159	4170
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	8	8	13	0.01%	15.2%	DLDITSPELR	99.7%	53.4	25	44.3	2	0	0	1158.60	261	270
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	8	8	13	0.01%	15.2%	EAWDLGVCR	99.7%	45.1	25	42.4	2	0	0	1105.51	352	360
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	8	8	13	0.01%	15.2%	IHAEFVQQK	99.7%	41.2	25	27.1	1	0	0	1099.59	178	186
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	8	8	13	0.01%	15.2%	LGDTQQSIPGNEER	99.7%	60.5	25	58.2	2	0	0	1543.73	311	324
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	8	8	13	0.01%	15.2%	LQVALGELR	99.7%	56.7	25	28.5	2	0	0	998.60	139	147
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	8	8	13	0.01%	15.2%	LQVALGELRR	99.5%	37.4	25	32.3	1	0	0	1154.70	139	148
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	8	8	13	0.01%	15.2%	NFLVEEEQR	99.7%	52.3	25	28.8	2	0	0	1163.57	187	195
E3 ubiquitin-protein ligase TRIM21	TRIM21	RO52_HUMAN	54.2	100.0%	8	8	13	0.01%	15.2%	SGFWTIWLWNK	99.7%	47.3	25	43	1	0	0	1437.73	375	385
E3 ubiquitin-protein ligase TRIP12	TRIP12	TRIPC_HUMAN	220.4	100.0%	3	3	4	0.00%	2.0%	IDPLALVQAIER	99.7%	83.4	25	83.3	1	0	0	1337.78	1289	1300
E3 ubiquitin-protein ligase TRIP12	TRIP12	TRIPC_HUMAN	220.4	100.0%	3	3	4	0.00%	2.0%	LVDLPLGLPFYK	98.6%	33.2	25	26.4	1	0	0	1374.80	1713	1724
E3 ubiquitin-protein ligase TRIP12	TRIP12	TRIPC_HUMAN	220.4	100.0%	3	3	4	0.00%	2.0%	SSAVVVDAIPVFLEK	99.7%	58.2	25	50.3	2	0	0	1573.88	515	529
E3 ubiquitin-protein ligase UBR4	UBR4	UBR4_HUMAN	573.8	100.0%	5	5	5	0.00%	1.1%	GVLPYVGNLITK	95.2%	28.1	25	21	1	0	0	1273.75	4204	4215
E3 ubiquitin-protein ligase UBR4	UBR4	UBR4_HUMAN	573.8	100.0%	5	5	5	0.00%	1.1%	IISLDLPVAEVYK	99.4%	37	25	37	1	0	0	1459.84	4414	4426
E3 ubiquitin-protein ligase UBR4	UBR4	UBR4_HUMAN	573.8	100.0%	5	5	5	0.00%	1.1%	QLLQLLTTYIVR	99.7%	48.5	25	48.5	1	0	0	1460.88	1490	1501
E3 ubiquitin-protein ligase UBR4	UBR4	UBR4_HUMAN	573.8	100.0%	5	5	5	0.00%	1.1%	TPVFIFER	98.9%	33.9	25	33.9	1	0	0	1008.55	4327	4334
E3 ubiquitin-protein ligase UBR4	UBR4	UBR4_HUMAN	573.8	100.0%	5	5	5	0.00%	1.1%	VCLNLPYFLR	99.7%	46.4	25	40.4	1	0	0	1294.70	259	268
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	13	13	24	0.02%	18.4%	AQFAEATQR	99.7%	46.4	25	38.3	2	0	0	1021.51	18	26
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	13	13	24	0.02%	18.4%	AVFVPDIYSR	97.9%	31.3	25	28.1	2	0	0	1166.62	242	251
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	13	13	24	0.02%	18.4%	CVPQIIAFLNSK	99.7%	39.8	25	39.8	2	0	0	1389.76	708	719
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	13	13	24	0.02%	18.4%	DLQEEVSNLYNNIR	99.6%	39.3	25	32.3	1	0	0	1706.83	539	552

E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	13	13	24	0.02%	18.4%	FFADDTQAALTK	99.7%	84.2	25	79.6	2	0	0	1327.65	560	571
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	13	13	24	0.02%	18.4%	FINDCTELFR	99.7%	43.2	25	42	1	0	0	1314.61	368	377
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	13	13	24	0.02%	18.4%	GVIFTEAFVAR	99.7%	80.4	25	76.2	2	0	0	1209.66	175	185
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	13	13	24	0.02%	18.4%	IISGHIDLDNR	99.6%	39	25	28.7	2	0	0	1252.66	164	174
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	13	13	24	0.02%	18.4%	LAADFQR	96.7%	29.6	25	22.2	2	0	0	820.43	11	17
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	13	13	24	0.02%	18.4%	LGIPDAVSYIK	99.7%	49.6	25	40.2	2	0	0	1175.67	275	285
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	13	13	24	0.02%	18.4%	QISTLESVSTSK	99.7%	48.5	25	45.7	2	0	0	1279.67	403	414
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	13	13	24	0.02%	18.4%	TQSTWVDSFFR	99.7%	53.6	25	52.8	2	0	0	1373.65	252	262
E3 UFM1-protein ligase 1	UFL1	UFL1_HUMAN	89.6	100.0%	13	13	24	0.02%	18.4%	TYDLPGNFLTQALTQR	99.7%	88.1	25	63.2	2	0	0	1837.94	145	160
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	14	17	29	0.03%	29.2%	ADQIETQQLMR	99.7%	57.9	25	43	4	0	0	1348.65	221	231
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	14	17	29	0.03%	29.2%	EHQISPGDFPSLR	99.7%	57.5	25	52.8	2	2	0	1482.73	345	357
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	14	17	29	0.03%	29.2%	ELVNNLGEIYQK	99.7%	85.1	25	85.1	2	0	0	1419.75	330	341
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	14	17	29	0.03%	29.2%	FQALKPK	95.6%	28.4	25	18.2	1	0	0	831.51	371	377
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	14	17	29	0.03%	29.2%	IINTPEVVR	99.7%	51.8	25	39.3	2	0	0	1040.61	243	251
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	14	17	29	0.03%	29.2%	KLNDLIK	99.5%	37.6	25	10.5	2	0	0	843.53	293	299
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	14	17	29	0.03%	29.2%	LLDTVDDMLANDIAR	99.7%	107	25	100	2	0	0	1674.84	378	392
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	14	17	29	0.03%	29.2%	LLPLEEHYR	99.7%	45.4	25	35.5	2	0	0	1169.63	33	41
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	14	17	29	0.03%	29.2%	LNAFGNAFLNR	99.7%	63.2	25	53.5	2	0	0	1236.65	125	135
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	14	17	29	0.03%	29.2%	MQELLQTQDFSK	99.7%	69.3	25	55.7	1	0	0	1467.72	359	370
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	14	17	29	0.03%	29.2%	QEESLMPSQVVK	99.7%	42	25	31.2	1	0	0	1390.69	399	410
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	14	17	29	0.03%	29.2%	SKLPNTVLGK	99.1%	35	25	35	2	0	0	1056.64	474	483
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	14	17	29	0.03%	29.2%	VYGALMWSLGK	99.7%	52.6	25	52.4	3	0	0	1240.64	232	242
EH domain-containing protein 1	EHD1	EHD1_HUMAN	60.6	100.0%	14	17	29	0.03%	29.2%	VYIGSFWSHPLLIPDNR	97.6%	25.5	25	24.4	0	1	0	2014.05	252	268
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	3	3	4	0.00%	10.0%	ADQVDTQQLMR	99.3%	36.2	25	23.1	1	0	0	1304.63	224	234
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	3	3	4	0.00%	10.0%	AGGADAVQTVTGGLR	99.7%	91.7	25	87	2	0	0	1372.72	15	29
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	3	3	4	0.00%	10.0%	KLNDLIK	99.5%	37.6	25	10.5	2	0	0	843.53	296	302
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	3	3	4	0.00%	10.0%	LPEIYIQLQR	99.7%	55.6	25	37.4	1	0	0	1272.73	338	347
EH domain-containing protein 4	EHD4	EHD4_HUMAN	61.2	100.0%	3	3	4	0.00%	10.0%	VYGALMWSLGK	99.7%	52.6	25	52.4	3	0	0	1240.64	235	245
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	16	22	62	0.06%	54.0%	AINTLNGLR	99.7%	59.9	25	52.1	4	0	0	971.56	77	85
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	16	22	62	0.06%	54.0%	DANLYISGLPR	99.7%	73.1	25	68.7	2	0	0	1218.65	105	115
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	16	22	62	0.06%	54.0%	DKVAGHSLGYGFVNYVTAK	99.7%	77.6	25	77.6	0	2	0	2026.04	54	72
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	16	22	62	0.06%	54.0%	DVEDMFSR	99.7%	48.3	25	30	3	0	0	998.42	121	128
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	16	22	62	0.06%	54.0%	FAANPNQNK	99.6%	38.3	25	27	5	0	0	1003.50	183	191
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	16	22	62	0.06%	54.0%	FGGPVHHQAQR	99.4%	30.7	25	21.6	2	4	0	1233.62	207	217
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	16	22	62	0.06%	54.0%	ILQVSFK	99.7%	46.6	25	0	2	0	0	834.51	314	320
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	16	22	62	0.06%	54.0%	LGDKILQVSFK	95.4%	28.3	25	28.3	1	0	0	1247.74	310	320
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	16	22	62	0.06%	54.0%	NVALLSQLYHSPAR	99.7%	87.7	25	77.9	2	2	0	1568.85	192	205
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	16	22	62	0.06%	54.0%	SEAEEAITSFNGHKPPGSSEPITVK	99.7%	75.7	25	72.1	0	3	0	2612.28	158	182
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	16	22	62	0.06%	54.0%	SLFSSIGEVESAK	99.7%	100	25	88.8	7	0	0	1353.69	38	50
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	16	22	62	0.06%	54.0%	TMTQKDVEDMFSR	99.7%	45.4	25	41	0	2	0	1619.70	116	128
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	16	22	62	0.06%	54.0%	TNLIVNYLPQNMTQDELR	99.7%	102	25	96.3	8	4	0	2162.09	20	37
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	16	22	62	0.06%	54.0%	VAGHSLGYGFVNYVTAK	99.7%	56.1	25	56.1	0	2	0	1782.92	56	72
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	16	22	62	0.06%	54.0%	VLVDQTTGLSR	99.7%	91.8	25	73.7	4	0	0	1188.66	137	147
ELAV-like protein 1	ELAVL1	ELAV1_HUMAN	36.1	100.0%	16	22	62	0.06%	54.0%	VSYARPSSEVIK	99.4%	37.1	25	23.4	3	0	0	1335.73	93	104
ELAV-like protein 2	ELAVL2	ELAV2_HUMAN	39.5	100.0%	7	7	15	0.01%	24.0%	AINTLNGLR	99.7%	59.9	25	52.1	4	0	0	971.56	96	104
ELAV-like protein 2	ELAVL2	ELAV2_HUMAN	39.5	100.0%	7	7	15	0.01%	24.0%	DANLYVSGLPK	99.7%	57.4	25	49.3	3	0	0	1176.63	124	134
ELAV-like protein 2	ELAVL2	ELAV2_HUMAN	39.5	100.0%	7	7	15	0.01%	24.0%	ELEQLFSQYGR	99.7%	52.5	25	52.5	1	0	0	1369.67	140	150
ELAV-like protein 2	ELAVL2	ELAV2_HUMAN	39.5	100.0%	7	7	15	0.01%	24.0%	ILVDQVTGISR	99.7%	86.1	25	69.3	2	0	0	1200.69	156	166
ELAV-like protein 2	ELAVL2	ELAV2_HUMAN	39.5	100.0%	7	7	15	0.01%	24.0%	RIEAEEAIK	98.9%	34	25	10.2	1	0	0	1058.58	176	184
ELAV-like protein 2	ELAVL2	ELAV2_HUMAN	39.5	100.0%	7	7	15	0.01%	24.0%	SLFGSIGEIESCK	99.7%	68.9	25	68.9	2	0	0	1426.69	57	69
ELAV-like protein 2	ELAVL2	ELAV2_HUMAN	39.5	100.0%	7	7	15	0.01%	24.0%	TNQAILSQLYQSPNR	99.7%	74.8	25	69.7	4	0	0	1732.90	210	224

ELAV-like protein 2	ELAVL2	ELAV2_HUMAN	39.5	100.0%	7	7	15	0.01%	24.0%	VLQVSFK	99.0%	34.6	25	28.6	2	0	0	820.49	346	352
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	10	13	31	0.03%	41.7%	AAVDAGFVPNDMQVGQTGK	99.7%	79.9	25	79.9	4	0	0	1904.92	250	268
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	10	13	31	0.03%	41.7%	ASSTSPVEISEWLDQK	99.7%	66.3	25	63	2	0	0	1776.87	188	203
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	10	13	31	0.03%	41.7%	GLLPEELTPLILATQK	99.7%	93.4	25	91.5	3	2	0	1736.02	86	101
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	10	13	31	0.03%	41.7%	GTSFDAAATSGGSASSEK	99.7%	115	25	106	2	0	0	1630.72	170	187
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	10	13	31	0.03%	41.7%	LEVAPISDIIAIK	99.7%	102	25	92.8	6	0	0	1381.83	127	139
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	10	13	31	0.03%	41.7%	LGGEVSCLVAGTK	99.7%	90.7	25	89.1	2	0	0	1290.67	47	59
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	10	13	31	0.03%	41.7%	LLYDLADQLHAAVGASR	99.7%	132	25	121	2	2	0	1812.96	233	249
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	10	13	31	0.03%	41.7%	SDRPELTGAK	99.7%	49.2	25	40.3	2	0	0	1073.56	207	216
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	10	13	31	0.03%	41.7%	SPDTFVR	99.7%	50	25	30	2	0	0	821.42	140	146
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	ETFA_HUMAN	35.1	100.0%	10	13	31	0.03%	41.7%	VLVAQHDVYK	99.7%	56.1	25	43.8	2	0	0	1171.65	76	85
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	19	0.02%	45.5%	EIDGGLETLR	99.7%	68.8	25	61.1	2	0	0	1102.57	165	174
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	19	0.02%	45.5%	EVIAVSCGPAQCQETIR	99.7%	86.5	25	86.5	2	0	0	1917.92	60	76
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	19	0.02%	45.5%	GIHVEVPPAEAER	99.6%	38.6	25	23.8	1	0	0	1403.73	86	98
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	19	0.02%	45.5%	IEVIKPGDLGVDLTSK	99.7%	72.2	25	72.2	2	0	0	1683.95	206	221
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	19	0.02%	45.5%	LGPLQVAR	99.7%	67.8	25	59.1	2	0	0	853.53	99	106
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	19	0.02%	45.5%	LKLPAVVTADLR	99.7%	51.9	25	51.9	1	0	0	1295.80	175	186
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	19	0.02%	45.5%	LPAVVTADLR	99.4%	36.4	25	35.9	2	0	0	1054.63	177	186
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	19	0.02%	45.5%	LSVISVEDPPQR	99.7%	61.1	25	59.9	2	0	0	1339.72	222	233
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	19	0.02%	45.5%	TALAMGADR	99.7%	42.8	25	30.6	1	0	0	905.45	77	85
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	19	0.02%	45.5%	TGVVTDGVK	99.6%	38.6	25	19.4	2	0	0	875.48	27	35
Electron transfer flavoprotein subunit beta	ETFB	ETFB_HUMAN	27.8	100.0%	11	11	19	0.02%	45.5%	VETTEDLVAK	99.7%	60.2	25	47.9	2	0	0	1104.58	239	248
ELMO domain-containing protein 2	ELMOD2	ELMD2_HUMAN	35.0	100.0%	4	5	8	0.01%	13.7%	IENSLTYSK	99.7%	42.8	25	39	2	0	0	1054.54	47	55
ELMO domain-containing protein 2	ELMOD2	ELMD2_HUMAN	35.0	100.0%	4	5	8	0.01%	13.7%	IFDTYVGAQR	99.7%	84.5	25	75.9	2	0	0	1169.60	34	43
ELMO domain-containing protein 2	ELMOD2	ELMD2_HUMAN	35.0	100.0%	4	5	8	0.01%	13.7%	MCLLQITGYK	99.7%	46.1	25	41.5	3	0	0	1242.62	97	106
ELMO domain-containing protein 2	ELMOD2	ELMD2_HUMAN	35.0	100.0%	4	5	8	0.01%	13.7%	NINPEKDASFK	99.0%	34.4	25	12.5	1	0	0	1262.64	82	92
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	232	0.22%	56.3%	DGNASGTTLLEALDCILPPTRPTDKPLR	99.7%	77.7	25	77.7	0	3	0	3021.57	220	247
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	232	0.22%	56.3%	EHALLAYTLGVK	99.7%	72.7	25	62.4	25	4	0	1314.74	135	146
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	232	0.22%	56.3%	EVSTYIKK	99.7%	48.7	25	40.6	3	0	0	967.55	173	180
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	232	0.22%	56.3%	FEKEAAEMGK	99.7%	50.8	25	39.5	3	0	0	1139.54	42	51
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	232	0.22%	56.3%	IGGIGTVPVGR	99.7%	97.2	25	88.5	21	0	0	1025.61	256	266
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	232	0.22%	56.3%	LPLQDVYK	99.7%	58	25	47.3	20	0	0	975.55	248	255
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	232	0.22%	56.3%	MDSTEPPYSQK	99.7%	45.2	25	43.5	1	0	0	1298.56	155	165
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	232	0.22%	56.3%	NMITGTSQADCAVLIVAAGVGEFEAGISK	99.7%	76.8	25	76.8	0	2	0	2925.43	101	129
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	232	0.22%	56.3%	QLIVGVNK	99.7%	40.1	25	22.2	13	0	0	870.54	147	154
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	232	0.22%	56.3%	QTVAVGVIK	99.7%	49	25	37.5	8	0	0	914.57	431	439
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	232	0.22%	56.3%	SGDAAIVDMVPGKPMCVESFSDYPPLGR	99.7%	66	25	66	0	6	0	2995.40	396	423
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	232	0.22%	56.3%	STTTGHLIYK	99.7%	52.5	25	42.1	29	0	0	1120.60	21	30
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	232	0.22%	56.3%	SVEMHHEALSEALPGDNVGFNVK	99.7%	78.8	25	72.1	0	4	0	2480.19	291	313
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	232	0.22%	56.3%	THINIVVIGHVDSGK	99.7%	114	25	114	11	26	0	1588.88	6	20
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	232	0.22%	56.3%	TIEKFEK	99.1%	34.9	25	22.1	1	0	0	894.49	38	44
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	232	0.22%	56.3%	VETGVLKPGMVVTFAPVNVTTEVK	99.7%	63.1	25	63.1	4	21	0	2515.38	267	290
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	232	0.22%	56.3%	YEEIVKEVSTYIK	99.7%	74.5	25	72.7	2	0	0	1600.85	167	179
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	232	0.22%	56.3%	YYVTIIDAPGHR	99.7%	69	25	66.6	13	8	0	1404.73	85	96
Elongation factor 1-alpha 1	EEF1A1	EF1A1_HUMAN	50.1	100.0%	19	29	232	0.22%	56.3%	YYVTIIDAPGHRDFIK	99.7%	62.9	25	62.9	2	2	0	1908.00	85	100
Elongation factor 1-delta	EEF1D	EF1D_HUMAN	31.1	100.0%	3	3	4	0.00%	17.4%	IASLEVENQSLR	99.7%	79.6	25	65.8	2	0	0	1358.73	84	95
Elongation factor 1-delta	EEF1D	EF1D_HUMAN	31.1	100.0%	3	3	4	0.00%	17.4%	SIQLDGLVWGASK	99.7%	51.2	25	49.1	1	0	0	1373.74	220	232
Elongation factor 1-delta	EEF1D	EF1D_HUMAN	31.1	100.0%	3	3	4	0.00%	17.4%	SLAGSSGPGASSGTSGDHGELVVR	98.7%	27.8	25	27.8	0	1	0	2185.05	60	83
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	26	0.02%	29.1%	AKDPFAHLPK	99.2%	35.6	25	30.1	1	0	0	1123.63	276	285
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	26	0.02%	29.1%	ALIAAQYSGAQVR	99.7%	100	25	100	3	0	0	1347.74	18	30
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	26	0.02%	29.1%	EYFSWEGAFQHVGK	99.7%	65.8	25	59.6	2	2	0	1684.78	415	428

Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	26	0.02%	29.1%	FAETQPK	98.3%	32.2	25	16.7	1	0	0	820.42	221	227
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	26	0.02%	29.1%	ILGLLDAYLK	99.7%	68.2	25	59.1	3	0	0	1118.68	138	147
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	26	0.02%	29.1%	KLDPGSEETQTLVR	99.7%	80.1	25	74.1	2	2	0	1572.82	401	414
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	26	0.02%	29.1%	MAQFDAK	97.3%	30.4	25	23.9	1	0	0	810.38	213	219
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	26	0.02%	29.1%	QVLEPSFR	97.1%	30	25	10.9	1	0	0	975.53	174	181
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	26	0.02%	29.1%	STFVLDEFKR	99.7%	50.1	25	43.2	2	0	0	1241.65	286	295
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	26	0.02%	29.1%	TFLVGER	99.7%	44.5	25	33.7	2	0	0	821.45	150	156
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	26	0.02%	29.1%	VLSAPPHFHFGQTNR	99.7%	41.6	25	40.1	0	2	0	1707.87	31	45
Elongation factor 1-gamma	EEF1G	EF1G_HUMAN	50.1	100.0%	12	14	26	0.02%	29.1%	WFLTCINQPQFR	99.7%	63.4	25	45.6	2	0	0	1609.79	190	201
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	ALLELQLEPEELYQTFQR	99.7%	69.4	25	69.4	1	0	0	2220.15	163	180
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	ARPFPDGLAEDIDKGEVSAR	99.7%	59.9	25	59.9	0	1	0	2143.08	606	625
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	AYLPVNESFGFTADLR	99.7%	102	25	102	2	0	0	1799.90	786	801
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	CLYASVLTAQPR	99.7%	73.2	25	69.9	2	0	0	1378.71	728	739
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	DSVVAGFQWATK	99.7%	50.2	25	42.6	1	0	0	1308.66	677	688
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	EGALCEENMR	99.7%	68.7	25	53.5	2	0	0	1208.50	689	698
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	EGIPALDNFLDKL	99.7%	54.7	25	51.6	3	0	0	1444.77	846	858
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	ETVSEESNVLCLSK	99.7%	90.4	25	80.8	2	0	0	1594.76	581	594
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	FSVSPVVR	95.6%	28.4	25	27.6	1	0	0	890.51	499	506
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	GEGQLGPAER	99.7%	42.2	25	35.3	2	0	0	1013.50	240	249
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	GGGQIIPTAR	99.7%	40.1	25	34	4	0	0	969.55	717	726
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	GHVFEESQVAGTPMFVVK	99.7%	36	25	32.6	0	1	0	1961.98	768	785
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	GPLMMYISK	99.7%	40.5	25	38.1	2	0	0	1039.53	392	400
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	GVQYLNEIK	99.7%	40.3	25	34	1	0	0	1063.58	668	676
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	IMGPNYTPGK	99.7%	50.7	25	45.9	2	0	0	1077.54	429	438
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	IMGPNYTPGKK	96.2%	29	25	24.6	1	0	0	1205.63	429	439
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	KEDLYLKPIQR	99.7%	45	25	45	0	2	0	1402.81	439	449
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	KIWCFGPDGTGPNILTDITK	95.6%	23.4	25	23.4	0	1	0	2233.13	648	667
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	NMSVIAHVDHGK	99.0%	34.5	25	28.9	1	0	0	1323.65	21	32
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	QFAEMYVAK	99.7%	46.6	25	43.7	2	0	0	1086.53	227	235
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	STLTDSLVCK	99.7%	63.2	25	57.9	2	0	0	1123.57	33	42
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	TFCQLILDPIFK	99.7%	65.8	25	64.8	4	0	0	1494.80	288	299
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	TGTITTFEHAHNMR	98.9%	28.6	25	26.7	0	1	0	1615.76	482	495
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	VFDAIMNFK	99.7%	58.1	25	54.7	2	0	0	1084.55	300	308
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	VFSGLVSTGLK	99.7%	90.4	25	76.4	4	0	0	1107.64	416	426
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	VNFTVDQIR	99.7%	84	25	63.7	5	0	0	1091.58	2	10
Elongation factor 2	EEF2	EF2_HUMAN	95.3	100.0%	26	26	50	0.05%	36.7%	YEWDVAEAR	99.7%	67.4	25	60.8	2	0	0	1138.52	639	647
Elongation factor Ts, mitochondrial	TSFM	EFTS_HUMAN	35.4	100.0%	3	4	6	0.01%	11.7%	GFLNSSELSGLPAGPDR	99.7%	68.4	25	59.4	2	0	0	1716.86	162	178
Elongation factor Ts, mitochondrial	TSFM	EFTS_HUMAN	35.4	100.0%	3	4	6	0.01%	11.7%	LGENMILK	99.7%	49.7	25	26	2	0	0	933.51	193	200
Elongation factor Ts, mitochondrial	TSFM	EFTS_HUMAN	35.4	100.0%	3	4	6	0.01%	11.7%	YGALVICETSEQK	99.7%	81.3	25	74.6	2	0	0	1497.73	234	246
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	34	90	0.08%	66.6%	ADAVQDSEMVELVELEIR	99.7%	97.3	25	96.2	3	1	0	2062.00	183	200
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	34	90	0.08%	66.6%	AEAGDNLGALVR	99.7%	90	25	72.8	5	0	0	1185.62	316	327
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	34	90	0.08%	66.6%	DKPHVNVGTIGHVDHGK	99.7%	55.4	25	54.9	0	2	0	1809.94	54	70
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	34	90	0.08%	66.6%	DLEKPFLLPVEAVYSVPGR	99.7%	70.6	25	70.6	5	3	0	2129.16	253	271
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	34	90	0.08%	66.6%	EHLLLAR	96.7%	29.5	25	23.9	1	0	0	851.51	163	169
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	34	90	0.08%	66.6%	ELAMPGEDLK	99.1%	34.8	25	31.1	3	0	0	1102.55	396	405
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	34	90	0.08%	66.6%	ELLTEFGYK	99.7%	47.1	25	42.7	2	0	0	1099.57	201	209
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	34	90	0.08%	66.6%	GDECELLGHSK	99.6%	38.7	25	38.3	1	0	0	1244.56	287	297
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	34	90	0.08%	66.6%	GEETPVIVGSALCALEGR	99.7%	43.5	25	43.5	1	0	0	1857.94	210	227
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	34	90	0.08%	66.6%	GITINAAHVEYSTAAR	99.7%	89.4	25	80.6	8	4	0	1673.86	105	120
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	34	90	0.08%	66.6%	GLVMVKPGSIKPHQK	99.7%	35.5	25	35.5	0	3	0	1618.95	337	351
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	34	90	0.08%	66.6%	GTVVTGTLER	99.7%	65.4	25	45.5	4	0	0	1032.57	272	281

Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	34	90	0.08%	66.6%	HYAHTDCPGHADYVK	99.7%	41.8	25	41.8	0	2	0	1770.77	121	135
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	34	90	0.08%	66.6%	IILPPEKELAMPGEDLK	99.7%	38.5	25	36.1	0	2	0	1909.04	389	405
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	34	90	0.08%	66.6%	KGDECELLGHSK	99.7%	64.1	25	55.9	2	2	0	1372.65	286	297
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	34	90	0.08%	66.6%	LLDAVDTYIPVPAR	99.7%	99.2	25	92.8	11	0	0	1542.85	239	252
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	34	90	0.08%	66.6%	NMITGTAPLDGCILVVAANDGPMPQTR	99.7%	37.6	25	34.6	0	1	0	2844.37	136	162
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	34	90	0.08%	66.6%	QIGVEHVVVYVNK	99.7%	62.4	25	52.1	2	0	0	1483.83	170	182
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	34	90	0.08%	66.6%	TIGTGLVTNTLAMTEEEK	99.7%	115	25	115	7	0	0	1907.96	430	447
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	34	90	0.08%	66.6%	TIGTGLVTNTLAMTEEEKNIK	94.9%	22.9	25	22.9	0	1	0	2263.19	430	450
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	34	90	0.08%	66.6%	TTLTAAITK	99.7%	56.2	25	43	2	0	0	919.55	71	79
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	34	90	0.08%	66.6%	TVVTGIEMFHK	99.7%	52.8	25	36.8	4	2	0	1261.66	301	311
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	34	90	0.08%	66.6%	VEAQVYILSK	99.7%	80	25	73	4	0	0	1149.65	352	361
Elongation factor Tu, mitochondrial	TUFM	EFTU_HUMAN	49.5	100.0%	24	34	90	0.08%	66.6%	YEEIDNAPEER	99.7%	66.3	25	61	2	0	0	1364.60	92	102
Elongator complex protein 3	ELP3	ELP3_HUMAN	62.3	100.0%	2	2	4	0.00%	4.9%	LEIGVQSVYEDVAR	99.7%	76.8	25	76.8	2	0	0	1577.82	243	256
Elongator complex protein 3	ELP3	ELP3_HUMAN	62.3	100.0%	2	2	4	0.00%	4.9%	SYSPSDLVELVAR	99.7%	78.1	25	68.9	2	0	0	1435.74	339	351
Emerin	EMD	EMD_HUMAN	29.0	100.0%	8	9	13	0.01%	41.3%	APGAGLGQDR	98.4%	32.4	25	24.9	1	0	0	941.48	212	221
Emerin	EMD	EMD_HUMAN	29.0	100.0%	8	9	13	0.01%	41.3%	DSAYQSITHYRPVSASR	99.5%	32	25	32	0	1	0	1937.95	158	174
Emerin	EMD	EMD_HUMAN	29.0	100.0%	8	9	13	0.01%	41.3%	GDADMYDLPK	99.7%	50.6	25	49.1	1	0	0	1140.49	69	78
Emerin	EMD	EMD_HUMAN	29.0	100.0%	8	9	13	0.01%	41.3%	GYNDDYYEESYFTTR	99.7%	69.3	25	69.3	2	0	0	1922.77	89	103
Emerin	EMD	EMD_HUMAN	29.0	100.0%	8	9	13	0.01%	41.3%	KEDALLYQSK	99.7%	60.6	25	48.1	2	0	0	1194.64	79	88
Emerin	EMD	EMD_HUMAN	29.0	100.0%	8	9	13	0.01%	41.3%	KIFEYETQR	99.7%	63.8	25	54.9	1	0	0	1213.62	37	45
Emerin	EMD	EMD_HUMAN	29.0	100.0%	8	9	13	0.01%	41.3%	LSPPSSSAASSYSFSDLNSTR	99.7%	88.6	25	87.1	2	0	0	2161.00	48	68
Emerin	EMD	EMD_HUMAN	29.0	100.0%	8	9	13	0.01%	41.3%	YNIPHGPVVGSTR	99.7%	34	25	29.9	1	2	0	1396.73	19	31
Endonuclease III-like protein 1	NTHL1	NTH_HUMAN	34.4	100.0%	2	2	3	0.00%	8.7%	DQVTAGAMQR	95.6%	28.5	25	24	1	0	0	1092.51	144	153
Endonuclease III-like protein 1	NTHL1	NTH_HUMAN	34.4	100.0%	2	2	3	0.00%	8.7%	GLTVDSILQTDDATLGK	99.7%	92.6	25	92.6	2	0	0	1746.91	158	174
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	5	5	8	0.01%	9.0%	DISTNYYASQK	99.7%	53.1	25	53.1	3	0	0	1289.60	672	682
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	5	5	8	0.01%	9.0%	ELISNASDALDK	99.7%	76.4	25	64.3	8	0	0	1275.64	103	114
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	5	5	8	0.01%	9.0%	ELISNASDALDKIR	99.7%	87.1	25	74.5	7	2	0	1544.83	103	116
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	5	5	8	0.01%	9.0%	FAFQAEVNR	99.7%	45	25	31.9	2	0	0	1081.54	76	84
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	5	5	8	0.01%	9.0%	GVVDSDDLPLNVSR	99.7%	60.3	25	58.3	1	0	0	1485.75	435	448
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	5	5	8	0.01%	9.0%	SGTSEFLNK	96.6%	29.5	25	18.2	1	0	0	982.48	169	177
Endoplasmin	HSP90B1	ENPL_HUMAN	92.5	100.0%	5	5	8	0.01%	9.0%	YSQFINFPIYVWSSK	99.7%	60.6	25	60.6	1	0	0	1878.94	271	285
Enhancer of mRNA-decapping protein 3	EDC3	EDC3_HUMAN	56.1	100.0%	5	6	9	0.01%	11.4%	AAVAWANQNR	99.3%	36.1	25	19.6	2	0	0	1100.56	427	436
Enhancer of mRNA-decapping protein 3	EDC3	EDC3_HUMAN	56.1	100.0%	5	6	9	0.01%	11.4%	AAVFEEIDTYER	99.7%	74.7	25	65.4	1	0	0	1442.68	216	227
Enhancer of mRNA-decapping protein 3	EDC3	EDC3_HUMAN	56.1	100.0%	5	6	9	0.01%	11.4%	AGDITELK	99.7%	42.7	25	13	1	0	0	846.46	56	63
Enhancer of mRNA-decapping protein 3	EDC3	EDC3_HUMAN	56.1	100.0%	5	6	9	0.01%	11.4%	KPASSSSAPQNIPK	99.7%	79.1	25	74.7	2	0	0	1411.75	106	119
Enhancer of mRNA-decapping protein 3	EDC3	EDC3_HUMAN	56.1	100.0%	5	6	9	0.01%	11.4%	MLESITNELSLFSK	99.7%	83.8	25	83.8	3	0	0	1627.82	374	387
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	5	7	13	0.01%	45.2%	ADTQTYQPYNK	99.4%	36.5	25	34.3	2	0	0	1328.61	74	84
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	5	7	13	0.01%	45.2%	ADTQTYQPYNKDWIK	99.2%	35.3	25	33.7	2	0	0	1870.90	74	88
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	5	7	13	0.01%	45.2%	IYVLLRR	98.1%	31.8	25	14.9	2	0	0	932.60	91	97
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	5	7	13	0.01%	45.2%	MYEEHLKR	99.0%	34.4	25	28.4	3	0	0	1121.54	35	42
Enhancer of rudimentary homolog	ERH	ERH_HUMAN	12.3	100.0%	5	7	13	0.01%	45.2%	TYADYESVNECMEGVCK	99.7%	101	25	101	4	0	0	2070.81	18	34
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	5	7	16	0.02%	22.1%	AFAAGADIK	99.7%	47.5	25	31.4	2	0	0	863.46	93	101
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	5	7	16	0.02%	22.1%	AQFAQPEILIGTIPGAGGTQR	99.7%	99.7	25	96.7	2	1	0	2125.14	158	178
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	5	7	16	0.02%	22.1%	EGMTAFVEK	99.3%	35.9	25	25.3	2	0	0	1011.48	274	282
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	5	7	16	0.02%	22.1%	NNTVGLIQLNRPK	99.7%	95.9	25	95.9	2	0	0	1466.84	44	56
Enoyl-CoA hydratase, mitochondrial	ECHS1	ECHM_HUMAN	31.4	100.0%	5	7	16	0.02%	22.1%	SLAMEMVLTGDR	99.7%	78.3	25	29.5	7	0	0	1338.64	186	197
ER lumen protein retaining receptor 1	KDELR1	ERD21_HUMAN	24.5	100.0%	3	3	5	0.00%	19.8%	ATYDGNHDTFR	99.7%	47.8	25	47.3	2	0	0	1296.56	84	94
ER lumen protein retaining receptor 1	KDELR1	ERD21_HUMAN	24.5	100.0%	3	3	5	0.00%	19.8%	SQVLFAVVFTAR	99.7%	90	25	90	2	0	0	1337.76	36	47
ER lumen protein retaining receptor 1	KDELR1	ERD21_HUMAN	24.5	100.0%	3	3	5	0.00%	19.8%	TGEAETITSHYLFALGVYR	99.2%	29.6	25	29.5	0	1	0	2128.07	141	159
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	8	8	12	0.01%	9.6%	ADGLLGMFLK	99.7%	46.2	25	34.4	1	0	0	1064.58	477	486
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	8	8	12	0.01%	9.6%	FASLEFSPGSK	99.7%	51.8	25	43.2	1	0	0	1169.58	42	52

ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	8	8	12	0.01%	9.6%	FNVEDGEIVQQVR	99.7%	88.2	25	78.5	1	0	0	1532.77	202	214
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	8	8	12	0.01%	9.6%	LFGIESSSGTILWK	99.7%	79.8	25	74.7	1	0	0	1537.83	545	558
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	8	8	12	0.01%	9.6%	NVIAALNSR	99.6%	38.6	25	37.3	1	0	0	957.55	61	69
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	8	8	12	0.01%	9.6%	RPEIPTEQSR	99.6%	38.2	25	27.9	1	0	0	1212.63	882	891
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	8	8	12	0.01%	9.6%	SLQTLALETEWELR	99.7%	57.7	25	51.2	2	0	0	1688.89	244	257
ER membrane protein complex subunit 1	EMC1	EMC1_HUMAN	111.8	100.0%	8	8	12	0.01%	9.6%	TFIGIFLIDGVTGR	99.7%	74.7	25	67.2	4	0	0	1508.85	755	768
ER membrane protein complex subunit 3	EMC3	EMC3_HUMAN	30.0	100.0%	2	2	5	0.00%	11.1%	AGPELLLDSNIR	99.7%	51.6	25	43.1	1	0	0	1297.71	2	13
ER membrane protein complex subunit 3	EMC3	EMC3_HUMAN	30.0	100.0%	2	2	5	0.00%	11.1%	SIYSLILGQDNAADQSR	99.7%	104	25	102	4	0	0	1850.92	181	197
ER membrane protein complex subunit 4	EMC4	EMC4_HUMAN	20.1	100.0%	4	4	10	0.01%	27.9%	CWDIALGPLK	99.6%	39.2	25	28.6	2	0	0	1172.61	69	78
ER membrane protein complex subunit 4	EMC4	EMC4_HUMAN	20.1	100.0%	4	4	10	0.01%	27.9%	GSGQGDSLYPVGYLDK	99.7%	61.3	25	58.9	4	0	0	1655.79	35	50
ER membrane protein complex subunit 4	EMC4	EMC4_HUMAN	20.1	100.0%	4	4	10	0.01%	27.9%	QVPDTSVQETDR	98.0%	31.6	25	30.6	2	0	0	1374.65	51	62
ER membrane protein complex subunit 4	EMC4	EMC4_HUMAN	20.1	100.0%	4	4	10	0.01%	27.9%	WAIELSGPGGGSR	99.7%	66.1	25	55.6	2	0	0	1286.65	17	29
ER membrane protein complex subunit 7	EMC7	EMC7_HUMAN	26.5	99.8%	2	2	2	0.00%	9.5%	SSGPPSYFIK	99.7%	39.8	25	30.6	1	0	0	1082.55	142	151
ER membrane protein complex subunit 7	EMC7	EMC7_HUMAN	26.5	99.8%	2	2	2	0.00%	9.5%	VLVDGEEHVGFLK	99.7%	59.1	25	55.5	1	0	0	1441.77	67	79
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	3	4	10	0.01%	21.1%	ADAEYYAAHK	99.7%	44	25	44	3	0	0	1138.52	258	267
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	3	4	10	0.01%	21.1%	DLNLMAPGLTIQAVR	99.7%	57.6	25	47.6	5	0	0	1627.88	155	169
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	3	4	10	0.01%	21.1%	EALEPSGENVIQNK	99.7%	88.4	25	86.4	2	0	0	1527.77	329	342
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	3	4	10	0.01%	21.1%	ISEIEDAAFLAR	99.7%	93.9	25	80.5	4	0	0	1334.70	242	253
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	3	4	10	0.01%	21.1%	SVQTTLQTDEVK	99.7%	92	25	73.7	6	0	0	1348.70	61	72
Erlin-1	ERLIN1	ERLN1_HUMAN	38.9	100.0%	3	4	10	0.01%	21.1%	VVEKEAETER	99.7%	43.3	25	42.3	2	0	0	1189.61	202	211
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	13	30	0.03%	41.3%	DIPNMFMDSAGSVSK	99.7%	92.2	25	86.5	4	0	0	1598.72	300	314
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	13	30	0.03%	41.3%	IEEGHIGVYYR	99.7%	51	25	39.6	2	0	0	1335.67	26	36
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	13	30	0.03%	41.3%	IEVVNFLVPNAVYDIVK	99.6%	38.4	25	36.4	1	0	0	1932.08	89	105
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	13	30	0.03%	41.3%	ISEIEDAAFLAR	99.7%	93.9	25	80.5	4	0	0	1334.70	242	253
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	13	30	0.03%	41.3%	KISEIEDAAFLAR	99.7%	80.7	25	72.8	2	0	0	1462.79	241	253
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	13	30	0.03%	41.3%	LALQQDLTSMAPGLVIQAVR	98.7%	33.3	25	33.3	1	0	0	2124.18	150	169
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	13	30	0.03%	41.3%	LTPEYLQLMK	99.6%	38.4	25	35.9	1	0	0	1251.67	276	285
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	13	30	0.03%	41.3%	NYELMESEK	97.4%	30.5	25	25.1	1	0	0	1142.50	182	190
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	13	30	0.03%	41.3%	SVQTTLQTDEVK	99.7%	92	25	73.7	6	0	0	1348.70	61	72
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	13	30	0.03%	41.3%	VAQVAEITYGQK	99.7%	96	25	92.5	4	0	0	1306.70	221	232
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	13	30	0.03%	41.3%	VTKPNIPEAIR	99.7%	39.6	25	39.6	2	0	0	1237.73	170	180
Erlin-2	ERLIN2	ERLN2_HUMAN	37.8	100.0%	12	13	30	0.03%	41.3%	VVEKEAETER	99.7%	43.3	25	42.3	2	0	0	1189.61	202	211
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	13	29	0.03%	33.0%	GVFVQSVLPYFVATK	99.7%	50.2	25	50.2	3	0	0	1654.92	224	238
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	13	29	0.03%	33.0%	IRKPTLDKPSPETFVK	99.5%	32.1	25	32.1	0	2	0	1856.06	242	257
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	13	29	0.03%	33.0%	ISYSLFTALR	99.7%	95.6	25	82.1	2	0	0	1170.65	26	35
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	13	29	0.03%	33.0%	KPTLDKPSPETFVK	99.7%	70.2	25	70	1	2	0	1586.88	244	257
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	13	29	0.03%	33.0%	MININILSVCK	99.7%	83.2	25	75.2	4	0	0	1304.71	157	167
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	13	29	0.03%	33.0%	MTQLVLPGMVER	99.7%	70	25	57.1	7	0	0	1389.72	168	179
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	13	29	0.03%	33.0%	SYAEELAK	98.4%	32.5	25	18	2	0	0	910.45	65	72
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	13	29	0.03%	33.0%	TFVDFFSQCLHEEYR	99.7%	68.8	25	68.8	2	2	0	1977.88	207	221
Estradiol 17-beta-dehydrogenase 12	HSD17B12	DHB12_HUMAN	34.3	100.0%	9	13	29	0.03%	33.0%	TIAVDFASEDIYDKIK	99.7%	85.7	25	85.7	2	0	0	1827.94	104	119
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	7	7	11	0.01%	30.0%	DLLGTVWGGPANLEAIAK	99.7%	47.6	25	47.6	2	0	0	1824.99	284	301
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	7	7	11	0.01%	30.0%	ELYLEEALQNER	99.7%	56.3	25	48.7	1	0	0	1506.74	272	283
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	7	7	11	0.01%	30.0%	LVEIIGSR	99.7%	54.3	25	51.3	2	0	0	886.54	199	206
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	7	7	11	0.01%	30.0%	NALNIGMVEEVLQSSDETK	99.7%	78.3	25	78.3	2	0	0	2077.01	222	240
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	7	7	11	0.01%	30.0%	NTFSSGSDLNAVK	99.7%	59.7	25	55	1	0	0	1339.65	109	121
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	7	7	11	0.01%	30.0%	QFIQGPPEVIR	99.7%	48.6	25	20.6	2	0	0	1283.71	251	261
Ethylmalonyl-CoA decarboxylase	ECHDC1	ECHD1_HUMAN	33.7	100.0%	7	7	11	0.01%	30.0%	VIELENWTEGK	99.6%	38.6	25	38.6	1	0	0	1317.67	90	100
Etoposide-induced protein 2.4 homolog	EI24	EI24_HUMAN	39.0	99.8%	2	2	2	0.00%	5.9%	TFLQDLAR	99.7%	53.6	25	41.7	1	0	0	963.53	7	14
Etoposide-induced protein 2.4 homolog	EI24	EI24_HUMAN	39.0	99.8%	2	2	2	0.00%	5.9%	VFIPVLQSVTAR	99.7%	43.7	25	41	1	0	0	1329.79	92	103
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	14	20	38	0.04%	48.5%	ATQALVLAPTR	99.5%	38.1	25	38.1	2	0	0	1140.67	100	110

Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	14	20	38	0.04%	48.5%	DFTVSAMHGDMDQKER	99.7%	43.1	25	43.1	0	3	0	1898.80	296	311
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	14	20	38	0.04%	48.5%	GFKDQIYDIFQK	99.7%	61.4	25	55.8	2	0	0	1501.77	191	202
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	14	20	38	0.04%	48.5%	GIDVQQVSLVINYDLPTNR	99.7%	44.7	25	42.5	1	0	0	2144.13	335	353
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	14	20	38	0.04%	48.5%	GIYAYGFEKPSAIQQR	99.7%	76.8	25	76.3	2	0	0	1827.94	46	61
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	14	20	38	0.04%	48.5%	GVAINMVTEEDKR	99.7%	55.2	25	55.2	2	0	0	1461.74	370	382
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	14	20	38	0.04%	48.5%	KEELTLEGIR	99.7%	57.2	25	43.8	2	0	0	1187.66	238	247
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	14	20	38	0.04%	48.5%	KVDWLTEK	96.0%	28.8	25	14.2	1	0	0	1018.56	284	291
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	14	20	38	0.04%	48.5%	LNSNTQVVLLSATMPSDVLEVTK	99.7%	60.8	25	60.8	2	0	0	2475.30	203	225
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	14	20	38	0.04%	48.5%	LQMEAPHIIVGTPGR	99.7%	64.2	25	64.2	4	4	0	1634.87	147	161
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	14	20	38	0.04%	48.5%	MFVLDEADEMLSR	99.7%	115	25	109	8	0	0	1555.71	178	190
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	14	20	38	0.04%	48.5%	VFDMLNRR	96.7%	29.6	25	16.1	1	0	0	1050.55	162	169
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	14	20	38	0.04%	48.5%	VLITTDLLAR	99.7%	70.1	25	63.8	2	0	0	1114.68	325	334
Eukaryotic initiation factor 4A-I	EIF4A1	IF4A1_HUMAN	46.2	100.0%	14	20	38	0.04%	48.5%	VVMALGDYMGASCHACIGGTNVR	99.7%	35.3	25	35.3	0	2	0	2471.09	119	141
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	13	26	0.02%	32.4%	ELAVQIQK	99.7%	48.8	25	34.7	2	0	0	928.55	117	124
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	13	26	0.02%	32.4%	ETQALILAPTR	99.7%	82.9	25	66.5	2	0	0	1212.69	106	116
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	13	26	0.02%	32.4%	GFKEQIYDVYR	99.7%	61.4	25	61.4	2	0	0	1417.71	196	206
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	13	26	0.02%	32.4%	GIYAYGFEKPSAIQQR	99.7%	76.8	25	76.3	2	0	0	1827.94	52	67
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	13	26	0.02%	32.4%	GRDVIAQSQSGTGK	99.7%	98.1	25	91.6	2	2	0	1403.72	75	88
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	13	26	0.02%	32.4%	KGVAINFVK	99.7%	59.3	25	51.8	2	0	0	975.60	374	382
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	13	26	0.02%	32.4%	KLDYGQHVVAGTPGR	99.7%	39.3	25	33.3	0	2	0	1597.84	152	166
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	13	26	0.02%	32.4%	KVDWLTEK	96.0%	28.8	25	14.2	1	0	0	1018.56	289	296
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	13	26	0.02%	32.4%	LDYGQHVVAGTPGR	99.7%	49.5	25	46.5	1	2	0	1469.75	153	166
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	13	26	0.02%	32.4%	MLVLDEADEMLNK	99.7%	77.8	25	77.8	3	0	0	1536.73	183	195
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	13	26	0.02%	32.4%	QFFVAVER	99.7%	42.8	25	26	2	0	0	995.53	253	260
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	13	26	0.02%	32.4%	RDELTLEGIK	99.7%	40.8	25	27.1	2	0	0	1173.65	243	252
Eukaryotic initiation factor 4A-III	EIF4A3	IF4A3_HUMAN	46.9	100.0%	11	13	26	0.02%	32.4%	VLISTDVWAR	99.7%	54.2	25	48.5	2	0	0	1159.65	330	339
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	5	6	14	0.01%	25.9%	AIVQQWLEYR	99.7%	54.6	25	47.7	4	0	0	1305.70	69	78
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	5	6	14	0.01%	25.9%	EYLLGSTAEEK	99.7%	62.9	25	58.4	4	0	0	1239.61	58	68
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	5	6	14	0.01%	25.9%	FIVDLTVQEKEK	98.4%	32.5	25	25.5	1	0	0	1448.80	127	138
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	5	6	14	0.01%	25.9%	NDIHTLLK	99.0%	34.7	25	21.9	2	0	0	953.54	89	96
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	MCA3_HUMAN	19.8	100.0%	5	6	14	0.01%	25.9%	QANKEYLLGSTAEEK	99.7%	74.6	25	71.6	2	1	0	1680.84	54	68
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	5	6	15	0.01%	18.4%	AGLNCSTENMPIK	99.7%	39.5	25	38.7	2	0	0	1450.67	214	226
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	5	6	15	0.01%	18.4%	GVFNVQMEPK	99.7%	41.4	25	25.8	3	0	0	1164.57	267	276
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	5	6	15	0.01%	18.4%	NECVVVIR	99.7%	41.2	25	32.7	3	0	0	988.52	68	75
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	5	6	15	0.01%	18.4%	TEGLSVLSQAMAVIK	99.7%	68.8	25	63.5	1	0	0	1546.85	245	259
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	IF2A_HUMAN	36.1	100.0%	5	6	15	0.01%	18.4%	VVTDTDETELAR	99.7%	87.9	25	77.2	6	0	0	1348.66	277	288
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	IF2G_HUMAN	51.1	100.0%	4	5	7	0.01%	10.6%	GVTIKPTVDDD	99.7%	68.3	25	68.2	1	0	0	1159.58	462	472
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	IF2G_HUMAN	51.1	100.0%	4	5	7	0.01%	10.6%	IVLTNPVCTEVGEK	99.7%	49.2	25	49.2	2	0	0	1558.81	427	440
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	IF2G_HUMAN	51.1	100.0%	4	5	7	0.01%	10.6%	LTPLSHEVISR	98.8%	33.6	25	33.1	2	0	0	1251.71	28	38
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	IF2G_HUMAN	51.1	100.0%	4	5	7	0.01%	10.6%	VGQEIEVRPGIVSK	99.7%	42	25	38.9	1	1	0	1510.86	290	303
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	ANEFLEVGK	99.7%	44.3	25	34.5	2	0	0	1006.52	15	23
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	ANEFLEVGKK	99.1%	34.9	25	15.5	3	0	0	1134.62	15	24
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	AVEDIHGLFSLSK	99.7%	79.1	25	77.9	2	0	0	1415.75	252	264
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	EDAPIGPHLQSMPSEQIR	99.7%	51.8	25	51.8	0	5	0	2004.98	503	520
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	EEELREYQER	99.7%	40.1	25	26.7	2	0	0	1380.64	838	847
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	ELEIEERER	96.4%	29.2	25	1.42	1	0	0	1202.60	862	870
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	EQPEKEPELQQYVPQLQNNTILR	97.7%	25.7	25	19	0	1	0	2794.44	416	438
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	FCLQYTR	99.7%	42	25	37.1	5	0	0	987.47	184	190
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	FLWESYR	99.7%	40	25	26.6	2	0	0	1000.49	152	158
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	FNVLQYVVPEVK	99.7%	75.6	25	66.4	8	0	0	1434.80	377	388
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	GLDDDRGPR	95.5%	28.4	25	25.4	1	0	0	1000.48	1072	1080

Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	GLDEDRGSWR	96.5%	29.3	25	20.2	2	0	0	1190.56	1021	1030
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	IGLINDMVR	99.7%	60.9	25	47.2	7	0	0	1046.57	368	376
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	ILQEHEQIK	99.7%	49.1	25	43.8	4	0	0	1137.63	624	632
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	ILQEHEQIKK	99.2%	30.1	25	18.5	0	1	0	1265.72	624	633
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	ITTMQLER	99.7%	62.7	25	43.1	4	0	0	991.52	733	740
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	KGPEADSEWR	98.7%	33.4	25	26.4	2	0	0	1174.55	901	910
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	KIDYFER	99.7%	39.4	25	22.6	3	0	0	970.50	694	700
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	KLCDNLR	96.7%	29.5	25	16	1	0	0	918.48	196	202
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	KQPALDVLYDVMK	99.7%	40.2	25	40.2	2	0	0	1535.81	24	36
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	LATLLGLQAPPTR	99.7%	52.5	25	47.6	4	0	0	1350.81	355	367
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	LEEIPLIK	96.8%	29.6	25	15.9	2	0	0	954.59	704	711
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	LESLNIQR	99.7%	52.7	25	19.1	4	0	0	972.55	582	589
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	LGDSSLSR	99.7%	74.3	25	58.8	2	0	0	834.43	878	885
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	LKQFEER	96.9%	29.8	25	7.43	2	0	0	949.51	776	782
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	LLDMDGIIVEK	99.7%	82.6	25	68.4	8	0	0	1245.68	341	351
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	LLLTPWVK	99.7%	43.9	25	21.8	4	0	0	969.61	144	151
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	LLQQVSQIYQSIEFSR	99.7%	63.2	25	31.8	2	0	0	1939.03	439	454
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	LTSLVPFVDAFQLER	99.7%	95.2	25	95.2	6	0	0	1734.94	455	469
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	LYHDIAQQAFK	99.7%	62.5	25	49.4	3	0	0	1333.69	173	183
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	MHLSQIQR	99.7%	44.3	25	37.7	5	0	0	1028.53	203	210
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	MLEDRDLFVMR	98.4%	27	25	23.6	0	1	0	1440.70	753	763
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	NICQQVNIK	99.7%	47.1	25	26	4	0	0	1116.58	76	84
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	NLTQDEMQR	99.7%	43.1	25	41.8	5	0	0	1134.52	309	317
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	NMDDDRLSR	98.3%	32.3	25	22.4	1	0	0	1121.50	1142	1150
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	NQLTAMSSVLAK	99.7%	97.7	25	84.5	9	0	0	1262.68	521	532
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	PAYFQRPENALK	99.7%	48.9	25	36.5	1	0	0	1433.75	2	13
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	PAYFQRPENALKR	97.4%	25.3	25	16.4	0	1	0	1589.85	2	14
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	QCLDLLR	99.4%	36.8	25	3.94	2	0	0	917.49	159	165
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	QPALDVLYDVMK	99.7%	43.5	25	34.3	3	0	0	1391.72	25	36
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	RGPAEESSSWR	99.7%	46	25	46	2	0	0	1261.59	1250	1260
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	RLEEIPLIK	98.5%	32.7	25	27.8	1	0	0	1110.69	703	711
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	RLGDSSLSR	94.9%	27.9	25	9.01	1	0	0	990.53	877	885
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	RVPPPALSR	97.9%	31.4	25	28.2	2	0	0	992.60	1329	1337
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	SGNALFHASTLHR	99.7%	52.5	25	50.5	1	6	0	1410.72	286	298
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	SLEDVVR	99.3%	36	25	8.83	2	0	0	817.44	85	91
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	TLSFGSDLNYATR	99.7%	90.8	25	82	4	0	0	1444.71	490	502
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	VLLATLSIPITPER	99.7%	72.6	25	72.6	9	0	0	1522.92	322	335
Eukaryotic translation initiation factor 3 subunit A	EIF3A	EIF3A_HUMAN	166.6	100.0%	49	57	157	0.15%	32.6%	VSTVFWK	98.9%	34.1	25	23.5	2	0	0	866.48	279	285
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	34	81	0.08%	34.6%	AQAVSEDAGGNEGR	99.7%	99.7	25	99.7	6	0	0	1360.61	121	134
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	34	81	0.08%	34.6%	DQYSVIFESGDR	99.7%	107	25	106	2	0	0	1415.64	304	315
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	34	81	0.08%	34.6%	ETIIAFAWEPNGSK	99.7%	71.9	25	68.5	2	0	0	1562.79	563	576
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	34	81	0.08%	34.6%	FAVLHGEAPR	99.7%	57.7	25	49.9	2	0	0	1096.59	577	586
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	34	81	0.08%	34.6%	FSHQGVQLIDFSPCER	99.7%	76.8	25	76.8	2	2	0	1919.91	371	386
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	34	81	0.08%	34.6%	GIALWGGEK	99.7%	44.4	25	35.8	2	0	0	930.50	356	364
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	34	81	0.08%	34.6%	GTQGVVTNFEIFR	99.7%	74.9	25	74.9	6	0	0	1467.76	536	548
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	34	81	0.08%	34.6%	GTYLATFHQR	99.7%	70.3	25	61.9	5	0	0	1193.61	346	355
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	34	81	0.08%	34.6%	GYIFLEYASPAHAVDAVK	99.7%	82.5	25	82.5	3	2	0	1951.00	231	248
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	34	81	0.08%	34.6%	ISVSFYHVK	99.5%	37.2	25	28.8	2	0	0	1079.59	587	595
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	34	81	0.08%	34.6%	ITNDFYPEEDGK	99.7%	62.3	25	62.3	2	0	0	1427.63	217	228
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	34	81	0.08%	34.6%	ITNDFYPEEDGKTK	99.7%	58.1	25	58.1	2	2	0	1656.78	217	230
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	34	81	0.08%	34.6%	MAQELYMEQK	99.7%	87.4	25	68.9	5	0	0	1270.58	763	772

Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	34	81	0.08%	34.6%	MTLDTLSIYETPSMGLLDK	99.7%	68.8	25	63.7	2	0	0	2128.06	441	459
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	34	81	0.08%	34.6%	MTLDTLSIYETPSMGLLDKK	99.7%	39.5	25	39.5	0	3	0	2256.15	441	460
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	34	81	0.08%	34.6%	NADGYKLDK	96.4%	29.2	25	23.6	1	0	0	1023.51	249	257
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	34	81	0.08%	34.6%	NGDYLCVK	99.7%	54.3	25	39.9	1	0	0	968.45	522	529
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	34	81	0.08%	34.6%	NLFNVVDCK	99.7%	50.5	25	43.3	2	0	0	1108.55	508	516
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	34	81	0.08%	34.6%	QVPVDVVEMK	99.7%	46.9	25	41.7	3	0	0	1143.61	553	562
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	34	81	0.08%	34.6%	TMMEDFRK	99.7%	42.5	25	34.8	2	0	0	1057.48	752	759
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	34	81	0.08%	34.6%	TSIFWNDVKDPVSIEER	99.7%	97.8	25	96.6	2	4	0	2035.01	316	332
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	34	81	0.08%	34.6%	VDNAYWLWTFQGR	99.7%	75.6	25	69.5	2	0	0	1655.80	677	689
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	34	81	0.08%	34.6%	VNLFTDFDK	99.7%	47	25	41.2	2	0	0	1098.55	263	271
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	34	81	0.08%	34.6%	VTLMQLPTR	99.7%	73.5	25	57.4	6	0	0	1058.60	493	501
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	34	81	0.08%	34.6%	YVVTSVSWWSHK	99.7%	43.5	25	38.1	2	0	0	1478.74	665	676
Eukaryotic translation initiation factor 3 subunit B	EIF3B	EIF3B_HUMAN	92.5	100.0%	26	34	81	0.08%	34.6%	YWLEEAECR	99.7%	50.9	25	47.4	2	0	0	1255.54	295	303
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN,EIFCL_HUMAN	105.3	100.0%	10	10	18	0.02%	10.3%	DFESHITSYK	96.3%	29.1	25	23.5	2	0	0	1226.57	151	160
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN,EIFCL_HUMAN	105.3	100.0%	10	10	18	0.02%	10.3%	ELLGQGLLLR	99.7%	64.8	25	49.1	2	0	0	1111.68	644	653
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN,EIFCL_HUMAN	105.3	100.0%	10	10	18	0.02%	10.3%	FEELTNLIR	99.7%	62.7	25	38.8	2	0	0	1134.62	57	65
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN,EIFCL_HUMAN	105.3	100.0%	10	10	18	0.02%	10.3%	GCILTLVER	99.7%	55.5	25	40.8	2	0	0	1060.58	442	450
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN,EIFCL_HUMAN	105.3	100.0%	10	10	18	0.02%	10.3%	GTEITHAVVIK	99.7%	61.8	25	49.9	2	0	0	1167.67	321	331
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN,EIFCL_HUMAN	105.3	100.0%	10	10	18	0.02%	10.3%	KLNEILQAR	99.7%	51.3	25	30	1	0	0	1084.65	332	340
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN,EIFCL_HUMAN	105.3	100.0%	10	10	18	0.02%	10.3%	LGSLVENNER	99.7%	66.1	25	49.7	2	0	0	1130.58	863	872
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN,EIFCL_HUMAN	105.3	100.0%	10	10	18	0.02%	10.3%	LNEILQAR	99.7%	51.8	25	38.1	2	0	0	956.55	333	340
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN,EIFCL_HUMAN	105.3	100.0%	10	10	18	0.02%	10.3%	SIVDKEGVPR	99.7%	39.4	25	33.3	1	0	0	1099.61	95	104
Eukaryotic translation initiation factor 3 subunit C	EIF3C	EIF3C_HUMAN,EIFCL_HUMAN	105.3	100.0%	10	10	18	0.02%	10.3%	TEPTAQQNLALQLAEK	99.7%	108	25	107	2	0	0	1754.93	847	862
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	14	18	29	0.03%	34.7%	GAVIATELK	99.2%	35.3	25	15.6	2	0	0	901.54	418	426
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	14	18	29	0.03%	34.7%	GAVIATELKNNSYK	99.7%	77.4	25	55.8	2	0	0	1507.81	418	431
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	14	18	29	0.03%	34.7%	IFHTVTTTDDPVIR	99.7%	66.7	25	63.8	2	2	0	1614.85	223	236
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	14	18	29	0.03%	34.7%	LGDDIDLIVR	99.7%	87.8	25	69.4	4	0	0	1128.63	365	374
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	14	18	29	0.03%	34.7%	NLAMEATYINHNFSQQCLR	99.7%	47.7	25	47.7	0	2	0	2310.08	311	329
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	14	18	29	0.03%	34.7%	NMLQFNLQILPK	99.7%	54.8	25	46	1	0	0	1474.81	113	124
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	14	18	29	0.03%	34.7%	SVYSWDIVVQR	99.7%	54.1	25	53	1	0	0	1351.70	261	271
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	14	18	29	0.03%	34.7%	TLNEWDSR	98.1%	31.9	25	26.6	1	0	0	1020.47	395	402
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	14	18	29	0.03%	34.7%	TQGNVFATDAILATLMSCTR	99.7%	72.4	25	72.4	2	0	0	2170.06	241	260
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	14	18	29	0.03%	34.7%	VADWTGATYQDKR	99.7%	68.2	25	64.6	3	1	0	1510.73	42	54
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	14	18	29	0.03%	34.7%	WTCCALLAGSEYLK	99.7%	40.5	25	37.9	2	0	0	1671.79	435	448
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	14	18	29	0.03%	34.7%	YLEVSEPQDIECCGALEYYDK	99.7%	75	25	74.3	1	0	0	2581.11	184	204
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	14	18	29	0.03%	34.7%	YLILKDPNK	99.7%	43.9	25	36.7	1	0	0	1103.65	506	514
Eukaryotic translation initiation factor 3 subunit D	EIF3D	EIF3D_HUMAN	64.0	100.0%	14	18	29	0.03%	34.7%	YNFPNPNPFVEDDMDKNEIASVAYR	99.7%	54.9	25	54.9	0	2	0	2961.34	335	359
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	45	0.04%	49.0%	EIYNEKELLQGK	99.7%	60.5	25	44.9	2	0	0	1463.77	30	41
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	45	0.04%	49.0%	FQYECGNYSGAAEYLYFFR	99.7%	80.1	25	80.1	1	0	0	2385.03	137	155
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	45	0.04%	49.0%	IAHFLDR	99.7%	39.6	25	30.6	2	0	0	871.48	10	16
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	45	0.04%	49.0%	LDLLSDTNMVDFAMDVYK	99.7%	97.3	25	64.3	3	0	0	2105.98	42	59
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	45	0.04%	49.0%	LFIFETFCR	99.7%	67.7	25	58.3	2	0	0	1232.61	338	346
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	45	0.04%	49.0%	LGHVVMGNNAVSPYQQVIEK	99.7%	56.9	25	52.3	0	2	0	2199.12	388	407
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	45	0.04%	49.0%	LKETIDNNSVSSPLQSLQQR	99.7%	49	25	49	0	2	0	2257.18	192	211
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	45	0.04%	49.0%	LNMTPEEAER	99.6%	38.4	25	36.6	1	0	0	1189.55	360	369
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	45	0.04%	49.0%	MFEDPETTR	99.7%	45.3	25	29	4	0	0	1141.48	94	102
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	45	0.04%	49.0%	MLFDYLADK	99.7%	51	25	37.1	4	0	0	1115.54	112	120
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	45	0.04%	49.0%	NLYSDDIPHALR	99.7%	66.8	25	60.3	2	2	0	1413.71	60	71
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	45	0.04%	49.0%	QEYLDTLYR	99.7%	40	25	34.2	2	0	0	1200.59	125	133
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	45	0.04%	49.0%	QLQAETEPIVK	99.7%	49.8	25	31.3	2	0	0	1255.69	83	93
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	45	0.04%	49.0%	RTTVVAQLK	99.2%	35.4	25	31.2	2	0	0	1015.63	74	82

Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	45	0.04%	49.0%	SEAPNWATQDSGFY	99.7%	53.5	25	53.5	2	0	0	1572.66	432	445
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	45	0.04%	49.0%	SQMLAMNIEK	99.7%	61.2	25	53.2	4	0	0	1164.58	415	424
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	45	0.04%	49.0%	TTVVAQLK	98.1%	31.7	25	16.6	1	0	0	859.52	75	82
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	45	0.04%	49.0%	WIVNLIR	99.7%	42.4	25	17.2	2	0	0	913.56	370	376
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	45	0.04%	49.0%	YLTTAVITNK	99.7%	63.1	25	52.4	2	0	0	1123.64	256	265
Eukaryotic translation initiation factor 3 subunit E	EIF3E	EIF3E_HUMAN	52.2	100.0%	20	25	45	0.04%	49.0%	YLTTAVITNKDVR	99.7%	62.3	25	55.9	1	0	0	1493.83	256	268
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	8	9	16	0.02%	26.3%	AYVSTLMGVPGR	99.7%	43.8	25	38.5	4	0	0	1250.66	215	226
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	8	9	16	0.02%	26.3%	FLMSLVNQVPK	99.7%	78.9	25	59.6	2	0	0	1275.71	307	317
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	8	9	16	0.02%	26.3%	IGVDLIMK	99.7%	41.6	25	40.2	1	0	0	904.52	247	254
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	8	9	16	0.02%	26.3%	LHPVILASIVDSYER	99.7%	44	25	44	0	2	0	1711.94	94	108
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	8	9	16	0.02%	26.3%	TMGVMFTPLTVK	99.7%	41.7	25	36.7	1	0	0	1324.70	227	238
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	8	9	16	0.02%	26.3%	VIGLSSDLQQVGGASAR	99.7%	129	25	124	2	0	0	1657.89	262	278
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	8	9	16	0.02%	26.3%	VIGTLLGTVDK	99.7%	63.4	25	52.5	2	0	0	1115.67	116	126
Eukaryotic translation initiation factor 3 subunit F	EIF3F	EIF3F_HUMAN	37.6	100.0%	8	9	16	0.02%	26.3%	YAYYDTER	99.7%	44.6	25	41.8	2	0	0	1080.46	239	246
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	7	7	13	0.01%	19.7%	EKLPGELEPVQATQNK	99.7%	34	25	32.1	0	2	0	1780.94	194	209
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	7	7	13	0.01%	19.7%	ELAEQLGLSTGEK	99.7%	57.6	25	56.7	2	0	0	1374.71	181	193
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	7	7	13	0.01%	19.7%	ELAEQLGLSTGEKEK	99.7%	55.2	25	48.3	1	0	0	1631.85	181	195
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	7	7	13	0.01%	19.7%	ETDLQELFRPFGSISR	99.7%	41.5	25	41.5	0	2	0	1894.97	252	267
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	7	7	13	0.01%	19.7%	GFAFISFHR	99.7%	44.8	25	36.2	2	0	0	1081.56	281	289
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	7	7	13	0.01%	19.7%	LPGELEPVQATQNK	99.7%	58.9	25	58.9	2	0	0	1523.81	196	209
Eukaryotic translation initiation factor 3 subunit G	EIF3G	EIF3G_HUMAN	35.6	100.0%	7	7	13	0.01%	19.7%	VTNLSEDTR	99.4%	37	25	24.6	2	0	0	1034.51	243	251
Eukaryotic translation initiation factor 3 subunit H	EIF3H	EIF3H_HUMAN	39.9	99.8%	2	3	4	0.00%	8.8%	EGTGSTATSSSSTAGAAGK	99.7%	54.2	25	48.9	2	0	0	1627.74	6	24
Eukaryotic translation initiation factor 3 subunit H	EIF3H	EIF3H_HUMAN	39.9	99.8%	2	3	4	0.00%	8.8%	LFMAQALQEYNN	99.1%	35.1	25	35.1	2	0	0	1441.68	341	352
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	11	14	28	0.03%	40.0%	DMTMFVTASK	99.7%	68.9	25	62	5	0	0	1130.52	199	208
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	11	14	28	0.03%	40.0%	DPIVNVWYSVNGER	99.7%	62.5	25	62.5	2	0	0	1647.81	31	44
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	11	14	28	0.03%	40.0%	EGDLLFTVAK	99.7%	59.3	25	51	2	0	0	1092.59	21	30
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	11	14	28	0.03%	40.0%	GHFGPINSVAFHPDGK	97.8%	26	25	26	0	1	0	1679.83	283	298
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	11	14	28	0.03%	40.0%	HVLTGSADNSCR	99.7%	70.7	25	66.2	2	0	0	1316.60	66	77
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	11	14	28	0.03%	40.0%	LFDSTTLEHQK	99.7%	48.7	25	35.3	2	2	0	1318.66	214	224
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	11	14	28	0.03%	40.0%	LWDCETGK	95.6%	28.5	25	28.5	1	0	0	1008.45	78	85
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	11	14	28	0.03%	40.0%	MKPILLQGHER	99.7%	49.5	25	49.5	0	4	0	1337.74	1	11
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	11	14	28	0.03%	40.0%	SGEVLVNVK	99.7%	70.6	25	55.3	2	0	0	944.54	177	185
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	11	14	28	0.03%	40.0%	SYSSGGEDGYVR	99.7%	41.7	25	40.9	3	0	0	1276.54	299	310
Eukaryotic translation initiation factor 3 subunit I	EIF3I	EIF3I_HUMAN	36.5	100.0%	11	14	28	0.03%	40.0%	TCGFDFGGNIIMFSTDK	99.7%	61.7	25	61.7	2	0	0	1909.85	98	114
Eukaryotic translation initiation factor 3 subunit K	EIF3K	EIF3K_HUMAN	25.1	100.0%	3	4	7	0.01%	16.5%	GIDRYNPENLATLER	99.7%	83.9	25	83.4	2	2	0	1760.89	17	31
Eukaryotic translation initiation factor 3 subunit K	EIF3K	EIF3K_HUMAN	25.1	100.0%	3	4	7	0.01%	16.5%	YNPENLATLER	99.7%	40	25	29.5	2	0	0	1319.66	21	31
Eukaryotic translation initiation factor 3 subunit K	EIF3K	EIF3K_HUMAN	25.1	100.0%	3	4	7	0.01%	16.5%	YVETQAKENAYDLEANLAVLK	99.1%	29.3	25	29.3	0	1	0	2382.22	32	52
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	53	0.05%	36.5%	EPFLQQLK	99.7%	60.4	25	35.8	2	0	0	1002.56	438	445
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	53	0.05%	36.5%	IDESIHLQLR	99.7%	64.4	25	54.4	2	2	0	1223.67	382	391
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	53	0.05%	36.5%	KSEEEIDFLR	99.7%	60.2	25	53.6	2	0	0	1265.64	207	216
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	53	0.05%	36.5%	LAGFLDLTEQEFR	99.7%	97.7	25	95.3	4	0	0	1538.79	475	487
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	53	0.05%	36.5%	LHSLLGDYYQAIK	99.7%	62.8	25	50.9	2	2	0	1520.81	280	292
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	53	0.05%	36.5%	LYTTMPVAK	99.7%	43	25	28.2	2	0	0	1039.55	466	474
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	53	0.05%	36.5%	MLGYFSLVGLLR	99.7%	68	25	59.3	3	0	0	1384.77	268	279
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	53	0.05%	36.5%	QLEVYTSGGDPESVAGEYGR	99.7%	123	25	123	2	0	0	2113.97	243	262
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	53	0.05%	36.5%	QYEQQTYQVIPEVIK	99.7%	82	25	82	2	0	0	1865.96	39	53
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	53	0.05%	36.5%	RYGDFFIR	99.5%	37.2	25	29.1	2	0	0	1073.55	538	545
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	53	0.05%	36.5%	SEEEIDFLR	99.7%	56.1	25	44.7	2	0	0	1137.54	208	216
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	53	0.05%	36.5%	TTYKYEMINK	99.7%	47.3	25	42.3	2	0	0	1290.64	353	362
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	53	0.05%	36.5%	VFANILLYIQR	99.7%	61.2	25	59.2	2	0	0	1349.79	335	345
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	53	0.05%	36.5%	VFSDEVQQQAQLSTIR	99.7%	109	25	109	6	0	0	1848.95	446	461

Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	53	0.05%	36.5%	VLENIELNKK	99.7%	63.1	25	53.4	2	0	0	1199.70	293	302
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	53	0.05%	36.5%	VSGGPSLEQR	99.7%	57.3	25	47.3	2	0	0	1029.53	144	153
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	53	0.05%	36.5%	VSSDVIDQK	99.7%	54.8	25	31.6	3	0	0	990.51	79	87
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	53	0.05%	36.5%	VYEIQDIYENSWTK	99.7%	110	25	106	2	0	0	1787.85	88	101
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	53	0.05%	36.5%	VYELQASR	99.7%	57.5	25	44.7	3	0	0	965.51	71	78
Eukaryotic translation initiation factor 3 subunit L	EIF3L	EIF3L_HUMAN	66.7	100.0%	20	22	53	0.05%	36.5%	YGDFFIR	99.7%	51.9	25	33.9	2	0	0	917.45	539	545
Eukaryotic translation initiation factor 4 gamma 1	EIF4G1	IF4G1_HUMAN	175.5	100.0%	3	3	4	0.00%	2.4%	ALPSEELNR	98.8%	33.6	25	26.7	1	0	0	1028.54	1437	1445
Eukaryotic translation initiation factor 4 gamma 1	EIF4G1	IF4G1_HUMAN	175.5	100.0%	3	3	4	0.00%	2.4%	EAVGDLLDAFK	99.7%	51	25	47.2	2	0	0	1177.61	525	535
Eukaryotic translation initiation factor 4 gamma 1	EIF4G1	IF4G1_HUMAN	175.5	100.0%	3	3	4	0.00%	2.4%	ITKPGSIDSNNQLFAPGGR	97.6%	25.6	25	25.6	0	1	0	1972.02	1072	1090
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	13	0.01%	11.1%	FLLQDTVELR	99.7%	51.3	25	37.9	1	0	0	1233.68	296	305
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	13	0.01%	11.1%	GLSFLFPLLK	99.7%	53	25	52.1	3	0	0	1134.69	723	732
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	13	0.01%	11.1%	LAEDAPNFDGPAAEGQPGQK	99.7%	88.1	25	88.1	1	0	0	2011.94	139	158
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	13	0.01%	11.1%	LEVDIPLVK	99.4%	36.6	25	36.6	2	0	0	1025.62	632	640
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	13	0.01%	11.1%	SDFFLEGPFMPPR	99.7%	50.3	25	42.2	2	0	0	1539.73	348	360
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	13	0.01%	11.1%	SYLAQFAAR	99.7%	51.8	25	47.9	1	0	0	1026.54	641	649
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	13	0.01%	11.1%	TAGNSEFLGK	96.9%	29.8	25	25	1	0	0	1023.51	32	41
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	13	0.01%	11.1%	TNPPLIQEKPAK	97.5%	30.7	25	30.7	1	0	0	1335.76	521	532
Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	IF4G2_HUMAN	102.4	100.0%	9	9	13	0.01%	11.1%	VIILSLDR	99.5%	37.2	25	30.8	1	0	0	928.58	585	592
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	6	8	26	0.02%	12.9%	AASIFGGAKPVDTAAR	99.7%	68.3	25	67.1	5	3	0	1531.82	357	372
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	6	8	26	0.02%	12.9%	GLNISAVR	99.7%	60	25	32.5	4	0	0	829.49	118	125
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	6	8	26	0.02%	12.9%	SILPTAPR	99.3%	35.9	25	23	2	0	0	854.51	71	78
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	6	8	26	0.02%	12.9%	SQSSDTEQQSPTSGGGK	99.7%	118	25	118	4	0	0	1680.73	495	511
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	6	8	26	0.02%	12.9%	STPKEDDSSASTSQSTR	99.7%	57	25	57	2	2	0	1783.79	340	356
Eukaryotic translation initiation factor 4B	EIF4B	IF4B_HUMAN	69.2	100.0%	6	8	26	0.02%	12.9%	VAPAQPSEEGPGR	99.7%	53.6	25	53	4	0	0	1294.64	512	524
Eukaryotic translation initiation factor 5B	EIF5B	IF2P_HUMAN	138.8	99.9%	2	2	2	0.00%	2.2%	HFEATDILVSK	96.1%	28.9	25	23.6	1	0	0	1259.66	1175	1185
Eukaryotic translation initiation factor 5B	EIF5B	IF2P_HUMAN	138.8	99.9%	2	2	2	0.00%	2.2%	TSEVPYAGINIGPVHK	99.7%	43.2	25	42.6	1	0	0	1681.89	1000	1015
Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	ECSIT	ECSIT_HUMAN	49.1	100.0%	3	3	3	0.00%	10.7%	ALVPFEDLFGQAPGGER	98.8%	33.6	25	32.5	1	0	0	1802.91	68	84
Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	ECSIT	ECSIT_HUMAN	49.1	100.0%	3	3	3	0.00%	10.7%	DLAVYNQLLNIFPK	99.7%	51.3	25	51.3	1	0	0	1647.91	125	138
Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	ECSIT	ECSIT_HUMAN	49.1	100.0%	3	3	3	0.00%	10.7%	DLPQDPVELAMFGLR	99.7%	79.9	25	76.8	1	0	0	1700.87	218	232
Exocyst complex component 2	EXOC2	EXOC2_HUMAN	104.1	100.0%	4	4	7	0.01%	5.2%	ASNTADTLFQEVLGR	99.7%	95.8	25	83.4	2	0	0	1621.82	249	263
Exocyst complex component 2	EXOC2	EXOC2_HUMAN	104.1	100.0%	4	4	7	0.01%	5.2%	FLFNLPLNIER	99.7%	42.8	25	36.1	2	0	0	1375.77	282	292
Exocyst complex component 2	EXOC2	EXOC2_HUMAN	104.1	100.0%	4	4	7	0.01%	5.2%	LVLSQLPNFWK	99.7%	59.4	25	58.8	2	0	0	1344.77	458	468
Exocyst complex component 2	EXOC2	EXOC2_HUMAN	104.1	100.0%	4	4	7	0.01%	5.2%	VIEAVSEELSR	99.7%	48.3	25	31.5	1	0	0	1231.65	828	838
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	7	7	9	0.01%	11.2%	DASVPLIDVTNLPTPR	99.7%	87.9	25	76.8	2	0	0	1707.93	224	239
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	7	7	9	0.01%	11.2%	EGNYAIVANVESMDYDPLVVK	99.7%	62.2	25	62.2	1	0	0	2326.13	796	816
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	7	7	9	0.01%	11.2%	ESEVLIGNLGDK	99.7%	75.7	25	69.1	1	0	0	1273.66	682	693
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	7	7	9	0.01%	11.2%	NIFLNQVLAEINK	99.7%	44.7	25	41.1	1	0	0	1515.85	534	546
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	7	7	9	0.01%	11.2%	NIFVLQQNLTNITMSR	99.7%	68.9	25	68.9	1	0	0	1892.01	873	888
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	7	7	9	0.01%	11.2%	SGELQGGPDDNLIEGGGTK	99.7%	70.3	25	70.3	1	0	0	1843.87	468	486
Exocyst complex component 4	EXOC4	EXOC4_HUMAN	110.5	100.0%	7	7	9	0.01%	11.2%	STTQVADSGYQR	99.7%	57.9	25	57	2	0	0	1312.61	314	325
Exocyst complex component 8	EXOC8	EXOC8_HUMAN	81.8	99.8%	2	2	2	0.00%	3.7%	QNASFLYETVLPVVEK	99.7%	56.5	25	56.5	1	0	0	1836.97	676	691
Exocyst complex component 8	EXOC8	EXOC8_HUMAN	81.8	99.8%	2	2	2	0.00%	3.7%	RFEEGVGKPAK	99.7%	33.7	25	31.5	0	1	0	1217.66	692	702
Exosome complex component CSL4	EXOSC1	EXOS1_HUMAN	21.5	99.8%	2	2	3	0.00%	12.8%	SFRPGDIVLAK	99.6%	38.7	25	21.4	1	0	0	1202.69	121	131
Exosome complex component CSL4	EXOSC1	EXOS1_HUMAN	21.5	99.8%	2	2	3	0.00%	12.8%	SSENGALPVVSVVR	99.7%	72.6	25	72.2	2	0	0	1413.77	44	57
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	4	4	6	0.01%	17.3%	GGGPAGAGGEAPAALR	99.7%	64.9	25	62.6	2	0	0	1308.67	78	93
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	4	4	6	0.01%	17.3%	GSAYLEAGGTK	97.8%	31.1	25	24.4	1	0	0	1053.52	51	61
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	4	4	6	0.01%	17.3%	LYPVLQQSLVR	99.7%	67.6	25	61.7	2	0	0	1315.77	251	261
Exosome complex component MTR3	EXOSC6	EXOS6_HUMAN	28.2	100.0%	4	4	6	0.01%	17.3%	VLCAVSGPR	99.7%	42.4	25	32.4	1	0	0	958.51	62	70
Exosome complex component RRP4	EXOSC2	EXOS2_HUMAN	32.8	100.0%	4	4	6	0.01%	17.4%	LDSVLLLSSMNLPGGELR	98.6%	33	25	33	1	0	0	1914.04	104	121
Exosome complex component RRP4	EXOSC2	EXOS2_HUMAN	32.8	100.0%	4	4	6	0.01%	17.4%	LIASVAGSVER	99.7%	62.9	25	51.3	1	0	0	1101.63	52	62
Exosome complex component RRP4	EXOSC2	EXOS2_HUMAN	32.8	100.0%	4	4	6	0.01%	17.4%	NCIISLVTQR	99.7%	63	25	55.2	2	0	0	1203.65	239	248

Exosome complex component RRP4	EXOSC2	EXOS2_HUMAN	32.8	100.0%	4	4	6	0.01%	17.4%	YIGEVGDIVVGR	99.7%	68.4	25	61.1	2	0	0	1276.69	76	87
Exosome complex component RRP41	EXOSC4	EXOS4_HUMAN	26.4	99.8%	2	2	4	0.00%	9.0%	ALAVVYGPHEIR	99.7%	48.9	25	45.6	2	0	0	1324.74	48	59
Exosome complex component RRP41	EXOSC4	EXOS4_HUMAN	26.4	99.8%	2	2	4	0.00%	9.0%	VLEAAAQAAR	99.7%	85.2	25	69.6	2	0	0	999.56	213	222
Exosome complex component RRP43	EXOSC8	EXOS8_HUMAN	30.0	99.8%	2	2	3	0.00%	10.9%	LGNTTVICGVK	99.7%	50.4	25	44.7	2	0	0	1161.63	53	63
Exosome complex component RRP43	EXOSC8	EXOS8_HUMAN	30.0	99.8%	2	2	3	0.00%	10.9%	TTTVNIGSISTADGSALVK	99.7%	76.8	25	76.8	1	0	0	1834.98	34	52
Exosome complex component RRP46	EXOSC5	EXOS5_HUMAN	25.2	99.9%	2	2	4	0.00%	11.1%	AVLTFALDSVER	99.7%	88.3	25	58.2	2	0	0	1320.72	179	190
Exosome complex component RRP46	EXOSC5	EXOS5_HUMAN	25.2	99.9%	2	2	4	0.00%	11.1%	NTCEAVVLGTLHPR	99.7%	80.9	25	80.9	2	0	0	1566.81	100	113
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	10	10	22	0.02%	12.5%	AIEEGIPAFTCEEYVK	98.6%	32.9	25	29.6	1	0	0	1855.88	184	199
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	10	10	22	0.02%	12.5%	ASLTYAEAQLR	99.7%	52.1	25	39.3	2	0	0	1222.64	586	596
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	10	10	22	0.02%	12.5%	IEDTVFHVFDK	99.7%	48	25	42.3	2	0	0	1349.67	896	906
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	10	10	22	0.02%	12.5%	IIFSEHLPLSK	99.7%	41.3	25	41.3	2	0	0	1283.74	226	236
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	10	10	22	0.02%	12.5%	LLAVAIGADCTYPELTDK	99.7%	58.2	25	57.1	2	0	0	1949.99	790	807
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	10	10	22	0.02%	12.5%	NAIVVLIPK	99.7%	40.6	25	40.6	2	0	0	966.63	858	866
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	10	10	22	0.02%	12.5%	NVIVLQTVLQEVR	99.7%	75	25	75	6	0	0	1510.90	87	99
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	10	10	22	0.02%	12.5%	SLTANPELIDR	99.3%	35.9	25	26.4	2	0	0	1228.65	200	210
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	10	10	22	0.02%	12.5%	YADVIVHR	99.7%	45.7	25	40	2	0	0	972.53	782	789
Exosome complex exonuclease RRP44	DIS3	RRP44_HUMAN	109.0	100.0%	10	10	22	0.02%	12.5%	YGLEGTVFFEEK	99.7%	72.5	25	67.5	1	0	0	1418.68	867	878
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	5	5	8	0.01%	6.1%	AAAEQAISVR	99.7%	55.8	25	29.7	2	0	0	1015.55	759	768
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	5	5	8	0.01%	6.1%	FALGSVVAVTK	99.7%	80.3	25	76.3	2	0	0	1091.65	38	48
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	5	5	8	0.01%	6.1%	LAQVQVQK	99.5%	37.3	25	16.5	1	0	0	913.55	726	733
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	5	5	8	0.01%	6.1%	TEDFIIDTLELR	99.7%	98.1	25	88.4	2	0	0	1464.76	335	346
Exosome component 10	EXOSC10	EXOSX_HUMAN	100.8	100.0%	5	5	8	0.01%	6.1%	VGILLDEASGVNK	99.7%	59.2	25	49.2	1	0	0	1314.73	124	136
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	AIIASNIMYIVGQYPR	99.7%	93.4	25	89.5	4	2	0	1824.97	538	553
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	AVGHPFVIQLGR	99.7%	45.2	25	37.9	2	2	0	1293.74	701	712
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	DFEEYPEHR	99.1%	35.2	25	31	1	0	0	1221.52	837	845
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	EFAGEDTSDLFLEER	99.7%	106	25	90.9	2	0	0	1757.79	1024	1038
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	EPEVLSTMAIIVNK	99.7%	98.8	25	94	4	0	0	1543.84	797	810
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	ESPFSTSASPLLSGSQHFDVPPR	98.3%	26.9	25	26.9	0	1	0	2443.19	383	405
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	ETLVYLTHLDYVDTER	99.7%	96.7	25	92.2	2	2	0	1966.98	459	474
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	FLNVPMFR	99.7%	47.4	25	43.2	2	0	0	1023.54	254	261
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	FLNWIPLGYIFETK	99.7%	65.2	25	65.2	2	0	0	1740.94	232	245
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	FLVTVIK	99.7%	44.1	25	14.1	2	0	0	819.53	516	522
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	HWPTFISDIVGASR	99.7%	50.5	25	44.6	2	2	0	1585.81	145	158
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	IYLDMLNVYK	99.7%	69.8	25	67.2	5	0	0	1271.67	713	722
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	LDINLLDNVVNCLYHGEGAQQR	99.7%	92.1	25	88	0	2	0	2541.25	23	44
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	LFVTGLFSLNQDIPAFK	99.7%	43.7	25	43.7	1	0	0	1910.04	996	1012
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	LHNQVNGTEWSWK	99.7%	63.9	25	58.5	1	0	0	1598.77	480	492
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	LISGWVSR	99.7%	53.5	25	34.3	2	0	0	917.52	758	765
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	LISTLIYK	99.7%	48.6	25	43.8	2	0	0	950.59	246	253
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	LLSEEVFDFSSGQITQVK	99.7%	100	25	100	5	2	0	2027.03	173	190
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	LNMILVQILK	99.7%	75.4	25	62.2	4	0	0	1184.74	130	139
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	LVLDSIIWAFK	99.7%	86.3	25	86.3	2	0	0	1304.76	873	883
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	MAKPEEVLVVENDQGEVVR	99.7%	56.9	25	55.3	0	4	0	2157.09	424	442
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	MAQEVLTHLK	99.7%	64.1	25	54.8	4	0	0	1185.63	45	54
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	NVDILKDPETVK	99.7%	44	25	34.3	1	2	0	1370.75	675	686
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	PAIMTMLADHAAR	99.7%	63.8	25	61.5	0	1	0	1397.70	2	14
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	QLLDFSQK	99.7%	44.3	25	35.5	2	0	0	978.53	15	22
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	QLYLPMLFK	99.4%	36.5	25	25.9	2	0	0	1152.65	407	415
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	QMLPLNTNIR	99.7%	63.9	25	53.3	4	0	0	1199.66	296	305
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	SAFPHLQDAQVK	99.7%	51.5	25	45.2	2	0	0	1340.70	984	995
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	TSESLCQNNMVILK	99.7%	97.1	25	81.9	4	0	0	1636.80	159	172

Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	TSSDPTCVEK	99.6%	38.6	25	20	2	0	0	1123.49	113	122
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	TSSDPTCVEKEK	99.7%	53.1	25	42.5	2	0	0	1380.63	113	124
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	VDTILEFSQNMNTK	99.7%	96.4	25	96.4	4	0	0	1655.79	63	76
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	YMLLPNQVWDSIIQQATK	99.7%	86.3	25	61.1	2	0	0	2148.12	657	674
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	YVVGLIIK	99.7%	46.5	25	32.8	2	0	0	904.59	105	112
Exportin-1	XPO1	XPO1_HUMAN	123.4	100.0%	35	51	98	0.09%	40.7%	YYGLQILENVIK	99.7%	84.6	25	84.6	2	0	0	1452.81	77	88
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	AACDLVR	99.7%	42.3	25	30.4	2	0	0	804.40	385	391
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	AADEEAFEDNSEEYIR	99.7%	115	25	115	2	0	0	1887.79	356	371
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	AADEEAFEDNSEEYIRR	99.7%	49.1	25	49.1	1	2	0	2043.89	356	372
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	ALTLPGSSENEYIMK	99.7%	100	25	96.3	4	0	0	1668.82	560	574
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	ANIVHLMLSSPEQIQK	99.7%	83.4	25	79.3	2	4	0	1807.97	94	109
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	ATIELCSTHANDASALR	99.7%	97.9	25	97.8	2	2	0	1829.88	190	206
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	DAAIYLVTSLASK	99.7%	98.4	25	94.8	2	0	0	1351.75	428	440
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	DLEGSDIDTR	99.7%	48.3	25	40.1	2	0	0	1120.51	373	382
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	DLEGSDIDTRR	99.6%	39.1	25	29.1	2	0	0	1276.61	373	383
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	EDFPQKWPDLLTEMVNR	99.7%	37.6	25	37.6	0	2	0	2118.03	121	137
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	EHDPVGQMVNNPK	99.7%	79.2	25	79.2	2	0	0	1480.69	913	925
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	FQSGDFHVINGVLR	99.7%	34.5	25	32	0	2	0	1588.82	138	151
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	GSNTIASAAADK	99.7%	50	25	43.5	2	0	0	1105.55	715	726
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	GSNTIASAAADKIPGLLGVFQK	99.7%	78.3	25	78.3	2	2	0	2158.19	715	736
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	IHLAQSLHK	99.7%	42.1	25	39.2	2	0	0	1046.61	926	934
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	IIIPEIQK	97.6%	30.8	25	0	1	0	0	953.60	825	832
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	ILFSSLILISK	99.7%	80.6	25	80.6	2	0	0	1233.78	207	217
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	IVEDEPNKICEADR	99.7%	76.8	25	76.8	2	2	0	1687.80	76	89
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	KICAVGITK	99.7%	41.2	25	32.7	2	0	0	989.58	840	848
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	LLQAFLER	99.7%	55.5	25	39.7	5	0	0	989.58	707	714
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	LLQTDDEEEAGLLELLK	99.7%	114	25	106	3	0	0	1929.01	252	268
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	LLTECPPMMDTEYTK	99.7%	70.3	25	70.1	4	0	0	1828.82	849	863
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	LSTACPGR	95.3%	28.2	25	22.2	1	0	0	861.42	935	942
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	LVLDAFALPLTNLFK	99.7%	76.9	25	76.2	2	0	0	1674.98	175	189
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	MFGMVLEK	97.2%	30.2	25	23.2	1	0	0	970.47	817	824
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	NLFEDQNTLTSICEK	99.7%	94.5	25	94.5	2	0	0	1811.85	332	346
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	QIFILLFQR	99.7%	68.5	25	67.2	4	0	0	1177.71	769	777
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	QLSDAISIIGR	99.7%	72.5	25	57.8	2	0	0	1172.66	110	120
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	SANVNEFPVLK	99.7%	49.2	25	31	2	0	0	1217.65	471	481
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	SNELWTEIK	99.7%	62.8	25	48.5	2	0	0	1119.57	166	174
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	SQICDNAALYAQK	99.7%	81.8	25	61.8	2	0	0	1481.71	269	281
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	TGNIPALVR	99.7%	62	25	58.2	4	0	0	940.56	698	706
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	TLDPDPAIR	98.0%	31.7	25	28.7	1	0	0	997.53	18	26
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	VIVPNMEFR	97.9%	31.3	25	19.3	1	0	0	1104.59	347	355
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	WPDLLTEMVNR	99.7%	55.3	25	55.3	2	0	0	1373.69	127	137
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	YDEEFQR	99.5%	37.4	25	37.4	2	0	0	986.42	282	288
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	YGALALQEIFDGIQPK	99.7%	98.3	25	98.3	5	0	0	1762.94	801	816
Exportin-2	CSE1L	XPO2_HUMAN	110.4	100.0%	38	46	96	0.09%	42.0%	YIMIFR	97.7%	30.9	25	18.8	1	0	0	842.46	487	492
Exportin-4	XPO4	XPO4_HUMAN	130.1	100.0%	3	3	3	0.00%	3.1%	AQETDSPLFLATR	99.7%	68.1	25	50	1	0	0	1448.74	1039	1051
Exportin-4	XPO4	XPO4_HUMAN	130.1	100.0%	3	3	3	0.00%	3.1%	IPQLPEDLFK	95.5%	28.4	25	21.7	1	0	0	1199.67	995	1004
Exportin-4	XPO4	XPO4_HUMAN	130.1	100.0%	3	3	3	0.00%	3.1%	SPPLNFLSSPVQR	99.7%	47.1	25	47.1	1	0	0	1441.78	737	749
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	11	11	23	0.02%	10.3%	AGGFVVGYTSSGNPIFR	99.7%	124	25	124	2	0	0	1728.87	746	762
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	11	11	23	0.02%	10.3%	ALDMLDAEK	98.8%	33.7	25	23.2	1	0	0	1021.49	802	810
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	11	11	23	0.02%	10.3%	AVMEQIPEIQK	99.7%	52.2	25	45.5	2	0	0	1285.68	1113	1123
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	11	11	23	0.02%	10.3%	AVTVMMDPNSTQR	99.7%	46.9	25	42.4	2	0	0	1449.68	16	28

Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	11	11	23	0.02%	10.3%	DIQQTLTQNMER	99.7%	49.1	25	45.2	1	0	0	1492.71	177	188
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	11	11	23	0.02%	10.3%	DPLLLAIIPK	99.7%	55.2	25	55.2	6	0	0	1092.70	387	396
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	11	11	23	0.02%	10.3%	FCEEFKEK	96.9%	29.9	25	14.6	2	0	0	1116.50	36	43
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	11	11	23	0.02%	10.3%	IVVEMIKR	97.9%	31.4	25	13.5	1	0	0	987.60	119	126
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	11	11	23	0.02%	10.3%	LLDNLLALIR	99.7%	60.1	25	42.6	3	0	0	1153.73	772	781
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	11	11	23	0.02%	10.3%	NPCTEQILK	94.5%	27.6	25	20.9	1	0	0	1102.56	763	771
Exportin-5	XPO5	XPO5_HUMAN	136.3	100.0%	11	11	23	0.02%	10.3%	VLSDVDAFIAYVGTDQK	99.7%	44.8	25	44.8	2	0	0	1840.93	688	704
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	21	21	31	0.03%	23.6%	AALSGSYVNFGVFR	99.7%	101	25	101	2	0	0	1487.76	841	854
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	21	21	31	0.03%	23.6%	ALVEFTNSPDCLSK	99.7%	50.6	25	41.2	1	0	0	1580.76	33	46
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	21	21	31	0.03%	23.6%	DSSLFDIFTLSCNLLK	99.7%	74.2	25	66.5	1	0	0	1872.94	183	198
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	21	21	31	0.03%	23.6%	GIAFAFNAK	99.7%	39.7	25	31.8	1	0	0	938.51	728	736
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	21	21	31	0.03%	23.6%	GSSSYSQLLAATCLTK	99.7%	63.1	25	57.9	1	0	0	1686.84	54	69
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	21	21	31	0.03%	23.6%	IYIGDQVQK	99.5%	37.3	25	26.7	1	0	0	1063.58	560	568
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	21	21	31	0.03%	23.6%	LAASVPYVK	96.6%	29.5	25	29.5	2	0	0	947.56	387	395
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	21	21	31	0.03%	23.6%	LATFVTQALIQLYAR	99.7%	56	25	56	1	0	0	1707.98	100	114
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	21	21	31	0.03%	23.6%	LESVHIILR	99.7%	68.1	25	68.1	2	0	0	1079.66	418	426
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	21	21	31	0.03%	23.6%	LLLSIPHSDLLDYPK	98.1%	31.7	25	31.7	1	0	0	1723.96	871	885
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	21	21	31	0.03%	23.6%	LMAELVHNR	99.7%	55.9	25	50.5	1	0	0	1082.58	774	782
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	21	21	31	0.03%	23.6%	LQFDVSSPNGILLFR	99.7%	58.7	25	55.1	2	0	0	1705.93	786	800
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	21	21	31	0.03%	23.6%	LYGDDALDNALQTFIK	99.7%	102	25	102	2	0	0	1796.91	855	870
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	21	21	31	0.03%	23.6%	NSIVNSQPPEK	99.7%	53.6	25	46.3	2	0	0	1212.62	1021	1031
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	21	21	31	0.03%	23.6%	NYVLNYLATRPK	99.7%	66.2	25	66.2	2	0	0	1451.80	88	99
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	21	21	31	0.03%	23.6%	QLYETTDTTTR	99.7%	53.3	25	50.7	1	0	0	1328.63	17	27
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	21	21	31	0.03%	23.6%	SNYQLGELVK	99.7%	49.3	25	43.6	2	0	0	1150.61	339	348
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	21	21	31	0.03%	23.6%	TLQLLNDLSIGYSSVR	99.7%	59.3	25	58.9	1	0	0	1778.96	613	628
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	21	21	31	0.03%	23.6%	TNNPLPLEQR	99.7%	56.4	25	46.9	2	0	0	1181.63	74	83
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	21	21	31	0.03%	23.6%	VENYPEVIR	99.7%	43.8	25	36.9	2	0	0	1118.58	349	357
Exportin-7	XPO7	XPO7_HUMAN	123.9	100.0%	21	21	31	0.03%	23.6%	VLQLMNLTDSR	99.7%	59.5	25	52	1	0	0	1289.69	527	537
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	19	23	42	0.04%	24.1%	ALAYFEQLK	99.7%	50.4	25	49.5	2	0	0	1082.59	21	29
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	19	23	42	0.04%	24.1%	ANVEAIMLAVMK	99.7%	98.8	25	90.2	2	0	0	1289.70	370	381
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	19	23	42	0.04%	24.1%	DGPVGFADFVYK	99.7%	58.6	25	58.6	2	0	0	1314.64	860	871
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	19	23	42	0.04%	24.1%	DLQEFIPLINQITAK	99.7%	94.7	25	85.1	2	0	0	1742.97	738	752
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	19	23	42	0.04%	24.1%	DVVHTSEEAR	99.7%	44.4	25	37	2	0	0	1142.54	157	166
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	19	23	42	0.04%	24.1%	EEACDCLFEVVNK	99.7%	74.5	25	74.5	1	0	0	1612.70	241	253
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	19	23	42	0.04%	24.1%	FFCFQVLEHQVK	99.7%	72.9	25	72.9	2	2	0	1581.79	54	65
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	19	23	42	0.04%	24.1%	FMEVEVAIR	99.7%	59.3	25	51	2	0	0	1093.57	443	451
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	19	23	42	0.04%	24.1%	GVDLYLR	99.7%	39.3	25	32.2	1	0	0	835.47	138	144
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	19	23	42	0.04%	24.1%	ISPDAWQVCAEALAQR	99.7%	88.3	25	88.3	2	0	0	1814.89	30	45
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	19	23	42	0.04%	24.1%	LAQVSPELLLASVR	99.7%	98.7	25	98.7	4	0	0	1495.88	415	428
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	19	23	42	0.04%	24.1%	LMLAQDEER	99.4%	36.4	25	23.9	2	0	0	1104.54	635	643
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	19	23	42	0.04%	24.1%	NAQEALQAIETK	99.7%	79.4	25	68.4	2	0	0	1315.69	317	328
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	19	23	42	0.04%	24.1%	QASLADCLNHAVGFASR	99.7%	47.1	25	44.4	0	1	0	1816.88	644	660
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	19	23	42	0.04%	24.1%	QMNPFIEDILNR	99.7%	57.8	25	53.5	3	0	0	1489.75	558	569
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	19	23	42	0.04%	24.1%	TCFIILSK	99.7%	47	25	37.9	2	0	0	981.54	844	851
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	19	23	42	0.04%	24.1%	VFSSTLQNWQTTR	99.7%	79.7	25	74	2	0	0	1567.79	430	442
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	19	23	42	0.04%	24.1%	VLVTVIQGAVEYPDPIAQK	99.7%	98.6	25	98.6	2	2	0	2040.14	825	843
Exportin-T	XPOT	XPOT_HUMAN	110.0	100.0%	19	23	42	0.04%	24.1%	YSELTTVQQQLIR	99.7%	83.8	25	79.6	2	0	0	1578.85	68	80
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	4	4	7	0.01%	5.8%	ALALLEDEER	99.7%	54.9	25	42.6	1	0	0	1158.60	163	172
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	4	4	7	0.01%	5.8%	ITVPLVSEVQIAQLR	99.7%	99.3	25	99.3	2	0	0	1665.99	365	379
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	4	4	7	0.01%	5.8%	LLDEWFTLDEVPK	99.7%	73.9	25	64.1	2	0	0	1604.82	484	496
Extended synaptotagmin-2	ESYT2	ESYT2_HUMAN	102.4	100.0%	4	4	7	0.01%	5.8%	SSSSLLASPGHISVK	97.3%	30.4	25	21.2	2	0	0	1469.80	736	750

FACT complex subunit SPT16	SUPT16H	SP16H_HUMAN	119.9	100.0%	4	4	7	0.01%	5.3%	AASITSEVFNK	99.7%	68	25	66.8	1	0	0	1166.61	186	196
FACT complex subunit SPT16	SUPT16H	SP16H_HUMAN	119.9	100.0%	4	4	7	0.01%	5.3%	APGEQTVPALNLQNAFR	99.7%	52.1	25	52.1	2	0	0	1825.96	607	623
FACT complex subunit SPT16	SUPT16H	SP16H_HUMAN	119.9	100.0%	4	4	7	0.01%	5.3%	INFYCPGSALGR	99.7%	50.4	25	45.8	1	0	0	1354.66	570	581
FACT complex subunit SPT16	SUPT16H	SP16H_HUMAN	119.9	100.0%	4	4	7	0.01%	5.3%	NEGNIFPNPEATFVK	99.7%	72.3	25	51.5	3	0	0	1676.83	582	596
FACT complex subunit SSRP1	SSRP1	SSRP1_HUMAN	81.1	100.0%	3	3	5	0.00%	4.8%	ADVIQATGDAICIFR	99.7%	90.7	25	86	2	0	0	1649.83	189	203
FACT complex subunit SSRP1	SSRP1	SSRP1_HUMAN	81.1	100.0%	3	3	5	0.00%	4.8%	FDEISFVNFAR	99.7%	81.6	25	77.3	2	0	0	1344.66	371	381
FACT complex subunit SSRP1	SSRP1	SSRP1_HUMAN	81.1	100.0%	3	3	5	0.00%	4.8%	IPYTTVLR	97.0%	29.9	25	23.1	1	0	0	962.57	234	241
F-actin-capping protein subunit alpha-1	CAPZA1	CAZA1_HUMAN	32.9	99.8%	2	2	4	0.00%	8.7%	FTITPPTAQVVGVLK	98.8%	33.8	25	33.8	2	0	0	1570.92	179	193
F-actin-capping protein subunit alpha-1	CAPZA1	CAZA1_HUMAN	32.9	99.8%	2	2	4	0.00%	8.7%	LLLNNDNLLR	99.7%	72.4	25	53.2	2	0	0	1197.70	38	47
Fanconi anemia group D2 protein	FANCD2	FACD2_HUMAN	166.5	100.0%	2	2	2	0.00%	1.8%	DGGPVTSQESGQK	98.1%	31.8	25	31.8	1	0	0	1289.60	711	723
Fanconi anemia group D2 protein	FANCD2	FACD2_HUMAN	166.5	100.0%	2	2	2	0.00%	1.8%	SEDKESLTEDASK	99.7%	42.8	25	36.5	1	0	0	1438.65	10	22
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	22	0.02%	14.5%	AMFANQLDAR	99.7%	46.7	25	44.7	1	0	0	1136.55	524	533
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	22	0.02%	14.5%	DLQLLQGSK	99.7%	47.4	25	27.8	2	0	0	1001.56	340	348
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	22	0.02%	14.5%	DVPLTAEEVEFVVEK	99.7%	87.9	25	68.3	1	0	0	1703.87	183	197
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	22	0.02%	14.5%	EGDLTNLLQNQAVK	99.7%	87.7	25	74	2	0	0	1542.81	26	39
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	22	0.02%	14.5%	ETGHVSGPDGQNPEK	99.7%	66.7	25	64.2	2	0	0	1551.70	855	869
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	22	0.02%	14.5%	GSPCSEEAGTLR	99.5%	37.2	25	37.2	1	0	0	1263.56	53	64
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	22	0.02%	14.5%	IFQNLCDITR	99.7%	50.3	25	35.5	1	0	0	1279.65	870	879
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	22	0.02%	14.5%	IQQFLR	97.6%	30.8	25	0	1	0	0	804.47	927	932
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	22	0.02%	14.5%	SADFSQSTSIGIK	99.7%	64.8	25	64.8	1	0	0	1340.67	726	738
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	22	0.02%	14.5%	SISLLCLEGLQK	99.7%	55.6	25	35.4	1	0	0	1360.75	903	914
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	22	0.02%	14.5%	SLLNLLSSQEEDFNSK	99.7%	84.8	25	80.2	2	0	0	1823.90	965	980
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	22	0.02%	14.5%	TAAPTVCLLVLSQAEK	99.7%	52.4	25	52.4	2	0	0	1700.93	1079	1094
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	22	0.02%	14.5%	TIETSPSLSR	98.8%	33.8	25	26.9	1	0	0	1090.57	403	412
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	22	0.02%	14.5%	VLEEVDWLITK	98.4%	32.4	25	27.5	1	0	0	1344.74	1095	1105
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	22	0.02%	14.5%	YAVNVALQK	99.5%	38	25	32.8	2	0	0	1005.57	841	849
Fanconi anemia group I protein	FANCI	FANCI_HUMAN	149.3	100.0%	16	16	22	0.02%	14.5%	YTSIPTSVEESGKK	99.1%	35.1	25	30.6	1	0	0	1525.77	885	898
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	18	22	46	0.04%	44.6%	AAQVMGPPDR	99.7%	65.5	25	61.4	3	0	0	1057.51	300	309
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	18	22	46	0.04%	44.6%	AEGFVDALHR	99.7%	53.7	25	46.8	2	0	0	1114.56	16	25
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	18	22	46	0.04%	44.6%	DGFGGLAAAR	99.7%	72.6	25	44	2	0	0	934.47	328	337
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	18	22	46	0.04%	44.6%	EMVLEIIR	99.7%	55.7	25	0	1	0	0	1002.57	226	233
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	18	22	46	0.04%	44.6%	FAVGIVIGR	99.7%	62.8	25	47	2	0	0	931.57	263	271
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	18	22	46	0.04%	44.6%	GDWSVGAPGGVQEITYTVPADK	99.7%	80.2	25	78.4	2	0	0	2247.09	344	365
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	18	22	46	0.04%	44.6%	GVPQQIEVAR	99.7%	56.5	25	51.6	2	0	0	1096.61	409	418
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	18	22	46	0.04%	44.6%	IDSIPHLNNSTPLVDPSVYGYGVQK	99.7%	68	25	68	0	2	0	2713.38	33	57
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	18	22	46	0.04%	44.6%	IQFKPDDGISPER	99.7%	54.3	25	49.5	2	4	0	1501.76	287	299
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	18	22	46	0.04%	44.6%	IQIASESSGIPERPCVLTGTPESIEQAK	99.7%	50.7	25	50.7	0	1	0	2997.52	111	138
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	18	22	46	0.04%	44.6%	LLGQIVDR	99.7%	45.6	25	36	3	0	0	913.55	140	147
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	18	22	46	0.04%	44.6%	MGGGSIEVSVPR	99.7%	91.5	25	86.2	2	0	0	1204.60	251	262
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	18	22	46	0.04%	44.6%	MVGFIIGR	99.5%	37.6	25	35	3	0	0	908.50	88	95
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	18	22	46	0.04%	44.6%	MVMIQDGPLPTGADKPLR	99.7%	48.7	25	48.7	0	4	0	1971.00	196	213
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	18	22	46	0.04%	44.6%	QQVAFYGQTLGQAQAHSQEQ	99.7%	84.8	25	84.6	1	0	0	2219.05	553	572
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	18	22	46	0.04%	44.6%	RPLDDGVGNQLGALVHQR	99.7%	71.4	25	68.7	0	4	0	1945.04	58	75
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	18	22	46	0.04%	44.6%	SINQQSGAHVELQR	99.7%	66.2	25	58.8	3	1	0	1566.80	379	392
Far upstream element-binding protein 3	FUBP3	FUBP3_HUMAN	61.6	100.0%	18	22	46	0.04%	44.6%	TVITEEFKVPDK	99.7%	56	25	45.1	2	0	0	1405.76	76	87
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	3	3	7	0.01%	6.7%	ATPEQYQILK	98.1%	31.8	25	22.7	2	0	0	1190.64	344	353
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	3	3	7	0.01%	6.7%	GLTVVVAFR	99.7%	49.3	25	31	3	0	0	961.58	127	135
Farnesyl pyrophosphate synthase	FDPS	FPPS_HUMAN	48.3	100.0%	3	3	7	0.01%	6.7%	IGTDIQDNK	99.4%	37	25	30	2	0	0	1003.51	324	332
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	7	8	12	0.01%	20.0%	DLTQEQTEK	99.6%	38.5	25	30.5	2	0	0	1091.52	8	16
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	7	8	12	0.01%	20.0%	ENTYPFLAMIMLK	99.7%	54.4	25	48.6	2	0	0	1570.80	227	239
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	7	8	12	0.01%	20.0%	FQIEANFPR	98.8%	33.8	25	9.84	1	0	0	1121.57	401	409

FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	7	8	12	0.01%	20.0%	FTYYTILDIFR	99.7%	77.5	25	70.3	2	0	0	1451.76	105	115
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	7	8	12	0.01%	20.0%	HTLEQHNWNIEAAVQDR	99.7%	55.5	25	55.5	0	1	0	2060.99	34	50
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	7	8	12	0.01%	20.0%	QQQDEAYLASLR	99.7%	84.2	25	70.7	2	0	0	1421.70	291	302
FAS-associated factor 2	FAF2	FAF2_HUMAN	52.6	100.0%	7	8	12	0.01%	20.0%	VTDPVGDIVSFMHSFEEK	99.7%	57.5	25	57.5	1	1	0	2036.96	129	146
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	14	15	20	0.02%	25.4%	DAPIALKR	96.4%	29.2	25	0.42	1	0	0	883.54	320	327
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	14	15	20	0.02%	25.4%	DIISELLTSDDMK	99.7%	86	25	81.1	4	0	0	1479.73	523	535
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	14	15	20	0.02%	25.4%	GLADYVAATFDIWK	97.9%	31.3	25	27.4	1	0	0	1569.79	402	415
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	14	15	20	0.02%	25.4%	ILVDQQVWK	99.7%	41.1	25	36.7	1	0	0	1128.64	295	303
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	14	15	20	0.02%	25.4%	IVEDPESLNMK	96.6%	29.5	25	18.7	1	0	0	1274.63	444	454
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	14	15	20	0.02%	25.4%	IYSVEALPVAAVNVQSTQ	99.7%	83.6	25	82.2	1	0	0	1889.00	693	710
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	14	15	20	0.02%	25.4%	LGIPQNTILVQTLLR	99.7%	52.5	25	52.1	2	0	0	1679.02	242	256
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	14	15	20	0.02%	25.4%	NQVLPLSDVDTTSATDIQR	99.7%	131	25	126	1	0	0	2073.05	615	633
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	14	15	20	0.02%	25.4%	SAYCLGSSHPR	99.7%	53.3	25	53.3	2	0	0	1234.56	642	652
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	14	15	20	0.02%	25.4%	SLILLDECSK	96.7%	29.5	25	23.3	1	0	0	1177.61	359	368
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	14	15	20	0.02%	25.4%	VAEVLSSLLGGEGHFSK	98.9%	28.6	25	22.1	0	1	0	1729.91	578	594
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	14	15	20	0.02%	25.4%	VAVLCVSR	99.7%	43.5	25	32	1	0	0	903.51	634	641
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	14	15	20	0.02%	25.4%	VNLNHEVSNEDVLTK	99.7%	46.8	25	46	0	2	0	1710.87	133	147
FAST kinase domain-containing protein 2	FASTKD2	FAKD2_HUMAN	81.5	100.0%	14	15	20	0.02%	25.4%	VVLDNIHGCPLR	99.7%	73	25	54.8	1	0	0	1392.74	369	380
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	34	0.03%	8.4%	AALQEELQLCK	99.7%	47.8	25	34.5	2	0	0	1302.67	1132	1142
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	34	0.03%	8.4%	AGLYGLPR	99.7%	42.4	25	36.2	1	0	0	846.48	42	49
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	34	0.03%	8.4%	AQVADVVVSR	99.7%	60.4	25	41.4	2	0	0	1043.58	1073	1082
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	34	0.03%	8.4%	DGAWGAFR	96.8%	29.7	25	13.9	1	0	0	879.41	1508	1515
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	34	0.03%	8.4%	DNLEFFLAGIGR	99.7%	79.6	25	49.1	2	0	0	1351.70	791	802
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	34	0.03%	8.4%	EDGLAQQQTQLNLR	99.7%	82	25	77	1	0	0	1613.82	2207	2220
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	34	0.03%	8.4%	FDASFFGVHPK	99.7%	56.3	25	32.4	2	0	0	1251.62	60	70
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	34	0.03%	8.4%	GLVQALQTK	99.7%	49.9	25	29.3	1	0	0	957.57	1143	1151
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	34	0.03%	8.4%	HGLYLPTR	98.9%	34.3	25	30.8	1	0	0	956.53	1044	1051
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	34	0.03%	8.4%	LLEQGLR	99.2%	35.3	25	0	3	0	0	828.49	437	443
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	34	0.03%	8.4%	LPEDPLLSGLLDSPALK	99.7%	85.3	25	85.3	2	0	0	1778.00	1209	1225
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	34	0.03%	8.4%	LQVVDQPLPVR	99.7%	58.9	25	58.9	2	0	0	1263.74	374	384
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	34	0.03%	8.4%	QEPLLIGSTK	99.7%	39.7	25	39.3	2	0	0	1085.62	317	326
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	34	0.03%	8.4%	SDEAVKPFGLK	98.0%	31.5	25	25	1	0	0	1190.64	523	533
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	34	0.03%	8.4%	SEGVVAVLLTK	99.7%	56.7	25	51.7	2	0	0	1115.67	225	235
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	34	0.03%	8.4%	SFYGSTLFLCR	99.7%	59.8	25	46.4	2	0	0	1350.65	1394	1404
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	34	0.03%	8.4%	TGTVSLEVR	99.7%	50.2	25	40.5	2	0	0	961.53	928	936
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	34	0.03%	8.4%	VLEALLPLK	99.7%	44.1	25	44.1	1	0	0	995.65	2383	2391
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	34	0.03%	8.4%	VVVQVLAEEPEAVLK	99.7%	96.6	25	73.7	3	0	0	1622.94	1852	1866
Fatty acid synthase	FASN	FAS_HUMAN	273.4	100.0%	20	20	34	0.03%	8.4%	VYQWDDPDPR	94.8%	27.8	25	7.63	1	0	0	1290.58	958	967
Filaggrin-2	FLG2	FILA2_HUMAN	248.1	99.8%	2	2	18	0.02%	1.0%	FSNSSSSNEFSK	99.7%	54.6	25	54.6	4	0	0	1320.57	404	415
Filaggrin-2	FLG2	FILA2_HUMAN	248.1	99.8%	2	2	18	0.02%	1.0%	SVVTVIDVFYK	99.7%	78.3	25	69.8	14	0	0	1269.71	7	17
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	17	17	22	0.02%	8.4%	AFGPGLQGGSAGSPAR	99.7%	57.4	25	54	1	0	0	1429.72	1072	1087
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	17	17	22	0.02%	8.4%	ALTQTGGPHVK	99.6%	39.2	25	30.5	2	0	0	1108.61	1284	1294
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	17	17	22	0.02%	8.4%	ANLPQSFQVDTSK	99.7%	44.1	25	41.2	1	0	0	1434.72	1465	1477
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	17	17	22	0.02%	8.4%	AWGPGLEGGVVGK	99.7%	53.2	25	47.9	2	0	0	1226.65	581	593
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	17	17	22	0.02%	8.4%	EGPYSISVLYGDEEVPR	99.7%	99.5	25	99.5	1	0	0	1909.92	1516	1532
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	17	17	22	0.02%	8.4%	IANLQTDLSDGLR	99.7%	71.9	25	61.2	1	0	0	1415.75	64	76
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	17	17	22	0.02%	8.4%	LLGWIQNK	99.7%	46.1	25	33.3	2	0	0	971.57	172	179
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	17	17	22	0.02%	8.4%	LYSVSYLLK	98.9%	34.1	25	13.6	1	0	0	1085.62	2613	2621
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	17	17	22	0.02%	8.4%	SPFSVAVSPSLDLSK	99.7%	74.8	25	71.5	2	0	0	1533.82	959	973
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	17	17	22	0.02%	8.4%	TGVELGKPTHFTVNAK	98.1%	26.4	25	26.4	0	1	0	1698.92	885	900
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	17	17	22	0.02%	8.4%	VEPGLGADNSVVR	96.2%	29	25	20.4	1	0	0	1312.69	1020	1032

Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	17	17	22	0.02%	8.4%	VHGPGIQSGTTNKPNK	95.8%	23.5	25	10	0	1	0	1634.86	1360	1375
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	17	17	22	0.02%	8.4%	VNVGAGSHPNK	99.4%	36.8	25	33	2	0	0	1079.56	761	771
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	17	17	22	0.02%	8.4%	VPVHDVTDASK	99.7%	48.1	25	41.3	1	0	0	1167.60	1440	1450
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	17	17	22	0.02%	8.4%	VTAQGPGLEPSGNIANK	99.7%	72.2	25	71.4	1	0	0	1652.86	384	400
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	17	17	22	0.02%	8.4%	VTVLFAGQHIAK	99.2%	35.2	25	28.1	1	0	0	1283.75	356	367
Filamin-A	FLNA	FLNA_HUMAN	280.7	100.0%	17	17	22	0.02%	8.4%	YGGDEIPFSPYR	99.7%	48.6	25	22.1	1	0	0	1400.65	1622	1633
Flap endonuclease 1	FEN1	FEN1_HUMAN	42.6	100.0%	2	2	4	0.00%	5.8%	KLPIQEFHLSR	99.4%	30.7	25	28.7	0	2	0	1367.78	201	211
Flap endonuclease 1	FEN1	FEN1_HUMAN	42.6	100.0%	2	2	4	0.00%	5.8%	LIADVAPSAIR	99.7%	58.7	25	45.2	2	0	0	1125.66	9	19
Fragile X mental retardation protein 1	FMR1	FMR1_HUMAN	71.2	100.0%	4	5	7	0.01%	11.1%	EDLMGLAIGTHGANIQQAR	99.7%	67.6	25	63	0	4	0	1995.01	227	245
Fragile X mental retardation protein 1	FMR1	FMR1_HUMAN	71.2	100.0%	4	5	7	0.01%	11.1%	LIQEIVDK	99.2%	35.7	25	16.2	2	0	0	957.56	303	310
Fragile X mental retardation protein 1	FMR1	FMR1_HUMAN	71.2	100.0%	4	5	7	0.01%	11.1%	LQIDEQLR	99.7%	48.9	25	32.6	2	0	0	1014.56	435	442
Fragile X mental retardation protein 1	FMR1	FMR1_HUMAN	71.2	100.0%	4	5	7	0.01%	11.1%	QIGASSRPPPNR	98.1%	26.4	25	23.8	1	1	0	1279.69	443	454
Fragile X mental retardation protein 1	FMR1	FMR1_HUMAN	71.2	100.0%	4	5	7	0.01%	11.1%	SFLEFAEDVIQVPR	99.7%	65.3	25	62.8	1	0	0	1649.85	277	290
Fragile X mental retardation protein 1	FMR1	FMR1_HUMAN	71.2	100.0%	4	5	7	0.01%	11.1%	VRIEAENEK	99.7%	49.4	25	38.8	2	0	0	1087.57	316	324
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	10	12	20	0.02%	20.1%	AGYSTDESSSSSLHATR	99.7%	95.7	25	86.3	1	1	0	1755.78	407	423
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	10	12	20	0.02%	20.1%	EDLMGLAIGTHGANIQQAR	99.7%	67.6	25	63	0	4	0	1995.01	237	255
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	10	12	20	0.02%	20.1%	EEGMVPFIFVGTR	99.7%	65.1	25	60	2	0	0	1497.74	339	351
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	10	12	20	0.02%	20.1%	IYGETPEACR	99.7%	47.4	25	38.5	2	0	0	1195.54	274	283
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	10	12	20	0.02%	20.1%	LQIDEQLR	99.7%	48.9	25	32.6	2	0	0	1014.56	379	386
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	10	12	20	0.02%	20.1%	LRPVNPNPLATK	99.7%	49.8	25	45.2	2	0	0	1319.78	122	133
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	10	12	20	0.02%	20.1%	SYLEFSEDSVQVPR	99.7%	71.4	25	67.4	2	0	0	1655.79	287	300
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	10	12	20	0.02%	20.1%	TGGPAYGPSSDVSTASETESEKR	95.5%	23.3	25	23.3	0	1	0	2313.05	438	460
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	10	12	20	0.02%	20.1%	VIQEIVDK	99.6%	39	25	23.9	2	0	0	943.55	313	320
Fragile X mental retardation syndrome-related protein 2	FXR2	FXR2_HUMAN	74.2	100.0%	10	12	20	0.02%	20.1%	YNSSSISSVLK	99.7%	44.7	25	38.5	1	0	0	1184.62	502	512
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	3	3	5	0.00%	9.6%	AAQEEYVKR	99.0%	34.5	25	26.1	1	0	0	1093.56	323	331
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	3	3	5	0.00%	9.6%	GILAADESTGSIAK	99.7%	82.5	25	73.5	2	0	0	1332.70	29	42
Fructose-bisphosphate aldolase A	ALDOA	ALDOA_HUMAN	39.4	100.0%	3	3	5	0.00%	9.6%	PYQYPALTPEQK	99.5%	37.2	25	31.8	2	0	0	1434.73	2	13
Fumarylacetoacetate hydrolase domain-containing protein 2A	FAHD2A	FAH2A_HUMAN	34.6	99.8%	2	2	3	0.00%	8.0%	DSVADPHNLK	98.3%	32.2	25	28.1	1	0	0	1095.54	225	234
Fumarylacetoacetate hydrolase domain-containing protein 2A	FAHD2A	FAH2A_HUMAN	34.6	99.8%	2	2	3	0.00%	8.0%	TFDTFCPLGPALVTK	99.7%	59.2	25	52.9	2	0	0	1666.85	210	224
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	5	5	13	0.01%	15.6%	EEFGAEPELAVSAPGR	99.7%	41.8	25	41.8	2	0	0	1658.80	22	37
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	5	5	13	0.01%	15.6%	EVQLEELEAAR	99.7%	73.9	25	66.2	4	0	0	1286.66	257	267
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	5	5	13	0.01%	15.6%	QPQVAELLAEAR	99.7%	40.7	25	39.8	1	0	0	1324.72	6	17
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	5	5	13	0.01%	15.6%	SLETSLVPLSDPK	99.7%	49.9	25	35	4	0	0	1385.75	205	217
Galactokinase	GALK1	GALK1_HUMAN	42.3	100.0%	5	5	13	0.01%	15.6%	TAQAAAALR	99.7%	66.6	25	53.5	2	0	0	872.49	288	296
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	7	7	12	0.01%	8.8%	AASAPYFEVLEK	99.7%	53.3	25	41.5	1	0	0	1324.68	382	393
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	7	7	12	0.01%	8.8%	LWFYIQPAMR	99.7%	45.5	25	39.8	1	0	0	1324.69	324	333
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	7	7	12	0.01%	8.8%	NLDPLVYLLSK	99.7%	57.8	25	52	2	0	0	1274.74	77	87
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	7	7	12	0.01%	8.8%	TFLVDPNLDLSIR	99.7%	60.4	25	47	2	0	0	1502.82	245	257
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	7	7	12	0.01%	8.8%	VLLDFLMEEK	99.7%	61.8	25	50.1	2	0	0	1236.65	498	507
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	7	7	12	0.01%	8.8%	WPLSLIINR	99.7%	50.3	25	50.3	2	0	0	1111.66	624	632
Gamma-tubulin complex component 2	TUBGCP2	GCP2_HUMAN	102.5	100.0%	7	7	12	0.01%	8.8%	YTIVQQQIPSFLQK	99.7%	69.8	25	69.8	2	0	0	1692.93	432	445
Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	4	4	5	0.00%	4.8%	ALEDITASIAMAVIQQK	99.7%	53.4	25	46.3	1	0	0	1817.97	398	414
Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	4	4	5	0.00%	4.8%	EWGEELQAVLR	99.7%	42.5	25	34.7	1	0	0	1329.68	326	336
Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	4	4	5	0.00%	4.8%	IFIQTLEANACR	99.7%	73.1	25	66.2	1	0	0	1435.74	673	684
Gem-associated protein 4	GEMIN4	GEMI4_HUMAN	120.0	100.0%	4	4	5	0.00%	4.8%	SIAEGIGPEER	99.7%	50.3	25	42.8	2	0	0	1157.58	1037	1047
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	12	12	17	0.02%	9.4%	GVLQTAAER	99.7%	57.3	25	37.8	2	0	0	944.52	934	942
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	12	12	17	0.02%	9.4%	GVVFCYWFNR	99.6%	38.6	25	38.3	1	0	0	1347.63	132	141
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	12	12	17	0.02%	9.4%	LSGEAFDINK	99.7%	59.8	25	47.7	2	0	0	1093.55	515	524
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	12	12	17	0.02%	9.4%	SIFSLDTPEQYQEAFQK	99.7%	49	25	49	1	0	0	2030.97	1166	1182
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	12	12	17	0.02%	9.4%	SLEAFFLYGR	99.7%	69.2	25	62.5	3	0	0	1202.62	1275	1284
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	12	12	17	0.02%	9.4%	TSVFLVR	97.9%	31.4	25	10.7	1	0	0	821.49	34	40

Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	12	12	17	0.02%	9.4%	TVAEVQETLAEMIR	99.7%	52.8	25	52.8	2	0	0	1589.82	1373	1386
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	12	12	17	0.02%	9.4%	TVIESSPESPVTITEPYR	99.7%	70.2	25	70.2	1	0	0	2005.01	616	633
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	12	12	17	0.02%	9.4%	VGPGAGESPGTPPFR	97.6%	30.8	25	30.8	1	0	0	1425.71	41	55
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	12	12	17	0.02%	9.4%	VIGELVGHTER	99.7%	55.5	25	55.5	1	0	0	1209.66	56	66
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	12	12	17	0.02%	9.4%	VYEAVELLK	99.4%	36.4	25	36.4	1	0	0	1063.60	991	999
Gem-associated protein 5	GEMIN5	GEMI5_HUMAN	168.6	100.0%	12	12	17	0.02%	9.4%	YPSATNNTPAK	98.9%	34	25	13.6	1	0	0	1163.57	1188	1198
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	8	8	9	0.01%	4.7%	IASNVLNTK	95.4%	28.2	25	11.6	1	0	0	959.55	1278	1286
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	8	8	9	0.01%	4.7%	LCYMGLLQFGPTEK	99.6%	38.2	25	20.5	1	0	0	1656.81	972	985
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	8	8	9	0.01%	4.7%	NAVIVDTTICDPHYNLAR	99.7%	37	25	37	0	1	0	2072.02	999	1016
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	8	8	9	0.01%	4.7%	NLIIEAVTNLR	99.7%	65	25	60.5	2	0	0	1255.74	619	629
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	8	8	9	0.01%	4.7%	NLSEEGLLR	99.0%	34.6	25	22.5	1	0	0	1030.55	665	673
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	8	8	9	0.01%	4.7%	NPQAYLNYK	99.4%	36.8	25	31.5	1	0	0	1110.56	1326	1334
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	8	8	9	0.01%	4.7%	NSNLEIPDTLQELFAR	99.7%	46.6	25	46.6	1	0	0	1859.95	1384	1399
General transcription factor 3C polypeptide 1	GTF3C1	TF3C1_HUMAN	238.9	100.0%	8	8	9	0.01%	4.7%	NWIWTSYIINQAK	99.1%	35	25	35	1	0	0	1636.85	1130	1142
General transcription factor 3C polypeptide 2	GTF3C2	TF3C2_HUMAN	100.7	99.8%	2	2	4	0.00%	2.1%	DLDRPESQSPK	99.7%	44.2	25	39.5	2	0	0	1271.62	159	169
General transcription factor 3C polypeptide 2	GTF3C2	TF3C2_HUMAN	100.7	99.8%	2	2	4	0.00%	2.1%	SPLFSVQR	99.7%	52	25	37.6	2	0	0	933.52	355	362
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	3	3	5	0.00%	4.1%	AIFAVLTSVLTK	99.7%	98.9	25	98.9	2	0	0	1262.77	611	622
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	3	3	5	0.00%	4.1%	ISLSTLQQQLGQPEK	99.7%	64	25	53.5	1	0	0	1669.91	494	508
General transcription factor 3C polypeptide 3	GTF3C3	TF3C3_HUMAN	101.3	100.0%	3	3	5	0.00%	4.1%	YNLAVVWLR	99.7%	76.9	25	59.2	2	0	0	1133.65	453	461
General transcription factor 3C polypeptide 4	GTF3C4	TF3C4_HUMAN	92.0	100.0%	3	3	4	0.00%	4.6%	NEAPEGNLGDFAEFQR	99.7%	57.9	25	57.9	1	0	0	1793.81	226	241
General transcription factor 3C polypeptide 4	GTF3C4	TF3C4_HUMAN	92.0	100.0%	3	3	4	0.00%	4.6%	NYQVQFVTLK	99.7%	47.4	25	38.6	2	0	0	1239.67	507	516
General transcription factor 3C polypeptide 4	GTF3C4	TF3C4_HUMAN	92.0	100.0%	3	3	4	0.00%	4.6%	QLIPIFTDVALK	99.7%	45.1	25	29.3	1	0	0	1357.81	449	460
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	11	12	21	0.02%	24.7%	DPYCHPVCANR	99.6%	38.3	25	36.5	2	0	0	1388.58	68	78
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	11	12	21	0.02%	24.7%	EGYNNPPISGENLIGLSR	99.7%	72.5	25	63.9	2	0	0	1929.97	192	209
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	11	12	21	0.02%	24.7%	FSTSSLLLR	99.7%	57.9	25	42.8	2	0	0	1023.58	79	87
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	11	12	21	0.02%	24.7%	HGYAPSDLPVK	99.7%	44.1	25	44.1	2	0	0	1183.61	329	339
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	11	12	21	0.02%	24.7%	IYADPTKR	98.6%	33	25	21.5	1	0	0	963.53	52	59
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	11	12	21	0.02%	24.7%	IYQVLDFR	99.7%	65.7	25	58	2	0	0	1053.57	315	322
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	11	12	21	0.02%	24.7%	LDAPVDYFYRPETQHR	99.7%	46.9	25	46.9	0	1	0	2006.97	176	191
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	11	12	21	0.02%	24.7%	LFDIRPIWSR	95.8%	23.5	25	18.9	0	1	0	1302.73	257	266
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	11	12	21	0.02%	24.7%	MLPTLGGEEGVSR	99.7%	59.9	25	53.1	4	0	0	1345.68	39	51
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	11	12	21	0.02%	24.7%	QGLGPSGTSGAR	99.7%	64.5	25	50.8	2	0	0	1087.55	368	379
General transcription factor 3C polypeptide 5	GTF3C5	TF3C5_HUMAN	59.6	100.0%	11	12	21	0.02%	24.7%	STYNYSLPITVK	99.7%	60	25	56.3	2	0	0	1385.73	343	354
General transcription factor II-I	GTF2I	GTF2I_HUMAN	112.4	100.0%	2	2	3	0.00%	2.1%	FAQALGLTEAVK	99.7%	75	25	52.8	2	0	0	1247.70	583	594
General transcription factor II-I	GTF2I	GTF2I_HUMAN	112.4	100.0%	2	2	3	0.00%	2.1%	RPSTYGIPR	98.5%	32.9	25	17.3	1	0	0	1046.57	410	418
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	DSEQVAELKQELATLK	98.3%	32.3	25	32.3	1	0	0	1801.95	783	798
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	EQDDLLVLLADQDQK	99.7%	107	25	80.3	2	0	0	1742.88	905	919
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	EQDLQLEELR	99.1%	35.2	25	13.1	1	0	0	1272.64	661	670
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	GVMGGQSAGPQHTEAETIQK	99.7%	35	25	35	0	2	0	2041.96	6	25
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	IVAFENAFER	99.7%	70.6	25	64.4	2	0	0	1195.61	203	212
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	LMDLLADSR	99.7%	68.9	25	51.7	4	0	0	1033.53	171	179
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	LSALLQETK	99.7%	52	25	41.2	2	0	0	1002.58	850	858
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	NDGVLLLQALTR	99.7%	93	25	87.6	2	0	0	1312.76	184	195
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	NQELLQSQLTEK	99.7%	76.6	25	73.9	1	0	0	1430.75	745	756
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	QSEDLGSQFTEIFIK	99.7%	101	25	95.4	2	0	0	1741.86	105	119
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	SQLNSQSVEITK	99.7%	72.4	25	65.2	2	0	0	1333.70	799	810
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	SSQTSGTNEQSSAIVSAR	99.7%	133	25	113	2	0	0	1809.86	765	782
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	SVEVQGETETIIATK	99.7%	99.4	25	82.3	1	0	0	1604.84	828	842
General vesicular transport factor p115	USO1	USO1_HUMAN	107.9	100.0%	14	15	25	0.02%	19.1%	VASSTLLDDRR	98.4%	32.5	25	18.9	1	0	0	1232.66	30	40
Geranylgeranyl transferase type-2 subunit alpha	RABGGTA	PGTA_HUMAN	65.1	100.0%	3	3	5	0.00%	5.5%	FLLENSVLK	99.7%	45.6	25	19.6	2	0	0	1062.62	429	437
Geranylgeranyl transferase type-2 subunit alpha	RABGGTA	PGTA_HUMAN	65.1	100.0%	3	3	5	0.00%	5.5%	LYQSATQAVFQK	99.7%	61.9	25	55.5	2	0	0	1383.73	27	38

Geranylgeranyl transferase type-2 subunit alpha	RABGGTA	PGTA_HUMAN	65.1	100.0%	3	3	5	0.00%	5.5%	VIWTAGDVQK	95.8%	28.6	25	22.7	1	0	0	1116.60	320	329
Glomulin	GLMN	GLMN_HUMAN	68.2	100.0%	5	5	8	0.01%	9.6%	GLELLENSLLR	99.7%	62.6	25	47.8	3	0	0	1256.72	335	345
Glomulin	GLMN	GLMN_HUMAN	68.2	100.0%	5	5	8	0.01%	9.6%	IEDNSLLYQYLEIK	99.7%	40	25	38.7	1	0	0	1740.91	346	359
Glomulin	GLMN	GLMN_HUMAN	68.2	100.0%	5	5	8	0.01%	9.6%	SFLTVPQGLVK	99.7%	47.2	25	47.2	1	0	0	1188.70	360	370
Glomulin	GLMN	GLMN_HUMAN	68.2	100.0%	5	5	8	0.01%	9.6%	STSEENIGIK	99.4%	36.8	25	30.1	2	0	0	1077.54	585	594
Glomulin	GLMN	GLMN_HUMAN	68.2	100.0%	5	5	8	0.01%	9.6%	VMTLCPIETLR	99.7%	39.5	25	22.5	1	0	0	1332.70	371	381
Glucose-6-phosphate isomerase	GPI	G6PI_HUMAN	63.1	100.0%	3	3	4	0.00%	8.4%	ILLANFLAQTEALMR	99.7%	93.9	25	88.7	2	0	0	1703.95	424	438
Glucose-6-phosphate isomerase	GPI	G6PI_HUMAN	63.1	100.0%	3	3	4	0.00%	8.4%	TLAQLNPESSLFIIASK	99.7%	41.3	25	41.3	1	0	0	1832.02	195	211
Glucose-6-phosphate isomerase	GPI	G6PI_HUMAN	63.1	100.0%	3	3	4	0.00%	8.4%	VFEGNRPTNSIVFTK	99.6%	38.4	25	23.3	1	0	0	1708.90	467	481
Glutamate--cysteine ligase regulatory subunit	GCLM	GSH0_HUMAN	30.7	100.0%	3	3	3	0.00%	13.9%	INPDEREEMK	98.9%	34.1	25	34.1	1	0	0	1260.59	81	90
Glutamate--cysteine ligase regulatory subunit	GCLM	GSH0_HUMAN	30.7	100.0%	3	3	3	0.00%	13.9%	LFIVESNSSSSTR	99.7%	41	25	38.5	1	0	0	1426.72	95	107
Glutamate--cysteine ligase regulatory subunit	GCLM	GSH0_HUMAN	30.7	100.0%	3	3	3	0.00%	13.9%	TLNEWSSQINPDLVR	99.7%	56.6	25	56.6	1	0	0	1771.90	50	64
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	7	7	13	0.01%	26.5%	AQTGAPCLSFDIVR	99.7%	51.3	25	48.7	2	0	0	1534.77	60	73
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	7	7	13	0.01%	26.5%	DPEAGDVEADPGLADLPQQLLFVHQGETELK	99.7%	99.8	25	99.8	0	2	0	3331.63	388	418
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	7	7	13	0.01%	26.5%	EGEELVMDEEAYVLYHR	99.7%	33.4	25	33.4	0	1	0	2081.95	43	59
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	7	7	13	0.01%	26.5%	GQVEVFALR	99.7%	51.4	25	35.7	2	0	0	1018.57	173	181
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	7	7	13	0.01%	26.5%	LLQVVEEPQALAAFLR	99.7%	120	25	116	2	0	0	1797.03	183	198
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	7	7	13	0.01%	26.5%	REPFLLSGGDDGALK	99.7%	51.9	25	51.9	0	2	0	1574.82	319	333
Glutamate-rich WD repeat-containing protein 1	GRWD1	GRWD1_HUMAN	49.4	100.0%	7	7	13	0.01%	26.5%	VSWLGEEPVAGVWSEK	99.7%	77.8	25	77.8	2	0	0	1772.89	157	172
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	4	4	5	0.00%	6.9%	GYDFESETDTETIAK	99.7%	85.7	25	85.7	2	0	0	1705.74	140	154
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	4	4	5	0.00%	6.9%	GYDVDFPR	99.7%	42.4	25	42.4	1	0	0	968.45	683	690
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	4	4	5	0.00%	6.9%	LSTDHIPILYR	99.7%	41.6	25	40	1	0	0	1327.74	217	227
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	GFPT1_HUMAN	78.8	100.0%	4	4	5	0.00%	6.9%	VIQQLEGAFALVFK	99.7%	69.7	25	69.7	1	0	0	1562.89	177	190
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	27	0.03%	22.6%	AINFNFGYAK	99.7%	50.9	25	39	2	0	0	1144.58	283	292
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	27	0.03%	22.6%	DVLNDTAPR	99.7%	44.1	25	35.4	2	0	0	1000.51	559	567
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	27	0.03%	22.6%	EAATQAQQTLGSTIDK	99.7%	103	25	99.4	2	0	0	1661.83	35	50
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	27	0.03%	22.6%	FDDTNPEKEEAK	99.7%	72.6	25	61.7	2	0	0	1422.64	302	313
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	27	0.03%	22.6%	FSEGEATLR	99.7%	58.6	25	43.5	2	0	0	1009.49	395	403
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	27	0.03%	22.6%	GFHQVPFAPIVFIER	99.7%	33.9	25	32.9	0	2	0	1756.95	602	616
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	27	0.03%	22.6%	GPSGCVESLEVTCR	99.7%	68.5	25	68.5	1	0	0	1550.69	653	666
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	27	0.03%	22.6%	HTGYVIELQHVVK	99.7%	44.4	25	42.3	0	2	0	1522.84	640	652
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	27	0.03%	22.6%	ILQLVATGAVR	99.7%	95.3	25	87.1	2	0	0	1140.71	499	509
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	27	0.03%	22.6%	LAWGQPVGLR	99.7%	59.5	25	49	2	0	0	1096.63	630	639
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	27	0.03%	22.6%	LFTLTALR	99.7%	70.3	25	50	2	0	0	934.57	516	523
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	27	0.03%	22.6%	LGYFSVDPDSHQGK	99.7%	39.8	25	39.8	1	0	0	1549.73	746	759
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	27	0.03%	22.6%	LSFLVSYIASK	99.7%	88.4	25	83.2	2	0	0	1227.70	69	79
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	27	0.03%	22.6%	NSALSAQLR	99.7%	76.2	25	65.3	2	0	0	959.53	26	34
Glutamine--tRNA ligase	QARS	SYQ_HUMAN	87.8	100.0%	15	15	27	0.03%	22.6%	SHPLDPIDTVDFER	99.7%	44.7	25	44.7	1	0	0	1640.79	96	109
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	4	4	10	0.01%	9.7%	FLEATLR	96.3%	29.1	25	12.9	1	0	0	849.48	118	124
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	4	4	10	0.01%	9.7%	TEELPLGR	96.4%	29.2	25	21.6	1	0	0	914.49	59	66
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	4	4	10	0.01%	9.7%	TPGSPGNLQVR	99.7%	56.4	25	48	3	0	0	1125.60	106	116
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	QPCTL_HUMAN	42.9	100.0%	4	4	10	0.01%	9.7%	VPLIGSLPEAR	99.7%	60.1	25	56.8	5	0	0	1151.68	70	80
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	10	13	25	0.02%	37.3%	GALQNIIPASTGAAK	99.7%	86.6	25	83.9	5	0	0	1411.79	201	215
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	10	13	25	0.02%	37.3%	IISNASCTTNCLAPLAK	99.7%	110	25	107	2	0	0	1833.92	146	162
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	10	13	25	0.02%	37.3%	LTGMAFR	97.2%	30.3	25	22	1	0	0	811.41	228	234
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	10	13	25	0.02%	37.3%	LVINGNPITIFQER	99.7%	74.5	25	68.7	2	0	0	1613.90	67	80
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	10	13	25	0.02%	37.3%	LVINGNPITIFQERDPSK	99.3%	30.7	25	27.4	0	1	0	2041.11	67	84
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	10	13	25	0.02%	37.3%	VIISAPSADAPMFVMGVNHEK	97.9%	26.1	25	26.1	0	1	0	2245.10	119	139
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	10	13	25	0.02%	37.3%	VPTANVSVVDLTCR	99.7%	99.2	25	95.6	2	2	0	1530.79	235	248
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	10	13	25	0.02%	37.3%	VVDLMAHMASK	99.7%	49.3	25	40.8	1	0	0	1201.61	324	334
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	10	13	25	0.02%	37.3%	VVDLMAHMASKE	99.7%	73.6	25	63	6	1	0	1330.65	324	335

Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	G3P_HUMAN	36.1	100.0%	10	13	25	0.02%	37.3%	WGDAGAEYVVESTGVFTTMEK	99.7%	82.4	25	82.4	1	0	0	2293.03	87	107
Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	GPD1L_HUMAN	38.4	100.0%	4	4	6	0.01%	13.7%	ICDEITGR	95.0%	27.9	25	22	1	0	0	963.46	103	110
Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	GPD1L_HUMAN	38.4	100.0%	4	4	6	0.01%	13.7%	LQGPQTSAEVYR	99.7%	55	25	55	2	0	0	1348.69	299	310
Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	GPD1L_HUMAN	38.4	100.0%	4	4	6	0.01%	13.7%	LTDIINNDHENVK	99.7%	43.1	25	38.5	1	0	0	1524.77	52	64
Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	GPD1L_HUMAN	38.4	100.0%	4	4	6	0.01%	13.7%	VCIVGSGNWGSAVAK	99.7%	46.3	25	38.6	2	0	0	1504.76	8	22
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	5	5	9	0.01%	10.3%	LPFAAAQIGNSFR	99.7%	73.9	25	68.9	2	0	0	1391.74	319	331
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	5	5	9	0.01%	10.3%	SPITGNDLSPPVSFNLMFK	99.7%	44.8	25	39.3	2	0	0	2064.05	265	283
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	5	5	9	0.01%	10.3%	TLYVEEVVPNVIEPSFGLGR	99.7%	55.4	25	55.4	2	0	0	2218.18	564	583
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	5	5	9	0.01%	10.3%	TVNVVQFEPSK	99.7%	45.9	25	40.7	2	0	0	1247.66	491	501
Glycine--tRNA ligase	GARS	SYG_HUMAN	83.2	100.0%	5	5	9	0.01%	10.3%	VPLVAEKPLKEPK	97.8%	25.9	25	25.9	0	1	0	1447.89	478	490
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	15	0.01%	16.1%	DYFFALAHTVR	99.7%	55.2	25	47.6	1	0	0	1339.68	51	61
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	15	0.01%	16.1%	GLAGLGDVAEVR	99.7%	87.7	25	80.1	2	0	0	1156.63	18	29
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	15	0.01%	16.1%	IGEEFLTDLSQLK	99.7%	77.2	25	65.2	2	0	0	1492.79	508	520
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	15	0.01%	16.1%	IGEEFLTDLSQLKK	98.5%	27.2	25	27.2	0	1	0	1620.88	508	521
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	15	0.01%	16.1%	LLPLVSDEVFIR	99.7%	55.2	25	53	2	0	0	1400.81	522	533
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	15	0.01%	16.1%	LVTSIGDVVNHDPVVGDR	99.7%	42.4	25	40.6	0	2	0	1891.99	623	640
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	15	0.01%	16.1%	NLAENISR	99.6%	38.7	25	15	3	0	0	916.48	271	278
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	15	0.01%	16.1%	VEDVEALDR	99.7%	46.5	25	36.9	2	0	0	1045.52	716	724
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	15	0.01%	16.1%	VIFLENYR	99.7%	57.9	25	47.2	2	0	0	1053.57	643	650
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	15	0.01%	16.1%	VLYPNDNFFEGK	99.7%	66.1	25	66.1	2	0	0	1442.70	279	290
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	15	0.01%	16.1%	WLLLCNPGLADTIVEK	99.7%	67.9	25	67.9	2	0	0	1841.98	492	507
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	15	0.01%	16.1%	YEFGIFNQK	99.3%	35.9	25	34	1	0	0	1145.56	162	170
Glycogen phosphorylase, brain form	PYGB	PYGB_HUMAN	96.7	100.0%	9	9	15	0.01%	16.1%	YGNPWEK	96.2%	29	25	21.8	2	0	0	893.42	186	192
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	APNDFNLR	99.7%	50.8	25	39.8	2	0	0	946.47	249	256
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	DFNVGDYIQAVLDR	99.7%	96.8	25	91.9	2	0	0	1624.80	257	270
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	DFSELEPDKFQNK	99.7%	59.7	25	53.9	1	0	0	1596.75	471	483
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	DGWQVEEADDWLR	99.7%	73.3	25	60.6	1	0	0	1618.71	173	185
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	DIINMLFYHDR	99.6%	38.6	25	32.2	1	0	0	1436.70	761	771
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	DYYFALAHTVR	99.7%	59.7	25	49.6	2	0	0	1355.67	51	61
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	EYAQNIWNVEPSDLK	99.7%	59.7	25	54.3	2	0	0	1805.87	820	834
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	EYYEALPELK	99.7%	40.5	25	33.4	2	0	0	1254.63	731	740
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	FSQFLETEYK	99.7%	71.5	25	66	2	0	0	1291.62	546	555
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	GIVGVENVAELK	99.7%	53.7	25	42.9	2	0	0	1227.69	18	29
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	GIVGVENVAELKK	99.7%	65.9	25	64.2	2	1	0	1355.79	18	30
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	HLEIIYEINQK	99.7%	61.1	25	50.5	2	0	0	1399.76	400	410
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	IDDVAALDK	99.7%	50.2	25	45.2	1	0	0	959.50	716	724
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	IDDVAALDKK	99.7%	57	25	38.6	2	0	0	1087.60	716	725
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	IFVDIEK	96.0%	28.8	25	14.3	1	0	0	863.49	353	359
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	IFVDIEKLPWSK	99.1%	29.5	25	27.9	0	1	0	1474.83	353	364
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	IGEDYVK	96.9%	29.8	25	16.2	1	0	0	823.42	508	514
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	INPSSMFDVQVK	99.7%	80	25	65.6	2	0	0	1364.69	558	569
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	LHSFLGDDVFLR	99.7%	66.7	25	56.9	2	2	0	1418.74	522	533
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	LITSVADVVNNDPMVGSK	99.7%	121	25	118	4	0	0	1858.96	623	640
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	LVIDQIDNGFFSPK	99.7%	83.3	25	81.6	2	0	0	1592.83	741	754
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	MSLIEEEGSKR	99.7%	55.2	25	40.8	3	0	0	1278.64	429	439
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	NLAENISR	99.6%	38.7	25	15	3	0	0	916.48	271	278
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	SRPEFMLPVHFYGK	99.7%	38.7	25	36.8	0	2	0	1707.87	193	206
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	TFAYTNHTVLPEALER	99.7%	39.3	25	36.8	0	2	0	1861.94	372	387
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	VFADYEAYVK	99.7%	61.4	25	58.4	2	0	0	1204.59	774	783
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	VIFLENYR	99.7%	57.9	25	47.2	2	0	0	1053.57	643	650
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	VIPATDLSEQISTAGTEASGTGNMK	99.7%	37.6	25	37.6	0	3	0	2494.20	657	681

Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	VLYPNDNFFEGK	99.7%	66.1	25	66.1	2	0	0	1442.70	279	290
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	VSQLYMNPK	99.7%	63.2	25	51.1	2	0	0	1079.56	788	796
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	WLLLCNPGLAELIAEK	97.1%	30.1	25	30.1	1	0	0	1840.00	492	507
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	WPVDLVEK	99.7%	40.9	25	32.2	2	0	0	985.54	388	395
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	YEYGIFNQK	99.4%	37.1	25	36.5	2	0	0	1161.56	162	170
Glycogen phosphorylase, liver form	PYGL	PYGL_HUMAN	97.2	100.0%	34	40	68	0.06%	43.3%	YGNPWEK	96.2%	29	25	21.8	2	0	0	893.42	186	192
Glycylpeptide N-tetradecanoyltransferase 1	NMT1	NMT1_HUMAN	56.8	100.0%	3	3	3	0.00%	8.1%	AIELFSVGQGPAK	99.7%	63.8	25	58.7	1	0	0	1316.72	95	107
Glycylpeptide N-tetradecanoyltransferase 1	NMT1	NMT1_HUMAN	56.8	100.0%	3	3	3	0.00%	8.1%	GFDVFNALDLMENK	99.2%	35.3	25	35.3	1	0	0	1628.76	446	459
Glycylpeptide N-tetradecanoyltransferase 1	NMT1	NMT1_HUMAN	56.8	100.0%	3	3	3	0.00%	8.1%	GSETDSAQDQPVK	98.8%	33.6	25	33.6	1	0	0	1361.62	68	80
Glyoxylate reductase/hydroxypyruvate reductase	GRHPR	GRHPR_HUMAN	35.7	100.0%	3	3	6	0.01%	11.0%	ILDAAGANLK	99.7%	74.1	25	59.8	2	0	0	985.57	67	76
Glyoxylate reductase/hydroxypyruvate reductase	GRHPR	GRHPR_HUMAN	35.7	100.0%	3	3	6	0.01%	11.0%	NTMSLLAANNLLAGLR	99.7%	53.6	25	44.9	2	0	0	1687.92	303	318
Glyoxylate reductase/hydroxypyruvate reductase	GRHPR	GRHPR_HUMAN	35.7	100.0%	3	3	6	0.01%	11.0%	RLPEAIEEVK	99.7%	55.9	25	42.6	2	0	0	1183.67	125	134
GMP synthase [glutamine-hydrolyzing]	GMPS	GUAA_HUMAN	76.7	100.0%	2	2	3	0.00%	5.6%	ELFVQSEIFPLETPAFAIK	99.7%	50.7	25	50.7	1	0	0	2179.17	47	65
GMP synthase [glutamine-hydrolyzing]	GMPS	GUAA_HUMAN	76.7	100.0%	2	2	3	0.00%	5.6%	EPPTDVTPTFLTTGVLSTLR	99.7%	81.9	25	81.9	2	0	0	2145.14	570	589
Golgi phosphoprotein 3	GOLPH3	GOLP3_HUMAN	33.8	99.8%	2	2	2	0.00%	9.4%	QLLDLDPEVECLK	99.7%	44	25	44	1	0	0	1571.80	270	282
Golgi phosphoprotein 3	GOLPH3	GOLP3_HUMAN	33.8	99.8%	2	2	2	0.00%	9.4%	SDAPTGDVLLDEALK	99.7%	93.6	25	93.6	1	0	0	1543.79	124	138
Golgin subfamily A member 7	GOLGA7	GOGA7_HUMAN	15.8	99.8%	2	2	3	0.00%	19.0%	IYAPQGLLLTDPIER	99.7%	46.3	25	46.3	2	0	0	1698.94	104	118
Golgin subfamily A member 7	GOLGA7	GOGA7_HUMAN	15.8	99.8%	2	2	3	0.00%	19.0%	TLNNLYAEAEK	99.7%	45.9	25	45.4	1	0	0	1265.64	49	59
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	7	7	9	0.01%	4.8%	AASSSSPGSPVASSPSR	99.7%	68.9	25	63.5	1	0	0	1531.73	1776	1792
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	7	7	9	0.01%	4.8%	ENYVWNVLLHR	99.7%	51.5	25	46.9	2	0	0	1442.75	896	906
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	7	7	9	0.01%	4.8%	GATPEGIFLR	99.7%	41.1	25	18.4	1	0	0	1060.58	907	916
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	7	7	9	0.01%	4.8%	GGGPSALWEITWER	99.7%	49.6	25	43.2	1	0	0	1558.77	1691	1704
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	7	7	9	0.01%	4.8%	SEDTTGPITGLALTSVNK	99.7%	100	25	96.2	2	0	0	1803.93	74	91
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	7	7	9	0.01%	4.8%	SLEETIIQK	99.7%	50	25	45	1	0	0	1060.59	945	953
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	GBF1_HUMAN	206.5	100.0%	7	7	9	0.01%	4.8%	VLNSLTQQEK	99.7%	43.7	25	33.6	1	0	0	1159.63	596	605
GPI transamidase component PIG-T	PIGT	PIGT_HUMAN	65.7	100.0%	5	5	6	0.01%	8.5%	ALGQLISK	95.0%	27.9	25	21.1	1	0	0	829.51	72	79
GPI transamidase component PIG-T	PIGT	PIGT_HUMAN	65.7	100.0%	5	5	6	0.01%	8.5%	GELSTLLYNTHPYR	99.7%	53.2	25	53.2	1	0	0	1663.84	366	379
GPI transamidase component PIG-T	PIGT	PIGT_HUMAN	65.7	100.0%	5	5	6	0.01%	8.5%	LYVHTLTITSK	99.7%	47.9	25	40.6	1	0	0	1275.73	395	405
GPI transamidase component PIG-T	PIGT	PIGT_HUMAN	65.7	100.0%	5	5	6	0.01%	8.5%	TRWDSELQR	99.7%	47.3	25	22.2	1	0	0	1190.59	52	60
GPI transamidase component PIG-T	PIGT	PIGT_HUMAN	65.7	100.0%	5	5	6	0.01%	8.5%	VSIQFER	99.7%	47.3	25	15.8	2	0	0	878.47	442	448
GPI-anchor transamidase	PIGK	GPI8_HUMAN	45.3	99.8%	2	2	2	0.00%	5.3%	KVEITTETIK	98.2%	32	25	23	1	0	0	1161.67	309	318
GPI-anchor transamidase	PIGK	GPI8_HUMAN	45.3	99.8%	2	2	2	0.00%	5.3%	SYEVTVENFLR	99.7%	66.7	25	60.2	1	0	0	1356.68	123	133
G-rich sequence factor 1	GRSF1	GRSF1_HUMAN	53.1	99.8%	2	2	4	0.00%	6.9%	GLPFQANAQDIINFFAPLKPVR	99.7%	55.6	25	51.5	0	2	0	2456.35	407	428
G-rich sequence factor 1	GRSF1	GRSF1_HUMAN	53.1	99.8%	2	2	4	0.00%	6.9%	SSPVVNDGVVR	99.7%	48.7	25	35	2	0	0	1128.60	243	253
Growth arrest and DNA damage-inducible proteins-interacting protein 1	GADD45GIP1	G45IP_HUMAN	25.4	99.8%	2	2	4	0.00%	11.7%	FQELLQDLEK	99.7%	48.2	25	28.6	2	0	0	1262.66	175	184
Growth arrest and DNA damage-inducible proteins-interacting protein 1	GADD45GIP1	G45IP_HUMAN	25.4	99.8%	2	2	4	0.00%	11.7%	LQAEAQELLGYQVDPR	99.7%	81.9	25	81.9	2	0	0	1829.94	156	171
GTPase-activating protein and VPS9 domain-containing protein 1	GAPVD1	GAPD1_HUMAN	165.0	100.0%	3	3	4	0.00%	2.8%	AVETPPLSSVNLLEGLSR	99.7%	68.7	25	68.4	2	0	0	1882.03	387	404
GTPase-activating protein and VPS9 domain-containing protein 1	GAPVD1	GAPD1_HUMAN	165.0	100.0%	3	3	4	0.00%	2.8%	ILEDTQFVDGYK	99.7%	62.2	25	62.2	1	0	0	1427.71	76	87
GTPase-activating protein and VPS9 domain-containing protein 1	GAPVD1	GAPD1_HUMAN	165.0	100.0%	3	3	4	0.00%	2.8%	LIASSLVAGEK	99.7%	39.4	25	34.5	1	0	0	1087.64	109	119
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	11	31	0.03%	41.7%	FNVWDTAGQEK	99.7%	64.6	25	58.5	5	0	0	1294.61	61	71
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	11	31	0.03%	41.7%	GPIKFNVWDTAGQEK	99.7%	81.3	25	81.3	2	2	0	1689.86	57	71
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	11	31	0.03%	41.7%	HLTGEFEK	99.7%	39.6	25	34.3	2	0	0	960.48	30	37
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	11	31	0.03%	41.7%	HLTGEFEKK	96.1%	28.9	25	18.4	1	0	0	1088.57	30	38
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	11	31	0.03%	41.7%	KYVATLGVEVHPLVFHTNR	99.7%	73.8	25	66.3	0	1	0	2180.20	38	56
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	11	31	0.03%	41.7%	LVLVGDGGTGK	99.7%	71.4	25	20.5	2	0	0	1015.58	13	23
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	11	31	0.03%	41.7%	NLQYYDISAK	99.7%	50.6	25	50.6	8	0	0	1214.61	143	152
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	11	31	0.03%	41.7%	SNYNFEKPFLWLAR	99.7%	48.9	25	48.9	0	4	0	1784.91	153	166
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	11	31	0.03%	41.7%	VCENIPIVLCGNK	99.7%	73.8	25	63.4	2	0	0	1515.77	111	123
GTP-binding nuclear protein Ran	RAN	RAN_HUMAN	24.4	100.0%	10	11	31	0.03%	41.7%	YVATLGVEVHPLVFHTNR	99.7%	52.8	25	52.8	0	2	0	2052.10	39	56
GTP-binding protein 10	GTPBP10	GTPBA_HUMAN	42.9	100.0%	3	3	5	0.00%	8.0%	ILVAQGGLGGK	99.7%	41.4	25	31.5	1	0	0	1012.62	116	126
GTP-binding protein 10	GTPBP10	GTPBA_HUMAN	42.9	100.0%	3	3	5	0.00%	8.0%	LLTNFLPLK	99.7%	51	25	40	2	0	0	1058.66	127	135

GTP-binding protein 10	GTPBP10	GTPBA_HUMAN	42.9	100.0%	3	3	5	0.00%	8.0%	TAFETIILLTK	99.7%	65.3	25	61.2	2	0	0	1249.74	249	259
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	7	9	17	0.02%	33.7%	ALAESWNAAFLESSAK	99.7%	107	25	107	2	0	0	1694.84	136	151
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	7	9	17	0.02%	33.7%	ENQTAVDVFR	99.7%	68.3	25	54.2	2	0	0	1178.58	152	161
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	7	9	17	0.02%	33.7%	IAILGYR	98.5%	32.8	25	26.5	2	0	0	805.49	9	15
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	7	9	17	0.02%	33.7%	IILEAEKMDGAASQGK	99.7%	72.1	25	72.1	2	2	0	1676.85	163	178
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	7	9	17	0.02%	33.7%	KIAILGYR	99.7%	51	25	36	2	0	0	933.59	8	15
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	7	9	17	0.02%	33.7%	VQIPIMLVGNK	99.3%	36.4	25	26.1	3	0	0	1211.72	110	120
GTP-binding protein Rheb	RHEB	RHEB_HUMAN	20.5	100.0%	7	9	17	0.02%	33.7%	VQIPIMLVGNKK	98.0%	31.5	25	31.5	2	0	0	1355.81	110	121
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	GBB2_HUMAN	37.3	100.0%	4	4	8	0.01%	15.3%	ACGDSTLTQITAGLDPVGR	99.7%	73.9	25	63.9	2	0	0	1931.95	24	42
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	GBB2_HUMAN	37.3	100.0%	4	4	8	0.01%	15.3%	LIIWDSYTTNK	99.7%	75.3	25	62.4	2	0	0	1353.71	79	89
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	GBB2_HUMAN	37.3	100.0%	4	4	8	0.01%	15.3%	LLVSASQDGK	99.7%	47.6	25	37.1	2	0	0	1017.56	69	78
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	GBB2_HUMAN	37.3	100.0%	4	4	8	0.01%	15.3%	TFVSGACDASIK	99.7%	84.1	25	70.6	2	0	0	1255.60	198	209
Guanine nucleotide-binding protein subunit alpha-11	GNA11	GNA11_HUMAN	42.1	99.8%	2	2	2	0.00%	7.2%	IATLGYLPTQQDVLR	98.8%	33.6	25	33.6	1	0	0	1687.94	167	181
Guanine nucleotide-binding protein subunit alpha-11	GNA11	GNA11_HUMAN	42.1	99.8%	2	2	2	0.00%	7.2%	LLLLGTGESGK	99.7%	43.8	25	21.9	1	0	0	1087.64	42	52
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	17	43	0.04%	57.7%	DETNYGIPQR	99.7%	64.5	25	54.3	2	0	0	1192.56	48	57
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	17	43	0.04%	57.7%	DGQAMLWDLNEGK	99.7%	82.9	25	82.9	2	0	0	1492.67	213	225
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	17	43	0.04%	57.7%	DKTIIMWK	97.2%	30.1	25	18.8	2	0	0	1034.57	37	44
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	17	43	0.04%	57.7%	DVLSVAFSSDNR	99.7%	80.3	25	79.2	6	0	0	1309.64	107	118
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	17	43	0.04%	57.7%	FSPNSSNPIIVSCGWDK	99.7%	74.9	25	60.9	2	0	0	1907.90	156	172
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	17	43	0.04%	57.7%	HLYTLDGGDIINALCFSPNR	99.7%	104	25	104	2	2	0	2276.11	226	245
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	17	43	0.04%	57.7%	IIVDELKQEVISTSSK	99.7%	89.4	25	89.4	3	2	0	1789.00	265	280
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	17	43	0.04%	57.7%	LTRDETNYGIPQR	99.4%	37.1	25	31.6	2	0	0	1562.79	45	57
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	17	43	0.04%	57.7%	LWDLTTGTTTR	99.7%	82.7	25	79	3	0	0	1264.65	89	99
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	17	43	0.04%	57.7%	LWNTLGVCK	99.7%	44.5	25	34.2	2	0	0	1090.57	131	139
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	17	43	0.04%	57.7%	TNHIGHTGYLNTVTVSPDGSLCASGGK	99.7%	127	25	127	0	2	0	2743.31	186	212
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	17	43	0.04%	57.7%	VWQVTIGTR	99.7%	71	25	60.7	5	0	0	1059.59	309	317
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	17	43	0.04%	57.7%	YTVQDESHSEWVSCVR	99.7%	76.1	25	76.1	2	2	0	1981.87	140	155
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	GBLP_HUMAN	35.1	100.0%	14	17	43	0.04%	57.7%	YWLCAATGPSIK	99.7%	72.2	25	64.4	2	0	0	1366.68	246	257
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	11	13	24	0.02%	26.4%	ELPTVVFR	99.6%	38.5	25	31.9	2	0	0	960.55	198	205
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	11	13	24	0.02%	26.4%	ENLESWLNYLK	97.0%	30	25	29.1	1	0	0	1408.71	186	196
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	11	13	24	0.02%	26.4%	GGIPNVEGAAK	99.3%	36.3	25	33.3	1	0	0	1012.54	378	388
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	11	13	24	0.02%	26.4%	KDPGVPNSAPFK	99.7%	47.2	25	43.1	2	0	0	1256.66	46	57
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	11	13	24	0.02%	26.4%	KLVLILNK	99.7%	41.9	25	41.9	1	0	0	940.66	172	179
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	11	13	24	0.02%	26.4%	LLGGFQETCSK	99.7%	47.5	25	47.5	2	0	0	1239.60	243	253
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	11	13	24	0.02%	26.4%	QITIIDSPSFIVSPLNSSSALALR	99.7%	105	25	105	1	1	0	2529.39	300	323
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	11	13	24	0.02%	26.4%	SGFNLEELEK	99.7%	70.7	25	58	2	0	0	1165.57	425	434
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	11	13	24	0.02%	26.4%	SPASIEVVKPMEAASAILSQADAR	99.7%	51.7	25	48.2	0	3	0	2441.27	324	347
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	11	13	24	0.02%	26.4%	VGVIGFPNVGK	99.7%	49.1	25	39.2	6	0	0	1086.63	257	267
Guanine nucleotide-binding protein-like 3	GNL3	GNL3_HUMAN	62.0	100.0%	11	13	24	0.02%	26.4%	VIEASDVVLEVLDAR	99.7%	98	25	79.1	2	0	0	1627.89	137	151
H/ACA ribonucleoprotein complex subunit 1	GAR1	GAR1_HUMAN	22.3	100.0%	3	3	6	0.01%	10.6%	DFYFSVK	98.7%	33.3	25	24.1	2	0	0	905.44	122	128
H/ACA ribonucleoprotein complex subunit 1	GAR1	GAR1_HUMAN	22.3	100.0%	3	3	6	0.01%	10.6%	FYIDPYK	99.7%	41.7	25	35.5	2	0	0	945.47	144	150
H/ACA ribonucleoprotein complex subunit 1	GAR1	GAR1_HUMAN	22.3	100.0%	3	3	6	0.01%	10.6%	VDEIFGQLR	99.7%	52	25	40.2	2	0	0	1076.57	113	121
H/ACA ribonucleoprotein complex subunit 2	NHP2	NHP2_HUMAN	17.2	99.8%	2	3	12	0.01%	19.0%	NLPYVYIPSK	99.7%	42.6	25	33	4	0	0	1193.66	102	111
H/ACA ribonucleoprotein complex subunit 2	NHP2	NHP2_HUMAN	17.2	99.8%	2	3	12	0.01%	19.0%	TYQELLVNQNPIAQPLASR	99.7%	96.1	25	95.7	4	4	0	2155.15	23	41
H/ACA ribonucleoprotein complex subunit 3	NOP10	NOP10_HUMAN	7.7	99.8%	2	3	5	0.00%	31.2%	FSPDDKYSR	99.7%	46	25	15	1	0	0	1114.52	35	43
H/ACA ribonucleoprotein complex subunit 3	NOP10	NOP10_HUMAN	7.7	99.8%	2	3	5	0.00%	31.2%	VLMTQQPRPVL	99.7%	52.4	25	52.4	4	0	0	1281.73	54	64
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	15	18	30	0.03%	31.7%	AGLESGAEPGDGDSDTTK	99.7%	42	25	41.8	2	0	0	1706.74	481	498
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	15	18	30	0.03%	31.7%	ALETLTGALFQRPPLIAAVK	99.7%	40.9	25	40.9	1	2	0	2109.24	172	191
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	15	18	30	0.03%	31.7%	APQVVAEAAK	99.7%	46.1	25	41.1	2	0	0	983.55	434	443
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	15	18	30	0.03%	31.7%	DSAVNAICYGAK	99.7%	62.3	25	58.3	2	0	0	1268.59	303	314
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	15	18	30	0.03%	31.7%	EIGDYIR	96.9%	29.8	25	18.5	1	0	0	865.44	82	88

H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	15	18	30	0.03%	31.7%	EVVAEVVK	99.7%	44.5	25	36.3	2	0	0	872.51	426	433
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	15	18	30	0.03%	31.7%	HGKPTDSTPATWK	96.1%	23.8	25	19	0	1	0	1425.71	401	413
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	15	18	30	0.03%	31.7%	IMLPGVLR	98.9%	34.2	25	18.3	4	0	0	914.55	315	322
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	15	18	30	0.03%	31.7%	LDTSQWPLLLK	99.7%	89.5	25	76.5	2	0	0	1313.75	47	57
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	15	18	30	0.03%	31.7%	LGIFWVSCEAGTYIR	99.7%	90.4	25	90.4	2	0	0	1771.88	213	227
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	15	18	30	0.03%	31.7%	LHNAIEGGTQLSR	99.7%	82.4	25	82.4	2	2	0	1395.73	159	171
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	15	18	30	0.03%	31.7%	MIEYDPER	96.4%	29.2	25	29.2	1	0	0	1052.47	204	211
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	15	18	30	0.03%	31.7%	MIEYDPERR	99.5%	37.2	25	32.3	1	0	0	1208.57	204	212
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	15	18	30	0.03%	31.7%	QEYVDYSESAK	99.7%	43.1	25	40.4	2	0	0	1318.58	414	424
H/ACA ribonucleoprotein complex subunit 4	DKC1	DKC1_HUMAN	57.7	100.0%	15	18	30	0.03%	31.7%	RVVYPLEK	97.9%	31.3	25	16.3	1	0	0	1003.59	284	291
HCLS1-associated protein X-1	HAX1	HAX1_HUMAN	31.6	100.0%	4	4	8	0.01%	19.0%	GFFGFPGPR	99.7%	49	25	48.4	2	0	0	981.49	9	17
HCLS1-associated protein X-1	HAX1	HAX1_HUMAN	31.6	100.0%	4	4	8	0.01%	19.0%	IFGGVLESDAR	99.7%	84.7	25	71.3	2	0	0	1163.61	140	150
HCLS1-associated protein X-1	HAX1	HAX1_HUMAN	31.6	100.0%	4	4	8	0.01%	19.0%	TREDNDLDSQVSQEGLGPVLQPQPK	99.7%	46.6	25	46.6	0	2	0	2750.36	181	205
HCLS1-associated protein X-1	HAX1	HAX1_HUMAN	31.6	100.0%	4	4	8	0.01%	19.0%	YPDSHQPR	99.2%	35.3	25	24.1	2	0	0	999.46	132	139
HEAT repeat-containing protein 1	HEATR1	HEAT1_HUMAN	242.4	100.0%	7	7	10	0.01%	3.8%	GWEEALENVIK	99.7%	69.4	25	61.9	2	0	0	1287.66	639	649
HEAT repeat-containing protein 1	HEATR1	HEAT1_HUMAN	242.4	100.0%	7	7	10	0.01%	3.8%	ITSEMGSASQANIR	99.7%	40.3	25	40.3	1	0	0	1480.71	1792	1805
HEAT repeat-containing protein 1	HEATR1	HEAT1_HUMAN	242.4	100.0%	7	7	10	0.01%	3.8%	LDDTYSFQVINK	99.7%	41.3	25	33.8	1	0	0	1442.72	1337	1348
HEAT repeat-containing protein 1	HEATR1	HEAT1_HUMAN	242.4	100.0%	7	7	10	0.01%	3.8%	LVPDLLAIVQR	99.7%	52.4	25	44.8	2	0	0	1236.77	1644	1654
HEAT repeat-containing protein 1	HEATR1	HEAT1_HUMAN	242.4	100.0%	7	7	10	0.01%	3.8%	TLATTLAPR	99.5%	37.5	25	31.5	1	0	0	943.56	1812	1820
HEAT repeat-containing protein 1	HEATR1	HEAT1_HUMAN	242.4	100.0%	7	7	10	0.01%	3.8%	VSLLNEQFLPLIR	99.7%	60	25	50.8	2	0	0	1541.91	418	430
HEAT repeat-containing protein 1	HEATR1	HEAT1_HUMAN	242.4	100.0%	7	7	10	0.01%	3.8%	VVESGGPEILK	99.4%	37	25	32.7	1	0	0	1127.63	1534	1544
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	13	13	24	0.02%	21.3%	AIQDAILEVLK	99.7%	84.5	25	77	2	0	0	1212.72	804	814
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	13	13	24	0.02%	21.3%	ALAVHLLDLGLR	99.7%	74.1	25	74.1	2	0	0	1290.79	94	105
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	13	13	24	0.02%	21.3%	ATDTINSQGQFPSYLETVTK	99.7%	75.6	25	75.6	1	0	0	2200.08	636	655
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	13	13	24	0.02%	21.3%	CSLLDPFAAVR	99.7%	60.3	25	50.1	2	0	0	1248.64	173	183
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	13	13	24	0.02%	21.3%	DVQETLMPQVLTTLEEDSK	99.7%	56.1	25	56.1	1	0	0	2176.07	697	715
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	13	13	24	0.02%	21.3%	EGSGLFPDLLVR	99.7%	47.4	25	40.6	2	0	0	1302.71	815	826
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	13	13	24	0.02%	21.3%	LFDDVPQVR	99.7%	60.5	25	52.8	2	0	0	1088.57	254	262
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	13	13	24	0.02%	21.3%	LIPLLLSSLNDEVPEVR	99.7%	81.8	25	80.6	2	0	0	1907.09	286	302
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	13	13	24	0.02%	21.3%	LLPGLEADSKPGR	99.7%	50.9	25	47.6	2	0	0	1352.75	34	46
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	13	13	24	0.02%	21.3%	MAAASTLVTWLQCVK	99.7%	49.6	25	49.6	1	0	0	1678.87	761	775
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	13	13	24	0.02%	21.3%	SAELVGTFVSPEVFLK	99.7%	70.3	25	63.3	4	0	0	1722.93	423	438
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	13	13	24	0.02%	21.3%	SVDDVLSHFAQR	99.7%	46.4	25	31.3	1	0	0	1373.68	242	253
HEAT repeat-containing protein 2	HEATR2	HEAT2_HUMAN	93.5	100.0%	13	13	24	0.02%	21.3%	TPSASGLLVLASAMR	99.7%	101	25	92.6	2	0	0	1473.81	447	461
HEAT repeat-containing protein 3	HEATR3	HEAT3_HUMAN	74.6	99.7%	2	3	3	0.00%	3.5%	DIMTPLVALLK	99.7%	43.1	25	36.5	2	0	0	1213.72	122	132
HEAT repeat-containing protein 3	HEATR3	HEAT3_HUMAN	74.6	99.7%	2	3	3	0.00%	3.5%	LGPLLLDPSLAVR	94.8%	27.8	25	27.8	1	0	0	1363.83	84	96
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	AAAIGIDLGTTYSCVGVFQHGK	99.7%	51.4	25	48.3	0	1	0	2265.13	4	25
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	AFYPEEISSMVLTK	99.7%	84.3	25	84.1	6	0	0	1630.80	113	126
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	AQIHDLVLVGGSTR	99.7%	97.6	25	88.8	2	2	0	1465.81	329	342
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	ARFEELCSDLFR	99.7%	60.1	25	53.6	2	2	0	1542.74	300	311
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	ATAGDTHLGGEDFDNR	99.7%	87.2	25	87.2	2	3	0	1675.73	221	236
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	DAGVIAGLNVLR	99.7%	109	25	92.2	4	0	0	1197.70	160	171
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	DNNLLGR	99.5%	37.2	25	32.3	2	0	0	801.42	452	458
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK	99.7%	61.5	25	61.5	0	1	0	3055.49	598	628
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	FEELCSDLFR	99.7%	42.9	25	42.9	2	0	0	1315.60	302	311
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	FGDPVVQSDMK	99.7%	63.1	25	63.1	2	0	0	1222.58	78	88
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	HWPFQVINDGDKPK	99.7%	46.7	25	46.7	0	1	0	1680.85	89	102
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	IINEPTAAAIAYGLDR	99.7%	119	25	112	3	4	0	1687.90	172	187
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	ITITNDKGR	99.7%	46.4	25	34.2	2	0	0	1017.57	501	509
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	KFGDPVVQSDMK	99.7%	42.1	25	42.1	2	0	0	1350.67	77	88
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	LDKAQIHDLVLVGGSTR	99.7%	64.2	25	64.2	0	2	0	1822.02	326	342

Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	LLQDFFNGR	99.7%	60.2	25	45.1	4	0	0	1109.57	349	357
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	LSKEEIER	99.7%	52.6	25	29.1	2	0	0	1003.54	510	517
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	LVNHFVEEFK	98.4%	32.5	25	28.3	1	0	0	1261.66	237	246
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	LVNHFVEEFKR	99.7%	39.8	25	38.6	0	2	0	1417.76	237	247
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	NALESYAFNMK	99.7%	77.4	25	77.4	9	0	0	1287.60	540	550
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	NQVALNPQNTVFDAK	99.7%	108	25	103	2	0	0	1658.85	57	71
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	NQVALNPQNTVFDAKR	98.6%	27.7	25	26.9	0	1	0	1814.95	57	72
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	SAVEDEGLK	97.1%	30.1	25	26.8	1	0	0	947.47	551	559
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	TTPSYVAFTDTER	99.7%	91.9	25	86.8	7	0	0	1487.70	37	49
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	VEIIANDQGNR	99.7%	72.3	25	0	2	0	0	1228.63	26	36
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	VQVSYKGETK	99.7%	48.5	25	43.4	2	0	0	1138.61	103	112
Heat shock 70 kDa protein 1A/1B	HSPA1A	HSP71_HUMAN	70.1	100.0%	24	30	71	0.07%	45.1%	YKAEDEVQR	99.7%	44.9	25	37.9	4	0	0	1137.55	525	533
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	8	8	12	0.01%	15.4%	AFSDPFVEAEK	99.7%	43.3	25	35.8	1	0	0	1239.59	74	84
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	8	8	12	0.01%	15.4%	AGGIETIANEYSDR	99.7%	53.1	25	52.3	1	0	0	1495.70	20	33
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	8	8	12	0.01%	15.4%	EFSITDVVPYPISLR	99.7%	50.9	25	50.9	2	0	0	1735.93	391	405
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	8	8	12	0.01%	15.4%	FQESEERPK	99.7%	41.6	25	29.8	2	0	0	1149.55	689	697
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	8	8	12	0.01%	15.4%	GCALQCAILSPAFK	99.7%	82.6	25	64.2	2	0	0	1535.77	375	388
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	8	8	12	0.01%	15.4%	LEDTENWLYEDGEDQPK	99.2%	35.2	25	35.2	1	0	0	2080.90	652	668
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	8	8	12	0.01%	15.4%	SNLAYDIVQLPTGLTGIK	99.7%	63.7	25	63.7	1	0	0	1903.05	85	102
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	8	8	12	0.01%	15.4%	TSTVDLPIENQLLWQIDR	99.7%	66.2	25	62.3	2	0	0	2141.12	574	591
Heat shock 70 kDa protein 4	HSPA4	HSP74_HUMAN	94.3	100.0%	8	8	12	0.01%	15.4%	VLATAFDTTLGGR	99.7%	111	25	102	2	0	0	1321.71	222	234
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	ARFEELNADLFR	99.7%	43.5	25	34.8	0	2	0	1480.75	300	311
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	DAGTIAGLNVLR	99.7%	105	25	96.6	3	0	0	1199.67	160	171
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	EIAEAYLGK	99.7%	50.2	25	39.7	2	0	0	993.53	129	137
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	FEELNADLFR	99.7%	61.2	25	54.6	2	0	0	1253.62	302	311
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	GPAVGIDLGTTYSCVGVFQHGK	99.7%	49.4	25	49	0	2	0	2263.12	4	25
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	HWPFMVVNDAGRPK	99.7%	40.2	25	40.2	0	2	0	1653.83	89	102
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	IINEPTAAAIAYGLDK	99.7%	129	25	127	2	0	0	1659.90	172	187
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	IINEPTAAAIAYGLDKK	99.7%	85.1	25	85.1	2	0	0	1787.99	172	188
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	ITITNDKGR	99.7%	46.4	25	34.2	2	0	0	1017.57	501	509
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	LDKSQIHDIVLVGGSTR	99.7%	48.3	25	48.3	0	2	0	1838.01	326	342
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	LLQDFFNGK	99.7%	51.2	25	34.4	2	0	0	1081.57	349	357
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	LSKEDIER	99.7%	56.1	25	13.9	2	0	0	989.53	510	517
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	MKEIAEAYLGK	99.7%	60.5	25	53.4	4	2	0	1268.66	127	137
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	MVNHFIAEFK	99.7%	48.3	25	38.9	3	3	0	1235.62	237	246
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	NQVAMNPTNTVFDAK	99.7%	105	25	102	4	0	0	1665.79	57	71
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	NQVAMNPTNTVFDAKR	98.8%	28.2	25	28.2	0	2	0	1805.90	57	72
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	NSLESYAFNMK	99.7%	60	25	60	2	0	0	1319.59	540	550
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	RFDDAVVQSDMK	99.7%	52.3	25	45.1	2	0	0	1410.67	77	88
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	SFYPEEVSSMVLTK	99.7%	84.6	25	84.6	4	0	0	1616.79	113	126
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	SINPDEAVAYGAAVQAAILSGDK	99.7%	97.6	25	97.6	2	1	0	2260.15	362	384
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	SQIHDIVLVGGSTR	99.7%	77.2	25	71.8	2	2	0	1481.81	329	342
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	STAGDTHLGGEDFDNR	99.7%	72.5	25	72.5	2	2	0	1691.73	221	236
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	TTPSYVAFTDTER	99.7%	91.9	25	86.8	7	0	0	1487.70	37	49
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	TVTNAVVTVPAYFNDSQR	99.7%	75.2	25	73.7	2	2	0	1982.00	138	155
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	VCNPIITK	99.1%	35	25	12.4	2	0	0	944.52	602	609
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	VEIIANDQGNR	99.7%	72.3	25	0	2	0	0	1228.63	26	36
Heat shock cognate 71 kDa protein	HSPA8	HSP7C_HUMAN	70.9	100.0%	27	38	79	0.07%	45.4%	VQVEYKGETK	99.7%	45.4	25	38.1	2	0	0	1180.62	103	112
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	13	14	27	0.03%	17.1%	AGGIETIANEFSDR	99.7%	77	25	77	2	0	0	1479.71	20	33
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	13	14	27	0.03%	17.1%	DISTTLNADEAVAR	99.7%	96.8	25	89.9	2	0	0	1475.73	361	374
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	13	14	27	0.03%	17.1%	FQEAEERPK	99.7%	45.3	25	29.4	2	0	0	1133.56	706	714

Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	13	14	27	0.03%	17.1%	GCALQCAILSPAFK	99.7%	82.6	25	64.2	2	0	0	1535.77	375	388
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	13	14	27	0.03%	17.1%	IEVPLYSLLEQTHLK	99.0%	28.9	25	28.9	0	1	0	1783.00	317	331
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	13	14	27	0.03%	17.1%	KSLDQDPVVR	99.7%	39.3	25	34.1	2	0	0	1156.63	772	781
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	13	14	27	0.03%	17.1%	LKETAENSLK	99.7%	42.7	25	25.9	2	0	0	1132.62	125	134
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	13	14	27	0.03%	17.1%	LVEHFCAEFK	99.7%	33.8	25	33.8	1	1	0	1279.61	240	249
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	13	14	27	0.03%	17.1%	SLDQDPVVR	99.5%	37.5	25	26.7	2	0	0	1028.54	773	781
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	13	14	27	0.03%	17.1%	SQFEELCAELLQK	99.7%	59.7	25	55.1	2	0	0	1594.78	304	316
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	13	14	27	0.03%	17.1%	SVLDAAQIVGLNCLR	99.7%	106	25	100	2	0	0	1628.88	155	169
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	13	14	27	0.03%	17.1%	VLGTAFDPFLGGK	99.7%	82.9	25	65.3	5	0	0	1321.72	222	234
Heat shock protein 105 kDa	HSPH1	HS105_HUMAN	96.9	100.0%	13	14	27	0.03%	17.1%	YNHIDESEMK	97.5%	30.7	25	25.6	1	0	0	1281.54	740	749
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	11	12	20	0.02%	23.0%	AFLDALQNQAEASSK	99.7%	120	25	116	2	0	0	1592.79	182	196
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	11	12	20	0.02%	23.0%	AQLLQPTLEINPR	99.7%	72.8	25	72.3	2	0	0	1492.85	635	647
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	11	12	20	0.02%	23.0%	EGIVTATEQEVKEDIAK	99.7%	74.1	25	73	1	0	0	1859.96	450	466
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	11	12	20	0.02%	23.0%	ELGSSVALYSR	99.7%	54.2	25	49.6	2	0	0	1181.62	358	368
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	11	12	20	0.02%	23.0%	ELISNASDALEK	99.7%	76.5	25	67.5	2	0	0	1289.66	115	126
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	11	12	20	0.02%	23.0%	ELLQESALIR	99.7%	71.3	25	58.5	2	0	0	1171.67	403	412
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	11	12	20	0.02%	23.0%	FFEDYGLFMR	99.7%	68.3	25	68.3	3	0	0	1324.60	440	449
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	11	12	20	0.02%	23.0%	GVVDSEDIPLNLSR	99.7%	115	25	0	12	0	0	1513.79	389	402
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	11	12	20	0.02%	23.0%	LVSDGQALPEMEIHLQTNAEK	99.3%	30.2	25	30.2	0	1	0	2339.16	131	151
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	11	12	20	0.02%	23.0%	SDCKEFSSEAR	99.7%	50.6	25	30.9	1	0	0	1315.56	259	269
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	11	12	20	0.02%	23.0%	TDAPLNIR	99.7%	43.6	25	32.4	2	0	0	899.49	333	340
Heat shock protein 75 kDa, mitochondrial	TRAP1	TRAP1_HUMAN	80.1	100.0%	11	12	20	0.02%	23.0%	YESSALPSGQLTSLSEYASR	99.7%	130	25	114	2	0	0	2146.03	470	489
Heat shock protein beta-1	HSPB1	HSPB1_HUMAN	22.8	100.0%	2	2	3	0.00%	13.2%	LATQSNEITIPVTFESR	99.7%	42.6	25	42.6	1	0	0	1905.99	172	188
Heat shock protein beta-1	HSPB1	HSPB1_HUMAN	22.8	100.0%	2	2	3	0.00%	13.2%	LFDQAFGLPR	99.7%	63.3	25	58.2	2	0	0	1163.62	28	37
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	ADLINNLGTIAK	99.7%	75.6	25	65	23	0	0	1242.71	101	112
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	ALLFVPR	99.7%	47.2	25	0	4	0	0	815.51	339	345
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	DNSTMGYMAAK	99.7%	51.5	25	43.1	4	0	0	1188.50	621	631
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	DQVANSAFVER	99.7%	79.3	25	72.3	6	0	0	1235.60	500	510
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	EDQTEYLEER	99.7%	62.4	25	55.3	4	0	0	1311.57	192	201
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	EGLELPEDEEEK	98.0%	31.5	25	31.5	2	0	0	1416.64	547	558
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	EGLELPEDEEEKK	99.7%	43.2	25	40.4	2	0	0	1544.73	547	559
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	EKYIDQEELNK	99.7%	55.6	25	44.4	2	0	0	1408.70	282	292
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	ELHINLIPNK	97.8%	31.2	25	30.3	2	0	0	1190.69	75	84
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	ELHINLIPNKQDR	99.7%	43.8	25	41.7	2	2	0	1589.88	75	87
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	ELISNSSDALDK	99.7%	72.3	25	62	2	0	0	1291.64	47	58
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	ELISNSSDALDKIR	99.7%	81.8	25	70.9	2	0	0	1560.82	47	60
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	FENLCK	98.6%	33.1	25	21.6	2	0	0	810.38	568	573
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	FYEQFSK	99.7%	46	25	23.5	2	0	0	948.45	437	443
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	GVVDSEDLPLNISR	99.7%	115	25	0	12	0	0	1513.79	387	400
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	HFSVEGQLEFR	99.7%	73	25	69.4	9	2	0	1348.66	328	338
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	HIYYITGETK	99.7%	53.8	25	51.5	2	0	0	1224.63	490	499
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	HLEINPDHSIIETLR	99.7%	76.6	25	76.6	2	2	0	1786.94	633	647
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	HNDDEQYAWESSAGGSFTVR	99.7%	125	25	125	4	4	0	2255.96	154	173
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	HSQFIGYPITLFVEK	99.7%	79.1	25	79.1	2	2	0	1778.95	210	224
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	IRYESLTDPSK	99.7%	45.2	25	36.4	2	2	0	1308.68	59	69
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	KLSELLR	96.3%	29.1	25	13.8	1	0	0	858.54	458	464
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	LGIHEDSQNR	99.7%	54.5	25	45.9	3	0	0	1168.57	447	456
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	LGIHEDSQNRK	98.7%	28	25	22.9	0	1	0	1296.67	447	457
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	LVTSPCCIVTSTYGWTANMER	99.7%	97.2	25	97.2	4	2	0	2446.12	592	612
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	NPDDITNEEYGEFYK	99.7%	96.4	25	89.3	2	0	0	1833.78	300	314
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	RAPFDLFENR	99.7%	46.1	25	44.8	2	0	0	1264.64	346	355

Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	SLTNDWEDHLAVK	99.7%	81.4	25	74.2	7	2	0	1527.74	315	327
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	TKFENLCK	99.3%	36	25	30.1	1	0	0	1039.52	566	573
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	TLTIVDTGIGMTK	99.7%	113	25	0	21	0	0	1365.73	88	100
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	VILHLKEDQTEYLEER	99.7%	86.6	25	82.3	3	6	0	2015.04	186	201
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	YESLTDPSK	99.7%	41.6	25	36.4	3	0	0	1039.49	61	69
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	YESLTDPSKLDSGK	99.7%	74.7	25	55	4	2	0	1539.75	61	74
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	YIDQEELNK	99.7%	60.2	25	40.1	12	0	0	1151.56	284	292
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	YYTSASGDEMVSLK	99.7%	81.6	25	72.4	4	0	0	1550.70	465	478
Heat shock protein HSP 90-alpha	HSP90AA1	HS90A_HUMAN	84.7	100.0%	20	27	58	0.05%	45.2%	YYTSASGDEMVSLKDYCTR	98.4%	27.1	25	27.1	0	2	0	2261.97	465	483
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	ADLINNLGTIAK	99.7%	75.6	25	65	23	0	0	1242.71	96	107
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	AKFENLCK	98.6%	33.1	25	21.5	1	0	0	1009.51	558	565
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	ALLFIPR	99.7%	46.6	25	16.3	11	0	0	829.53	331	337
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	APFDLFENK	99.7%	49.5	25	45	4	0	0	1080.54	339	347
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	APFDLFENKK	99.7%	56.4	25	49.5	2	0	0	1208.63	339	348
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	CLELFSELAEDKENYK	99.7%	68.4	25	68.2	1	2	0	1987.93	412	427
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	DNSTMGYMMAK	99.7%	76.2	25	76.2	13	0	0	1248.51	613	623
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	EDQTEYLEER	99.7%	62.4	25	55.3	4	0	0	1311.57	187	196
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	EGLELPEDEEEK	98.0%	31.5	25	31.5	2	0	0	1416.64	539	550
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	EGLELPEDEEEKK	99.7%	43.2	25	40.4	2	0	0	1544.73	539	551
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	EKYIDQEELNK	99.7%	55.6	25	44.4	2	0	0	1408.70	274	284
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	ELISNASDALDK	99.7%	76.4	25	64.3	8	0	0	1275.64	42	53
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	ELISNASDALDKIR	99.7%	87.1	25	74.5	7	2	0	1544.83	42	55
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	ELKIDIIPNPQER	99.7%	59	25	54	3	0	0	1564.87	70	82
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	EQVANSAFVER	99.7%	74.1	25	64.5	13	0	0	1249.62	492	502
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	FENLCK	98.6%	33.1	25	21.6	2	0	0	810.38	560	565
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	FYEAFSK	99.3%	36.2	25	28	3	0	0	891.42	429	435
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	GFEVVYMTEPIDEYCVQQLK	99.7%	103	25	54	8	4	0	2464.14	507	526
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	GVVDSEDLPLNISR	99.7%	115	25	0	12	0	0	1513.79	379	392
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	HFSVEGQLEFR	99.7%	73	25	69.4	9	2	0	1348.66	320	330
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	HLEINPDHPIVETLR	99.7%	74.8	25	68.2	2	4	0	1782.95	625	639
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	HNDDEQYAWESSAGGSFTVR	99.7%	125	25	125	4	4	0	2255.96	149	168
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	HSQFIGYPITLYLEK	99.7%	79.1	25	0	3	4	0	1808.96	205	219
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	IDIIPNPQER	99.7%	49.9	25	42.2	6	0	0	1194.65	73	82
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	IRYESLTDPSK	99.7%	45.2	25	36.4	2	2	0	1308.68	54	64
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	KFYEAFSK	97.0%	30	25	19.9	1	0	0	1019.52	428	435
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	KHLEINPDHPIVETLR	99.3%	30.7	25	30.7	0	2	0	1911.04	624	639
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	LGIHEDSTNR	99.7%	56	25	56	5	0	0	1141.56	439	448
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	LGIHEDSTNRR	99.7%	42.7	25	41.5	1	4	0	1297.66	439	449
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	LVSSPCCIVTSTYGWTANMER	99.7%	97.7	25	97.7	6	4	0	2448.10	584	604
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	NPDDITQEEYGEFYK	99.7%	90.5	25	90.5	10	0	0	1847.80	292	306
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	RAPFDLFENK	99.7%	51.9	25	28.4	6	0	0	1236.64	338	347
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	RLSELLR	99.5%	37.6	25	14.9	3	0	0	886.55	450	456
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	SIYYITGESK	99.7%	73.7	25	64.5	7	0	0	1160.58	482	491
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	SLTNDWEDHLAVK	99.7%	81.4	25	74.2	7	2	0	1527.74	307	319
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	TLTLVDTGIGMTK	99.7%	113	25	0	21	0	0	1365.73	83	95
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	VFIMDSCDELIPEYLNFIR	99.7%	75.4	25	75.4	2	0	0	2390.14	360	378
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	VILHLKEDQTEYLEER	99.7%	86.6	25	82.3	3	6	0	2015.04	181	196
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	YESLTDPSK	99.7%	41.6	25	36.4	3	0	0	1039.49	56	64
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	YESLTDPSKLDSGK	99.7%	74.7	25	55	4	2	0	1539.75	56	69
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	YHTSQSGDEMTSLSEYVSR	99.7%	104	25	104	5	11	0	2176.95	457	475
Heat shock protein HSP 90-beta	HSP90AB1	HS90B_HUMAN	83.3	100.0%	42	64	298	0.28%	53.7%	YIDQEELNK	99.7%	60.2	25	40.1	12	0	0	1151.56	276	284

Helicase-like transcription factor	HLTF	HLTF_HUMAN	113.9	100.0%	2	2	3	0.00%	2.0%	MSELSSSRPK	99.7%	42.1	25	31.9	2	0	0	1121.56	377	386
Helicase-like transcription factor	HLTF	HLTF_HUMAN	113.9	100.0%	2	2	3	0.00%	2.0%	VILDEGHAIR	99.7%	43.2	25	34.7	1	0	0	1122.63	554	563
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	9	9	19	0.02%	18.1%	ALPLIVGAQLIHADK	99.7%	54.4	25	54.4	2	0	0	1558.93	15	29
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	9	9	19	0.02%	18.1%	GASGSFVVVQK	99.7%	57	25	41.4	2	0	0	1078.59	223	233
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	9	9	19	0.02%	18.1%	GQLEQITGK	99.2%	35.3	25	6.23	3	0	0	973.53	312	320
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	9	9	19	0.02%	18.1%	KYVSQYYPK	99.7%	43	25	31.7	1	0	0	1175.61	283	291
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	9	9	19	0.02%	18.1%	LEDVLPLAFTR	99.7%	62.7	25	39.7	3	0	0	1273.72	259	269
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	9	9	19	0.02%	18.1%	MDAILTEAIK	99.5%	37.8	25	32.3	2	0	0	1120.59	161	170
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	9	9	19	0.02%	18.1%	SGASVVAIR	99.7%	70.8	25	45.8	2	0	0	859.50	176	184
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	9	9	19	0.02%	18.1%	SSAVDPEPQVK	99.7%	58.1	25	41.6	2	0	0	1156.58	248	258
Heterochromatin protein 1-binding protein 3	HP1BP3	HP1B3_HUMAN	61.2	100.0%	9	9	19	0.02%	18.1%	TIPSWATLSASQLAR	99.7%	99.3	25	99.2	2	0	0	1601.86	132	146
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	4	5	31	0.03%	15.4%	DLKDYFTK	97.6%	30.8	25	18.2	5	0	0	1029.53	84	91
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	4	5	31	0.03%	15.4%	EVYQQQQYGSGGR	99.7%	90.6	25	84.9	16	0	0	1499.69	233	245
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	4	5	31	0.03%	15.4%	FGEVVDCTIK	99.7%	69.2	25	0	20	0	0	1167.57	92	101
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	4	5	31	0.03%	15.4%	GFGFILFK	99.7%	39.6	25	31.9	3	0	0	928.53	111	118
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	ROAA_HUMAN	36.2	100.0%	4	5	31	0.03%	15.4%	MFVGGLSWDTSK	99.7%	56.5	25	52	7	0	0	1343.63	71	82
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	6	9	36	0.03%	28.5%	AEIIADKQSGK	99.7%	56.8	25	35.7	4	0	0	1159.63	127	137
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	6	9	36	0.03%	28.5%	AVPKEDIYSGGGGGGSR	99.7%	103	25	92	4	1	0	1606.78	173	189
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	6	9	36	0.03%	28.5%	EDIYSGGGGGGSR	99.7%	78.8	25	74.2	4	0	0	1211.53	177	189
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	6	9	36	0.03%	28.5%	GDVAEGDLIEHFSQFGTVEK	99.7%	91.2	25	91.2	6	6	0	2178.04	107	126
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	6	9	36	0.03%	28.5%	GFGFVYFQNHDAADK	99.7%	73	25	73	3	2	0	1715.78	140	154
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	6	9	36	0.03%	28.5%	KLFVGGLK	98.9%	34	25	0	3	0	0	861.56	99	106
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	ROA0_HUMAN	30.8	100.0%	6	9	36	0.03%	28.5%	LFIGGLNVQTSESGLR	99.7%	141	25	134	6	0	0	1690.91	9	24
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	14	25	139	0.13%	41.7%	DYFEQYGK	99.7%	43.2	25	43	3	0	0	1049.46	123	130
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	14	25	139	0.13%	41.7%	EDSQRPGAHLTVK	99.7%	57	25	46.3	10	1	0	1437.74	93	105
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	14	25	139	0.13%	41.7%	EDSQRPGAHLTVKK	99.7%	47.5	25	40.8	2	1	0	1565.84	93	106
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	14	25	139	0.13%	41.7%	GFAFVTFDDHDSVDK	99.7%	79.7	25	77.9	5	2	0	1699.76	147	161
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	14	25	139	0.13%	41.7%	IEVIEIMTDR	99.7%	75.5	25	70.4	16	0	0	1218.64	131	140
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	14	25	139	0.13%	41.7%	IFVGGIKEDTEEHHLR	99.7%	66.7	25	0	0	9	0	1879.97	107	122
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	14	25	139	0.13%	41.7%	KIFVGGIK	98.9%	34	25	0	3	0	0	861.56	106	113
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	14	25	139	0.13%	41.7%	KLFIGGLSFETTDESLR	99.7%	70.3	25	68	5	5	0	1913.00	15	31
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	14	25	139	0.13%	41.7%	LFIGGLSFETTDESLR	99.7%	125	25	115	22	0	0	1784.91	16	31
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	14	25	139	0.13%	41.7%	NQGGYGGSSSSSSYGSGR	99.7%	123	25	123	10	0	0	1694.70	353	370
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	14	25	139	0.13%	41.7%	RGFAFVTFDDHDSVDK	99.7%	37.3	25	37.3	0	2	0	1855.86	146	161
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	14	25	139	0.13%	41.7%	SESPKEPEQLR	99.7%	48.6	25	30.9	4	3	0	1299.65	4	14
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	14	25	139	0.13%	41.7%	SHFEQWGTLTDCVVMR	99.7%	89.6	25	89.6	4	8	0	1965.89	32	47
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	14	25	139	0.13%	41.7%	SSGPYGGGGQYFAKPR	99.7%	102	25	98.5	26	5	0	1628.78	337	352
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	14	25	139	0.13%	41.7%	YHTVNGHNCEVR	99.7%	64	25	63.3	2	2	0	1485.67	167	178
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	ROA1_HUMAN	38.7	100.0%	14	25	139	0.13%	41.7%	YHTVNGHNCEVRK	98.1%	26.5	25	26.5	0	1	0	1613.76	167	179
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	9	14	88	0.08%	28.3%	EDSVKPGAHLTVK	99.7%	60.3	25	51	15	1	0	1380.75	114	126
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	9	14	88	0.08%	28.3%	EDTEEYNLR	99.7%	64	25	64	5	0	0	1168.51	135	143
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	9	14	88	0.08%	28.3%	GFAFVTFDDHDTVDK	99.7%	56.8	25	56.8	1	1	0	1713.78	168	182
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	9	14	88	0.08%	28.3%	IETIEVMEDR	99.7%	76.1	25	65.2	26	0	0	1234.60	152	161
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	9	14	88	0.08%	28.3%	IFVGGIKEDTEEYNLR	99.7%	86.1	25	78.3	8	9	0	1882.95	128	143
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	9	14	88	0.08%	28.3%	KIFVGGIK	98.9%	34	25	0	3	0	0	861.56	127	134
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	9	14	88	0.08%	28.3%	LFIGGLSFETTDDSLR	99.7%	77.3	25	70.4	2	0	0	1770.89	37	52
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	9	14	88	0.08%	28.3%	SSGSPYGGGYGSGGGSGGYGSR	99.7%	151	25	151	13	0	0	1910.79	355	376
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	9	14	88	0.08%	28.3%	WGTLTDCVVMR	99.7%	51.3	25	39.7	6	0	0	1337.63	58	68
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	ROA3_HUMAN	39.6	100.0%	9	14	88	0.08%	28.3%	YGKIETIEVMEDR	97.7%	25.7	25	21.2	0	1	0	1598.77	149	161
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	26	91	0.09%	38.6%	DLKDYFSK	99.1%	34.8	25	25.5	2	0	0	1015.51	112	119
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	26	91	0.09%	38.6%	ESESVDKVMDQK	99.7%	53.5	25	40.1	2	1	0	1394.65	147	158

Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	26	91	0.09%	38.6%	EYFGGFGEVESIELPMDNK	99.7%	82.3	25	82.3	4	0	0	2160.98	200	218
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	26	91	0.09%	38.6%	EYFGGFGEVESIELPMDNKTNK	99.7%	66.9	25	65.8	0	2	0	2520.16	200	221
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	26	91	0.09%	38.6%	FGEVVDCTLK	99.7%	69.2	25	0	20	0	0	1167.57	120	129
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	26	91	0.09%	38.6%	FGEVVDCTLKLDPITGR	99.7%	72.1	25	68	2	2	0	1919.99	120	136
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	26	91	0.09%	38.6%	GFCFITFK	97.7%	31.1	25	27	2	0	0	1019.50	224	231
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	26	91	0.09%	38.6%	GFCFITFKEEEPVK	99.7%	82.1	25	80.2	2	1	0	1730.85	224	237
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	26	91	0.09%	38.6%	GFGFVLFK	99.7%	57.2	25	51.2	13	0	0	914.51	139	146
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	26	91	0.09%	38.6%	IDASKNEEDEGHSNSSPR	99.7%	90.8	25	90.8	2	2	0	1971.86	68	85
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	26	91	0.09%	38.6%	IFVGGLSPDTPEEK	99.7%	84.8	25	76	16	0	0	1488.76	184	197
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	26	91	0.09%	38.6%	IFVGGLSPDTPEEKIR	99.7%	34.9	25	33.3	0	2	0	1757.94	184	199
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	26	91	0.09%	38.6%	IREYFGGFGEVESIELPMDNK	99.7%	63.2	25	62.4	2	2	0	2430.16	198	218
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	26	91	0.09%	38.6%	KYHNVGLSK	99.7%	53.5	25	40.8	2	0	0	1045.58	243	251
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	26	91	0.09%	38.6%	MFIGGLSWDTTK	99.7%	75	25	70.4	4	0	0	1355.67	99	110
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	26	91	0.09%	38.6%	MFIGGLSWDTTKK	99.7%	72	25	71.1	4	0	0	1483.76	99	111
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	HNRPD_HUMAN	38.4	100.0%	17	26	91	0.09%	38.6%	YHNVGLSK	99.7%	43.7	25	28.4	2	0	0	917.48	244	251
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	10	23	0.02%	21.2%	DAASVDKVLELK	99.7%	56.8	25	43.4	2	0	0	1287.72	198	209
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	10	23	0.02%	21.2%	DLTEYLSR	99.7%	48.2	25	31	4	0	0	996.50	163	170
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	10	23	0.02%	21.2%	FGEVVDCTIK	99.7%	69.2	25	0	20	0	0	1167.57	171	180
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	10	23	0.02%	21.2%	FGEVVDCTIKTDPVTGR	99.7%	90.5	25	87.6	1	0	0	1893.94	171	187
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	10	23	0.02%	21.2%	GFCFITYTDEEPVK	99.7%	46.3	25	46.3	1	0	0	1705.78	275	288
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	10	23	0.02%	21.2%	GFCFITYTDEEPVKK	99.7%	67.1	25	67.1	2	0	0	1833.87	275	289
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	10	23	0.02%	21.2%	GFGFVLFK	99.7%	57.2	25	51.2	13	0	0	914.51	190	197
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	10	23	0.02%	21.2%	MFIGGLSWDTSK	99.7%	70.8	25	65.8	5	0	0	1341.65	150	161
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	10	23	0.02%	21.2%	MFIGGLSWDTSKK	99.7%	87.2	25	80.3	6	0	0	1469.75	150	162
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	HNRDL_HUMAN	46.4	100.0%	8	10	23	0.02%	21.2%	VFVGGLSPDTSEEQIK	99.7%	55.7	25	54.2	2	0	0	1705.86	235	250
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	7	9	21	0.02%	33.0%	ATENDIYNFFSPLNPVR	99.7%	97.6	25	97.6	18	2	0	1996.98	300	316
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	7	9	21	0.02%	33.0%	DLSYCLSGMYDHR	99.7%	54.7	25	54.7	2	0	0	1632.68	263	275
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	7	9	21	0.02%	33.0%	GLPFGCTK	98.3%	32.1	25	9.16	1	0	0	879.44	117	124
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	7	9	21	0.02%	33.0%	HSGPNSADSANDGFVR	99.7%	98.5	25	96.9	2	2	0	1630.72	99	114
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	7	9	21	0.02%	33.0%	ITGEAFVQFASQELAEK	99.7%	81.3	25	74.2	6	0	0	1867.94	151	167
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	7	9	21	0.02%	33.0%	QSGEAFVELGSEDDVK	99.7%	105	25	102	2	0	0	1709.79	53	68
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	7	9	21	0.02%	33.0%	VHIEIGPDGR	99.7%	56.6	25	55.2	11	0	0	1092.58	317	326
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	7	9	21	0.02%	33.0%	VTGEADVEFATHEEAVAAMSK	99.7%	49.8	25	49.8	0	2	0	2208.01	327	347
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	HNRPF_HUMAN	45.7	100.0%	7	9	21	0.02%	33.0%	YGDSEFTVQSTTGHCVHMR	99.7%	66.5	25	66.5	0	4	0	2211.95	276	294
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	13	20	105	0.10%	47.0%	ATENDIYNFFSPLNPVR	99.7%	97.6	25	97.6	18	2	0	1996.98	300	316
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	13	20	105	0.10%	47.0%	DLNYCFSGMSDHR	99.7%	69.9	25	69.9	8	0	0	1601.65	263	275
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	13	20	105	0.10%	47.0%	EGRPSGEAFVELESEDEVK	99.7%	118	25	109	4	4	0	2106.98	50	68
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	13	20	105	0.10%	47.0%	GAYGGGYGGYDDYNGYNDGYGFGSDR	99.7%	95.4	25	95.4	1	0	0	2717.05	234	259
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	13	20	105	0.10%	47.0%	GLPWSCSADEVQR	99.7%	77.9	25	75.3	5	0	0	1504.69	17	29
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	13	20	105	0.10%	47.0%	HTGPNSPDTANDGFVR	99.7%	67.2	25	61.9	6	9	0	1684.77	99	114
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	13	20	105	0.10%	47.0%	IQNGAQGIR	99.7%	67.9	25	52.1	5	0	0	956.53	36	44
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	13	20	105	0.10%	47.0%	SNNVEMDWVLK	99.7%	60.8	25	54.5	6	0	0	1334.64	88	98
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	13	20	105	0.10%	47.0%	STGEAFVQFASQEIAEK	99.7%	95.1	25	95.1	10	0	0	1841.89	151	167
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	13	20	105	0.10%	47.0%	VHIEIGPDGR	99.7%	56.6	25	55.2	11	0	0	1092.58	317	326
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	13	20	105	0.10%	47.0%	VTGEADVEFATHEDAVAAMSK	99.7%	42.3	25	29.8	0	5	0	2194.00	327	347
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	13	20	105	0.10%	47.0%	YGDGGSTFQSTTGHCVHMR	99.7%	82.4	25	82.4	0	8	0	2097.89	276	294
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	HNRH1_HUMAN	49.2	100.0%	13	20	105	0.10%	47.0%	YVELFLNSTAGASGGAYEHR	97.9%	26.1	25	24.6	0	3	0	2142.03	356	375
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	6	8	17	0.02%	33.9%	ATENDIYNFFSPLNPMR	99.7%	89.4	25	89.4	6	0	0	2028.95	300	316
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	6	8	17	0.02%	33.9%	DLNYCFSGMSDHR	99.7%	69.9	25	69.9	8	0	0	1601.65	263	275
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	6	8	17	0.02%	33.9%	EGRPSGEAFVELESEEEVK	96.0%	23.7	25	22.8	0	1	0	2121.00	50	68
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	6	8	17	0.02%	33.9%	HTGPNSPDTANDGFVR	99.7%	67.2	25	61.9	6	9	0	1684.77	99	114

Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	6	8	17	0.02%	33.9%	IQNGTSGIR	97.5%	30.6	25	19.2	2	0	0	945.51	36	44
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	6	8	17	0.02%	33.9%	SNSVEMDWVLK	99.7%	54.1	25	42.2	2	0	0	1307.63	88	98
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	6	8	17	0.02%	33.9%	STGEAFVQFASQEIAEK	99.7%	95.1	25	95.1	10	0	0	1841.89	151	167
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	6	8	17	0.02%	33.9%	VHIEIGPDGR	99.7%	56.6	25	55.2	11	0	0	1092.58	317	326
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	6	8	17	0.02%	33.9%	VTGEADVEFATHEDAVAAMAK	99.7%	37	25	4.27	0	2	0	2178.00	327	347
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	HNRH2_HUMAN	49.3	100.0%	6	8	17	0.02%	33.9%	YGDGGSSFQSTTGHCVHMR	99.7%	73.2	25	73.2	0	4	0	2083.87	276	294
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	13	45	0.04%	37.0%	ATENDIANFFSPLNPIR	99.7%	62.3	25	60.5	9	0	0	1918.97	206	222
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	13	45	0.04%	37.0%	ATGEADVEFVTHEDAVAAMSK	99.7%	74.3	25	52.8	2	4	0	2194.00	233	253
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	13	45	0.04%	37.0%	DGMDNQGGYGSVGR	99.7%	71.9	25	65.8	4	0	0	1412.59	288	301
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	13	45	0.04%	37.0%	EIAENALGK	99.7%	50.7	25	45.4	2	0	0	944.50	68	76
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	13	45	0.04%	37.0%	HNGPNDASDGTVR	99.7%	44	25	33.6	2	0	0	1339.60	7	19
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	13	45	0.04%	37.0%	STGEAFVQFASK	99.7%	92.6	25	86.8	11	0	0	1271.63	56	67
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	13	45	0.04%	37.0%	VHIDIGADGR	99.7%	54.5	25	39.1	4	0	0	1052.55	223	232
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	13	45	0.04%	37.0%	YIEIFR	98.7%	33.3	25	0	2	0	0	840.46	85	90
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	HNRH3_HUMAN	36.9	100.0%	9	13	45	0.04%	37.0%	YIELFLNSTPGGGSGMGGSGMGGYGR	99.7%	81.4	25	81.4	4	1	0	2554.13	262	287
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	20	29	106	0.10%	41.5%	DLAGSIIGK	99.7%	59.2	25	42.4	4	0	0	873.50	397	405
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	20	29	106	0.10%	41.5%	DYDDMSPR	99.7%	42.8	25	42.8	2	0	0	998.39	279	286
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	20	29	106	0.10%	41.5%	GGDLMAYDR	99.7%	51	25	47.5	6	0	0	997.44	317	325
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	20	29	106	0.10%	41.5%	GGDLMAYDRR	98.9%	34.2	25	20.8	3	0	0	1153.54	317	326
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	20	29	106	0.10%	41.5%	GSDFDCELR	99.7%	53.2	25	52.9	4	0	0	1098.45	140	148
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	20	29	106	0.10%	41.5%	GSYGDLGGPIITTQVTIPK	99.7%	91.7	25	89	4	0	0	1917.03	378	396
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	20	29	106	0.10%	41.5%	IDEPLEGSEDR	99.7%	79.3	25	69.6	4	0	0	1259.58	423	433
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	20	29	106	0.10%	41.5%	IDEPLEGSEDRIITITGTQDQIQNAQYLLQNSVK	99.7%	85.3	25	85.3	0	2	0	3829.95	423	456
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	20	29	106	0.10%	41.5%	IILDLISESPIK	99.7%	96.2	25	82.5	16	0	0	1340.80	208	219
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	20	29	106	0.10%	41.5%	IITITGTQDQIQNAQYLLQNSVK	99.7%	84.5	25	84.5	4	4	0	2589.39	434	456
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	20	29	106	0.10%	41.5%	ILSISADIETIGEILK	99.7%	125	25	116	4	0	0	1714.98	87	102
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	20	29	106	0.10%	41.5%	ILSISADIETIGEILKK	99.7%	125	25	125	4	2	0	1843.08	87	103
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	20	29	106	0.10%	41.5%	LFQECCPHSTDR	99.7%	89.8	25	89.8	4	2	0	1549.65	180	191
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	20	29	106	0.10%	41.5%	LLIHQSLAGGIIGVK	99.7%	66.4	25	66.4	2	4	0	1518.94	149	163
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	20	29	106	0.10%	41.5%	NLPLPPPPPPR	99.7%	50.3	25	34.6	4	0	0	1194.70	306	316
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	20	29	106	0.10%	41.5%	NTDEMVELR	99.7%	73.8	25	60.5	8	0	0	1106.51	38	46
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	20	29	106	0.10%	41.5%	RDYDDMSPR	99.2%	35.6	25	35.6	2	0	0	1154.49	278	286
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	20	29	106	0.10%	41.5%	RPAEDMEEEQAFKR	99.7%	88.9	25	88.9	1	7	0	1735.81	22	35
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	20	29	106	0.10%	41.5%	SRNTDEMVELR	99.7%	53.1	25	36.6	2	2	0	1349.65	36	46
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	HNRPK_HUMAN	51.0	100.0%	20	29	106	0.10%	41.5%	VVLIGGKPDR	99.7%	50.2	25	50.2	5	0	0	1053.64	192	201
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	20	33	147	0.14%	47.0%	AITHLNNNFMFGQK	99.7%	84.1	25	80.4	8	7	0	1634.81	435	448
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	20	33	147	0.14%	47.0%	ASLNGADIYSGCCTLK	99.7%	93.9	25	89.8	4	0	0	1729.79	249	264
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	20	33	147	0.14%	47.0%	FSTPEQAAK	96.4%	29.2	25	22.6	1	0	0	978.49	485	493
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	20	33	147	0.14%	47.0%	IEYAKPTR	99.7%	57.5	25	50.6	11	0	0	977.54	265	272
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	20	33	147	0.14%	47.0%	ISRPGDSDDSR	99.7%	40.9	25	36	4	5	0	1204.56	179	189
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	20	33	147	0.14%	47.0%	LCFSTAQHAS	99.7%	51.5	25	51.5	6	0	0	1121.50	580	589
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	20	33	147	0.14%	47.0%	LNVCVSK	99.7%	46.2	25	31.9	4	0	0	819.44	449	455
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	20	33	147	0.14%	47.0%	MGPPVGGHR	99.7%	50.8	25	38.9	5	0	0	907.46	345	353
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	20	33	147	0.14%	47.0%	NDQDTWDYTNPNLSGQGDPGSNPNKR	99.7%	111	25	111	0	4	0	2890.26	278	303
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	20	33	147	0.14%	47.0%	NGVQAMVEFDSVQSAQR	99.7%	129	25	126	6	0	0	1865.88	230	246
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	20	33	147	0.14%	47.0%	NPNGPYPYTLK	99.7%	40.5	25	26.4	4	0	0	1263.64	569	579
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	20	33	147	0.14%	47.0%	QPAIMPGQSYGLEDGSCSYK	99.7%	103	25	102	4	0	0	2187.97	456	475
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	20	33	147	0.14%	47.0%	QPAIMPGQSYGLEDGSCSYKDFSESR	99.7%	69.4	25	69.4	0	5	0	2925.27	456	481
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	20	33	147	0.14%	47.0%	SDALETLGFLNHYQMK	99.7%	78.5	25	78.5	8	6	0	1866.91	553	568
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	20	33	147	0.14%	47.0%	SKPGAAMVEMADGYAVDR	99.7%	92.6	25	85.8	8	16	0	1899.86	417	434
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	20	33	147	0.14%	47.0%	SSSGLLEWESK	99.7%	71.9	25	58.3	5	0	0	1222.60	542	552

Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	20	33	147	0.14%	47.0%	TDNAGDQHGGGGGGGGAGAAGGGGGGENYDDPHK	99.6%	32.8	25	32.8	0	1	0	2981.20	63	97
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	20	33	147	0.14%	47.0%	TPASPVVHIR	99.7%	62.5	25	60.4	6	0	0	1076.62	98	107
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	20	33	147	0.14%	47.0%	VFNVFCLYGNVEK	99.7%	102	25	93.9	18	0	0	1588.78	399	411
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	HNRPL_HUMAN	64.1	100.0%	20	33	147	0.14%	47.0%	YYGGGSEGGR	99.7%	43.3	25	43.3	1	0	0	1002.43	47	56
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	ACQIFVR	99.4%	36.6	25	26	2	0	0	893.47	652	658
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	ADILEDKDGK	99.7%	56.6	25	43.6	6	0	0	1103.56	233	242
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	AFITNIPFDVK	99.7%	66.6	25	47.6	9	0	0	1264.69	73	83
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	DKFNECGHVLYADIK	99.7%	78.1	25	70	2	0	0	1808.86	671	685
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	EKVGEVTYVELLMDAEGK	99.7%	34.6	25	26.4	0	1	0	2026.01	93	110
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	EVFSMAGVVVR	99.7%	70.7	25	64.3	2	0	0	1193.63	222	232
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	FEPYANPTKR	97.9%	31.4	25	17.2	1	0	0	1222.62	61	70
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	FESPEVAER	99.7%	45.8	25	36.4	5	0	0	1063.51	699	707
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	FGSGMNMGR	99.7%	59.2	25	14.2	12	0	0	972.40	363	371
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	GCAVVEFK	99.7%	48.3	25	30.6	3	0	0	909.45	113	120
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	GCGVVKFESPEVAER	99.0%	29.1	25	29.1	0	1	0	1663.81	693	707
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	GGNRFEPYANPTK	99.6%	38.6	25	18.5	2	2	0	1450.71	57	69
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	GIGMGNIGPAGMGMEGIGFGINK	99.7%	103	25	103	9	2	0	2226.04	323	345
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	GNFGGSFAGSFGGAGGHAPGVAR	99.7%	120	25	120	2	4	0	2034.95	628	650
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	INEILSNALK	99.7%	71.7	25	51.7	6	0	0	1114.65	372	381
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	INEILSNALKR	99.7%	61.4	25	54	2	0	0	1270.75	372	382
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	KACQIFVR	99.7%	60.2	25	42.7	2	0	0	1021.56	651	658
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	LGSTVFVANLDYK	99.7%	77.4	25	68.7	4	0	0	1426.76	202	214
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	LKEVFSMAGVVVR	99.7%	96.3	25	87	4	8	0	1434.81	220	232
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	MGAGLGHGMDR	99.7%	83.1	25	77	7	0	0	1117.49	419	429
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	MGAGMGFGLER	99.7%	88.3	25	72.5	12	0	0	1157.51	486	496
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	MGANNLER	99.7%	67.5	25	59.4	4	0	0	904.43	558	565
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	MGANSLER	99.7%	67.1	25	59.8	6	0	0	877.42	571	578
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	MGGMEGPFGGGMENMGR	99.7%	88.5	25	88.5	11	0	0	1714.68	346	362
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	MGLAMGGGGGASFDR	99.7%	99.7	25	50.4	10	0	0	1399.61	607	621
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	MGLSMER	99.7%	55.8	25	43.3	8	0	0	823.38	525	531
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	MGLVMDR	99.7%	53.6	25	49.4	6	0	0	821.40	437	443
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	MGPAMGPALGAGIER	99.7%	82.4	25	78.8	10	0	0	1459.70	592	606
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	MGPLGLDHMASSIER	99.7%	87.6	25	75.9	8	6	0	1629.77	457	471
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	MGPVMDR	99.0%	34.7	25	22.9	2	0	0	821.36	544	550
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	MVPAGMGAGLER	99.7%	64.3	25	60.4	6	0	0	1188.59	532	543
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	NLPFDFTWK	99.3%	35.9	25	29.8	2	0	0	1167.58	659	667
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	QGGGGGGGSVPGIER	99.7%	96.2	25	94.9	6	0	0	1284.63	389	403
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	VGEVTYVELLMDAEGK	99.7%	100	25	100	9	0	0	1752.87	95	110
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	HNRPM_HUMAN	77.5	100.0%	35	55	206	0.19%	48.9%	WQSLKDLVK	99.5%	37.8	25	31.9	2	0	0	1116.64	84	92
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	AGPIWDLR	99.7%	62.6	25	48.7	5	0	0	927.50	185	192
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	AIEALKEFNEDGALAVLQQFK	99.7%	45.9	25	45.9	0	2	0	2334.23	61	81
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	DLFEDELVPLFEK	99.7%	107	25	95.7	14	0	0	1593.80	172	184
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	DSDLSHVQNK	99.7%	46.7	25	32.3	4	0	0	1142.54	82	91
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	DYAFIHFDER	99.7%	57.5	25	44.2	2	0	0	1312.60	372	381
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	DYAFIHFDERDGAVK	98.2%	26.6	25	26.6	0	2	0	1782.84	372	386
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	EFNEDGALAVLQQFK	99.7%	62.2	25	62.2	5	0	0	1708.85	67	81
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	EQILEEFSK	99.6%	39	25	6.25	4	0	0	1122.57	257	265
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	GFCFLEYEDHK	99.7%	54.9	25	54.9	10	3	0	1444.62	287	297
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	GFCFLEYEDHKTAAQAR	99.7%	34.9	25	34.9	0	1	0	2042.94	287	303
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	GYAFVTFCTK	99.7%	71.4	25	71.4	7	0	0	1193.57	204	213
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	HIGVCISVANNR	99.7%	67.6	25	0	7	2	0	1339.69	233	244

Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	KYGGPPPDSVYSGQQPSVGTEIFVGK	99.7%	68.9	25	68.9	0	2	0	2694.34	143	168
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	LDEIYVAGLVAHSDLDER	99.7%	121	25	121	2	0	0	2015.01	43	60
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	LFVGSIPK	99.7%	46.7	25	28.6	7	0	0	860.52	245	252
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	LKDYAFIHFDER	99.7%	73.9	25	68.6	2	3	0	1553.77	370	381
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	LMMDPLTGLNR	99.7%	72	25	65.5	23	0	0	1260.64	193	203
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	LYNNHEIR	99.7%	46.5	25	31.6	5	0	0	1058.54	222	229
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	NLANTVTEEILEK	99.7%	96.7	25	87.1	9	0	0	1473.78	344	356
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	QTNNQNWGSQPIAQQPLQGGDHSGNYGYK	99.7%	97.6	25	97	0	2	0	3187.46	579	607
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	SAFLCGVMK	99.7%	50.4	25	41.3	14	0	0	1012.50	92	100
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	SENQEFYQDTFGQQWK	99.7%	86.2	25	86.2	2	0	0	2034.88	608	623
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	TGYTLDVTTGQR	99.7%	71.5	25	68	10	0	0	1311.65	131	142
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	TKEQILEEFSK	99.7%	74.3	25	74.3	10	2	0	1351.71	255	265
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	VAEKLDEIYVAGLVAHSDLDER	99.7%	48.2	25	43.8	0	1	0	2442.25	39	60
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	VTEGLTDVILYHQPDDK	99.7%	82.6	25	82.6	4	3	0	1942.98	266	282
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	VWGNVGTVEWADPIEDPDPEVMAK	99.7%	65.8	25	65.8	4	3	0	2654.24	313	336
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	HNRPQ_HUMAN	69.6	100.0%	28	39	182	0.17%	50.4%	YGGPPPDSVYSGQQPSVGTEIFVGK	99.7%	82.6	25	82.6	2	4	0	2566.25	144	168
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	18	26	144	0.14%	42.3%	AGPIWDLR	99.7%	62.6	25	48.7	5	0	0	927.50	188	195
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	18	26	144	0.14%	42.3%	DLYEDELVPLFEK	99.7%	84.8	25	79.9	16	0	0	1609.80	175	187
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	18	26	144	0.14%	42.3%	DYAFVHFEDR	99.7%	51.8	25	49.7	6	0	0	1298.58	375	384
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	18	26	144	0.14%	42.3%	EFNEEGALSVLQQFK	99.7%	105	25	94.5	7	0	0	1738.86	70	84
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	18	26	144	0.14%	42.3%	ENILEEFSK	99.7%	46.7	25	38	2	0	0	1108.55	260	268
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	18	26	144	0.14%	42.3%	GFCFLEYEDHK	99.7%	54.9	25	54.9	10	3	0	1444.62	290	300
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	18	26	144	0.14%	42.3%	GYAFITFCGK	99.7%	81.5	25	72.7	7	0	0	1163.56	207	216
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	18	26	144	0.14%	42.3%	HLGVCISVANNR	99.7%	67.6	25	0	7	2	0	1339.69	236	247
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	18	26	144	0.14%	42.3%	LCDSYEIRPGK	99.7%	65.3	25	50.9	7	2	0	1337.65	225	235
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	18	26	144	0.14%	42.3%	LFVGSIPK	99.7%	46.7	25	28.6	7	0	0	860.52	248	255
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	18	26	144	0.14%	42.3%	LKDYAFVHFEDR	99.7%	91	25	89.2	2	8	0	1539.76	373	384
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	18	26	144	0.14%	42.3%	LMMDPLSGQNR	99.7%	67.7	25	46.9	22	0	0	1261.60	196	206
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	18	26	144	0.14%	42.3%	NLATTVTEEILEK	99.7%	111	25	101	13	0	0	1460.78	347	359
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	18	26	144	0.14%	42.3%	SAFLCGVMK	99.7%	50.4	25	41.3	14	0	0	1012.50	95	103
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	18	26	144	0.14%	42.3%	SFSEFGK	97.4%	30.5	25	24.9	2	0	0	801.38	360	366
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	18	26	144	0.14%	42.3%	SFSEFGKLER	99.7%	48.1	25	38.3	2	0	0	1199.61	360	369
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	18	26	144	0.14%	42.3%	STAYEDYYYHPPPR	99.7%	77.1	25	76.8	3	5	0	1758.78	428	441
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	18	26	144	0.14%	42.3%	TGYTLDVTTGQR	99.7%	71.5	25	68	10	0	0	1311.65	134	145
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	18	26	144	0.14%	42.3%	TKENILEEFSK	99.7%	74.3	25	61.3	8	0	0	1337.69	258	268
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	18	26	144	0.14%	42.3%	TLIEAGLPQK	99.7%	63.8	25	63.8	4	0	0	1069.63	32	41
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	18	26	144	0.14%	42.3%	VQESTKGPDEAK	99.7%	70.3	25	64.7	6	1	0	1288.64	115	126
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	18	26	144	0.14%	42.3%	VTEGLVDVILYHQPDDK	99.7%	86.1	25	83.5	6	6	0	1941.00	269	285
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	18	26	144	0.14%	42.3%	VWGNVVTVEWADPVEEPDPEVMAK	99.7%	75.3	25	75.3	3	0	0	2696.29	316	339
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	HNRPR_HUMAN	70.9	100.0%	18	26	144	0.14%	42.3%	YGGPPPDSVYSGVQPGIGTEVFVGK	99.7%	96.7	25	96.7	2	4	0	2507.25	147	171
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	AEGGGGGGRPGAPAAGDGK	99.7%	49.8	25	46.7	2	2	0	1538.73	216	234
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	AEGGGGGGRPGAPAAGDGKTEQK	99.7%	60	25	60	0	2	0	2024.97	216	238
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	AEVEGKDLPEHAVLK	99.7%	40.5	25	40.5	0	1	0	1634.88	621	635
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	DCEVVMMIGLPGAGK	99.7%	87.4	25	15	8	0	0	1592.75	496	510
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	DIDIHEVR	99.7%	45.5	25	36.4	11	0	0	996.51	353	360
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	DLPEHAVLK	99.6%	39.3	25	29.1	7	0	0	1021.57	627	635
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	EKPYFPIPEEYTFIQNVPLEDR	99.0%	29.1	25	29.1	0	1	0	2724.36	463	484
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	FIEIAAR	99.7%	44.9	25	28	13	0	0	819.47	566	572
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	GKVCFEMK	98.7%	33.4	25	24.9	3	0	0	998.48	332	339
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	GYFEYIEENK	99.7%	59.5	25	53	4	0	0	1291.58	256	265
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	GYFEYIEENKYSR	99.7%	75	25	75	8	3	0	1697.78	256	268

Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	KAEGGGGGGRPGAPAAGDGK	99.3%	30.3	25	30.3	1	4	0	1666.83	215	234
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	KAVVVCPK	98.9%	33.9	25	14.1	1	0	0	900.53	602	609
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	KDCEVVMMIGLPGAGK	99.7%	93.9	25	93.9	6	6	0	1704.85	495	510
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	KMCLFAGFQR	99.7%	44	25	33.6	2	2	0	1273.62	592	601
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	LLEQYKEESK	99.7%	60.4	25	51	13	0	0	1266.66	665	674
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	LNTLLQR	99.7%	61	25	28.7	4	0	0	857.52	552	558
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	LQAALDDEEAGGRPAMEPGNGSLDLGGDSAGR	99.7%	91.2	25	91.2	0	4	0	3142.43	38	69
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	MCLFAGFQR	99.7%	77.1	25	73.4	16	0	0	1145.52	593	601
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	MMVAGFK	98.5%	32.7	25	11.3	4	0	0	799.38	537	543
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	MMVAGFKK	95.2%	28.1	25	22.9	1	0	0	911.48	537	544
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	NFILDQTNVSAAAQR	99.7%	129	25	117	19	2	0	1647.84	576	590
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	NGQDLGVAFK	99.7%	57.7	25	46.5	8	0	0	1048.54	424	433
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	RNFILDQTNVSAAAQR	99.7%	39.5	25	35.6	0	2	0	1803.95	575	590
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	SSGPTSLFAVTVAPPGAR	99.7%	68.3	25	61.9	13	2	0	1714.91	187	204
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	TCNCETEDYGEK	99.7%	48.7	25	48.7	2	0	0	1505.55	388	399
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	VCFEMK	97.3%	30.3	25	15.5	1	0	0	813.36	334	339
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	VSELKEELK	99.7%	43.4	25	25.2	2	0	0	1074.60	13	21
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	VTEKIPVR	99.7%	51.9	25	44.7	4	0	0	941.58	340	347
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	HNRPU_HUMAN	90.6	100.0%	30	43	204	0.19%	33.1%	YNILGTNTIMDK	99.7%	90.7	25	76.9	20	0	0	1398.69	525	536
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	11	12	37	0.03%	17.3%	AIVICPTDEDLKDR	96.9%	24.6	25	22.2	0	1	0	1644.83	528	541
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	11	12	37	0.03%	17.3%	EALGGQALYPHVLVK	99.7%	79.6	25	70.8	6	0	0	1594.90	361	375
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	11	12	37	0.03%	17.3%	HLPSTEPDPHVVR	99.7%	44.3	25	41.6	0	6	0	1483.77	271	283
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	11	12	37	0.03%	17.3%	INEEISVK	99.6%	38.6	25	16.9	1	0	0	931.51	263	270
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	11	12	37	0.03%	17.3%	NCAVEFNFGQR	99.7%	64.8	25	64.8	4	0	0	1341.60	376	386
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	11	12	37	0.03%	17.3%	NPPGASTYNK	98.6%	33.1	25	31.3	1	0	0	1048.51	722	731
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	11	12	37	0.03%	17.3%	NYILDQTNVYGSAQR	99.7%	138	25	131	6	0	0	1741.85	501	515
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	11	12	37	0.03%	17.3%	QGAPTSFLPPEASQLKPDR	99.7%	60.4	25	60.4	0	2	0	2039.06	147	165
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	11	12	37	0.03%	17.3%	QNQFYDTQVIK	99.7%	51.2	25	21.4	2	0	0	1383.69	107	117
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	11	12	37	0.03%	17.3%	VCFEMK	97.3%	30.3	25	15.5	1	0	0	813.36	257	262
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	11	12	37	0.03%	17.3%	WDVLIQQATQCLNR	99.7%	103	25	102	4	0	0	1744.88	477	490
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	HNRL1_HUMAN	95.7	100.0%	11	12	37	0.03%	17.3%	YNILGTNAIMDK	99.7%	56	25	49.4	4	0	0	1352.69	450	461
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	20	46	0.04%	22.6%	ANFSLPEK	99.7%	49.3	25	34.6	2	0	0	905.47	594	601
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	20	46	0.04%	22.6%	DLLVQQASQCLSK	99.7%	112	25	109	3	0	0	1489.77	509	521
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	20	46	0.04%	22.6%	DRYGGQPLFSEK	99.7%	49.8	25	34.6	2	0	0	1396.69	262	273
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	20	46	0.04%	22.6%	EGCTEVSLLR	99.7%	50.5	25	28	4	0	0	1163.57	306	315
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	20	46	0.04%	22.6%	EVEGDDVPESIMLEMK	99.7%	66.1	25	64.8	4	0	0	1820.83	578	593
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	20	46	0.04%	22.6%	FPTLWSGAR	99.7%	43.6	25	32.8	4	0	0	1034.54	274	282
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	20	46	0.04%	22.6%	GLEEPEMDPK	99.7%	43.9	25	42.7	4	0	0	1144.52	497	506
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	20	46	0.04%	22.6%	MKGLEEPEMDPK	99.7%	43.3	25	43.3	1	0	0	1435.64	495	506
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	20	46	0.04%	22.6%	NCVVELNFGQK	99.7%	74.7	25	64.4	2	0	0	1307.64	407	417
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	20	46	0.04%	22.6%	NFILDQCNVYNSGQR	99.7%	93.1	25	90.3	2	0	0	1827.84	532	546
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	20	46	0.04%	22.6%	NYYGYQGYR	99.7%	55.7	25	49.1	2	0	0	1183.52	739	747
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	20	46	0.04%	22.6%	SGDETPGSEVPGDK	99.7%	54.5	25	51.7	3	0	0	1374.60	161	174
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	20	46	0.04%	22.6%	TIEECEVILMVGLPGSGK	99.3%	36.1	25	36.1	1	0	0	1931.98	448	465
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	20	46	0.04%	22.6%	VTQNLPMK	99.7%	39.7	25	15.8	4	0	0	930.51	298	305
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	20	46	0.04%	22.6%	YGGQPLFSEK	99.7%	45.4	25	37.5	2	0	0	1125.56	264	273
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	HNRL2_HUMAN	85.1	100.0%	16	20	46	0.04%	22.6%	YNVLGAETVLNQMR	99.7%	106	25	101	6	0	0	1607.82	481	494
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	22	33	231	0.22%	61.5%	DYFEEYGK	98.1%	31.7	25	31.7	2	0	0	1050.44	130	137
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	22	33	231	0.22%	61.5%	EESGKPGAHVTVK	99.7%	69.7	25	61.9	17	0	0	1338.70	100	112
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	22	33	231	0.22%	61.5%	EESGKPGAHVTVKK	99.7%	49.5	25	40.3	2	0	0	1466.80	100	113
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	22	33	231	0.22%	61.5%	GFGDGYNGYGGGPGGGNFGGSPGYGGGR	99.7%	127	25	127	4	3	0	2495.04	239	266

Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	22	33	231	0.22%	61.5%	GFGFVTFDDHDPVDK	99.7%	98.1	25	96.4	8	6	0	1695.77	154	168
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	22	33	231	0.22%	61.5%	GFGFVTFDDHDPVDKIVLQK	99.7%	64.9	25	64.9	2	4	0	2277.16	154	173
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	22	33	231	0.22%	61.5%	GGGGNFGPGPGSNFR	99.7%	60.9	25	60.1	22	0	0	1377.63	214	228
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	22	33	231	0.22%	61.5%	GGNFGFGDSR	99.7%	73	25	69.2	25	0	0	1013.44	204	213
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	22	33	231	0.22%	61.5%	IDTIEIITDR	99.7%	101	25	93.8	11	0	0	1188.65	138	147
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	22	33	231	0.22%	61.5%	KLFIGGLSFETTEESLR	99.7%	58.1	25	58.1	4	5	0	1927.02	22	38
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	22	33	231	0.22%	61.5%	KLFVGGIK	98.9%	34	25	0	3	0	0	861.56	113	120
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	22	33	231	0.22%	61.5%	LFIGGLSFETTEESLR	99.7%	126	25	126	28	0	0	1798.92	23	38
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	22	33	231	0.22%	61.5%	LFVGGIKEDTEEHHLR	99.7%	66.7	25	0	0	9	0	1879.97	114	129
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	22	33	231	0.22%	61.5%	LTDCVVMR	99.7%	64.4	25	56.9	14	0	0	993.49	47	54
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	22	33	231	0.22%	61.5%	LTDCVVMRDPASK	99.7%	69.2	25	55.4	3	0	0	1491.73	47	59
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	22	33	231	0.22%	61.5%	NMGGPYGGGNYGPGGSGGSGGYGGR	99.7%	148	25	148	15	7	0	2205.90	326	350
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	22	33	231	0.22%	61.5%	NYYEQWGK	99.7%	42.2	25	42.2	7	0	0	1087.48	39	46
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	22	33	231	0.22%	61.5%	QEMQEVQSSR	99.7%	78.2	25	77.1	7	0	0	1221.55	191	200
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	22	33	231	0.22%	61.5%	RGFGFVTFDDHDPVDK	99.7%	33.8	25	33.8	0	2	0	1851.87	153	168
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	22	33	231	0.22%	61.5%	TLETVPLER	99.7%	62.2	25	62.2	14	0	0	1057.59	4	12
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	22	33	231	0.22%	61.5%	YHTINGHNAEVR	99.7%	70.8	25	56.9	2	3	0	1410.69	174	185
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	ROA2_HUMAN	37.4	100.0%	22	33	231	0.22%	61.5%	YHTINGHNAEVRK	98.3%	26.9	25	26.7	1	1	0	1538.78	174	186
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	12	17	267	0.25%	33.3%	GDDLQAIKK	99.7%	43.9	25	29.7	6	0	0	987.55	190	198
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	12	17	267	0.25%	33.3%	GFAFVQYVNER	99.7%	89.4	25	89.3	32	0	0	1329.66	51	61
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	12	17	267	0.25%	33.3%	KSDVEAIFSK	99.7%	66.4	25	55.1	30	0	0	1123.60	30	39
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	12	17	267	0.25%	33.3%	LKGDDLQAIK	99.7%	41.5	25	33.1	11	0	0	1100.63	188	197
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	12	17	267	0.25%	33.3%	MIAGQVLDINLAAEPK	99.7%	133	25	133	61	9	0	1682.91	74	89
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	12	17	267	0.25%	33.3%	MYSYPAR	99.2%	35.4	25	22.8	14	0	0	887.41	136	142
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	12	17	267	0.25%	33.3%	NDKSEEEQSSSSVK	99.7%	56.6	25	56.6	2	0	0	1553.69	230	243
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	12	17	267	0.25%	33.3%	QKVDSLLENLEK	99.7%	58	25	49.6	16	2	0	1415.77	205	216
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	12	17	267	0.25%	33.3%	SDVEAIFSK	99.7%	75.7	25	66.5	19	0	0	995.50	31	39
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	12	17	267	0.25%	33.3%	VDSLLENLEK	99.7%	67.9	25	50	13	0	0	1159.62	207	216
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	12	17	267	0.25%	33.3%	VFIGNLNTLVVK	99.7%	96.1	25	95.7	42	0	0	1316.79	18	29
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	HNRPC_HUMAN	33.7	100.0%	12	17	267	0.25%	33.3%	VPPPPPIAR	99.3%	36	25	34.7	10	0	0	943.57	143	151
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	15	23	0.02%	18.5%	AAQLCGAGMAAVVDK	99.7%	71.9	25	65.2	1	0	0	1461.72	830	844
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	15	23	0.02%	18.5%	AILQQLGLNSTCDDSILVK	99.7%	44.5	25	44.5	1	0	0	2088.10	802	820
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	15	23	0.02%	18.5%	ASGVEGADVVK	99.7%	50	25	30.7	2	0	0	1031.54	177	187
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	15	23	0.02%	18.5%	CNVSFLLSEDGSGK	99.7%	65	25	57.9	1	0	0	1512.70	886	899
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	15	23	0.02%	18.5%	FLLSESGSGK	99.7%	42.8	25	24.2	2	0	0	1024.53	442	451
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	15	23	0.02%	18.5%	FLSQIESDR	99.7%	66.6	25	52	2	0	0	1094.55	786	794
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	15	23	0.02%	18.5%	GAALITAVGVR	99.7%	71.4	25	61.4	1	0	0	1027.63	900	910
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	15	23	0.02%	18.5%	GAAMVTAVAYR	99.7%	80.6	25	66.6	2	0	0	1125.57	452	462
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	15	23	0.02%	18.5%	GDFIALDLGGSSFR	99.7%	86	25	86	2	0	0	1454.73	78	91
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	15	23	0.02%	18.5%	HIDLVEGDEGR	99.7%	49.5	25	49.5	1	0	0	1239.60	244	254
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	15	23	0.02%	18.5%	IDEAILITWTK	99.7%	60.3	25	59.1	2	0	0	1302.73	163	173
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	15	23	0.02%	18.5%	LALLQVR	99.7%	40.5	25	22.4	2	0	0	812.54	795	801
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	15	23	0.02%	18.5%	LSDETLIDIMTR	99.7%	73	25	66.8	2	0	0	1406.72	31	42
Hexokinase-1	HK1	HXK1_HUMAN	102.5	100.0%	14	15	23	0.02%	18.5%	SANLVAATLGAILNR	99.7%	72.7	25	65.7	1	1	0	1483.86	382	396
High mobility group protein B1	HMGB1	HMGB1_HUMAN	24.9	99.8%	2	2	2	0.00%	11.6%	IKGEHPGLSIGDVAK	98.9%	28.6	25	26.9	0	1	0	1520.84	113	127
High mobility group protein B1	HMGB1	HMGB1_HUMAN	24.9	99.8%	2	2	2	0.00%	11.6%	TYIPPKGETK	97.4%	30.6	25	22.7	1	0	0	1133.62	77	86
Histidine triad nucleotide-binding protein 2, mitochondrial	HINT2	HINT2_HUMAN	17.2	99.8%	2	2	3	0.00%	19.0%	AQQATPGGAAPTIFSR	99.7%	47.9	25	40.8	2	0	0	1572.81	43	58
Histidine triad nucleotide-binding protein 2, mitochondrial	HINT2	HINT2_HUMAN	17.2	99.8%	2	2	3	0.00%	19.0%	DVAPQAPVHFLVIPK	98.2%	31.9	25	31.9	1	0	0	1630.93	80	94
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	9	13	21	0.02%	22.4%	ISICSSDKR	99.5%	37.2	25	24.6	1	0	0	1065.54	405	413
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	9	13	21	0.02%	22.4%	LGCFNLTIK	99.7%	63	25	47.2	2	0	0	1065.58	271	279
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	9	13	21	0.02%	22.4%	LHISPSNMTNQNTNEYLEK	99.7%	46.2	25	46.2	0	3	0	2233.06	343	361

Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	9	13	21	0.02%	22.4%	MTHNLLLNYGLYR	99.7%	52	25	52	1	0	0	1607.84	37	49
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	9	13	21	0.02%	22.4%	SFNLPMLMLGGGGYTIR	99.7%	54.8	25	54	2	0	0	1826.93	290	306
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	9	13	21	0.02%	22.4%	SIRPDNMSEYSK	99.7%	48.3	25	35.9	4	1	0	1426.66	78	89
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	9	13	21	0.02%	22.4%	VMTVSFHK	99.7%	50.5	25	42.8	2	0	0	948.50	193	200
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	9	13	21	0.02%	22.4%	YGEYFPGTGDLR	99.7%	66	25	64.7	4	0	0	1374.63	201	212
Histone deacetylase 1	HDAC1	HDAC1_HUMAN	55.1	100.0%	9	13	21	0.02%	22.4%	YYAVNYPLR	99.7%	43.8	25	34.7	1	0	0	1158.59	221	229
Histone deacetylase 2	HDAC2	HDAC2_HUMAN	55.4	100.0%	4	4	6	0.01%	20.3%	LGCFNLTVK	99.7%	59.8	25	52.8	2	0	0	1051.56	272	280
Histone deacetylase 2	HDAC2	HDAC2_HUMAN	55.4	100.0%	4	4	6	0.01%	20.3%	LHISPSNMTNQNTPEYMEK	99.7%	38.5	25	38.5	0	2	0	2250.02	344	362
Histone deacetylase 2	HDAC2	HDAC2_HUMAN	55.4	100.0%	4	4	6	0.01%	20.3%	MTHNLLLNYGLYR	99.7%	52	25	52	1	0	0	1607.84	38	50
Histone deacetylase 2	HDAC2	HDAC2_HUMAN	55.4	100.0%	4	4	6	0.01%	20.3%	SIRPDNMSEYSK	99.7%	48.3	25	35.9	4	1	0	1426.66	79	90
Histone deacetylase 2	HDAC2	HDAC2_HUMAN	55.4	100.0%	4	4	6	0.01%	20.3%	TFNLPLLMLGGGGYTIR	99.7%	50.1	25	50.1	1	0	0	1838.98	291	307
Histone deacetylase 2	HDAC2	HDAC2_HUMAN	55.4	100.0%	4	4	6	0.01%	20.3%	VMTVSFHK	99.7%	50.5	25	42.8	2	0	0	948.50	194	201
Histone deacetylase 2	HDAC2	HDAC2_HUMAN	55.4	100.0%	4	4	6	0.01%	20.3%	YGEYFPGTGDLR	99.7%	66	25	64.7	4	0	0	1374.63	202	213
Histone deacetylase 2	HDAC2	HDAC2_HUMAN	55.4	100.0%	4	4	6	0.01%	20.3%	YYAVNFPMR	99.7%	59	25	59	1	0	0	1160.56	222	230
Histone deacetylase complex subunit SAP18	SAP18	SAP18_HUMAN	17.6	100.0%	3	6	12	0.01%	15.7%	GTDDSMTLQSQK	99.7%	75.8	25	62.3	4	0	0	1310.59	115	126
Histone deacetylase complex subunit SAP18	SAP18	SAP18_HUMAN	17.6	100.0%	3	6	12	0.01%	15.7%	KGTDDSMTLQSQK	99.7%	76.8	25	67.6	4	0	0	1438.68	114	126
Histone deacetylase complex subunit SAP18	SAP18	SAP18_HUMAN	17.6	100.0%	3	6	12	0.01%	15.7%	VKEIGSTMSGR	99.7%	43.8	25	35.1	4	0	0	1164.60	103	113
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	8	11	121	0.11%	22.8%	ALAAAGYDVEK	99.7%	76.9	25	67.1	27	0	0	1107.57	65	75
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	8	11	121	0.11%	22.8%	ALAAAGYDVEKNNSR	99.7%	87.6	25	87.6	8	3	0	1578.79	65	79
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	8	11	121	0.11%	22.8%	ASGPPVSELITK	99.7%	74.4	25	67.7	23	0	0	1198.67	35	46
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	8	11	121	0.11%	22.8%	KALAAAGYDVEK	99.7%	67.8	25	57.6	2	1	0	1235.66	64	75
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	8	11	121	0.11%	22.8%	KASGPPVSELITK	99.7%	69.8	25	64.7	24	2	0	1326.76	34	46
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	8	11	121	0.11%	22.8%	SGVSLAALK	99.7%	63.8	25	39.2	5	0	0	845.51	55	63
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	8	11	121	0.11%	22.8%	SGVSLAALKK	99.7%	76.6	25	71.9	25	0	0	973.60	55	64
Histone H1.4	HIST1H1E	H14_HUMAN	21.9	100.0%	8	11	121	0.11%	22.8%	SLVSKGTLVQTK	99.7%	45.8	25	43.3	1	0	0	1260.75	86	97
Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	6	6	21	0.02%	23.5%	ALVQNDTLLQVK	99.7%	86.2	25	74.4	3	0	0	1341.77	95	106
Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	6	6	21	0.02%	23.5%	GAPAAATAPAPTAHK	99.7%	82.5	25	78.4	6	0	0	1331.71	129	143
Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	6	6	21	0.02%	23.5%	KVPWFDQQNGR	99.4%	36.9	25	31.7	2	0	0	1374.69	76	86
Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	6	6	21	0.02%	23.5%	RGAPAAATAPAPTAHK	99.7%	44.4	25	44.4	0	2	0	1487.81	128	143
Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	6	6	21	0.02%	23.5%	YSQLVVETIR	99.7%	93.5	25	74.3	6	0	0	1207.67	48	57
Histone H1x	H1FX	H1X_HUMAN	22.5	100.0%	6	6	21	0.02%	23.5%	YSQLVVETIRR	97.9%	31.3	25	27.4	2	0	0	1363.77	48	58
Histone H2A type 1-B/E	HIST1H2AB	H2A1B_HUMAN,H2AC_HUMAN,H2A3_HUMAN	14.1	100.0%	5	6	30	0.03%	35.4%	AGLQFPVGR	99.7%	65.5	25	51.1	14	0	0	944.53	22	30
Histone H2A type 1-B/E	HIST1H2AB	H2A1B_HUMAN,H2AC_HUMAN,H2A3_HUMAN	14.1	100.0%	5	6	30	0.03%	35.4%	HLQLAIR	99.7%	40.8	25	27.9	3	0	0	850.53	83	89
Histone H2A type 1-B/E	HIST1H2AB	H2A1B_HUMAN,H2AC_HUMAN,H2A3_HUMAN	14.1	100.0%	5	6	30	0.03%	35.4%	HLQLAIRNDEELNK	99.7%	39.2	25	38.6	0	2	0	1692.90	83	96
Histone H2A type 1-B/E	HIST1H2AB	H2A1B_HUMAN,H2AC_HUMAN,H2A3_HUMAN	14.1	100.0%	5	6	30	0.03%	35.4%	NDEELNKLLGR	99.7%	64.7	25	47.9	2	0	0	1300.69	90	100
Histone H2A type 1-B/E	HIST1H2AB	H2A1B_HUMAN,H2AC_HUMAN,H2A3_HUMAN	14.1	100.0%	5	6	30	0.03%	35.4%	VTIAQGGVLPNIQAVLLPK	99.7%	54.9	25	54.9	7	2	0	1931.17	101	119
Histone H2A.V	H2AFV	H2AV_HUMAN,H2AZ_HUMAN	13.5	99.8%	2	3	5	0.00%	31.2%	AGLQFPVGR	99.7%	65.5	25	51.1	14	0	0	944.53	24	32
Histone H2A.V	H2AFV	H2AV_HUMAN,H2AZ_HUMAN	13.5	99.8%	2	3	5	0.00%	31.2%	ATIAGGGVIPHIHK	99.7%	60.9	25	59.7	1	2	0	1370.79	103	116
Histone H2A.V	H2AFV	H2AV_HUMAN,H2AZ_HUMAN	13.5	99.8%	2	3	5	0.00%	31.2%	GDEELDSLIK	99.7%	63.3	25	53.1	2	0	0	1118.56	93	102
Histone H2A.V	H2AFV	H2AV_HUMAN,H2AZ_HUMAN	13.5	99.8%	2	3	5	0.00%	31.2%	HLQLAIR	99.7%	40.8	25	27.9	3	0	0	850.53	86	92
Histone H2B type 1-C/E/F/G/I	HIST1H2BC	————————	13.9	100.0%	4	5	32	0.03%	27.0%	AMGIMNSFVNDIFER	99.7%	100	25	99.1	18	0	0	1743.82	59	73
Histone H2B type 1-C/E/F/G/I	HIST1H2BC	————————	13.9	100.0%	4	5	32	0.03%	27.0%	ESYSVYVYK	99.3%	36.3	25	36.3	2	0	0	1137.55	36	44
Histone H2B type 1-C/E/F/G/I	HIST1H2BC	————————	13.9	100.0%	4	5	32	0.03%	27.0%	KESYSVYVYK	99.7%	60.8	25	54.4	3	0	0	1265.64	35	44
Histone H2B type 1-C/E/F/G/I	HIST1H2BC	————————	13.9	100.0%	4	5	32	0.03%	27.0%	LLLPGELAK	99.7%	63.7	25	34.2	9	0	0	953.60	101	109
Histone H3.1t	HIST3H3	H3T_HUMAN,H31_HUMAN,H32_HUMAN,H33_HUMAN	15.5	100.0%	4	4	21	0.02%	19.9%	EIAQDFK	98.6%	33.2	25	22.1	2	0	0	850.43	74	80
Histone H3.1t	HIST3H3	H3T_HUMAN,H31_HUMAN,H32_HUMAN,H33_HUMAN	15.5	100.0%	4	4	21	0.02%	19.9%	EIAQDFKTDLR	99.7%	41.1	25	30.8	8	0	0	1335.69	74	84
Histone H3.1t	HIST3H3	H3T_HUMAN,H31_HUMAN,H32_HUMAN,H33_HUMAN	15.5	100.0%	4	4	21	0.02%	19.9%	STELLIR	99.7%	49	25	34.7	9	0	0	831.49	58	64
Histone H3.1t	HIST3H3	H3T_HUMAN,H31_HUMAN,H32_HUMAN,H33_HUMAN	15.5	100.0%	4	4	21	0.02%	19.9%	YRPGTVALR	95.0%	27.9	25	26.1	2	0	0	1032.59	42	50
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	9	36	0.03%	51.5%	DAVTYTEHAK	99.7%	51.8	25	51.2	6	0	0	1134.54	69	78
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	9	36	0.03%	51.5%	DNIQGITKPAIR	99.7%	66.3	25	51.1	8	4	0	1325.75	25	36
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	9	36	0.03%	51.5%	ISGLIYEETR	99.7%	64.2	25	58.2	6	0	0	1180.62	47	56

Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	9	36	0.03%	51.5%	TVTAMDVVYALK	99.7%	52.1	25	43.1	3	0	0	1326.70	81	92
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	9	36	0.03%	51.5%	TVTAMDVVYALKR	99.7%	57.7	25	57.7	4	0	0	1466.80	81	93
Histone H4	HIST1H4A	H4_HUMAN	11.4	100.0%	6	9	36	0.03%	51.5%	VFLENVIR	99.7%	57.5	25	44.9	5	0	0	989.58	61	68
Histone-binding protein RBBP4	RBBP4	RBBP4_HUMAN	47.7	100.0%	2	2	3	0.00%	3.5%	LMIWDTR	99.7%	39.6	25	35.6	2	0	0	934.48	252	258
Histone-binding protein RBBP4	RBBP4	RBBP4_HUMAN	47.7	100.0%	2	2	3	0.00%	3.5%	LNVWDLSK	99.7%	40	25	26.2	1	0	0	974.53	342	349
Hornerin	HRNR	HORN_HUMAN	282.4	100.0%	5	6	32	0.03%	3.4%	GPYESGSGHSSGLGHQESR	99.7%	59	25	59	0	3	0	1928.85	572	590
Hornerin	HRNR	HORN_HUMAN	282.4	100.0%	5	6	32	0.03%	3.4%	GPYESGSGHSSGLGHR	99.7%	91	25	89.5	7	18	0	1584.72	1038	1053
Hornerin	HRNR	HORN_HUMAN	282.4	100.0%	5	6	32	0.03%	3.4%	GSGSGQSPSSGQHGTGFGR	97.1%	24.9	25	24.9	0	1	0	1747.77	430	448
Hornerin	HRNR	HORN_HUMAN	282.4	100.0%	5	6	32	0.03%	3.4%	HGSGSGQSSSYSPYGSGSGWSSSR	99.7%	70.1	25	70.1	0	1	0	2348.98	1484	1507
Hornerin	HRNR	HORN_HUMAN	282.4	100.0%	5	6	32	0.03%	3.4%	QSLGHGQHGSGSGQSPSPSR	99.3%	30.5	25	30.5	0	2	0	1947.90	992	1011
Huntingtin	HTT	HD_HUMAN	347.6	100.0%	3	3	3	0.00%	1.1%	LFEPLVIK	94.5%	27.6	25	14.5	1	0	0	958.60	1424	1431
Huntingtin	HTT	HD_HUMAN	347.6	100.0%	3	3	3	0.00%	1.1%	NSGVPAFLTPLLR	99.1%	34.8	25	33.5	1	0	0	1384.79	2381	2393
Huntingtin	HTT	HD_HUMAN	347.6	100.0%	3	3	3	0.00%	1.1%	QIADIILPMLAK	98.7%	33.5	25	24	1	0	0	1325.79	1609	1620
Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	HMGCL_HUMAN	34.4	100.0%	3	3	5	0.00%	11.7%	AAQSANISVR	99.5%	37.5	25	28.3	1	0	0	1016.55	156	165
Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	HMGCL_HUMAN	34.4	100.0%	3	3	5	0.00%	11.7%	EVVIFGAASELFTK	99.7%	73.5	25	72.1	2	0	0	1510.82	123	136
Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	HMGCL_HUMAN	34.4	100.0%	3	3	5	0.00%	11.7%	FPGINYPVLTPNLK	99.7%	55	25	49	2	0	0	1572.88	98	111
Hydroxysteroid dehydrogenase-like protein 2	HSDL2	HSDL2_HUMAN	45.4	100.0%	4	4	11	0.01%	13.6%	KVDIIADAAYSIFQKPK	99.7%	52	25	52	0	2	0	1907.06	220	236
Hydroxysteroid dehydrogenase-like protein 2	HSDL2	HSDL2_HUMAN	45.4	100.0%	4	4	11	0.01%	13.6%	LAGCTVFITGASR	99.7%	82.6	25	64.5	4	0	0	1352.70	8	20
Hydroxysteroid dehydrogenase-like protein 2	HSDL2	HSDL2_HUMAN	45.4	100.0%	4	4	11	0.01%	13.6%	LLGTIYTAAEEIEAVGGK	99.7%	106	25	104	3	0	0	1834.98	50	67
Hydroxysteroid dehydrogenase-like protein 2	HSDL2	HSDL2_HUMAN	45.4	100.0%	4	4	11	0.01%	13.6%	SGAVEETFR	99.7%	52.4	25	45.7	2	0	0	995.48	307	315
Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	HPRT_HUMAN	24.6	100.0%	4	5	7	0.01%	21.6%	NVLIVEDIIDTGK	99.6%	39.1	25	39.1	2	0	0	1428.79	129	141
Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	HPRT_HUMAN	24.6	100.0%	4	5	7	0.01%	21.6%	TMQTLLSLVR	99.7%	71.2	25	41.3	2	0	0	1161.67	142	151
Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	HPRT_HUMAN	24.6	100.0%	4	5	7	0.01%	21.6%	VFIPHGLIMDR	98.6%	27.5	25	25	0	2	0	1313.70	35	45
Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	HPRT_HUMAN	24.6	100.0%	4	5	7	0.01%	21.6%	VIGGDDLSTLTGK	99.7%	40.1	25	40.1	1	0	0	1275.68	116	128
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	18	30	0.03%	19.3%	AANSLEAFIFETQDK	99.7%	65.9	25	50.9	2	0	0	1683.82	739	753
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	18	30	0.03%	19.3%	AEAGPEGVAPAPEGEK	99.7%	80.1	25	73	2	0	0	1508.72	670	685
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	18	30	0.03%	19.3%	AEAGPEGVAPAPEGEKK	99.7%	43.4	25	43.4	2	2	0	1636.82	670	686
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	18	30	0.03%	19.3%	DAVITVPVFFNQAER	98.6%	33.2	25	28.5	1	0	0	1705.89	171	185
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	18	30	0.03%	19.3%	DAVVYPILVEFTR	99.7%	81.6	25	78.5	2	0	0	1521.83	439	451
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	18	30	0.03%	19.3%	EAGMQPQLQIR	98.6%	33.2	25	28.4	1	0	0	1270.66	252	262
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	18	30	0.03%	19.3%	EVEEEPGIHSLK	99.7%	43.3	25	33.4	1	0	0	1366.69	452	463
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	18	30	0.03%	19.3%	EVQYLLNK	97.4%	30.5	25	13.4	2	0	0	1006.56	901	908
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	18	30	0.03%	19.3%	FFGDSAASMAIK	99.7%	82.9	25	76.6	2	0	0	1244.60	80	91
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	18	30	0.03%	19.3%	LAGLFNEQR	99.7%	59.4	25	50.4	2	0	0	1047.56	283	291
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	18	30	0.03%	19.3%	LGNTISSLFGGGTTPDAK	99.7%	112	25	110	2	0	0	1735.89	577	594
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	18	30	0.03%	19.3%	LYQPEYQEVSTEEQREEISGK	96.2%	23.9	25	21.6	0	1	0	2542.19	754	774
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	18	30	0.03%	19.3%	TLGGLEMELR	99.7%	75.8	25	62.4	3	0	0	1118.59	269	278
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	18	30	0.03%	19.3%	TPVIVTLK	99.6%	39.3	25	39.3	1	0	0	870.57	68	75
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	18	30	0.03%	19.3%	VAIVKPGVPMEIVLNK	98.9%	28.4	25	26.8	0	2	0	1723.02	47	62
Hypoxia up-regulated protein 1	HYOU1	HYOU1_HUMAN	111.3	100.0%	16	18	30	0.03%	19.3%	YFQHLLGK	99.7%	39.4	25	31.4	2	0	0	1005.55	99	106
Ig kappa chain V-II region RPMI 6410	IGKV2-30	KV206_HUMAN	14.7	99.8%	2	3	216	0.20%	12.0%	FSGSGSGTDFTLK	99.7%	101	25	0	202	0	0	1303.62	87	99
Ig kappa chain V-II region RPMI 6410	IGKV2-30	KV206_HUMAN	14.7	99.8%	2	3	216	0.20%	12.0%	FSGSGSGTDFTLKISR	99.7%	106	25	0	5	9	0	1659.83	87	102
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	11	13	21	0.02%	29.9%	ASLSLIEK	99.7%	50.8	25	41.6	2	0	0	860.51	487	494
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	11	13	21	0.02%	29.9%	EATWTMSNITAGR	99.7%	56.6	25	56.6	3	0	0	1437.68	354	366
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	11	13	21	0.02%	29.9%	EKQPPIDNIIR	99.7%	35.3	25	28.6	0	1	0	1322.74	107	117
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	11	13	21	0.02%	29.9%	GINSSNVENQLQATQAAR	99.7%	117	25	108	2	0	0	1900.95	84	101
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	11	13	21	0.02%	29.9%	LLGASELPIVTPALR	99.7%	58.6	25	58.6	2	0	0	1549.93	301	315
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	11	13	21	0.02%	29.9%	NKNPAPPIDAVEQILPTLVR	99.7%	58.4	25	58.4	2	0	0	2185.23	239	258
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	11	13	21	0.02%	29.9%	NLTWTLSNLCR	99.7%	67	25	0	2	0	0	1377.69	228	238
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	11	13	21	0.02%	29.9%	NNQGTVNWSVDDIVK	99.7%	100	25	100	2	0	0	1688.82	69	83
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	11	13	21	0.02%	29.9%	NPAPPIDAVEQILPTLVR	99.7%	87.2	25	87.2	1	1	0	1943.10	241	258

Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	11	13	21	0.02%	29.9%	QDQIQQVVNHGLVPFLVSVLSK	99.7%	73.1	25	72.8	0	2	0	2448.36	367	388
Importin subunit alpha-1	KPNA2	IMA1_HUMAN	57.9	100.0%	11	13	21	0.02%	29.9%	YGAVDPLLALLAVPDMSSLACGYLR	99.7%	35.4	25	35.3	0	1	0	2665.37	203	227
Importin subunit alpha-5	KPNA1	IMA5_HUMAN	60.2	100.0%	5	5	8	0.01%	12.6%	EACWTISNITAGNR	99.7%	81.4	25	81.4	2	0	0	1592.75	357	370
Importin subunit alpha-5	KPNA1	IMA5_HUMAN	60.2	100.0%	5	5	8	0.01%	12.6%	EPNPPIDEVISTPGVVAR	99.7%	59.6	25	59.6	1	0	0	1890.00	113	130
Importin subunit alpha-5	KPNA1	IMA5_HUMAN	60.2	100.0%	5	5	8	0.01%	12.6%	IVQVALNGLENILR	99.7%	49.1	25	49.1	2	0	0	1551.92	439	452
Importin subunit alpha-5	KPNA1	IMA5_HUMAN	60.2	100.0%	5	5	8	0.01%	12.6%	LVELLMHNDYK	99.0%	34.5	25	34.5	1	0	0	1374.71	301	311
Importin subunit alpha-5	KPNA1	IMA5_HUMAN	60.2	100.0%	5	5	8	0.01%	12.6%	NAVWALSNLCR	99.7%	61.8	25	59.5	2	0	0	1303.66	231	241
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	20	43	0.04%	25.0%	AAVENLPTFLVELSR	99.7%	99.9	25	98.8	5	0	0	1658.91	28	42
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	20	43	0.04%	25.0%	DTAAWTVGR	99.7%	63.6	25	50.6	2	0	0	976.48	426	434
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	20	43	0.04%	25.0%	ESCLEAYTGIVQGLK	99.7%	99.9	25	94.3	2	0	0	1667.83	763	777
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	20	43	0.04%	25.0%	GDQENVHPDVMLVQPR	99.7%	51.7	25	51.7	0	2	0	1849.89	778	793
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	20	43	0.04%	25.0%	LAATNALLNSLEFTK	99.7%	125	25	120	5	0	0	1605.88	192	206
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	20	43	0.04%	25.0%	LLETTDRPDGHQNNLR	99.7%	44.9	25	40.6	1	2	0	1878.94	510	525
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	20	43	0.04%	25.0%	NSLTSKDPDIK	97.4%	30.5	25	9.38	1	0	0	1217.64	63	73
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	20	43	0.04%	25.0%	SDYDMVDYLNELR	99.7%	76.6	25	76.6	2	0	0	1632.72	750	762
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	20	43	0.04%	25.0%	SNEILTAIIQGMR	99.7%	92.8	25	84.8	4	0	0	1445.78	170	182
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	20	43	0.04%	25.0%	SSAYESLMEIVK	99.7%	84.9	25	79.4	2	0	0	1356.67	526	537
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	20	43	0.04%	25.0%	TTLVIMER	99.7%	47.1	25	36.5	3	0	0	978.53	550	557
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	20	43	0.04%	25.0%	TVSPDRLELEAAQK	99.7%	65	25	55.1	2	0	0	1556.83	10	23
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	20	43	0.04%	25.0%	VAAGLQIK	99.7%	50.9	25	36.9	2	0	0	799.50	55	62
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	20	43	0.04%	25.0%	VAALQNLVK	99.5%	37.2	25	32	2	0	0	955.59	235	243
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	20	43	0.04%	25.0%	VLANPGNSQVAR	99.7%	65.3	25	61.8	2	0	0	1225.66	43	54
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	20	43	0.04%	25.0%	YLEVVLNTLQQASQAQVDK	99.7%	120	25	120	2	0	0	2147.13	731	749
Importin subunit beta-1	KPNB1	IMB1_HUMAN	97.2	100.0%	17	20	43	0.04%	25.0%	YMEAFKPFLGIGLK	99.7%	42.5	25	42.5	2	0	0	1613.88	646	659
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	7	7	11	0.01%	7.7%	ALLTFYHVTK	99.6%	38.2	25	32.3	2	0	0	1192.67	147	156
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	7	7	11	0.01%	7.7%	EITTEGQVQVLK	99.7%	45.8	25	37.3	1	0	0	1344.74	739	750
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	7	7	11	0.01%	7.7%	FIVQCMNLIK	99.2%	35.7	25	23	1	0	0	1265.67	316	325
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	7	7	11	0.01%	7.7%	LTVDDFEFR	99.7%	65	25	57	2	0	0	1141.55	541	549
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	7	7	11	0.01%	7.7%	NFEDSSPETLEAHK	99.7%	69.1	25	61.6	2	0	0	1603.72	338	351
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	7	7	11	0.01%	7.7%	SIGTDNVCR	99.7%	53	25	49.4	2	0	0	1021.47	255	263
Importin-11	IPO11	IPO11_HUMAN	112.5	100.0%	7	7	11	0.01%	7.7%	VAPHALSEEEK	99.7%	41.9	25	36.3	1	0	0	1209.61	77	87
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	45	0.04%	19.8%	ACYALENFVENLGPK	99.7%	69.2	25	69.2	2	0	0	1724.83	458	472
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	45	0.04%	19.8%	AQELQAVLGLS	99.7%	43.9	25	43.9	2	0	0	1128.63	1071	1081
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	45	0.04%	19.8%	ATEQLQIVLR	99.7%	67.7	25	39.5	2	0	0	1170.68	24	33
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	45	0.04%	19.8%	DNICGALAR	99.7%	43.3	25	32	1	0	0	989.48	959	967
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	45	0.04%	19.8%	ELLLPDTER	96.2%	29	25	21.7	1	0	0	1085.58	12	20
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	45	0.04%	19.8%	EVMPLLLAYLK	99.7%	67.2	25	56	7	0	0	1289.75	435	445
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	45	0.04%	19.8%	GLEDPSQVVR	99.7%	41.3	25	27.8	2	0	0	1099.57	402	411
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	45	0.04%	19.8%	ICSLILADNK	98.5%	32.8	25	24.9	1	0	0	1146.62	1026	1035
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	45	0.04%	19.8%	ILCCLTFLVK	99.7%	40.8	25	35	1	0	0	1266.70	267	276
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	45	0.04%	19.8%	LAELCGVLK	99.7%	62.9	25	51.4	3	0	0	1002.57	793	801
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	45	0.04%	19.8%	LIMAMQTLIPIDEAK	99.7%	46.1	25	8	4	0	0	1702.91	206	220
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	45	0.04%	19.8%	LLECPHLNVR	97.6%	30.8	25	25.1	2	0	0	1250.67	705	714
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	45	0.04%	19.8%	LLMASPTR	99.4%	37	25	26.7	2	0	0	904.49	968	975
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	45	0.04%	19.8%	LLPPLLQIVCK	97.5%	30.7	25	30.7	1	0	0	1293.80	391	401
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	45	0.04%	19.8%	LLPVLLSTAQEADPEVR	99.7%	69.1	25	69.1	3	0	0	1851.02	900	916
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	45	0.04%	19.8%	NVALGNAIR	99.7%	46.7	25	35.1	1	0	0	927.54	256	264
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	45	0.04%	19.8%	SLILTALQR	99.7%	59.2	25	46.5	2	0	0	1014.63	82	90
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	45	0.04%	19.8%	TLTTMAPYLSTEDVPLAR	99.7%	80.7	25	79.3	4	0	0	1979.02	183	200
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	45	0.04%	19.8%	VRDNICGALAR	98.4%	32.5	25	27	1	0	0	1244.65	957	967
Importin-4	IPO4	IPO4_HUMAN	118.7	100.0%	20	24	45	0.04%	19.8%	VVPSYMQAVNR	99.7%	50.7	25	50.7	3	0	0	1279.65	751	761

Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	22	26	77	0.07%	27.3%	ATAAFILANEHNVALFK	99.7%	67.9	25	59.7	2	0	0	1829.99	196	212
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	22	26	77	0.07%	27.3%	EFQQYLPVVMGPLMK	99.7%	64.3	25	59.9	2	0	0	1779.92	618	632
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	22	26	77	0.07%	27.3%	EGFVEYTEQVVK	99.7%	71.3	25	61.7	2	0	0	1427.71	694	705
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	22	26	77	0.07%	27.3%	FLFDSVSSQNVGLR	99.7%	104	25	101	8	0	0	1568.81	135	148
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	22	26	77	0.07%	27.3%	FMQDASDVMQLLLK	99.7%	109	25	100	6	0	0	1638.82	573	586
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	22	26	77	0.07%	27.3%	FVPYYDLFMPSLK	99.7%	64.8	25	0	8	0	0	1635.81	527	539
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	22	26	77	0.07%	27.3%	HIVENAVQK	99.2%	35.4	25	33.8	2	0	0	1037.57	540	548
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	22	26	77	0.07%	27.3%	LQELIQK	99.5%	37.6	25	5.52	2	0	0	871.52	497	503
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	22	26	77	0.07%	27.3%	LVLEQVVTSIASVADTAEEK	99.7%	97	25	92.1	2	4	0	2102.12	507	526
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	22	26	77	0.07%	27.3%	NLIDEDGNNQWPEGLK	99.7%	74.5	25	74.5	1	0	0	1841.87	119	134
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	22	26	77	0.07%	27.3%	QAEETYENIPGQSK	99.7%	74.6	25	68.8	2	0	0	1593.74	28	41
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	22	26	77	0.07%	27.3%	QMAAVLLR	99.7%	53.9	25	35.1	2	0	0	901.53	60	67
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	22	26	77	0.07%	27.3%	SLLIPYLDNLVK	99.7%	46.5	25	27.8	3	0	0	1387.82	476	487
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	22	26	77	0.07%	27.3%	SLVEIADTVPK	99.7%	95.8	25	87.3	8	0	0	1171.66	239	249
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	22	26	77	0.07%	27.3%	STACQMLVCYAK	99.7%	51.7	25	51.7	2	0	0	1431.64	679	690
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	22	26	77	0.07%	27.3%	TIECISLIGLAVGK	99.7%	109	25	104	5	0	0	1473.83	557	570
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	22	26	77	0.07%	27.3%	VAAAESMPLLLECAR	99.7%	69.6	25	63.8	2	0	0	1630.83	721	735
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	22	26	77	0.07%	27.3%	VCDIAAELAR	99.7%	56.2	25	27.4	5	0	0	1117.57	109	118
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	22	26	77	0.07%	27.3%	VIAALLQTMEDQGNQR	99.7%	108	25	107	3	0	0	1786.91	442	457
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	22	26	77	0.07%	27.3%	VQAHAAAALINFTEDCPK	99.7%	54	25	54	0	2	0	1955.96	458	475
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	22	26	77	0.07%	27.3%	VSDILHSIFSSYK	99.7%	64.4	25	60.2	2	1	0	1495.78	842	854
Importin-5	IPO5	IPO5_HUMAN	123.6	100.0%	22	26	77	0.07%	27.3%	YAACNAVGQMATDFAPGFQK	99.7%	51.7	25	46.4	1	0	0	2146.97	417	436
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	59	0.06%	23.2%	ACWVLHYFCEVK	99.7%	61.3	25	59.4	2	0	0	1611.74	476	487
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	59	0.06%	23.2%	AFAVGVQQVLLK	99.7%	93.2	25	79.2	6	0	0	1272.77	295	306
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	59	0.06%	23.2%	AIFQTIQNR	99.7%	54.7	25	47.3	7	0	0	1090.60	964	972
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	59	0.06%	23.2%	DGALHMIGSLAEILLK	97.1%	30	25	30	1	0	0	1680.94	430	445
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	59	0.06%	23.2%	ENIVEAIIHSPELIR	99.7%	77.2	25	64.6	2	2	0	1732.96	93	107
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	59	0.06%	23.2%	ETENDDLTNVIQK	99.7%	75	25	68.1	4	0	0	1518.73	552	564
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	59	0.06%	23.2%	EYNEFAEVFLK	99.7%	70.5	25	68.4	4	0	0	1388.67	284	294
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	59	0.06%	23.2%	FIQLLSDQSDQSVLIQK	99.7%	110	25	109	2	0	0	1962.05	185	201
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	59	0.06%	23.2%	FKSDQNLQTALELTR	98.4%	27.2	25	25.7	0	1	0	1763.93	488	502
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	59	0.06%	23.2%	GIDQCIPLFVEAALER	99.7%	101	25	96.7	2	0	0	1830.94	753	768
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	59	0.06%	23.2%	LLEVIILQCK	99.7%	78.7	25	78.7	6	0	0	1228.73	741	750
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	59	0.06%	23.2%	NPVWYQALTHGLNEEQR	99.7%	37.1	25	37	0	2	0	2055.00	973	989
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	59	0.06%	23.2%	QLQDIATLADQR	99.7%	43	25	34.3	2	0	0	1371.72	991	1002
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	59	0.06%	23.2%	SDQNLQTALELTR	99.7%	82.2	25	55.7	4	0	0	1488.77	490	502
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	59	0.06%	23.2%	SPLVAAMQHFLPVLK	99.7%	85.4	25	85.4	2	0	0	1650.94	168	182
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	59	0.06%	23.2%	TMGFCYQILTEPNADPR	99.7%	74.7	25	74.7	2	0	0	2012.92	411	427
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	59	0.06%	23.2%	VLTGVAGEDAECHAAK	99.7%	97.6	25	97.6	3	1	0	1627.77	725	740
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	59	0.06%	23.2%	WALHILAR	99.7%	49.5	25	42.6	2	0	0	979.58	263	270
Importin-7	IPO7	IPO7_HUMAN	119.5	100.0%	19	22	59	0.06%	23.2%	YLEMIYSMCK	99.7%	59.5	25	48.4	2	0	0	1337.59	714	723
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	5	6	9	0.01%	6.6%	EYFEFSEFFLK	99.7%	48	25	48	1	0	0	1485.69	285	295
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	5	6	9	0.01%	6.6%	IAAENELNQSYK	99.7%	78.1	25	78.1	1	0	0	1379.68	20	31
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	5	6	9	0.01%	6.6%	IINFAPSLLR	99.7%	48.4	25	33	3	0	0	1143.69	32	41
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	5	6	9	0.01%	6.6%	LLEVIILQCK	99.7%	78.7	25	78.7	6	0	0	1228.73	741	750
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	5	6	9	0.01%	6.6%	TALQEVYTLAEHR	99.7%	58.8	25	56	1	1	0	1530.79	989	1001
Importin-8	IPO8	IPO8_HUMAN	119.9	100.0%	5	6	9	0.01%	6.6%	TYAVGIQQVLLK	99.7%	88.7	25	82.8	2	0	0	1332.79	296	307
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	10	14	25	0.02%	13.2%	EALVDTLTGILSPVQEVR	99.7%	49.1	25	44.7	2	0	0	1940.07	23	40
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	10	14	25	0.02%	13.2%	ELGENLDQILR	99.7%	48.9	25	44.1	1	0	0	1299.69	777	787
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	10	14	25	0.02%	13.2%	EVTDTQMPLVAPVILPEMYK	99.7%	54.1	25	53.5	3	0	0	2290.17	176	195
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	10	14	25	0.02%	13.2%	FRPPETTER	98.6%	32.9	25	18.4	2	0	0	1132.57	96	104

Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	10	14	25	0.02%	13.2%	IFTMAEVYGIR	99.7%	72.4	25	58.1	3	0	0	1299.68	196	206
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	10	14	25	0.02%	13.2%	LIINELSNVMEANAAR	99.7%	108	25	107	4	0	0	1773.92	920	935
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	10	14	25	0.02%	13.2%	LIPTLVSIMQAPADK	99.7%	67.2	25	57.8	3	0	0	1612.90	647	661
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	10	14	25	0.02%	13.2%	LLQHGINADDKR	98.4%	32.6	25	27.5	1	0	0	1379.74	866	877
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	10	14	25	0.02%	13.2%	WTNIPLLVK	99.7%	40.2	25	23.1	2	0	0	1083.66	908	916
Importin-9	IPO9	IPO9_HUMAN	116.0	100.0%	10	14	25	0.02%	13.2%	YSNDPVVASLAQDIFK	99.7%	98.2	25	85.5	4	0	0	1766.90	616	631
Inactive hydroxysteroid dehydrogenase-like protein 1	HSDL1	HSDL1_HUMAN	37.0	99.8%	2	2	2	0.00%	5.5%	AYAEELASR	97.3%	30.4	25	26.4	1	0	0	1009.49	82	90
Inactive hydroxysteroid dehydrogenase-like protein 1	HSDL1	HSDL1_HUMAN	37.0	99.8%	2	2	2	0.00%	5.5%	GLNIILISR	97.2%	30.2	25	29.7	1	0	0	998.64	91	99
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	5	5	10	0.01%	31.4%	ALLELQEYFGSLAA	99.7%	72.4	25	71.3	2	0	0	1524.79	181	194
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	5	5	10	0.01%	31.4%	IDLPEYQGEPDEISIQK	99.7%	61.8	25	59.1	2	0	0	1973.97	40	56
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	5	5	10	0.01%	31.4%	IVFVTGNAK	99.7%	53.3	25	46.7	2	0	0	948.55	10	18
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	5	5	10	0.01%	31.4%	KIVFVTGNAK	98.7%	33.3	25	33.3	2	0	0	1076.65	9	18
Inosine triphosphate pyrophosphatase	ITPA	ITPA_HUMAN	21.4	100.0%	5	5	10	0.01%	31.4%	SAYALCTFALSTGDPSQPVR	99.7%	88.9	25	88.9	2	0	0	2141.03	111	130
Inosine-5'-monophosphate dehydrogenase 2	IMPDH2	IMDH2_HUMAN	55.8	100.0%	3	3	5	0.00%	7.0%	EANEILQR	99.1%	35	25	8.3	2	0	0	972.51	196	203
Inosine-5'-monophosphate dehydrogenase 2	IMPDH2	IMDH2_HUMAN	55.8	100.0%	3	3	5	0.00%	7.0%	LPIVNEDDELVAIIAR	99.7%	74.6	25	74.6	1	0	0	1779.99	209	224
Inosine-5'-monophosphate dehydrogenase 2	IMPDH2	IMDH2_HUMAN	55.8	100.0%	3	3	5	0.00%	7.0%	VAQGVSGAVQDK	99.7%	59.3	25	50.1	2	0	0	1158.61	439	450
Insulin receptor substrate 4	IRS4	IRS4_HUMAN	133.8	100.0%	3	3	6	0.01%	2.6%	AAVSAFPTDSLER	99.7%	49	25	43.3	3	0	0	1363.69	1098	1110
Insulin receptor substrate 4	IRS4	IRS4_HUMAN	133.8	100.0%	3	3	6	0.01%	2.6%	ANPLSLDSAR	99.7%	67.9	25	57.2	2	0	0	1043.55	985	994
Insulin receptor substrate 4	IRS4	IRS4_HUMAN	133.8	100.0%	3	3	6	0.01%	2.6%	LLQEEEQER	99.7%	52.5	25	41.7	1	0	0	1173.57	1074	1082
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	25	40	136	0.13%	47.7%	AIETFSGK	99.7%	43.4	25	43.1	3	0	0	852.45	53	60
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	25	40	136	0.13%	47.7%	AIETFSGKVELQGK	99.7%	71.6	25	67.5	2	0	0	1506.82	53	66
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	25	40	136	0.13%	47.7%	AISVHSTPEGCSSACK	99.7%	90	25	85.7	4	4	0	1690.75	243	258
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	25	40	136	0.13%	47.7%	DQTPDENDQVIVK	99.7%	76	25	69.8	4	0	0	1500.72	526	538
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	25	40	136	0.13%	47.7%	EEVKLETHIR	99.7%	57.5	25	47.8	3	2	0	1253.68	484	493
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	25	40	136	0.13%	47.7%	IIGHFYASQMAQR	99.7%	59.5	25	59.5	8	8	0	1521.76	539	551
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	25	40	136	0.13%	47.7%	ILAHNNFVGR	99.7%	54.3	25	51.2	4	0	0	1140.63	281	290
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	25	40	136	0.13%	47.7%	IRDILAQVK	99.7%	50.7	25	26.9	4	0	0	1055.66	553	561
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	25	40	136	0.13%	47.7%	ISYSGQFLVK	99.7%	68.9	25	65.4	3	0	0	1141.63	27	36
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	25	40	136	0.13%	47.7%	ITISSLQDLTLYNPER	99.7%	80.2	25	71.9	4	0	0	1862.99	310	325
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	25	40	136	0.13%	47.7%	LEIEHSVPK	99.7%	41.4	25	36	2	0	0	1051.58	68	76
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	25	40	136	0.13%	47.7%	LKEENFFGPK	99.7%	46.2	25	46.2	4	3	0	1208.63	474	483
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	25	40	136	0.13%	47.7%	LLVPTQYVGAIIGK	99.7%	104	25	104	10	1	0	1471.89	200	213
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	25	40	136	0.13%	47.7%	LNGHQLENHALK	99.7%	39.6	25	38	2	2	0	1373.73	139	150
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	25	40	136	0.13%	47.7%	LYIGNLNESVTPADLEK	99.7%	90.5	25	76.7	4	0	0	1875.97	4	20
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	25	40	136	0.13%	47.7%	MILEIMHK	99.7%	45.9	25	36.3	4	0	0	1014.55	259	266
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	25	40	136	0.13%	47.7%	MVIITGPPEAQFK	99.7%	72.7	25	64.7	8	0	0	1446.77	453	465
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	25	40	136	0.13%	47.7%	QGSPVAAGAPAK	99.7%	75.7	25	73.8	4	0	0	1053.57	179	190
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	25	40	136	0.13%	47.7%	QQQVDIPLR	99.7%	52.3	25	37.4	4	0	0	1096.61	191	199
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	25	40	136	0.13%	47.7%	RLEIEHSVPK	99.7%	38.6	25	37.8	3	4	0	1207.68	67	76
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	25	40	136	0.13%	47.7%	SGYAFVDCPDEHWAMK	99.7%	77.9	25	77.9	4	3	0	1928.79	37	52
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	25	40	136	0.13%	47.7%	TADEVPLK	99.7%	44.6	25	31.3	4	0	0	872.47	273	280
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	25	40	136	0.13%	47.7%	TVNELQNLTAAEVVVPR	99.7%	99.1	25	86.5	7	4	0	1853.01	509	525
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	25	40	136	0.13%	47.7%	VSYIPDEQIAQGPENGR	99.7%	91.8	25	91.8	4	0	0	1872.91	151	167
Insulin-like growth factor 2 mRNA-binding protein 1	IGF2BP1	IF2B1_HUMAN	63.5	100.0%	25	40	136	0.13%	47.7%	VSYIPDEQIAQGPENGRR	99.3%	36	25	35.6	1	1	0	2029.01	151	168
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	14	16	45	0.04%	35.9%	DQTPDENEEVIVR	99.7%	81.3	25	63.9	2	0	0	1543.72	548	560
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	14	16	45	0.04%	35.9%	EEVKLEAHIR	98.9%	34.1	25	32.4	1	0	0	1223.67	506	515
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	14	16	45	0.04%	35.9%	IAPAEGPDVSER	99.7%	60.4	25	60.4	4	0	0	1240.62	463	474
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	14	16	45	0.04%	35.9%	IIGHFFASQTAQR	99.7%	69.7	25	63.5	2	2	0	1475.78	561	573
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	14	16	45	0.04%	35.9%	ILVPTQFVGAIIGK	99.7%	101	25	0	5	1	0	1455.89	198	211
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	14	16	45	0.04%	35.9%	IMEVDYSVSK	99.7%	39.8	25	39.8	2	0	0	1170.57	68	77
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	14	16	45	0.04%	35.9%	ISYIPDEEVSSPSPPQR	99.7%	69.4	25	69.1	4	0	0	1900.93	152	168

Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	14	16	45	0.04%	35.9%	ITISSLQDLSIYNPER	99.7%	88.2	25	82.3	3	0	0	1848.97	308	323
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	14	16	45	0.04%	35.9%	KLPLAGQVLLK	98.3%	32.3	25	17.2	2	0	0	1179.78	27	37
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	14	16	45	0.04%	35.9%	LAEEIPLK	99.7%	53.4	25	42.5	3	0	0	912.54	271	278
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	14	16	45	0.04%	35.9%	LSGHQFENYSFK	99.7%	48.3	25	44.8	3	4	0	1456.69	140	151
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	14	16	45	0.04%	35.9%	LYIGNLSPAVTADDLR	99.7%	68.4	25	68.1	4	0	0	1717.91	5	20
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	14	16	45	0.04%	35.9%	MILEIMQK	96.8%	29.7	25	10.1	1	0	0	1005.55	257	264
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	14	16	45	0.04%	35.9%	MVIITGPPEAQFK	99.7%	72.7	25	64.7	8	0	0	1446.77	475	487
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	14	16	45	0.04%	35.9%	SGYAFVDYPDQNWAIR	99.7%	98.4	25	98.4	4	0	0	1901.88	38	53
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	14	16	45	0.04%	35.9%	TVNELQNLTSAEVIVPR	99.7%	54.5	25	41.9	2	0	0	1883.02	531	547
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	IF2B2_HUMAN	66.1	100.0%	14	16	45	0.04%	35.9%	YPQGVASQR	99.7%	54.4	25	37.8	3	0	0	1005.51	589	597
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	21	27	64	0.06%	48.4%	ALQSGPPQSR	99.7%	42.4	25	29	2	0	0	1040.55	568	577
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	21	27	64	0.06%	48.4%	DQTPDENDQVVVK	99.7%	72.9	25	65.3	2	0	0	1486.70	526	538
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	21	27	64	0.06%	48.4%	EAQDIKFTEEIPLK	99.7%	61.6	25	50.8	2	0	0	1660.88	267	280
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	21	27	64	0.06%	48.4%	EEVKLEAHIR	98.9%	34.1	25	32.4	1	0	0	1223.67	484	493
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	21	27	64	0.06%	48.4%	FTEEIPLK	96.9%	29.8	25	22.9	2	0	0	976.54	273	280
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	21	27	64	0.06%	48.4%	IAPAEAPDAK	99.7%	61.3	25	61.3	4	0	0	982.52	441	450
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	21	27	64	0.06%	48.4%	IELHGKPIEVEHSVPK	99.7%	53.2	25	53.2	0	2	0	1812.00	61	76
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	21	27	64	0.06%	48.4%	IKEENFVSPK	99.7%	50.1	25	33.2	4	0	0	1190.64	474	483
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	21	27	64	0.06%	48.4%	ILAHNNFVGR	99.7%	54.3	25	51.2	4	0	0	1140.63	281	290
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	21	27	64	0.06%	48.4%	IPVSGPFLVK	99.7%	45.7	25	45.6	4	0	0	1056.65	27	36
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	21	27	64	0.06%	48.4%	ITGHFYACQVAQR	99.7%	74.7	25	64.6	2	2	0	1550.75	539	551
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	21	27	64	0.06%	48.4%	ITISPLQELTLYNPER	99.7%	93.1	25	93.1	5	1	0	1887.02	310	325
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	21	27	64	0.06%	48.4%	LLVPTQFVGAIIGK	99.7%	101	25	0	5	1	0	1455.89	200	213
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	21	27	64	0.06%	48.4%	LNGFQLENFTLK	99.7%	63.2	25	55.7	2	0	0	1423.76	139	150
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	21	27	64	0.06%	48.4%	LYIGNLSENAAPSDLESIFK	99.7%	89.7	25	89.7	4	0	0	2181.11	4	23
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	21	27	64	0.06%	48.4%	MVIITGPPEAQFK	99.7%	72.7	25	64.7	8	0	0	1446.77	453	465
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	21	27	64	0.06%	48.4%	QALDKLNGFQLENFTLK	96.5%	24.2	25	24.2	0	1	0	1979.06	134	150
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	21	27	64	0.06%	48.4%	SILEIMHK	99.5%	37.2	25	22.3	2	0	0	970.54	259	266
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	21	27	64	0.06%	48.4%	SITILSTPEGTSAACK	99.7%	95.1	25	90.6	3	0	0	1635.83	243	258
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	21	27	64	0.06%	48.4%	TGYAFVDCPDESWALK	99.7%	69.7	25	69.7	2	0	0	1858.83	37	52
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	21	27	64	0.06%	48.4%	TVNELQNLSSAEVVVPR	99.7%	95	25	80	2	2	0	1854.99	509	525
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	21	27	64	0.06%	48.4%	VAYIPDEMAAQQNPLQQPR	99.7%	94.3	25	91.5	3	2	0	2169.08	151	169
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	IF2B3_HUMAN	63.7	100.0%	21	27	64	0.06%	48.4%	VPSFAAGR	99.7%	51.4	25	42.6	2	0	0	804.44	494	501
Integrator complex subunit 11	CPSF3L	INT11_HUMAN	67.7	100.0%	3	3	6	0.01%	5.7%	VLIPVFALGR	99.7%	55.5	25	55.5	2	0	0	1084.69	235	244
Integrator complex subunit 11	CPSF3L	INT11_HUMAN	67.7	100.0%	3	3	6	0.01%	5.7%	VPIYFSTGLTEK	99.7%	73.6	25	73.6	2	0	0	1354.73	263	274
Integrator complex subunit 11	CPSF3L	INT11_HUMAN	67.7	100.0%	3	3	6	0.01%	5.7%	VTPLGAGQDVGR	99.7%	69.8	25	65.6	2	0	0	1169.63	6	17
Interferon-induced protein with tetratricopeptide repeats 5	IFIT5	IFIT5_HUMAN	55.8	99.8%	2	2	2	0.00%	5.6%	IDPENAEFLTALCELR	99.7%	47.6	25	47.6	1	0	0	1890.93	464	479
Interferon-induced protein with tetratricopeptide repeats 5	IFIT5	IFIT5_HUMAN	55.8	99.8%	2	2	2	0.00%	5.6%	LALYNLLAYVK	99.7%	47.5	25	43.8	1	0	0	1280.76	51	61
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	100.0%	7	7	12	0.01%	15.6%	DLKPSNIFLVDTK	99.7%	45.9	25	39.5	2	0	0	1489.83	414	426
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	100.0%	7	7	12	0.01%	15.6%	EIELIGSGGFGQVFK	99.7%	102	25	96.7	2	0	0	1580.83	269	283
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	100.0%	7	7	12	0.01%	15.6%	IGDFGLVTSLK	99.7%	94.9	25	83.6	2	0	0	1149.65	430	440
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	100.0%	7	7	12	0.01%	15.6%	KPEDRPNTSEILR	96.3%	24	25	6.35	0	1	0	1554.82	522	534
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	100.0%	7	7	12	0.01%	15.6%	LAVEILNK	99.7%	46.3	25	25.8	2	0	0	899.56	70	77
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	100.0%	7	7	12	0.01%	15.6%	LAYLQILSEETSVK	99.7%	114	25	114	2	0	0	1593.87	160	173
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	E2AK2_HUMAN	62.1	100.0%	7	7	12	0.01%	15.6%	VLALELFEQITK	99.7%	52.5	25	52.5	1	0	0	1403.81	389	400
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	12	20	55	0.05%	42.8%	AAEAAINILK	99.7%	66.9	25	50	8	0	0	1013.60	91	100
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	12	20	55	0.05%	42.8%	ANASICFAVPDPLMPDPSK	99.7%	83.5	25	83.5	6	0	0	2045.97	101	119
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	12	20	55	0.05%	42.8%	EDSGTFSLGK	99.7%	65.8	25	59.8	4	0	0	1040.49	16	25
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	12	20	55	0.05%	42.8%	HRAEAPPLER	99.7%	39.6	25	32.2	2	0	0	1175.63	6	15
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	12	20	55	0.05%	42.8%	LESFMETGK	99.7%	51.8	25	45.1	5	0	0	1041.49	165	173
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	12	20	55	0.05%	42.8%	LPEYTLSQEGGPAHK	99.7%	76.3	25	73.2	2	2	0	1626.81	142	156

Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	12	20	55	0.05%	42.8%	LPEYTLSQEGGPAHKR	99.7%	92.4	25	92.3	2	2	0	1782.91	142	157
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	12	20	55	0.05%	42.8%	SDVQIHVPTFTFR	99.7%	58.6	25	58.6	2	4	0	1546.80	57	69
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	12	20	55	0.05%	42.8%	SLLSIPNTDYIQLLSEIAK	99.7%	46.3	25	46.3	2	0	0	2118.17	232	250
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	12	20	55	0.05%	42.8%	TPIQVLHEYGMK	99.7%	66.7	25	58.9	4	4	0	1431.73	34	45
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	12	20	55	0.05%	42.8%	VTVGDITCTGEGTSK	99.7%	113	25	113	4	0	0	1524.72	70	84
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	PRKRA_HUMAN	34.4	100.0%	12	20	55	0.05%	42.8%	VTVGDITCTGEGTSKK	99.7%	65.8	25	59.1	2	0	0	1652.82	70	85
Interferon-related developmental regulator 2	IFRD2	IFRD2_HUMAN	54.8	99.8%	2	2	3	0.00%	5.1%	DIFGLGPVLLLDATALK	99.7%	73.2	25	73.2	1	0	0	1756.03	455	471
Interferon-related developmental regulator 2	IFRD2	IFRD2_HUMAN	54.8	99.8%	2	2	3	0.00%	5.1%	LLPDFLLER	99.7%	47	25	25.5	2	0	0	1115.65	171	179
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	17	27	105	0.10%	47.7%	AQDPSEVLTMLTNETGFEISSSDATVK	99.7%	56.5	25	56.5	2	1	0	2870.36	148	174
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	17	27	105	0.10%	47.7%	GTMTTGHNVADLVVILK	99.7%	85.9	25	74.1	5	6	0	1768.96	111	127
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	17	27	105	0.10%	47.7%	ILITTVPPNLR	99.7%	52.9	25	52.9	12	0	0	1236.77	175	185
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	17	27	105	0.10%	47.7%	ILPTLEAVAALGNK	99.7%	91.3	25	86.2	12	2	0	1409.84	128	141
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	17	27	105	0.10%	47.7%	ILPTLEAVAALGNKVVESLR	99.7%	75.3	25	75.3	2	0	0	2093.23	128	147
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	17	27	105	0.10%	47.7%	ILSHGGFR	99.7%	47.1	25	31.3	2	0	0	886.49	320	327
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	17	27	105	0.10%	47.7%	KGTMTTGHNVADLVVILK	99.7%	42	25	42	0	4	0	1897.06	110	127
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	17	27	105	0.10%	47.7%	KLDPELHLDIK	99.7%	55.5	25	29.5	2	4	0	1320.75	186	196
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	17	27	105	0.10%	47.7%	LDPELHLDIK	99.7%	48.6	25	38.6	2	0	0	1192.66	187	196
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	17	27	105	0.10%	47.7%	NQDLAPNSAEQASILSLVTK	99.7%	137	25	137	7	5	0	2099.10	61	80
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	17	27	105	0.10%	47.7%	QPLALNVAYR	99.7%	53.7	25	42.5	9	0	0	1144.65	260	269
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	17	27	105	0.10%	47.7%	RNQDLAPNSAEQASILSLVTK	99.7%	75.9	25	69.2	0	2	0	2255.20	60	80
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	17	27	105	0.10%	47.7%	VHTVMTLEQQDMVCYTAQTLVR	99.7%	76.4	25	76.4	0	2	0	2655.26	298	319
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	17	27	105	0.10%	47.7%	VKPAPDETSFSEALLK	99.7%	74.9	25	71.3	4	4	0	1731.92	44	59
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	17	27	105	0.10%	47.7%	VKPAPDETSFSEALLKR	99.7%	81.5	25	77.9	2	0	0	1888.02	44	60
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	17	27	105	0.10%	47.7%	VLQSALAAIR	99.7%	85.8	25	75.5	10	0	0	1041.64	197	206
Interleukin enhancer-binding factor 2	ILF2	ILF2_HUMAN	43.1	100.0%	17	27	105	0.10%	47.7%	WFEENASQSTVK	99.7%	62.7	25	59	4	0	0	1425.66	210	221
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	AEPPQAMNALMR	99.7%	56.8	25	53.7	11	0	0	1328.65	397	408
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	AVSDWIDEQEK	99.7%	71.2	25	58.8	2	0	0	1319.61	44	54
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	AYAALAALEK	99.7%	90.4	25	64.3	22	0	0	1020.57	578	587
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	CLAALASLR	99.7%	72.1	25	54	7	0	0	974.55	203	211
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	EATDAIGHLDR	99.7%	73.3	25	52.1	10	0	0	1197.59	298	308
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	EDITQSAQHALR	99.7%	68.5	25	57	7	2	0	1368.69	312	323
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	EKPTTALLDK	95.0%	28	25	18.7	1	0	0	1115.63	118	127
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	EPPLSLTIHLTSPVVR	99.7%	79.5	25	79.5	2	2	0	1759.01	162	177
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	FNYSGSGGR	99.7%	68.5	25	56.5	4	0	0	944.42	807	815
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	FVMEVEVDGQK	99.7%	69.9	25	68.9	12	0	0	1296.61	555	565
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	GDLDLELVLLCK	99.7%	77.8	25	73.6	3	0	0	1387.75	106	117
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	GWPLELLCEK	99.7%	70.1	25	0	11	0	0	1244.63	248	257
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	GYNHGQGSYSYSNSYNSPGGGGGSDYNYESK	99.7%	96.4	25	96.4	0	2	0	3253.30	776	806
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	HGKNPVMELNEK	99.5%	31.6	25	29.7	0	2	0	1411.70	524	535
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	IFVNDDR	99.7%	46.8	25	20.8	2	0	0	878.44	6	12
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	IFVNDDRHVMAK	99.7%	60.6	25	41.7	4	3	0	1444.74	6	17
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	LAAFGQLHK	99.7%	58.4	25	46.8	13	0	0	984.56	324	332
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	LFPDTPLALDANK	99.7%	64.6	25	59.1	12	0	0	1414.76	588	600
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	LFPDTPLALDANKK	99.7%	68	25	62.9	6	1	0	1542.85	588	601
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	LNQLKPGLQYK	99.7%	57.1	25	44.2	7	3	0	1301.76	409	419
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	LVSQTGPVHAPIFTMSVEVDGNSFEASGPSK	99.7%	76.8	25	76.8	0	2	0	3204.55	420	450
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	NADHSMNYQYR	99.7%	54.9	25	54.9	4	4	0	1414.58	884	894
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	NENPVDYTVQIPPSTTYAITPMK	99.7%	73.4	25	73.4	4	3	0	2595.27	349	371
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	NPVMELNEK	99.7%	50.3	25	43.9	10	0	0	1073.53	527	535
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	NPVMELNEKR	99.7%	54	25	43	3	0	0	1229.63	527	536
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	NTKEPPLSLTIHLTSPVVR	99.7%	56.5	25	56.5	0	2	0	2102.20	159	177

Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	RPMEEDGEEKSPSK	99.7%	41.2	25	41.2	0	8	0	1618.74	372	385
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	SCVIVIR	99.7%	46.9	25	0	2	0	0	846.49	225	231
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	SGGNSYGSGGASYNPGSHGGYGGGSGGGSSYQGK	99.7%	37.7	25	37.7	0	1	0	3012.24	816	849
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	SIGTANRPMGAGEALR	99.7%	56.6	25	51.9	2	3	0	1600.82	258	273
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	SIGTANRPMGAGEALRR	99.7%	35.8	25	33.4	0	5	0	1756.92	258	274
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	VLAGETLSVNDPPDVLDR	99.7%	111	25	110	11	1	0	1909.99	183	200
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	VLECLASGIVMPDGSGIYDPCEK	99.7%	91.8	25	91.8	3	2	0	2526.16	275	297
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	VLGMDPLPSK	99.7%	55.2	25	46.4	9	0	0	1056.58	333	342
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	VLQDMGLPTGAEGR	99.7%	90.9	25	76.7	17	0	0	1443.73	461	474
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	VPTWGPLR	99.7%	54.2	25	25.1	4	0	0	925.53	240	247
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	YELISETGGSHDK	99.7%	67.8	25	51.9	2	0	0	1435.67	541	553
Interleukin enhancer-binding factor 3	ILF3	ILF3_HUMAN	95.3	100.0%	38	64	261	0.24%	50.3%	YELISETGGSHDKR	99.7%	72.6	25	68.8	6	2	0	1591.77	541	554
Iron-sulfur protein NUBPL	NUBPL	NUBPL_HUMAN	34.1	99.8%	2	2	4	0.00%	10.7%	AIGLLDVDVYGPSVPK	99.7%	92.9	25	92.9	2	0	0	1642.91	100	115
Iron-sulfur protein NUBPL	NUBPL	NUBPL_HUMAN	34.1	99.8%	2	2	4	0.00%	10.7%	STTAVNLALALAANDSSK	99.7%	63.5	25	63.5	2	0	0	1746.92	82	99
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	3	3	10	0.01%	9.0%	CSDFTEEICR	99.7%	68.2	25	63.8	2	0	0	1316.52	351	360
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	3	3	10	0.01%	9.0%	NVTAIQGPGGK	99.7%	55.7	25	53.2	2	0	0	1041.57	67	77
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	IDH3A_HUMAN	39.6	100.0%	3	3	10	0.01%	9.0%	TPYTDVNIVTIR	99.7%	78.6	25	71.7	6	0	0	1391.75	135	146
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	5	8	22	0.02%	16.9%	DMGGYSTTTDFIK	99.7%	57.1	25	53.7	4	0	0	1435.64	362	374
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	5	8	22	0.02%	16.9%	EQTEGEYSSLEHESAR	99.7%	73.1	25	69.3	4	1	0	1851.80	165	180
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	5	8	22	0.02%	16.9%	GELASYDMR	99.7%	48.4	25	48.4	2	0	0	1057.46	123	131
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	5	8	22	0.02%	16.9%	HNNLDLVIIR	99.7%	42	25	36.2	1	0	0	1206.70	155	164
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	IDH3B_HUMAN	42.2	100.0%	5	8	22	0.02%	16.9%	NIANPTAMLLSASNMLR	99.7%	98.3	25	98.3	10	0	0	1848.93	318	334
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	21	35	0.03%	36.9%	ATDFVADR	99.1%	35	25	27.1	2	0	0	894.43	181	188
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	21	35	0.03%	36.9%	CATITPDEAR	96.8%	29.6	25	22.6	1	0	0	1133.53	113	122
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	21	35	0.03%	36.9%	DIFQEIFDK	98.3%	32.2	25	21.8	1	0	0	1154.57	264	272
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	21	35	0.03%	36.9%	DQTDDQVTIDSALATQK	99.7%	117	25	114	2	0	0	1848.88	90	106
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	21	35	0.03%	36.9%	FKDIFQEIFDK	99.7%	65.2	25	52.4	2	0	0	1429.74	262	272
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	21	35	0.03%	36.9%	GKLDGNQDLIR	99.7%	57.9	25	43.1	2	0	0	1228.66	383	393
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	21	35	0.03%	36.9%	IIWQFIK	97.6%	30.8	25	25.5	1	0	0	947.57	61	67
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	21	35	0.03%	36.9%	LIDDMVAQVLK	99.7%	86.5	25	69.2	4	0	0	1244.69	289	299
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	21	35	0.03%	36.9%	LILPHVDIQLK	99.7%	50.2	25	34.1	2	1	0	1288.80	70	80
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	21	35	0.03%	36.9%	LNEHFLNTTDFLDTIK	99.7%	75.9	25	70.8	2	2	0	1920.97	427	442
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	21	35	0.03%	36.9%	NILGGTVFR	99.7%	47.9	25	36.9	2	0	0	976.56	141	149
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	21	35	0.03%	36.9%	NILGGTVFREPIICK	99.7%	54.7	25	50.4	1	0	0	1716.95	141	155
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	21	35	0.03%	36.9%	TIEAEAAHGTVTR	99.7%	86.4	25	79.6	2	0	0	1355.69	341	353
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	21	35	0.03%	36.9%	VAKPVVEMDGDEMTR	99.7%	66	25	66	1	2	0	1708.79	46	60
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	21	35	0.03%	36.9%	VCVETVESGAMTK	99.7%	115	25	108	3	0	0	1426.66	401	413
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	IDHP_HUMAN	50.9	100.0%	16	21	35	0.03%	36.9%	YFDLGLPNR	99.7%	48.9	25	42.1	2	0	0	1094.56	81	89
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	22	26	50	0.05%	19.1%	APLKPYPVSPSDK	99.7%	55.6	25	52.8	2	2	0	1398.76	1039	1051
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	22	26	50	0.05%	19.1%	AVPSWFVR	99.7%	42.6	25	32.2	2	0	0	961.53	411	418
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	22	26	50	0.05%	19.1%	DVLLPWYNAYR	99.7%	42.2	25	35.3	2	0	0	1409.72	651	661
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	22	26	50	0.05%	19.1%	EIVVIHQDPEALK	99.7%	81	25	74.5	2	0	0	1490.82	849	861
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	22	26	50	0.05%	19.1%	ESVDHLTIPSR	99.7%	55.1	25	36.7	2	0	0	1253.65	501	511
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	22	26	50	0.05%	19.1%	FLIQNVLR	99.7%	39.7	25	24.5	4	0	0	1002.61	662	669
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	22	26	50	0.05%	19.1%	FVDILTNWYVR	99.7%	71.6	25	67.1	2	0	0	1425.75	726	736
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	22	26	50	0.05%	19.1%	GSELEITLTR	99.7%	76.8	25	48.6	2	0	0	1118.61	1062	1071
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	22	26	50	0.05%	19.1%	LESDYEILER	99.7%	78.9	25	69.4	2	0	0	1266.62	269	278
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	22	26	50	0.05%	19.1%	LFLNETQTQEITEDIPVK	99.7%	95.8	25	94.1	2	0	0	2118.10	1227	1244
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	22	26	50	0.05%	19.1%	LLILMEAR	99.7%	65.8	25	47.2	4	0	0	958.58	255	262
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	22	26	50	0.05%	19.1%	LYLINSPVVR	99.7%	70.8	25	63	2	0	0	1173.70	625	634
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	22	26	50	0.05%	19.1%	LYTVVPR	97.0%	30	25	13.2	1	0	0	847.50	716	722

Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	22	26	50	0.05%	19.1%	MGITEYNNQCR	99.7%	46	25	43.7	2	0	0	1385.59	111	121
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	22	26	50	0.05%	19.1%	NVIVNGLVLASDGQK	99.7%	97.2	25	97.2	2	0	0	1526.85	586	600
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	22	26	50	0.05%	19.1%	QLSSEELEQFQK	99.7%	69	25	64	2	0	0	1465.72	918	929
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	22	26	50	0.05%	19.1%	TESAVSQMQSVIELGR	99.7%	91.7	25	83.4	4	0	0	1734.87	818	833
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	22	26	50	0.05%	19.1%	TVYVSVLPTTADF	97.7%	30.9	25	22.8	1	0	0	1412.73	1250	1262
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	22	26	50	0.05%	19.1%	VCMDFNIIR	99.5%	37.8	25	28.9	1	0	0	1183.56	335	343
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	22	26	50	0.05%	19.1%	VENMVDQLLR	99.7%	84.4	25	68.2	4	0	0	1216.64	419	428
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	22	26	50	0.05%	19.1%	VREELIDK	97.2%	30.2	25	14.5	1	0	0	1001.56	809	816
Isoleucine--tRNA ligase, cytoplasmic	IARS	SYIC_HUMAN	144.5	100.0%	22	26	50	0.05%	19.1%	YIIEELNVR	99.7%	65.7	25	15.9	2	0	0	1148.63	869	877
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	28	50	0.05%	26.1%	ASPLLPANHVTMAK	99.7%	55.1	25	48.1	2	0	0	1465.78	373	386
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	28	50	0.05%	26.1%	AVLEEGTDVVIK	99.7%	88.7	25	78.1	2	0	0	1272.70	434	445
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	28	50	0.05%	26.1%	CGFSELYSWQR	99.7%	63	25	61.1	1	0	0	1432.63	91	101
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	28	50	0.05%	26.1%	DQLGGWFQSSLLTSVAAR	99.7%	90.8	25	90.8	2	0	0	1935.99	626	643
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	28	50	0.05%	26.1%	DSFLGSIPGK	99.7%	85.4	25	70	2	0	0	1020.54	887	896
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	28	50	0.05%	26.1%	EAQNLSAMEIR	99.7%	63.7	25	53.5	4	0	0	1261.62	171	181
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	28	50	0.05%	26.1%	ELSNFYFSIIK	99.7%	61.2	25	53.2	2	0	0	1360.71	793	803
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	28	50	0.05%	26.1%	EMTADVIELK	99.7%	49.5	25	29.4	4	0	0	1148.59	948	957
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	28	50	0.05%	26.1%	EPPYGADVLR	99.7%	43.6	25	37.5	2	0	0	1116.57	688	697
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	28	50	0.05%	26.1%	FLINLEGGDIR	99.7%	70.4	25	50.4	2	0	0	1246.68	960	970
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	28	50	0.05%	26.1%	FLINLEGGDIREESSYK	99.7%	89.7	25	89.7	1	2	0	1969.99	960	976
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	28	50	0.05%	26.1%	FPLLKPSPK	99.7%	40.8	25	34.3	2	0	0	1026.63	273	281
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	28	50	0.05%	26.1%	QQPDTELEIQQK	99.7%	58.3	25	50.2	1	0	0	1456.73	79	90
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	28	50	0.05%	26.1%	SCQTALVEILDVIVR	99.7%	108	25	106	2	2	0	1715.94	818	832
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	28	50	0.05%	26.1%	SGDLYVLAADK	99.7%	84	25	75.3	2	0	0	1151.59	326	336
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	28	50	0.05%	26.1%	SYKPVFWSPSSR	99.7%	43	25	40.3	2	0	0	1440.73	239	250
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	28	50	0.05%	26.1%	TALAEAELEYNPEHVSR	99.7%	72.4	25	70.1	1	2	0	1928.93	251	267
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	28	50	0.05%	26.1%	TGWISTSSIWK	99.7%	55	25	46.7	2	0	0	1265.65	861	871
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	28	50	0.05%	26.1%	TKDEYLINSQTTEHIVK	99.7%	49.5	25	49.5	0	2	0	2019.04	539	555
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	28	50	0.05%	26.1%	TVIVHGFTLGEK	99.7%	66.2	25	58.5	2	0	0	1300.73	650	661
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	28	50	0.05%	26.1%	VWGVPIPVFHHK	99.7%	41.3	25	39.6	0	2	0	1415.79	527	538
Isoleucine--tRNA ligase, mitochondrial	IARS2	SYIM_HUMAN	113.8	100.0%	22	28	50	0.05%	26.1%	YTAESSDTLCPR	99.7%	69.3	25	69.3	2	0	0	1399.62	993	1004
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	4	4	6	0.01%	6.0%	LAEPSQLLK	97.4%	30.5	25	9.87	1	0	0	998.59	116	124
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	4	4	6	0.01%	6.0%	LLNDEDPVVVTK	99.7%	65.5	25	59.1	3	0	0	1341.73	150	161
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	4	4	6	0.01%	6.0%	LNYGIPAIVK	99.4%	36.5	25	23.3	1	0	0	1087.65	478	487
Junction plakoglobin	JUP	PLAK_HUMAN	81.7	100.0%	4	4	6	0.01%	6.0%	NEGTATYAAAVLFR	99.7%	59.2	25	51.2	1	0	0	1483.75	638	651
Katanin p60 ATPase-containing subunit A1	KATNA1	KTNA1_HUMAN	56.0	100.0%	4	4	5	0.00%	10.4%	DIISQNPNVR	99.7%	40.4	25	33.1	1	0	0	1155.61	198	207
Katanin p60 ATPase-containing subunit A1	KATNA1	KTNA1_HUMAN	56.0	100.0%	4	4	5	0.00%	10.4%	EAVVLPMWMPEFFK	99.7%	56.3	25	56.3	1	0	0	1723.86	223	236
Katanin p60 ATPase-containing subunit A1	KATNA1	KTNA1_HUMAN	56.0	100.0%	4	4	5	0.00%	10.4%	FYSPATIFIDEIDSICSR	99.7%	79.2	25	79.2	2	0	0	2134.02	299	316
Katanin p60 ATPase-containing subunit A1	KATNA1	KTNA1_HUMAN	56.0	100.0%	4	4	5	0.00%	10.4%	SVSAADIER	99.7%	46.7	25	30.8	1	0	0	947.48	472	480
KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	KHDR1_HUMAN	48.2	100.0%	3	4	8	0.01%	8.8%	ILGPQGNTIKR	99.7%	51.8	25	46.1	2	0	0	1196.71	176	186
KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	KHDR1_HUMAN	48.2	100.0%	3	4	8	0.01%	8.8%	KDDEENYLDLFSHK	99.7%	45.7	25	45.7	0	2	0	1752.81	139	152
KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	KHDR1_HUMAN	48.2	100.0%	3	4	8	0.01%	8.8%	SGSMDPSGAHPSVR	99.7%	46.8	25	40	2	2	0	1400.62	18	31
Kinesin-like protein KIF11	KIF11	KIF11_HUMAN	119.2	99.8%	2	2	4	0.00%	2.4%	LNLVDLAGSENIGR	99.7%	89.7	25	86.8	2	0	0	1470.79	261	274
Kinesin-like protein KIF11	KIF11	KIF11_HUMAN	119.2	99.8%	2	2	4	0.00%	2.4%	TVLQELINVLK	99.7%	50.6	25	42.2	2	0	0	1269.78	619	629
Kinesin-like protein KIF22	KIF22	KIF22_HUMAN	73.3	99.8%	2	2	5	0.00%	3.8%	ALMDLLQLTR	99.7%	73.1	25	51	2	0	0	1173.67	150	159
Kinesin-like protein KIF22	KIF22	KIF22_HUMAN	73.3	99.8%	2	2	5	0.00%	3.8%	VLDLLDPASGDLVIR	99.7%	70.7	25	66.9	3	0	0	1595.90	184	198
Kinesin-like protein KIF23	KIF23	KIF23_HUMAN	110.1	99.9%	2	2	2	0.00%	2.5%	ALLQEFDNAVLSK	99.7%	78.7	25	69	1	0	0	1447.78	524	536
Kinesin-like protein KIF23	KIF23	KIF23_HUMAN	110.1	99.9%	2	2	2	0.00%	2.5%	STEEAFEVFWR	99.7%	55.9	25	55.9	1	0	0	1400.65	272	282
Kinetochore-associated protein 1	KNTC1	KNTC1_HUMAN	250.8	99.8%	2	2	4	0.00%	1.0%	LGISFQPVFR	99.7%	51.3	25	42.1	2	0	0	1163.66	1414	1423
Kinetochore-associated protein 1	KNTC1	KNTC1_HUMAN	250.8	99.8%	2	2	4	0.00%	1.0%	VLAPELIPSILEK	99.7%	51.7	25	51.7	2	0	0	1421.86	727	739
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	4	4	7	0.01%	12.3%	GLLEESSFATLFPK	99.7%	76.4	25	72.8	2	0	0	1538.81	53	66

KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	4	4	7	0.01%	12.3%	ILQDDVACDIIK	99.7%	58.5	25	52.9	2	0	0	1402.73	135	146
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	4	4	7	0.01%	12.3%	LGALTAEEIALK	99.7%	63	25	34.3	1	0	0	1228.71	358	369
KRR1 small subunit processome component homolog	KRR1	KRR1_HUMAN	43.7	100.0%	4	4	7	0.01%	12.3%	TFDPYIIIR	99.7%	53.1	25	46	2	0	0	1137.63	107	115
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	4	4	5	0.00%	9.9%	FIPEITISDILR	99.7%	68	25	64.4	2	0	0	1416.81	388	399
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	4	4	5	0.00%	9.9%	GDYLLLKPEK	99.4%	36.9	25	30.1	1	0	0	1175.67	283	292
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	4	4	5	0.00%	9.9%	ISELSGCTPDPR	99.6%	38.5	25	37.7	1	0	0	1331.63	266	277
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	L2HDH_HUMAN	50.3	100.0%	4	4	5	0.00%	9.9%	LIVAVEQEEIPR	99.7%	60.1	25	36.4	1	0	0	1395.78	137	148
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	4	4	8	0.01%	17.4%	IAWALSR	99.7%	40.5	25	30.3	2	0	0	816.47	89	95
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	4	4	8	0.01%	17.4%	KSLDFYTR	99.7%	49	25	19.9	2	0	0	1029.54	44	51
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	4	4	8	0.01%	17.4%	RFEELGVK	99.7%	44	25	19.2	2	0	0	977.54	141	148
Lactoylglutathione lyase	GLO1	LGUL_HUMAN	20.8	100.0%	4	4	8	0.01%	17.4%	VLGMTLIQK	99.7%	54.7	25	50	2	0	0	1002.60	52	60
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	27	0.03%	13.7%	KFADGEVVR	99.7%	50.7	25	39.4	2	0	0	1020.55	5	13
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	27	0.03%	13.7%	LTPLILKPFGNSISR	99.7%	57	25	57	3	1	0	1655.98	117	131
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	27	0.03%	13.7%	NDLSPASSGNAVYDFFIGR	99.7%	93.1	25	93.1	9	0	0	2029.96	354	372
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	27	0.03%	13.7%	NLLVSGWWGFVR	99.7%	76.9	25	76.1	4	0	0	1433.77	533	544
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	27	0.03%	13.7%	TFEVTPIR	99.5%	37.8	25	34.2	4	0	0	962.53	196	203
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	27	0.03%	13.7%	VVEGTPLIDGR	99.7%	59.7	25	53.5	2	0	0	1155.64	280	290
Lamin-B receptor	LBR	LBR_HUMAN	70.7	100.0%	7	8	27	0.03%	13.7%	YNGEPEHIER	99.7%	50.6	25	35	2	0	0	1243.57	132	141
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	23	27	48	0.04%	37.5%	AGGPTTPLSPTR	99.7%	67.2	25	59.6	4	0	0	1154.62	15	26
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	23	27	48	0.04%	37.5%	ALYETELADAR	99.7%	93.7	25	65.9	2	0	0	1251.62	80	90
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	23	27	48	0.04%	37.5%	CQSLTEDLEFRK	99.7%	39.3	25	39.3	0	1	0	1525.73	198	209
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	23	27	48	0.04%	37.5%	DAALATALGDK	94.8%	27.8	25	20.1	1	0	0	1045.55	146	156
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	23	27	48	0.04%	37.5%	DAALATALGDKK	99.7%	71.8	25	43.8	3	0	0	1173.65	146	157
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	23	27	48	0.04%	37.5%	DQMQQQLNDYEQLLDVK	99.7%	77.3	25	76.2	1	0	0	2108.00	351	367
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	23	27	48	0.04%	37.5%	ESDLNGAQIK	97.9%	31.4	25	22.4	1	0	0	1074.54	125	134
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	23	27	48	0.04%	37.5%	IGDTSVSYK	99.7%	68.2	25	68.2	2	0	0	969.49	475	483
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	23	27	48	0.04%	37.5%	IQELEDLLAK	99.7%	64.7	25	32.3	4	0	0	1171.66	321	330
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	23	27	48	0.04%	37.5%	KESDLNGAQIK	99.7%	48.6	25	32.3	1	0	0	1202.64	124	134
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	23	27	48	0.04%	37.5%	KLLEGEEER	99.5%	37.9	25	22.2	1	0	0	1102.57	379	387
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	23	27	48	0.04%	37.5%	KQLADETLLK	98.8%	33.7	25	26.5	1	0	0	1158.67	182	191
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	23	27	48	0.04%	37.5%	LAQALHEMR	99.7%	55.1	25	48	4	0	0	1084.56	242	250
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	23	27	48	0.04%	37.5%	LLEGEEERLK	99.7%	51	25	36	2	0	0	1215.66	380	389
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	23	27	48	0.04%	37.5%	LQEKEELR	99.7%	50.3	25	22.6	2	0	0	1044.57	30	37
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	23	27	48	0.04%	37.5%	LQIELGK	98.2%	31.9	25	0	1	0	0	800.49	103	109
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	23	27	48	0.04%	37.5%	LSSEMNTSTVNSAR	99.7%	119	25	107	4	0	0	1496.70	277	290
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	23	27	48	0.04%	37.5%	LYKEELEQTYHAK	99.7%	83.9	25	73.4	2	1	0	1651.83	259	271
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	23	27	48	0.04%	37.5%	MRIESLSSQLSNLQK	99.7%	68.5	25	66.9	1	1	0	1749.92	298	312
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	23	27	48	0.04%	37.5%	NQNSWGTGEDVK	99.7%	53.1	25	53.1	2	0	0	1334.60	517	528
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	23	27	48	0.04%	37.5%	QIEYEYK	99.7%	44.5	25	37.1	2	0	0	972.47	235	241
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	23	27	48	0.04%	37.5%	QLADETLLK	99.7%	52.5	25	37.5	2	0	0	1030.58	183	191
Lamin-B1	LMNB1	LMNB1_HUMAN	66.4	100.0%	23	27	48	0.04%	37.5%	SLETENSALQLQVTEREEVR	99.7%	59.3	25	59.3	0	2	0	2331.18	52	71
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	12	13	24	0.02%	26.7%	AGGPATPLSPTR	99.7%	63.5	25	54	2	0	0	1124.61	9	20
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	12	13	24	0.02%	26.7%	ALELENDRLLLK	99.7%	60.2	25	51.6	2	0	0	1426.83	46	57
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	12	13	24	0.02%	26.7%	ATSSSSGSLSATGR	99.7%	107	25	102	2	0	0	1268.61	397	410
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	12	13	24	0.02%	26.7%	CQSLQEELDFRK	99.7%	40.3	25	40.3	0	1	0	1552.74	192	203
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	12	13	24	0.02%	26.7%	EGELTVAQGR	99.7%	52.5	25	32.5	3	0	0	1059.54	119	128
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	12	13	24	0.02%	26.7%	GLESDVAELR	99.7%	84.2	25	63.4	2	0	0	1088.56	152	161
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	12	13	24	0.02%	26.7%	ISEKEEVTTR	99.7%	60.2	25	34.1	2	0	0	1191.62	58	67
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	12	13	24	0.02%	26.7%	KLLEGEEER	99.5%	37.9	25	22.2	1	0	0	1102.57	373	381
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	12	13	24	0.02%	26.7%	LELEQTYQAK	99.2%	35.3	25	31.7	2	0	0	1222.63	256	265
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	12	13	24	0.02%	26.7%	LLEGEEERLK	99.7%	51	25	36	2	0	0	1215.66	374	383

Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	12	13	24	0.02%	26.7%	LQEKEELR	99.7%	50.3	25	22.6	2	0	0	1044.57	24	31
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	12	13	24	0.02%	26.7%	LQIEIGK	98.2%	31.9	25	0	1	0	0	800.49	97	103
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	12	13	24	0.02%	26.7%	LSSDQNDKAASAAR	99.7%	44.6	25	33.2	1	0	0	1433.70	271	284
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	12	13	24	0.02%	26.7%	QVLEGEEIAYK	99.7%	72.9	25	64.7	2	0	0	1278.66	486	496
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	12	13	24	0.02%	26.7%	RLVEVDSSR	99.4%	37	25	27.1	2	0	0	1060.57	220	228
Lamin-B2	LMNB2	LMNB2_HUMAN	67.7	100.0%	12	13	24	0.02%	26.7%	VKDLESLFHR	99.7%	47.4	25	37.6	1	2	0	1243.68	129	138
Lanosterol synthase	LSS	ERG7_HUMAN	83.3	99.8%	2	2	2	0.00%	3.7%	LSAAEDPLVQSLR	98.0%	31.5	25	24	1	0	0	1398.76	248	260
Lanosterol synthase	LSS	ERG7_HUMAN	83.3	99.8%	2	2	2	0.00%	3.7%	STVFGTALNYVSLR	99.7%	64.5	25	60.4	1	0	0	1527.82	149	162
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	15	17	34	0.03%	15.0%	AVTPVPTKTEEVSNLK	99.6%	32.4	25	26.3	0	1	0	1712.94	524	539
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	15	17	34	0.03%	15.0%	DYEAGQLYGLEK	99.7%	48.7	25	25.5	1	0	0	1385.66	981	992
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	15	17	34	0.03%	15.0%	ETESAPGSPR	99.7%	45.2	25	42.3	6	0	0	1030.48	514	523
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	15	17	34	0.03%	15.0%	FQHPSHELLK	98.5%	32.7	25	23.9	1	0	0	1235.65	872	881
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	15	17	34	0.03%	15.0%	FQQVPTDALANK	99.7%	66.6	25	59.4	4	0	0	1331.70	742	753
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	15	17	34	0.03%	15.0%	FWSFFLR	99.7%	50.1	25	48.4	2	0	0	1002.52	918	924
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	15	17	34	0.03%	15.0%	ILIVTQTPHYMR	99.7%	67.3	25	60.1	2	2	0	1487.80	643	654
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	15	17	34	0.03%	15.0%	LFGAPEPSTIAR	99.7%	45.2	25	17.2	2	0	0	1258.68	754	765
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	15	17	34	0.03%	15.0%	LGIGQSQEMNTLFR	99.7%	65.3	25	60.7	4	0	0	1593.81	904	917
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	15	17	34	0.03%	15.0%	LQEYLGK	97.9%	31.3	25	13.5	2	0	0	850.47	1011	1017
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	15	17	34	0.03%	15.0%	QIEYYFSVDNLER	99.7%	46.9	25	46.8	1	0	0	1675.80	410	422
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	15	17	34	0.03%	15.0%	SLPTTVPESPNYR	99.6%	39.3	25	36.1	2	0	0	1460.74	766	778
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	15	17	34	0.03%	15.0%	THFDYQFGYR	99.7%	40.2	25	40.2	1	0	0	1333.60	357	366
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	15	17	34	0.03%	15.0%	VVEIVDEK	99.2%	35.2	25	25.4	1	0	0	930.51	466	473
La-related protein 1	LARP1	LARP1_HUMAN	123.5	100.0%	15	17	34	0.03%	15.0%	YGLECLFR	99.7%	59.6	25	56.9	2	0	0	1057.51	949	956
La-related protein 4B	LARP4B	LAR4B_HUMAN	80.6	99.8%	2	2	3	0.00%	3.4%	EISESTPVEEVEALFK	98.2%	31.9	25	31.9	1	0	0	1806.90	242	257
La-related protein 4B	LARP4B	LAR4B_HUMAN	80.6	99.8%	2	2	3	0.00%	3.4%	VVAEPQTQR	96.8%	29.6	25	22.8	2	0	0	1027.55	9	17
La-related protein 7	LARP7	LARP7_HUMAN	66.9	100.0%	3	3	5	0.00%	7.0%	AIEFLNNPPEEAPR	99.7%	70.8	25	65.4	2	0	0	1596.80	182	195
La-related protein 7	LARP7	LARP7_HUMAN	66.9	100.0%	3	3	5	0.00%	7.0%	DRVEASSLPEVR	96.9%	29.8	25	25.7	1	0	0	1357.71	280	291
La-related protein 7	LARP7	LARP7_HUMAN	66.9	100.0%	3	3	5	0.00%	7.0%	VNATGPQFVSGVIVK	99.7%	86.3	25	79.1	2	0	0	1515.85	444	458
Lethal(2) giant larvae protein homolog 1	LLGL1	L2GL1_HUMAN	115.4	99.8%	2	2	4	0.00%	2.4%	APVVAIAVLDGR	99.7%	95.7	25	88.7	3	0	0	1180.70	788	799
Lethal(2) giant larvae protein homolog 1	LLGL1	L2GL1_HUMAN	115.4	99.8%	2	2	4	0.00%	2.4%	TGPLPWPAGFQPR	97.7%	31	25	25.9	1	0	0	1423.75	578	590
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	AFAETHIK	99.7%	47.3	25	40.6	2	0	0	916.49	1091	1098
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	AGDMENAENILTVMR	99.7%	82.2	25	77.5	4	0	0	1663.78	245	259
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	AGYPQYVSEILEK	99.7%	85	25	71.1	2	0	0	1496.76	315	327
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	CVANNQVETLEK	99.7%	52.8	25	46.8	2	0	0	1404.68	930	941
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	DAHLLVESK	99.7%	56.1	25	45.3	2	0	0	1011.55	641	649
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	EKDIQEESTFSSR	99.7%	72.9	25	65.2	2	0	0	1555.72	65	77
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	EQNIVFNAETYSNLIK	99.7%	87.6	25	85.3	2	0	0	1882.95	1060	1075
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	GAYDIFLNAK	99.7%	63	25	53.9	2	0	0	1111.58	1050	1059
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	GDVENIEVVQK	99.7%	65.2	25	56.5	2	0	0	1229.64	1153	1163
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	GFTLNDAANSR	99.7%	77.2	25	63.1	2	0	0	1165.56	1099	1109
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	IPENIYR	97.7%	31	25	14.5	2	0	0	904.49	618	624
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	IQEENVIPR	99.7%	68.2	25	59.6	2	0	0	1097.60	981	989
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	ISIMAER	99.6%	39.1	25	28.4	1	0	0	835.43	1237	1243
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	KIIETPGIR	99.7%	48.5	25	37.6	2	0	0	1026.63	909	917
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	LDDLFLKR	99.7%	52.7	25	39.6	2	0	0	1019.59	1351	1358
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	LDSSAVLDTGK	99.7%	70.8	25	64.1	2	0	0	1105.57	740	750
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	LIASYCNVGDIEGASK	99.7%	111	25	105	2	0	0	1696.82	203	218
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	LIITQVR	98.4%	32.4	25	13.4	1	0	0	842.55	1110	1116
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	LLMSEDYFTQAMEVK	99.7%	64.9	25	52.1	3	0	0	1836.84	1076	1090
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	LQDAINILK	99.7%	59.3	25	51	2	0	0	1027.61	764	772
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	LVEKGETDLIQK	99.7%	54.3	25	44.5	2	0	0	1372.77	865	876

Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	MEEANIQPNR	99.7%	47.2	25	39.5	2	0	0	1201.56	188	197
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	MLNGLEDSIGLSK	99.7%	73.3	25	67	4	0	0	1376.71	1164	1176
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	MVFINNIALAQIK	99.7%	71.6	25	71.6	4	0	0	1490.84	1177	1189
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	NVQGIIEILK	99.7%	57	25	56.7	2	0	0	1126.68	454	463
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	SCGSLLPELK	99.7%	54.5	25	40.6	2	0	0	1103.58	129	138
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	SEAANGNLDFVLSFLK	99.7%	47.1	25	47.1	1	0	0	1724.89	514	529
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	SGGLGGSHALLLLR	99.7%	47.7	25	35.8	1	2	0	1350.79	115	128
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	SNTLPISLQSIR	99.7%	78.8	25	54.9	2	0	0	1328.75	530	541
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	SYVSEKDVTSAK	99.7%	63.3	25	63.3	2	0	0	1313.66	1327	1338
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	TVLDQQQTPSR	99.7%	72.8	25	58.5	2	0	0	1272.65	1129	1139
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	TVQLTSSELESTLETLK	99.7%	98.5	25	90.2	2	0	0	1878.99	656	672
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	LPPRC_HUMAN	157.9	100.0%	33	38	71	0.07%	26.8%	VYLQNEYK	99.7%	39.9	25	33.8	2	0	0	1056.54	171	178
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	12	12	20	0.02%	22.3%	FLALEGNPLR	99.7%	41.9	25	31.7	1	0	0	1129.64	338	347
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	12	12	20	0.02%	22.3%	FLPEFPSCSLLK	99.5%	37.4	25	24.3	2	0	0	1437.74	257	268
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	12	12	20	0.02%	22.3%	GTAAILEYLR	99.7%	60.5	25	43	2	0	0	1106.62	588	597
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	12	12	20	0.02%	22.3%	LDLSNNDISSLPYSLGNLHLK	99.7%	50.5	25	47.6	0	2	0	2313.21	317	337
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	12	12	20	0.02%	22.3%	LQTINLSFNR	99.7%	71.6	25	59.9	2	0	0	1205.66	497	506
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	12	12	20	0.02%	22.3%	LTFLDLR	99.7%	41.3	25	36.2	2	0	0	877.51	474	480
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	12	12	20	0.02%	22.3%	MLPEVLYR	96.8%	29.7	25	25.9	1	0	0	1020.55	509	516
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	12	12	20	0.02%	22.3%	NLSEVPQCVWR	99.7%	45.6	25	41.7	1	0	0	1387.68	47	57
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	12	12	20	0.02%	22.3%	QATLIPDEVFDAVK	99.7%	43.7	25	23.5	2	0	0	1545.82	410	423
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	12	12	20	0.02%	22.3%	SNIVTSINFSK	99.7%	46.8	25	40.3	1	0	0	1209.65	424	434
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	12	12	20	0.02%	22.3%	SVPDEIILLR	99.7%	64.5	25	45.9	2	0	0	1154.68	303	312
Leucine-rich repeat-containing protein 40	LRRC40	LRC40_HUMAN	68.3	100.0%	12	12	20	0.02%	22.3%	TLLLDGNPFR	99.5%	38	25	33.6	2	0	0	1145.63	569	578
Leucine-rich repeat-containing protein 47	LRRC47	LRC47_HUMAN	63.5	99.8%	2	2	4	0.00%	5.0%	NALGPGLSPELGPLPALR	99.7%	41.4	25	41.4	2	0	0	1772.01	85	102
Leucine-rich repeat-containing protein 47	LRRC47	LRC47_HUMAN	63.5	99.8%	2	2	4	0.00%	5.0%	TAATLATHELR	99.7%	80.9	25	70.5	2	0	0	1183.64	371	381
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	15	16	28	0.03%	15.0%	FDDPLLGPR	99.7%	65.5	25	52.1	2	0	0	1029.54	1118	1126
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	15	16	28	0.03%	15.0%	GTGVVTSVPSDSPDDIAALR	99.7%	75	25	75	2	0	0	1956.99	385	404
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	15	16	28	0.03%	15.0%	ILDLQLEFDEK	99.7%	85.2	25	83.5	2	0	0	1362.72	1007	1017
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	15	16	28	0.03%	15.0%	MIDAGDALIYMEPEK	99.7%	68.6	25	68.6	2	0	0	1695.80	498	512
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	15	16	28	0.03%	15.0%	SFITTDVNPYYDSFVR	99.7%	79.8	25	79.8	2	0	0	1923.91	204	219
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	15	16	28	0.03%	15.0%	SGPASTFNDR	98.2%	32	25	20.9	1	0	0	1051.48	786	795
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	15	16	28	0.03%	15.0%	SLGLSDEEIVK	99.7%	44.5	25	37.4	1	0	0	1189.63	163	173
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	15	16	28	0.03%	15.0%	STGNFLTLTQAIDK	99.7%	97.2	25	89.8	2	0	0	1508.80	720	733
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	15	16	28	0.03%	15.0%	TGFFEFQAAK	99.7%	60.7	25	51.9	2	0	0	1145.56	823	832
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	15	16	28	0.03%	15.0%	VDIGDTIIYLVH	99.7%	89.2	25	87	1	0	0	1357.74	1165	1176
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	15	16	28	0.03%	15.0%	VFASELNAGIIK	99.7%	95.8	25	85.3	2	0	0	1261.72	796	807
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	15	16	28	0.03%	15.0%	VFEVNASNLEK	99.7%	74.2	25	69.5	2	0	0	1249.64	29	39
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	15	16	28	0.03%	15.0%	VIASELGSMPELK	99.7%	60.1	25	48.5	3	0	0	1373.73	971	983
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	15	16	28	0.03%	15.0%	VIASELGSMPELKK	99.7%	48	25	37.3	2	0	0	1501.83	971	984
Leucine--tRNA ligase, cytoplasmic	LARS	SYLC_HUMAN	134.5	100.0%	15	16	28	0.03%	15.0%	VIYVLPMLTIK	99.7%	54.6	25	54.6	2	0	0	1289.79	371	381
Leukotriene A-4 hydrolase	LTA4H	LKHA4_HUMAN	69.3	99.8%	2	2	3	0.00%	5.1%	LVVDLTDIDPDVAYSSVPYEK	99.7%	68.9	25	68.9	2	0	0	2338.17	366	386
Leukotriene A-4 hydrolase	LTA4H	LKHA4_HUMAN	69.3	99.8%	2	2	3	0.00%	5.1%	TFGETHPFTK	99.7%	51.8	25	50.1	1	0	0	1164.57	356	365
Leydig cell tumor 10 kDa protein homolog	C19orf53	L10K_HUMAN	10.6	99.8%	2	2	3	0.00%	8.1%	NLEVGIR	99.7%	40.8	25	19.9	2	0	0	800.46	52	58
Leydig cell tumor 10 kDa protein homolog	C19orf53	L10K_HUMAN	10.6	99.8%	2	2	3	0.00%	8.1%	NLEVGIRK	98.2%	32	25	17.4	1	0	0	928.56	52	59
LINE-1 retrotransposable element ORF1 protein	L1RE1	LORF1_HUMAN	40.1	99.8%	2	2	2	0.00%	7.1%	LTADLSAETLQAR	99.7%	71.8	25	64.8	1	0	0	1388.74	249	261
LINE-1 retrotransposable element ORF1 protein	L1RE1	LORF1_HUMAN	40.1	99.8%	2	2	2	0.00%	7.1%	QANVQIQEIQR	99.7%	46.6	25	45.3	1	0	0	1326.71	192	202
Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	DBT	ODB2_HUMAN	53.5	99.8%	2	3	4	0.00%	4.8%	LSFMPFFLK	99.4%	36.9	25	27.3	2	0	0	1129.61	305	313
Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	DBT	ODB2_HUMAN	53.5	99.8%	2	3	4	0.00%	4.8%	SYLENPAFMLLDLK	99.7%	47.7	25	47.7	2	0	0	1669.85	469	482
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	9	9	11	0.01%	3.6%	DLSKPIGALNPK	98.5%	32.8	25	32.8	1	0	0	1252.73	2268	2279
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	9	9	11	0.01%	3.6%	EAVEAQIR	99.7%	42.3	25	26.4	1	0	0	915.49	2465	2472

Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	9	9	11	0.01%	3.6%	EIFVDFAPFLSR	99.7%	66.8	25	62.2	2	0	0	1440.75	1813	1824
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	9	9	11	0.01%	3.6%	IQNPQILK	96.2%	29	25	17.9	1	0	0	953.58	813	820
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	9	9	11	0.01%	3.6%	LSSAIAFTYNPR	99.7%	52.8	25	48.2	1	0	0	1339.70	413	424
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	9	9	11	0.01%	3.6%	NPLGSTHPEATLK	99.7%	45.8	25	34.4	1	0	0	1364.72	1998	2010
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	9	9	11	0.01%	3.6%	SAAAIALPPIAK	99.7%	43.6	25	34.9	1	0	0	1122.69	213	224
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	9	9	11	0.01%	3.6%	VGVGTSFGLPQTR	99.7%	55	25	55	1	0	0	1318.71	2183	2195
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	LRBA_HUMAN	319.1	100.0%	9	9	11	0.01%	3.6%	YGPDAFFNFPGK	99.7%	74	25	72	2	0	0	1359.64	201	212
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	29	156	0.15%	60.8%	DLADELALVDVIEDK	99.7%	125	25	122	3	0	0	1657.85	43	57
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	29	156	0.15%	60.8%	DQLIYNLLK	99.7%	64.7	25	46.3	8	0	0	1119.64	6	14
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	29	156	0.15%	60.8%	DQLIYNLLKEEQTPQNK	99.7%	106	25	101	4	4	0	2074.08	6	22
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	29	156	0.15%	60.8%	DYNVTANSK	99.7%	59.6	25	59.6	7	0	0	1011.47	82	90
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	29	156	0.15%	60.8%	FIIPNVVK	99.6%	38.8	25	28.3	6	0	0	929.58	119	126
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	29	156	0.15%	60.8%	GEMMDLQHGSLFLR	99.7%	88.2	25	88.2	7	7	0	1633.78	60	73
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	29	156	0.15%	60.8%	GYTSWAIGLSVADLAESIMK	99.7%	76.4	25	76.4	2	0	0	2128.06	246	265
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	29	156	0.15%	60.8%	ITVVGVGAVGMACAISILMK	99.7%	67	25	67	7	1	0	1990.09	23	42
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	29	156	0.15%	60.8%	IVSGKDYNVTANSK	99.7%	85.9	25	85.9	3	2	0	1495.78	77	90
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	29	156	0.15%	60.8%	KSADTLWGIQK	94.6%	22.6	25	17.7	0	1	0	1246.68	318	328
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	29	156	0.15%	60.8%	LKGEMMDLQHGSLFLR	97.8%	25.9	25	25.9	0	1	0	1906.95	58	73
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	29	156	0.15%	60.8%	LLIVSNPVDILTYVAWK	99.7%	112	25	0	8	2	0	1944.12	133	149
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	29	156	0.15%	60.8%	LVIITAGAR	99.7%	76	25	47.7	20	0	0	913.58	91	99
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	29	156	0.15%	60.8%	QVVESAYEVIK	99.7%	71.8	25	64.2	9	0	0	1264.68	233	243
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	29	156	0.15%	60.8%	RVHPVSTMIK	99.7%	42.8	25	33.4	3	0	0	1167.67	269	278
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	29	156	0.15%	60.8%	SADTLWGIQK	99.7%	66.2	25	56.2	6	0	0	1118.58	319	328
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	29	156	0.15%	60.8%	TLHPDLGTDK	98.7%	33.4	25	33.4	2	0	0	1096.56	213	222
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	29	156	0.15%	60.8%	TLHPDLGTDKDK	96.3%	29.1	25	29.1	1	0	0	1339.69	213	224
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	29	156	0.15%	60.8%	VIGSGCNLDSAR	99.7%	78.2	25	71.4	20	0	0	1248.60	158	169
L-lactate dehydrogenase A chain	LDHA	LDHA_HUMAN	36.7	100.0%	20	29	156	0.15%	60.8%	VTLTSEEEAR	99.7%	79.4	25	72.4	22	0	0	1134.56	306	315
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	14	24	121	0.11%	46.7%	EKLIAPVAEEEATVPNNK	99.7%	99.1	25	92.9	2	2	0	1952.03	6	23
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	14	24	121	0.11%	46.7%	FIIPQIVK	99.7%	44.3	25	39.2	6	0	0	957.61	120	127
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	14	24	121	0.11%	46.7%	GEMMDLQHGSLFLQTPK	99.7%	65	25	62.8	6	8	0	1931.94	61	77
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	14	24	121	0.11%	46.7%	GLTSVINQK	99.7%	61.7	25	48.2	8	0	0	959.55	300	308
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	14	24	121	0.11%	46.7%	ITVVGVGQVGMACAISILGK	99.7%	127	25	127	14	4	0	1973.09	24	43
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	14	24	121	0.11%	46.7%	IVADKDYSVTANSK	99.7%	86.2	25	79	10	2	0	1510.77	78	91
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	14	24	121	0.11%	46.7%	IVVVTAGVR	99.7%	69.4	25	55.3	7	0	0	913.58	92	100
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	14	24	121	0.11%	46.7%	KSADTLWDIQK	99.7%	63.1	25	56	2	0	0	1304.68	319	329
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	14	24	121	0.11%	46.7%	LIAPVAEEEATVPNNK	99.7%	101	25	89.6	14	2	0	1694.90	8	23
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	14	24	121	0.11%	46.7%	LKDDEVAQLK	99.7%	59.1	25	27.9	2	0	0	1158.64	309	318
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	14	24	121	0.11%	46.7%	LKGEMMDLQHGSLFLQTPK	97.9%	26.1	25	25.1	0	1	0	2205.10	59	77
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	14	24	121	0.11%	46.7%	MVVESAYEVIK	99.7%	84.6	25	77.5	21	0	0	1267.66	234	244
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	14	24	121	0.11%	46.7%	SADTLWDIQK	99.7%	69.2	25	52.9	7	0	0	1176.59	320	329
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	14	24	121	0.11%	46.7%	SLADELALVDVLEDK	99.7%	105	25	83.3	3	0	0	1629.86	44	58
L-lactate dehydrogenase B chain	LDHB	LDHB_HUMAN	36.6	100.0%	14	24	121	0.11%	46.7%	VIGSGCNLDSAR	99.7%	78.2	25	71.4	20	0	0	1248.60	159	170
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	6	6	12	0.01%	7.8%	DIIALNPLYR	99.7%	64.8	25	47.1	2	0	0	1187.68	302	311
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	6	6	12	0.01%	7.8%	EIFDIAFPDEQAEALAVER	99.7%	62.5	25	55.1	2	0	0	2163.06	941	959
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	6	6	12	0.01%	7.8%	ILEFIAVSQLR	99.7%	62.7	25	52	2	0	0	1288.76	501	511
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	6	6	12	0.01%	7.8%	LAQPYVGVFLK	99.7%	45.6	25	32.6	2	0	0	1234.72	159	169
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	6	6	12	0.01%	7.8%	LSSDVLTLLIK	99.7%	79.8	25	66.9	2	0	0	1201.74	691	701
Lon protease homolog, mitochondrial	LONP1	LONM_HUMAN	106.5	100.0%	6	6	12	0.01%	7.8%	TENPLILIDEVDK	99.7%	39.9	25	39.9	2	0	0	1498.80	582	594
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	8	8	14	0.01%	15.3%	AKPVNSKPDSAYR	99.7%	41.3	25	39.5	1	0	0	1432.75	57	69
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	8	8	14	0.01%	15.3%	HIITVDGKPPTWSEFPK	99.7%	36.2	25	36.2	0	1	0	1952.03	233	249
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	8	8	14	0.01%	15.3%	IGYSSPQTLADQSSK	99.7%	86.2	25	86.2	2	0	0	1581.78	349	363

Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	8	8	14	0.01%	15.3%	LKDIVSLVPR	99.7%	51.9	25	45.4	2	0	0	1139.71	221	230
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	8	8	14	0.01%	15.3%	LLLCGGAPLSATTQR	99.7%	93	25	86.7	2	0	0	1557.84	447	461
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	8	8	14	0.01%	15.3%	LQAGEYVSLGK	99.7%	41.9	25	36.2	2	0	0	1164.63	586	596
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	8	8	14	0.01%	15.3%	LSPEPWTPETGLVTDAFK	99.7%	78.4	25	78.4	2	0	0	1988.00	682	699
Long-chain-fatty-acid--CoA ligase 3	ACSL3	ACSL3_HUMAN	80.4	100.0%	8	8	14	0.01%	15.3%	NTPLCDSFVFR	99.7%	42.9	25	42.9	2	0	0	1355.64	425	435
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	12	12	26	0.02%	30.1%	EGIILFK	95.0%	28	25	2.29	1	0	0	819.50	270	276
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	12	12	26	0.02%	30.1%	FVETPGQK	96.3%	29.1	25	17.6	2	0	0	905.47	167	174
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	12	12	26	0.02%	30.1%	GSIFVVFDSIESAK	99.7%	93.8	25	90.8	4	0	0	1498.78	152	165
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	12	12	26	0.02%	30.1%	GSIFVVFDSIESAKK	99.7%	68.3	25	67.7	2	0	0	1626.87	152	166
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	12	12	26	0.02%	30.1%	ICHQIEYYFGDFNLPR	99.7%	46.4	25	46.4	0	2	0	2071.97	17	32
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	12	12	26	0.02%	30.1%	IIEDQQESLNK	99.7%	85	25	73.7	4	0	0	1316.67	318	328
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	12	12	26	0.02%	30.1%	KFVETPGQK	97.0%	30	25	28.5	1	0	0	1033.57	166	174
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	12	12	26	0.02%	30.1%	LDEGWVPLEIMIK	98.0%	31.6	25	18.7	1	0	0	1542.82	42	54
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	12	12	26	0.02%	30.1%	LTTDFNVIVEALSK	99.7%	109	25	106	4	0	0	1549.85	61	74
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	12	12	26	0.02%	30.1%	QKLEEDAEMK	99.5%	37.6	25	34.2	1	0	0	1236.58	215	224
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	12	12	26	0.02%	30.1%	SPSKPLPEVTDEYKNDVK	99.7%	35.5	25	35.5	0	2	0	2046.04	92	109
Lupus La protein	SSB	LA_HUMAN	46.8	100.0%	12	12	26	0.02%	30.1%	YKETDLLILFK	99.7%	48.8	25	47.1	2	0	0	1382.79	175	185
Lymphoid-specific helicase	HELLS	HELLS_HUMAN	97.1	100.0%	3	3	3	0.00%	3.9%	EVVVYAPLSK	99.7%	45.7	25	43.5	1	0	0	1104.63	465	474
Lymphoid-specific helicase	HELLS	HELLS_HUMAN	97.1	100.0%	3	3	3	0.00%	3.9%	MEQQQLEEQK	99.7%	48.5	25	42.4	1	0	0	1306.59	86	95
Lymphoid-specific helicase	HELLS	HELLS_HUMAN	97.1	100.0%	3	3	3	0.00%	3.9%	NSIDASEEKPVMR	95.7%	28.6	25	28.6	1	0	0	1491.71	114	126
Lysine-rich nucleolar protein 1	KNOP1	KNOP1_HUMAN	51.6	99.8%	2	2	2	0.00%	5.7%	GAGLGFSTAPNK	98.7%	33.4	25	29.5	1	0	0	1119.58	431	442
Lysine-rich nucleolar protein 1	KNOP1	KNOP1_HUMAN	51.6	99.8%	2	2	2	0.00%	5.7%	VEAPEYIPISDDPK	99.7%	42	25	41.6	1	0	0	1572.78	250	263
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	7	7	10	0.01%	13.6%	IAPELYHK	99.2%	35.4	25	11.2	1	0	0	970.54	298	305
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	7	7	10	0.01%	13.6%	INMVEELEK	96.6%	29.5	25	19.3	1	0	0	1104.56	394	402
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	7	7	10	0.01%	13.6%	LPETNLFETEETRK	99.3%	30.5	25	28.9	0	2	0	1706.86	408	421
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	7	7	10	0.01%	13.6%	MLVVGGIDR	99.7%	54.7	25	46.9	2	0	0	959.53	306	314
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	7	7	10	0.01%	13.6%	RGDIIGVQGNPGK	99.7%	65.3	25	61.1	1	0	0	1310.72	178	190
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	7	7	10	0.01%	13.6%	VAMFLTDSNNIK	99.7%	50.5	25	50.5	1	0	0	1352.69	554	565
Lysine--tRNA ligase	KARS	SYK_HUMAN	68.1	100.0%	7	7	10	0.01%	13.6%	YSHLQPGDHLTDITLK	99.4%	31.2	25	21.8	0	2	0	1837.94	112	127
Lysophosphatidylcholine acyltransferase 1	LPCAT1	PCAT1_HUMAN	59.2	100.0%	4	4	6	0.01%	12.2%	DIPIWGTLIQYIRPVFVSR	97.9%	26.1	25	22.7	0	1	0	2273.28	159	177
Lysophosphatidylcholine acyltransferase 1	LPCAT1	PCAT1_HUMAN	59.2	100.0%	4	4	6	0.01%	12.2%	ITFADFHR	99.3%	35.9	25	27.7	2	0	0	1006.51	471	478
Lysophosphatidylcholine acyltransferase 1	LPCAT1	PCAT1_HUMAN	59.2	100.0%	4	4	6	0.01%	12.2%	TALGVAELTVTDLFR	99.7%	50.4	25	49.3	1	0	0	1605.88	447	461
Lysophosphatidylcholine acyltransferase 1	LPCAT1	PCAT1_HUMAN	59.2	100.0%	4	4	6	0.01%	12.2%	TCLITFKPGAFIPGAPVQPVVLR	99.7%	43	25	43	0	2	0	2481.41	215	237
Lysosomal protective protein	CTSA	PPGB_HUMAN	54.5	100.0%	4	4	6	0.01%	8.1%	EFSHIAFLTIK	99.5%	37.9	25	36.2	2	0	0	1305.72	443	453
Lysosomal protective protein	CTSA	PPGB_HUMAN	54.5	100.0%	4	4	6	0.01%	8.1%	FLNKQPY	96.9%	29.8	25	21.6	1	0	0	909.48	474	480
Lysosomal protective protein	CTSA	PPGB_HUMAN	54.5	100.0%	4	4	6	0.01%	8.1%	SMNSQYLK	99.6%	38.1	25	28.2	1	0	0	970.47	376	383
Lysosomal protective protein	CTSA	PPGB_HUMAN	54.5	100.0%	4	4	6	0.01%	8.1%	YGDSGEQIAGFVK	99.7%	83.9	25	77	2	0	0	1370.66	430	442
Magnesium transporter protein 1	MAGT1	MAGT1_HUMAN	38.0	100.0%	3	3	6	0.01%	8.1%	GFSAEQIAR	99.7%	43.5	25	32	2	0	0	978.50	160	168
Magnesium transporter protein 1	MAGT1	MAGT1_HUMAN	38.0	100.0%	3	3	6	0.01%	8.1%	RGDTYELQVR	99.7%	46.9	25	39.6	2	0	0	1236.63	150	159
Magnesium transporter protein 1	MAGT1	MAGT1_HUMAN	38.0	100.0%	3	3	6	0.01%	8.1%	YSSAFTNR	99.7%	46	25	38.9	2	0	0	945.44	106	113
Malate dehydrogenase, cytoplasmic	MDH1	MDHC_HUMAN	36.4	99.8%	2	2	3	0.00%	7.8%	LGVTANDVK	99.7%	44.5	25	32.8	2	0	0	916.51	171	179
Malate dehydrogenase, cytoplasmic	MDH1	MDHC_HUMAN	36.4	99.8%	2	2	3	0.00%	7.8%	VIVVGNPANTNCLTASK	99.7%	59.9	25	59.9	1	0	0	1757.92	126	142
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	4	4	7	0.01%	18.0%	IFGVTTLDIVR	99.7%	42.2	25	29.4	2	0	0	1233.72	166	176
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	4	4	7	0.01%	18.0%	SQETECTYFSTPLLLGK	99.7%	91.2	25	91.2	2	0	0	1973.95	280	296
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	4	4	7	0.01%	18.0%	VAVLGASGGIGQPLSLLLK	99.7%	107	25	107	2	0	0	1793.09	27	45
Malate dehydrogenase, mitochondrial	MDH2	MDHM_HUMAN	35.5	100.0%	4	4	7	0.01%	18.0%	VDFPQDQLTALTGR	99.7%	58.6	25	58	1	0	0	1560.80	216	229
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	2	2	3	0.00%	6.4%	IPAEVLILNSIVLPHK	99.7%	34.5	25	34.5	0	1	0	1756.07	393	408
Mannose-1-phosphate guanyltransferase alpha	GMPPA	GMPPA_HUMAN	46.3	100.0%	2	2	3	0.00%	6.4%	LLPAITILGCR	99.7%	42.5	25	42.5	2	0	0	1226.73	380	390
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	ALWFQGR	96.3%	29.1	25	20.6	2	0	0	877.47	556	562
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	DDWEEKR	98.7%	33.5	25	11.1	2	0	0	977.43	176	182
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	DLDELSR	96.2%	29	25	24.2	1	0	0	847.42	121	127

Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	DLDELSRYPEDK	99.7%	53.7	25	45.3	4	1	0	1479.70	121	132
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	DLSAAGIGLLAAATQSLSMPASLGR	99.7%	53.3	25	53.3	1	0	0	2387.26	20	44
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	DSFDDRGPSLNPVLDYDHGSR	99.7%	55.2	25	55.2	0	3	0	2362.07	187	207
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	EDAMAMVDHCLK	99.7%	68.1	25	66.9	4	0	0	1419.61	543	554
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	EDAMAMVDHCLKK	96.5%	24.2	25	24.2	0	1	0	1547.70	543	555
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	FDQKQELGR	99.7%	47.6	25	40.4	5	0	0	1120.57	488	496
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	FDSEYER	99.7%	42.1	25	42.1	4	0	0	945.39	246	252
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	GAPPSSNIEDFHGLLPK	99.7%	61.8	25	60.8	4	0	0	1778.91	271	287
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	GDADQASNILASFGLSAR	99.7%	96	25	96	4	1	0	1792.88	103	120
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	GNLGAGNGNLQGPR	99.7%	84.8	25	84.8	6	0	0	1324.67	374	387
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	GPGPLQER	99.7%	49.9	25	43.2	5	0	0	853.45	256	263
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	GPLPLSSQHR	99.7%	54.8	25	51.4	4	0	0	1091.60	93	102
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	GPSLNPVLDYDHGSR	99.7%	102	25	102	4	4	0	1626.79	193	207
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	GYPHLCSICDLPVHSNK	99.7%	45.6	25	45.6	0	2	0	1996.94	288	304
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	IGPYQPNVPVGIDYVIPK	99.7%	64.3	25	64.3	7	0	0	1969.08	781	798
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	IKNYILMR	99.2%	35.5	25	24.2	4	0	0	1050.61	523	530
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	ITPENLPQILLQLK	99.7%	70.9	25	67.7	5	0	0	1619.97	133	146
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	LCSLFYTNEEVAK	99.7%	75.4	25	69.5	6	0	0	1573.76	805	817
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	MDYEDDRLR	99.7%	40	25	31.8	6	0	0	1212.53	217	225
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	NTHCSSLPHYQK	99.7%	51.3	25	51.3	4	1	0	1471.67	818	829
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	NYILMR	99.6%	38.4	25	26	5	0	0	809.43	525	530
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	RTEEGPTLSYGR	99.7%	59.2	25	48.3	4	1	0	1365.68	149	160
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	SFQQSSLSR	99.7%	50.3	25	37.6	2	0	0	1039.52	4	12
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	SQAFIEMETR	99.7%	64.8	25	57.4	9	0	0	1211.57	533	542
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	SQESGYYDR	99.7%	62.9	25	62.9	4	0	0	1104.46	208	216
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	TEEGPTLSYGR	99.7%	66.7	25	57	4	0	0	1209.57	150	160
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	VIHLSNLPHSGYSDSAVLK	99.7%	88.9	25	85.2	1	6	0	2037.08	497	515
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	VVHIMDFQR	99.7%	50.6	25	42.7	9	0	0	1144.59	399	407
Matrin-3	MATR3	MATR3_HUMAN	94.6	100.0%	32	42	143	0.13%	41.1%	YQLLQLVEPFGVISNHLILNK	99.7%	38.4	25	38.4	0	3	0	2438.38	413	433
Mediator of DNA damage checkpoint protein 1	MDC1	MDC1_HUMAN	226.7	100.0%	4	4	7	0.01%	3.2%	GIPILSLDWLHQSR	99.7%	48	25	48	1	0	0	1634.90	1944	1957
Mediator of DNA damage checkpoint protein 1	MDC1	MDC1_HUMAN	226.7	100.0%	4	4	7	0.01%	3.2%	NQLVTPEPTSR	99.3%	36.2	25	23	2	0	0	1241.65	1585	1595
Mediator of DNA damage checkpoint protein 1	MDC1	MDC1_HUMAN	226.7	100.0%	4	4	7	0.01%	3.2%	TPEPVVPTAPEPHPTTSTDQPVTPK	99.7%	38.4	25	38.4	0	2	0	2623.33	1608	1632
Mediator of DNA damage checkpoint protein 1	MDC1	MDC1_HUMAN	226.7	100.0%	4	4	7	0.01%	3.2%	VGLPLLSPEFLLTGVLK	99.7%	42	25	42	2	0	0	1796.09	2055	2071
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	5	5	6	0.01%	4.1%	EVGNALLNVVLK	99.5%	37.4	25	22.9	1	0	0	1268.76	1121	1132
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	5	5	6	0.01%	4.1%	FLELLPVSK	96.4%	29.2	25	29.2	1	0	0	1045.63	974	982
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	5	5	6	0.01%	4.1%	FLTEVLLPIVK	99.7%	48.6	25	41.7	1	0	0	1271.80	1230	1240
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	5	5	6	0.01%	4.1%	LFDLLYPEK	99.7%	47.9	25	41.6	2	0	0	1137.62	398	406
Mediator of RNA polymerase II transcription subunit 23	MED23	MED23_HUMAN	156.5	100.0%	5	5	6	0.01%	4.1%	SSVALAPALVETYSR	99.7%	58.9	25	54.5	1	0	0	1563.84	555	569
Melanoma-associated antigen D2	MAGED2	MAGD2_HUMAN	65.0	100.0%	5	5	9	0.01%	11.7%	EAPATQASSTTQLTDTQVLAAENK	99.7%	52.4	25	52.4	0	2	0	2475.22	77	100
Melanoma-associated antigen D2	MAGED2	MAGD2_HUMAN	65.0	100.0%	5	5	9	0.01%	11.7%	EYTDVYPEIIER	99.7%	49.1	25	49.1	1	0	0	1526.74	312	323
Melanoma-associated antigen D2	MAGED2	MAGD2_HUMAN	65.0	100.0%	5	5	9	0.01%	11.7%	GPIAFWAR	99.7%	54.7	25	51.4	2	0	0	917.50	220	227
Melanoma-associated antigen D2	MAGED2	MAGD2_HUMAN	65.0	100.0%	5	5	9	0.01%	11.7%	SSEAVIWEVLR	99.7%	69.7	25	40.7	2	0	0	1288.69	386	396
Melanoma-associated antigen D2	MAGED2	MAGD2_HUMAN	65.0	100.0%	5	5	9	0.01%	11.7%	VPNSNPPEYEFFWGLR	99.7%	67.5	25	66	2	0	0	1951.93	431	446
Melanoma-associated antigen G1	NDNL2	MAGG1_HUMAN	34.3	99.8%	2	2	3	0.00%	7.6%	DGFAEEAPSTSR	99.7%	42	25	27.8	1	0	0	1266.56	41	52
Melanoma-associated antigen G1	NDNL2	MAGG1_HUMAN	34.3	99.8%	2	2	3	0.00%	7.6%	VSELVQFLLIK	99.5%	37.5	25	28.1	2	0	0	1288.79	89	99
Metaxin-2	MTX2	MTX2_HUMAN	29.8	100.0%	3	3	3	0.00%	16.0%	LGTQPYFFNK	99.7%	39.6	25	37.7	1	0	0	1214.62	197	206
Metaxin-2	MTX2	MTX2_HUMAN	29.8	100.0%	3	3	3	0.00%	16.0%	NYSNLLAFCR	99.7%	51.6	25	44.7	1	0	0	1257.60	238	247
Metaxin-2	MTX2	MTX2_HUMAN	29.8	100.0%	3	3	3	0.00%	16.0%	VPFIHVGNQVVSELGPIVQFVK	99.7%	66.3	25	66.3	0	1	0	2406.35	72	93
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	38.8%	ADKNEVAAEVAK	99.7%	61.9	25	35.3	2	2	0	1244.65	864	875
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	38.8%	AEVLISTVGPEDCVVPFLTRPK	99.7%	57.8	25	57.8	0	2	0	2427.30	26	47
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	38.8%	ALEEGLTPQEICDK	99.2%	35.6	25	34.4	1	0	0	1602.77	322	335

Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	38.8%	ALTHIDHSLSR	99.7%	44.6	25	43.1	2	2	0	1249.66	120	130
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	38.8%	FFGGYVPEMVLTPDDQR	99.7%	84.8	25	78.8	4	0	0	1970.93	664	680
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	38.8%	FVEGVCPFCGYEEAR	99.7%	71	25	71	2	0	0	1819.78	400	414
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	38.8%	GFVLQDTVEQLR	99.7%	82.7	25	63.4	4	0	0	1404.75	377	388
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	38.8%	GLESLPPLRPQQNPVLPVAGER	99.7%	35.1	25	29.7	0	2	0	2367.31	243	264
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	38.8%	GVGVFGDMAQDTGIPADIWR	99.7%	128	25	128	4	0	0	2121.01	599	618
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	38.8%	ITQDIFQQLLK	99.7%	80.8	25	65.5	6	0	0	1346.77	365	375
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	38.8%	KGEDVLGSVR	99.7%	52	25	43.5	2	0	0	1059.58	109	118
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	38.8%	LENDQIESLR	99.7%	75.6	25	61.6	2	0	0	1216.62	805	814
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	38.8%	LFVSDGVPGCLPVLAAAGR	99.7%	79.6	25	72.4	2	0	0	1899.02	3	21
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	38.8%	LINAVELK	99.7%	56.6	25	41.2	2	0	0	899.56	424	431
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	38.8%	NNSELLNNLGNFINR	99.7%	108	25	103	2	0	0	1731.88	642	656
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	38.8%	NPEQVDLYQFMAK	99.7%	79.6	25	79.6	4	0	0	1582.76	542	554
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	38.8%	QLAVAEGKPPEAPK	99.7%	64.5	25	62.3	2	0	0	1434.80	882	895
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	38.8%	QPQPSPAEGR	99.2%	35.6	25	34.4	1	0	0	1066.53	205	214
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	38.8%	QQGVLALRPYLQK	99.7%	55	25	47.8	2	0	0	1513.89	192	204
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	38.8%	QWNTLYLCGTDEYGTATETK	99.7%	106	25	106	2	0	0	2351.05	302	321
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	38.8%	RLEEWLGR	99.7%	43.3	25	25.9	2	0	0	1058.57	460	467
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	38.8%	SCPVVQSSQHLFLDLPK	99.7%	73.7	25	67.1	2	0	0	1955.01	440	456
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	38.8%	TLPGSDWTPNAQFITR	99.7%	93.8	25	90.7	2	0	0	1803.90	468	483
Methionine--tRNA ligase, cytoplasmic	MARS	SYMC_HUMAN	101.1	100.0%	24	29	62	0.06%	38.8%	VPVLQLDSGNYLFSTSAICR	99.7%	153	25	153	2	0	0	2240.14	48	67
Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	MCCC2	MCCB_HUMAN	61.3	99.8%	2	2	2	0.00%	5.5%	AFYGDTLVTGFAR	99.7%	76.4	25	69.1	1	0	0	1417.71	349	361
Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	MCCC2	MCCB_HUMAN	61.3	99.8%	2	2	2	0.00%	5.5%	ISVMGGEQAANVLATITK	99.7%	53.7	25	53.7	1	0	0	1802.97	470	487
Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	MCCC1	MCCA_HUMAN	80.5	99.8%	2	2	4	0.00%	3.3%	ESLCQAALGLILK	99.7%	82	25	70	2	0	0	1415.79	506	518
Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	MCCC1	MCCA_HUMAN	80.5	99.8%	2	2	4	0.00%	3.3%	IIEEAPAPGIK	99.7%	51.3	25	47.8	2	0	0	1137.65	285	295
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	18	208	0.20%	37.7%	AHAAQVTCVAASPHK	99.7%	102	25	101	15	20	0	1547.77	165	179
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	18	208	0.20%	37.7%	AHAAQVTCVAASPHKDSVFLSCSEDNR	99.7%	88.6	25	88.6	0	2	0	2957.36	165	191
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	18	208	0.20%	37.7%	CWAGSLWLFK	99.7%	49.1	25	45.1	3	0	0	1267.63	53	62
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	18	208	0.20%	37.7%	DSVFLSCSEDNR	99.7%	78.4	25	72.5	15	0	0	1428.61	180	191
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	18	208	0.20%	37.7%	ETPPPLVPPAAR	99.7%	42.5	25	35.5	4	0	0	1244.70	4	15
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	18	208	0.20%	37.7%	EWNLPPNAPACMER	99.7%	64	25	64	17	0	0	1700.75	16	29
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	18	208	0.20%	37.7%	FCKYEHDDIVSTVSVLSSGTQAVSGSK	99.7%	95.4	25	90.5	0	2	0	2901.39	119	145
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	18	208	0.20%	37.7%	ILLWDTR	99.7%	53.3	25	48.2	25	0	0	916.53	192	198
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	18	208	0.20%	37.7%	KETPPPLVPPAAR	99.7%	50.6	25	45.1	4	0	0	1372.79	3	15
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	18	208	0.20%	37.7%	SDGALLLGASSLSGR	99.7%	130	25	123	41	0	0	1403.75	38	52
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	18	208	0.20%	37.7%	VWDLAQQVVLSSYR	99.7%	105	25	98.4	14	2	0	1663.88	151	164
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	18	208	0.20%	37.7%	YEHDDIVSTVSVLSSGTQAVSGSK	99.7%	115	25	115	12	18	0	2466.20	122	145
Methylosome protein 50	WDR77	MEP50_HUMAN	36.7	100.0%	13	18	208	0.20%	37.7%	YRSDGALLLGASSLSGR	99.7%	87.3	25	86.8	5	9	0	1722.91	36	52
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	6	8	32	0.03%	44.3%	DRSDCLGEHLYVMVNAK	99.7%	33.4	25	33.4	0	2	0	2006.94	69	85
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	6	8	32	0.03%	44.3%	GLGTGTLYIAESR	99.7%	101	25	81.9	10	0	0	1337.71	31	43
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	6	8	32	0.03%	44.3%	LEGMLSQSVSSQYNMAGVR	99.7%	115	25	106	7	3	0	2056.98	188	206
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	6	8	32	0.03%	44.3%	QQPDTEAVLNGK	99.7%	66.7	25	64.1	4	0	0	1299.65	19	30
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	6	8	32	0.03%	44.3%	SFPPPGPAEGLLR	99.7%	45	25	40.3	4	0	0	1337.72	6	18
Methylosome subunit pICln	CLNS1A	ICLN_HUMAN	26.2	100.0%	6	8	32	0.03%	44.3%	TEDSIRDYEDGMEVDTTPTVAGQFEDADVDH	99.7%	62.4	25	62.4	0	2	0	3473.45	207	237
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	3	3	8	0.01%	8.7%	GVSAVVVGADR	99.7%	64.5	25	41.2	2	0	0	1029.57	239	249
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	3	3	8	0.01%	8.7%	TALTTTISSR	99.7%	64.4	25	54	2	0	0	1050.58	351	360
Methylthioribose-1-phosphate isomerase	MRI1	MTNA_HUMAN	39.1	100.0%	3	3	8	0.01%	8.7%	VGTYQLAIVAK	99.7%	63.7	25	57.6	4	0	0	1162.68	260	270
Methyltransferase-like protein 13	METTL13	MET13_HUMAN	78.8	99.8%	2	2	4	0.00%	3.3%	LAEAVQER	99.0%	34.5	25	12.9	2	0	0	915.49	242	249
Methyltransferase-like protein 13	METTL13	MET13_HUMAN	78.8	99.8%	2	2	4	0.00%	3.3%	LATPELLETAQALER	99.7%	87.4	25	73.9	2	0	0	1654.90	660	674
Microsomal glutathione S-transferase 1	MGST1	MGST1_HUMAN	17.6	100.0%	4	7	16	0.02%	27.1%	IYHTIAYLTPLPQPNR	99.7%	81.8	25	81.8	2	2	0	1897.03	115	130
Microsomal glutathione S-transferase 1	MGST1	MGST1_HUMAN	17.6	100.0%	4	7	16	0.02%	27.1%	KVFANPEDCVAFGK	99.7%	44.9	25	38.5	2	2	0	1581.77	42	55

Microsomal glutathione S-transferase 1	MGST1	MGST1_HUMAN	17.6	100.0%	4	7	16	0.02%	27.1%	MMLMSTATAFYR	99.7%	82.5	25	82.5	7	0	0	1422.66	27	38
Microsomal glutathione S-transferase 1	MGST1	MGST1_HUMAN	17.6	100.0%	4	7	16	0.02%	27.1%	VFANPEDCVAFGK	99.7%	41	25	36.5	1	0	0	1453.68	43	55
Microtubule-associated protein 1S	MAP1S	MAP1S_HUMAN	112.2	99.8%	2	2	2	0.00%	2.4%	AVLDALLASK	99.7%	41.9	25	36	1	0	0	1000.60	991	1000
Microtubule-associated protein 1S	MAP1S	MAP1S_HUMAN	112.2	99.8%	2	2	2	0.00%	2.4%	GDNLETLVLLNPSDK	97.4%	30.5	25	30.5	1	0	0	1627.85	82	96
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	5	5	7	0.01%	1.2%	ALEFGEPVLLVGDTGCGK	99.7%	71.1	25	65.7	1	0	0	1861.94	1379	1396
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	5	5	7	0.01%	1.2%	FMLFATQNPPGLYGGR	99.7%	68.2	25	68.2	2	0	0	1768.88	1189	1204
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	5	5	7	0.01%	1.2%	IISAISELLER	99.7%	72.6	25	60.5	2	0	0	1243.73	4574	4584
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	5	5	7	0.01%	1.2%	SLLQAWGLILR	99.7%	41.1	25	33.8	1	0	0	1269.77	2860	2870
Midasin	MDN1	MDN1_HUMAN	632.8	100.0%	5	5	7	0.01%	1.2%	TSLVEYLAAVTGR	99.7%	72.9	25	62	1	0	0	1379.75	336	348
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	11	11	17	0.02%	15.9%	ADPLALAAEK	99.7%	47.5	25	36.8	1	0	0	998.55	61	70
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	11	11	17	0.02%	15.9%	AMVEAVQLIADGK	99.7%	82.8	25	77	2	0	0	1344.72	197	209
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	11	11	17	0.02%	15.9%	DLGEEALNEYLK	99.7%	60.9	25	51.2	2	0	0	1393.68	904	915
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	11	11	17	0.02%	15.9%	GVINIIPGSGGIAGQR	99.7%	45.3	25	45.3	2	0	0	1508.85	642	657
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	11	11	17	0.02%	15.9%	IPQPEEGATYEGIQK	99.7%	97.6	25	0	2	0	0	1659.82	213	227
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	11	11	17	0.02%	15.9%	LGFTGSTPIGK	99.7%	41.9	25	41.2	1	0	0	1077.59	667	677
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	11	11	17	0.02%	15.9%	LLQYCETGVK	99.7%	43.3	25	34.6	1	0	0	1210.61	779	788
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	11	11	17	0.02%	15.9%	SAACLAAGNTLVLKPAQVTPLTALK	99.7%	51.6	25	45.1	0	2	0	2508.42	605	629
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	11	11	17	0.02%	15.9%	SPLIIFNDCELDK	99.7%	56.9	25	48	1	0	0	1563.77	699	711
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	11	11	17	0.02%	15.9%	TDVAAPFGGVK	99.1%	35.1	25	30.8	1	0	0	1061.56	887	897
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	ALDH1L2	AL1L2_HUMAN	101.7	100.0%	11	11	17	0.02%	15.9%	VSYASLADVDK	99.7%	65.5	25	65.5	2	0	0	1167.59	474	484
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	20	38	0.04%	52.2%	AVIGMTAGATGAFVGTPAEVALIR	99.7%	126	25	126	4	2	0	2289.23	123	146
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	20	38	0.04%	52.2%	AVVVNAAQLASYSQSK	99.7%	96	25	92.6	3	1	0	1635.87	191	206
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	20	38	0.04%	52.2%	EEGVLTLWR	97.1%	30	25	22.6	1	0	0	1102.59	174	182
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	20	38	0.04%	52.2%	FLFGGLAGMGATVFVQPLDLVK	99.7%	53.5	25	52.4	2	1	0	2280.25	25	46
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	20	38	0.04%	52.2%	GIYTGLSAGLLR	99.7%	68.6	25	60.2	2	0	0	1220.70	79	90
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	20	38	0.04%	52.2%	ITREEGVLTLWR	94.9%	22.8	25	18.1	0	1	0	1472.82	171	182
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	20	38	0.04%	52.2%	LGIYTVLFER	99.7%	81.9	25	77.1	6	0	0	1210.68	99	108
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	20	38	0.04%	52.2%	LTGADGTPPGFLLK	99.7%	67.8	25	55.8	2	0	0	1386.76	109	122
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	20	38	0.04%	52.2%	MIDGKPEYK	95.1%	28	25	23.1	1	0	0	1096.53	252	260
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	20	38	0.04%	52.2%	MQLSGEGAK	98.7%	33.3	25	12.6	1	0	0	936.45	49	57
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	20	38	0.04%	52.2%	NGLDVLFK	99.7%	49.7	25	35.2	2	0	0	905.51	261	268
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	20	38	0.04%	52.2%	NVFNALIR	99.7%	42.8	25	24.4	4	0	0	946.55	163	170
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	20	38	0.04%	52.2%	TSFHALTSILK	99.7%	55.7	25	40	2	2	0	1217.69	63	73
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	M2OM_HUMAN	34.1	100.0%	14	20	38	0.04%	52.2%	YEGFFSLWK	95.6%	28.4	25	26.5	1	0	0	1176.57	272	280
Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20	MCAT_HUMAN	32.9	100.0%	3	3	5	0.00%	9.6%	EGITGLYR	99.3%	36	25	23.8	2	0	0	908.48	66	73
Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20	MCAT_HUMAN	32.9	100.0%	3	3	5	0.00%	9.6%	ELIRDEGVTSLYK	99.7%	41.6	25	40.9	2	0	0	1522.81	255	267
Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20	MCAT_HUMAN	32.9	100.0%	3	3	5	0.00%	9.6%	GTVLTLMR	99.6%	38.8	25	25.2	1	0	0	906.51	171	178
Mitochondrial carrier homolog 2	MTCH2	MTCH2_HUMAN	33.3	99.8%	2	2	2	0.00%	9.9%	GLFTGLTPR	99.7%	46.9	25	22.5	1	0	0	961.55	69	77
Mitochondrial carrier homolog 2	MTCH2	MTCH2_HUMAN	33.3	99.8%	2	2	2	0.00%	9.9%	VLQHYQESDKGEELGPGNVQK	97.2%	25	25	25	0	1	0	2355.16	91	111
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	26	0.02%	48.4%	FAIYETVR	99.7%	43.7	25	36.7	2	0	0	998.53	79	86
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	26	0.02%	48.4%	GALVTVGQLSCYDQAK	99.7%	96	25	96	2	0	0	1709.85	171	186
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	26	0.02%	48.4%	GEYQGVFHCAVETAK	99.7%	72	25	72	2	2	0	1695.78	232	246
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	26	0.02%	48.4%	GSQGPLPFHEK	99.7%	41.2	25	28.9	2	0	0	1196.61	92	102
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	26	0.02%	48.4%	LFSGATMASSR	99.7%	81.1	25	73.2	2	0	0	1143.55	160	170
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	26	0.02%	48.4%	LGPLAFYK	99.7%	52	25	46.7	2	0	0	908.52	247	254
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	26	0.02%	48.4%	NYAHALDGLYR	99.7%	55.5	25	55.5	2	0	0	1292.64	140	150
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	26	0.02%	48.4%	QMTYSLTR	99.7%	49.2	25	36.4	2	0	0	999.49	71	78
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	26	0.02%	48.4%	TDGILALYSGLSASLCR	99.7%	105	25	104	2	0	0	1796.92	54	70
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	26	0.02%	48.4%	VHLQTQQEVK	99.7%	51.7	25	44.2	2	0	0	1209.66	32	41
Mitochondrial dicarboxylate carrier	SLC25A10	DIC_HUMAN	31.3	100.0%	11	13	26	0.02%	48.4%	VLLGSVSGLAGGFVGTPADLVNVR	99.7%	84.8	25	84.8	2	2	0	2298.28	103	126
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	6	6	12	0.01%	30.1%	KLYPTVGKPSSS	99.6%	38.8	25	34.1	2	0	0	1263.69	155	166

Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	6	6	12	0.01%	30.1%	LYPTVGKPSSS	99.7%	43.8	25	28.3	2	0	0	1135.60	156	166
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	6	6	12	0.01%	30.1%	SVDFLLDSSLR	99.7%	78.9	25	60	2	0	0	1251.66	144	154
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	6	6	12	0.01%	30.1%	SVDFLLDSSLRK	99.7%	49.6	25	45.7	2	0	0	1379.75	144	155
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	6	6	12	0.01%	30.1%	VCAASLYVLGTATR	99.7%	91.5	25	85.4	1	0	0	1481.78	103	116
Mitochondrial fission process protein 1	MTFP1	MTFP1_HUMAN	18.0	100.0%	6	6	12	0.01%	30.1%	YLGYANEVGEAFR	99.7%	68.2	25	68.2	3	0	0	1488.71	21	33
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	9	9	15	0.01%	35.3%	GAAVNLTLVTPEK	99.7%	70.2	25	62	2	0	0	1312.75	68	80
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	9	9	15	0.01%	35.3%	GLGATLLR	98.5%	32.7	25	11.6	1	0	0	800.50	189	196
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	9	9	15	0.01%	35.3%	GVNEDTYSGILDCAR	99.7%	102	25	102	2	0	0	1669.75	259	273
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	9	9	15	0.01%	35.3%	HEGPSAFLK	99.7%	39.8	25	35.8	2	0	0	985.51	278	286
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	9	9	15	0.01%	35.3%	ILAAQGQLSAQGGAQPSVEAPAAPRPTATQLTR	99.7%	86	25	86	0	1	0	3256.74	143	175
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	9	9	15	0.01%	35.3%	IQLQDAGR	99.7%	44.2	25	22.9	2	0	0	900.49	129	136
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	9	9	15	0.01%	35.3%	LAANDFFR	99.7%	55.2	25	40.7	2	0	0	953.48	84	91
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	9	9	15	0.01%	35.3%	SEGYFGMYR	99.7%	42.1	25	34.6	1	0	0	1109.47	59	67
Mitochondrial glutamate carrier 1	SLC25A22	GHC1_HUMAN	34.5	100.0%	9	9	15	0.01%	35.3%	VYTSMSDCLIK	99.3%	36.3	25	27.4	2	0	0	1316.62	45	55
Mitochondrial import inner membrane translocase subunit Tim21	TIMM21	TIM21_HUMAN	28.2	99.8%	2	2	4	0.00%	8.5%	ENPGSGEYDFR	99.7%	67.9	25	64.2	2	0	0	1270.53	214	224
Mitochondrial import inner membrane translocase subunit Tim21	TIMM21	TIM21_HUMAN	28.2	99.8%	2	2	4	0.00%	8.5%	FYIEGSEPGK	99.6%	38.4	25	34.3	2	0	0	1126.54	195	204
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	4	4	9	0.01%	15.6%	AQGPQQQPGSEGPSYAK	99.7%	59.2	25	59.2	4	0	0	1729.81	48	64
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	4	4	9	0.01%	15.6%	IPDEFDNDPILVQQLR	99.7%	78.5	25	77	2	0	0	1911.98	98	113
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	4	4	9	0.01%	15.6%	QNLFLGSLTSR	96.1%	28.9	25	21.6	1	0	0	1235.67	335	345
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	TIM50_HUMAN	39.6	100.0%	4	4	9	0.01%	15.6%	TIALNGVEDVR	99.7%	68.1	25	56.9	2	0	0	1186.64	285	295
Mitochondrial import receptor subunit TOM22 homolog	TOMM22	TOM22_HUMAN	15.5	100.0%	2	4	9	0.01%	16.2%	LQMEQQQQLQQR	99.7%	73.5	25	62	5	0	0	1557.78	106	117
Mitochondrial import receptor subunit TOM22 homolog	TOMM22	TOM22_HUMAN	15.5	100.0%	2	4	9	0.01%	16.2%	LWGLTEMFPER	99.7%	43.8	25	40.8	4	0	0	1394.68	48	58
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	5	5	10	0.01%	17.2%	ELFPIQMEGVK	95.0%	27.9	25	20.5	1	0	0	1306.67	92	102
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	5	5	10	0.01%	17.2%	FVNWQVDGEYR	99.7%	44.2	25	44.2	2	0	0	1412.66	185	195
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	5	5	10	0.01%	17.2%	GSVDSNWIVGATLEK	99.7%	77.1	25	66.2	4	0	0	1575.80	316	330
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	5	5	10	0.01%	17.2%	MAIQTQQSK	99.0%	34.3	25	25.2	1	0	0	1050.53	176	184
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	TOM40_HUMAN	37.9	100.0%	5	5	10	0.01%	17.2%	MQDTSVSFGYQLDLPK	99.7%	78.7	25	78.7	2	0	0	1844.87	294	309
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	18	49	0.05%	26.5%	AAMDNSEIAGEKK	99.7%	40.1	25	37	1	0	0	1379.65	258	270
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	18	49	0.05%	26.5%	AVDEAADALLK	99.7%	70.8	25	53.8	4	0	0	1115.59	287	297
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	18	49	0.05%	26.5%	ELDSITPEVLPGWK	99.7%	80.3	25	79.7	4	0	0	1583.83	372	385
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	18	49	0.05%	26.5%	ERPPEEVAAR	99.7%	48.6	25	39.4	4	0	0	1153.60	196	205
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	18	49	0.05%	26.5%	EVAGAKPHITAAEGK	99.0%	29	25	29	2	1	0	1478.80	316	330
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	18	49	0.05%	26.5%	GIEQAVQSHAVAEEEAR	99.7%	53	25	52.6	0	4	0	1823.89	548	564
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	18	49	0.05%	26.5%	GVYSEETLR	99.7%	60.4	25	48.9	4	0	0	1053.52	624	632
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	18	49	0.05%	26.5%	ISSVSEVMK	94.9%	27.9	25	19	1	0	0	995.51	111	119
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	18	49	0.05%	26.5%	LFEMVLGPAAYNVPLPK	99.7%	45.4	25	43.6	2	0	0	1859.01	85	101
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	18	49	0.05%	26.5%	LHNMIVDLDNVVK	99.7%	71.8	25	69.2	2	0	0	1509.81	331	343
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	18	49	0.05%	26.5%	LSEQELQFR	99.7%	76.9	25	45.3	4	0	0	1149.59	517	525
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	18	49	0.05%	26.5%	SEFEQNLSEK	99.7%	47.1	25	39.4	3	0	0	1210.56	507	516
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	18	49	0.05%	26.5%	TSSAETPTIPLGSAVEAIK	99.7%	96.7	25	94.4	2	0	0	1872.00	582	600
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	18	49	0.05%	26.5%	TVEGALKER	99.5%	38	25	24.7	2	0	0	1002.56	276	284
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	18	49	0.05%	26.5%	VVSQYHELVVQAR	99.7%	79.6	25	75.9	4	2	0	1527.83	354	366
Mitochondrial inner membrane protein	IMMT	IMMT_HUMAN	83.7	100.0%	16	18	49	0.05%	26.5%	YSTSGSSGLTTGK	99.7%	65.7	25	64.6	3	0	0	1245.60	33	45
Mitochondrial ornithine transporter 1	SLC25A15	ORNT1_HUMAN	32.7	100.0%	3	3	5	0.00%	9.0%	IQVLSMSGK	97.7%	31	25	8.78	1	0	0	962.53	237	245
Mitochondrial ornithine transporter 1	SLC25A15	ORNT1_HUMAN	32.7	100.0%	3	3	5	0.00%	9.0%	SQNTVWSVIK	99.7%	56.8	25	45.2	2	0	0	1161.63	149	158
Mitochondrial ornithine transporter 1	SLC25A15	ORNT1_HUMAN	32.7	100.0%	3	3	5	0.00%	9.0%	TYSQVGFR	98.5%	32.7	25	21.8	2	0	0	957.48	54	61
Mitochondrial pyruvate carrier 2	MPC2	MPC2_HUMAN	14.3	100.0%	2	2	3	0.00%	15.7%	LLDKVELMLPEK	98.6%	27.7	25	15.3	0	1	0	1443.81	16	27
Mitochondrial pyruvate carrier 2	MPC2	MPC2_HUMAN	14.3	100.0%	2	2	3	0.00%	15.7%	YSLVIIPK	99.7%	41.6	25	41.6	2	0	0	932.58	85	92
Mitochondrial Rho GTPase 2	RHOT2	MIRO2_HUMAN	68.1	100.0%	4	4	6	0.01%	6.6%	ILLLGEAQVGK	99.7%	86.9	25	57.1	2	0	0	1140.70	7	17
Mitochondrial Rho GTPase 2	RHOT2	MIRO2_HUMAN	68.1	100.0%	4	4	6	0.01%	6.6%	NISELFYYAQK	98.4%	32.4	25	20	1	0	0	1375.69	154	164
Mitochondrial Rho GTPase 2	RHOT2	MIRO2_HUMAN	68.1	100.0%	4	4	6	0.01%	6.6%	SAFLQAFLGR	99.7%	70.8	25	62.1	2	0	0	1109.61	430	439

Mitochondrial Rho GTPase 2	RHOT2	MIRO2_HUMAN	68.1	100.0%	4	4	6	0.01%	6.6%	VPIILVGNK	99.5%	37.2	25	0	1	0	0	952.62	111	119
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	13	16	25	0.02%	38.0%	DSIIYLTADSPNVMTTFR	99.7%	99.4	25	99.2	4	0	0	2044.01	285	302
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	13	16	25	0.02%	38.0%	EVPEHITEEELK	99.7%	43.5	25	32.9	2	0	0	1452.72	107	118
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	13	16	25	0.02%	38.0%	HTGFLEISQHSQEFINR	99.7%	36.7	25	36.6	0	2	0	2043.00	381	397
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	13	16	25	0.02%	38.0%	LLETTEEDKQK	99.7%	58.5	25	47.1	2	0	0	1333.68	165	175
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	13	16	25	0.02%	38.0%	LNLATECLPLDK	99.7%	57.4	25	46.8	1	0	0	1386.73	329	340
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	13	16	25	0.02%	38.0%	NFLFLR	99.4%	36.9	25	11.8	2	0	0	809.47	176	181
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	13	16	25	0.02%	38.0%	NLTLDQMIR	98.6%	32.9	25	24.2	1	0	0	1103.59	350	358
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	13	16	25	0.02%	38.0%	NVDPFHIYFCNLK	99.7%	52.3	25	51	2	1	0	1666.80	237	249
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	13	16	25	0.02%	38.0%	SMQPGTSLAK	96.4%	29.2	25	19.9	1	0	0	1019.52	316	325
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	13	16	25	0.02%	38.0%	SSVQEECVSTISSSK	99.6%	38.3	25	38.3	1	0	0	1627.75	72	86
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	13	16	25	0.02%	38.0%	SSVQEECVSTISSSKDEDPLAATR	99.7%	49.2	25	49.2	0	2	0	2596.20	72	95
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	13	16	25	0.02%	38.0%	TLMECVSNTAK	99.7%	56.7	25	56.7	3	0	0	1253.59	119	129
Mitochondrial ribonuclease P protein 1	TRMT10C	MRRP1_HUMAN	47.3	100.0%	13	16	25	0.02%	38.0%	VYVIGSFVDK	99.7%	43.7	25	43.7	1	0	0	1126.61	306	315
Mitochondrial ribonuclease P protein 3	KIAA0391	MRRP3_HUMAN	67.3	100.0%	4	4	8	0.01%	7.7%	DVIDGGDQYRK	99.6%	38.6	25	30.1	1	0	0	1265.61	375	385
Mitochondrial ribonuclease P protein 3	KIAA0391	MRRP3_HUMAN	67.3	100.0%	4	4	8	0.01%	7.7%	EALLLLEDIKK	99.7%	52.8	25	47.4	2	0	0	1284.78	228	238
Mitochondrial ribonuclease P protein 3	KIAA0391	MRRP3_HUMAN	67.3	100.0%	4	4	8	0.01%	7.7%	ESQLLLNVVSQLAK	99.7%	102	25	102	3	0	0	1541.89	422	435
Mitochondrial ribonuclease P protein 3	KIAA0391	MRRP3_HUMAN	67.3	100.0%	4	4	8	0.01%	7.7%	LLDILSYLR	99.7%	68.7	25	68.7	2	0	0	1105.66	301	309
Mitochondrial thiamine pyrophosphate carrier	SLC25A19	TPC_HUMAN	35.5	100.0%	2	2	3	0.00%	5.9%	ALISPFDVIK	98.9%	34.3	25	33.3	2	0	0	1102.65	31	40
Mitochondrial thiamine pyrophosphate carrier	SLC25A19	TPC_HUMAN	35.5	100.0%	2	2	3	0.00%	5.9%	SEGPQVFYK	96.3%	29.1	25	19.5	1	0	0	1054.52	168	176
Mitochondrial translocator assembly and maintenance protein 41 homolog	TAMM41	TAM41_HUMAN	51.1	99.8%	2	2	3	0.00%	6.0%	ELYGSILQENPQVVYK	99.7%	79.8	25	78	2	0	0	1879.98	214	229
Mitochondrial translocator assembly and maintenance protein 41 homolog	TAMM41	TAM41_HUMAN	51.1	99.8%	2	2	3	0.00%	6.0%	IISVNEDVTLR	95.7%	28.6	25	26.4	1	0	0	1258.70	140	150
Mitotic spindle assembly checkpoint protein MAD2A	MAD2L1	MD2L1_HUMAN	23.5	99.8%	2	2	2	0.00%	9.3%	GIYPSETFTR	97.7%	30.9	25	28.4	1	0	0	1170.58	36	45
Mitotic spindle assembly checkpoint protein MAD2A	MAD2L1	MD2L1_HUMAN	23.5	99.8%	2	2	2	0.00%	9.3%	WQFDIECDK	96.9%	29.8	25	29.8	1	0	0	1240.53	100	108
Mitotic spindle-associated MMXD complex subunit MIP18	FAM96B	MIP18_HUMAN	17.7	99.8%	2	2	4	0.00%	17.2%	EIFDLIR	98.4%	32.6	25	21	2	0	0	905.51	45	51
Mitotic spindle-associated MMXD complex subunit MIP18	FAM96B	MIP18_HUMAN	17.7	99.8%	2	2	4	0.00%	17.2%	VGGGGVGGGLLENANPLIYQR	99.7%	75.6	25	75.6	2	0	0	2041.08	2	22
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	8	8	16	0.02%	8.3%	EDLILSLR	99.7%	47.7	25	15.8	2	0	0	958.56	239	246
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	8	8	16	0.02%	8.3%	EVFQTASER	99.7%	46.6	25	37.1	2	0	0	1066.52	308	316
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	8	8	16	0.02%	8.3%	FAEFLLPLLIEK	99.7%	77.6	25	68.1	4	0	0	1432.85	255	266
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	8	8	16	0.02%	8.3%	FQPFQDGSSGQR	96.2%	29	25	27.4	1	0	0	1353.62	701	712
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	8	8	16	0.02%	8.3%	GEWFLLGSPGS	99.0%	34.7	25	34.7	2	0	0	1149.56	1020	1030
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	8	8	16	0.02%	8.3%	LLQAAAGASAR	99.7%	84.3	25	76.8	2	0	0	1028.58	374	384
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	8	8	16	0.02%	8.3%	LPTPVLLPYKPQVIR	97.4%	25.2	25	25.2	0	2	0	1734.07	984	998
MMS19 nucleotide excision repair protein homolog	MMS19	MMS19_HUMAN	113.3	100.0%	8	8	16	0.02%	8.3%	NLLVAFR	98.0%	31.5	25	24.8	1	0	0	832.50	189	195
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	6	6	17	0.02%	22.8%	EFNLLDPK	98.9%	34.3	25	16.1	1	0	0	975.51	188	195
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	6	6	17	0.02%	22.8%	EFPSSFESLVR	99.7%	57.8	25	54.8	2	0	0	1297.64	135	145
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	6	6	17	0.02%	22.8%	ELVVLPR	99.2%	35.2	25	14.9	3	0	0	825.52	42	48
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	6	6	17	0.02%	22.8%	ITDFQFK	99.7%	42.4	25	14.6	4	0	0	898.47	35	41
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	6	6	17	0.02%	22.8%	KAYLEPEHTK	99.0%	28.8	25	28.8	0	3	0	1215.64	23	32
MOB kinase activator 2	MOB2	MOB2_HUMAN	26.9	100.0%	6	6	17	0.02%	22.8%	LVTDEDVFPTK	99.7%	73.2	25	69.2	4	0	0	1263.65	121	131
Monocarboxylate transporter 1	SLC16A1	MOT1_HUMAN	53.9	100.0%	4	5	14	0.01%	8.4%	DLHDANTDLIGR	99.7%	54.8	25	49.1	6	2	0	1339.66	225	236
Monocarboxylate transporter 1	SLC16A1	MOT1_HUMAN	53.9	100.0%	4	5	14	0.01%	8.4%	ESKEEETSIDVAGKPNEVTK	99.7%	42.7	25	42.7	0	3	0	2190.08	460	479
Monocarboxylate transporter 1	SLC16A1	MOT1_HUMAN	53.9	100.0%	4	5	14	0.01%	8.4%	KDLHDANTDLIGR	97.0%	24.7	25	24.7	0	1	0	1467.76	224	236
Monocarboxylate transporter 1	SLC16A1	MOT1_HUMAN	53.9	100.0%	4	5	14	0.01%	8.4%	LNDMYGDYK	99.7%	47.1	25	47.1	2	0	0	1118.48	412	420
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	21	22	40	0.04%	26.1%	AEIDLVCELAK	99.7%	67.7	25	55.9	2	0	0	1260.65	808	818
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	21	22	40	0.04%	26.1%	ASGLVPNVVVLVATVR	99.7%	59.1	25	59.1	2	1	0	1593.97	730	745
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	21	22	40	0.04%	26.1%	AVIELLEK	99.7%	49.7	25	16.2	2	0	0	914.56	206	213
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	21	22	40	0.04%	26.1%	DFILPISDVR	99.7%	57	25	46.6	2	0	0	1174.65	926	935
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	21	22	40	0.04%	26.1%	DIELSPEAQAK	99.7%	67.2	25	55.1	2	0	0	1200.61	881	891
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	21	22	40	0.04%	26.1%	DVDGVTDINLGK	99.7%	78.5	25	60	2	0	0	1245.63	178	189
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	21	22	40	0.04%	26.1%	EFSEIQLAR	99.7%	52.6	25	26.6	2	0	0	1092.57	531	539

Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	21	22	40	0.04%	26.1%	EIGLLADEIEIYGK	99.7%	87.4	25	84.5	2	0	0	1562.83	380	393
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	21	22	40	0.04%	26.1%	EVLSLLQEK	99.7%	47.5	25	40.7	2	0	0	1058.61	84	92
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	21	22	40	0.04%	26.1%	FQFLYDVQVPIVDK	99.7%	91.4	25	90.2	2	0	0	1710.91	855	868
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	21	22	40	0.04%	26.1%	IQNMVSSGR	99.7%	46.2	25	31.7	2	0	0	991.50	327	335
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	21	22	40	0.04%	26.1%	KITIGQGNTEK	98.7%	33.5	25	23.2	2	0	0	1188.66	586	596
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	21	22	40	0.04%	26.1%	LDIDPSTITWQR	99.7%	77	25	70.4	2	0	0	1444.74	564	575
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	21	22	40	0.04%	26.1%	LQPLSPVPSDIEISR	99.7%	56.4	25	54.5	2	0	0	1650.91	353	367
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	21	22	40	0.04%	26.1%	LVPLVNGVR	96.7%	29.6	25	26.7	1	0	0	966.61	522	530
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	21	22	40	0.04%	26.1%	MHGGGPSVTAGVPLKK	99.1%	29.5	25	29.5	0	1	0	1535.84	749	764
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	21	22	40	0.04%	26.1%	SGQPVTADDLGVTGALTVLMK	99.7%	100	25	100	1	0	0	2089.09	639	659
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	21	22	40	0.04%	26.1%	TDPSTLTEEEVSK	99.7%	70.1	25	64.4	2	0	0	1435.68	548	560
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	21	22	40	0.04%	26.1%	TIAQAVYGAK	99.7%	63.7	25	52	2	0	0	1021.57	871	880
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	21	22	40	0.04%	26.1%	VLNALKPEK	97.6%	30.8	25	26.4	2	0	0	1011.62	169	177
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	C1TM_HUMAN	105.8	100.0%	21	22	40	0.04%	26.1%	YVLVAGITPTPLGEGK	99.7%	84.8	25	84.8	2	0	0	1614.91	414	429
Motile sperm domain-containing protein 2	MOSPD2	MSPD2_HUMAN	59.7	100.0%	5	5	9	0.01%	11.4%	EISVNDLNESSIPR	99.7%	92.2	25	83	1	0	0	1572.79	74	87
Motile sperm domain-containing protein 2	MOSPD2	MSPD2_HUMAN	59.7	100.0%	5	5	9	0.01%	11.4%	IVIFDMPWLMNAAFK	99.7%	40.2	25	40.2	2	0	0	1827.92	182	196
Motile sperm domain-containing protein 2	MOSPD2	MSPD2_HUMAN	59.7	100.0%	5	5	9	0.01%	11.4%	LIAFWLER	99.7%	56.5	25	45	2	0	0	1047.60	128	135
Motile sperm domain-containing protein 2	MOSPD2	MSPD2_HUMAN	59.7	100.0%	5	5	9	0.01%	11.4%	TLIVLTNVTK	99.7%	68.2	25	68.2	2	0	0	1101.69	348	357
Motile sperm domain-containing protein 2	MOSPD2	MSPD2_HUMAN	59.7	100.0%	5	5	9	0.01%	11.4%	TWLGPEAVSLLK	99.7%	50.1	25	28	2	0	0	1313.75	200	211
mRNA export factor	RAE1	RAE1L_HUMAN	41.0	100.0%	3	3	4	0.00%	9.5%	CWEVQDSGQTIPK	99.7%	41.7	25	33.4	2	0	0	1547.72	68	80
mRNA export factor	RAE1	RAE1L_HUMAN	41.0	100.0%	3	3	4	0.00%	9.5%	NAAEELKPR	98.9%	34.3	25	27.6	1	0	0	1027.55	357	365
mRNA export factor	RAE1	RAE1L_HUMAN	41.0	100.0%	3	3	4	0.00%	9.5%	SSNPMMVLQLPER	99.7%	40.2	25	25.3	1	0	0	1533.74	160	172
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	6	7	11	0.01%	28.5%	EGDVLTPEQAR	96.6%	29.4	25	29.4	1	0	0	1214.60	178	188
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	6	7	11	0.01%	28.5%	GEVGLLFTNR	99.7%	66.3	25	58.1	2	0	0	1105.60	98	107
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	6	7	11	0.01%	28.5%	GVVTLLSDYEVCK	99.7%	81.8	25	70.9	1	0	0	1482.75	165	177
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	6	7	11	0.01%	28.5%	SPSDEYKDNLHQVSK	99.7%	40.1	25	40.1	0	2	0	1746.83	80	94
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	6	7	11	0.01%	28.5%	YLFIFSVANMR	99.7%	49.7	25	49.7	4	0	0	1360.71	39	49
mRNA turnover protein 4 homolog	MRTO4	MRT4_HUMAN	27.6	100.0%	6	7	11	0.01%	28.5%	YTEMDYAR	99.5%	37.8	25	37.8	1	0	0	1064.44	119	126
Multidrug resistance-associated protein 1	ABCC1	MRP1_HUMAN	171.6	99.8%	2	2	4	0.00%	1.6%	ITIIPQDPVLFSGSLR	99.7%	62.6	25	59.5	2	0	0	1756.00	1370	1385
Multidrug resistance-associated protein 1	ABCC1	MRP1_HUMAN	171.6	99.8%	2	2	4	0.00%	1.6%	TPSGNLVNR	99.4%	36.9	25	36.9	2	0	0	957.51	1067	1075
Multidrug resistance-associated protein 4	ABCC4	MRP4_HUMAN	149.5	99.8%	2	2	3	0.00%	1.7%	IQTFLLLDEISQR	99.7%	47.3	25	45.4	1	0	0	1575.87	386	398
Multidrug resistance-associated protein 4	ABCC4	MRP4_HUMAN	149.5	99.8%	2	2	3	0.00%	1.7%	SSLISALFR	99.7%	66.6	25	18.7	2	0	0	993.57	1082	1090
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	4	4	7	0.01%	11.8%	ACGNFGIPCELR	97.4%	30.6	25	27.9	1	0	0	1393.64	287	298
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	4	4	7	0.01%	11.8%	ASILNTWISLK	99.7%	53.8	25	47.1	2	0	0	1245.72	404	414
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	4	4	7	0.01%	11.8%	EIVLADVIDNDSWR	99.7%	87.8	25	81.7	2	0	0	1644.82	202	215
Multifunctional protein ADE2	PAICS	PUR6_HUMAN	47.1	100.0%	4	4	7	0.01%	11.8%	TKEVYELLDSPGK	99.7%	68.8	25	67	2	0	0	1478.77	18	30
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	AGALHAQVER	99.7%	40.3	25	26.7	1	0	0	1051.56	897	906
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	ALVDILSEVSK	99.7%	98.8	25	92.9	2	0	0	1173.67	180	190
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	AQDSSLHMPER	97.3%	30.3	25	30.3	1	0	0	1286.58	433	443
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	ATLQEILPEVLK	99.7%	57.6	25	45.3	2	0	0	1353.80	191	202
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	EIPSATQSPISK	99.7%	48	25	44.1	2	0	0	1257.67	1156	1167
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	EVVEQGLLK	99.7%	53.2	25	41	4	0	0	1014.58	287	295
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	FLSPPALQGYVAWLR	99.7%	51.2	25	42.6	1	0	0	1717.94	397	411
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	GNTAEGCVHETQEK	99.7%	60.5	25	57.6	2	0	0	1559.68	936	949
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	HPFSFPLENQAR	98.3%	26.9	25	26.9	0	1	0	1442.72	499	510
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	HQACLLLQK	99.3%	36	25	24.4	2	0	0	1110.61	1028	1036
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	HYGEHVCTAK	97.5%	25.4	25	25.4	0	1	0	1201.54	332	341
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	KPTSQIPETK	99.7%	41.1	25	30	4	0	0	1128.63	489	498
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	LITGLGVGR	99.7%	63.3	25	41.4	2	0	0	885.55	77	85
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	LLEYLR	99.6%	38.5	25	23.3	2	0	0	806.48	57	62
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	LLGAALPLLTK	99.7%	53.6	25	53.6	3	0	0	1109.73	308	318

Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	LPAIALDLLR	99.7%	60.7	25	48.5	2	0	0	1094.69	264	273
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	LVGSVNLFSDENVPR	99.7%	96	25	87.3	4	0	0	1645.85	232	246
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	MQFWPASYLCFR	99.7%	52.1	25	52.1	4	0	0	1605.73	296	307
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	NSPLTVPMFLSLFSR	99.7%	46.4	25	46.4	1	0	0	1724.90	990	1004
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	QLMGQVLAK	99.7%	52	25	34	2	0	0	987.57	1054	1062
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	RYCHDLGER	95.9%	23.6	25	19.1	0	1	0	1205.55	888	896
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	SCFEDPEWK	99.6%	39.3	25	39.3	1	0	0	1197.49	1045	1053
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	SPAPGAPTR	99.0%	34.6	25	20.9	3	0	0	853.45	1232	1240
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	SPLSALAR	99.7%	63.2	25	30.4	2	0	0	814.48	1290	1297
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	SPSLLQSGAK	99.7%	42.1	25	35	1	0	0	987.55	1308	1317
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	VLDLVEVLVTK	99.7%	101	25	101	2	0	0	1227.76	828	838
Myb-binding protein 1A	MYBBP1A	MBB1A_HUMAN	148.9	100.0%	27	28	57	0.05%	21.8%	VYSTALSSFLTK	99.7%	90.9	25	78.9	4	0	0	1316.71	977	988
Myosin light polypeptide 6	MYL6	MYL6_HUMAN	16.9	100.0%	6	6	13	0.01%	47.7%	ALGQNPTNAEVLK	99.7%	61.9	25	49.9	2	0	0	1354.73	38	50
Myosin light polypeptide 6	MYL6	MYL6_HUMAN	16.9	100.0%	6	6	13	0.01%	47.7%	EAFQLFDR	99.7%	43.9	25	41.6	3	0	0	1025.51	14	21
Myosin light polypeptide 6	MYL6	MYL6_HUMAN	16.9	100.0%	6	6	13	0.01%	47.7%	HVLVTLGEK	98.9%	34.2	25	32.5	4	0	0	995.59	111	119
Myosin light polypeptide 6	MYL6	MYL6_HUMAN	16.9	100.0%	6	6	13	0.01%	47.7%	ILYSQCGDVMR	99.7%	51.5	25	51.5	2	0	0	1357.62	27	37
Myosin light polypeptide 6	MYL6	MYL6_HUMAN	16.9	100.0%	6	6	13	0.01%	47.7%	NKDQGTYEDYVEGLR	99.7%	71	25	69.7	1	0	0	1786.82	80	94
Myosin light polypeptide 6	MYL6	MYL6_HUMAN	16.9	100.0%	6	6	13	0.01%	47.7%	VFDKEGNGTVMGAEIR	96.2%	23.9	25	0	0	1	0	1722.85	95	110
Myosin regulatory light chain 12A	MYL12A	ML12A_HUMAN,ML12B_HUMAN	19.8	100.0%	3	3	8	0.01%	18.7%	FTDEEVDELYR	99.7%	66.5	25	66.5	2	0	0	1415.63	133	143
Myosin regulatory light chain 12A	MYL12A	ML12A_HUMAN,ML12B_HUMAN	19.8	100.0%	3	3	8	0.01%	18.7%	GNFNYIEFTR	99.7%	72.3	25	68.8	4	0	0	1260.60	151	160
Myosin regulatory light chain 12A	MYL12A	ML12A_HUMAN,ML12B_HUMAN	19.8	100.0%	3	3	8	0.01%	18.7%	LNGTDPEDVIR	99.7%	54.1	25	46.7	2	0	0	1228.62	93	103
Myosin-10	MYH10	MYH10_HUMAN	229.0	100.0%	3	3	4	0.00%	2.5%	ALELDPNLYR	99.7%	42.2	25	39.5	2	0	0	1203.64	753	762
Myosin-10	MYH10	MYH10_HUMAN	229.0	100.0%	3	3	4	0.00%	2.5%	LDPHLVLDQLR	99.7%	40.8	25	34.3	1	0	0	1318.75	690	700
Myosin-10	MYH10	MYH10_HUMAN	229.0	100.0%	3	3	4	0.00%	2.5%	QLLQANPILESFGNAK	99.7%	66.6	25	66.6	1	0	0	1742.94	217	232
Myosin-10	MYH10	MYH10_HUMAN	229.0	100.0%	3	3	4	0.00%	2.5%	SDLLLEGFNNYR	99.7%	42.4	25	42.4	1	0	0	1440.71	297	308
Myosin-9	MYH9	MYH9_HUMAN	226.5	100.0%	3	3	4	0.00%	2.1%	LDPHLVLDQLR	99.7%	40.8	25	34.3	1	0	0	1318.75	683	693
Myosin-9	MYH9	MYH9_HUMAN	226.5	100.0%	3	3	4	0.00%	2.1%	QLLQANPILEAFGNAK	99.7%	75	25	68	2	0	0	1726.95	210	225
Myosin-9	MYH9	MYH9_HUMAN	226.5	100.0%	3	3	4	0.00%	2.1%	VISGVLQLGNIVFK	99.7%	46.7	25	46.7	1	0	0	1486.90	342	355
N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	DDAH2	DDAH2_HUMAN	29.6	99.8%	2	2	2	0.00%	9.1%	GGGDLPNSQEALQK	99.7%	54.8	25	53.5	1	0	0	1413.70	238	251
N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	DDAH2	DDAH2_HUMAN	29.6	99.8%	2	2	2	0.00%	9.1%	TVVAGSSDAAQK	99.3%	36.1	25	33.4	1	0	0	1133.58	183	194
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	13	0.01%	9.3%	AGFVPVYLR	99.0%	34.5	25	22.9	2	0	0	1021.58	726	734
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	13	0.01%	9.3%	ASEVFLQR	99.7%	71.1	25	48.7	1	0	0	949.51	521	528
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	13	0.01%	9.3%	EELEALFLPYDLK	99.1%	35.1	25	32.2	1	0	0	1579.83	811	823
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	13	0.01%	9.3%	ILIENGVAER	99.7%	61.2	25	50.1	2	0	0	1113.63	12	21
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	13	0.01%	9.3%	LDYLGVSYGLTPR	99.7%	72.3	25	56.9	2	0	0	1453.77	706	718
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	13	0.01%	9.3%	LFNEVQEK	96.5%	29.3	25	15.1	1	0	0	1006.52	905	912
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	13	0.01%	9.3%	QQSAQSQVSTTAENK	99.7%	73.2	25	68.1	1	0	0	1606.77	433	447
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	13	0.01%	9.3%	SLFVVVGDR	99.7%	51.2	25	41	2	0	0	991.56	24	32
N-acetyltransferase 10	NAT10	NAT10_HUMAN	115.7	100.0%	9	9	13	0.01%	9.3%	TEAHQDVVGR	99.7%	43.7	25	43.7	1	0	0	1111.55	173	182
N-acetyltransferase 14	NAT14	NAT14_HUMAN	21.7	100.0%	3	3	4	0.00%	19.4%	APSHLSVR	99.1%	34.9	25	34.9	1	0	0	866.48	2	9
N-acetyltransferase 14	NAT14	NAT14_HUMAN	21.7	100.0%	3	3	4	0.00%	19.4%	AWAGGMGEPR	99.7%	51.7	25	51.7	1	0	0	1031.47	153	162
N-acetyltransferase 14	NAT14	NAT14_HUMAN	21.7	100.0%	3	3	4	0.00%	19.4%	GSGDVCGVLALAPGTNAGDGAR	99.7%	66.5	25	66.5	2	0	0	2014.96	103	124
N-acylneuraminate cytidylyltransferase	CMAS	NEUA_HUMAN	48.4	99.8%	2	2	2	0.00%	6.5%	EVTEPLNLNPAK	97.7%	31	25	27.9	1	0	0	1324.71	189	200
N-acylneuraminate cytidylyltransferase	CMAS	NEUA_HUMAN	48.4	99.8%	2	2	2	0.00%	6.5%	VGLSGAPADACSTAQK	99.7%	46.5	25	46.5	1	0	0	1532.74	384	399
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	5	5	10	0.01%	6.4%	AQYPIADLVK	99.0%	34.4	25	19.4	2	0	0	1117.63	940	949
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	5	5	10	0.01%	6.4%	FFTGQITAAGK	99.7%	60.7	25	55.9	3	0	0	1140.60	214	224
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	5	5	10	0.01%	6.4%	MATQASTLYSNNITK	99.7%	53.2	25	53.2	1	0	0	1658.81	380	394
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	5	5	10	0.01%	6.4%	TSGTLISFIYPAQNPELLNK	99.7%	57	25	57	2	0	0	2206.18	147	166
NAD(P) transhydrogenase, mitochondrial	NNT	NNTM_HUMAN	113.9	100.0%	5	5	10	0.01%	6.4%	VALSPAGVQNLVK	99.7%	80	25	71.5	2	0	0	1295.77	72	84
NAD(P)H-hydrate epimerase	APOA1BP	NNRE_HUMAN	31.7	99.8%	2	2	3	0.00%	10.4%	GNAGGIQPDLLISLTAPK	97.4%	30.5	25	30.5	1	0	0	1764.99	228	245
NAD(P)H-hydrate epimerase	APOA1BP	NNRE_HUMAN	31.7	99.8%	2	2	3	0.00%	10.4%	LFGYEPTIYYPK	99.7%	47.8	25	38.1	2	0	0	1490.76	133	144

NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4	NDUFAF4	NDUF4_HUMAN	20.3	99.8%	2	2	3	0.00%	11.4%	EQISLYPEVK	99.6%	38.9	25	35.1	2	0	0	1205.64	42	51
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4	NDUFAF4	NDUF4_HUMAN	20.3	99.8%	2	2	3	0.00%	11.4%	IMQEYQLEQK	99.7%	42.6	25	32.8	1	0	0	1325.64	138	147
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	4	4	5	0.00%	11.0%	CEVLQYSAR	99.6%	38.7	25	33.4	1	0	0	1125.54	253	261
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	4	4	5	0.00%	11.0%	LQSWLYSSR	96.2%	29	25	10.3	1	0	0	1139.58	131	139
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	4	4	5	0.00%	11.0%	VITVDGNICTGK	99.7%	65.8	25	61.2	2	0	0	1276.66	59	70
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	NDUAA_HUMAN	40.8	100.0%	4	4	5	0.00%	11.0%	VVEDIEYLK	97.9%	31.4	25	27.6	1	0	0	1107.59	269	277
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	100.0%	5	6	14	0.01%	36.6%	FNVTGTPEQYVPYSTTR	99.7%	64.9	25	64.9	4	0	0	1959.94	115	131
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	100.0%	5	6	14	0.01%	36.6%	GLQQITGHGGLR	99.7%	65.4	25	60.2	3	2	0	1236.68	10	21
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	100.0%	5	6	14	0.01%	36.6%	VGTLVGEDK	99.7%	51.1	25	16.7	2	0	0	917.49	35	43
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	100.0%	5	6	14	0.01%	36.6%	VGTLVGEDKYGNK	98.9%	34.2	25	34.2	1	0	0	1379.72	35	47
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	NDUAC_HUMAN	17.1	100.0%	5	6	14	0.01%	36.6%	YYEDNKQFFGR	99.7%	54.2	25	54.2	2	0	0	1466.67	48	58
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	NDUAD_HUMAN	16.7	100.0%	5	6	11	0.01%	30.6%	ENLEEEAIIMK	99.7%	77	25	77	4	0	0	1334.65	89	99
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	NDUAD_HUMAN	16.7	100.0%	5	6	11	0.01%	30.6%	IALLPLLQAETDR	99.7%	51.4	25	51.4	2	0	0	1452.84	69	81
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	NDUAD_HUMAN	16.7	100.0%	5	6	11	0.01%	30.6%	LQIEDFEAR	99.7%	55.9	25	46.1	2	0	0	1120.56	60	68
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	NDUAD_HUMAN	16.7	100.0%	5	6	11	0.01%	30.6%	RLQIEDFEAR	94.7%	27.8	25	22.5	1	0	0	1276.66	59	68
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	NDUAD_HUMAN	16.7	100.0%	5	6	11	0.01%	30.6%	VGESVFHTTR	99.7%	74.7	25	62.6	2	0	0	1132.57	106	115
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	NDUFA4	NDUA4_HUMAN	9.4	100.0%	3	3	5	0.00%	32.1%	FYSVNVDYSK	99.7%	58.8	25	51.5	2	0	0	1221.58	64	73
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	NDUFA4	NDUA4_HUMAN	9.4	100.0%	3	3	5	0.00%	32.1%	LGPNDQYK	99.7%	41.5	25	29	1	0	0	934.46	56	63
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	NDUFA4	NDUA4_HUMAN	9.4	100.0%	3	3	5	0.00%	32.1%	NNPEPWNK	98.6%	33.1	25	33.1	2	0	0	998.47	48	55
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	NDUA5_HUMAN	13.5	100.0%	3	4	8	0.01%	31.0%	ILDVLEEIPK	99.7%	54.8	25	48.1	2	0	0	1168.68	31	40
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	NDUA5_HUMAN	13.5	100.0%	3	4	8	0.01%	31.0%	KYTEQITNEK	99.7%	40.5	25	32.2	2	0	0	1253.64	46	55
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	NDUA5_HUMAN	13.5	100.0%	3	4	8	0.01%	31.0%	TTGLVGLAVCNTPHER	99.7%	66.7	25	66.7	2	2	0	1724.88	8	23
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	NDUFA6	NDUA6_HUMAN	17.9	100.0%	3	4	8	0.01%	18.8%	FFHETEAPRPK	99.7%	44.1	25	40.3	2	2	0	1358.69	132	142
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	NDUFA6	NDUA6_HUMAN	17.9	100.0%	3	4	8	0.01%	18.8%	GKIELEETIK	97.0%	29.9	25	21.3	1	0	0	1159.66	112	121
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	NDUFA6	NDUA6_HUMAN	17.9	100.0%	3	4	8	0.01%	18.8%	VVDLLVIK	99.7%	49.6	25	49.2	3	0	0	898.60	104	111
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	12	13	23	0.02%	38.5%	DAFPEAIIVKPSDIFGR	99.6%	38.7	25	38.7	2	0	0	1875.00	193	209
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	12	13	23	0.02%	38.5%	FGPIPLGSLGWK	97.7%	31	25	29.9	2	0	0	1271.71	223	234
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	12	13	23	0.02%	38.5%	FLNSFASMHR	95.5%	28.4	25	19.8	1	0	0	1225.58	213	222
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	12	13	23	0.02%	38.5%	MGSQVIIPYR	99.7%	59.5	25	54.5	4	0	0	1163.62	76	85
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	12	13	23	0.02%	38.5%	NFDFEDVFVK	99.7%	48.4	25	15.6	2	0	0	1259.59	138	147
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	12	13	23	0.02%	38.5%	QPVYVVDVSK	99.7%	57.2	25	54.2	2	0	0	1133.62	238	247
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	12	13	23	0.02%	38.5%	SFAFVGPSR	99.7%	49.6	25	37.5	2	0	0	967.50	262	270
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	12	13	23	0.02%	38.5%	SSVSGIVATVFGATGFLGR	99.7%	69.5	25	69.5	2	0	0	1825.98	49	67
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	12	13	23	0.02%	38.5%	VFEISPFEPWITR	99.7%	71	25	62.8	2	0	0	1620.84	304	316
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	12	13	23	0.02%	38.5%	VVQHSNVVINLIGR	99.7%	61.3	25	61.3	1	0	0	1547.90	119	132
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	12	13	23	0.02%	38.5%	WLSAEIEDVKPAK	99.7%	63.2	25	50	1	0	0	1485.79	361	373
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	NDUA9_HUMAN	42.5	100.0%	12	13	23	0.02%	38.5%	YVVNHLGR	98.9%	34.2	25	26.6	2	0	0	957.53	68	75
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	NDUFB4	NDUB4_HUMAN	15.2	100.0%	4	5	14	0.01%	41.1%	EYLLQYNDPNRR	99.7%	41.3	25	39.3	1	2	0	1580.78	46	57
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	NDUFB4	NDUB4_HUMAN	15.2	100.0%	4	5	14	0.01%	41.1%	GLIENPALLR	99.7%	68.2	25	57.9	4	0	0	1095.65	58	67
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	NDUFB4	NDUB4_HUMAN	15.2	100.0%	4	5	14	0.01%	41.1%	TINVYPNFRPTPK	99.7%	53	25	50.9	4	0	0	1546.84	73	85
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	NDUFB4	NDUB4_HUMAN	15.2	100.0%	4	5	14	0.01%	41.1%	TLPETLDPAEYNISPETR	99.7%	85.3	25	85.3	3	0	0	2046.00	13	30
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	99.8%	2	2	3	0.00%	4.3%	EAYEAGLIGK	99.7%	47.7	25	45.1	1	0	0	1050.55	175	184
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	NDUV1_HUMAN	50.8	99.8%	2	2	3	0.00%	4.3%	GGAGFPTGLK	96.3%	29.1	25	24.1	2	0	0	904.49	89	98
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	4	4	6	0.01%	11.4%	GEFGVYLVSDGSSRPYR	98.5%	32.9	25	31.8	1	0	0	1888.92	405	421
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	4	4	6	0.01%	11.4%	MFEFYER	99.3%	36.2	25	33.3	2	0	0	1021.44	210	216
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	4	4	6	0.01%	11.4%	NITLNFGPQHPAAHGVLR	99.7%	37.5	25	36.8	0	2	0	1942.04	79	96
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	NDUS2_HUMAN	52.5	100.0%	4	4	6	0.01%	11.4%	TYLQALPYFDR	98.0%	31.6	25	31.6	1	0	0	1386.71	128	138
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	15	0.01%	39.4%	AANWYER	99.7%	45.1	25	45.1	2	0	0	909.42	162	168
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	15	0.01%	39.4%	DFPLSGYVELR	99.7%	66.5	25	52	2	0	0	1295.66	201	211
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	15	0.01%	39.4%	ESAGADTRPTVRPR	98.9%	28.4	25	24.8	0	1	0	1512.79	37	50
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	15	0.01%	39.4%	FDLNSPWEAFPVYR	99.7%	42.5	25	42.5	2	0	0	1740.84	233	246

NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	15	0.01%	39.4%	ILTDYGFEGHPFR	99.7%	81.1	25	81.1	2	0	0	1551.76	187	199
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	15	0.01%	39.4%	QLSAFGEYVAEILPK	99.7%	65	25	65	2	0	0	1664.89	57	71
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	15	0.01%	39.4%	SLVDLTAVDVPTR	99.7%	96.3	25	92.9	2	0	0	1385.76	110	122
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	NDUS3_HUMAN	30.2	100.0%	8	8	15	0.01%	39.4%	TYTDELTPIESAVSVFK	99.7%	56.7	25	50.4	2	0	0	1899.96	145	161
NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	NDUFS6	NDUS6_HUMAN	13.7	99.8%	2	2	4	0.00%	21.8%	TGTCGYCGLQFR	98.5%	32.7	25	32.5	2	0	0	1419.61	109	120
NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	NDUFS6	NDUS6_HUMAN	13.7	99.8%	2	2	4	0.00%	21.8%	VIACDGGGGALGHPK	99.7%	54	25	42.5	2	0	0	1408.70	84	98
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	NDUS7_HUMAN	23.6	100.0%	4	6	17	0.02%	17.8%	LDDLVNWAR	99.7%	76.8	25	61.8	4	0	0	1101.57	67	75
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	NDUS7_HUMAN	23.6	100.0%	4	6	17	0.02%	17.8%	LQIWYR	96.1%	28.9	25	21.5	1	0	0	878.49	207	212
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	NDUS7_HUMAN	23.6	100.0%	4	6	17	0.02%	17.8%	QSDVMIVAGTLTNK	99.7%	122	25	109	8	0	0	1492.77	116	129
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	NDUS7_HUMAN	23.6	100.0%	4	6	17	0.02%	17.8%	VYDQMPEPR	99.7%	55.5	25	55.5	4	0	0	1134.52	137	145
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	NDUS8_HUMAN	23.7	100.0%	3	5	10	0.01%	18.1%	GLGMTLSYLFR	99.7%	67.9	25	66.7	3	0	0	1257.67	67	77
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	NDUS8_HUMAN	23.7	100.0%	3	5	10	0.01%	18.1%	LCEAICPAQAITIEAEPR	99.7%	81.8	25	81.8	2	1	0	2042.00	116	133
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	NDUS8_HUMAN	23.7	100.0%	3	5	10	0.01%	18.1%	TLLWTELFR	99.7%	58.3	25	51.2	4	0	0	1178.66	58	66
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	15	27	0.03%	26.3%	ALSEIAGMTLPYDTLDQVR	99.7%	84.7	25	84.7	3	0	0	2093.06	625	643
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	15	27	0.03%	26.3%	FASEIAGVDDLGTTGR	99.7%	121	25	118	2	0	0	1608.79	185	200
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	15	27	0.03%	26.3%	FAYDGLKR	97.8%	31.2	25	23.3	1	0	0	969.52	292	299
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	15	27	0.03%	26.3%	FEAPLFNAR	99.7%	52.1	25	43.2	2	0	0	1064.55	409	417
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	15	27	0.03%	26.3%	GLLTYTSWEDALSR	99.7%	110	25	105	2	0	0	1611.80	312	325
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	15	27	0.03%	26.3%	GWNILTNSEK	99.2%	35.3	25	26.8	1	0	0	1161.59	99	108
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	15	27	0.03%	26.3%	ILQDIASGSHPFSQVLK	99.7%	51.7	25	51.7	0	2	0	1840.00	451	467
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	15	27	0.03%	26.3%	LVNQQLLADPLVPPQLTIK	99.7%	56	25	56	2	0	0	2100.24	674	692
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	15	27	0.03%	26.3%	NDGAAILAAVSSIAQK	99.7%	118	25	115	3	0	0	1528.83	484	499
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	15	27	0.03%	26.3%	SATYVNTEGR	99.7%	49.7	25	45.3	2	0	0	1097.52	593	602
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	15	27	0.03%	26.3%	VALIGSPVDLTYTYDHLGDSPK	98.1%	26.4	25	26.4	0	2	0	2361.20	429	450
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	15	27	0.03%	26.3%	VAVTPPGLAR	99.2%	35.6	25	35.1	2	0	0	980.59	608	617
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	15	27	0.03%	26.3%	VLFLLGADGGCITR	99.7%	92.1	25	85.6	2	0	0	1491.80	544	557
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	NDUS1_HUMAN	79.5	100.0%	14	15	27	0.03%	26.3%	VMNILHR	97.9%	31.3	25	25.6	1	0	0	882.50	512	518
NADH-ubiquinone oxidoreductase chain 1	MT-ND1	NU1M_HUMAN	35.7	99.8%	2	2	3	0.00%	8.5%	GPNVVGPYGLLQPFADAMK	99.7%	50.4	25	50.4	1	0	0	1974.02	36	54
NADH-ubiquinone oxidoreductase chain 1	MT-ND1	NU1M_HUMAN	35.7	99.8%	2	2	3	0.00%	8.5%	ILGYMQLR	99.7%	53.1	25	45.3	2	0	0	993.56	27	34
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	7	8	22	0.02%	31.1%	AMIENFNAK	99.6%	39.3	25	38.9	2	0	0	1053.50	97	105
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	7	8	22	0.02%	31.1%	DLTQMADELRR	99.1%	35.2	25	27.5	2	0	0	1347.67	150	160
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	7	8	22	0.02%	31.1%	HVVLGAIENKVESK	99.7%	34.1	25	34.1	0	3	0	1522.86	170	183
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	7	8	22	0.02%	31.1%	MEEDPDDVPHGHITSLAVK	99.7%	63.9	25	61.6	0	5	0	2105.98	60	78
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	7	8	22	0.02%	31.1%	YVSLHVR	99.7%	40.4	25	30.5	3	0	0	873.49	106	112
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	7	8	22	0.02%	31.1%	YYADGEDAYAMK	99.7%	54.5	25	54.5	4	0	0	1396.57	137	148
N-alpha-acetyltransferase 10	NAA10	NAA10_HUMAN	26.5	100.0%	7	8	22	0.02%	31.1%	YYADGEDAYAMKR	99.7%	63.9	25	61.6	3	0	0	1568.67	137	149
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	29	52	0.05%	25.6%	AIELATTLDESLTNR	99.7%	111	25	93.4	2	0	0	1646.86	783	797
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	29	52	0.05%	25.6%	ALKPANMLER	99.7%	51.4	25	35.5	2	0	0	1142.64	267	276
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	29	52	0.05%	25.6%	DLSLLQIQMR	99.7%	88	25	76.8	4	0	0	1216.67	119	128
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	29	52	0.05%	25.6%	EALEHLCTYEK	99.7%	49.1	25	33.8	2	0	0	1392.65	208	218
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	29	52	0.05%	25.6%	EEAYELVR	99.3%	35.8	25	24.6	2	0	0	1008.50	63	70
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	29	52	0.05%	25.6%	FAEHGETLAMK	99.7%	47	25	40	4	1	0	1233.59	42	52
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	29	52	0.05%	25.6%	FLLMLQSVK	99.7%	48.6	25	28.3	4	0	0	1078.63	688	696
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	29	52	0.05%	25.6%	GCPPVFNTLR	99.6%	38.9	25	25.2	2	0	0	1160.59	321	330
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	29	52	0.05%	25.6%	GLTLNCLGK	99.7%	40.2	25	26.6	2	0	0	975.53	53	61
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	29	52	0.05%	25.6%	IAIEIYLK	99.7%	51.6	25	46.5	2	0	0	962.59	560	567
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	29	52	0.05%	25.6%	ILEEFRK	99.5%	38.1	25	31.8	2	0	0	934.54	170	176
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	29	52	0.05%	25.6%	IYEEAWTK	98.7%	33.2	25	26.4	2	0	0	1039.51	279	286
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	29	52	0.05%	25.6%	KEEAYELVR	99.7%	52.5	25	42.1	2	0	0	1136.59	62	70
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	29	52	0.05%	25.6%	LEDAADVYR	99.7%	73.1	25	67	2	0	0	1051.51	240	248
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	29	52	0.05%	25.6%	LFGATNPK	98.9%	34	25	14.4	1	0	0	847.47	741	748

N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	29	52	0.05%	25.6%	LFNTAVCESK	99.7%	66.1	25	56.7	2	0	0	1168.57	715	724
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	29	52	0.05%	25.6%	LPLNFLSGEK	99.7%	51.1	25	39.5	2	0	0	1117.63	296	305
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	29	52	0.05%	25.6%	MVYYLDPSSQK	99.7%	54.5	25	44	4	0	0	1346.63	771	781
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	29	52	0.05%	25.6%	NFNETFLK	96.9%	29.8	25	13.2	1	0	0	1012.51	749	756
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	29	52	0.05%	25.6%	NPENWAYYK	99.7%	59.4	25	57.6	2	0	0	1184.54	254	262
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	29	52	0.05%	25.6%	RLPLNFLSGEK	99.7%	40.9	25	35.7	1	0	0	1273.73	295	305
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	29	52	0.05%	25.6%	VAIIEELVVGYETSLK	99.7%	65.3	25	65.3	2	0	0	1762.98	339	354
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	29	52	0.05%	25.6%	VETPLEEAIK	97.3%	30.4	25	17.3	1	0	0	1128.61	650	659
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	NAA15_HUMAN	101.3	100.0%	24	29	52	0.05%	25.6%	WMDEAQALDTADR	99.7%	77.2	25	77.2	1	0	0	1521.66	430	442
N-alpha-acetyltransferase 20	NAA20	NAA20_HUMAN	20.4	100.0%	5	6	11	0.01%	30.3%	AFTCDDLFR	99.7%	45.1	25	39.8	2	0	0	1144.51	6	14
N-alpha-acetyltransferase 20	NAA20	NAA20_HUMAN	20.4	100.0%	5	6	11	0.01%	30.3%	LMELLEEISER	99.7%	86.7	25	79.1	4	0	0	1377.69	92	102
N-alpha-acetyltransferase 20	NAA20	NAA20_HUMAN	20.4	100.0%	5	6	11	0.01%	30.3%	QLGYSVYR	99.7%	43.8	25	34.4	2	0	0	985.51	125	132
N-alpha-acetyltransferase 20	NAA20	NAA20_HUMAN	20.4	100.0%	5	6	11	0.01%	30.3%	SIIPLPHPVRPEDIE	99.7%	43.4	25	43.4	1	0	0	1711.94	164	178
N-alpha-acetyltransferase 20	NAA20	NAA20_HUMAN	20.4	100.0%	5	6	11	0.01%	30.3%	VSNQVAVNMYK	99.7%	55.5	25	55.5	2	0	0	1252.64	114	124
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	14.5%	DIQYPFLGPVPTR	99.7%	52.8	25	45.8	2	0	0	1502.80	748	760
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	14.5%	DTSEYIIQAYK	99.7%	66.2	25	63.9	2	0	0	1330.65	576	586
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	14.5%	IPEFIAFR	99.7%	56.5	25	36.9	2	0	0	992.56	593	600
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	14.5%	LALPADIR	99.7%	42.6	25	26.5	2	0	0	868.53	402	409
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	14.5%	LGDPEELMFQYFK	99.7%	51.7	25	50.3	1	0	0	1616.77	345	357
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	14.5%	LLLQQLEATLETGK	99.7%	71.7	25	71.7	1	0	0	1556.89	729	742
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	14.5%	LLLQQLEATLETGKR	99.6%	32.8	25	27.6	0	2	0	1712.99	729	743
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	14.5%	LNNSLHFAQVR	98.6%	27.7	25	24.4	0	1	0	1298.70	603	613
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	14.5%	LSLEEETLWLR	99.7%	60.2	25	54.7	2	0	0	1388.74	678	688
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	14.5%	LTSEIQSR	99.3%	35.9	25	21.4	2	0	0	933.50	224	231
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	14.5%	SLLDQLKDVFSK	99.7%	76.5	25	65.6	2	0	0	1392.77	807	818
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	14.5%	TMFLPLAER	96.3%	29.1	25	26.3	1	0	0	1077.58	171	179
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	14.5%	VFVDLLPATQCTK	98.9%	33.9	25	29.6	2	0	0	1491.79	371	383
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	NAA25_HUMAN	112.3	100.0%	14	14	24	0.02%	14.5%	YQEALDVIR	99.7%	47.2	25	37.2	2	0	0	1106.58	209	217
Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACA	NACAM_HUMAN,NACA_HUMAN	205.4	99.8%	2	2	3	0.00%	1.4%	IEDLSQQAQLAAAEK	99.7%	106	25	97.5	2	0	0	1614.83	1991	2005
Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACA	NACAM_HUMAN,NACA_HUMAN	205.4	99.8%	2	2	3	0.00%	1.4%	SPASDTYIVFGEAK	99.7%	93	25	89.7	1	0	0	1484.73	1977	1990
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	7	7	11	0.01%	7.5%	AAEDLFVNIR	99.7%	57.1	25	47.5	2	0	0	1147.61	306	315
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	7	7	11	0.01%	7.5%	ASLGLADHR	99.7%	67.6	25	56	2	0	0	939.50	502	510
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	7	7	11	0.01%	7.5%	ELATVLSDQPGLLGPK	99.7%	86.4	25	86.4	2	0	0	1637.91	352	367
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	7	7	11	0.01%	7.5%	LVVENVDVLTQMR	99.7%	61.4	25	61.4	1	0	0	1531.82	869	881
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	7	7	11	0.01%	7.5%	MFQQCLELPSQSR	97.1%	30.1	25	20.9	1	0	0	1623.76	552	564
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	7	7	11	0.01%	7.5%	NNNQQLAQLQK	99.7%	50.2	25	42.8	1	0	0	1298.68	71	81
Nck-associated protein 1	NCKAP1	NCKP1_HUMAN	128.8	100.0%	7	7	11	0.01%	7.5%	SLSELLGPYGMK	99.6%	38.9	25	30.8	2	0	0	1294.67	838	849
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	9	9	18	0.02%	22.7%	DAAAVGNHVAK	99.7%	62.1	25	48.5	2	0	0	1052.55	353	363
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	9	9	18	0.02%	22.7%	EGQGNLPVR	96.2%	29	25	25.3	2	0	0	969.51	318	326
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	9	9	18	0.02%	22.7%	FTVVVATQLPESTSLR	99.7%	94.5	25	94.5	2	0	0	1747.96	123	138
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	9	9	18	0.02%	22.7%	GTIPDMIADSGK	98.7%	33.2	25	25	2	0	0	1204.59	327	338
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	9	9	18	0.02%	22.7%	LADVLWNSQIPLLICR	99.7%	73.4	25	73.4	2	0	0	1911.05	139	154
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	9	9	18	0.02%	22.7%	LLCSNSAFLR	99.7%	49.1	25	35	2	0	0	1180.61	382	391
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	9	9	18	0.02%	22.7%	TYGLVGYMR	99.7%	54.1	25	41.2	2	0	0	1059.53	155	163
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	9	9	18	0.02%	22.7%	YGAAEPHTIAAFLGGAAAQEVIK	99.7%	35.4	25	33.1	0	2	0	2285.19	485	507
NEDD8-activating enzyme E1 regulatory subunit	NAE1	ULA1_HUMAN	60.2	100.0%	9	9	18	0.02%	22.7%	YPGVSNYQVEEDIGK	99.7%	71.5	25	71.5	2	0	0	1697.80	442	456
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	4	4	6	0.01%	5.6%	ATLEMVNHEK	98.7%	33.3	25	25	1	0	0	1171.58	159	168
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	4	4	6	0.01%	5.6%	EIEAEIQALR	99.7%	57.4	25	41.3	1	0	0	1171.63	128	137
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	4	4	6	0.01%	5.6%	EYQDLLNVK	99.7%	55.2	25	43.9	6	0	0	1121.58	383	391
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	4	4	6	0.01%	5.6%	LRDDTEAAIR	99.7%	45.3	25	33.4	2	0	0	1159.61	195	204
Neurofilament medium polypeptide	NEFM	NFM_HUMAN	102.5	100.0%	4	4	6	0.01%	5.6%	VQSLQDEVAFLR	99.7%	70.6	25	59.3	2	0	0	1404.75	224	235

Neutral alpha-glucosidase AB	GANAB	GANAB_HUMAN	106.9	99.8%	2	2	2	0.00%	2.2%	SLLLSVNAR	99.6%	38.2	25	28	1	0	0	972.58	165	173
Neutral alpha-glucosidase AB	GANAB	GANAB_HUMAN	106.9	99.8%	2	2	2	0.00%	2.2%	VLLVLELQGLQK	99.7%	39.7	25	39.7	1	0	0	1352.85	85	96
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	8	8	39	0.04%	18.9%	EVLDSFLDLAR	99.7%	83.5	25	74.9	8	0	0	1277.67	179	189
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	8	8	39	0.04%	18.9%	GPAGDATVASEK	99.7%	51.3	25	44.4	1	0	0	1102.54	526	537
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	8	8	39	0.04%	18.9%	IVEMEDVGLLFAR	99.7%	77.5	25	76.6	4	0	0	1491.79	289	301
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	8	8	39	0.04%	18.9%	LGPEGELLIR	99.7%	83	25	76.4	2	0	0	1096.64	248	257
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	8	8	39	0.04%	18.9%	LSAFVFPGELLLR	99.7%	73.5	25	72.8	6	0	0	1461.85	86	98
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	8	8	39	0.04%	18.9%	NIFPSNLVSAAFR	99.7%	55.5	25	49.5	7	0	0	1435.77	190	202
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	8	8	39	0.04%	18.9%	SELPLDPLPVPTEEGNPLLK	99.7%	76	25	76	7	0	0	2158.16	503	522
Neutral amino acid transporter B(0)	SLC1A5	AAAT_HUMAN	56.6	100.0%	8	8	39	0.04%	18.9%	STEPELIQVK	99.7%	59.6	25	53.1	4	0	0	1143.63	493	502
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	8	9	18	0.02%	12.6%	EGLGLDVER	99.7%	53.6	25	46	2	0	0	987.51	589	597
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	8	9	18	0.02%	12.6%	GAVEDVISR	99.7%	54.8	25	38.5	3	0	0	945.50	525	533
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	8	9	18	0.02%	12.6%	LLTDGYACEVR	99.7%	57.2	25	52.3	2	0	0	1296.63	235	245
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	8	9	18	0.02%	12.6%	MTVEYVYER	99.7%	52	25	52	2	0	0	1189.56	464	472
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	8	9	18	0.02%	12.6%	SESHTDLTFSR	99.7%	37.3	25	37.3	1	2	0	1279.59	616	626
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	8	9	18	0.02%	12.6%	SGEGIREPISVK	99.1%	34.8	25	18.2	2	0	0	1271.70	572	583
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	8	9	18	0.02%	12.6%	TNPEYIYAPLK	99.7%	53.1	25	48.1	2	0	0	1308.68	212	222
NF-kappa-B-repressing factor	NKRF	NKRF_HUMAN	77.7	100.0%	8	9	18	0.02%	12.6%	VILESEVIAEAVGVK	99.7%	72.6	25	64.5	2	0	0	1555.89	482	496
NHP2-like protein 1	NHP2L1	NH2L1_HUMAN	14.2	100.0%	3	3	3	0.00%	31.2%	ACGVSRPVIACSVTIK	99.0%	34.5	25	32.8	1	0	0	1717.91	92	107
NHP2-like protein 1	NHP2L1	NH2L1_HUMAN	14.2	100.0%	3	3	3	0.00%	31.2%	LLDLVQQSCNYK	99.7%	52.8	25	51.9	1	0	0	1480.75	22	33
NHP2-like protein 1	NHP2L1	NH2L1_HUMAN	14.2	100.0%	3	3	3	0.00%	31.2%	QQIQSIQQSIER	99.7%	41.3	25	32.9	1	0	0	1457.77	114	125
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	8	8	15	0.01%	17.4%	AVSDWLIASVEGR	99.7%	86.4	25	62.5	2	0	0	1402.73	195	207
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	8	8	15	0.01%	17.4%	DPEFVFYDQLK	99.7%	74.9	25	59.4	2	0	0	1400.67	501	511
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	8	8	15	0.01%	17.4%	ELETVAAHQFPEVR	99.7%	72	25	61.6	2	0	0	1625.83	340	353
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	8	8	15	0.01%	17.4%	IIAEALTR	99.7%	50.2	25	27	2	0	0	886.54	417	424
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	8	8	15	0.01%	17.4%	LLDFSYEQYQK	99.7%	71.8	25	71.8	2	0	0	1433.69	89	99
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	8	8	15	0.01%	17.4%	QSAGAVVIILPR	98.4%	32.6	25	17.3	1	0	0	1223.75	103	114
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	8	8	15	0.01%	17.4%	QTQAASASQGSASAAEVLLR	99.7%	122	25	118	1	0	0	1945.99	158	177
Nicalin	NCLN	NCLN_HUMAN	63.0	100.0%	8	8	15	0.01%	17.4%	TMAAEVLSR	99.7%	52.4	25	46.2	3	0	0	977.51	74	82
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	16	19	33	0.03%	43.4%	AVPEGFVIPR	99.7%	61.3	25	52.4	2	0	0	1084.62	118	127
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	16	19	33	0.03%	43.4%	DVYKEHFQDDVFNEK	99.7%	37.9	25	37.9	0	2	0	1912.87	85	99
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	16	19	33	0.03%	43.4%	EHFQDDVFNEK	99.7%	48.2	25	40.9	1	0	0	1407.62	89	99
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	16	19	33	0.03%	43.4%	GTDTVAGLALIK	99.7%	74.7	25	41.5	2	0	0	1158.67	217	228
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	16	19	33	0.03%	43.4%	GVSSQETAGIGASAHLVNFK	99.7%	45.3	25	44	0	1	0	1973.01	197	216
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	16	19	33	0.03%	43.4%	GWNYILEK	99.7%	50.7	25	34.1	2	0	0	1022.53	100	107
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	16	19	33	0.03%	43.4%	KFPVTENSK	98.9%	34	25	22	2	0	0	1049.56	331	339
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	16	19	33	0.03%	43.4%	MWSIENIAFGSGGGLLQK	99.7%	115	25	107	2	2	0	1923.96	372	389
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	16	19	33	0.03%	43.4%	STQAPLIIRPDSGNPLDTVLK	99.7%	56.7	25	56.7	1	0	0	2235.23	303	323
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	16	19	33	0.03%	43.4%	SYSFDEIRK	99.3%	35.9	25	24.1	2	0	0	1144.56	470	478
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	16	19	33	0.03%	43.4%	TPAGNFVTLEEGKGDLEEYGQDLLHTVFK	99.7%	97.7	25	97.7	0	2	0	3207.58	435	463
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	16	19	33	0.03%	43.4%	VIQGDGVDINTLQEIVEGMK	99.7%	145	25	144	4	0	0	2158.11	350	369
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	16	19	33	0.03%	43.4%	VKYEETVFYGLQYILNK	99.7%	74.1	25	74.1	1	2	0	2107.11	52	68
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	16	19	33	0.03%	43.4%	YDGHLPIEIK	98.8%	33.7	25	23	1	0	0	1184.63	108	117
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	16	19	33	0.03%	43.4%	YEETVFYGLQYILNK	99.7%	85.9	25	80.4	2	0	0	1879.95	54	68
Nicotinamide phosphoribosyltransferase	NAMPT	NAMPT_HUMAN	55.5	100.0%	16	19	33	0.03%	43.4%	YLLETSGNLDGLEYK	99.7%	86.4	25	81.9	2	0	0	1714.85	175	189
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	20	56	0.05%	31.8%	AAPGAEFAPNKR	99.7%	64.2	25	61.3	4	0	0	1228.64	457	468
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	20	56	0.05%	31.8%	AGEVFIHK	99.7%	50.8	25	32.8	6	0	0	900.49	100	107
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	20	56	0.05%	31.8%	AVVIVDDR	99.7%	39.8	25	28.1	4	0	0	886.50	177	184
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	20	56	0.05%	31.8%	EKLEMEMEAAR	99.7%	44.4	25	33.5	2	0	0	1336.62	294	304
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	20	56	0.05%	31.8%	FACHSASLTVR	99.7%	54.9	25	52.2	4	5	0	1248.62	143	153
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	20	56	0.05%	31.8%	FAQPGSFEYEYAMR	99.7%	82.5	25	81.4	5	0	0	1711.74	257	270

Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	20	56	0.05%	31.8%	FGQAATMEGIGAIGGTPPAFNR	99.7%	105	25	105	3	4	0	2163.07	435	456
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	20	56	0.05%	31.8%	GIVEFSGKPAAR	99.7%	43.6	25	43.6	3	0	0	1231.68	191	202
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	20	56	0.05%	31.8%	LFVGNLPPDITEEEMR	99.7%	77.7	25	77.7	2	0	0	1859.92	76	91
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	20	56	0.05%	31.8%	MEELHNQEVQK	99.7%	61.9	25	23	5	0	0	1384.65	326	336
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	20	56	0.05%	31.8%	MGQMAMGGAMGINNR	99.7%	67.6	25	67.6	3	0	0	1602.65	384	398
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	20	56	0.05%	31.8%	RMEELHNQEVQK	96.8%	24.5	25	21.7	0	1	0	1540.75	325	336
Non-POU domain-containing octamer-binding protein	NONO	NONO_HUMAN	54.2	100.0%	13	20	56	0.05%	31.8%	VELDNMPLR	99.7%	68.6	25	50.2	5	0	0	1086.56	127	135
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	7	7	16	0.02%	10.5%	ATNDEIFSILK	99.7%	63.4	25	54.2	2	0	0	1250.66	512	522
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	7	7	16	0.02%	10.5%	DGVLEEQIER	99.2%	35.5	25	17.6	1	0	0	1187.59	685	694
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	7	7	16	0.02%	10.5%	IFANTESYLK	99.7%	57.3	25	41.4	2	0	0	1185.62	195	204
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	7	7	16	0.02%	10.5%	ILDIVPPTFSALCPANPTCIYK	99.7%	41.7	25	40.4	1	0	0	2490.28	465	486
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	7	7	16	0.02%	10.5%	NLFLVIFQR	99.7%	64.2	25	64.2	6	0	0	1149.68	708	716
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	7	7	16	0.02%	10.5%	NYNFGGEFVEAMIR	99.7%	102	25	97.5	3	0	0	1646.76	97	110
Nuclear cap-binding protein subunit 1	NCBP1	NCBP1_HUMAN	91.8	100.0%	7	7	16	0.02%	10.5%	VMFEVWR	99.6%	38.5	25	36.4	1	0	0	966.49	589	595
Nuclear cap-binding protein subunit 2	NCBP2	NCBP2_HUMAN	18.0	99.8%	2	2	3	0.00%	15.4%	SDSYVELSQYR	99.7%	61.5	25	50.8	2	0	0	1346.62	11	21
Nuclear cap-binding protein subunit 2	NCBP2	NCBP2_HUMAN	18.0	99.8%	2	2	3	0.00%	15.4%	TACGFCFVEYYSR	99.7%	80.6	25	80.6	1	0	0	1659.69	79	91
Nuclear export mediator factor NEMF	NEMF	NEMF_HUMAN	123.0	100.0%	2	2	3	0.00%	1.9%	AAEPLLTLER	99.6%	38.4	25	36.7	1	0	0	1112.63	160	169
Nuclear export mediator factor NEMF	NEMF	NEMF_HUMAN	123.0	100.0%	2	2	3	0.00%	1.9%	LTEIVASAPK	99.7%	65.6	25	57.5	2	0	0	1028.60	170	179
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	16	16	22	0.02%	8.4%	AADALEEQQR	99.7%	54.7	25	45.1	1	0	0	1130.54	725	734
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	16	16	22	0.02%	8.4%	AVQAQGGESQQEAQR	99.7%	91	25	85.7	2	0	0	1586.75	1574	1588
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	16	16	22	0.02%	8.4%	DSAQTSVTQAQR	99.7%	75	25	64.9	2	0	0	1291.62	632	643
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	16	16	22	0.02%	8.4%	ELVKEPAR	99.2%	35.6	25	26.9	2	0	0	941.54	936	943
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	16	16	22	0.02%	8.4%	FQVATDALK	98.7%	33.3	25	7.65	1	0	0	992.54	1700	1708
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	16	16	22	0.02%	8.4%	HQVEQLSSSLK	99.7%	46	25	42	2	0	0	1255.66	551	561
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	16	16	22	0.02%	8.4%	LADDLSTLQEK	99.7%	57	25	43.4	1	0	0	1232.64	898	908
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	16	16	22	0.02%	8.4%	LDFVCSFLQK	99.6%	38.2	25	27.3	1	0	0	1256.63	61	70
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	16	16	22	0.02%	8.4%	LEILQQQLQVANEAR	99.7%	100	25	100	1	0	0	1752.96	617	631
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	16	16	22	0.02%	8.4%	LGHELQQAGLK	99.2%	35.8	25	33.2	1	0	0	1193.66	1655	1665
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	16	16	22	0.02%	8.4%	LLQAETASNSAR	99.7%	81.5	25	73.8	2	0	0	1260.65	1271	1282
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	16	16	22	0.02%	8.4%	QELTSQAER	99.5%	37.7	25	24.1	1	0	0	1061.52	1313	1321
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	16	16	22	0.02%	8.4%	QFLEVELDQAR	99.7%	43.5	25	31.5	1	0	0	1347.69	1463	1473
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	16	16	22	0.02%	8.4%	SAPASQASLR	99.1%	35.2	25	25.4	2	0	0	987.52	1840	1849
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	16	16	22	0.02%	8.4%	SQAGVSSGAPPGR	98.9%	34	25	28.5	1	0	0	1170.59	1887	1899
Nuclear mitotic apparatus protein 1	NUMA1	NUMA1_HUMAN	238.3	100.0%	16	16	22	0.02%	8.4%	VLEGSELELAK	98.9%	34.2	25	24.4	1	0	0	1187.65	87	97
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	14	0.01%	10.4%	AIYAALSGNLK	99.7%	65.6	25	43	2	0	0	1120.64	426	436
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	14	0.01%	10.4%	EADLDVATITK	99.7%	66.3	25	57.6	2	0	0	1175.62	627	637
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	14	0.01%	10.4%	EYLGANWTLEK	99.7%	50.8	25	44.6	1	0	0	1323.66	481	491
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	14	0.01%	10.4%	GHLDALTADVK	99.7%	53.5	25	53.5	2	0	0	1139.61	804	814
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	14	0.01%	10.4%	IDVIDWLVFDPAQR	99.7%	55.5	25	55.5	1	0	0	1686.89	672	685
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	14	0.01%	10.4%	LLASLYR	99.4%	36.8	25	14	1	0	0	835.50	221	227
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	14	0.01%	10.4%	SGFGEISSPVIR	99.7%	42.1	25	38.2	2	0	0	1248.66	4	15
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	14	0.01%	10.4%	TVVEALFQR	99.7%	56.9	25	53.3	2	0	0	1062.59	251	259
Nuclear pore complex protein Nup107	NUP107	NU107_HUMAN	106.4	100.0%	9	9	14	0.01%	10.4%	VFEELQATDK	99.7%	75.2	25	64.2	1	0	0	1179.59	492	501
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	12	12	25	0.02%	12.2%	AAFLQYCR	99.7%	56.4	25	37.2	2	0	0	1028.50	524	531
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	12	12	25	0.02%	12.2%	DGIQLSEYLPEVK	99.7%	40.5	25	38.6	2	0	0	1490.77	1111	1123
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	12	12	25	0.02%	12.2%	DLLQADQLGSLK	99.7%	83.9	25	69.9	2	0	0	1300.71	1124	1135
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	12	12	25	0.02%	12.2%	EYEIPSNLTPADVFFR	99.7%	53.1	25	52.1	4	0	0	1897.93	676	691
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	12	12	25	0.02%	12.2%	GLPLGSAVSSPVLFSPVGR	99.7%	76.2	25	76.2	2	0	0	1840.03	36	54
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	12	12	25	0.02%	12.2%	LLLCEHAEK	98.4%	32.6	25	32.6	2	0	0	1112.58	638	646
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	12	12	25	0.02%	12.2%	NETIAQEDKIK	99.7%	47.4	25	32.5	2	0	0	1288.67	510	520
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	12	12	25	0.02%	12.2%	NSGLVSITSR	99.7%	77.2	25	75.5	2	0	0	1033.56	467	476

Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	12	12	25	0.02%	12.2%	SNPYFEFVLK	99.5%	38.1	25	30.6	1	0	0	1243.64	1136	1145
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	12	12	25	0.02%	12.2%	SSFYSLTSSNISK	99.7%	94.3	25	79.2	2	0	0	1420.70	284	296
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	12	12	25	0.02%	12.2%	TFGSSLPVK	99.7%	42.3	25	35.8	2	0	0	935.52	83	91
Nuclear pore complex protein Nup133	NUP133	NU133_HUMAN	129.0	100.0%	12	12	25	0.02%	12.2%	VAYPQADSNLR	99.7%	42	25	33.8	2	0	0	1233.62	788	798
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	8	8	13	0.01%	6.6%	DLLILQQLLMR	99.7%	71.5	25	70.1	1	0	0	1355.81	733	743
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	8	8	13	0.01%	6.6%	EFTVCSIGTANAVAGAVK	99.6%	38.1	25	36.2	1	0	0	1794.91	61	78
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	8	8	13	0.01%	6.6%	GFNPAQPLNIR	99.7%	39.4	25	32.1	1	0	0	1226.66	690	700
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	8	8	13	0.01%	6.6%	LLSTYLER	99.7%	60.5	25	44.1	2	0	0	994.56	1291	1298
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	8	8	13	0.01%	6.6%	LPLTPVFEGLAFK	99.5%	37.8	25	37.7	2	0	0	1431.82	1237	1249
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	8	8	13	0.01%	6.6%	SEDGEIVSTPR	99.7%	60.8	25	54.2	2	0	0	1189.57	949	959
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	8	8	13	0.01%	6.6%	SFVELSGAER	99.7%	68.4	25	61.2	2	0	0	1094.55	44	53
Nuclear pore complex protein Nup160	NUP160	NU160_HUMAN	162.1	100.0%	8	8	13	0.01%	6.6%	TAPLLLSYYLIK	99.7%	62.5	25	55.3	2	0	0	1394.83	766	777
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	25	29	50	0.05%	14.4%	AQIEQVIANCEHK	99.7%	78.9	25	78.9	2	0	0	1539.76	1207	1219
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	25	29	50	0.05%	14.4%	ASTEGVAIQGQQGTR	99.7%	77.4	25	71.8	2	0	0	1502.76	70	84
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	25	29	50	0.05%	14.4%	DACDGHEIGR	99.7%	60.5	25	56.3	2	0	0	1129.47	1484	1493
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	25	29	50	0.05%	14.4%	DLPSADSVQYR	99.7%	52.2	25	40.7	2	0	0	1250.60	572	582
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	25	29	50	0.05%	14.4%	ENLFMDLLR	99.7%	67.5	25	51	3	0	0	1150.59	860	868
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	25	29	50	0.05%	14.4%	FQDDNVEGDKVSK	99.7%	51.7	25	33.8	1	0	0	1480.69	1733	1745
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	25	29	50	0.05%	14.4%	FTDELMEQGLTYK	99.7%	103	25	103	3	0	0	1574.74	173	185
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	25	29	50	0.05%	14.4%	ILCCISCNSNIQIK	97.4%	30.5	25	22.9	1	0	0	1722.83	919	932
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	25	29	50	0.05%	14.4%	IQQGALELLR	99.7%	59.5	25	55.6	2	0	0	1140.67	1566	1575
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	25	29	50	0.05%	14.4%	KADNVVNIAR	99.7%	59.3	25	45.2	2	0	0	1099.62	892	901
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	25	29	50	0.05%	14.4%	KPVSTTNLQDPGVLGCPR	99.7%	40.9	25	40.9	0	2	0	1939.01	1013	1030
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	25	29	50	0.05%	14.4%	LAWALALR	99.7%	67.9	25	52.5	2	0	0	913.56	331	338
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	25	29	50	0.05%	14.4%	LLDIEGLYSK	99.7%	39.5	25	38.5	1	0	0	1150.64	1979	1988
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	25	29	50	0.05%	14.4%	LPGLQATVR	99.7%	60.1	25	58.8	2	0	0	954.57	322	330
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	25	29	50	0.05%	14.4%	LTAPEDVFSK	99.7%	45.1	25	38.3	2	0	0	1106.57	1452	1461
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	25	29	50	0.05%	14.4%	LVGDFTHDQSISQK	99.7%	76.6	25	72.5	2	0	0	1574.78	933	946
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	25	29	50	0.05%	14.4%	MLALALLDR	99.7%	70.9	25	57.2	4	0	0	1015.60	1494	1502
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	25	29	50	0.05%	14.4%	QCLGLLSR	97.1%	30	25	15	1	0	0	946.51	1714	1721
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	25	29	50	0.05%	14.4%	QYIATIHSR	99.7%	44.2	25	31.8	2	0	0	1088.58	305	313
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	25	29	50	0.05%	14.4%	SVSGFLHFDTATK	99.7%	64.1	25	59	2	0	0	1409.71	1165	1177
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	25	29	50	0.05%	14.4%	TLQSLLTPQPPLLK	99.7%	40.5	25	30.9	2	0	0	1548.94	1535	1548
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	25	29	50	0.05%	14.4%	TWTLELSPELASMTTR	99.7%	60.5	25	54.8	3	0	0	1851.92	157	172
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	25	29	50	0.05%	14.4%	VGNALWR	99.6%	39.1	25	21.9	1	0	0	815.45	24	30
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	25	29	50	0.05%	14.4%	YLYHGNTNPELAFESAK	99.4%	30.9	25	30.9	0	2	0	1953.93	902	918
Nuclear pore complex protein Nup205	NUP205	NU205_HUMAN	227.9	100.0%	25	29	50	0.05%	14.4%	YSFIQALVR	99.7%	65.6	25	50.5	2	0	0	1096.61	1993	2001
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	7	7	11	0.01%	14.0%	DAAFATLVSDR	99.7%	81.4	25	72.1	2	0	0	1165.58	495	505
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	7	7	11	0.01%	14.0%	DVDVYSQILR	99.7%	52	25	46.5	1	0	0	1207.63	60	69
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	7	7	11	0.01%	14.0%	EADASPASAGICR	99.7%	54.4	25	53.5	1	0	0	1304.59	219	231
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	7	7	11	0.01%	14.0%	FADAASLLLSLMTSR	99.7%	60.5	25	57.7	2	0	0	1595.85	553	567
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	7	7	11	0.01%	14.0%	LGSALSWSIR	99.7%	104	25	83	2	0	0	1089.61	483	492
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	7	7	11	0.01%	14.0%	SEMVPSCPFIYIIR	97.8%	31.1	25	22.5	1	0	0	1727.85	45	58
Nuclear pore complex protein Nup85	NUP85	NUP85_HUMAN	75.0	100.0%	7	7	11	0.01%	14.0%	TMPILSPGNTQTLTELELK	99.7%	87.4	25	87.4	2	0	0	2086.11	239	257
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	44	0.04%	30.4%	AFDIIER	94.7%	27.8	25	21.4	1	0	0	863.46	710	716
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	44	0.04%	30.4%	AQHQLGEFK	99.0%	34.7	25	30.6	1	0	0	1057.54	341	349
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	44	0.04%	30.4%	AVYCIIGR	99.7%	40.3	25	32.2	2	0	0	951.51	389	396
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	44	0.04%	30.4%	CGDLLAASQVVNR	99.7%	77	25	65.2	2	0	0	1402.71	328	340
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	44	0.04%	30.4%	DNALLSAIEESR	99.7%	96.3	25	91.2	2	0	0	1317.66	107	118
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	44	0.04%	30.4%	EALQYFYFLR	99.7%	64.8	25	59.2	3	0	0	1349.69	546	555
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	44	0.04%	30.4%	ESMLVEWEQVK	99.7%	46	25	34.5	2	0	0	1377.67	131	141

Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	44	0.04%	30.4%	FTSDTKPIINK	99.7%	53.8	25	47.2	2	0	0	1263.69	601	611
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	44	0.04%	30.4%	GLDISHISQR	99.7%	49.7	25	47.7	4	0	0	1125.60	68	77
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	44	0.04%	30.4%	LESLSAATTFEPLEPVKDTDIQGFLK	99.7%	59	25	59	0	2	0	2849.48	78	103
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	44	0.04%	30.4%	LLMLYTR	99.7%	40	25	39.8	2	0	0	909.52	531	537
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	44	0.04%	30.4%	LLSPVVPQISAPQSNK	99.7%	58.2	25	58.2	2	0	0	1677.95	645	660
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	44	0.04%	30.4%	LTLSQFQK	99.7%	59	25	52.7	3	0	0	964.55	435	442
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	44	0.04%	30.4%	LVPLNQESVEER	99.7%	66.5	25	58.5	2	0	0	1412.74	719	730
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	44	0.04%	30.4%	NLQEIQQAGER	99.7%	65.4	25	32.3	2	0	0	1285.65	32	42
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	44	0.04%	30.4%	QALAYLEQSYK	99.7%	46.2	25	44.2	1	0	0	1313.67	257	267
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	44	0.04%	30.4%	QMTDVLLTPATDALK	99.7%	78.2	25	61.2	2	0	0	1616.86	229	243
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	44	0.04%	30.4%	SSGQSAQLLSHEPGDPPCLR	99.7%	65.7	25	58	0	2	0	2136.01	505	524
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	44	0.04%	30.4%	TLITFAGMIPYR	99.7%	74.1	25	52.4	5	0	0	1382.75	791	802
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	44	0.04%	30.4%	TWFQEYMNSK	99.7%	47.4	25	47.4	1	0	0	1333.59	350	359
Nuclear pore complex protein Nup93	NUP93	NUP93_HUMAN	93.5	100.0%	21	22	44	0.04%	30.4%	VIEDRDSQLR	94.7%	27.7	25	17.6	1	0	0	1230.64	777	786
Nuclear pore complex protein Nup98-Nup96	NUP98	NUP98_HUMAN	197.6	100.0%	3	3	9	0.01%	2.2%	GFLEDLAPPER	95.2%	28.1	25	17.6	1	0	0	1243.63	1669	1679
Nuclear pore complex protein Nup98-Nup96	NUP98	NUP98_HUMAN	197.6	100.0%	3	3	9	0.01%	2.2%	LALLLSQFVGSQSVR	99.7%	106	25	106	4	0	0	1617.93	1358	1372
Nuclear pore complex protein Nup98-Nup96	NUP98	NUP98_HUMAN	197.6	100.0%	3	3	9	0.01%	2.2%	NSPVEAVFSYLTGK	99.7%	90.7	25	83.1	4	0	0	1511.77	1328	1341
Nuclear pore glycoprotein p62	NUP62	NUP62_HUMAN	53.3	99.8%	2	2	3	0.00%	4.6%	ELEDLLSPLEELVK	99.7%	43.9	25	32.1	2	0	0	1626.88	402	415
Nuclear pore glycoprotein p62	NUP62	NUP62_HUMAN	53.3	99.8%	2	2	3	0.00%	4.6%	LAENIDAQLK	99.7%	40.2	25	27	1	0	0	1114.61	436	445
Nuclear pore membrane glycoprotein 210	NUP210	PO210_HUMAN	205.1	100.0%	3	3	4	0.00%	2.0%	AVDPTSGQLYGLAR	99.7%	57.3	25	53.1	1	0	0	1447.75	1259	1272
Nuclear pore membrane glycoprotein 210	NUP210	PO210_HUMAN	205.1	100.0%	3	3	4	0.00%	2.0%	VFGAPEVLENLEVK	99.7%	79.8	25	71.2	2	0	0	1543.84	1711	1724
Nuclear pore membrane glycoprotein 210	NUP210	PO210_HUMAN	205.1	100.0%	3	3	4	0.00%	2.0%	VGQALELPLR	99.7%	46	25	44.8	1	0	0	1095.65	549	558
Nuclear receptor coactivator 5	NCOA5	NCOA5_HUMAN	65.5	100.0%	3	4	5	0.00%	6.2%	DPYGFGDSR	99.6%	38.9	25	29.6	1	0	0	1013.43	14	22
Nuclear receptor coactivator 5	NCOA5	NCOA5_HUMAN	65.5	100.0%	3	4	5	0.00%	6.2%	MADEAILQER	99.7%	63.1	25	46.9	3	0	0	1175.57	316	325
Nuclear receptor coactivator 5	NCOA5	NCOA5_HUMAN	65.5	100.0%	3	4	5	0.00%	6.2%	RFDAERPVDCSVIVVNK	95.0%	22.9	25	19.8	0	1	0	2004.03	191	207
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	8	9	15	0.01%	17.3%	AQFFVEDASTASALK	99.7%	111	25	98.8	2	0	0	1584.79	159	173
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	8	9	15	0.01%	17.3%	AWLLSMIQSK	99.7%	73.8	25	59.7	2	0	0	1176.64	133	142
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	8	9	15	0.01%	17.3%	GSYFGTENLK	96.5%	29.3	25	14.4	2	0	0	1115.54	375	384
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	8	9	15	0.01%	17.3%	IIEENIPELLSLNLSNNR	99.7%	69.3	25	69.3	2	1	0	2081.12	259	276
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	8	9	15	0.01%	17.3%	ILNLSGNELK	99.3%	36.3	25	30.9	2	0	0	1100.63	295	304
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	8	9	15	0.01%	17.3%	LDDMSSIVQK	99.7%	40.2	25	33.8	1	0	0	1151.56	280	289
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	8	9	15	0.01%	17.3%	LNVVAFLNELPK	99.7%	95.9	25	92.1	2	0	0	1356.79	460	471
Nuclear RNA export factor 1	NXF1	NXF1_HUMAN	70.2	100.0%	8	9	15	0.01%	17.3%	TFIAVPASNSGLCIVNDELFVR	99.7%	93	25	93	1	0	0	2422.24	516	537
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	14	16	43	0.04%	54.6%	AADPPAENSSAPEAEQGGAE	99.2%	35.4	25	35.4	2	0	0	1897.80	305	324
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	14	16	43	0.04%	54.6%	EDGNEEDKENQGDETQGQQPPQR	99.7%	35.8	25	35.8	0	2	0	2628.10	257	279
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	14	16	43	0.04%	54.6%	EDVFVHQTAIK	99.7%	57	25	51.8	2	0	0	1286.67	82	92
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	14	16	43	0.04%	54.6%	EDVFVHQTAIKK	99.7%	42	25	34	1	0	0	1414.77	82	93
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	14	16	43	0.04%	54.6%	GAEAANVTGPGGVPVQGSK	99.7%	127	25	127	4	0	0	1695.87	119	137
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	14	16	43	0.04%	54.6%	NDTKEDVFVHQTAIK	99.7%	75.9	25	70.6	2	5	0	1744.89	78	92
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	14	16	43	0.04%	54.6%	NEGSESAPEGQAQQR	99.7%	76.8	25	73.5	2	0	0	1587.70	171	185
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	14	16	43	0.04%	54.6%	NGYGFINR	99.7%	51.4	25	43.7	4	0	0	940.46	70	77
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	14	16	43	0.04%	54.6%	NYQQNYQNSESGEKNEGSESAPEGQAQQR	99.7%	74	25	74	0	2	0	3257.40	157	185
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	14	16	43	0.04%	54.6%	RPENPKPQDGKETK	99.6%	32.7	25	32.7	0	2	0	1623.85	291	304
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	14	16	43	0.04%	54.6%	RPQYSNPPVQGEVMEGADNQGAGEQGRPVR	99.7%	82.1	25	82.1	0	4	0	3223.53	205	234
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	14	16	43	0.04%	54.6%	RRPENPKPQDGK	97.5%	25.4	25	25.2	0	2	0	1421.76	290	301
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	14	16	43	0.04%	54.6%	SVGDGETVEFDVVEGEK	99.7%	111	25	103	7	0	0	1795.82	102	118
Nuclease-sensitive element-binding protein 1	YBX1	YBOX1_HUMAN	35.9	100.0%	14	16	43	0.04%	54.6%	SVGDGETVEFDVVEGEKGAEAANVTGPGGVPVQGSK	99.7%	93.1	25	93.1	0	2	0	3472.67	102	137
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	13	27	0.03%	14.6%	DREIQLEISGK	99.7%	58.6	25	53.3	2	0	0	1287.69	627	637
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	13	27	0.03%	14.6%	EEGTPLTLYYSHWR	99.7%	55.7	25	52.8	2	0	0	1751.84	610	623
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	13	27	0.03%	14.6%	LFHEVVQAFR	99.7%	41.5	25	38.6	2	2	0	1245.67	169	178
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	13	27	0.03%	14.6%	LSNVNLQEK	99.7%	47.1	25	37	2	0	0	1044.57	508	516

Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	13	27	0.03%	14.6%	MLQPSSSPLWGK	99.7%	59.4	25	49.7	4	0	0	1330.68	234	245
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	13	27	0.03%	14.6%	NSVPVTVAMVER	99.7%	73.2	25	62.9	2	0	0	1301.69	145	156
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	13	27	0.03%	14.6%	QVQQLLGK	99.7%	41.6	25	33.6	1	0	0	913.55	569	576
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	13	27	0.03%	14.6%	SPDKPGGSPSASR	99.7%	35.6	25	34.4	1	2	0	1242.61	49	61
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	13	27	0.03%	14.6%	VLAFLVLSR	99.7%	76.9	25	76.9	5	0	0	1017.65	311	319
Nucleolar complex protein 2 homolog	NOC2L	NOC2L_HUMAN	84.9	100.0%	10	13	27	0.03%	14.6%	VQENSAYICSR	99.7%	75.4	25	72.9	2	0	0	1326.61	577	587
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	10	10	19	0.02%	16.1%	DLSSSEPVHAK	99.7%	50.5	25	45.3	2	0	0	1169.58	113	123
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	10	10	19	0.02%	16.1%	FAAHLIAGAPSEGSGALKPELSR	99.7%	52.1	25	52.1	0	2	0	2279.21	707	729
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	10	10	19	0.02%	16.1%	FLQGDSFLNEDLNQLIK	99.7%	90.9	25	82.4	2	0	0	1994.02	761	777
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	10	10	19	0.02%	16.1%	FYLENLEQMVK	99.7%	61.1	25	44.8	1	0	0	1413.71	307	317
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	10	10	19	0.02%	16.1%	IRPLTEAEK	98.8%	33.6	25	22.3	2	0	0	1056.60	275	283
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	10	10	19	0.02%	16.1%	KPIPLENPK	95.6%	28.4	25	28.4	1	0	0	1035.62	60	68
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	10	10	19	0.02%	16.1%	LGQASLGVIK	99.7%	75.1	25	35.6	2	0	0	985.60	394	403
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	10	10	19	0.02%	16.1%	LVIVSLMELFK	99.7%	42	25	36.9	2	0	0	1291.77	257	267
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	10	10	19	0.02%	16.1%	SPLLPAVLEGLAK	99.7%	55.9	25	55.9	3	0	0	1307.79	512	524
Nucleolar complex protein 3 homolog	NOC3L	NOC3L_HUMAN	92.6	100.0%	10	10	19	0.02%	16.1%	YSSEVATESPLDFTK	99.7%	66.6	25	66.6	2	0	0	1673.79	779	793
Nucleolar complex protein 4 homolog	NOC4L	NOC4L_HUMAN	58.5	100.0%	5	6	11	0.01%	9.7%	ELALSALLK	99.7%	52.3	25	43	2	0	0	957.60	116	124
Nucleolar complex protein 4 homolog	NOC4L	NOC4L_HUMAN	58.5	100.0%	5	6	11	0.01%	9.7%	LFGALLER	99.7%	64.4	25	39.5	2	0	0	918.54	56	63
Nucleolar complex protein 4 homolog	NOC4L	NOC4L_HUMAN	58.5	100.0%	5	6	11	0.01%	9.7%	LGELLGHPSFQVK	99.7%	43.2	25	29.9	1	2	0	1424.79	103	115
Nucleolar complex protein 4 homolog	NOC4L	NOC4L_HUMAN	58.5	100.0%	5	6	11	0.01%	9.7%	REPTVSSFYVK	96.7%	29.5	25	23.8	2	0	0	1312.69	222	232
Nucleolar complex protein 4 homolog	NOC4L	NOC4L_HUMAN	58.5	100.0%	5	6	11	0.01%	9.7%	RLEAVLASR	99.7%	49	25	33.3	2	0	0	1014.61	17	25
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	8	8	13	0.01%	13.1%	ADVDVQPYAFTTK	99.7%	73.6	25	73.6	2	0	0	1454.72	191	203
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	8	8	13	0.01%	13.1%	FTQQNYHDR	99.7%	46.2	25	38.7	2	0	0	1208.54	53	61
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	8	8	13	0.01%	13.1%	IAELSEDDQK	99.1%	34.9	25	34.9	1	0	0	1147.55	296	305
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	8	8	13	0.01%	13.1%	LALGQINIAK	99.7%	57.8	25	54.3	2	0	0	1040.65	94	103
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	8	8	13	0.01%	13.1%	LPTIDPNTR	99.7%	51.5	25	43	2	0	0	1026.56	161	169
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	8	8	13	0.01%	13.1%	LSQILTDFPK	99.7%	59.4	25	52.1	2	0	0	1161.65	62	71
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	8	8	13	0.01%	13.1%	QSLEYLEQVR	99.0%	34.6	25	23.5	1	0	0	1264.65	146	155
Nucleolar GTP-binding protein 1	GTPBP4	NOG1_HUMAN	74.0	100.0%	8	8	13	0.01%	13.1%	TLLLCGYPNVGK	99.7%	64.4	25	64.1	1	0	0	1334.71	170	181
Nucleolar MIF4G domain-containing protein 1	NOM1	NOM1_HUMAN	96.3	100.0%	5	5	6	0.01%	7.4%	ASGAGSEFQDQTR	99.7%	67.7	25	67.7	1	0	0	1353.60	532	544
Nucleolar MIF4G domain-containing protein 1	NOM1	NOM1_HUMAN	96.3	100.0%	5	5	6	0.01%	7.4%	DGLDYILGALESGK	99.7%	80.4	25	80.3	1	0	0	1450.74	214	227
Nucleolar MIF4G domain-containing protein 1	NOM1	NOM1_HUMAN	96.3	100.0%	5	5	6	0.01%	7.4%	TAGPEQGPGLGGR	99.7%	48.3	25	42.8	1	0	0	1196.60	101	113
Nucleolar MIF4G domain-containing protein 1	NOM1	NOM1_HUMAN	96.3	100.0%	5	5	6	0.01%	7.4%	TRPSAAATAAAR	99.1%	34.9	25	30.4	1	0	0	1143.62	160	171
Nucleolar MIF4G domain-containing protein 1	NOM1	NOM1_HUMAN	96.3	100.0%	5	5	6	0.01%	7.4%	TYNPFYAFLASK	99.7%	44	25	44	2	0	0	1421.71	702	713
Nucleolar pre-ribosomal-associated protein 1	URB1	NPA1P_HUMAN	254.4	100.0%	3	3	4	0.00%	1.7%	AEAAGLIGWLK	99.7%	73.6	25	58.2	2	0	0	1128.64	2116	2126
Nucleolar pre-ribosomal-associated protein 1	URB1	NPA1P_HUMAN	254.4	100.0%	3	3	4	0.00%	1.7%	ILLTLVANPYSYTDK	99.7%	49.8	25	49.8	1	0	0	1710.93	703	717
Nucleolar pre-ribosomal-associated protein 1	URB1	NPA1P_HUMAN	254.4	100.0%	3	3	4	0.00%	1.7%	ISTINILLSTLK	99.7%	44.9	25	40.3	1	0	0	1315.82	237	248
Nucleolar protein 16	NOP16	NOP16_HUMAN	21.2	100.0%	5	5	9	0.01%	30.3%	AMEVDIEERPK	99.7%	65.9	25	51.1	2	0	0	1316.65	75	85
Nucleolar protein 16	NOP16	NOP16_HUMAN	21.2	100.0%	5	5	9	0.01%	30.3%	DEKNYYQDTPK	99.7%	46.9	25	41.4	2	0	0	1400.63	136	146
Nucleolar protein 16	NOP16	NOP16_HUMAN	21.2	100.0%	5	5	9	0.01%	30.3%	FGYSVNR	98.1%	31.9	25	27.1	2	0	0	842.42	13	19
Nucleolar protein 16	NOP16	NOP16_HUMAN	21.2	100.0%	5	5	9	0.01%	30.3%	QNLAEMGLAVDPNR	99.7%	71.3	25	70.5	2	0	0	1543.75	51	64
Nucleolar protein 16	NOP16	NOP16_HUMAN	21.2	100.0%	5	5	9	0.01%	30.3%	YMVENHGEDYK	99.7%	43.7	25	43.7	1	0	0	1384.58	121	131
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	11	13	22	0.02%	21.0%	GLTDLSACK	99.1%	34.8	25	27.3	1	0	0	964.48	135	143
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	11	13	22	0.02%	21.0%	IDCFSEVPTSVFGEK	99.7%	61	25	55.7	1	0	0	1714.80	382	396
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	11	13	22	0.02%	21.0%	IINDNATYCR	99.7%	46.6	25	46.6	2	0	0	1239.58	203	212
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	11	13	22	0.02%	21.0%	LAQFIGNR	99.7%	44.8	25	29.2	2	0	0	918.52	213	220
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	11	13	22	0.02%	21.0%	LLLETHLPSK	99.0%	34.7	25	26.6	2	0	0	1150.68	78	87
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	11	13	22	0.02%	21.0%	LREQVEER	98.6%	33.2	25.3	11.5	2	0	0	1058.56	397	404
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	11	13	22	0.02%	21.0%	MSQVAPSLSALIGEAVGAR	99.7%	118	25	116	4	0	0	1856.99	289	307
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	11	13	22	0.02%	21.0%	STPKEETVNDPEEAGHR	96.1%	23.8	25	23.8	0	1	0	1895.87	537	553
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	11	13	22	0.02%	21.0%	VLLGVGDPK	99.7%	57.1	25	40.4	2	0	0	897.54	91	99

Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	11	13	22	0.02%	21.0%	VVSLSEYR	99.7%	53.4	25	41.2	2	0	0	952.51	271	278
Nucleolar protein 56	NOP56	NOP56_HUMAN	66.1	100.0%	11	13	22	0.02%	21.0%	YGLIFHSTFIGR	99.7%	43.5	25	39.7	1	2	0	1410.75	348	359
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	9	11	19	0.02%	22.3%	EAHEPLAVADAK	99.7%	40.4	25	33.2	2	0	0	1250.64	82	93
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	9	11	19	0.02%	22.3%	FQDTAEALAAFTALMEGK	99.7%	129	25	129	3	0	0	1929.93	50	67
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	9	11	19	0.02%	22.3%	HAASTVQILGAEK	99.7%	49.4	25	49.4	2	0	0	1324.72	311	323
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	9	11	19	0.02%	22.3%	IISDNLTYCK	99.7%	58.3	25	58.3	2	0	0	1226.61	197	206
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	9	11	19	0.02%	22.3%	LIAHAGSLLNLAK	99.7%	62	25	62	1	2	0	1320.80	298	310
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	9	11	19	0.02%	22.3%	LSELLPEEVEAEVK	99.7%	62.2	25	58.9	2	0	0	1584.84	222	235
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	9	11	19	0.02%	22.3%	SQMDGLIPGVEPR	99.7%	70.6	25	69.7	2	0	0	1414.70	121	133
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	9	11	19	0.02%	22.3%	TQLYEYLQNR	99.7%	55.2	25	55.2	2	0	0	1327.66	269	278
Nucleolar protein 58	NOP58	NOP58_HUMAN	59.6	100.0%	9	11	19	0.02%	22.3%	TYDPSGDSTLPTCSK	99.7%	87.9	25	87.9	1	0	0	1628.71	427	441
Nucleolar protein 9	NOP9	NOP9_HUMAN	69.4	99.8%	2	2	4	0.00%	4.6%	GSSVDGSPLLLFLR	99.7%	85.8	25	71.6	2	0	0	1460.81	311	324
Nucleolar protein 9	NOP9	NOP9_HUMAN	69.4	99.8%	2	2	4	0.00%	4.6%	TLLQVLGGTILESER	99.7%	94.2	25	90	2	0	0	1628.92	209	223
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	AAVIGDVIR	99.7%	64.4	25	50.8	4	0	0	913.55	424	432
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	AEPSEVDMNSPK	99.7%	48.7	25	35.5	1	0	0	1319.58	62	73
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	APQVLVLAPTR	99.7%	65.5	25	65.5	3	0	0	1164.71	260	270
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	DSEDNPQTLLFSATCPHWVFNVAK	99.7%	76.8	25	76.8	0	2	0	2776.30	364	387
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	DVESYIHR	99.7%	49.8	25	33	2	0	0	1018.50	517	524
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	EAQELSQNSAIK	99.7%	66.2	25	52.1	3	0	0	1317.66	450	461
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	EEYQLVQVEQK	99.7%	70.8	25	64.5	2	0	0	1392.70	545	555
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	EGAFSNFPISEETIK	99.7%	71.2	25	70.4	6	0	0	1668.81	185	199
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	ELKEQLGEEIDSK	99.7%	61.9	25	55.2	2	1	0	1517.77	656	668
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	GAVEALAAALAHISGATSVDQR	99.7%	84.6	25	84.6	1	2	0	2108.11	606	627
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	GRAPQVLVLAPTR	99.7%	68.5	25	68.5	2	0	0	1377.83	258	270
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	GVTFLFPIQAK	99.7%	72.8	25	51.5	2	0	0	1220.70	205	215
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	IGVPSATEIIK	99.5%	37.4	25	32.6	4	0	0	1127.67	563	573
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	KAEPSEVDMNSPK	99.7%	48.8	25	48.7	2	1	0	1447.67	61	73
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	KEAQELSQNSAIK	98.2%	26.6	25	20.6	0	1	0	1445.76	449	461
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	KLSVACFYGGTPYGGQFER	99.7%	43.9	25	37.6	0	2	0	2137.02	286	304
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	LGVCFDVPTASVTEIQEK	99.7%	85.4	25	78.5	2	0	0	1992.99	679	696
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	LLDSVPPTAISHFK	99.5%	37.2	25	25	2	1	0	1524.84	582	595
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	LSVACFYGGTPYGGQFER	99.7%	73.7	25	66.4	2	0	0	2008.92	287	304
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	NEEPSEEEIDAPKPK	99.7%	77.3	25	69.9	2	1	0	1711.80	117	131
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	NGIDILVGTPGR	99.7%	82.9	25	74	3	0	0	1211.67	307	318
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	NGSFGVLVATNVAAR	99.7%	85.1	25	83.7	2	0	0	1475.80	485	499
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	QDAQSLHGDIPQK	99.7%	79.4	25	74.8	2	0	0	1436.71	462	474
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	SDAGLESDTAMK	99.7%	86	25	85.6	4	0	0	1240.54	7	18
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	SDKTEEIAEEEETVFPK	99.7%	87.2	25	77.4	2	1	0	1980.93	38	54
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	STYEQVDLIGK	99.7%	87.6	25	76.1	2	0	0	1252.64	392	402
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	STYEQVDLIGKK	99.7%	64.1	25	46.4	2	0	0	1380.74	392	403
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	TAITVEHLAIK	99.7%	67.9	25	62.8	4	0	0	1195.70	407	417
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	TFSFAIPLIEK	99.7%	64.6	25	62.9	3	0	0	1265.71	237	247
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	TGVCICFYQHK	99.7%	43.7	25	43.7	2	1	0	1412.65	534	544
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	TIIFCETKK	99.1%	35	25	20.6	1	0	0	1139.61	441	449
Nucleolar RNA helicase 2	DDX21	DDX21_HUMAN	87.3	100.0%	32	40	84	0.08%	46.9%	WQLSVATEQPELEGPR	99.7%	72.4	25	71.2	2	0	0	1839.92	703	718
Nucleolar transcription factor 1	UBTF	UBF1_HUMAN	89.4	99.8%	2	2	4	0.00%	3.4%	FLESLPEEEQQR	99.7%	67.4	25	62	2	0	0	1504.73	361	372
Nucleolar transcription factor 1	UBTF	UBF1_HUMAN	89.4	99.8%	2	2	4	0.00%	3.4%	TLTELILDAQEHVK	99.7%	79.8	25	79.8	2	0	0	1609.88	84	97
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	32	185	0.17%	33.0%	ALELTGLK	99.7%	57.8	25	36.5	8	0	0	844.51	363	370
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	32	185	0.17%	33.0%	ALVATPGKK	97.0%	29.9	25	28.1	1	0	0	884.56	117	125
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	32	185	0.17%	33.0%	EAMEDGEIDGNK	99.7%	65.5	25	63.2	4	0	0	1307.54	628	639
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	32	185	0.17%	33.0%	EAMEDGEIDGNKVTLDWAKPK	99.7%	79.9	25	79.9	0	9	0	2346.13	628	648

Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	32	185	0.17%	33.0%	ESFDGSVR	97.6%	30.9	25	17.7	2	0	0	896.41	590	597
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	32	185	0.17%	33.0%	EVFEDAAEIR	99.7%	74	25	58.1	8	0	0	1178.57	411	420
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	32	185	0.17%	33.0%	FGYVDFESAEDLEK	99.7%	109	25	106	8	0	0	1648.74	349	362
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	32	185	0.17%	33.0%	GFGFVDFNSEEDAK	99.7%	88.5	25	87.5	15	0	0	1561.68	611	624
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	32	185	0.17%	33.0%	GIAYIEFK	99.7%	52.1	25	39.1	4	0	0	940.51	430	437
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	32	185	0.17%	33.0%	GLSEDTTEETLK	99.7%	87.8	25	75.3	6	0	0	1322.63	578	589
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	32	185	0.17%	33.0%	GLSEDTTEETLKESFDGSVR	99.7%	103	25	103	5	6	0	2200.03	578	597
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	32	185	0.17%	33.0%	GYAFIEFASFEDAK	99.7%	110	25	101	8	0	0	1594.74	524	537
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	32	185	0.17%	33.0%	KFGYVDFESAEDLEK	99.7%	98.9	25	84.1	5	3	0	1776.83	348	362
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	32	185	0.17%	33.0%	LELQGPR	99.7%	44.7	25	35.4	8	0	0	812.46	555	561
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	32	185	0.17%	33.0%	NDLAVVDVR	99.7%	88.7	25	77.7	13	0	0	1000.54	334	342
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	32	185	0.17%	33.0%	QKVEGTEPTTAFNLFVGNLNFNK	99.7%	47.8	25	47.5	0	4	0	2568.31	296	318
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	32	185	0.17%	33.0%	SISLYYTGEK	99.7%	57.7	25	46.5	13	0	0	1160.58	458	467
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	32	185	0.17%	33.0%	TEADAEKTFEEK	99.7%	74.4	25	66.4	5	0	0	1397.64	438	449
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	32	185	0.17%	33.0%	TGISDVFAK	99.7%	72.6	25	55.3	11	0	0	937.50	325	333
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	32	185	0.17%	33.0%	TLVLSNLSYSATEETLQEVFEK	99.7%	135	25	135	5	2	0	2501.27	487	508
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	32	185	0.17%	33.0%	VAVATPAKK	98.5%	32.8	25	22.7	1	0	0	884.56	72	80
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	32	185	0.17%	33.0%	VEGTEPTTAFNLFVGNLNFNK	99.7%	104	25	104	7	5	0	2312.16	298	318
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	32	185	0.17%	33.0%	VFGNEIK	96.9%	29.9	25	10.4	4	0	0	806.44	371	377
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	32	185	0.17%	33.0%	VTLDWAKPK	99.7%	53.8	25	44.7	4	0	0	1057.60	640	648
Nucleolin	NCL	NUCL_HUMAN	76.6	100.0%	25	32	185	0.17%	33.0%	VTQDELKEVFEDAAEIR	99.7%	111	25	105	5	6	0	1991.99	404	420
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	7	11	63	0.06%	25.2%	GPSSVEDIK	99.7%	57.8	25	52.7	12	0	0	931.47	240	248
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	7	11	63	0.06%	25.2%	GPSSVEDIKAK	99.7%	84.3	25	66	10	0	0	1130.61	240	250
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	7	11	63	0.06%	25.2%	LLSISGKR	99.7%	44	25	33	2	0	0	873.55	135	142
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	7	11	63	0.06%	25.2%	MQASIEK	99.2%	35.6	25	23.5	3	0	0	822.40	251	257
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	7	11	63	0.06%	25.2%	MSVQPTVSLGGFEITPPVVLR	99.7%	102	25	102	14	4	0	2243.21	81	101
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	7	11	63	0.06%	25.2%	MTDQEAIQDLWQWR	99.7%	55.3	25	55.3	6	0	0	1835.84	278	291
Nucleophosmin	NPM1	NPM_HUMAN	32.6	100.0%	7	11	63	0.06%	25.2%	VDNDENEHQLSLR	99.7%	81.2	25	79.1	12	0	0	1568.73	33	45
Nucleoporin NDC1	NDC1	NDC1_HUMAN	76.3	99.8%	2	2	3	0.00%	4.5%	LSTPDVVSPFGTPFGSSVMNR	99.7%	42	25	42	1	0	0	2195.08	438	458
Nucleoporin NDC1	NDC1	NDC1_HUMAN	76.3	99.8%	2	2	3	0.00%	4.5%	VLIMYFFSK	99.7%	51.3	25	40.3	2	0	0	1147.62	537	545
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	9	9	11	0.01%	6.0%	ALLLVPASVNCLR	99.5%	37.2	25	37.2	1	0	0	1425.82	1142	1154
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	9	9	11	0.01%	6.0%	CTLLLILLR	99.7%	52.4	25	46.2	1	0	0	1114.70	1160	1168
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	9	9	11	0.01%	6.0%	ELWTILLGR	99.7%	52.2	25	41.8	2	0	0	1100.65	15	23
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	9	9	11	0.01%	6.0%	HTLNPEETSSVVR	96.8%	29.7	25	29.7	1	0	0	1468.74	331	343
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	9	9	11	0.01%	6.0%	LAFSVTNNVIR	99.7%	45.5	25	41.4	1	0	0	1233.69	816	826
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	9	9	11	0.01%	6.0%	LSMSLMEQLLK	99.7%	41	25	38.2	2	0	0	1292.70	1399	1409
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	9	9	11	0.01%	6.0%	QLFLDVLDGTK	98.6%	33.2	25	26.7	1	0	0	1248.68	1131	1141
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	9	9	11	0.01%	6.0%	VFSAFITVLQMK	99.0%	34.4	25	34.4	1	0	0	1399.77	1206	1217
Nucleoporin NUP188 homolog	NUP188	NU188_HUMAN	196.0	100.0%	9	9	11	0.01%	6.0%	VQRPPSAASAAPSSSK	99.7%	45.7	25	40.6	1	0	0	1540.81	1518	1533
Nucleoside diphosphate kinase 6	NME6	NDK6_HUMAN	21.1	100.0%	3	3	4	0.00%	18.3%	GSFGLTDTR	99.0%	34.3	25	24.4	1	0	0	953.47	117	125
Nucleoside diphosphate kinase 6	NME6	NDK6_HUMAN	21.1	100.0%	3	3	4	0.00%	18.3%	LVEFMASGPIR	99.7%	46.8	25	41.2	1	0	0	1235.65	72	82
Nucleoside diphosphate kinase 6	NME6	NDK6_HUMAN	21.1	100.0%	3	3	4	0.00%	18.3%	NTTHGSDSVVSASR	99.7%	45.7	25	45.5	2	0	0	1417.67	126	139
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	11	32	0.03%	46.7%	DRPFFAGLVK	99.7%	39.4	25	31.4	1	0	0	1149.64	57	66
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	11	32	0.03%	46.7%	GDFCIQVGR	99.7%	63.4	25	55.4	4	0	0	1051.50	106	114
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	11	32	0.03%	46.7%	GLVGEIIK	99.7%	52.9	25	41.1	2	0	0	828.52	19	26
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	11	32	0.03%	46.7%	GLVGEIIKR	99.7%	45.2	25	42.6	4	0	0	984.62	19	27
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	11	32	0.03%	46.7%	NIIHGSDSVESAEK	98.9%	34	25	23.1	1	0	0	1485.72	115	128
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	11	32	0.03%	46.7%	TFIAIKPDGVQR	99.7%	52.6	25	52.4	4	1	0	1344.76	7	18
Nucleoside diphosphate kinase A	NME1	NDKA_HUMAN	17.1	100.0%	7	11	32	0.03%	46.7%	VMLGETNPADSKPGTIR	99.7%	79.5	25	77.7	8	7	0	1801.91	89	105
Nucleoside diphosphate kinase, mitochondrial	NME4	NDKM_HUMAN	20.7	100.0%	5	7	9	0.01%	32.1%	AMIGHTDSAEAAPGTIR	99.7%	38.7	25	38.7	1	1	0	1713.82	122	138
Nucleoside diphosphate kinase, mitochondrial	NME4	NDKM_HUMAN	20.7	100.0%	5	7	9	0.01%	32.1%	GDFSVHISR	99.7%	44.9	25	32	2	0	0	1017.51	139	147

Nucleoside diphosphate kinase, mitochondrial	NME4	NDKM_HUMAN	20.7	100.0%	5	7	9	0.01%	32.1%	LVGDVIQR	99.6%	39.2	25	28.5	1	0	0	899.53	53	60
Nucleoside diphosphate kinase, mitochondrial	NME4	NDKM_HUMAN	20.7	100.0%	5	7	9	0.01%	32.1%	NVIHASDSVEGAQR	99.7%	54.4	25	41.4	1	1	0	1482.73	148	161
Nucleoside diphosphate kinase, mitochondrial	NME4	NDKM_HUMAN	20.7	100.0%	5	7	9	0.01%	32.1%	TLVAVKPDGVQR	99.7%	48.7	25	43.6	2	0	0	1282.75	40	51
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	5	6	22	0.02%	22.0%	FYEEVHDLER	99.7%	48.2	25	43.8	6	0	0	1336.62	95	104
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	5	6	22	0.02%	22.0%	GIPEFWLTVFK	99.7%	65.7	25	61.5	6	0	0	1336.73	166	176
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	5	6	22	0.02%	22.0%	LDGLVETPTGYIESLPR	99.7%	86.3	25	84.1	7	0	0	1859.98	56	72
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	5	6	22	0.02%	22.0%	NVDLLSDMVQEHDEPILK	99.7%	64.1	25	64.1	1	2	0	2095.04	177	194
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	5	6	22	0.02%	22.0%	QLTVQMMQNPQILAALQER	99.7%	75.8	25	75.8	1	0	0	2212.16	37	55
Nucleosome assembly protein 1-like 1	NAP1L1	NP1L1_HUMAN	45.4	100.0%	5	6	22	0.02%	22.0%	YAVLYQPLFDK	99.7%	48.2	25	48.2	5	0	0	1356.72	106	116
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	8	8	19	0.02%	26.7%	FYEEVHDLER	99.7%	48.2	25	43.8	6	0	0	1336.62	84	93
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	8	8	19	0.02%	26.7%	GIPEFWFTIFR	99.7%	54.3	25	54.3	1	0	0	1412.74	158	168
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	8	8	19	0.02%	26.7%	LDNVPHTPSSYIETLPK	99.7%	33.6	25	33.6	0	1	0	1910.99	45	61
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	8	8	19	0.02%	26.7%	LTDQVMQNPR	99.7%	68.4	25	62.7	3	0	0	1201.60	27	36
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	8	8	19	0.02%	26.7%	NVDMLSELVQEYDEPILK	99.7%	49.3	25	49.3	1	0	0	2151.05	169	186
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	8	8	19	0.02%	26.7%	QVPNESFFNFFNPLK	99.7%	53.3	25	46.9	2	0	0	1827.91	283	297
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	8	8	19	0.02%	26.7%	VLAALQER	99.7%	58.5	25	40.7	4	0	0	899.53	37	44
Nucleosome assembly protein 1-like 4	NAP1L4	NP1L4_HUMAN	42.8	100.0%	8	8	19	0.02%	26.7%	YAALYQPLFDK	99.7%	51.3	25	49.5	1	0	0	1328.69	95	105
Oligosaccharyltransferase complex subunit OSTC	OSTC	OSTC_HUMAN	16.8	99.8%	2	2	10	0.01%	14.1%	MKLPGYLMG	99.7%	50	25	34.1	4	0	0	1025.52	141	149
Oligosaccharyltransferase complex subunit OSTC	OSTC	OSTC_HUMAN	16.8	99.8%	2	2	10	0.01%	14.1%	VPFLVLECPNLK	99.7%	73.8	25	69.3	6	0	0	1428.79	7	18
Origin recognition complex subunit 3	ORC3	ORC3_HUMAN	82.3	100.0%	6	7	10	0.01%	10.8%	AVSELELLGFIKPTK	99.7%	69.5	25	63.6	2	0	0	1644.96	683	697
Origin recognition complex subunit 3	ORC3	ORC3_HUMAN	82.3	100.0%	6	7	10	0.01%	10.8%	ENVVNFIDCLVR	99.7%	70.1	25	70.1	2	0	0	1477.75	553	564
Origin recognition complex subunit 3	ORC3	ORC3_HUMAN	82.3	100.0%	6	7	10	0.01%	10.8%	LLLTTQFPFK	99.2%	35.2	25	20.5	1	0	0	1207.71	292	301
Origin recognition complex subunit 3	ORC3	ORC3_HUMAN	82.3	100.0%	6	7	10	0.01%	10.8%	NLFDNLIEFLQK	99.7%	43.2	25	33.1	1	0	0	1493.80	68	79
Origin recognition complex subunit 3	ORC3	ORC3_HUMAN	82.3	100.0%	6	7	10	0.01%	10.8%	SKEEESVHVTQR	99.7%	47.6	25	45.9	1	2	0	1428.71	164	175
Origin recognition complex subunit 3	ORC3	ORC3_HUMAN	82.3	100.0%	6	7	10	0.01%	10.8%	TTSSQWQSPPVVVILK	99.7%	46.6	25	46.6	1	0	0	1769.98	205	220
Origin recognition complex subunit 4	ORC4	ORC4_HUMAN	50.4	99.8%	2	2	3	0.00%	3.9%	LDILELLEK	99.7%	68.4	25	62.5	2	0	0	1085.65	196	204
Origin recognition complex subunit 4	ORC4	ORC4_HUMAN	50.4	99.8%	2	2	3	0.00%	3.9%	SVQEVLQK	97.4%	30.6	25	17.7	1	0	0	930.53	261	268
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	4	4	7	0.01%	10.1%	ESQVSILQSLFGER	99.7%	86.2	25	86.2	2	0	0	1592.83	12	25
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	4	4	7	0.01%	10.1%	LLAILYSIVDSR	99.7%	55.2	25	55.2	1	0	0	1362.80	362	373
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	4	4	7	0.01%	10.1%	LLLEQILNK	99.7%	64.5	25	50.3	2	0	0	1083.68	71	79
Origin recognition complex subunit 5	ORC5	ORC5_HUMAN	50.3	100.0%	4	4	7	0.01%	10.1%	TYVTQTLLK	99.4%	36.8	25	34.1	2	0	0	1066.61	44	52
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	23	51	0.05%	51.7%	AFYNNVLGEYEEYITK	99.7%	67.2	25	61.5	2	0	0	1952.93	114	129
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	23	51	0.05%	51.7%	DNGLLAKPTHGDIIR	99.7%	49.6	25	49.6	0	2	0	1619.89	399	413
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	23	51	0.05%	51.7%	EDELRESIEIINK	99.7%	69.9	25	55.5	1	0	0	1587.82	422	434
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	23	51	0.05%	51.7%	FAPPLVIKEDELR	99.7%	69.1	25	66.3	2	0	0	1526.86	414	426
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	23	51	0.05%	51.7%	GIYLWDVEGR	99.7%	59.5	25	45.8	3	0	0	1207.61	67	76
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	23	51	0.05%	51.7%	GLLNAIVIK	99.7%	62	25	51.6	2	0	0	940.62	375	383
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	23	51	0.05%	51.7%	HQVLFIADEIQTGLAR	99.7%	97.2	25	89.7	2	2	0	1810.98	256	271
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	23	51	0.05%	51.7%	IVFAAGNFWGR	99.7%	70.7	25	70.7	6	0	0	1237.65	170	180
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	23	51	0.05%	51.7%	KTVQGPPTSDDIFER	99.7%	75.6	25	75.6	2	2	0	1689.84	32	46
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	23	51	0.05%	51.7%	LPSDVVTAVR	99.7%	77.3	25	64	4	0	0	1056.60	363	372
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	23	51	0.05%	51.7%	NELMKLPSDVVTAVR	97.5%	25.4	25	25.4	0	1	0	1687.90	358	372
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	23	51	0.05%	51.7%	SQVDKLTLTSR	99.7%	58	25	50.9	2	2	0	1247.70	103	113
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	23	51	0.05%	51.7%	TVQGPPTSDDIFER	99.7%	92.2	25	81.3	2	0	0	1561.75	33	46
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	23	51	0.05%	51.7%	VAIAALEVLEEENLAENADK	99.7%	107	25	102	2	0	0	2141.10	332	351
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	23	51	0.05%	51.7%	VLPMNTGVEAGETACK	99.7%	87.7	25	84.8	4	0	0	1692.79	136	151
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	23	51	0.05%	51.7%	WLAVDYENVRPDIVLLGK	99.7%	75.3	25	75.3	2	2	0	2100.15	275	292
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	23	51	0.05%	51.7%	YFDFLSSYSAVNQGHCHPK	99.7%	40.7	25	40.7	0	2	0	2257.01	78	96
Ornithine aminotransferase, mitochondrial	OAT	OAT_HUMAN	48.5	100.0%	18	23	51	0.05%	51.7%	YGAHNYHPLPVALER	99.7%	50.9	25	50.9	2	0	0	1736.89	50	64
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	13	14	25	0.02%	34.5%	AGTEPSDAIR	95.2%	28.1	25	23.3	1	0	0	1016.50	266	275
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	13	14	25	0.02%	34.5%	CQIIYPR	98.6%	33	25	16.9	1	0	0	949.49	341	347

Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	13	14	25	0.02%	34.5%	ELEMIGFIENNVSK	99.7%	95.4	25	88	2	0	0	1622.81	355	368
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	13	14	25	0.02%	34.5%	HSNVVILTTSNITEK	99.7%	49.5	25	49.5	0	2	0	1655.90	290	304
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	13	14	25	0.02%	34.5%	IDVAFVDR	99.7%	61.1	25	39.6	2	0	0	934.50	305	312
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	13	14	25	0.02%	34.5%	IYLSCLEELMK	99.7%	65.4	25	56	2	0	0	1398.70	330	340
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	13	14	25	0.02%	34.5%	LSLLLNDISR	99.7%	63.5	25	42	2	0	0	1143.67	369	378
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	13	14	25	0.02%	34.5%	NVQSVSIIDTELK	99.7%	73.3	25	63.9	2	0	0	1445.78	69	81
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	13	14	25	0.02%	34.5%	QQLLTLR	99.7%	43.3	25	24.2	2	0	0	871.54	348	354
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	13	14	25	0.02%	34.5%	QYIGPPSAAAIFK	99.7%	51.6	25	47.5	2	0	0	1362.74	317	329
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	13	14	25	0.02%	34.5%	VVLLHGPPGTGK	99.7%	57.4	25	57.4	2	0	0	1174.69	174	185
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	13	14	25	0.02%	34.5%	VVNAVLTQIDQIKR	99.7%	79.9	25	79.9	2	2	0	1596.94	276	289
Pachytene checkpoint protein 2 homolog	TRIP13	PCH2_HUMAN	48.6	100.0%	13	14	25	0.02%	34.5%	YGQLIEINSHSLFSK	99.7%	35.2	25	26.5	0	1	0	1735.90	206	220
Paired amphipathic helix protein Sin3a	SIN3A	SIN3A_HUMAN	145.2	99.8%	2	2	4	0.00%	1.5%	AADIIDGLR	96.0%	28.8	25	15.5	2	0	0	943.52	677	685
Paired amphipathic helix protein Sin3a	SIN3A	SIN3A_HUMAN	145.2	99.8%	2	2	4	0.00%	1.5%	LLFSNTAAQK	99.7%	48	25	34.7	2	0	0	1092.60	866	875
Parafibromin	CDC73	CDC73_HUMAN	60.6	100.0%	2	2	4	0.00%	4.3%	GDEVIFGEFSWPK	99.7%	47.5	25	47.5	2	0	0	1510.72	22	34
Parafibromin	CDC73	CDC73_HUMAN	60.6	100.0%	2	2	4	0.00%	4.3%	NIFAILQSVK	99.7%	48.5	25	42.7	2	0	0	1132.67	248	257
PC4 and SFRS1-interacting protein	PSIP1	PSIP1_HUMAN	60.1	99.8%	2	2	4	0.00%	3.0%	GQEEKQPK	97.9%	31.4	25	23.3	2	0	0	943.48	221	228
PC4 and SFRS1-interacting protein	PSIP1	PSIP1_HUMAN	60.1	99.8%	2	2	4	0.00%	3.0%	IDNLDVNR	99.7%	41.1	25	11.9	2	0	0	958.50	365	372
PCI domain-containing protein 2	PCID2	PCID2_HUMAN	46.0	99.8%	2	2	3	0.00%	6.5%	AIDSSNLKDDYSTAQR	98.6%	27.8	25	26	0	1	0	1783.85	194	209
PCI domain-containing protein 2	PCID2	PCID2_HUMAN	46.0	99.8%	2	2	3	0.00%	6.5%	MILIYLLPVK	99.7%	80.5	25	80.5	2	0	0	1202.76	250	259
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	11	12	22	0.02%	20.3%	AGHQFGVTWR	99.7%	40	25	28.7	2	0	0	1158.58	230	239
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	11	12	22	0.02%	20.3%	AIGIEPSLATYHHIIR	98.7%	27.9	25	27.9	0	2	0	1790.99	362	377
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	11	12	22	0.02%	20.3%	AYEQALNLYTELLNNR	99.7%	78.2	25	69.9	2	0	0	1924.98	271	286
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	11	12	22	0.02%	20.3%	DIAEPHIPCLMPEYFEPQIK	99.4%	30.8	25	27.2	0	1	0	2427.17	131	150
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	11	12	22	0.02%	20.3%	FIGPDQHR	99.6%	38.6	25	29.4	2	0	0	969.49	447	454
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	11	12	22	0.02%	20.3%	SAYESQPIR	99.7%	40.3	25	29.3	2	0	0	1050.52	557	565
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	11	12	22	0.02%	20.3%	SELLNELMDSAK	99.7%	86.7	25	82.3	4	0	0	1349.66	608	619
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	11	12	22	0.02%	20.3%	SPALQVLR	99.7%	64.2	25	58.9	2	0	0	883.54	351	358
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	11	12	22	0.02%	20.3%	VEGTDVTGIEEVVIPK	99.7%	98.5	25	91.1	2	0	0	1684.90	46	61
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	11	12	22	0.02%	20.3%	VKPNLQTFNTILK	99.2%	35.8	25	31.3	1	0	0	1515.89	328	340
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	PTCD3_HUMAN	78.6	100.0%	11	12	22	0.02%	20.3%	VMSDFAINQEQK	99.7%	95.5	25	95.5	2	0	0	1409.67	649	660
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	12	24	0.02%	58.2%	EGMNIVEAMER	99.7%	55.7	25	53.6	5	0	0	1294.58	134	144
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	12	24	0.02%	58.2%	FEDENFILK	99.7%	42.4	25	27.3	2	0	0	1154.57	83	91
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	12	24	0.02%	58.2%	IIPGFMCQGGDFTR	99.7%	54.5	25	54.5	4	0	0	1614.74	56	69
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	12	24	0.02%	58.2%	KITIADCGQLE	99.7%	65.7	25	56.5	2	0	0	1247.63	155	165
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	12	24	0.02%	58.2%	SIYGEKFEDENFILK	99.7%	74.6	25	68.4	2	0	0	1831.91	77	91
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	12	24	0.02%	58.2%	TEWLDGKHVVFGK	96.1%	23.8	25	19.8	0	1	0	1515.80	119	131
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	12	24	0.02%	58.2%	VKEGMNIVEAMER	99.7%	66.8	25	66.8	2	0	0	1505.75	132	144
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	12	24	0.02%	58.2%	VNPTVFFDIAVDGEPLGR	99.7%	64.4	25	61.3	2	0	0	1946.00	2	19
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	12	24	0.02%	58.2%	VSFELFADK	99.7%	62.9	25	54.1	2	0	0	1055.54	20	28
Peptidyl-prolyl cis-trans isomerase A	PPIA	PPIA_HUMAN	18.0	100.0%	10	12	24	0.02%	58.2%	VSFELFADKVPK	99.7%	58	25	57.6	2	0	0	1379.76	20	31
Peptidyl-prolyl cis-trans isomerase B	PPIB	PPIB_HUMAN	23.7	100.0%	3	3	4	0.00%	18.1%	DTNGSQFFITTVK	99.7%	63.6	25	56	2	0	0	1457.73	146	158
Peptidyl-prolyl cis-trans isomerase B	PPIB	PPIB_HUMAN	23.7	100.0%	3	3	4	0.00%	18.1%	SIYGERFPDENFK	99.3%	36.2	25	31.8	1	0	0	1601.76	117	129
Peptidyl-prolyl cis-trans isomerase B	PPIB	PPIB_HUMAN	23.7	100.0%	3	3	4	0.00%	18.1%	TVDNFVALATGEK	99.7%	83.5	25	77.7	1	0	0	1364.71	72	84
Peptidyl-prolyl cis-trans isomerase H	PPIH	PPIH_HUMAN	19.2	100.0%	3	4	8	0.01%	18.6%	IELFADVVPK	99.7%	56.2	25	50.9	2	0	0	1130.65	29	38
Peptidyl-prolyl cis-trans isomerase H	PPIH	PPIH_HUMAN	19.2	100.0%	3	4	8	0.01%	18.6%	IIDGLLVMR	99.7%	62.5	25	46.3	4	0	0	1029.61	144	152
Peptidyl-prolyl cis-trans isomerase H	PPIH	PPIH_HUMAN	19.2	100.0%	3	4	8	0.01%	18.6%	KIENVPTGPNNKPK	99.7%	35.3	25	34.1	0	2	0	1535.85	153	166
Peptidyl-prolyl cis-trans isomerase-like 1	PPIL1	PPIL1_HUMAN	18.2	100.0%	4	5	7	0.01%	26.5%	DFMIQGGDPTGTGR	99.7%	58.7	25	54.4	1	0	0	1467.65	59	72
Peptidyl-prolyl cis-trans isomerase-like 1	PPIL1	PPIL1_HUMAN	18.2	100.0%	4	5	7	0.01%	26.5%	IIKDFMIQGGDPTGTGR	99.7%	42	25	34.6	1	2	0	1821.92	56	72
Peptidyl-prolyl cis-trans isomerase-like 1	PPIL1	PPIL1_HUMAN	18.2	100.0%	4	5	7	0.01%	26.5%	VCQGIGMVNR	99.7%	58.7	25	41.6	2	0	0	1149.55	132	141
Peptidyl-prolyl cis-trans isomerase-like 1	PPIL1	PPIL1_HUMAN	18.2	100.0%	4	5	7	0.01%	26.5%	VGMVETNSQDRPVDDVK	95.6%	28.4	25	28.4	1	0	0	1904.90	142	158
Peptidyl-tRNA hydrolase ICT1, mitochondrial	ICT1	ICT1_HUMAN	23.6	100.0%	3	3	4	0.00%	15.5%	FHLATAEWIAEPVR	99.7%	45.6	25	40.4	1	0	0	1639.86	103	116

Peptidyl-tRNA hydrolase ICT1, mitochondrial	ICT1	ICT1_HUMAN	23.6	100.0%	3	3	4	0.00%	15.5%	NLADCLQK	99.2%	35.4	25	26.4	1	0	0	961.48	146	153
Peptidyl-tRNA hydrolase ICT1, mitochondrial	ICT1	ICT1_HUMAN	23.6	100.0%	3	3	4	0.00%	15.5%	QADSDIPLDR	99.7%	73.2	25	52.4	2	0	0	1129.55	67	76
Periodic tryptophan protein 2 homolog	PWP2	PWP2_HUMAN	102.5	99.8%	2	2	3	0.00%	2.6%	AGTLLPVIQFLQK	99.7%	49.3	25	43.3	2	0	0	1427.86	838	850
Periodic tryptophan protein 2 homolog	PWP2	PWP2_HUMAN	102.5	99.8%	2	2	3	0.00%	2.6%	LVQEALEAVPR	97.1%	30.1	25	24.5	1	0	0	1224.69	774	784
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	8	8	21	0.02%	42.2%	ADEGISFR	96.9%	29.8	25	18	1	0	0	894.43	121	128
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	8	8	21	0.02%	42.2%	GLFIIDDKGILR	99.7%	69.1	25	69.1	6	0	0	1359.80	129	140
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	8	8	21	0.02%	42.2%	IGHPAPNFK	97.1%	30	25	28	1	0	0	980.53	8	16
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	8	8	21	0.02%	42.2%	LVQAFQFTDK	99.7%	54.1	25	45	2	0	0	1196.63	159	168
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	8	8	21	0.02%	42.2%	QGGLGPMNIPLVSDPKR	98.9%	28.5	25	28.5	0	2	0	1794.95	94	110
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	8	8	21	0.02%	42.2%	QITVNDLPVGR	99.7%	80.3	25	71.9	3	0	0	1211.67	141	151
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	8	8	21	0.02%	42.2%	SVDETLR	99.1%	34.9	25	21.4	2	0	0	819.42	152	158
Peroxiredoxin-1	PRDX1	PRDX1_HUMAN	22.1	100.0%	8	8	21	0.02%	42.2%	TIAQDYGVLK	99.7%	49.5	25	42.2	4	0	0	1107.60	111	120
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	5	6	9	0.01%	29.8%	ATAVVDGAFKEVK	99.7%	53.1	25	38.7	2	0	0	1334.73	17	29
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	5	6	9	0.01%	29.8%	EGGLGPLNIPLLADVTR	99.7%	76.5	25	76.5	2	0	0	1734.98	93	109
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	5	6	9	0.01%	29.8%	GLFIIDGK	94.8%	27.8	25	27.8	1	0	0	862.50	128	135
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	5	6	9	0.01%	29.8%	KEGGLGPLNIPLLADVTR	99.6%	38.9	25	38.9	1	1	0	1863.07	92	109
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	5	6	9	0.01%	29.8%	LSEDYGVLK	99.7%	57.5	25	45.1	2	0	0	1023.54	111	119
Peroxiredoxin-2	PRDX2	PRDX2_HUMAN	21.9	100.0%	5	6	9	0.01%	29.8%	QITVNDLPVGR	99.7%	80.3	25	71.9	3	0	0	1211.67	140	150
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	8	8	15	0.01%	37.1%	DFTPVCTTELGR	99.7%	58.9	25	51.6	4	0	0	1395.66	42	53
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	8	8	15	0.01%	37.1%	DINAYNCEEPTEK	99.7%	40.8	25	40.8	1	0	0	1582.67	85	97
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	8	8	15	0.01%	37.1%	LPFPIIDDR	99.7%	57.1	25	49.9	2	0	0	1085.60	98	106
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	8	8	15	0.01%	37.1%	LSILYPATTGR	97.2%	30.3	25	19.5	2	0	0	1191.67	145	155
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	8	8	15	0.01%	37.1%	NFDEILR	98.3%	32.2	25	10.6	1	0	0	906.47	156	162
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	8	8	15	0.01%	37.1%	PGGLLLGDVAPNFEANTTVGR	99.7%	95.9	25	93.4	2	0	0	2098.09	2	22
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	8	8	15	0.01%	37.1%	VVFVFGPDK	99.7%	39.8	25	34.2	1	0	0	1007.56	133	141
Peroxiredoxin-6	PRDX6	PRDX6_HUMAN	25.0	100.0%	8	8	15	0.01%	37.1%	VVFVFGPDKK	99.7%	56.8	25	56.8	2	0	0	1135.65	133	142
Peroxisomal multifunctional enzyme type 2	HSD17B4	DHB4_HUMAN	79.7	100.0%	3	3	4	0.00%	5.4%	IDVVVNNAGILR	99.7%	58.5	25	51.1	1	0	0	1282.75	93	104
Peroxisomal multifunctional enzyme type 2	HSD17B4	DHB4_HUMAN	79.7	100.0%	3	3	4	0.00%	5.4%	LGLLGLANSLAIEGR	99.6%	39.3	25	39.3	2	0	0	1496.88	169	183
Peroxisomal multifunctional enzyme type 2	HSD17B4	DHB4_HUMAN	79.7	100.0%	3	3	4	0.00%	5.4%	VVLVTGAGAGLGR	99.7%	59.8	25	55.1	1	0	0	1169.70	11	23
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	14	0.01%	11.1%	EALAFIIR	99.7%	39.6	25	25.4	2	0	0	932.56	341	348
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	14	0.01%	11.1%	GSATNYITR	99.7%	68.5	25	57.5	2	0	0	982.50	12	20
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	14	0.01%	11.1%	LAALEEQR	99.7%	47.7	25	41.5	2	0	0	929.51	496	503
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	14	0.01%	11.1%	LAALSASLAR	99.7%	72.5	25	41.3	2	0	0	972.58	276	285
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	14	0.01%	11.1%	LAQEEESEAKR	99.7%	50.2	25	44.3	2	0	0	1289.63	524	534
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	14	0.01%	11.1%	LEGQAQAEAK	99.7%	61.7	25	45.4	2	0	0	1044.53	250	259
Pescadillo homolog	PES1	PESC_HUMAN	68.0	100.0%	7	7	14	0.01%	11.1%	LQLSLADFR	99.7%	54.2	25	44.6	2	0	0	1062.59	27	35
PHD finger protein 6	PHF6	PHF6_HUMAN	41.3	100.0%	2	2	4	0.00%	4.7%	AEFGDFDIK	99.7%	46.4	25	42.2	2	0	0	1041.49	258	266
PHD finger protein 6	PHF6	PHF6_HUMAN	41.3	100.0%	2	2	4	0.00%	4.7%	TVLQEIKR	99.7%	59.2	25	20.2	2	0	0	986.60	267	274
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	14	16	32	0.03%	38.0%	DQHDTFFLR	99.7%	45.2	25	32.2	1	0	0	1178.56	272	280
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	14	16	32	0.03%	38.0%	DQHDTFFLRDPAEALQLPMDYVQR	99.7%	54.9	25	54.9	0	2	0	2905.39	272	295
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	14	16	32	0.03%	38.0%	FKPAYNPYTEPSMEVFSYHQGLK	99.7%	49.2	25	47.7	0	2	0	2733.30	405	427
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	14	16	32	0.03%	38.0%	HWELTAEGEEIAR	99.7%	70.4	25	51.6	2	2	0	1540.74	60	72
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	14	16	32	0.03%	38.0%	LDAEPRPPPTQEAA	94.7%	27.8	25	21.3	1	0	0	1491.74	495	508
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	14	16	32	0.03%	38.0%	LGITQLR	99.7%	57	25	34	4	0	0	800.50	398	404
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	14	16	32	0.03%	38.0%	LLAEVTLK	96.6%	29.5	25	17.5	2	0	0	886.56	164	171
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	14	16	32	0.03%	38.0%	QETELSPEMISSGSWR	99.7%	63.9	25	60.5	1	0	0	1852.84	188	203
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	14	16	32	0.03%	38.0%	RLEASDGGLDSAELAAELGMEHQAVVGAVK	99.7%	70.8	25	70.8	0	2	0	3039.51	13	42
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	14	16	32	0.03%	38.0%	SLQALGEVIEAELR	99.7%	116	25	111	4	0	0	1527.84	43	56
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	14	16	32	0.03%	38.0%	THSQGGYGSQGYK	99.7%	67.5	25	67.5	2	0	0	1369.61	299	311
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	14	16	32	0.03%	38.0%	VNLQMVYDSPLCR	99.7%	77.7	25	76.6	2	0	0	1594.77	482	494
Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	14	16	32	0.03%	38.0%	VVDSMEDEVQR	99.7%	69	25	63.3	4	0	0	1322.59	128	138

Phenylalanine--tRNA ligase alpha subunit	FARSA	SYFA_HUMAN	57.6	100.0%	14	16	32	0.03%	38.0%	YGINNIR	99.7%	46.1	25	28.2	1	0	0	849.46	469	475
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	15	15	24	0.02%	28.0%	ALVAIGTHDLDTLSGPFTYTAK	99.7%	35.5	25	35.5	0	1	0	2291.19	155	176
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	15	15	24	0.02%	28.0%	ASEGPAFFPGR	99.7%	69.3	25	54	2	0	0	1135.55	537	547
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	15	15	24	0.02%	28.0%	DLLFQALGR	99.7%	69.9	25	49.8	2	0	0	1032.58	9	17
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	15	15	24	0.02%	28.0%	DRYDSFIELQEK	99.7%	53.6	25	41.1	2	0	0	1542.74	134	145
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	15	15	24	0.02%	28.0%	HLCAVYYNK	98.5%	32.9	25	26.5	1	0	0	1167.56	496	504
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	15	15	24	0.02%	28.0%	IKAPVYK	96.6%	29.4	25	7.53	1	0	0	818.51	91	97
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	15	15	24	0.02%	28.0%	IRPFAVAAVLR	99.7%	42.2	25	42.2	1	0	0	1212.76	117	127
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	15	15	24	0.02%	28.0%	LFEISDIVIK	99.7%	49.1	25	33.5	2	0	0	1176.69	474	483
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	15	15	24	0.02%	28.0%	LGVLHPDVITK	99.7%	40	25	40	2	0	0	1191.71	561	571
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	15	15	24	0.02%	28.0%	LIITEETAK	99.7%	48.5	25	36.2	2	0	0	1017.58	108	116
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	15	15	24	0.02%	28.0%	NIFIECTGTDFTK	99.7%	88.9	25	88.9	2	0	0	1545.73	250	262
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	15	15	24	0.02%	28.0%	NPGFEIIHGLLDR	99.7%	44	25	42.2	1	0	0	1480.79	505	517
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	15	15	24	0.02%	28.0%	TAEFQVAR	99.7%	50.3	25	41	1	0	0	921.48	444	451
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	15	15	24	0.02%	28.0%	TTLLPGLLK	98.5%	32.6	25	24.9	2	0	0	955.62	452	460
Phenylalanine--tRNA ligase beta subunit	FARSB	SYFB_HUMAN	66.1	100.0%	15	15	24	0.02%	28.0%	YDLLCLEGLVR	99.7%	59.9	25	51.8	2	0	0	1350.71	72	82
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	23	67	0.06%	36.7%	EKGSSASLVLK	98.4%	32.5	25	21	1	0	0	1118.64	294	304
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	23	67	0.06%	36.7%	FACFER	97.2%	30.2	25	30.2	2	0	0	829.37	235	240
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	23	67	0.06%	36.7%	FGFYEVFK	99.3%	36.3	25	34.7	4	0	0	1036.51	138	145
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	23	67	0.06%	36.7%	GIFNGFSVTLK	99.7%	77	25	69.1	5	0	0	1182.65	102	112
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	23	67	0.06%	36.7%	GIFNGFSVTLKEDGVR	99.7%	72.7	25	69.3	2	0	0	1738.91	102	117
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	23	67	0.06%	36.7%	GSSASLVLK	99.5%	37.9	25	27.4	3	0	0	861.50	296	304
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	23	67	0.06%	36.7%	GSSASLVLKR	99.7%	54.2	25	26.8	4	0	0	1017.61	296	305
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	23	67	0.06%	36.7%	GVAPLWMR	99.7%	45.5	25	34.5	6	0	0	945.50	219	226
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	23	67	0.06%	36.7%	GWAPTFLGYSMQGLCK	99.7%	93.5	25	93.5	6	0	0	1831.85	122	137
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	23	67	0.06%	36.7%	IQTQPGYANTLR	99.7%	73.4	25	59.6	9	0	0	1361.72	190	201
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	23	67	0.06%	36.7%	LPRPPPPEMPESLK	99.7%	47.7	25	47.7	1	2	0	1587.86	342	355
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	23	67	0.06%	36.7%	LPRPPPPEMPESLKK	99.7%	43.3	25	42.2	0	2	0	1731.95	342	356
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	23	67	0.06%	36.7%	MQVDPQK	99.7%	40.5	25	22.3	1	0	0	845.42	93	99
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	23	67	0.06%	36.7%	MQVDPQKYK	98.1%	31.7	25	20.6	2	0	0	1152.57	93	101
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	23	67	0.06%	36.7%	MYKEEGLK	99.6%	39.3	25	28.7	6	0	0	997.50	207	214
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	23	67	0.06%	36.7%	TVEALYK	99.2%	35.5	25	17.7	3	0	0	823.46	241	247
Phosphate carrier protein, mitochondrial	SLC25A3	MPCP_HUMAN	40.1	100.0%	17	23	67	0.06%	36.7%	VLYSNMLGEENTYLWR	99.7%	93.8	25	93.8	8	0	0	1987.96	146	161
Phosphatidylethanolamine-binding protein 1	PEBP1	PEBP1_HUMAN	21.1	99.8%	2	2	2	0.00%	18.2%	GNDISSGTVLSDYVGSGPPK	99.7%	76.8	25	73.5	1	0	0	1949.95	94	113
Phosphatidylethanolamine-binding protein 1	PEBP1	PEBP1_HUMAN	21.1	99.8%	2	2	2	0.00%	18.2%	LYTLVLTDPDAPSR	99.7%	43.5	25	40.2	1	0	0	1560.83	63	76
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	6	7	12	0.01%	34.8%	AATALLEAGLAR	99.7%	92.4	25	77.6	2	0	0	1156.67	2	13
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	6	7	12	0.01%	34.8%	GVITMNEEYETR	99.7%	67.8	25	67.8	3	0	0	1457.66	67	78
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	6	7	12	0.01%	34.8%	IDPTVLLGALPLR	99.7%	84.9	25	80.4	2	0	0	1377.85	41	53
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	6	7	12	0.01%	34.8%	LGVEQLR	99.7%	48.4	25	24.5	2	0	0	814.48	90	96
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	6	7	12	0.01%	34.8%	LSTVDMTGIPTLDNLQK	99.7%	50.7	25	49	1	0	0	1845.96	97	113
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	PTPM1_HUMAN	22.8	100.0%	6	7	12	0.01%	34.8%	QLVQDENVR	99.7%	46.6	25	35.7	2	0	0	1100.57	58	66
Phosphatidylinositide phosphatase SAC1	SACM1L	SAC1_HUMAN	67.0	100.0%	5	5	8	0.01%	8.2%	ELSAQPEVHR	99.4%	36.8	25	29.3	2	0	0	1165.60	175	184
Phosphatidylinositide phosphatase SAC1	SACM1L	SAC1_HUMAN	67.0	100.0%	5	5	8	0.01%	8.2%	LEEQDEFEK	98.3%	32.1	25	16	1	0	0	1166.52	424	432
Phosphatidylinositide phosphatase SAC1	SACM1L	SAC1_HUMAN	67.0	100.0%	5	5	8	0.01%	8.2%	QVIINLINQK	99.7%	44.9	25	36.7	1	0	0	1182.72	302	311
Phosphatidylinositide phosphatase SAC1	SACM1L	SAC1_HUMAN	67.0	100.0%	5	5	8	0.01%	8.2%	TNVIQSLLAR	99.7%	60.8	25	45.7	2	0	0	1114.66	396	405
Phosphatidylinositide phosphatase SAC1	SACM1L	SAC1_HUMAN	67.0	100.0%	5	5	8	0.01%	8.2%	YFDWILISR	99.7%	51.1	25	40	2	0	0	1212.64	205	213
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	34	0.03%	30.5%	AALQALGVAEGGER	99.7%	93.6	25	83.2	2	0	0	1341.71	36	49
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	34	0.03%	30.5%	ALGATFGPLLLR	99.7%	60	25	47.9	4	0	0	1228.74	245	256
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	34	0.03%	30.5%	APGPGPPPAAR	99.7%	42.8	25	36.3	2	0	0	987.54	718	728
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	34	0.03%	30.5%	DQYLVWLTQK	99.7%	56	25	51.1	1	0	0	1293.68	575	584
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	34	0.03%	30.5%	DTPDGTFLVR	98.6%	33.2	25	29.6	2	0	0	1120.56	346	355

Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	34	0.03%	30.5%	EAAGPVGPALEPPTLPLHR	96.6%	24.3	25	24.3	0	1	0	1922.05	200	218
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	34	0.03%	30.5%	EYDQLYEEYTR	99.7%	39.7	25	39.7	2	0	0	1508.65	459	469
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	34	0.03%	30.5%	FLLQHLGR	99.7%	48.7	25	44.9	2	0	0	983.58	224	231
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	34	0.03%	30.5%	HESLAQYNAK	99.7%	42.5	25	37.5	2	0	0	1160.57	407	416
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	34	0.03%	30.5%	IFEEQGQTQEK	99.7%	67.6	25	58.1	2	0	0	1336.64	490	500
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	34	0.03%	30.5%	INEWLGIK	99.7%	44.9	25	27.3	1	0	0	972.55	591	598
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	34	0.03%	30.5%	SFLLALPAPLVTPEASAEAR	99.7%	106	25	101	4	0	0	2053.13	176	195
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	34	0.03%	30.5%	TAIEAFNETIK	99.7%	69.8	25	64.8	2	0	0	1236.65	479	489
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	34	0.03%	30.5%	TATGFGFAEPYNLYGSLK	99.7%	69.7	25	59.8	2	0	0	1935.95	673	690
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	34	0.03%	30.5%	TDWSLSDVDQWDTAALADGIK	99.7%	64.3	25	61.3	2	0	0	2307.08	155	175
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	34	0.03%	30.5%	TGLDSESHYRPELPAPR	99.7%	42.5	25	42.5	0	2	0	1924.95	138	154
Phosphatidylinositol 3-kinase regulatory subunit beta	PIK3R2	P85B_HUMAN	81.5	100.0%	17	17	34	0.03%	30.5%	TQAEEMLSGKR	98.6%	33.1	25	28.7	1	0	0	1265.62	630	640
Phosphatidylinositol 4-kinase alpha	PI4KA	PI4KA_HUMAN	231.3	99.8%	2	2	3	0.00%	1.2%	TLLLSLLATEIER	99.7%	58.8	25	58.8	2	0	0	1471.87	1432	1444
Phosphatidylinositol 4-kinase alpha	PI4KA	PI4KA_HUMAN	231.3	99.8%	2	2	3	0.00%	1.2%	VMEPILQILQQK	98.0%	31.6	25	31.6	1	0	0	1439.83	575	586
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	99.8%	2	2	11	0.01%	4.5%	GVDASGETTYKK	99.7%	46.8	25	40.6	5	0	0	1255.62	62	73
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	PI51C_HUMAN	73.3	99.8%	2	2	11	0.01%	4.5%	QAQGAQSTSDEKRPVGQK	99.7%	62.5	25	62.5	0	6	0	1914.96	334	351
Phosphatidylserine decarboxylase proenzyme	PISD	PISD_HUMAN	46.7	100.0%	3	3	5	0.00%	8.6%	GSYNDFSFVTHTNR	99.7%	83.7	25	83.7	2	0	0	1644.74	347	360
Phosphatidylserine decarboxylase proenzyme	PISD	PISD_HUMAN	46.7	100.0%	3	3	5	0.00%	8.6%	GVTYSLESFLGPR	99.7%	69.6	25	67.8	2	0	0	1425.74	210	222
Phosphatidylserine decarboxylase proenzyme	PISD	PISD_HUMAN	46.7	100.0%	3	3	5	0.00%	8.6%	ILNFGQVK	95.9%	28.8	25	7.85	1	0	0	918.54	194	201
Phosphatidylserine synthase 1	PTDSS1	PTSS1_HUMAN	55.5	100.0%	4	4	6	0.01%	10.1%	AVLQFTPASWTYVR	99.7%	64	25	64	2	0	0	1638.86	263	276
Phosphatidylserine synthase 1	PTDSS1	PTSS1_HUMAN	55.5	100.0%	4	4	6	0.01%	10.1%	ILFIGGITAPTVR	99.7%	68.7	25	67.9	2	0	0	1357.82	324	336
Phosphatidylserine synthase 1	PTDSS1	PTSS1_HUMAN	55.5	100.0%	4	4	6	0.01%	10.1%	SLMYWLDPNLR	99.7%	51.8	25	49.8	1	0	0	1407.71	128	138
Phosphatidylserine synthase 1	PTDSS1	PTSS1_HUMAN	55.5	100.0%	4	4	6	0.01%	10.1%	TLSKDDVNYK	98.4%	32.5	25	24	1	0	0	1182.60	9	18
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	4	4	14	0.01%	8.7%	AFVRPSGTEDVVR	99.7%	50.8	25	49.4	0	4	0	1432.75	493	505
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	4	4	14	0.01%	8.7%	MGLLAVLR	99.7%	79.4	25	58	4	0	0	872.54	42	49
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	4	4	14	0.01%	8.7%	QAVTPPGLQEAINDLVK	99.7%	52.6	25	52	4	0	0	1792.98	470	486
Phosphoacetylglucosamine mutase	PGM3	AGM1_HUMAN	59.9	100.0%	4	4	14	0.01%	8.7%	VISTTDAER	99.4%	36.8	25	28.4	2	0	0	991.51	461	469
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	20	46	0.04%	35.2%	AIDTTQLFSLPK	99.7%	85.4	25	73.5	3	0	0	1333.74	589	600
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	20	46	0.04%	35.2%	DEAGHFLWPGFGENAR	99.7%	36.2	25	35.3	0	2	0	1802.82	538	553
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	20	46	0.04%	35.2%	DFWEQEVR	99.7%	41.6	25	27.2	2	0	0	1108.51	601	608
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	20	46	0.04%	35.2%	EGALDLSGLR	99.7%	49.5	25	43.6	3	0	0	1030.55	579	588
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	20	46	0.04%	35.2%	EIISFGSGYGGNSLLGK	99.7%	104	25	104	2	0	0	1698.87	245	261
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	20	46	0.04%	35.2%	ETPIGLVPK	99.7%	40.3	25	40.3	2	0	0	953.57	570	578
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	20	46	0.04%	35.2%	EVLAELEALER	99.7%	81.2	25	74.3	2	0	0	1271.68	625	635
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	20	46	0.04%	35.2%	GQLGNWMSPADFQR	99.7%	74.5	25	74.5	4	0	0	1606.74	129	142
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	20	46	0.04%	35.2%	GVPLVYEAFNWR	99.7%	62.1	25	56	2	0	0	1450.75	458	469
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	20	46	0.04%	35.2%	HGVFVGSAMR	96.6%	29.4	25	21.9	1	0	0	1060.54	470	479
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	20	46	0.04%	35.2%	IFHVNWFR	96.8%	29.7	25	19.3	1	0	0	1118.59	529	536
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	20	46	0.04%	35.2%	LGTPVLQALGDGDFVK	99.7%	103	25	94.2	4	0	0	1629.89	194	209
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	20	46	0.04%	35.2%	SYLTEQVNQDLPK	99.7%	102	25	93.5	2	0	0	1534.77	612	624
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	20	46	0.04%	35.2%	TLIGHVPDQR	99.7%	46	25	30	2	0	0	1135.62	235	244
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	20	46	0.04%	35.2%	TMYVLPFSMGPVGSPLSR	99.7%	91.3	25	74.2	7	0	0	1954.98	156	173
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	20	46	0.04%	35.2%	VLDWICR	99.7%	43.6	25	40	2	0	0	961.49	554	560
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	20	46	0.04%	35.2%	VLSGDLGQLPTGIR	99.7%	103	25	94	2	0	0	1425.81	32	45
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	20	46	0.04%	35.2%	YNNCWLAR	98.8%	33.7	25	25.3	2	0	0	1096.50	89	96
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	PCKGM_HUMAN	70.7	100.0%	19	20	46	0.04%	35.2%	YVAAAFPSACGK	96.5%	29.4	25	29.4	1	0	0	1241.60	297	308
Phosphoglycerate mutase 1	PGAM1	PGAM1_HUMAN,PGAM2_HUMAN	28.8	100.0%	4	4	6	0.01%	17.7%	ALPFWNEEIVPQIK	96.3%	29.1	25	29.1	1	0	0	1683.91	163	176
Phosphoglycerate mutase 1	PGAM1	PGAM1_HUMAN,PGAM2_HUMAN	28.8	100.0%	4	4	6	0.01%	17.7%	AMEAVAAQGK	98.0%	31.7	25	27.7	1	0	0	975.49	242	251
Phosphoglycerate mutase 1	PGAM1	PGAM1_HUMAN,PGAM2_HUMAN	28.8	100.0%	4	4	6	0.01%	17.7%	HYGGLTGLNK	99.6%	38.5	25	24.7	2	0	0	1059.56	91	100
Phosphoglycerate mutase 1	PGAM1	PGAM1_HUMAN,PGAM2_HUMAN	28.8	100.0%	4	4	6	0.01%	17.7%	VLIAAHGNSLR	99.7%	56.6	25	56.6	2	0	0	1150.67	181	191
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	5	5	10	0.01%	19.9%	FIAGTGCLVR	99.7%	47	25	24	2	0	0	1093.58	211	220

Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	5	5	10	0.01%	19.9%	FIFDCVSQEYGINPER	99.7%	75.8	25	69.9	2	0	0	1973.91	239	254
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	5	5	10	0.01%	19.9%	GETAVPGAPEALR	99.7%	49.7	25	33.6	2	0	0	1267.66	42	54
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	5	5	10	0.01%	19.9%	LGFITNNSSK	99.7%	41.2	25	29.5	2	0	0	1080.57	63	72
Phosphoglycolate phosphatase	PGP	PGP_HUMAN	34.0	100.0%	5	5	10	0.01%	19.9%	TILTLTGVSTLGDVK	99.7%	90.2	25	90.2	2	0	0	1517.88	276	290
Phosphoinositide 3-kinase regulatory subunit 4	PIK3R4	PI3R4_HUMAN	153.1	99.8%	2	2	3	0.00%	1.6%	FLELVQLK	98.0%	31.6	25	19	1	0	0	989.60	496	503
Phosphoinositide 3-kinase regulatory subunit 4	PIK3R4	PI3R4_HUMAN	153.1	99.8%	2	2	3	0.00%	1.6%	VVTLLSDPENIVK	99.7%	49	25	36	2	0	0	1426.82	541	553
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	99.9%	2	2	6	0.01%	7.6%	EIQGFFSFPVDNLR	99.7%	53	25	53	4	0	0	1668.84	139	152
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	KPRA_HUMAN	39.4	99.9%	2	2	6	0.01%	7.6%	NIIGVIPYFPYSK	99.1%	34.8	25	34.6	2	0	0	1510.83	91	103
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	4	4	7	0.01%	13.3%	GGLVLFSANSNSSCMELSK	99.7%	67.9	25	67.9	2	0	0	2016.94	18	36
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	4	4	7	0.01%	13.3%	TVDISMILSEAIR	99.7%	67.9	25	64.2	2	0	0	1463.78	338	350
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	4	4	7	0.01%	13.3%	VQIQESVR	99.7%	46.9	25	32.5	2	0	0	958.53	61	68
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	KPRB_HUMAN	40.9	100.0%	4	4	7	0.01%	13.3%	VQVYQEPNR	99.7%	40.8	25	30.3	1	0	0	1132.57	49	57
Phosphoribosyltransferase domain-containing protein 1	PRTFDC1	PRDC1_HUMAN	25.7	99.8%	2	2	2	0.00%	10.7%	DIGYSDIMVLCVLK	99.7%	58.9	25	48	1	0	0	1625.83	63	76
Phosphoribosyltransferase domain-containing protein 1	PRTFDC1	PRDC1_HUMAN	25.7	99.8%	2	2	2	0.00%	10.7%	FCADLVEHLK	99.1%	34.8	25	34.1	1	0	0	1231.61	81	90
Plasma membrane calcium-transporting ATPase 1	ATP2B1	AT2B1_HUMAN	138.8	100.0%	3	3	5	0.00%	3.7%	EASDIILTDDNFTSIVK	99.7%	85.3	25	81.6	2	0	0	1880.95	824	840
Plasma membrane calcium-transporting ATPase 1	ATP2B1	AT2B1_HUMAN	138.8	100.0%	3	3	5	0.00%	3.7%	SSPTDKHTLVK	99.7%	42	25	36.7	1	0	0	1212.66	768	778
Plasma membrane calcium-transporting ATPase 1	ATP2B1	AT2B1_HUMAN	138.8	100.0%	3	3	5	0.00%	3.7%	YGDLLPADGILIQGNDLK	99.7%	46.9	25	30.5	2	0	0	1915.02	220	237
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	22	22	31	0.03%	4.9%	ALQALEELR	98.1%	31.8	25	24.5	1	0	0	1042.59	1671	1679
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	22	22	31	0.03%	4.9%	APVPASELLASGVLSR	99.7%	68	25	68	2	0	0	1566.89	3447	3462
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	22	22	31	0.03%	4.9%	AQLEPVASPAK	98.6%	33.1	25	33.1	1	0	0	1110.62	1428	1438
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	22	22	31	0.03%	4.9%	ESADPLGAWLQDAR	99.7%	44	25	38.5	2	0	0	1528.74	1351	1364
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	22	22	31	0.03%	4.9%	GLLSAEVAR	99.3%	36.2	25	18.5	2	0	0	915.53	3850	3858
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	22	22	31	0.03%	4.9%	IISLETYNLLR	99.7%	58.2	25	48.9	2	0	0	1334.77	3794	3804
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	22	22	31	0.03%	4.9%	LAAEQELIR	99.7%	41.6	25	23.3	2	0	0	1042.59	1846	1854
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	22	22	31	0.03%	4.9%	LISLFQAMK	96.2%	29	25	22.9	1	0	0	1050.60	4159	4167
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	22	22	31	0.03%	4.9%	LKAEATEAAR	98.3%	32.3	25	29.3	2	0	0	1059.58	2349	2358
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	22	22	31	0.03%	4.9%	LLEAAAQSTK	99.7%	51.8	25	38.2	1	0	0	1031.57	4600	4609
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	22	22	31	0.03%	4.9%	LQAEEVAQQK	99.7%	50.2	25	33.5	2	0	0	1143.60	1783	1792
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	22	22	31	0.03%	4.9%	LQEAGILSAEELQR	99.7%	86.7	25	83.7	1	0	0	1556.83	2795	2808
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	22	22	31	0.03%	4.9%	LTVDEAVR	99.2%	35.4	25	18.6	1	0	0	902.49	3213	3220
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	22	22	31	0.03%	4.9%	QLLEEELAR	96.4%	29.2	25	22.2	1	0	0	1100.59	1867	1875
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	22	22	31	0.03%	4.9%	SDEGQLSPATR	95.8%	28.6	25	26.7	1	0	0	1160.55	714	724
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	22	22	31	0.03%	4.9%	SIQEELQQLR	99.7%	55.7	25	35.4	1	0	0	1243.66	1554	1563
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	22	22	31	0.03%	4.9%	SKEQAELEAAR	99.7%	49.8	25	40.1	1	0	0	1231.63	2098	2108
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	22	22	31	0.03%	4.9%	SLVPAAELLESR	99.7%	48.3	25	38.3	2	0	0	1284.72	3116	3127
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	22	22	31	0.03%	4.9%	SQVEEELFSVR	99.7%	65.6	25	62	1	0	0	1322.66	2361	2371
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	22	22	31	0.03%	4.9%	SSIAGLLLK	99.6%	38.2	25	25.4	1	0	0	901.57	2833	2841
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	22	22	31	0.03%	4.9%	VLADPSDDTK	99.3%	35.9	25	26	1	0	0	1060.52	2979	2988
Plectin	PLEC	PLEC_HUMAN	531.8	100.0%	22	22	31	0.03%	4.9%	VPVDVAYR	99.7%	47.6	25	39.6	2	0	0	918.50	2961	2968
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	14	16	26	0.02%	45.5%	ASVHTLSGHTNAVATVR	99.7%	78.1	25	73.5	1	2	0	1720.91	321	337
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	14	16	26	0.02%	45.5%	CIAVEPGNQWFVTGSADR	99.7%	131	25	130	2	0	0	2006.94	209	226
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	14	16	26	0.02%	45.5%	CQAAEPQIITGSHDTTIR	99.7%	40.6	25	40.6	0	1	0	1997.97	338	355
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	14	16	26	0.02%	45.5%	GPQNATDSYVHK	99.7%	64.5	25	54.8	2	2	0	1316.62	69	80
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	14	16	26	0.02%	45.5%	HYTFASGSPDNIK	99.7%	67	25	65.5	2	0	0	1436.68	384	396
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	14	16	26	0.02%	45.5%	LKLSLTGHISTVR	99.0%	29	25	28.7	0	1	0	1424.86	238	250
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	14	16	26	0.02%	45.5%	LRNEYGPVLHMPTSK	99.7%	39	25	34.7	0	2	0	1741.91	48	62
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	14	16	26	0.02%	45.5%	LWDLVAGK	99.7%	51.1	25	31.5	2	0	0	901.51	356	363
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	14	16	26	0.02%	45.5%	MPSESAAQSLAVALPLQTK	99.7%	77.9	25	77.9	1	0	0	1958.03	117	135
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	14	16	26	0.02%	45.5%	QYPANQGQEVEYFVAGTHPYPPGPGVALTADTK	99.7%	43.7	25	43.7	0	1	0	3502.69	81	113
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	14	16	26	0.02%	45.5%	SPYLFSCGEDK	99.7%	55.7	25	55.7	2	0	0	1302.57	258	268
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	14	16	26	0.02%	45.5%	TGYNFQR	99.7%	50.7	25	31.8	2	0	0	885.42	443	449

Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	14	16	26	0.02%	45.5%	VHAAVQPGSLDSESGIFACAFDQSESR	99.7%	63.6	25	63.6	0	2	0	2865.31	450	476
Pleiotropic regulator 1	PLRG1	PLRG1_HUMAN	57.2	100.0%	14	16	26	0.02%	45.5%	VYREDDTATEETHPVSWKPEIIK	95.3%	23.1	25	23.1	0	1	0	2743.36	488	510
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	17	17	36	0.03%	20.0%	AEPVEVVAPR	99.7%	45.9	25	41.4	2	0	0	1066.59	487	496
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	17	17	36	0.03%	20.0%	AMVEYEIDLQK	99.7%	66.3	25	61.1	2	0	0	1338.66	685	695
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	17	17	36	0.03%	20.0%	ASLCISTK	99.7%	40.7	25	26.7	1	0	0	879.46	426	433
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	17	17	36	0.03%	20.0%	ELLIFNK	98.8%	33.8	25	3.16	1	0	0	876.52	263	269
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	17	17	36	0.03%	20.0%	GIYFADMVSK	99.7%	57.1	25	43.5	2	0	0	1130.56	894	903
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	17	17	36	0.03%	20.0%	HPDVEVDGFSELR	94.9%	27.9	25	18.8	1	0	0	1499.71	66	78
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	17	17	36	0.03%	20.0%	IAPPEAPVTGYMFGK	98.6%	33	25	23.8	1	0	0	1593.80	879	893
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	17	17	36	0.03%	20.0%	KGDEVDGVDEVAK	99.7%	75.9	25	67.2	2	0	0	1360.66	209	221
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	17	17	36	0.03%	20.0%	KPPLLNNADSVQAK	99.7%	81.4	25	79.6	2	0	0	1494.83	748	761
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	17	17	36	0.03%	20.0%	LQLLEDDKENR	99.7%	52.7	25	46.2	2	0	0	1372.71	572	582
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	17	17	36	0.03%	20.0%	MAIMVQSPMFDGK	99.7%	73	25	64.7	2	0	0	1454.68	35	47
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	17	17	36	0.03%	20.0%	QQVPSGESAILDR	99.7%	60.2	25	48.7	3	0	0	1399.72	270	282
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	17	17	36	0.03%	20.0%	TLGDFAAEYAK	99.7%	65.5	25	63.6	3	0	0	1185.58	109	119
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	17	17	36	0.03%	20.0%	TTNFAGILSQGLR	99.7%	100	25	91.2	3	0	0	1377.75	866	878
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	17	17	36	0.03%	20.0%	VFSATLGLVDIVK	99.7%	77	25	52.1	4	0	0	1361.80	552	564
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	17	17	36	0.03%	20.0%	VVDRDSEEAEIIR	98.9%	33.9	25	22.1	1	0	0	1530.78	803	815
Poly [ADP-ribose] polymerase 1	PARP1	PARP1_HUMAN	113.1	100.0%	17	17	36	0.03%	20.0%	VVSEDFLQDVSASTK	99.7%	120	25	116	4	0	0	1624.81	453	467
Poly(A) RNA polymerase, mitochondrial	MTPAP	PAPD1_HUMAN	66.2	100.0%	3	3	4	0.00%	6.5%	FSHQASGFQCDLTTNNR	98.1%	26.3	25	26.3	0	1	0	1982.88	315	331
Poly(A) RNA polymerase, mitochondrial	MTPAP	PAPD1_HUMAN	66.2	100.0%	3	3	4	0.00%	6.5%	NVSQSQLQK	99.5%	37.8	25	25.3	1	0	0	1031.55	489	497
Poly(A) RNA polymerase, mitochondrial	MTPAP	PAPD1_HUMAN	66.2	100.0%	3	3	4	0.00%	6.5%	SPPILPTLDSLK	99.6%	38.8	25	38	2	0	0	1280.75	392	403
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	8	20	0.02%	26.4%	AITIAGVPQSVTECVK	99.2%	35.7	25	35.7	1	0	0	1672.89	145	160
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	8	20	0.02%	26.4%	ESTGAQVQVAGDMLPNSTER	99.7%	88.2	25	83.8	7	0	0	2089.98	125	144
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	8	20	0.02%	26.4%	IANPVEGSSGR	99.7%	55	25	54.1	2	0	0	1086.55	315	325
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	8	20	0.02%	26.4%	IITLTGPTNAIFK	99.7%	41.5	25	37.8	2	0	0	1388.82	58	70
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	8	20	0.02%	26.4%	INISEGNCPER	99.7%	47.1	25	46.8	4	0	0	1288.60	47	57
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	8	20	0.02%	26.4%	LVVPATQCGSLIGK	99.7%	40.7	25	24	2	0	0	1442.80	102	115
Poly(rC)-binding protein 1	PCBP1	PCBP1_HUMAN	37.5	100.0%	7	8	20	0.02%	26.4%	QGANINEIR	99.7%	58.6	25	43.5	2	0	0	1014.53	298	306
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	16	0.02%	23.3%	AITIAGIPQSIIECVK	99.7%	43.8	25	30.6	3	0	0	1712.96	145	160
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	16	0.02%	23.3%	ESTGAQVQVAGDMLPNSTER	99.7%	88.2	25	83.8	7	0	0	2089.98	125	144
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	16	0.02%	23.3%	IANPVEGSTDR	99.7%	49.1	25	49.1	3	0	0	1158.58	323	333
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	16	0.02%	23.3%	IITLAGPTNAIFK	99.7%	69.3	25	69.3	6	0	0	1358.80	58	70
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	16	0.02%	23.3%	INISEGNCPER	99.7%	47.1	25	46.8	4	0	0	1288.60	47	57
Poly(rC)-binding protein 2	PCBP2	PCBP2_HUMAN	38.6	100.0%	4	4	16	0.02%	23.3%	LVVPASQCGSLIGK	99.7%	79.1	25	78.3	4	0	0	1428.79	102	115
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	12	16	30	0.03%	29.2%	AQSSQDAVSSMNLFDLGGQYLR	99.7%	113	25	113	4	0	0	2387.13	277	298
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	12	16	30	0.03%	29.2%	AVTPPMPLLTPATPGGLPPAAAVAAAAATAK	99.7%	44.8	25	44.8	0	5	0	2810.55	302	332
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	12	16	30	0.03%	29.2%	GYGFIEYEK	99.7%	47.9	25	46.7	2	0	0	1105.52	268	276
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	12	16	30	0.03%	29.2%	IYVASVHQDLSDDDIK	99.7%	83.4	25	77.3	1	1	0	1817.89	228	243
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	12	16	30	0.03%	29.2%	KQESTVMVLR	99.7%	50.9	25	44.2	4	0	0	1206.65	458	467
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	12	16	30	0.03%	29.2%	KVVAEVYDQER	99.7%	72.2	25	70.4	2	0	0	1335.69	541	551
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	12	16	30	0.03%	29.2%	LGLPPLTPEQQEALQK	99.7%	75.1	25	73	2	0	0	1761.97	54	69
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	12	16	30	0.03%	29.2%	QGEEEDAEIIVK	99.7%	55.5	25	39.3	2	0	0	1359.66	503	514
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	12	16	30	0.03%	29.2%	SIDMSWDSVTMK	99.7%	78.7	25	78	2	0	0	1399.62	157	168
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	12	16	30	0.03%	29.2%	SVFEAFGK	97.0%	30	25	21.4	1	0	0	884.45	244	251
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	12	16	30	0.03%	29.2%	VVAEVYDQER	99.7%	63.7	25	59.2	2	0	0	1207.60	542	551
Poly(U)-binding-splicing factor PUF60	PUF60	PUF60_HUMAN	59.9	100.0%	12	16	30	0.03%	29.2%	VYVGSIYYELGEDTIR	99.7%	91.6	25	86.2	2	0	0	1876.93	131	146
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	AKEFTNVYIK	99.7%	48.7	25	43	6	4	0	1212.66	187	196
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	ALDTMNFDVIK	99.7%	87.2	25	79.1	25	0	0	1266.64	68	78
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	ALYDTFSAFGNILSCK	99.7%	129	25	127	15	1	0	1806.87	114	129
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	AVDEMNGKELNGK	99.7%	41.8	25	37.3	1	0	0	1404.68	247	259

Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	EFSPFGTITSAK	99.7%	73.5	25	58	10	0	0	1284.65	313	324
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	EFTNVYIK	99.7%	51.2	25	36.1	4	0	0	1013.53	189	196
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	EREAELGAR	99.1%	35	25	24.8	4	0	0	1030.53	178	186
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	FGPALSVK	99.7%	57	25	16	10	0	0	818.48	214	221
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	FSPAGPILSIR	99.7%	79.9	25	75	11	0	0	1157.67	31	41
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	GFGFVCFSSPEEATK	99.7%	96.9	25	96.9	9	0	0	1662.75	334	348
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	GFGFVSFER	99.7%	55.3	25	34.4	10	0	0	1045.51	232	240
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	GYGFVHFETQEAAER	99.7%	78.2	25	77.8	6	6	0	1740.80	139	153
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	IMWSQR	95.7%	28.6	25	0	1	0	0	836.41	84	89
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	ITGMLLEIDNSELLHMLESPESLR	99.7%	75.2	25	75.2	0	3	0	2772.38	581	604
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	IVATKPLYVALAQR	99.7%	92.6	25	91.7	8	8	0	1542.94	357	370
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	KEFSPFGTITSAK	99.7%	91.3	25	90.2	7	5	0	1412.74	312	324
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	KSGVGNIFIK	99.4%	36.9	25	35.2	3	0	0	1062.63	95	104
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	LFPLIQAMHPTLAGK	99.7%	86.5	25	84.8	9	1	0	1636.92	566	580
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	LKDLFGK	94.6%	27.6	25	14.5	1	0	0	820.49	207	213
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	MNGMLLNDR	99.7%	64.5	25	53.6	7	0	0	1063.50	158	166
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	MNGMLLNDRK	99.7%	49.1	25	40.1	4	0	0	1191.60	158	167
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	NFGEDMDDER	99.5%	37.3	25	37.3	3	0	0	1227.46	197	206
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	NFGEDMDDERLK	99.7%	59.4	25	52.2	2	0	0	1468.64	197	208
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	NLDDGIDDER	99.7%	66.7	25	53.9	8	0	0	1161.50	300	309
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	NLDDGIDDERLR	99.7%	65.2	25	52.9	6	4	0	1430.69	300	311
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	QAHLTNQYMQR	99.7%	65.1	25	55.7	9	9	0	1405.66	375	385
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	RSLGYAYVNFQQPADAER	99.7%	71.5	25	69.7	2	3	0	2085.01	50	67
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	SGVGNIFIK	99.7%	81.4	25	54.3	10	0	0	934.54	96	104
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	SKGFGFVCFSSPEEATK	99.7%	65.8	25	64.6	1	2	0	1877.87	332	348
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	SKVDEAVAVLQAHQAK	99.7%	114	25	108	2	4	0	1693.92	605	620
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	SLGYAYVNFQQPADAER	99.7%	105	25	105	17	0	0	1928.91	51	67
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	VANTSTQTMGPRPAAAAAAATPAVR	99.7%	48.7	25	48.7	0	2	0	2397.23	482	506
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	VDEAVAVLQAHQAK	99.7%	70.2	25	70.2	2	1	0	1478.80	607	620
Polyadenylate-binding protein 1	PABPC1	PABP1_HUMAN	70.7	100.0%	34	53	276	0.26%	50.2%	YQGVNLYVK	99.7%	52	25	43.2	10	0	0	1083.58	291	299
Polyadenylate-binding protein 2	PABPN1	PABP2_HUMAN	32.7	100.0%	8	10	22	0.02%	19.0%	ELQNEVEK	99.7%	39.3	25	11.2	2	0	0	988.49	138	145
Polyadenylate-binding protein 2	PABPN1	PABP2_HUMAN	32.7	100.0%	8	10	22	0.02%	19.0%	EMEEEAEKLK	99.7%	43.2	25	35.3	1	0	0	1235.58	128	137
Polyadenylate-binding protein 2	PABPN1	PABP2_HUMAN	32.7	100.0%	8	10	22	0.02%	19.0%	GFAYIEFSDK	99.7%	59	25	48.3	2	0	0	1176.56	214	223
Polyadenylate-binding protein 2	PABPN1	PABP2_HUMAN	32.7	100.0%	8	10	22	0.02%	19.0%	GFAYIEFSDKESVR	99.7%	69.9	25	55.9	2	2	0	1647.80	214	227
Polyadenylate-binding protein 2	PABPN1	PABP2_HUMAN	32.7	100.0%	8	10	22	0.02%	19.0%	LKELQNEVEK	99.4%	37.1	25	10.4	2	0	0	1229.67	136	145
Polyadenylate-binding protein 2	PABPN1	PABP2_HUMAN	32.7	100.0%	8	10	22	0.02%	19.0%	TSLALDESLFR	99.7%	71.9	25	68.3	5	0	0	1251.66	228	238
Polyadenylate-binding protein 2	PABPN1	PABP2_HUMAN	32.7	100.0%	8	10	22	0.02%	19.0%	VREMEEEAEK	99.5%	37.4	25	32.5	2	0	0	1249.57	126	135
Polyadenylate-binding protein 2	PABPN1	PABP2_HUMAN	32.7	100.0%	8	10	22	0.02%	19.0%	VTILCDKFSGHPK	99.7%	66.9	25	61.5	2	2	0	1501.78	201	213
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	AHLTNQYMQR	99.7%	53.6	25	53.2	3	0	0	1261.61	376	385
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	AKEFTNVYIK	99.7%	48.7	25	43	6	4	0	1212.66	187	196
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	ALDTMNFDVIK	99.7%	87.2	25	79.1	25	0	0	1266.64	68	78
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	ALYDTFSAFGNILSCK	99.7%	129	25	127	15	1	0	1806.87	114	129
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	AVEEMNGKEISGK	99.7%	54.7	25	49.1	2	0	0	1407.68	247	259
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	EFSPFGSITSAK	99.7%	64.5	25	63.8	5	0	0	1270.63	313	324
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	EFTNVYIK	99.7%	51.2	25	36.1	4	0	0	1013.53	189	196
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	FSPAGPVLSIR	99.7%	71.4	25	60.8	13	0	0	1143.65	31	41
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	GFGFVCFSSPEEATK	99.7%	96.9	25	96.9	9	0	0	1662.75	334	348
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	GFGFVSYEK	99.7%	46.8	25	26	2	0	0	1033.50	232	240
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	GFGFVSYEKHEDANK	99.7%	63.5	25	63.3	1	2	0	1727.80	232	246
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	GYAFVHFETQEAADK	99.7%	86.1	25	86.1	2	2	0	1712.79	139	153
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	GYAFVHFETQEAADKAIEK	99.7%	44.6	25	44.6	0	2	0	2154.05	139	157

Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	IMWSQR	95.7%	28.6	25	0	1	0	0	836.41	84	89
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	ITGMLLEIDNSELLHMLESPESLR	99.7%	75.2	25	75.2	0	3	0	2772.38	590	613
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	IVGSKPLYVALAQR	99.7%	78	25	59.5	2	3	0	1514.91	357	370
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	KAHLTNQYMQR	99.7%	63.5	25	63.5	4	3	0	1405.70	375	385
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	KEFSPFGSITSAK	99.7%	52.4	25	43.4	1	0	0	1398.73	312	324
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	LFPLIQTMHSNLAGK	99.7%	81.7	25	78.9	6	0	0	1669.91	575	589
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	MNGMLLNDR	99.7%	64.5	25	53.6	7	0	0	1063.50	158	166
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	MNGMLLNDRK	99.7%	49.1	25	40.1	4	0	0	1191.60	158	167
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	NFGEEVDDESLKELFSQFGK	99.7%	97.2	25	97.2	2	2	0	2318.08	197	216
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	NLDDTIDDEK	99.7%	44.4	25	44.4	2	0	0	1177.52	300	309
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	NLDDTIDDEKLR	99.7%	60.7	25	53.7	2	0	0	1446.71	300	311
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	RSLGYAYVNFQQPADAER	99.7%	71.5	25	69.7	2	3	0	2085.01	50	67
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	SGVGNVFIK	99.7%	81.7	25	36.4	2	0	0	920.52	96	104
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	SKGFGFVCFSSPEEATK	99.7%	65.8	25	64.6	1	2	0	1877.87	332	348
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	SKVDEAVAVLQAHHAK	99.7%	59.5	25	58.3	0	2	0	1702.92	614	629
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	SLGYAYVNFQQPADAER	99.7%	105	25	105	17	0	0	1928.91	51	67
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	VMLEDGR	99.7%	39.9	25	28.9	2	0	0	835.40	325	331
Polyadenylate-binding protein 4	PABPC4	PABP4_HUMAN	70.8	100.0%	19	27	73	0.07%	46.0%	YQGVNLYIK	99.7%	48.7	25	40.8	6	0	0	1097.60	291	299
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	4	4	7	0.01%	14.1%	IFSLSGTLETVR	99.7%	83.9	25	72.6	2	0	0	1322.73	286	297
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	4	4	7	0.01%	14.1%	LENLDSDVVQLR	99.7%	89.8	25	79.5	2	0	0	1400.74	269	280
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	4	4	7	0.01%	14.1%	SQTEAVTFLANHDDSR	99.7%	75.4	25	75.4	1	0	0	1790.83	150	165
Polymerase delta-interacting protein 2	POLDIP2	PDIP2_HUMAN	42.0	100.0%	4	4	7	0.01%	14.1%	VLETVGVFEVPK	99.7%	64.1	25	63.6	2	0	0	1316.75	61	72
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	17	24	49	0.05%	55.7%	AQAALQAVNSVQSGNLALAASAAAVDAGMAMAGQSPVLR	99.7%	106	25	106	0	2	0	3680.88	147	185
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	17	24	49	0.05%	55.7%	DYGNSPLHR	99.7%	45.3	25	32.3	2	0	0	1058.50	429	437
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	17	24	49	0.05%	55.7%	ELKTDSSPNQAR	99.7%	39.8	25	27.1	2	0	0	1345.67	135	146
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	17	24	49	0.05%	55.7%	ENALVQMADGNQAQLAMSHLNGHK	99.7%	38.4	25	38.4	0	1	0	2577.23	375	398
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	17	24	49	0.05%	55.7%	GQPIYIQFSNHK	99.7%	75.1	25	68.9	3	0	0	1431.74	123	134
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	17	24	49	0.05%	55.7%	HQNVQLPR	99.7%	45.3	25	36.9	2	0	0	991.54	411	418
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	17	24	49	0.05%	55.7%	IAIPGLAGAGNSVLLVSNLNPER	99.7%	111	25	111	3	2	0	2275.28	326	348
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	17	24	49	0.05%	55.7%	IIVENLFYPVTLDVLHQIFSK	99.7%	64.9	25	64.9	1	2	0	2488.39	186	206
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	17	24	49	0.05%	55.7%	KLPIDVTEGEVISLGLPFGK	99.7%	114	25	114	2	2	0	2112.20	65	84
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	17	24	49	0.05%	55.7%	LPIDVTEGEVISLGLPFGK	99.7%	87.7	25	87.7	1	0	0	1984.10	66	84
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	17	24	49	0.05%	55.7%	LSLDGQNIYNACCTLR	99.7%	111	25	111	2	0	0	1897.89	239	254
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	17	24	49	0.05%	55.7%	NFQNIFPPSATLHLSNIPPSVSEEDLK	99.7%	40.9	25	38.8	0	6	0	2994.52	445	471
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	17	24	49	0.05%	55.7%	NNQFQALLQYADPVSAQHAK	99.7%	105	25	105	2	2	0	2243.12	219	238
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	17	24	49	0.05%	55.7%	NQAFIEMNTEEAANTMVNYYTSVTPVLR	99.7%	39.2	25	1.57	0	1	0	3222.51	95	122
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	17	24	49	0.05%	55.7%	VLFSSNGGVVK	99.7%	63.9	25	56.6	2	0	0	1106.62	472	482
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	17	24	49	0.05%	55.7%	VTNLLMLK	99.7%	59.6	25	0	4	0	0	931.56	85	92
Polypyrimidine tract-binding protein 1	PTBP1	PTBP1_HUMAN	57.2	100.0%	17	24	49	0.05%	55.7%	VTPQSLFILFGVYGDVQR	99.7%	94.7	25	94.7	2	3	0	2039.10	349	366
Polypyrimidine tract-binding protein 3	PTBP3	PTBP3_HUMAN	59.7	100.0%	5	5	6	0.01%	12.3%	HQAVQLPR	99.7%	45.8	25	39	2	0	0	948.54	432	439
Polypyrimidine tract-binding protein 3	PTBP3	PTBP3_HUMAN	59.7	100.0%	5	5	6	0.01%	12.3%	KIPCDVTEAEIISLGLPFGK	96.3%	24	25	24	0	1	0	2187.17	65	84
Polypyrimidine tract-binding protein 3	PTBP3	PTBP3_HUMAN	59.7	100.0%	5	5	6	0.01%	12.3%	NLFIEAGCSVK	99.7%	41.2	25	38.3	1	0	0	1237.62	493	503
Polypyrimidine tract-binding protein 3	PTBP3	PTBP3_HUMAN	59.7	100.0%	5	5	6	0.01%	12.3%	SQPVYIQYSNHR	97.5%	30.7	25	30.7	1	0	0	1491.73	123	134
Polypyrimidine tract-binding protein 3	PTBP3	PTBP3_HUMAN	59.7	100.0%	5	5	6	0.01%	12.3%	TDNLPNQAR	98.5%	32.9	25	21.9	1	0	0	1028.51	138	146
Polypyrimidine tract-binding protein 3	PTBP3	PTBP3_HUMAN	59.7	100.0%	5	5	6	0.01%	12.3%	VTNLLMLK	99.7%	59.6	25	0	4	0	0	931.56	85	92
Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	FIP1_HUMAN	66.5	100.0%	4	4	6	0.01%	10.3%	AEFTSPPSLFK	99.7%	44.1	25	33.8	2	0	0	1223.63	255	265
Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	FIP1_HUMAN	66.5	100.0%	4	4	6	0.01%	10.3%	RLPGAIDVIGQTITISR	99.7%	49.5	25	49.5	0	1	0	1810.05	309	325
Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	FIP1_HUMAN	66.5	100.0%	4	4	6	0.01%	10.3%	TGAPQYGSYGTAPVNLNIK	99.7%	91.8	25	89	2	0	0	1950.99	105	123
Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	FIP1_HUMAN	66.5	100.0%	4	4	6	0.01%	10.3%	TGNSEKETALPSTK	99.5%	37.2	25	32.1	1	0	0	1462.74	241	254
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	5	7	19	0.02%	48.0%	GTAYVVYEDIFDAK	99.7%	85.9	25	82.9	4	0	0	1590.77	58	71
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	5	7	19	0.02%	48.0%	ITAEEMYDIFGK	99.7%	79.2	25	72	7	0	0	1416.67	30	41

Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	5	7	19	0.02%	48.0%	NACDHLSGFNVCNR	99.7%	57.6	25	57.6	2	2	0	1663.71	72	85
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	5	7	19	0.02%	48.0%	YGINTDPPK	99.6%	38.5	25	32.1	2	0	0	1004.50	117	125
Pre-mRNA branch site protein p14	SF3B14	PM14_HUMAN	14.6	100.0%	5	7	19	0.02%	48.0%	YLVVLYYNANR	99.7%	76.6	25	75	2	0	0	1387.74	86	96
Pre-mRNA-processing factor 17	CDC40	PRP17_HUMAN	65.5	100.0%	8	8	13	0.01%	18.0%	FKENDASNIDGFLGPWAK	95.6%	23.3	25	16.5	0	1	0	2008.98	181	198
Pre-mRNA-processing factor 17	CDC40	PRP17_HUMAN	65.5	100.0%	8	8	13	0.01%	18.0%	IVQWDIR	99.4%	37.1	25	24.5	2	0	0	929.52	400	406
Pre-mRNA-processing factor 17	CDC40	PRP17_HUMAN	65.5	100.0%	8	8	13	0.01%	18.0%	LWDTETGQCISR	99.7%	78.5	25	74.9	2	0	0	1465.67	358	369
Pre-mRNA-processing factor 17	CDC40	PRP17_HUMAN	65.5	100.0%	8	8	13	0.01%	18.0%	SGEIVQEYDR	99.7%	54.4	25	47.9	2	0	0	1195.56	407	416
Pre-mRNA-processing factor 17	CDC40	PRP17_HUMAN	65.5	100.0%	8	8	13	0.01%	18.0%	SYLHIPQDVGVNLR	99.6%	32.5	25	32.5	0	1	0	1610.87	253	266
Pre-mRNA-processing factor 17	CDC40	PRP17_HUMAN	65.5	100.0%	8	8	13	0.01%	18.0%	TFATYGYALDPSLDNHQVSAK	99.7%	59.8	25	59.8	0	2	0	2298.10	131	151
Pre-mRNA-processing factor 17	CDC40	PRP17_HUMAN	65.5	100.0%	8	8	13	0.01%	18.0%	VITCGWDGLIK	99.7%	41.2	25	32.3	1	0	0	1261.66	566	576
Pre-mRNA-processing factor 17	CDC40	PRP17_HUMAN	65.5	100.0%	8	8	13	0.01%	18.0%	VWEWDIPVDFK	99.7%	51.5	25	45.8	2	0	0	1433.71	444	454
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	15	20	39	0.04%	46.6%	ALQDEWDAVMLHSFTLR	99.7%	61	25	61	2	2	0	2032.00	77	93
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	15	20	39	0.04%	46.6%	ATVLTTER	99.7%	58.3	25	46.4	2	0	0	890.49	180	187
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	15	20	39	0.04%	46.6%	FIASTGMDR	99.7%	66.1	25	54.7	4	0	0	997.48	489	497
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	15	20	39	0.04%	46.6%	ILTGGADKNVVVFDK	99.7%	87.7	25	82.2	2	2	0	1575.87	237	251
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	15	20	39	0.04%	46.6%	IWDLKER	98.7%	33.5	25	13.7	2	0	0	959.53	376	382
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	15	20	39	0.04%	46.6%	IWSVPNASCVQVVR	99.7%	82.4	25	74.9	2	0	0	1614.84	290	303
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	15	20	39	0.04%	46.6%	KVTSVVFHPSQDLVFSASPDATIR	99.7%	86.1	25	86.1	0	2	0	2601.37	266	289
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	15	20	39	0.04%	46.6%	QELSHALYQHDAACR	99.7%	62.1	25	62.1	0	2	0	1798.83	101	115
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	15	20	39	0.04%	46.6%	SSEQILATLK	99.7%	63.3	25	40.1	2	0	0	1089.62	252	261
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	15	20	39	0.04%	46.6%	TLQLDNNFEVK	99.7%	62.5	25	51.7	2	0	0	1320.68	429	439
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	15	20	39	0.04%	46.6%	TNVANFPGHSGPITSIAFSENGYYLATAADDSSVK	99.7%	123	25	123	0	2	0	3601.71	383	417
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	15	20	39	0.04%	46.6%	TVPEELVKPEELSK	99.7%	67.4	25	59.4	2	0	0	1597.87	193	206
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	15	20	39	0.04%	46.6%	VTDETSGCSLTCAQFHPDGLIFGTGTMDSQIK	99.7%	90.5	25	90.5	0	3	0	3473.57	344	375
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	15	20	39	0.04%	46.6%	VTSVVFHPSQDLVFSASPDATIR	99.7%	55.3	25	50	0	2	0	2473.27	267	289
Pre-mRNA-processing factor 19	PRPF19	PRP19_HUMAN	55.2	100.0%	15	20	39	0.04%	46.6%	YIAENGTDPINNQPLSEEQLIDIK	99.7%	81.7	25	81.7	2	2	0	2714.35	33	56
Pre-mRNA-processing factor 40 homolog A	PRPF40A	PR40A_HUMAN	108.8	100.0%	5	5	9	0.01%	7.2%	ELEDLEGYQNTIVAGSLITK	99.7%	50.4	25	50.4	1	0	0	2193.13	214	233
Pre-mRNA-processing factor 40 homolog A	PRPF40A	PR40A_HUMAN	108.8	100.0%	5	5	9	0.01%	7.2%	EPAFEDITLESER	99.7%	84.7	25	75	2	0	0	1535.72	777	789
Pre-mRNA-processing factor 40 homolog A	PRPF40A	PR40A_HUMAN	108.8	100.0%	5	5	9	0.01%	7.2%	FTNMLGQPGSTALDLFK	99.5%	37.4	25	33.3	1	0	0	1855.93	646	662
Pre-mRNA-processing factor 40 homolog A	PRPF40A	PR40A_HUMAN	108.8	100.0%	5	5	9	0.01%	7.2%	LAFNSLLEK	99.7%	46.9	25	38.6	4	0	0	1034.59	719	727
Pre-mRNA-processing factor 40 homolog A	PRPF40A	PR40A_HUMAN	108.8	100.0%	5	5	9	0.01%	7.2%	STTLDAGNIK	98.4%	32.4	25	16	1	0	0	1019.54	709	718
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	22	24	42	0.04%	25.4%	AAELETDIR	99.7%	53.5	25	16.5	2	0	0	1017.52	379	387
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	22	24	42	0.04%	25.4%	AAQDLCEEALR	99.7%	40.9	25	33.2	1	0	0	1275.60	693	703
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	22	24	42	0.04%	25.4%	AAVELEEPEDAR	99.7%	61.3	25	61.2	2	0	0	1328.63	409	420
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	22	24	42	0.04%	25.4%	AEVLWLMGAK	99.7%	61	25	48.5	2	0	0	1117.61	607	616
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	22	24	42	0.04%	25.4%	AGSVATCQAVMR	99.7%	43.7	25	41.4	3	0	0	1266.59	516	527
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	22	24	42	0.04%	25.4%	AIYAYALQVFPSK	99.7%	76.6	25	65.5	2	0	0	1470.80	561	573
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	22	24	42	0.04%	25.4%	AVIGIGIEEEDRK	99.7%	68.3	25	67.1	2	0	0	1428.77	528	540
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	22	24	42	0.04%	25.4%	AVVAQAVR	99.7%	40.3	25	34.1	2	0	0	813.49	360	367
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	22	24	42	0.04%	25.4%	EQWIQDAEECDR	99.7%	71.3	25	71.3	1	0	0	1578.65	504	515
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	22	24	42	0.04%	25.4%	ESLEALLQR	99.7%	54	25	35.7	2	0	0	1058.58	591	599
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	22	24	42	0.04%	25.4%	ETNPHHPPAWIASAR	99.7%	40.5	25	40.5	0	2	0	1683.84	303	317
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	22	24	42	0.04%	25.4%	HGELWCAVSK	99.7%	45.4	25	37.5	2	0	0	1186.57	908	917
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	22	24	42	0.04%	25.4%	HIWITAAK	99.7%	43.8	25	31.7	2	0	0	939.54	465	472
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	22	24	42	0.04%	25.4%	HYEDFPK	99.1%	34.9	25	27	2	0	0	935.43	704	710
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	22	24	42	0.04%	25.4%	IDSDLGDAWAFFYK	99.7%	114	25	114	2	0	0	1647.77	870	883
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	22	24	42	0.04%	25.4%	IQQQFSDLKR	99.7%	33.8	25	23.6	1	1	0	1262.69	138	147
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	22	24	42	0.04%	25.4%	LESENDEYER	99.7%	58.9	25	58.9	2	0	0	1283.54	651	660
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	22	24	42	0.04%	25.4%	LEWVQDNIR	99.7%	51.1	25	37.3	2	0	0	1172.61	684	692
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	22	24	42	0.04%	25.4%	LSQVSDSVSGQTVVDPK	99.7%	135	25	112	2	0	0	1745.89	255	271
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	22	24	42	0.04%	25.4%	NPGLWLESVR	99.7%	55.4	25	50.2	2	0	0	1170.63	776	785

Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	22	24	42	0.04%	25.4%	SEDVWLEAAR	99.7%	62.9	25	55.1	1	0	0	1175.57	342	351
Pre-mRNA-processing factor 6	PRPF6	PRP6_HUMAN	106.9	100.0%	22	24	42	0.04%	25.4%	WLAGDVPAAR	99.7%	45.5	25	44.4	2	0	0	1055.56	619	628
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	ADWWTNTAHYNR	99.7%	57.5	25	57.5	2	0	0	1534.68	747	758
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	AISAANLHLR	99.7%	63.4	25	53.4	2	0	0	1065.62	2077	2086
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	ALDIPLVK	99.4%	37	25	35.2	2	0	0	868.55	421	428
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	ANPALYVLR	99.7%	52.4	25	44.7	2	0	0	1016.59	1736	1744
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	AQIAGYLYGVSPPDNPQVK	99.7%	79.6	25	71.1	2	0	0	2017.04	2122	2140
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	AVFWDIK	99.3%	36	25	21	1	0	0	878.48	1152	1158
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	DGVWNLQNEVTK	99.7%	64.4	25	56	1	0	0	1402.70	1211	1222
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	DINLQDEDWNEFNDINK	99.7%	104	25	104	2	0	0	2121.94	285	301
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	DLILADYGKK	99.4%	36.7	25	28.3	2	0	0	1135.64	1985	1994
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	DMNHTNSYGIIR	99.7%	49.2	25	41.2	2	0	0	1420.66	1021	1032
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	DNPNLLFNMCGFECR	99.7%	106	25	104	4	0	0	1886.80	1181	1195
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	EAVVNTQELLDLLVK	99.7%	102	25	94.3	1	0	0	1683.95	1276	1290
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	EELGLIEQAYDNPHEALSR	99.7%	86.4	25	86.4	0	2	0	2184.06	862	880
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	EQSQLTATQTR	99.7%	64.2	25	51.5	2	0	0	1262.63	2035	2045
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	FGDLILK	99.7%	50	25	30.1	2	0	0	805.48	1902	1908
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	FGNAFHLCR	99.7%	43.2	25	37.1	2	0	0	1121.53	540	548
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	FICISDLR	99.7%	56.3	25	43.8	2	0	0	1023.53	2114	2121
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	FNTGPVGK	98.7%	33.2	25	18.6	2	0	0	819.44	616	623
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	FPPVVFYTPK	99.7%	50.2	25	42.8	5	0	0	1194.66	1311	1320
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	FSPIPFPPLSYK	99.7%	41.6	25	41.6	2	0	0	1392.76	822	833
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	FTLWWSPTINR	99.7%	48.2	25	45	2	0	0	1420.74	1534	1544
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	GITPLLER	99.5%	37.9	25	25.1	1	0	0	898.54	643	650
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	GPGCGFWAAGWR	99.7%	78.2	25	74	2	0	0	1321.59	624	635
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	GSELQLPFQACLK	99.7%	67.6	25	53.5	2	0	0	1490.77	1886	1898
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	GTYFPTWEGLFWEK	99.7%	74.4	25	73.4	2	0	0	1760.83	1492	1505
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	GYLPSHYER	99.2%	35.7	25	32.6	2	0	0	1121.54	2250	2258
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	HGDEIITSTTSNYETQTFSSK	99.7%	52.5	25	52.5	0	2	0	2346.07	2050	2070
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	IDLTLLNR	99.7%	58.5	25	37	2	0	0	957.57	988	995
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	IIHTSVWAGQK	99.7%	52.4	25	45.8	2	0	0	1239.68	1821	1831
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	IMADNPSWDGEK	99.7%	72.8	25	72.8	4	0	0	1378.59	2199	2210
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	ISLIQIFR	99.7%	71.9	25	71.3	4	0	0	989.61	1571	1578
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	LIVDHNIADYMTAK	99.7%	65.9	25	65.9	4	2	0	1619.81	999	1012
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	LKEAYSVK	98.2%	32.1	25	17	2	0	0	937.54	846	853
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	LLILALER	99.7%	59.3	25	59.3	2	0	0	940.62	838	845
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	LTLEDLEDSWDR	99.7%	96.5	25	91.6	2	0	0	1491.70	1403	1414
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	LVVDSHVQYR	99.7%	82.3	25	74.4	2	0	0	1215.65	556	565
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	MNSSCADILLFASYK	99.7%	102	25	102	4	0	0	1719.81	1622	1636
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	NNVNVASLTQSEIR	99.7%	86.9	25	82.6	1	0	0	1544.80	1995	2008
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	NNVVINYK	99.7%	54.2	25	50.4	2	0	0	963.53	1013	1020
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	QGYNMLNLLIHR	98.7%	28	25	26.2	0	2	0	1471.78	499	510
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	QILMASGSTTFTK	99.7%	68	25	61.1	4	0	0	1400.71	1246	1258
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	QNPFWWTHQR	99.5%	37.3	25	34	1	0	0	1399.67	1450	1459
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	QQIAEIEK	99.0%	34.5	25	22.5	2	0	0	958.52	2024	2031
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	QTDVGITHFR	99.7%	66.3	25	55	2	0	0	1173.60	1345	1354
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	RALDIPLVK	99.7%	54.5	25	41	2	0	0	1024.65	420	428
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	SGLNQIPNR	99.0%	34.4	25	26.3	1	0	0	998.54	1524	1532
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	SGMSHEEDQLIPNLYR	99.7%	40.4	25	30.4	0	4	0	1904.88	1355	1370
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	SLPVEEQPK	99.3%	36	25	31.6	1	0	0	1026.55	1851	1859
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	SVTTVQWENSFVSVYSK	99.7%	58.7	25	58.7	2	0	0	1960.96	1164	1180

Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	TAEEVAALIR	99.7%	63.1	25	47.6	2	0	0	1072.60	1841	1850
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	TAQCFLR	99.4%	36.4	25	22.3	2	0	0	895.45	1225	1231
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	TGQLFLK	96.7%	29.5	25	18.2	2	0	0	806.48	1814	1820
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	TIIITCSFTPGSCTLTAYK	99.7%	105	25	105	2	0	0	2134.06	2211	2229
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	TILQHLSEAWR	99.7%	47	25	45.2	2	1	0	1353.73	708	718
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	TISSYTAFSR	99.7%	67.9	25	59.9	2	0	0	1132.56	1926	1935
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	TSYEEFTHK	99.7%	48.2	25	47.2	2	0	0	1141.52	1202	1210
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	VPGLPTPIENMILR	99.7%	39.6	25	39.6	4	0	0	1565.87	728	741
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	VQMLLSDR	99.7%	57.3	25	46.3	2	0	0	961.51	2259	2266
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	VWAEYALKR	99.7%	39.6	25	34.6	2	0	0	1135.63	1385	1393
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	VWLFFMR	99.6%	38.3	25	32.3	2	0	0	998.53	636	642
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	WLGNLLAR	94.9%	27.9	25	7.79	1	0	0	942.55	651	658
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	YIQPWESEFIDSQR	99.7%	71.8	25	69.3	2	0	0	1797.84	1371	1384
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	YLTEHPDPNNENIVGYNNK	96.8%	24.5	25	24.5	0	1	0	2231.04	1113	1131
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	YLTEHPDPNNENIVGYNNKK	99.7%	56.8	25	56.8	0	2	0	2359.13	1113	1132
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	YWIDIQLR	99.7%	49.7	25	43.2	2	0	0	1106.60	1660	1667
Pre-mRNA-processing-splicing factor 8	PRPF8	PRP8_HUMAN	273.6	100.0%	66	75	144	0.14%	30.8%	YYVLNALK	99.2%	35.3	25	28.2	2	0	0	983.56	453	460
Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16	DHX38	PRP16_HUMAN	140.5	100.0%	2	2	2	0.00%	1.9%	DATSDLAIIAR	99.7%	53.8	25	40.5	1	0	0	1145.62	435	445
Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16	DHX38	PRP16_HUMAN	140.5	100.0%	2	2	2	0.00%	1.9%	SLNTDVLFGLLR	96.7%	29.6	25	25.3	1	0	0	1347.76	658	669
Pre-mRNA-splicing factor CWC22 homolog	CWC22	CWC22_HUMAN	105.5	100.0%	3	3	4	0.00%	3.3%	FFGLLAGR	95.4%	28.3	25	21.2	1	0	0	880.50	506	513
Pre-mRNA-splicing factor CWC22 homolog	CWC22	CWC22_HUMAN	105.5	100.0%	3	3	4	0.00%	3.3%	LSEETTTSSSR	99.7%	82	25	73.8	2	0	0	1197.56	570	580
Pre-mRNA-splicing factor CWC22 homolog	CWC22	CWC22_HUMAN	105.5	100.0%	3	3	4	0.00%	3.3%	YTSDKDVPSER	99.5%	37.8	25	35	1	0	0	1296.61	784	794
Pre-mRNA-splicing factor SPF27	BCAS2	SPF27_HUMAN	26.1	100.0%	4	4	6	0.01%	20.9%	EAAAALVEEETRR	96.6%	29.5	25	15.7	1	0	0	1444.74	30	42
Pre-mRNA-splicing factor SPF27	BCAS2	SPF27_HUMAN	26.1	100.0%	4	4	6	0.01%	20.9%	QPIELLSMK	99.4%	36.8	25	34.8	1	0	0	1058.59	77	85
Pre-mRNA-splicing factor SPF27	BCAS2	SPF27_HUMAN	26.1	100.0%	4	4	6	0.01%	20.9%	RYELPAPSSGQK	99.7%	65.9	25	59.4	2	0	0	1332.69	86	97
Pre-mRNA-splicing factor SPF27	BCAS2	SPF27_HUMAN	26.1	100.0%	4	4	6	0.01%	20.9%	TIVQLENEIYQIK	99.7%	75	25	57.9	2	0	0	1590.87	198	210
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	13	14	25	0.02%	17.4%	AEQLAAEAER	99.7%	62.1	25	48.7	2	0	0	1087.54	776	785
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	13	14	25	0.02%	17.4%	AEQLAAEAERDQPLR	99.7%	53.8	25	50.4	2	0	0	1696.86	776	790
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	13	14	25	0.02%	17.4%	AIEVLSDEHAR	99.6%	39.3	25	39.3	1	0	0	1239.63	655	665
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	13	14	25	0.02%	17.4%	AVEPAQQYDMFNIYIK	99.7%	68.8	25	64.5	2	0	0	1929.94	622	637
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	13	14	25	0.02%	17.4%	EIINTYTEAVQTVDPFK	99.7%	110	25	110	4	0	0	1968.00	373	389
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	13	14	25	0.02%	17.4%	HENYDEALR	99.7%	40.3	25	40.3	2	0	0	1146.52	446	454
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	13	14	25	0.02%	17.4%	LEQQSVPAAVFGSLKED	99.7%	52.8	25	52.8	1	0	0	1817.93	839	855
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	13	14	25	0.02%	17.4%	LNQLYER	99.7%	41.3	25	31	2	0	0	935.49	53	59
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	13	14	25	0.02%	17.4%	LSPESAEEYIEYLK	99.7%	66.6	25	64.8	2	0	0	1670.82	175	188
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	13	14	25	0.02%	17.4%	LWCSLADYYIR	99.7%	58.2	25	56.2	2	0	0	1459.70	258	268
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	13	14	25	0.02%	17.4%	SSDRLDEAAQR	96.9%	29.9	25	25	1	1	0	1247.60	189	199
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	13	14	25	0.02%	17.4%	TTGAFWQTWK	99.0%	34.6	25	34.6	1	0	0	1225.60	699	708
Pre-mRNA-splicing factor SYF1	XAB2	SYF1_HUMAN	100.0	100.0%	13	14	25	0.02%	17.4%	VQSLNVDAIIR	99.7%	55.7	25	45.1	2	0	0	1227.71	235	245
pre-rRNA processing protein FTSJ3	FTSJ3	SPB1_HUMAN	96.6	100.0%	3	3	6	0.01%	3.9%	ILDPEGLALGAVIASSK	99.7%	81.1	25	78.9	4	0	0	1653.94	662	678
pre-rRNA processing protein FTSJ3	FTSJ3	SPB1_HUMAN	96.6	100.0%	3	3	6	0.01%	3.9%	LACDFLAR	99.6%	39.2	25	34.3	1	0	0	965.49	143	150
pre-rRNA processing protein FTSJ3	FTSJ3	SPB1_HUMAN	96.6	100.0%	3	3	6	0.01%	3.9%	TSVTDFLR	99.7%	42.4	25	33.1	1	0	0	938.49	252	259
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	7	7	11	0.01%	13.3%	AAQEFFQR	99.1%	35.1	25	30.1	1	0	0	996.49	222	229
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	7	7	11	0.01%	13.3%	DSPPEVAGAR	98.6%	33	25	23.7	1	0	0	998.49	543	552
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	7	7	11	0.01%	13.3%	IVVEFSSPNVAK	99.7%	54.1	25	39	2	0	0	1289.71	127	138
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	7	7	11	0.01%	13.3%	LELGDVQALSLWQK	99.7%	82.6	25	75	2	0	0	1599.87	230	243
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	7	7	11	0.01%	13.3%	LLGITPVCR	98.4%	32.4	25	23.1	1	0	0	1028.59	569	577
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	7	7	11	0.01%	13.3%	TVLQQVIEDGSK	99.7%	58	25	46.2	2	0	0	1316.71	100	111
Probable arginine--tRNA ligase, mitochondrial	RARS2	SYRM_HUMAN	65.5	100.0%	7	7	11	0.01%	13.3%	VGLAALIIQDFK	99.7%	68	25	63.4	2	0	0	1287.77	427	438
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	14	14	27	0.03%	33.6%	APILIATDVASR	99.7%	104	25	104	8	0	0	1226.71	469	480
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	14	14	27	0.03%	33.6%	APLPDLYPFGTMR	99.6%	38.9	25	38.9	2	0	0	1477.75	69	81

Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	14	14	27	0.03%	33.6%	DMVGIAQTGSGK	99.7%	85	25	77	2	0	0	1179.57	210	221
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	14	14	27	0.03%	33.6%	DWVLNEFR	99.7%	42.1	25	37.4	2	0	0	1078.53	458	465
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	14	14	27	0.03%	33.6%	ELAQQVQQVADDYGK	99.7%	100	25	98.5	2	0	0	1691.82	255	269
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	14	14	27	0.03%	33.6%	FVINYDYPNSSEDYVHR	99.7%	78.4	25	73.8	2	0	0	2117.96	489	505
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	14	14	27	0.03%	33.6%	GDGPICLVLAPTR	99.7%	71.2	25	68.6	4	0	0	1368.73	242	254
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	14	14	27	0.03%	33.6%	GLDVEDVK	99.7%	40.2	25	24.6	4	0	0	874.45	481	488
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	14	14	27	0.03%	33.6%	GTAYTFFTPGNLK	99.7%	48.3	25	43	2	0	0	1416.72	516	528
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	14	14	27	0.03%	33.6%	GVEICIATPGR	99.7%	59.2	25	38.3	2	0	0	1172.61	294	304
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	14	14	27	0.03%	33.6%	IVDQIRPDR	99.0%	34.7	25	19.7	2	0	0	1111.62	342	350
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	14	14	27	0.03%	33.6%	KIVDQIRPDR	97.1%	30	25	13.8	1	0	0	1239.72	341	350
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	14	14	27	0.03%	33.6%	LIDFLESGK	99.7%	51.7	25	42.5	2	0	0	1021.56	305	313
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	14	14	27	0.03%	33.6%	LMQLVDHR	98.9%	34.1	25	23.6	2	0	0	1027.54	548	555
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	14	14	27	0.03%	33.6%	LTPYEVDELRR	95.9%	28.7	25	18.8	1	0	0	1390.73	144	154
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	14	14	27	0.03%	33.6%	MLDMGFEPQIR	99.7%	72.5	25	66.6	7	0	0	1336.64	330	340
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	14	14	27	0.03%	33.6%	NFYVEHPEVAR	99.7%	48.7	25	44.6	2	0	0	1360.66	133	143
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	14	14	27	0.03%	33.6%	QLAEDFLR	99.7%	58.6	25	29.3	2	0	0	991.52	365	372
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	14	14	27	0.03%	33.6%	QTLMWSATWPK	99.7%	62.2	25	51.4	4	0	0	1348.67	351	361
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	14	14	27	0.03%	33.6%	SSQSSSQQFSGIGR	99.7%	98.8	25	93.2	2	0	0	1455.68	671	684
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	14	14	27	0.03%	33.6%	STCIYGGAPK	99.7%	58.7	25	47.5	4	0	0	1053.50	275	284
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	14	14	27	0.03%	33.6%	TIIFVETK	98.6%	33	25	33	1	0	0	950.56	421	428
Probable ATP-dependent RNA helicase DDX17	DDX17	DDX17_HUMAN	80.3	100.0%	14	14	27	0.03%	33.6%	VLEEANQAINPK	99.7%	77.6	25	73.6	3	0	0	1325.71	536	547
Probable ATP-dependent RNA helicase DDX20	DDX20	DDX20_HUMAN	92.2	100.0%	4	4	4	0.00%	5.3%	IPFNQALVFSNLHSR	99.7%	54.6	25	53	0	1	0	1742.93	307	321
Probable ATP-dependent RNA helicase DDX20	DDX20	DDX20_HUMAN	92.2	100.0%	4	4	4	0.00%	5.3%	TAQDLSSPR	99.7%	46.8	25	38.2	1	0	0	974.49	42	50
Probable ATP-dependent RNA helicase DDX20	DDX20	DDX20_HUMAN	92.2	100.0%	4	4	4	0.00%	5.3%	VLISTDLTSR	99.7%	39.7	25	39.7	1	0	0	1104.63	362	371
Probable ATP-dependent RNA helicase DDX20	DDX20	DDX20_HUMAN	92.2	100.0%	4	4	4	0.00%	5.3%	VVNSYPLAHK	94.5%	27.6	25	17.2	1	0	0	1127.62	282	291
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	100.0%	5	5	7	0.01%	6.5%	DIIGVAETGSGK	99.7%	60.4	25	53.7	2	0	0	1146.60	430	441
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	100.0%	5	5	7	0.01%	6.5%	ELAQQIEEETIK	99.7%	46.8	25	46.8	2	0	0	1430.74	479	490
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	100.0%	5	5	7	0.01%	6.5%	LIDVLENR	99.7%	39.6	25	38.5	1	0	0	971.55	529	536
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	100.0%	5	5	7	0.01%	6.5%	QAIPIGLQNR	99.7%	48.5	25	35.3	1	0	0	1109.64	420	429
Probable ATP-dependent RNA helicase DDX23	DDX23	DDX23_HUMAN	95.6	100.0%	5	5	7	0.01%	6.5%	TLEEKEQEEAR	99.7%	54.5	25	51.5	1	0	0	1361.65	329	339
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	7	7	9	0.01%	9.4%	ALQEFDLALR	99.7%	39.8	25	32.9	1	0	0	1175.64	667	676
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	7	7	9	0.01%	9.4%	EAIVAALLTR	99.7%	53.1	25	47	1	0	0	1056.64	451	460
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	7	7	9	0.01%	9.4%	EAVVQEPER	99.5%	37.3	25	31.1	1	0	0	1056.53	642	650
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	7	7	9	0.01%	9.4%	ELGIQVHSVTR	99.7%	59.7	25	48.2	2	0	0	1238.69	300	310
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	7	7	9	0.01%	9.4%	IFVNSNTDVAPFLR	99.7%	68.9	25	60.3	2	0	0	1592.84	423	436
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	7	7	9	0.01%	9.4%	SADFNPDFVFTEK	99.7%	48.2	25	43.3	1	0	0	1516.70	79	91
Probable ATP-dependent RNA helicase DDX27	DDX27	DDX27_HUMAN	89.8	100.0%	7	7	9	0.01%	9.4%	VLVLVPTR	97.5%	30.6	25	30.5	1	0	0	896.59	292	299
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	8	8	13	0.01%	18.1%	AQLVLVGATFPEGVGQLLNK	99.7%	68.5	25	68.5	2	0	0	2054.16	324	343
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	8	8	13	0.01%	18.1%	AQQEAPAVR	98.5%	32.7	25	12.9	1	0	0	969.51	112	120
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	8	8	13	0.01%	18.1%	GSFADLGLEPR	99.7%	48.4	25	40.4	1	0	0	1161.59	126	136
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	8	8	13	0.01%	18.1%	LLGQPSLDSLPIPAPR	99.7%	66.2	25	66.2	2	0	0	1673.96	190	205
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	8	8	13	0.01%	18.1%	RPELNQPAR	99.5%	37.2	25	30	2	0	0	1080.59	73	81
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	8	8	13	0.01%	18.1%	SPDEPLPVVR	98.8%	33.9	25	33.9	1	0	0	1108.60	28	37
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	8	8	13	0.01%	18.1%	VAELVHILK	99.7%	40.3	25	40.3	2	0	0	1021.64	378	386
Probable ATP-dependent RNA helicase DDX28	DDX28	DDX28_HUMAN	59.6	100.0%	8	8	13	0.01%	18.1%	VASPDAVTTITSSK	99.7%	54.4	25	46	2	0	0	1376.73	344	357
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	5	5	8	0.01%	9.8%	DVLVATDVASK	99.7%	59.8	25	44.4	1	0	0	1117.61	484	494
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	5	5	8	0.01%	9.8%	GVEAVAIHGGKDQEER	95.9%	23.6	25	22.2	0	1	0	1694.85	456	471
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	5	5	8	0.01%	9.8%	MVYLLECLQK	97.5%	30.7	25	26.7	2	0	0	1296.67	421	430
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	5	5	8	0.01%	9.8%	SALVKPVTINVGR	99.7%	37	25	36.3	0	3	0	1353.82	388	400
Probable ATP-dependent RNA helicase DDX41	DDX41	DDX41_HUMAN	69.8	100.0%	5	5	8	0.01%	9.8%	TPPPVLIFAEK	97.3%	30.4	25	27.5	1	0	0	1211.70	431	441
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	5	5	9	0.01%	13.4%	IQIEAIPLALQGR	99.7%	105	25	95.6	2	0	0	1421.85	50	62

Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	5	5	9	0.01%	13.4%	LFALVLTPTR	99.7%	45.4	25	41.5	2	0	0	1130.69	93	102
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	5	5	9	0.01%	13.4%	LIDHLENTK	99.7%	42.4	25	36.5	1	0	0	1082.58	153	161
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	5	5	9	0.01%	13.4%	LQQYYIFIPSK	99.7%	50	25	31.1	2	0	0	1399.76	238	248
Probable ATP-dependent RNA helicase DDX47	DDX47	DDX47_HUMAN	50.6	100.0%	5	5	9	0.01%	13.4%	TGAFALPILNALLETPQR	99.7%	79.1	25	79.1	2	0	0	1925.09	75	92
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	27	75	0.07%	37.8%	APILIATDVASR	99.7%	104	25	104	8	0	0	1226.71	392	403
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	27	75	0.07%	37.8%	DGWPAMGIHGDK	99.7%	43.3	25	37.6	2	0	0	1283.58	364	375
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	27	75	0.07%	37.8%	DWVLNEFK	96.0%	28.9	25	20.6	1	0	0	1050.53	381	388
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	27	75	0.07%	37.8%	ELAQQVQQVAAEYCR	99.7%	90.8	25	90.8	4	0	0	1792.86	178	192
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	27	75	0.07%	37.8%	FVINYDYPNSSEDYIHR	99.7%	75.8	25	60.3	1	2	0	2131.97	412	428
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	27	75	0.07%	37.8%	GDGPICLVLAPTR	99.7%	71.2	25	68.6	4	0	0	1368.73	165	177
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	27	75	0.07%	37.8%	GLDVEDVK	99.7%	40.2	25	24.6	4	0	0	874.45	404	411
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	27	75	0.07%	37.8%	GVEICIATPGR	99.7%	59.2	25	38.3	2	0	0	1172.61	217	227
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	27	75	0.07%	37.8%	IVDQIRPDR	99.0%	34.7	25	19.7	2	0	0	1111.62	265	273
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	27	75	0.07%	37.8%	KIVDQIRPDR	97.1%	30	25	13.8	1	0	0	1239.72	264	273
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	27	75	0.07%	37.8%	LIDFLECGK	99.7%	59.9	25	56.6	4	0	0	1094.56	228	236
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	27	75	0.07%	37.8%	LLQLVEDR	99.7%	64.8	25	48.8	4	0	0	985.57	471	478
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	27	75	0.07%	37.8%	LMEEIMSEKENK	99.7%	43.4	25	37.1	1	0	0	1480.70	332	343
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	27	75	0.07%	37.8%	MLDMGFEPQIR	99.7%	72.5	25	66.6	7	0	0	1336.64	253	263
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	27	75	0.07%	37.8%	NFYQEHPDLAR	99.7%	52.8	25	41.3	2	0	0	1389.65	57	67
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	27	75	0.07%	37.8%	QTLMWSATWPK	99.7%	62.2	25	51.4	4	0	0	1348.67	274	284
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	27	75	0.07%	37.8%	QVSDLISVLR	99.7%	74.6	25	57.7	4	0	0	1129.66	452	461
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	27	75	0.07%	37.8%	STCIYGGAPK	99.7%	58.7	25	47.5	4	0	0	1053.50	198	207
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	27	75	0.07%	37.8%	TAQEVETYR	99.7%	69.7	25	56.3	2	0	0	1096.53	69	77
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	27	75	0.07%	37.8%	TAQEVETYRR	96.7%	24.4	25	22.6	0	1	0	1252.63	69	78
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	27	75	0.07%	37.8%	TGTAYTFFTPNNIK	99.7%	82.3	25	67.5	4	0	0	1574.79	438	451
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	27	75	0.07%	37.8%	TIVFVETK	99.6%	38.2	25	29.6	3	0	0	936.54	344	351
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	27	75	0.07%	37.8%	TIVFVETKR	99.7%	58	25	56.8	2	0	0	1092.64	344	352
Probable ATP-dependent RNA helicase DDX5	DDX5	DDX5_HUMAN	69.1	100.0%	24	27	75	0.07%	37.8%	TTYLVLDEADR	99.7%	82.7	25	73.3	2	0	0	1295.65	242	252
Probable ATP-dependent RNA helicase DDX52	DDX52	DDX52_HUMAN	67.5	100.0%	4	5	9	0.01%	8.0%	ELASQIHR	99.7%	41.9	25	23.8	2	0	0	953.52	245	252
Probable ATP-dependent RNA helicase DDX52	DDX52	DDX52_HUMAN	67.5	100.0%	4	5	9	0.01%	8.0%	ELLASAPTGSGK	98.5%	32.8	25	32.8	2	0	0	1130.61	204	215
Probable ATP-dependent RNA helicase DDX52	DDX52	DDX52_HUMAN	67.5	100.0%	4	5	9	0.01%	8.0%	GFNPPVLVFVQSIER	99.7%	72.2	25	72.2	2	0	0	1701.93	410	424
Probable ATP-dependent RNA helicase DDX52	DDX52	DDX52_HUMAN	67.5	100.0%	4	5	9	0.01%	8.0%	TLAFSIPILMQLK	99.7%	55.9	25	55.9	3	0	0	1474.87	216	228
Probable ATP-dependent RNA helicase DDX56	DDX56	DDX56_HUMAN	61.6	99.8%	2	2	3	0.00%	4.4%	SLLFVNTLER	99.7%	73.7	25	65.3	1	0	0	1191.67	261	270
Probable ATP-dependent RNA helicase DDX56	DDX56	DDX56_HUMAN	61.6	99.8%	2	2	3	0.00%	4.4%	VANVSAAEDSVSQR	99.7%	95.7	25	87.5	2	0	0	1432.70	115	128
Probable ATP-dependent RNA helicase DHX36	DHX36	DHX36_HUMAN	114.8	100.0%	3	3	4	0.00%	4.8%	ASLLDDYQLPEILR	99.7%	87.2	25	82.2	2	0	0	1645.88	620	633
Probable ATP-dependent RNA helicase DHX36	DHX36	DHX36_HUMAN	114.8	100.0%	3	3	4	0.00%	4.8%	AVICAGLYPK	99.7%	40.1	25	31.7	1	0	0	1091.59	833	842
Probable ATP-dependent RNA helicase DHX36	DHX36	DHX36_HUMAN	114.8	100.0%	3	3	4	0.00%	4.8%	ISAISVAER	99.7%	49.1	25	29	1	0	0	945.54	267	275
Probable ATP-dependent RNA helicase DHX36	DHX36	DHX36_HUMAN	114.8	100.0%	3	3	4	0.00%	4.8%	TTQVTQFILDNYIER	99.7%	76.9	25	76.9	1	0	0	1840.94	237	251
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	8	8	10	0.01%	5.9%	APEPPPALIVR	99.7%	42.4	25	42.4	1	0	0	1159.68	797	807
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	8	8	10	0.01%	5.9%	EMFLEDILR	99.0%	34.4	25	5.8	1	0	0	1165.59	377	385
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	8	8	10	0.01%	5.9%	LAAIAVAER	99.6%	38.8	25	21.7	1	0	0	913.55	251	259
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	8	8	10	0.01%	5.9%	LASNALQEPSSFR	99.7%	84.4	25	75.8	2	0	0	1419.72	1069	1081
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	8	8	10	0.01%	5.9%	LSQSLGLVSK	99.7%	70	25	58.5	2	0	0	1031.61	81	90
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	8	8	10	0.01%	5.9%	SFDALNFVTMLK	99.6%	38.6	25	30.6	1	0	0	1385.71	713	724
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	8	8	10	0.01%	5.9%	TQLLGQLR	97.4%	30.4	25	16.5	1	0	0	928.56	938	945
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	YTDC2_HUMAN	160.3	100.0%	8	8	10	0.01%	5.9%	VVLIVGETGSGK	99.7%	47.8	25	47.8	1	0	0	1158.67	211	222
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	6	6	9	0.01%	5.7%	DSPTLSNSGIR	99.7%	58	25	51.4	1	0	0	1146.58	898	908
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	6	6	9	0.01%	5.7%	GFQEDSEIR	99.7%	43.3	25	34.3	1	0	0	1080.50	208	216
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	6	6	9	0.01%	5.7%	LGDASIAAPFTSK	99.7%	62.6	25	56.2	2	0	0	1277.67	951	963
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	6	6	9	0.01%	5.7%	SIDGSIVLPLAR	99.7%	48.8	25	46.8	2	0	0	1240.73	786	797
Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	6	6	9	0.01%	5.7%	SPQENLVPCDVLLLR	99.7%	63.5	25	62.2	2	0	0	1752.93	328	342

Probable cation-transporting ATPase 13A1	ATP13A1	AT131_HUMAN	133.0	100.0%	6	6	9	0.01%	5.7%	VLDLQADSR	98.6%	33	25	28.6	1	0	0	1016.54	372	380
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	6	6	9	0.01%	10.5%	DSKPHFTTVFQNSVYK	99.4%	31.2	25	31.2	0	2	0	1897.94	653	668
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	6	6	9	0.01%	10.5%	ICWTVTR	99.6%	38.5	25	20.2	1	0	0	935.48	133	139
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	6	6	9	0.01%	10.5%	LTEYPLVINTLK	99.7%	44.3	25	35.4	1	0	0	1403.81	92	103
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	6	6	9	0.01%	10.5%	TPLCNLLVK	99.7%	55.7	25	51	2	0	0	1057.61	644	652
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	6	6	9	0.01%	10.5%	VLEVVKE	99.7%	45	25	7	2	0	0	815.49	669	675
Probable C-mannosyltransferase DPY19L1	DPY19L1	D19L1_HUMAN	77.3	100.0%	6	6	9	0.01%	10.5%	YSTKPDAVFAGAMPTMASVK	99.7%	39.3	25	35.2	0	1	0	2104.01	544	563
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	7	7	12	0.01%	21.4%	LQVLVGDVLK	99.7%	55.2	25	24.7	2	0	0	1083.68	107	116
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	7	7	12	0.01%	21.4%	LSINTQLLAR	99.7%	70.5	25	56.9	2	0	0	1128.67	175	184
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	7	7	12	0.01%	21.4%	NNFRPPPK	98.5%	32.8	25	24.7	1	0	0	969.53	194	201
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	7	7	12	0.01%	21.4%	NPLIINSIIDK	99.7%	71.1	25	70.3	2	0	0	1239.73	41	51
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	7	7	12	0.01%	21.4%	SMDIDDFIR	99.6%	38.1	25	36.4	1	0	0	1111.51	292	300
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	7	7	12	0.01%	21.4%	SSAVQQLLEK	99.7%	57.3	25	31.9	2	0	0	1102.61	244	253
Probable dimethyladenosine transferase	DIMT1	DIM1_HUMAN	35.2	100.0%	7	7	12	0.01%	21.4%	VVACELDPR	99.7%	44.1	25	26.2	2	0	0	1058.53	81	89
Probable glutamate--tRNA ligase, mitochondrial	EARS2	SYEM_HUMAN	58.7	100.0%	3	3	5	0.00%	6.1%	GGPAGPYQQSQR	99.7%	42.8	25	42.8	2	0	0	1245.60	109	120
Probable glutamate--tRNA ligase, mitochondrial	EARS2	SYEM_HUMAN	58.7	100.0%	3	3	5	0.00%	6.1%	NMSQEQVAQK	99.7%	54.1	25	45.5	2	0	0	1162.55	169	178
Probable glutamate--tRNA ligase, mitochondrial	EARS2	SYEM_HUMAN	58.7	100.0%	3	3	5	0.00%	6.1%	TALYNYIFAK	99.4%	36.6	25	35.2	1	0	0	1203.64	56	65
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	12	12	20	0.02%	14.4%	ADLEGSLDSK	98.7%	33.4	25	27	1	0	0	1034.50	364	373
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	12	12	20	0.02%	14.4%	AMQDALADLPEWYGIK	99.7%	77.7	25	75	2	0	0	1820.89	251	266
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	12	12	20	0.02%	14.4%	EEVDLTGSVPVHAK	99.7%	68.3	25	56.4	1	0	0	1480.76	615	628
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	12	12	20	0.02%	14.4%	FYVLSMFPYPSGK	99.7%	84.2	25	84.2	2	0	0	1535.76	84	96
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	12	12	20	0.02%	14.4%	IPVPQQVAR	98.9%	34	25	32.8	1	0	0	1007.60	853	861
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	12	12	20	0.02%	14.4%	LLAQGLIK	95.7%	28.6	25	0	2	0	0	855.57	593	600
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	12	12	20	0.02%	14.4%	LPSGQYLQR	99.7%	59.8	25	45.6	2	0	0	1061.57	606	614
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	12	12	20	0.02%	14.4%	LSSSAEFTGMTR	99.7%	63.5	25	62.1	1	0	0	1286.60	408	419
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	12	12	20	0.02%	14.4%	QDAFLALTQK	99.7%	61.4	25	47.8	2	0	0	1134.62	420	429
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	12	12	20	0.02%	14.4%	TALINFLVQD	99.7%	67.4	25	64.1	2	0	0	1133.62	894	903
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	12	12	20	0.02%	14.4%	TDALPGVLR	99.7%	47.2	25	42.4	2	0	0	941.54	682	690
Probable leucine--tRNA ligase, mitochondrial	LARS2	SYLM_HUMAN	102.0	100.0%	12	12	20	0.02%	14.4%	VYTISDTIAR	99.7%	41.5	25	31.5	2	0	0	1138.61	104	113
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	99.9%	2	2	3	0.00%	7.2%	AVDPEDDFQR	95.5%	28.4	25	28.4	1	0	0	1191.53	95	104
Probable rRNA-processing protein EBP2	EBNA1BP2	EBP2_HUMAN	34.9	99.9%	2	2	3	0.00%	7.2%	QAQAAVLAVLPR	99.7%	40.3	25	32.4	2	0	0	1236.74	111	122
Probable serine carboxypeptidase CPVL	CPVL	CPVL_HUMAN	54.2	100.0%	4	4	9	0.01%	9.5%	FLSLPEVR	99.6%	39.3	25	29.5	2	0	0	960.55	332	339
Probable serine carboxypeptidase CPVL	CPVL	CPVL_HUMAN	54.2	100.0%	4	4	9	0.01%	9.5%	GGGHILPYDQPLR	97.2%	25	25	10.5	0	1	0	1422.75	445	457
Probable serine carboxypeptidase CPVL	CPVL	CPVL_HUMAN	54.2	100.0%	4	4	9	0.01%	9.5%	NNDFYVTGESYAGK	99.7%	87.2	25	87.2	4	0	0	1564.69	195	208
Probable serine carboxypeptidase CPVL	CPVL	CPVL_HUMAN	54.2	100.0%	4	4	9	0.01%	9.5%	SDSEVAGYIR	99.7%	75.9	25	65.2	2	0	0	1096.53	424	433
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	6	6	9	0.01%	24.2%	GPGMGAPLVSVAVVAR	97.3%	30.3	25	20.1	1	0	0	1496.83	79	94
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	6	6	9	0.01%	24.2%	ISNDPSPGYNIEQMAK	99.7%	91.9	25	90.2	1	0	0	1763.83	170	185
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	6	6	9	0.01%	24.2%	LVELPYTVK	96.4%	29.2	25	23.7	1	0	0	1061.62	190	198
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	6	6	9	0.01%	24.2%	PAVLGFEGSANK	99.7%	84.8	25	80.1	2	0	0	1189.62	2	13
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	6	6	9	0.01%	24.2%	TPLSDSGVTQR	99.7%	49.8	25	30	2	0	0	1160.59	313	323
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	OSGEP_HUMAN	36.4	100.0%	6	6	9	0.01%	24.2%	TYVTPPGTGFLPGDTAR	99.7%	85.4	25	79.2	2	0	0	1749.88	31	47
Probable tRNA pseudouridine synthase 1	TRUB1	TRUB1_HUMAN	37.3	99.9%	2	2	2	0.00%	7.2%	ELSSCANVLELTR	99.5%	38	25	31.5	1	0	0	1491.75	265	277
Probable tRNA pseudouridine synthase 1	TRUB1	TRUB1_HUMAN	37.3	99.9%	2	2	2	0.00%	7.2%	GVLVVGIGSGTK	99.7%	65.1	25	57.4	1	0	0	1086.65	126	137
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	18	19	32	0.03%	8.1%	ALTLQDLDNIWAAQAGK	99.7%	46.2	25	46.2	1	0	0	1827.96	425	441
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	18	19	32	0.03%	8.1%	DGQLWLCAPQAK	99.7%	54.2	25	48.1	2	0	0	1386.68	667	678
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	18	19	32	0.03%	8.1%	EIYTNLGPR	99.7%	54.5	25	44.7	2	0	0	1062.56	795	803
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	18	19	32	0.03%	8.1%	ELDMEPYTVAGVAK	99.3%	35.8	25	32.5	1	0	0	1522.75	1821	1834
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	18	19	32	0.03%	8.1%	ELLAFQTSEK	99.7%	44.3	25	36.1	2	0	0	1165.61	1436	1445
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	18	19	32	0.03%	8.1%	FNDYFEFPR	99.7%	56	25	47.6	2	0	0	1234.55	1812	1820
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	18	19	32	0.03%	8.1%	FSEYLLECPSAEVR	99.7%	74.7	25	73	2	0	0	1699.80	2100	2113
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	18	19	32	0.03%	8.1%	GDLLEGANAYHCEK	99.7%	56.3	25	56.3	1	0	0	1576.71	1760	1773

Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	18	19	32	0.03%	8.1%	GWLVDLLNK	99.7%	41	25	0	2	0	0	1057.60	219	227
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	18	19	32	0.03%	8.1%	HSGDYFTLLR	99.7%	50.7	25	42.7	2	0	0	1208.61	1371	1380
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	18	19	32	0.03%	8.1%	IIEDCSNSEETVK	99.7%	44.6	25	8.5	1	0	0	1523.69	2289	2301
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	18	19	32	0.03%	8.1%	LAQQISDEASR	99.7%	85.7	25	77.9	1	0	0	1217.61	1221	1231
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	18	19	32	0.03%	8.1%	LPPVLAIQLK	99.7%	48	25	45	2	0	0	1091.72	1789	1798
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	18	19	32	0.03%	8.1%	LYSVVSQLIR	99.7%	74.1	25	61.3	2	0	0	1177.69	2228	2237
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	18	19	32	0.03%	8.1%	SGGLPLVLSMLTR	99.7%	70.6	25	70.6	4	0	0	1343.77	1120	1132
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	18	19	32	0.03%	8.1%	VISSVSYYTHR	99.7%	80.3	25	76	1	0	0	1311.67	361	371
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	18	19	32	0.03%	8.1%	VLGGSFADQK	99.7%	48.9	25	39.2	2	0	0	1021.53	1713	1722
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	USP9X_HUMAN	292.3	100.0%	18	19	32	0.03%	8.1%	VVIQSNDDIASR	99.7%	60.9	25	60.9	2	0	0	1316.68	777	788
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	100.0%	8	8	12	0.01%	14.4%	FLGSGGFIGYAPNLSK	99.7%	108	25	99.3	2	0	0	1627.85	151	166
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	100.0%	8	8	12	0.01%	14.4%	FLLEYIAPMTEK	99.7%	75.3	25	73.6	2	0	0	1454.76	615	626
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	100.0%	8	8	12	0.01%	14.4%	IFQNLDGALDEVVLK	99.7%	99.3	25	83.9	2	0	0	1673.91	206	220
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	100.0%	8	8	12	0.01%	14.4%	LQLNYLGNYIPR	99.7%	52.6	25	52.6	1	0	0	1463.80	248	259
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	100.0%	8	8	12	0.01%	14.4%	LTHYHEGLPTTR	99.3%	30.6	25	30.6	0	2	0	1424.73	704	715
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	100.0%	8	8	12	0.01%	14.4%	SEDYVDIVQGR	99.7%	64.6	25	56.5	1	0	0	1280.61	431	441
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	100.0%	8	8	12	0.01%	14.4%	VGVDYEGGGCR	99.7%	85.7	25	78.8	1	0	0	1168.51	671	681
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	PLOD1_HUMAN	83.6	100.0%	8	8	12	0.01%	14.4%	VGVWNVPYISNIYLIK	99.7%	45.1	25	45.1	1	0	0	1878.05	443	458
Profilin-1	PFN1	PROF1_HUMAN	15.1	99.8%	2	3	5	0.00%	17.9%	DSLLQDGEFSMDLR	99.7%	62.2	25	62.2	3	0	0	1625.75	76	89
Profilin-1	PFN1	PROF1_HUMAN	15.1	99.8%	2	3	5	0.00%	17.9%	TDKTLVLLMGK	99.7%	52.3	25	47.7	2	0	0	1234.71	106	116
Profilin-2	PFN2	PROF2_HUMAN	15.0	99.8%	2	2	4	0.00%	19.3%	EGFFTNGLTLGAK	99.7%	46.3	25	46.3	2	0	0	1354.70	57	69
Profilin-2	PFN2	PROF2_HUMAN	15.0	99.8%	2	2	4	0.00%	19.3%	SQGGEPTYNVAVGR	99.7%	71.4	25	69.5	2	0	0	1434.70	92	105
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	11	11	18	0.02%	15.6%	DTIVLLCKPEPELNAAIPSANPAK	99.7%	37.8	25	37.1	0	1	0	2561.36	518	541
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	11	11	18	0.02%	15.6%	EILDESLR	97.7%	31.1	25	21	1	0	0	974.52	449	456
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	11	11	18	0.02%	15.6%	ELPELLQR	99.7%	46	25	43	2	0	0	997.57	439	446
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	11	11	18	0.02%	15.6%	ETVLSALSR	99.7%	47.6	25	40.7	1	0	0	975.55	165	173
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	11	11	18	0.02%	15.6%	FYNELTEILVR	99.7%	76.6	25	67.7	3	0	0	1396.75	676	686
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	11	11	18	0.02%	15.6%	LANQAADYFGDAFK	99.7%	51	25	51	1	0	0	1530.72	216	229
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	11	11	18	0.02%	15.6%	NIQVSHQEFSK	99.7%	44.3	25	41	2	0	0	1316.66	628	638
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	11	11	18	0.02%	15.6%	SLLSNLDEVKK	99.7%	55.5	25	27.1	2	0	0	1245.71	554	564
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	11	11	18	0.02%	15.6%	STPVNVPISQK	99.7%	40.9	25	40.9	2	0	0	1169.65	340	350
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	11	11	18	0.02%	15.6%	SVIEQGGIQTVDQLIK	99.7%	120	25	107	2	0	0	1727.95	423	438
Programmed cell death 6-interacting protein	PDCD6IP	PDC6I_HUMAN	96.0	100.0%	11	11	18	0.02%	15.6%	TSEVDLAKPLVK	99.1%	34.9	25	24	1	0	0	1299.75	12	23
Programmed cell death protein 10	PDCD10	PDC10_HUMAN	24.7	100.0%	2	2	3	0.00%	10.4%	AINVFVSANR	99.7%	55.1	25	40.8	1	0	0	1090.60	187	196
Programmed cell death protein 10	PDCD10	PDC10_HUMAN	24.7	100.0%	2	2	3	0.00%	10.4%	SVEVNFTESLLR	99.7%	65.9	25	59.2	2	0	0	1393.73	71	82
Programmed cell death protein 6	PDCD6	PDCD6_HUMAN	21.9	100.0%	5	7	12	0.01%	28.3%	AGVNFSEFTGVWK	99.7%	62.4	25	54.1	2	0	0	1441.71	78	90
Programmed cell death protein 6	PDCD6	PDCD6_HUMAN	21.9	100.0%	5	7	12	0.01%	28.3%	LSDQFHDILIR	99.7%	60	25	52.8	2	1	0	1356.73	126	136
Programmed cell death protein 6	PDCD6	PDCD6_HUMAN	21.9	100.0%	5	7	12	0.01%	28.3%	QALSGFGYR	99.7%	82.2	25	71.7	2	0	0	998.51	117	125
Programmed cell death protein 6	PDCD6	PDCD6_HUMAN	21.9	100.0%	5	7	12	0.01%	28.3%	SIISMFDRENK	99.7%	54.2	25	48.9	3	0	0	1339.67	67	77
Programmed cell death protein 6	PDCD6	PDCD6_HUMAN	21.9	100.0%	5	7	12	0.01%	28.3%	YITDWQNVFR	99.7%	55.1	25	49.9	2	0	0	1341.66	91	100
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	16	19	59	0.06%	59.9%	AAELIANSLATAGDGLIELR	99.7%	138	25	116	4	2	0	1998.09	220	239
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	16	19	59	0.06%	59.9%	AAIISAEGDSK	99.7%	71.8	25	67	3	0	0	1061.55	209	219
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	16	19	59	0.06%	59.9%	AVIFDRFR	99.1%	34.9	25	31.7	2	0	0	1023.57	36	43
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	16	19	59	0.06%	59.9%	DLQNVNITLR	99.7%	73.8	25	56.1	2	0	0	1185.66	84	93
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	16	19	59	0.06%	59.9%	EFTEAVEAK	99.7%	64.9	25	53	2	0	0	1023.50	178	186
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	16	19	59	0.06%	59.9%	FDAGELITQR	99.7%	75	25	61.5	12	0	0	1149.59	134	143
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	16	19	59	0.06%	59.9%	FVVEKAEQQK	96.5%	29.4	25	22.7	1	0	0	1205.65	198	207
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	16	19	59	0.06%	59.9%	IFTSIGEDYDER	99.7%	94.5	25	85.9	6	0	0	1444.66	106	117
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	16	19	59	0.06%	59.9%	ILFRPVASQLPR	99.7%	57.3	25	47.6	2	6	0	1396.84	94	105
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	16	19	59	0.06%	59.9%	KAAIISAEGDSK	99.7%	54	25	48	2	0	0	1189.64	208	219
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	16	19	59	0.06%	59.9%	KLEAAEDIAYQLSR	99.7%	131	25	128	2	2	0	1606.84	240	253

Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	16	19	59	0.06%	59.9%	LEAAEDIAYQLSR	99.7%	68.1	25	60.7	2	0	0	1478.75	241	253
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	16	19	59	0.06%	59.9%	NITYLPAGQSVLLQLPQ	99.3%	35.8	25	35.8	2	0	0	1855.03	256	272
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	16	19	59	0.06%	59.9%	QVAQQEAER	99.6%	38.4	25	25.2	1	0	0	1058.52	187	195
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	16	19	59	0.06%	59.9%	QVSDDLTER	99.7%	39.7	25	28.5	1	0	0	1062.51	149	157
Prohibitin	PHB	PHB_HUMAN	29.8	100.0%	16	19	59	0.06%	59.9%	VLPSITTEILK	99.7%	67.2	25	55.2	5	0	0	1213.74	118	128
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	22	108	0.10%	57.5%	AQFLVEK	99.4%	37	25	16	4	0	0	834.47	210	216
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	22	108	0.10%	57.5%	AQVSLLIR	99.7%	57.3	25	44.5	6	0	0	899.57	158	165
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	22	108	0.10%	57.5%	DLQMVNISLR	99.7%	71.4	25	53.7	8	0	0	1188.64	98	107
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	22	108	0.10%	57.5%	ESVFTVEGGHR	99.7%	98.3	25	80.6	4	3	0	1217.59	38	48
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	22	108	0.10%	57.5%	EYTAAVEAK	99.7%	62.3	25	62.3	4	0	0	981.49	192	200
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	22	108	0.10%	57.5%	FNASQLITQR	99.7%	80.8	25	64.2	8	0	0	1177.63	148	157
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	22	108	0.10%	57.5%	IGGVQQDTILAEGLHFR	99.7%	112	25	112	4	10	0	1853.99	55	71
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	22	108	0.10%	57.5%	IPWFQYPIIYDIR	99.7%	62.5	25	57.2	4	0	0	1723.92	72	84
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	22	108	0.10%	57.5%	IVQAEGEAEAAK	99.7%	90.1	25	78	4	0	0	1215.62	225	236
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	22	108	0.10%	57.5%	IYLTADNLVLNLQDESFTR	99.7%	124	25	124	4	2	0	2225.15	271	289
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	22	108	0.10%	57.5%	LGLDYEER	99.7%	78.6	25	55.3	7	0	0	994.48	124	131
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	22	108	0.10%	57.5%	LLLGAGAVAYGVR	99.7%	101	25	84.6	10	0	0	1259.75	25	37
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	22	108	0.10%	57.5%	MLGEALSK	99.7%	39.4	25	17.2	7	0	0	864.45	237	244
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	22	108	0.10%	57.5%	VLPSIVNEVLK	99.7%	55.5	25	42.8	7	0	0	1210.74	132	142
Prohibitin-2	PHB2	PHB2_HUMAN	33.3	100.0%	15	22	108	0.10%	57.5%	VLSRPNAQELPSMYQR	99.7%	59.6	25	51.9	4	8	0	1888.97	108	123
Prolactin-inducible protein	PIP	PIP_HUMAN	16.6	100.0%	4	4	17	0.02%	36.3%	ELGICPDDAAVIPIK	99.7%	45.5	25	45.1	2	0	0	1610.85	119	133
Prolactin-inducible protein	PIP	PIP_HUMAN	16.6	100.0%	4	4	17	0.02%	36.3%	FYTIEILKVE	99.7%	44.5	25	31.4	7	0	0	1254.70	137	146
Prolactin-inducible protein	PIP	PIP_HUMAN	16.6	100.0%	4	4	17	0.02%	36.3%	TVQIAAVVDVIR	99.7%	76.2	25	62.5	7	0	0	1283.77	107	118
Prolactin-inducible protein	PIP	PIP_HUMAN	16.6	100.0%	4	4	17	0.02%	36.3%	TYLISSIPLQGAFNYK	99.5%	37.2	25	37.2	1	0	0	1814.97	70	85
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	12	17	31	0.03%	55.2%	AEDNADTLALVFEAPNQEK	99.7%	86.8	25	86.8	2	0	0	2074.99	92	110
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	12	17	31	0.03%	55.2%	ATPLSSTVTLSMSADVPLVVEYK	99.7%	68.1	25	68.1	3	2	0	2424.26	218	240
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	12	17	31	0.03%	55.2%	DLSHIGDAVVISCAK	99.7%	70.1	25	70.1	2	1	0	1584.81	150	164
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	12	17	31	0.03%	55.2%	FSASGELGNGNIK	99.7%	98.4	25	91.7	2	0	0	1293.64	169	181
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	12	17	31	0.03%	55.2%	IADMGHLK	99.7%	45.3	25	37.8	2	0	0	884.47	241	248
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	12	17	31	0.03%	55.2%	LMDLDVEQLGIPEQEYSCVVK	99.7%	58.2	25	58.2	3	0	0	2481.19	118	138
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	12	17	31	0.03%	55.2%	LVQGSILK	99.6%	38.5	25	13.2	1	0	0	857.55	6	13
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	12	17	31	0.03%	55.2%	LVQGSILKK	99.7%	46.8	25	25.7	2	0	0	985.64	6	14
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	12	17	31	0.03%	55.2%	MPSGEFAR	99.7%	43.1	25	33.4	2	0	0	910.41	139	146
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	12	17	31	0.03%	55.2%	NLAMGVNLTSMSK	99.7%	111	25	110	6	0	0	1365.69	65	77
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	12	17	31	0.03%	55.2%	SEGFDTYR	99.7%	49.5	25	40.9	2	0	0	974.42	54	61
Proliferating cell nuclear antigen	PCNA	PCNA_HUMAN	28.8	100.0%	12	17	31	0.03%	55.2%	YLNFFTK	99.0%	34.6	25	16.3	1	0	0	932.49	211	217
Prolyl 3-hydroxylase 1	LEPRE1	P3H1_HUMAN	83.4	100.0%	5	5	6	0.01%	8.4%	AVGFSSGTENPHGVK	99.5%	37.8	25	37.8	1	0	0	1486.73	648	662
Prolyl 3-hydroxylase 1	LEPRE1	P3H1_HUMAN	83.4	100.0%	5	5	6	0.01%	8.4%	DLSFFGGLLR	99.7%	66.3	25	45.3	2	0	0	1124.61	106	115
Prolyl 3-hydroxylase 1	LEPRE1	P3H1_HUMAN	83.4	100.0%	5	5	6	0.01%	8.4%	LTNVAATSGDGYR	99.7%	62	25	60.5	1	0	0	1324.65	489	501
Prolyl 3-hydroxylase 1	LEPRE1	P3H1_HUMAN	83.4	100.0%	5	5	6	0.01%	8.4%	SPYNYLQVAYFK	99.7%	51.5	25	39	1	0	0	1492.75	144	155
Prolyl 3-hydroxylase 1	LEPRE1	P3H1_HUMAN	83.4	100.0%	5	5	6	0.01%	8.4%	TVTAEVQPQCGR	99.7%	55	25	53.6	1	0	0	1345.65	636	647
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	12	12	20	0.02%	26.4%	DPEGFVGHPVNAFK	99.7%	63.5	25	51	2	0	0	1513.74	73	86
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	12	12	20	0.02%	26.4%	FHDIISDAEIEIVK	99.7%	53.2	25	48.5	1	0	0	1628.85	340	353
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	12	12	20	0.02%	26.4%	GVAVDYLPER	99.7%	52.2	25	46.1	2	0	0	1118.58	277	286
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	12	12	20	0.02%	26.4%	HAACPVLVGNK	99.7%	54.6	25	45.9	2	0	0	1165.61	500	510
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	12	12	20	0.02%	26.4%	KLLELDPEHQR	99.7%	46.4	25	41.7	0	1	0	1377.75	230	240
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	12	12	20	0.02%	26.4%	LLELDPEHQR	99.7%	39.4	25	39.4	2	0	0	1249.65	231	240
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	12	12	20	0.02%	26.4%	LNTEWSELENLVLK	99.7%	71.3	25	60.5	1	0	0	1687.89	91	104
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	12	12	20	0.02%	26.4%	LQDTYNLDTDTISK	99.7%	105	25	97.9	2	0	0	1626.79	137	150
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	12	12	20	0.02%	26.4%	QLDEGEISTIDK	99.7%	55	25	48.8	1	0	0	1347.66	193	204
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	12	12	20	0.02%	26.4%	QYFPNDEDQVGAAK	99.7%	63.8	25	61.1	2	0	0	1581.72	119	132

Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	12	12	20	0.02%	26.4%	SAWLSGYENPVVSR	99.7%	80.1	25	74.1	2	0	0	1564.78	383	396
Prolyl 4-hydroxylase subunit alpha-1	P4HA1	P4HA1_HUMAN	61.1	100.0%	12	12	20	0.02%	26.4%	SFLTAEDCFELGK	99.7%	53.7	25	53.7	2	0	0	1516.70	160	172
Prolyl 4-hydroxylase subunit alpha-2	P4HA2	P4HA2_HUMAN	60.9	100.0%	3	3	6	0.01%	6.2%	GTAVFWYNLLR	98.5%	32.8	25	26.6	2	0	0	1339.72	481	491
Prolyl 4-hydroxylase subunit alpha-2	P4HA2	P4HA2_HUMAN	60.9	100.0%	3	3	6	0.01%	6.2%	QLDAGEEATTTK	99.7%	72	25	66.5	2	0	0	1263.61	195	206
Prolyl 4-hydroxylase subunit alpha-2	P4HA2	P4HA2_HUMAN	60.9	100.0%	3	3	6	0.01%	6.2%	TGVLTVASYR	99.7%	78.2	25	72.4	2	0	0	1066.59	371	380
Proteasomal ubiquitin receptor ADRM1	ADRM1	ADRM1_HUMAN	42.2	99.8%	2	2	4	0.00%	5.9%	SQSAAVTPSSTTSSTR	99.7%	63.4	25	58.2	2	0	0	1567.76	211	226
Proteasomal ubiquitin receptor ADRM1	ADRM1	ADRM1_HUMAN	42.2	99.8%	2	2	4	0.00%	5.9%	VPQCPSGR	98.1%	31.8	25	31.8	2	0	0	900.44	85	92
Proteasome activator complex subunit 3	PSME3	PSME3_HUMAN	29.5	99.8%	2	2	4	0.00%	11.8%	ITSEAEDLVANFFPK	99.7%	54.7	25	52.1	2	0	0	1680.85	22	36
Proteasome activator complex subunit 3	PSME3	PSME3_HUMAN	29.5	99.8%	2	2	4	0.00%	11.8%	TVESEAASYLDQISR	99.7%	77	25	46.1	2	0	0	1668.81	167	181
Proteasome assembly chaperone 3	PSMG3	PSMG3_HUMAN	13.1	99.8%	2	2	4	0.00%	18.0%	AVLLAVAVK	99.7%	40.9	25	29.6	2	0	0	883.60	94	102
Proteasome assembly chaperone 3	PSMG3	PSMG3_HUMAN	13.1	99.8%	2	2	4	0.00%	18.0%	NLVAFVSQEAGNR	99.7%	99.5	25	86.3	2	0	0	1404.72	81	93
Proteasome subunit alpha type-3	PSMA3	PSA3_HUMAN	28.4	100.0%	3	3	6	0.01%	12.2%	AVENSSTAIGIR	99.7%	77.2	25	69.7	2	0	0	1217.65	30	41
Proteasome subunit alpha type-3	PSMA3	PSA3_HUMAN	28.4	100.0%	3	3	6	0.01%	12.2%	SNFGYNIPLK	99.5%	37.5	25	35.9	2	0	0	1152.60	101	110
Proteasome subunit alpha type-3	PSMA3	PSA3_HUMAN	28.4	100.0%	3	3	6	0.01%	12.2%	VFQVEYAMK	99.7%	62.8	25	60	2	0	0	1114.56	21	29
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	6	8	18	0.02%	21.8%	ATCIGNNSAAAVSMLK	99.7%	113	25	94.4	4	0	0	1607.79	161	176
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	6	8	18	0.02%	21.8%	LLDEVFFSEK	99.7%	61.1	25	57.8	4	0	0	1226.63	55	64
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	6	8	18	0.02%	21.8%	LSAEKVEIATLTR	99.7%	85.5	25	75.8	2	2	0	1430.82	206	218
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	6	8	18	0.02%	21.8%	QAYTQFGGK	99.0%	34.7	25	30.2	1	0	0	999.49	119	127
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	6	8	18	0.02%	21.8%	TTIFSPEGR	99.7%	55.3	25	40.8	2	0	0	1007.52	9	17
Proteasome subunit alpha type-4	PSMA4	PSA4_HUMAN	29.5	100.0%	6	8	18	0.02%	21.8%	VEIATLTR	99.7%	64.4	25	46.9	3	0	0	902.53	211	218
Proteasome subunit alpha type-5	PSMA5	PSA5_HUMAN	26.4	100.0%	4	5	10	0.01%	22.4%	GPQLFHMDPSGTFVQCDAR	99.7%	40.7	25	40.7	0	1	0	2178.97	150	168
Proteasome subunit alpha type-5	PSMA5	PSA5_HUMAN	26.4	100.0%	4	5	10	0.01%	22.4%	GVNTFSPEGR	99.7%	54.3	25	45.8	2	0	0	1063.52	11	20
Proteasome subunit alpha type-5	PSMA5	PSA5_HUMAN	26.4	100.0%	4	5	10	0.01%	22.4%	ITSPLMEPSSIEK	99.7%	71.5	25	60.1	4	0	0	1447.74	54	66
Proteasome subunit alpha type-5	PSMA5	PSA5_HUMAN	26.4	100.0%	4	5	10	0.01%	22.4%	LFQVEYAIEAIK	99.7%	61.3	25	53.6	3	0	0	1423.78	21	32
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	5	6	11	0.01%	23.8%	ALLEVVQSGGK	99.7%	79.2	25	73.6	2	0	0	1100.63	194	204
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	5	6	11	0.01%	23.8%	GRDIVVLGVEK	99.7%	52.4	25	45.4	2	0	0	1184.70	37	47
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	5	6	11	0.01%	23.8%	LTVEDPVTVEYITR	99.7%	61.8	25	58.1	2	0	0	1634.86	96	109
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	5	6	11	0.01%	23.8%	NIELAVMR	99.7%	43.6	25	31.2	3	0	0	961.51	205	212
Proteasome subunit alpha type-7	PSMA7	PSA7_HUMAN	27.9	100.0%	5	6	11	0.01%	23.8%	NYTDEAIETDDLTIK	99.7%	130	25	129	2	0	0	1740.82	175	189
Proteasome subunit beta type-5	PSMB5	PSB5_HUMAN	28.5	100.0%	2	2	4	0.00%	10.3%	ATAGAYIASQTVK	99.7%	67.7	25	57.8	2	0	0	1280.68	79	91
Proteasome subunit beta type-5	PSMB5	PSB5_HUMAN	28.5	100.0%	2	2	4	0.00%	10.3%	DAYSGGAVNLYHVR	99.7%	39.8	25	39.8	2	0	0	1521.74	226	239
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	38	0.04%	14.2%	AGEQLAPFLPQLVPR	99.7%	77.2	25	67.1	2	0	0	1635.92	1112	1126
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	38	0.04%	14.2%	AIACVVTACSAELEK	99.7%	113	25	110	2	0	0	1621.79	1591	1605
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	38	0.04%	14.2%	ALSINTLVK	99.6%	38.2	25	23.3	1	0	0	958.59	1272	1280
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	38	0.04%	14.2%	ESSCLALNDLLR	99.7%	52.9	25	46.6	1	0	0	1390.70	1180	1191
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	38	0.04%	14.2%	FVDKTEWIK	99.7%	41.6	25	31.2	1	0	0	1165.63	691	699
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	38	0.04%	14.2%	HSVATAADLELK	99.7%	43.3	25	38.3	2	0	0	1254.67	274	285
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	38	0.04%	14.2%	IVAISCAADILK	99.7%	86.1	25	75	2	0	0	1273.72	1633	1644
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	38	0.04%	14.2%	LHLVESLLSR	99.6%	38.9	25	36.4	2	0	0	1166.69	838	847
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	38	0.04%	14.2%	LLLQGLMDSVEAK	99.7%	82.2	25	82.2	2	0	0	1416.78	880	892
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	38	0.04%	14.2%	LLSMAYSAVGK	99.7%	68.1	25	57.2	4	0	0	1139.61	415	425
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	38	0.04%	14.2%	LMSALLSGLTDR	99.7%	84.7	25	76.3	2	0	0	1276.69	1401	1412
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	38	0.04%	14.2%	LSSTQEGVR	99.7%	42.8	25	10.5	1	0	0	976.51	47	55
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	38	0.04%	14.2%	MSEQQDLER	99.2%	35.3	25	26.2	1	0	0	1151.50	771	779
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	38	0.04%	14.2%	NGPLPIPSEGSGFTK	99.1%	34.7	25	34.7	2	0	0	1500.77	823	837
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	38	0.04%	14.2%	SASPFNLAEKPK	99.7%	57.2	25	48	1	0	0	1288.69	157	168
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	38	0.04%	14.2%	SVPNQPSTNEILQAVLK	99.7%	43.3	25	43.3	1	0	0	1838.00	1606	1622
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	38	0.04%	14.2%	TEALSVIELLLK	99.7%	74.4	25	70.6	3	0	0	1328.80	1785	1796
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	38	0.04%	14.2%	TLMSSGQMAPSSSNK	99.7%	87.8	25	87.8	2	0	0	1557.69	632	646
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	38	0.04%	14.2%	TPDGQGLSTYK	99.7%	45.2	25	44.5	1	0	0	1166.57	1057	1067
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	38	0.04%	14.2%	TSCALTIHAIGR	99.7%	48.6	25	48.6	1	0	0	1299.68	1457	1468

Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	38	0.04%	14.2%	VYLGDIPLK	97.8%	31.3	25	25.7	2	0	0	1017.60	305	313
Proteasome-associated protein ECM29 homolog	ECM29	ECM29_HUMAN	204.3	100.0%	22	23	38	0.04%	14.2%	YLLLLAAGDPR	99.7%	74.8	25	67.4	2	0	0	1201.69	517	527
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	AAILPTSIFLTNK	99.7%	98	25	98	26	0	0	1388.81	228	240
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	AAILPTSIFLTNKK	99.7%	79.1	25	77.5	6	6	0	1516.91	228	241
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	ADIIVSELLGSFADNELSPECLDGAQHFLK	99.7%	102	25	95.4	0	1	0	3288.61	429	458
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	DDGVSIPGEYTSFLAPISSSK	99.7%	109	25	109	15	0	0	2170.06	459	479
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	DDIIENAPTTHTEEYSGEEK	99.7%	85.9	25	85.9	4	2	0	2278.00	165	184
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	DLNCVPEIADTLGAVAK	99.7%	91.4	25	89.3	22	2	0	1785.91	19	35
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	DPEAQFEMPYVVR	99.7%	74.1	25	74.1	2	0	0	1580.74	493	505
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	DPIKYSQYQQAIYK	99.7%	64.4	25	62.2	2	1	0	1744.89	330	343
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	DPMIDNNR	99.7%	39.6	25	34	2	0	0	974.44	527	534
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	DRDPEAQFEMPYVVR	99.7%	63	25	62.9	3	6	0	1851.87	491	505
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	DTNVQVLMVLGAGR	99.7%	107	25	93.4	2	0	0	1488.78	355	368
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	DWNTLIVGK	99.7%	56.5	25	41.5	11	0	0	1045.57	77	85
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	EFCSYLQYLEYLSQNRPPPNAYELFAK	99.7%	88.4	25	88.4	0	1	0	3340.60	276	302
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	EFIQEPAK	99.7%	44.1	25	31	13	0	0	961.50	53	60
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	EGQTICVR	99.7%	41.9	25	36.8	10	0	0	962.47	594	601
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	EWVAPEK	98.0%	31.5	25	28.2	1	0	0	858.44	422	428
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	GPLVNASLR	99.7%	61.3	25	53.3	10	0	0	926.54	369	377
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	GYEDYLQSPLQPLMDNLESQTYEVFEKDPIK	99.7%	66	25	66	0	4	0	3689.76	303	333
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	IAVALEIGADLPSNHVIDR	99.7%	104	25	104	6	8	0	2003.09	202	220
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	IKLYAVEK	99.1%	35	25	21.1	2	0	0	963.59	386	393
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	KGFPVLSK	99.7%	47.3	25	28.2	9	0	0	875.54	241	248
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	KVWYEWAVTAPVCSAIHNPTGR	99.7%	80.4	25	80.4	0	2	0	2542.27	610	631
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	LHNFHQLSAPQPCFTFSHPNR	99.7%	61.8	25	51.1	0	2	0	2535.21	506	526
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	LSPWIRPDSK	99.1%	34.8	25	28.6	6	0	0	1198.66	86	95
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	QGFDFLCMPVFHPR	99.7%	79.1	25	76.9	10	15	0	1750.82	36	49
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	REFIQEPAK	99.7%	43.2	25	29	2	0	0	1117.60	52	60
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	SDLLLSGR	99.7%	48.6	25	34	8	0	0	860.48	69	76
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	SDLLLSGRDWNTLIVGK	99.7%	85.3	25	85.3	2	2	0	1887.03	69	85
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	TLCDYSK	95.3%	28.2	25	27.7	1	0	0	886.40	194	200
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	TLCDYSKR	99.7%	49.8	25	37.1	3	0	0	1042.50	194	201
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	TWMWWHNFR	99.7%	40.8	25	36.9	11	6	0	1379.61	185	193
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	VPEEEKDTNVQVLMVLGAGR	99.7%	112	25	112	4	10	0	2184.13	349	368
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	VPLVAPEDLR	99.7%	62	25	59.4	14	0	0	1108.64	155	164
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	VPLVAPEDLRDDIIENAPTTHTEEYSGEEK	99.7%	88.5	25	88.5	0	4	0	3367.62	155	184
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	VWYEWAVTAPVCSAIHNPTGR	99.7%	75.7	25	75.7	2	2	0	2414.17	611	631
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	WLGEPIK	98.1%	31.7	25	21.8	3	0	0	842.48	221	227
Protein arginine N-methyltransferase 5	PRMT5	ANM5_HUMAN	72.7	100.0%	37	56	300	0.28%	62.5%	YSQYQQAIYK	99.7%	63.9	25	63.9	14	0	0	1291.63	334	343
Protein BUD31 homolog	BUD31	BUD31_HUMAN	17.0	100.0%	6	6	11	0.01%	40.3%	DTNFGTNCICR	99.7%	50.8	25	49.5	2	0	0	1357.56	110	120
Protein BUD31 homolog	BUD31	BUD31_HUMAN	17.0	100.0%	6	6	11	0.01%	40.3%	ELYEYCIK	95.6%	28.4	25	27.2	1	0	0	1117.52	73	80
Protein BUD31 homolog	BUD31	BUD31_HUMAN	17.0	100.0%	6	6	11	0.01%	40.3%	IIECTHCGCR	99.5%	37.8	25	37.8	2	0	0	1305.55	131	140
Protein BUD31 homolog	BUD31	BUD31_HUMAN	17.0	100.0%	6	6	11	0.01%	40.3%	KVESLWPIFR	99.7%	53.4	25	42.3	2	0	0	1274.73	42	51
Protein BUD31 homolog	BUD31	BUD31_HUMAN	17.0	100.0%	6	6	11	0.01%	40.3%	QGYENLCCLR	99.7%	49.2	25	43.4	2	0	0	1312.58	95	104
Protein BUD31 homolog	BUD31	BUD31_HUMAN	17.0	100.0%	6	6	11	0.01%	40.3%	YIFDLFYKR	99.7%	42.7	25	35.7	2	0	0	1264.67	59	67
Protein CIP2A	KIAA1524	CIP2A_HUMAN	102.2	100.0%	3	3	4	0.00%	3.7%	ALALAQADR	99.7%	46.1	25	37.6	1	0	0	928.52	648	656
Protein CIP2A	KIAA1524	CIP2A_HUMAN	102.2	100.0%	3	3	4	0.00%	3.7%	LITPLAFALTSDNR	99.7%	94.6	25	94.6	2	0	0	1531.85	509	522
Protein CIP2A	KIAA1524	CIP2A_HUMAN	102.2	100.0%	3	3	4	0.00%	3.7%	SLLLTVSQYK	99.7%	56.9	25	56.7	1	0	0	1151.67	9	18
Protein CMSS1	CMSS1	CMS1_HUMAN	31.9	100.0%	3	3	6	0.01%	10.8%	FLVFDWNWR	99.6%	38.5	25	33.4	2	0	0	1282.64	232	240
Protein CMSS1	CMSS1	CMS1_HUMAN	31.9	100.0%	3	3	6	0.01%	10.8%	QGGLNLSPLK	99.7%	78.4	25	65.1	2	0	0	1026.59	222	231
Protein CMSS1	CMSS1	CMS1_HUMAN	31.9	100.0%	3	3	6	0.01%	10.8%	VVHLGVGTPGR	99.7%	68.4	25	66.9	2	0	0	1091.63	205	215

Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	4	5	12	0.01%	9.3%	LLASANLEEVTMK	99.7%	93.8	25	89.8	4	0	0	1434.75	332	344
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	4	5	12	0.01%	9.3%	NVGQFSGFPFEK	99.7%	60	25	58.8	4	0	0	1356.66	126	137
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	4	5	12	0.01%	9.3%	SGVNSELVK	99.7%	48.3	25	32.5	2	0	0	932.50	169	177
Protein DEK	DEK	DEK_HUMAN	42.7	100.0%	4	5	12	0.01%	9.3%	SGVNSELVKR	99.7%	42.3	25	30.5	2	0	0	1088.61	169	178
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	3	3	6	0.01%	2.4%	ELGEYFLFDPK	99.7%	40.7	25	40.7	2	0	0	1357.67	1117	1127
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	3	3	6	0.01%	2.4%	LNAILFK	99.1%	35.2	25	18.2	2	0	0	818.51	937	943
Protein diaphanous homolog 1	DIAPH1	DIAP1_HUMAN	141.4	100.0%	3	3	6	0.01%	2.4%	TAQNLSIFLGSFR	99.7%	62.9	25	62.9	2	0	0	1453.78	856	868
Protein disulfide-isomerase	P4HB	PDIA1_HUMAN	57.1	100.0%	3	3	3	0.00%	10.2%	EADDIVNWLK	94.7%	27.7	25	23	1	0	0	1202.61	121	130
Protein disulfide-isomerase	P4HB	PDIA1_HUMAN	57.1	100.0%	3	3	3	0.00%	10.2%	TGPAATTLPDGAAAESLVESSEVAVIGFFK	99.7%	35.2	25	35.2	0	1	0	2935.49	133	162
Protein disulfide-isomerase	P4HB	PDIA1_HUMAN	57.1	100.0%	3	3	3	0.00%	10.2%	YKPESEELTAER	99.5%	38.1	25	32.8	1	0	0	1451.70	327	338
Protein DJ-1	PARK7	PARK7_HUMAN	19.9	99.9%	2	2	3	0.00%	16.4%	GAEEMETVIPVDVMR	99.7%	47.4	25	46.2	1	0	0	1675.80	13	27
Protein DJ-1	PARK7	PARK7_HUMAN	19.9	99.9%	2	2	3	0.00%	16.4%	VTVAGLAGKDPVQCSR	99.7%	41	25	39.7	0	2	0	1657.87	33	48
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	7	7	12	0.01%	6.5%	ADLTALFLPR	99.7%	70.4	25	63.8	2	0	0	1116.64	875	884
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	7	7	12	0.01%	6.5%	AVQGAQQPSLYQIR	99.7%	66	25	55.5	2	0	0	1558.83	1047	1060
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	7	7	12	0.01%	6.5%	GVDLSGNDFK	99.7%	42.9	25	37	1	0	0	1051.51	12	21
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	7	7	12	0.01%	6.5%	LAEDILNTMFDTSYSK	99.7%	62.8	25	62.8	1	0	0	1847.87	1116	1131
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	7	7	12	0.01%	6.5%	LLQSLLDTR	99.7%	55.6	25	43.6	2	0	0	1058.62	765	773
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	7	7	12	0.01%	6.5%	NQLTSLPSAICK	99.6%	38.6	25	17	2	0	0	1331.70	279	290
Protein flightless-1 homolog	FLII	FLII_HUMAN	144.8	100.0%	7	7	12	0.01%	6.5%	VPECLYTLPSLR	99.7%	53.8	25	45	2	0	0	1447.76	238	249
Protein jagunal homolog 1	JAGN1	JAGN1_HUMAN	21.1	100.0%	5	6	9	0.01%	18.0%	AAGTDGSDFQHR	99.7%	49.3	25	38.2	2	0	0	1261.56	9	20
Protein jagunal homolog 1	JAGN1	JAGN1_HUMAN	21.1	100.0%	5	6	9	0.01%	18.0%	KLLDSWFTSTQEK	96.0%	23.7	25	20.9	0	1	0	1582.81	168	180
Protein jagunal homolog 1	JAGN1	JAGN1_HUMAN	21.1	100.0%	5	6	9	0.01%	18.0%	LLDSWFTSTQEK	99.7%	71.6	25	69.2	2	0	0	1454.72	169	180
Protein jagunal homolog 1	JAGN1	JAGN1_HUMAN	21.1	100.0%	5	6	9	0.01%	18.0%	LLDSWFTSTQEKK	99.2%	35.2	25	31.9	1	0	0	1582.81	169	181
Protein jagunal homolog 1	JAGN1	JAGN1_HUMAN	21.1	100.0%	5	6	9	0.01%	18.0%	MSVGHLR	99.7%	40.7	25	26	3	0	0	799.42	55	61
Protein KRI1 homolog	KRI1	KRI1_HUMAN	82.6	100.0%	4	4	6	0.01%	8.5%	AFVEDSEDEDGAGEGGSSLLQK	99.7%	53.2	25	27.4	2	0	0	2239.98	166	187
Protein KRI1 homolog	KRI1	KRI1_HUMAN	82.6	100.0%	4	4	6	0.01%	8.5%	LLGPTVMLGGCEFSR	99.7%	58.9	25	58.9	2	0	0	1636.82	657	671
Protein KRI1 homolog	KRI1	KRI1_HUMAN	82.6	100.0%	4	4	6	0.01%	8.5%	LQAFGLNPK	98.9%	34.1	25	20.4	1	0	0	987.56	674	682
Protein KRI1 homolog	KRI1	KRI1_HUMAN	82.6	100.0%	4	4	6	0.01%	8.5%	LQETSSQSYVEEQK	99.7%	85	25	85	1	0	0	1655.78	145	158
Protein lin-28 homolog B	LIN28B	LN28B_HUMAN	27.1	100.0%	3	3	6	0.01%	17.6%	GGGEEPGKLPEPAEEESQVLR	98.6%	27.6	25	25.6	0	1	0	2208.08	9	29
Protein lin-28 homolog B	LIN28B	LN28B_HUMAN	27.1	100.0%	3	3	6	0.01%	17.6%	MGFGFISMINR	99.7%	64.2	25	60.4	2	0	0	1272.62	41	51
Protein lin-28 homolog B	LIN28B	LN28B_HUMAN	27.1	100.0%	3	3	6	0.01%	17.6%	NVAQPPASSQGR	99.4%	37.1	25	37.1	3	0	0	1211.61	168	179
Protein LLP homolog	LLPH	LLPH_HUMAN	15.2	99.8%	2	2	4	0.00%	17.1%	DVQEIATVVVPKPK	99.7%	61.2	25	61.2	2	0	0	1522.88	43	56
Protein LLP homolog	LLPH	LLPH_HUMAN	15.2	99.8%	2	2	4	0.00%	17.1%	LDGDVLMK	95.3%	28.2	25	19.5	2	0	0	906.46	35	42
Protein LYRIC	MTDH	LYRIC_HUMAN	63.8	99.8%	2	2	4	0.00%	4.1%	TISTSDPAEVLVK	99.7%	62	25	49.2	2	0	0	1359.74	492	504
Protein LYRIC	MTDH	LYRIC_HUMAN	63.8	99.8%	2	2	4	0.00%	4.1%	TVEVAEGEAVR	99.7%	72.8	25	58.1	2	0	0	1159.60	132	142
Protein mago nashi homolog 2	MAGOHB	MGN2_HUMAN,MGN_HUMAN	17.3	100.0%	3	3	5	0.00%	19.6%	IGSLIDVNQSK	99.7%	73.8	25	54.3	2	0	0	1173.65	106	116
Protein mago nashi homolog 2	MAGOHB	MGN2_HUMAN,MGN_HUMAN	17.3	100.0%	3	3	5	0.00%	19.6%	SVMEELKR	97.6%	30.8	25	18.8	1	0	0	991.52	57	64
Protein mago nashi homolog 2	MAGOHB	MGN2_HUMAN,MGN_HUMAN	17.3	100.0%	3	3	5	0.00%	19.6%	VFYYLVQDLK	99.7%	65.6	25	53.4	2	0	0	1287.70	123	132
Protein MON2 homolog	MON2	MON2_HUMAN	190.5	99.8%	2	2	3	0.00%	1.2%	LQLLLLNPLK	99.7%	55.2	25	51.6	2	0	0	1164.77	862	871
Protein MON2 homolog	MON2	MON2_HUMAN	190.5	99.8%	2	2	3	0.00%	1.2%	VLSIGLPVAR	99.4%	37.1	25	36.5	1	0	0	1024.65	1470	1479
Protein NipSnap homolog 1	NIPSNAP1	NIPS1_HUMAN	33.3	100.0%	4	5	9	0.01%	16.2%	DAHSTLLSK	97.2%	30.2	25	25	1	0	0	971.52	57	65
Protein NipSnap homolog 1	NIPSNAP1	NIPS1_HUMAN	33.3	100.0%	4	5	9	0.01%	16.2%	FSGGYPALMDCMNK	99.7%	40.2	25	40.2	2	0	0	1590.68	128	141
Protein NipSnap homolog 1	NIPSNAP1	NIPS1_HUMAN	33.3	100.0%	4	5	9	0.01%	16.2%	GWDENVYYTVPLVR	99.7%	52.5	25	50.9	2	0	0	1710.85	255	268
Protein NipSnap homolog 1	NIPSNAP1	NIPS1_HUMAN	33.3	100.0%	4	5	9	0.01%	16.2%	MGPNIYELR	99.7%	71	25	62	4	0	0	1092.55	180	188
Protein NipSnap homolog 2	GBAS	NIPS2_HUMAN	33.7	99.8%	2	2	4	0.00%	5.9%	ICQEVLPK	99.7%	44	25	22.8	2	0	0	986.53	92	99
Protein NipSnap homolog 2	GBAS	NIPS2_HUMAN	33.7	99.8%	2	2	4	0.00%	5.9%	SGPNIYELR	99.7%	76.4	25	64.7	2	0	0	1048.54	182	190
Protein odr-4 homolog	ODR4	ODR4_HUMAN	51.1	100.0%	3	3	4	0.00%	7.9%	DYVILATR	99.3%	36.4	25	26.1	1	0	0	950.53	39	46
Protein odr-4 homolog	ODR4	ODR4_HUMAN	51.1	100.0%	3	3	4	0.00%	7.9%	VFVPLPGSTVMLCDYK	99.4%	37	25	34.5	1	0	0	1825.92	346	361
Protein odr-4 homolog	ODR4	ODR4_HUMAN	51.1	100.0%	3	3	4	0.00%	7.9%	VLTQLLLNSDHR	99.7%	49.2	25	45.3	2	0	0	1408.79	256	267
Protein PBDC1	PBDC1	PBDC1_HUMAN	26.1	99.8%	2	2	3	0.00%	10.7%	FNGIVEDFNYGTLLR	99.7%	41.7	25	40.5	1	0	0	1757.89	108	122
Protein PBDC1	PBDC1	PBDC1_HUMAN	26.1	99.8%	2	2	3	0.00%	10.7%	IQFFAIEIAR	99.6%	38.8	25	33.8	2	0	0	1207.68	140	149

Protein pelota homolog	PELO	PELO_HUMAN	43.4	100.0%	3	3	3	0.00%	9.4%	FYEQVVQAIQR	99.1%	34.8	25	27.8	1	0	0	1380.73	185	195
Protein pelota homolog	PELO	PELO_HUMAN	43.4	100.0%	3	3	3	0.00%	9.4%	GTNIQENEYVK	97.5%	30.7	25	27.9	1	0	0	1294.63	85	95
Protein pelota homolog	PELO	PELO_HUMAN	43.4	100.0%	3	3	3	0.00%	9.4%	VQTESSTGSVGSNR	99.7%	89.9	25	79.7	1	0	0	1408.67	47	60
Protein phosphatase 1B	PPM1B	PPM1B_HUMAN	52.6	100.0%	2	2	3	0.00%	4.4%	IQNAGGSVMIQR	99.7%	49.3	25	44.6	2	0	0	1289.66	180	191
Protein phosphatase 1B	PPM1B	PPM1B_HUMAN	52.6	100.0%	2	2	3	0.00%	4.4%	NVIEAVYSR	95.1%	28	25	28	1	0	0	1050.56	361	369
Protein phosphatase 1F	PPM1F	PPM1F_HUMAN	49.8	99.8%	2	2	3	0.00%	6.8%	HVSLPSFNQLFGLSDPVNR	99.7%	39.7	25	39.7	0	2	0	2127.10	173	191
Protein phosphatase 1F	PPM1F	PPM1F_HUMAN	49.8	99.8%	2	2	3	0.00%	6.8%	YAAVHVHTNAAR	97.7%	25.7	25	24.7	0	1	0	1309.68	208	219
Protein PRRC2A	PRRC2A	PRC2A_HUMAN	228.9	100.0%	4	5	7	0.01%	2.9%	GGGTGGPNHPPAPR	98.5%	32.7	25	32.7	1	2	0	1271.62	1067	1080
Protein PRRC2A	PRRC2A	PRC2A_HUMAN	228.9	100.0%	4	5	7	0.01%	2.9%	GVGSGGQGPPPPR	99.7%	90.7	25	82.1	2	0	0	1162.60	905	917
Protein PRRC2A	PRRC2A	PRC2A_HUMAN	228.9	100.0%	4	5	7	0.01%	2.9%	LKAEPAAPPAAPSTPAPPPAVPK	96.0%	23.7	25	23.7	0	1	0	2175.22	504	526
Protein PRRC2A	PRRC2A	PRC2A_HUMAN	228.9	100.0%	4	5	7	0.01%	2.9%	QSSSEISLAVER	99.7%	44.9	25	43.4	1	0	0	1305.66	455	466
Protein RCC2	RCC2	RCC2_HUMAN	56.1	99.8%	2	2	2	0.00%	5.8%	AGGAAVVITEPEHTKER	96.8%	24.5	25	24.5	0	1	0	1764.92	78	94
Protein RCC2	RCC2	RCC2_HUMAN	56.1	99.8%	2	2	2	0.00%	5.8%	LGHAEQKDEMVPR	99.2%	30	25	28.2	0	1	0	1525.74	362	374
Protein RFT1 homolog	RFT1	RFT1_HUMAN	60.3	99.8%	2	2	2	0.00%	3.9%	GSQEVLGHAAR	99.7%	60.2	25	52	1	0	0	1124.58	2	12
Protein RFT1 homolog	RFT1	RFT1_HUMAN	60.3	99.8%	2	2	2	0.00%	3.9%	ITDLLPNITR	99.7%	56	25	49.1	1	0	0	1155.67	221	230
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	18	18	31	0.03%	11.0%	ACILCVHPR	99.7%	46.1	25	34.9	2	0	0	1125.57	329	337
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	18	18	31	0.03%	11.0%	AIFENTLSTYPK	99.7%	56.6	25	50.8	2	0	0	1383.72	1782	1793
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	18	18	31	0.03%	11.0%	AINIGQLVDVK	99.7%	69.7	25	57.3	2	0	0	1169.69	632	642
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	18	18	31	0.03%	11.0%	FAQLEFQLGDAER	99.7%	80.6	25	71.5	1	0	0	1523.75	1767	1779
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	18	18	31	0.03%	11.0%	FYNNVQGLVPK	99.7%	41	25	41	2	0	0	1278.68	561	571
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	18	18	31	0.03%	11.0%	GQEEVEMPSKEK	99.7%	51.6	25	48.1	1	0	0	1406.65	1446	1457
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	18	18	31	0.03%	11.0%	IPLLLTSLSFK	99.7%	61.4	25	61.4	2	0	0	1231.77	1178	1188
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	18	18	31	0.03%	11.0%	LGPSVVGLAR	99.7%	79.3	25	71.6	2	0	0	968.59	1343	1352
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	18	18	31	0.03%	11.0%	LKDGVLAYAR	99.7%	55.7	25	43.8	2	0	0	1105.64	386	395
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	18	18	31	0.03%	11.0%	TSIIEAQYLR	99.7%	68.1	25	62.4	2	0	0	1193.65	437	446
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	18	18	31	0.03%	11.0%	TTEPGVTGLLLAVEGPAAK	99.7%	88.7	25	88.3	4	0	0	1824.01	982	1000
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	18	18	31	0.03%	11.0%	VFYTGQVVK	97.5%	30.7	25	20.9	2	0	0	1040.58	585	593
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	18	18	31	0.03%	11.0%	VLCLSQSEGR	99.7%	39.7	25	33	2	0	0	1148.57	692	701
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	18	18	31	0.03%	11.0%	VLLCDPEAK	99.3%	35.9	25	28.7	1	0	0	1044.54	507	515
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	18	18	31	0.03%	11.0%	VTPNEGLTVSFPFGK	97.7%	30.9	25	22.2	1	0	0	1592.83	1240	1254
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	18	18	31	0.03%	11.0%	VVVLNCEPSKER	98.7%	33.4	25	33.4	1	0	0	1429.75	594	605
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	18	18	31	0.03%	11.0%	WLEVEIAPDIR	97.7%	31	25	22.9	1	0	0	1340.72	1165	1175
Protein RRP5 homolog	PDCD11	RRP5_HUMAN	208.7	100.0%	18	18	31	0.03%	11.0%	YHDIEPGAVVK	99.7%	54.6	25	49.3	1	0	0	1227.64	447	457
Protein S100-A8	S100A8	S10A8_HUMAN	10.8	99.8%	2	2	3	0.00%	23.7%	ALNSIIDVYHK	99.7%	40.3	25	39.1	2	0	0	1272.69	8	18
Protein S100-A8	S100A8	S10A8_HUMAN	10.8	99.8%	2	2	3	0.00%	23.7%	LLETECPQYIR	99.7%	47.8	25	38.5	1	0	0	1421.71	37	47
Protein SAAL1	SAAL1	SAAL1_HUMAN	53.6	100.0%	4	5	9	0.01%	9.9%	KPENSAESNTEETKR	99.7%	82.6	25	82.6	0	2	0	1719.81	369	383
Protein SAAL1	SAAL1	SAAL1_HUMAN	53.6	100.0%	4	5	9	0.01%	9.9%	TDLTQDDFHLK	99.7%	60.4	25	52.4	2	0	0	1332.64	384	394
Protein SAAL1	SAAL1	SAAL1_HUMAN	53.6	100.0%	4	5	9	0.01%	9.9%	VDLPLIDSLIR	99.7%	58.5	25	58.5	2	0	0	1253.75	348	358
Protein SAAL1	SAAL1	SAAL1_HUMAN	53.6	100.0%	4	5	9	0.01%	9.9%	VLQNMEQCQK	99.7%	55.7	25	45.2	3	0	0	1277.60	359	368
Protein SCO2 homolog, mitochondrial	SCO2	SCO2_HUMAN	29.8	99.8%	2	2	2	0.00%	10.5%	QGPAETGGQGQPQGPGLR	99.7%	44.4	25	44.4	1	0	0	1734.85	41	58
Protein SCO2 homolog, mitochondrial	SCO2	SCO2_HUMAN	29.8	99.8%	2	2	2	0.00%	10.5%	SAEQISDSVR	99.6%	39	25	8.77	1	0	0	1091.53	246	255
Protein SEC13 homolog	SEC13	SEC13_HUMAN	35.5	99.8%	2	2	3	0.00%	11.8%	DVAWAPSIGLPTSTIASCSQDGR	99.7%	54	25	53.6	2	0	0	2389.15	217	239
Protein SEC13 homolog	SEC13	SEC13_HUMAN	35.5	99.8%	2	2	3	0.00%	11.8%	ESVDGQWVCISDVNK	99.7%	41.8	25	41.8	1	0	0	1735.80	291	305
Protein SON	SON	SON_HUMAN	263.8	100.0%	4	4	6	0.01%	2.1%	AGIEGPLLASDVGR	99.7%	54.7	25	51.2	1	0	0	1354.73	1750	1763
Protein SON	SON	SON_HUMAN	263.8	100.0%	4	4	6	0.01%	2.1%	ILDSFAAAPVPTTTLVLK	99.7%	49.5	25	49.5	2	0	0	1857.07	241	258
Protein SON	SON	SON_HUMAN	263.8	100.0%	4	4	6	0.01%	2.1%	LGQDPYR	99.7%	46.4	25	40	2	0	0	848.43	944	950
Protein SON	SON	SON_HUMAN	263.8	100.0%	4	4	6	0.01%	2.1%	SVESTSPEPSK	99.7%	39.4	25	37.5	1	0	0	1147.55	278	288
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	9	12	19	0.02%	19.8%	AISYHLVQKPFSLTK	99.7%	38.1	25	28.7	0	2	0	1731.98	278	292
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	9	12	19	0.02%	19.8%	DFVAPHLAQPTGSQSPPPGSK	98.8%	28.4	25	28.2	0	1	0	2118.06	539	559
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	9	12	19	0.02%	19.8%	DVLLDVAYAYGK	99.7%	89.6	25	84.8	2	0	0	1326.69	293	304
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	9	12	19	0.02%	19.8%	ELQSVEQEVR	99.7%	67.3	25	49.5	2	0	0	1216.62	164	173

Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	9	12	19	0.02%	19.8%	LATDLLSLMPSLTSGEVAHCAK	99.7%	34.7	25	34.7	0	2	0	2330.17	316	337
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	9	12	19	0.02%	19.8%	LLGSLYALGIPK	99.7%	71.7	25	70.6	2	0	0	1244.76	149	160
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	9	12	19	0.02%	19.8%	LSFHQTQVSQR	99.7%	58.1	25	46.8	2	1	0	1330.69	305	315
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	9	12	19	0.02%	19.8%	LSHLLSEKPEDK	96.5%	29.3	25	20.7	1	0	0	1395.75	107	118
Protein TBRG4	TBRG4	TBRG4_HUMAN	70.7	100.0%	9	12	19	0.02%	19.8%	VLVMLAAQSR	99.7%	99	25	94.1	4	0	0	1087.63	261	270
Protein THEM6	THEM6	THEM6_HUMAN	23.9	100.0%	3	3	4	0.00%	13.9%	DGFVCALLR	98.3%	32.2	25	19.2	1	0	0	1050.54	142	150
Protein THEM6	THEM6	THEM6_HUMAN	23.9	100.0%	3	3	4	0.00%	13.9%	LLEPFEVR	99.5%	37.7	25	15.4	2	0	0	1002.56	113	120
Protein THEM6	THEM6	THEM6_HUMAN	23.9	100.0%	3	3	4	0.00%	13.9%	MESGLSDVTKDQ	99.7%	58.5	25	56.9	1	0	0	1325.59	197	208
Protein timeless homolog	TIMELESS	TIM_HUMAN	138.7	99.8%	2	2	3	0.00%	1.7%	FGGSYIVQGLK	99.7%	54.4	25	47.4	1	0	0	1168.64	278	288
Protein timeless homolog	TIMELESS	TIM_HUMAN	138.7	99.8%	2	2	3	0.00%	1.7%	LLALGLVAER	99.7%	64.2	25	64.2	2	0	0	1054.66	931	940
Protein transport protein Sec23A	SEC23A	SC23A_HUMAN	86.2	99.8%	2	2	4	0.00%	3.3%	MVVPVAALFTPLK	99.7%	49.9	25	49.9	2	0	0	1385.82	34	46
Protein transport protein Sec23A	SEC23A	SC23A_HUMAN	86.2	99.8%	2	2	4	0.00%	3.3%	YIDTEHGGSQAR	99.7%	49	25	40.3	2	0	0	1333.61	705	716
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	5	5	15	0.01%	8.6%	AFSPTTVNTGR	99.7%	49.9	25	33.4	5	0	0	1150.59	195	205
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	5	5	15	0.01%	8.6%	ETSMVHELNR	99.0%	34.5	25	31.1	1	0	0	1231.57	406	415
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	5	5	15	0.01%	8.6%	GQYNTYPIK	99.7%	50.5	25	33.9	3	0	0	1083.55	274	282
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	5	5	15	0.01%	8.6%	IIEVGDTPK	99.7%	52.3	25	45	4	0	0	971.54	99	107
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	S61A1_HUMAN	52.3	100.0%	5	5	15	0.01%	8.6%	IIEVGDTPKDR	99.7%	47	25	29.9	2	0	0	1242.67	99	109
Protein tyrosine phosphatase type IVA 1	PTP4A1	TP4A1_HUMAN	19.8	100.0%	3	3	5	0.00%	20.2%	FLITHNPTNATLNK	99.7%	45.6	25	41.4	2	0	0	1583.85	19	32
Protein tyrosine phosphatase type IVA 1	PTP4A1	TP4A1_HUMAN	19.8	100.0%	3	3	5	0.00%	20.2%	VCEATYDTTLVEK	99.7%	88.2	25	78.8	2	0	0	1528.72	48	60
Protein tyrosine phosphatase type IVA 1	PTP4A1	TP4A1_HUMAN	19.8	100.0%	3	3	5	0.00%	20.2%	YGVTTIVR	99.5%	37.8	25	0	1	0	0	908.52	40	47
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	10	11	17	0.02%	13.3%	ALIPLALEGTDVGQTK	99.7%	124	25	124	2	0	0	1625.91	692	707
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	10	11	17	0.02%	13.3%	DNALTLLIK	99.7%	40.2	25	16.2	1	0	0	1000.60	313	321
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	10	11	17	0.02%	13.3%	EVQDLFEAQGNDR	99.7%	54.4	25	54.4	1	0	0	1520.70	807	819
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	10	11	17	0.02%	13.3%	LDQAVLDLQR	99.7%	70.5	25	49.6	2	0	0	1170.65	108	117
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	10	11	17	0.02%	13.3%	LLDMGETDLMLAALR	99.7%	108	25	106	2	0	0	1661.86	203	217
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	10	11	17	0.02%	13.3%	LLVLYSGEDDELLQR	99.7%	94.2	25	85.5	2	0	0	1762.92	822	836
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	10	11	17	0.02%	13.3%	TESPVLTSSCR	94.7%	27.8	25	26.5	1	0	0	1236.59	654	664
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	10	11	17	0.02%	13.3%	TVATLSILGTR	99.7%	78.6	25	71.7	2	0	0	1131.67	230	240
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	10	11	17	0.02%	13.3%	VEQMFQILLDPEEK	99.7%	62.6	25	48.9	2	0	0	1718.87	153	166
Protein unc-45 homolog A	UNC45A	UN45A_HUMAN	103.1	100.0%	10	11	17	0.02%	13.3%	VFLALVEEVEDR	99.7%	75.6	25	75.1	2	0	0	1418.75	670	681
Protein virilizer homolog	KIAA1429	VIR_HUMAN	202.0	100.0%	5	5	6	0.01%	3.5%	DTGELASSFLEFMR	99.7%	58.5	25	54.5	1	0	0	1602.75	1389	1402
Protein virilizer homolog	KIAA1429	VIR_HUMAN	202.0	100.0%	5	5	6	0.01%	3.5%	EESPENLFLELEK	97.1%	30	25	29.3	1	0	0	1576.77	1446	1458
Protein virilizer homolog	KIAA1429	VIR_HUMAN	202.0	100.0%	5	5	6	0.01%	3.5%	ENSGAIEASVK	95.2%	28.1	25	15	1	0	0	1104.55	374	384
Protein virilizer homolog	KIAA1429	VIR_HUMAN	202.0	100.0%	5	5	6	0.01%	3.5%	LLELILLDQTVR	99.7%	75	25	75	2	0	0	1425.87	534	545
Protein virilizer homolog	KIAA1429	VIR_HUMAN	202.0	100.0%	5	5	6	0.01%	3.5%	WVTALEEIPSLIIK	99.6%	38.6	25	38.6	1	0	0	1611.94	400	413
Protein YIF1A	YIF1A	YIF1A_HUMAN	32.0	99.8%	2	2	4	0.00%	9.2%	TAALGPDSMGGPVPR	99.7%	47.3	25	42.4	2	0	0	1441.71	251	265
Protein YIF1A	YIF1A	YIF1A_HUMAN	32.0	99.8%	2	2	4	0.00%	9.2%	YFFAVDTAYVAK	99.7%	79.4	25	71.8	2	0	0	1394.70	93	104
Protein YIPF5	YIPF5	YIPF5_HUMAN	28.0	99.8%	2	2	4	0.00%	8.2%	QYAGYDYSQQGR	99.7%	62.5	25	62.1	2	0	0	1435.62	38	49
Protein YIPF5	YIPF5	YIPF5_HUMAN	28.0	99.8%	2	2	4	0.00%	8.2%	TLTVLHPLK	95.5%	28.4	25	28.4	2	0	0	1021.64	107	115
Protein zwilch homolog	ZWILCH	ZWILC_HUMAN	67.2	99.8%	2	2	3	0.00%	4.1%	FLLVLADGLR	99.7%	83.4	25	70.2	2	0	0	1116.68	271	280
Protein zwilch homolog	ZWILCH	ZWILC_HUMAN	67.2	99.8%	2	2	3	0.00%	4.1%	INLPVTALPPLWVR	99.7%	47.2	25	36.6	1	0	0	1588.96	126	139
Pumilio homolog 1	PUM1	PUM1_HUMAN	126.5	100.0%	4	4	6	0.01%	4.2%	DQYANYVVQK	99.7%	50.8	25	42	1	0	0	1227.60	1118	1127
Pumilio homolog 1	PUM1	PUM1_HUMAN	126.5	100.0%	4	4	6	0.01%	4.2%	FFEFGSLEQK	99.7%	47.8	25	31.2	2	0	0	1231.60	905	914
Pumilio homolog 1	PUM1	PUM1_HUMAN	126.5	100.0%	4	4	6	0.01%	4.2%	GNVLVLSQHK	99.7%	43.7	25	43.7	1	0	0	1094.63	1067	1076
Pumilio homolog 1	PUM1	PUM1_HUMAN	126.5	100.0%	4	4	6	0.01%	4.2%	SASSASSLFSPSSTLFSSSR	99.7%	64.6	25	64.6	2	0	0	1992.95	797	816
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	AFFESHPAPSAER	99.7%	43.6	25	43.6	2	2	0	1445.68	870	882
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	AGIISTVEVLK	99.7%	67.9	25	59.1	2	0	0	1129.68	628	638
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	ATFDISLVVPK	99.7%	82	25	74.7	2	0	0	1189.68	198	208
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	DAESIHQYLLQR	99.7%	65.4	25	59.5	2	0	0	1472.75	901	912
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	DNWEELYNR	99.2%	35.5	25	30.4	2	0	0	1238.54	833	841
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	DYFNVPYPLPK	99.7%	71.6	25	63.7	4	0	0	1352.69	294	304

Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	ETALLIDPK	99.7%	57.9	25	53.8	2	0	0	999.57	328	336
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	FALEVAAK	99.7%	46.5	25	29	2	0	0	848.49	280	287
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	FIKDNWEELYNR	99.7%	61.6	25	53.4	1	0	0	1626.79	830	841
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	GMNMYLTK	99.7%	45	25	39.8	2	0	0	957.45	460	467
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	HGDGTTLDIMLK	99.7%	43.8	25	34.6	1	0	0	1300.66	754	765
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	IDFVGELNDK	99.7%	55.4	25	33.1	2	0	0	1149.58	146	155
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	ILMDKPEMNVVLK	99.6%	38.2	25	31.2	2	0	0	1561.83	559	571
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	KPYPDDENLVEVK	99.7%	71	25	62.3	2	0	0	1545.78	222	234
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	LEAAAQVR	97.9%	31.4	25	22	2	0	0	857.48	80	87
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	LGLQNDLFSLAR	99.7%	92.2	25	73.8	5	0	0	1346.74	616	627
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	LGWDPKPGEGHLDALLR	99.3%	30.4	25	30.4	0	2	0	1873.99	690	706
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	LNLGTVGFYR	99.7%	67.3	25	60.1	4	0	0	1139.62	581	590
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	LSVEGFAVDK	99.4%	36.6	25	17.1	1	0	0	1064.56	854	863
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	NVKPDQWVK	98.3%	32.2	25	24.6	2	0	0	1113.61	572	580
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	QILSADLR	99.7%	68.1	25	45.6	2	0	0	915.53	737	744
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	SPVYLTVLK	99.7%	50.8	25	49.7	2	0	0	1019.61	745	753
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	TIQQCCENILLNAAWLK	99.7%	71.9	25	71.9	2	0	0	2075.04	883	899
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	TQYSSAMLESLLPGIR	99.7%	87.7	25	71.4	5	0	0	1765.92	591	606
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	VALSNMNVIDR	99.7%	88.8	25	80	4	0	0	1231.65	211	221
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	VLGATLLPDLIQK	99.7%	85.6	25	85.6	2	0	0	1380.85	782	794
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	VTLSFPSTLQTGTGTLK	99.7%	74.5	25	74.2	3	0	0	1750.96	129	145
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	YAAVTQFEATDAR	99.7%	105	25	102	2	0	0	1442.69	173	185
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	YQGGFLISR	99.7%	62.6	25	54.2	2	0	0	1040.55	842	850
Puromycin-sensitive aminopeptidase	NPEPPS	PSA_HUMAN	103.3	100.0%	30	33	71	0.07%	36.0%	YTTPSGEVR	96.9%	29.8	25	29.8	1	0	0	1009.49	164	172
Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial	CLPP	CLPP_HUMAN	30.2	99.8%	2	2	2	0.00%	14.8%	AYDIYSR	99.4%	37	25	20.5	1	0	0	887.43	72	78
Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial	CLPP	CLPP_HUMAN	30.2	99.8%	2	2	2	0.00%	14.8%	VLVHPPQDGEDEPTLVQKEPVEAAPAAEPVPAST	99.7%	66.1	25	64.3	0	1	0	3517.77	244	277
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	AIFQQPPVGVR	99.7%	55.2	25	50.2	4	0	0	1211.69	715	725
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	AIVLAAIFR	99.7%	72	25	72	3	0	0	973.62	886	894
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	ALTQFPLPK	99.1%	35.2	25	25.1	1	0	0	1014.60	238	246
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	ATISLSDSDLLR	99.7%	75.4	25	67.5	2	0	0	1290.69	1116	1127
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	AVAGWEEVLR	99.7%	55.1	25	44	2	0	0	1129.60	942	951
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	AVDSPNIK	99.4%	36.7	25	23.1	1	0	0	843.46	839	846
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	CNVIITQPR	95.1%	28	25	17.8	1	0	0	1100.59	484	492
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	DPFSSSLQNR	99.7%	59	25	51.8	3	0	0	1150.55	909	918
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	DSGPLSDPITGKPYVPLLEAEEVR	99.7%	52.8	25	51.1	0	1	0	2582.34	389	412
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	DVNTDFLLILLK	99.7%	86.4	25	61.4	4	0	0	1403.81	565	576
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	ENYLEENLLYAPSLR	99.7%	54.2	25	54.2	4	0	0	1823.92	959	973
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	EYLTTLGQR	99.7%	47.7	25	40.5	2	0	0	1080.57	865	873
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	FKPNSVTYR	99.7%	40.4	25	28.9	2	0	0	1111.59	1041	1049
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	GGALLFCTVGILLR	99.7%	67.8	25	59.1	2	0	0	1489.86	529	542
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	GSSFEMTDDDSAIR	99.7%	102	25	101	3	0	0	1530.64	224	237
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	GVLMAGLYPNLIQVR	99.7%	66.2	25	66.2	5	0	0	1643.93	1017	1031
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	IPQLLLER	99.7%	60.1	25	40.9	4	0	0	981.61	467	474
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	ISAVSVAQR	99.7%	75.2	25	30.9	4	0	0	930.54	494	502
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	LQEALGMHESK	99.7%	64.1	25	55.3	3	0	0	1242.61	688	698
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	LQSDDILPLGK	99.7%	57.8	25	40.3	2	0	0	1198.67	378	388
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	LVLMSATGDNER	99.7%	77.1	25	68.4	4	0	0	1305.65	587	598
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	MVPFQVPEILR	99.7%	44.7	25	37	4	0	0	1328.74	803	813
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	NELFDAAK	95.1%	28	25	15.6	1	0	0	907.45	131	138
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	NLLNSVIGR	99.7%	59.7	25	48.2	2	0	0	985.58	55	63
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	NLMQFHTVGTK	99.7%	51.6	25	39.2	4	0	0	1275.65	264	274

Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	NVGFQVR	99.6%	38.5	25	25.9	1	0	0	819.45	514	520
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	QAAAAACQLFK	98.7%	33.4	25	27.4	1	0	0	1178.60	112	122
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	RISAVSVAQR	99.7%	48.1	25	12.4	2	0	0	1086.64	493	502
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	SGNILLHK	99.7%	44.5	25	20.9	2	0	0	881.52	1052	1059
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	SVEVEGYGSK	99.7%	57.6	25	54.7	2	0	0	1054.51	96	105
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	TPLENLVLQAK	99.7%	67.5	25	67.5	4	0	0	1225.72	814	824
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	VIQIATSSSTAK	99.7%	95.9	25	88.2	2	0	0	1205.67	252	263
Putative ATP-dependent RNA helicase DHX30	DHX30	DHX30_HUMAN	133.9	100.0%	33	39	84	0.08%	29.4%	VSCLETVWVSR	99.7%	63.8	25	59.4	2	0	0	1335.67	763	773
Putative ATP-dependent RNA helicase DHX57	DHX57	DHX57_HUMAN	155.6	99.8%	2	2	3	0.00%	1.3%	ISAISVAER	99.7%	49.1	25	29	1	0	0	945.54	604	612
Putative ATP-dependent RNA helicase DHX57	DHX57	DHX57_HUMAN	155.6	99.8%	2	2	3	0.00%	1.3%	VPLEQLCLR	99.7%	45.3	25	37.9	2	0	0	1127.62	997	1005
Putative deoxyribose-phosphate aldolase	DERA	DEOC_HUMAN	35.2	99.8%	2	2	4	0.00%	8.5%	ETVNATFPVAIVMLR	99.7%	59.2	25	59.2	2	0	0	1660.91	224	238
Putative deoxyribose-phosphate aldolase	DERA	DEOC_HUMAN	35.2	99.8%	2	2	4	0.00%	8.5%	IGASTLLSDIER	99.7%	88.9	25	77.2	2	0	0	1274.70	288	299
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	25	26	73	0.07%	29.6%	AHILACAPSNSGADLLCQR	99.7%	42.8	25	40.8	0	1	0	2053.99	548	566
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	25	26	73	0.07%	29.6%	DGQLLIR	99.4%	36.5	25	1.8	2	0	0	814.48	136	142
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	25	26	73	0.07%	29.6%	EAGQCFESFLVVR	99.7%	69.4	25	66.1	4	0	0	1541.74	12	24
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	25	26	73	0.07%	29.6%	EGEGGLSLQVEPEWR	99.7%	61.1	25	54.9	2	0	0	1685.81	986	1000
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	25	26	73	0.07%	29.6%	EGNSPSFFNPEEAATVTSYLK	99.7%	84.3	25	84.3	3	0	0	2288.07	788	808
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	25	26	73	0.07%	29.6%	ETGDPGGQLVLAGDPR	99.7%	101	25	101	4	0	0	1581.79	667	682
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	25	26	73	0.07%	29.6%	GPDGYDPQFITK	99.7%	65.3	25	52	1	0	0	1337.64	716	727
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	25	26	73	0.07%	29.6%	HGLGYSLLER	99.7%	45.6	25	40.2	2	0	0	1144.61	696	705
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	25	26	73	0.07%	29.6%	HGVDVEVQGPHEAR	99.7%	75.9	25	71.5	0	4	0	1529.75	122	135
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	25	26	73	0.07%	29.6%	IANLAYVTK	99.7%	48.2	25	38.3	4	0	0	992.58	63	71
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	25	26	73	0.07%	29.6%	ISFGTPAPGFSSMLYGMK	99.7%	62.7	25	57	2	0	0	1890.91	45	62
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	25	26	73	0.07%	29.6%	KGEYVFPAK	99.7%	45.5	25	43.5	2	0	0	1038.56	602	610
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	25	26	73	0.07%	29.6%	KGPDGYDPQFITK	95.2%	28.1	25	25.9	1	0	0	1465.73	715	727
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	25	26	73	0.07%	29.6%	LDLQQGQNLLQGLSK	99.7%	80.5	25	72.2	4	0	0	1654.91	953	967
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	25	26	73	0.07%	29.6%	LLTLEVPGVTESRPSVLR	98.2%	26.6	25	26.6	0	1	0	1966.13	376	393
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	25	26	73	0.07%	29.6%	LLTYNSLYK	97.8%	31.2	25	28.3	2	0	0	1114.61	706	714
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	25	26	73	0.07%	29.6%	RFNVAVTR	99.7%	47	25	40.5	3	0	0	962.55	904	911
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	25	26	73	0.07%	29.6%	SLESNPEQLQAMR	99.7%	68.7	25	63.5	5	0	0	1502.73	496	508
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	25	26	73	0.07%	29.6%	SVGVISPYR	99.7%	43.8	25	29.9	4	0	0	977.54	826	834
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	25	26	73	0.07%	29.6%	SVILISTVR	99.7%	67	25	55.7	4	0	0	987.62	874	882
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	25	26	73	0.07%	29.6%	TVTLVEAIK	99.7%	41.3	25	30.5	4	0	0	973.59	531	539
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	25	26	73	0.07%	29.6%	VGSVEEFQGQER	99.7%	82.7	25	73.4	4	0	0	1364.64	862	873
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	25	26	73	0.07%	29.6%	VLITTLITAGR	99.7%	101	25	94.7	7	0	0	1157.73	618	628
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	25	26	73	0.07%	29.6%	VNFTFNR	99.1%	34.9	25	28.9	2	0	0	897.46	445	451
Putative helicase MOV-10	MOV10	MOV10_HUMAN	113.7	100.0%	25	26	73	0.07%	29.6%	WLLWPMLFPVAPR	99.7%	42.7	25	36.7	1	0	0	1641.90	467	479
Putative methyltransferase NSUN5	NSUN5	NSUN5_HUMAN	46.7	99.8%	2	2	6	0.01%	6.1%	VLVYELLLGK	99.7%	68.2	25	63.9	4	0	0	1146.71	73	82
Putative methyltransferase NSUN5	NSUN5	NSUN5_HUMAN	46.7	99.8%	2	2	6	0.01%	6.1%	YSAVLDAVIASAGLLR	99.7%	73.2	25	68	2	0	0	1618.92	46	61
Putative mitochondrial import inner membrane translocase subunit Tim23B	TIMM23B	TI23B_HUMAN,TIM23_HUMAN	21.9	100.0%	2	2	4	0.00%	10.5%	NVQILNMVTR	99.7%	62.7	25	33.2	2	0	0	1187.66	113	122
Putative mitochondrial import inner membrane translocase subunit Tim23B	TIMM23B	TI23B_HUMAN,TIM23_HUMAN	21.9	100.0%	2	2	4	0.00%	10.5%	YLVQDTDEFILPTGANK	99.7%	68.4	25	66.5	2	0	0	1923.97	52	68
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	8	9	13	0.01%	21.3%	ALDQSDNDMSAVYR	99.7%	86.2	25	86.2	2	0	0	1600.69	536	549
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	8	9	13	0.01%	21.3%	DLTIPESSTVK	99.0%	34.7	25	28.4	1	0	0	1189.63	180	190
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	8	9	13	0.01%	21.3%	DLVLGPSGVLQGIRPGK	99.7%	73.7	25	73.7	2	0	0	1706.00	339	355
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	8	9	13	0.01%	21.3%	FFGTEDHAWIK	99.0%	34.7	25	27.9	1	0	0	1350.65	46	56
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	8	9	13	0.01%	21.3%	FQQAVDAVEEFLR	99.7%	102	25	94.1	2	0	0	1551.78	79	91
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	8	9	13	0.01%	21.3%	GLYEDCSSCFQAMGK	99.7%	62.9	25	62.9	1	0	0	1752.70	408	422
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	8	9	13	0.01%	21.3%	LAIALGDAVNHPTPMAAAANEVYK	99.7%	47.9	25	47.6	0	2	0	2453.25	509	532
Putative oxidoreductase GLYR1	GLYR1	GLYR1_HUMAN	60.6	100.0%	8	9	13	0.01%	21.3%	TSFFLGEVGNAAK	99.7%	88.5	25	83	2	0	0	1340.68	423	435
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	12	16	45	0.04%	16.7%	DYYINIR	95.7%	28.5	25	22.3	1	0	0	956.48	684	690
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	12	16	45	0.04%	16.7%	EAMNDPLLER	99.7%	46.8	25	38.5	3	0	0	1187.57	244	253

Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	12	16	45	0.04%	16.7%	EVDDLGPEVGDIK	99.7%	73.4	25	69.2	3	0	0	1385.68	372	384
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	12	16	45	0.04%	16.7%	FTDILVR	99.7%	42	25	27.1	3	0	0	863.50	146	152
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	12	16	45	0.04%	16.7%	HQSFVLVGETGSGK	99.7%	83.1	25	83.1	2	1	0	1445.74	153	166
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	12	16	45	0.04%	16.7%	IRVESLLVTAISK	99.7%	86.8	25	86.8	2	0	0	1428.88	451	463
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	12	16	45	0.04%	16.7%	SLMSADNVR	99.2%	35.3	25	27.4	2	0	0	992.48	653	661
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	12	16	45	0.04%	16.7%	SNLGSVVLQLK	99.7%	80.7	25	72.9	6	0	0	1157.69	505	515
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	12	16	45	0.04%	16.7%	TCTDIKPEWLVK	99.7%	47.7	25	42.7	1	0	0	1489.77	749	760
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	12	16	45	0.04%	16.7%	TEMQDNTYPEILR	99.7%	61.4	25	55.7	1	0	0	1609.75	492	504
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	12	16	45	0.04%	16.7%	TLATDILMGVLK	99.7%	104	25	88.7	12	0	0	1290.73	266	277
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	DHX15_HUMAN	90.9	100.0%	12	16	45	0.04%	16.7%	YGVIILDEAHER	99.7%	66.5	25	62.9	4	4	0	1414.73	254	265
Putative ribonuclease	YBEY	YBEY_HUMAN	19.3	99.8%	2	2	3	0.00%	12.0%	AVLDELGRR	98.3%	32.3	25	21.9	1	0	0	1028.58	143	151
Putative ribonuclease	YBEY	YBEY_HUMAN	19.3	99.8%	2	2	3	0.00%	12.0%	FDLGIICVDNK	99.7%	78.6	25	70.1	2	0	0	1293.65	35	45
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	12	12	23	0.02%	18.2%	DLAQALINR	99.7%	50.8	25	39.3	2	0	0	1013.57	323	331
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	12	12	23	0.02%	18.2%	ELLLSAIDSVNATSK	99.7%	113	25	109	4	0	0	1560.85	493	507
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	12	12	23	0.02%	18.2%	GADSELSTVPSVTK	99.7%	61.6	25	33.9	3	0	0	1390.71	656	669
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	12	12	23	0.02%	18.2%	GISAGAVQTAGK	99.7%	74.5	25	63.5	2	0	0	1059.58	80	91
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	12	12	23	0.02%	18.2%	GPQPPTVSPIR	94.5%	27.6	25	27.6	1	0	0	1148.64	779	789
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	12	12	23	0.02%	18.2%	GVNLDPLGK	99.7%	40.9	25	38.8	1	0	0	912.52	332	340
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	12	12	23	0.02%	18.2%	IQDIVGILR	99.7%	65.7	25	38.6	2	0	0	1026.63	243	251
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	12	12	23	0.02%	18.2%	LGVTNTIISHYDGR	99.7%	57.7	25	57.7	1	0	0	1545.80	432	445
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	12	12	23	0.02%	18.2%	LVPTGLDFGQEGFTR	99.7%	88.9	25	82.8	4	0	0	1636.83	539	553
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	12	12	23	0.02%	18.2%	NTGVILANDANAER	99.7%	82.5	25	78.3	1	0	0	1457.73	408	421
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	12	12	23	0.02%	18.2%	SPEAKPLPGK	98.0%	31.5	25	26.8	1	0	0	1023.58	67	76
Putative ribosomal RNA methyltransferase NOP2	NOP2	NOP2_HUMAN	89.3	100.0%	12	12	23	0.02%	18.2%	TQASSSFQDSSQPAGK	99.7%	79.8	25	72.4	1	0	0	1625.74	670	685
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	7	7	10	0.01%	9.3%	FGVITEVDIK	99.7%	56.3	25	47.9	1	0	0	1120.63	397	406
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	7	7	10	0.01%	9.3%	ISHLSGSGSGDER	99.7%	39.3	25	38.7	2	0	0	1301.61	204	216
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	7	7	10	0.01%	9.3%	LQQLALGR	98.1%	31.8	25	20.2	1	0	0	898.55	307	314
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	7	7	10	0.01%	9.3%	LWVGGLGPWVPLAALAR	98.7%	33.2	25	33.2	1	0	0	1776.03	457	473
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	7	7	10	0.01%	9.3%	QDGGTAPVASASPK	99.7%	53.7	25	42.8	2	0	0	1285.64	770	783
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	7	7	10	0.01%	9.3%	SSGAASSAPGGGDGAEYK	99.6%	38.8	25	38.8	1	0	0	1568.68	153	170
Putative RNA-binding protein 15	RBM15	RBM15_HUMAN	107.2	100.0%	7	7	10	0.01%	9.3%	VGAGAGAAPFR	99.7%	64.7	25	51.6	2	0	0	973.52	349	359
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	7	7	17	0.02%	19.9%	AMLDQLMGTSR	99.7%	67	25	60.6	1	0	0	1254.58	9	19
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	7	7	17	0.02%	19.9%	LADHFGGK	99.5%	37.7	25	27	2	0	0	844.43	206	213
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	7	7	17	0.02%	19.9%	LAETQEEISAEVAAK	99.7%	112	25	106	4	0	0	1588.81	108	122
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	7	7	17	0.02%	19.9%	LHLGFIEIR	99.7%	40.9	25	38.5	2	0	0	1097.65	214	222
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	7	7	17	0.02%	19.9%	SSEEREAGEI	96.9%	29.9	25	24.4	2	0	0	1106.50	383	392
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	7	7	17	0.02%	19.9%	VEQLGAEGNVEESQK	99.7%	88.7	25	84.6	4	0	0	1616.78	140	154
Putative RNA-binding protein Luc7-like 2	LUC7L2	LC7L2_HUMAN	46.5	100.0%	7	7	17	0.02%	19.9%	VHELNEEIGK	99.7%	62.3	25	56.3	2	0	0	1167.60	126	135
Pyridoxal phosphate phosphatase	PDXP	PLPP_HUMAN	31.7	99.8%	2	2	3	0.00%	10.5%	LAGDPSAGDGAAPR	99.7%	60.5	25	59.6	2	0	0	1254.61	129	142
Pyridoxal phosphate phosphatase	PDXP	PLPP_HUMAN	31.7	99.8%	2	2	3	0.00%	10.5%	TPGTGSLAAAVETASGR	99.7%	41.2	25	40.7	1	0	0	1545.79	190	206
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	12	19	33	0.03%	48.0%	DNVSSPGGATIHALHVLESGGFR	95.9%	23.6	25	23.6	0	1	0	2321.16	229	251
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	12	19	33	0.03%	48.0%	EGATVYATGTHAQVEDGR	99.7%	86.7	25	86.7	2	2	0	1861.87	130	147
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	12	19	33	0.03%	48.0%	ELQSMADQEQVSPAAIK	99.7%	90.3	25	80.8	3	0	0	1860.90	267	283
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	12	19	33	0.03%	48.0%	ELQSMADQEQVSPAAIKK	99.7%	39.9	25	37.1	0	3	0	1973.00	267	284
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	12	19	33	0.03%	48.0%	GFTAAGVLAAHK	99.7%	71.8	25	63.7	2	0	0	1142.63	18	29
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	12	19	33	0.03%	48.0%	IMASSPDMDLATVSALR	99.7%	111	25	111	4	0	0	1777.88	30	46
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	12	19	33	0.03%	48.0%	IMASSPDMDLATVSALRK	99.7%	34.4	25	27.8	0	3	0	1921.97	30	47
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	12	19	33	0.03%	48.0%	LDSPAGTALSPSGHTK	99.7%	89.3	25	79.1	2	2	0	1538.78	292	307
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	12	19	33	0.03%	48.0%	LGAQALLGAAK	99.7%	90.6	25	83.9	2	0	0	1012.62	205	215
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	12	19	33	0.03%	48.0%	LSAFRPAPR	97.7%	31	25	23.6	2	0	0	1014.58	108	116
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	12	19	33	0.03%	48.0%	MLLHSEQHPGQLK	99.6%	33.2	25	29	0	3	0	1517.79	216	228

Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	12	19	33	0.03%	48.0%	SLLINAVEASCIR	99.7%	98.2	25	90.1	8	0	0	1445.78	252	264
Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	P5CR1_HUMAN	33.4	100.0%	12	19	33	0.03%	48.0%	VKLDSPAGTALSPSGHTK	99.7%	42.3	25	32	0	2	0	1765.94	290	307
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	12	14	35	0.03%	38.4%	ELQSMADQEK	99.7%	55.7	25	42.6	4	0	0	1194.53	267	276
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	12	14	35	0.03%	38.4%	GFTAAGILSAHK	99.7%	65.7	25	59.5	4	0	0	1172.64	18	29
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	12	14	35	0.03%	38.4%	IIASSPEMNLPTVSALR	99.7%	134	25	121	4	0	0	1814.97	30	46
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	12	14	35	0.03%	38.4%	ISPAALKK	99.7%	40.9	25	34.2	2	0	0	827.54	277	284
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	12	14	35	0.03%	38.4%	KLMAFQPAPK	99.1%	34.8	25	17.2	1	0	0	1130.64	107	116
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	12	14	35	0.03%	38.4%	LAIQLGAQALLGAAK	99.7%	69	25	69	2	0	0	1437.88	201	215
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	12	14	35	0.03%	38.4%	LESPTVSTLTPSSPGK	99.7%	87.3	25	66.3	2	0	0	1600.84	292	307
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	12	14	35	0.03%	38.4%	LMAFQPAPK	99.7%	54.5	25	43.9	2	0	0	1002.54	108	116
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	12	14	35	0.03%	38.4%	MGVNLTR	99.7%	40.9	25	10.1	2	0	0	806.42	48	54
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	12	14	35	0.03%	38.4%	MLLDSEQHPCQLK	99.7%	57.9	25	53.3	2	0	0	1614.76	216	228
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	12	14	35	0.03%	38.4%	SLLINAVEASCIR	99.7%	98.2	25	90.1	8	0	0	1445.78	252	264
Pyrroline-5-carboxylate reductase 2	PYCR2	P5CR2_HUMAN	33.6	100.0%	12	14	35	0.03%	38.4%	VKLESPTVSTLTPSSPGK	99.7%	81.8	25	74.2	2	0	0	1828.01	290	307
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	5	7	10	0.01%	21.5%	AATMSAVEAATCR	99.7%	67.1	25	67.1	3	0	0	1354.61	255	267
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	5	7	10	0.01%	21.5%	IAAQTLLGTAK	99.7%	87.8	25	87.8	2	0	0	1086.65	208	218
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	5	7	10	0.01%	21.5%	MAGAIAQGLIR	99.7%	75.5	25	68.3	3	0	0	1116.62	19	29
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	5	7	10	0.01%	21.5%	MGMPSSLAHR	99.7%	39.5	25	34	1	0	0	1086.52	198	207
Pyrroline-5-carboxylate reductase 3	PYCRL	P5CR3_HUMAN	28.6	100.0%	5	7	10	0.01%	21.5%	VEAQHILASAPTDR	98.9%	28.5	25	23.4	0	1	0	1507.79	33	46
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	4	4	6	0.01%	4.9%	AEAEAQAEELSFPR	99.7%	112	25	106	1	0	0	1547.73	929	942
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	4	4	6	0.01%	4.9%	DFTATFGPLDSLNTR	99.7%	63.9	25	58.2	2	0	0	1654.81	1022	1036
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	4	4	6	0.01%	4.9%	GANAVGYTNYPDNVVFK	99.7%	53.7	25	50.6	1	0	0	1828.89	645	661
Pyruvate carboxylase, mitochondrial	PC	PYC_HUMAN	129.6	100.0%	4	4	6	0.01%	4.9%	TSTAPAASPNVR	99.2%	35.5	25	23.3	2	0	0	1171.61	19	30
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	9	10	22	0.02%	26.7%	AHGFTFTR	99.0%	34.4	25	27.5	2	0	0	936.47	120	127
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	9	10	22	0.02%	26.7%	EILAELTGR	99.7%	49	25	35.9	2	0	0	1001.56	133	141
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	9	10	22	0.02%	26.7%	GPILMELQTYR	99.7%	63.1	25	63.1	2	0	0	1320.70	278	288
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	9	10	22	0.02%	26.7%	LEEGPPVTTVLTR	99.7%	68.1	25	60.8	6	0	0	1411.78	46	58
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	9	10	22	0.02%	26.7%	LPCIFICENNR	99.7%	57.1	25	54	1	0	0	1435.68	216	226
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	9	10	22	0.02%	26.7%	NFYGGNGIVGAQVPLGAGIALACK	99.7%	58.3	25	58.3	0	1	0	2347.22	159	182
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	9	10	22	0.02%	26.7%	TREEIQEVR	99.2%	35.6	25	11.4	2	0	0	1159.61	303	311
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	9	10	22	0.02%	26.7%	VDGMDILCVR	99.7%	55.2	25	48.8	2	0	0	1177.57	254	263
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	ODPA_HUMAN	43.3	100.0%	9	10	22	0.02%	26.7%	YGMGTSVER	99.7%	46.7	25	40.3	4	0	0	1015.45	227	235
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	17	38	0.04%	34.8%	DAINQGMDEELER	99.2%	35.4	25	35.4	1	0	0	1519.67	37	49
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	17	38	0.04%	34.8%	DAINQGMDEELERDEK	99.7%	69.5	25	66.8	2	1	0	1891.83	37	52
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	17	38	0.04%	34.8%	DFLIPIGK	98.4%	32.4	25	19.5	2	0	0	902.53	220	227
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	17	38	0.04%	34.8%	DIIFAIK	99.2%	35.2	25	20.9	1	0	0	819.50	348	354
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	17	38	0.04%	34.8%	DIIFAIKK	99.6%	38.4	25	26	2	0	0	947.59	348	355
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	17	38	0.04%	34.8%	EGVECEVINMR	99.7%	55.7	25	55.7	4	0	0	1335.60	259	269
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	17	38	0.04%	34.8%	ILEDNSIPQVK	99.7%	45.6	25	33	2	0	0	1255.69	337	347
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	17	38	0.04%	34.8%	IMEGPAFNFLDAPAVR	99.7%	81.4	25	81.4	8	0	0	1763.88	309	324
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	17	38	0.04%	34.8%	TYYMSGGLQPVPIVFR	99.7%	79.9	25	76	5	0	0	1827.95	130	145
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	17	38	0.04%	34.8%	VFLLGEEVAQYDGAYK	99.7%	107	25	100	4	0	0	1801.90	53	68
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	17	38	0.04%	34.8%	VTGADVPMPYAK	99.7%	49.9	25	48.2	4	0	0	1264.62	325	336
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	ODPB_HUMAN	39.2	100.0%	12	17	38	0.04%	34.8%	VVSPWNSEDAK	99.7%	64.1	25	43.3	2	0	0	1231.60	174	184
Pyruvate dehydrogenase protein X component, mitochondrial	PDHX	ODPX_HUMAN	54.1	100.0%	4	4	5	0.00%	8.4%	GIQEIADSVK	94.9%	27.9	25	25.9	1	0	0	1059.57	385	394
Pyruvate dehydrogenase protein X component, mitochondrial	PDHX	ODPX_HUMAN	54.1	100.0%	4	4	5	0.00%	8.4%	HSLDASQGTATGPR	99.2%	35.4	25	35.4	1	0	0	1397.68	195	208
Pyruvate dehydrogenase protein X component, mitochondrial	PDHX	ODPX_HUMAN	54.1	100.0%	4	4	5	0.00%	8.4%	VSVNDFIIK	99.4%	37	25	18	1	0	0	1034.59	326	334
Pyruvate dehydrogenase protein X component, mitochondrial	PDHX	ODPX_HUMAN	54.1	100.0%	4	4	5	0.00%	8.4%	VVDDELATR	99.3%	36.1	25	27.1	2	0	0	1017.52	477	485
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	AEGSDVANAVLDGADCIMLSGETAK	99.7%	126	25	126	4	4	0	2510.14	343	367
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	AGKPVICATQMLESMIK	99.7%	71.3	25	69.2	6	10	0	1908.96	320	336
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	CCSGAIIVLTK	99.7%	76.4	25	67.1	4	0	0	1221.63	423	433

Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	CDENILWLDYK	99.7%	85	25	83.5	2	0	0	1468.68	152	162
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	DPVQEAWAEDVDLR	99.7%	109	25	109	2	0	0	1642.77	476	489
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	EAEAAIYHLQLFEELR	98.7%	27.8	25	27.3	0	1	0	1931.99	384	399
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	EAEAAIYHLQLFEELRR	99.7%	53	25	53	0	4	0	2088.09	384	400
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	FDEILEASDGIMVAR	99.7%	88.3	25	88.3	1	0	0	1665.82	280	294
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	FGVEQDVDMVFASFIR	99.7%	127	25	127	13	6	0	1859.90	231	246
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	GADFLVTEVENGGSLGSK	99.7%	137	25	132	4	0	0	1779.88	189	206
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	GADFLVTEVENGGSLGSKK	99.7%	46.7	25	40.5	0	2	0	1907.97	189	207
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	GDLGIEIPAEK	99.7%	73.7	25	54.1	16	0	0	1141.61	295	305
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	GDVVIVLTGWRPGSGFTNTMR	99.7%	36.2	25	36.2	0	1	0	2279.16	506	526
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	GDYPLEAVR	99.7%	60.1	25	49.9	14	0	0	1019.52	368	376
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	GIFPVLCK	97.8%	31.2	25	10.8	1	0	0	933.52	468	475
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	GIFPVLCKDPVQEAWAEDVDLR	99.7%	57.1	25	57.1	0	4	0	2557.28	468	489
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	GSGTAEVELK	99.7%	57.5	25	35.9	2	0	0	990.51	126	135
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	GSGTAEVELKK	99.7%	59.7	25	44.6	10	0	0	1118.61	126	136
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	GVNLPGAAVDLPAVSEK	99.7%	123	25	121	5	0	0	1636.89	208	224
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	GVNLPGAAVDLPAVSEKDIQDLK	99.7%	81.4	25	81.4	2	2	0	2349.27	208	230
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	ITLDNAYMEK	99.7%	64.4	25	57.3	6	0	0	1197.58	142	151
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	IYVDDGLISLQVK	99.7%	98.2	25	98.2	11	0	0	1462.82	174	186
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	KGVNLPGAAVDLPAVSEK	99.7%	104	25	104	2	2	0	1764.99	207	224
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	LAPITSDPTEATAVGAVEASFK	99.7%	127	25	127	6	3	0	2175.12	401	422
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	LDIDSPPITAR	99.7%	67.6	25	60.2	15	0	0	1197.65	33	43
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	LNFSHGTHEYHAETIK	99.7%	74.4	25	59	2	4	0	1883.90	74	89
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	MQHLIAR	99.7%	41.1	25	29.2	8	0	0	868.48	377	383
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	NTGIICTIGPASR	99.7%	101	25	101	12	0	0	1359.71	44	56
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	RFDEILEASDGIMVAR	99.7%	74.7	25	70.8	6	8	0	1837.91	279	294
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	SVETLKEMIK	99.7%	47	25	34.3	6	0	0	1177.65	57	66
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	TATESFASDPILYRPVAVALDTK	99.7%	69.5	25	69.5	2	10	0	2465.29	93	115
Pyruvate kinase PKM	PKM	KPYM_HUMAN	57.9	100.0%	32	53	233	0.22%	68.4%	VNFAMNVGK	99.7%	62.1	25	55.9	10	0	0	979.50	490	498
Queuine tRNA-ribosyltransferase subunit QTRTD1	QTRTD1	QTRD1_HUMAN	46.7	100.0%	3	3	6	0.01%	8.7%	GVDLFESFFPYQVTER	99.7%	74	25	73	2	0	0	1933.93	267	282
Queuine tRNA-ribosyltransferase subunit QTRTD1	QTRTD1	QTRD1_HUMAN	46.7	100.0%	3	3	6	0.01%	8.7%	LQEESEVLQK	99.2%	35.5	25	23.4	2	0	0	1202.63	177	186
Queuine tRNA-ribosyltransferase subunit QTRTD1	QTRTD1	QTRD1_HUMAN	46.7	100.0%	3	3	6	0.01%	8.7%	SLLFLDNCLR	99.7%	53.1	25	42.3	2	0	0	1250.66	167	176
Rab3 GTPase-activating protein non-catalytic subunit	RAB3GAP2	RBGPR_HUMAN	156.0	99.8%	2	2	3	0.00%	1.8%	VAQFLVIYAPR	99.6%	38.4	25	38.4	1	0	0	1276.74	461	471
Rab3 GTPase-activating protein non-catalytic subunit	RAB3GAP2	RBGPR_HUMAN	156.0	99.8%	2	2	3	0.00%	1.8%	VVSAAVQAQHSATK	99.7%	58.7	25	58.7	2	0	0	1396.75	1220	1233
Rab-like protein 2A	RABL2A	RBL2A_HUMAN,RBL2B_HUMAN	26.1	99.8%	2	2	3	0.00%	11.0%	IICLGDSAVGK	99.7%	44.8	25	38.9	1	0	0	1132.60	24	34
Rab-like protein 2A	RABL2A	RBL2A_HUMAN,RBL2B_HUMAN	26.1	99.8%	2	2	3	0.00%	11.0%	TILVDFWDTAGQER	99.7%	102	25	93.3	2	0	0	1650.81	69	82
Rab-like protein 3	RABL3	RABL3_HUMAN	26.4	99.8%	2	2	3	0.00%	8.1%	WSLEALNR	99.7%	43.8	25	32.7	1	0	0	988.52	109	116
Rab-like protein 3	RABL3	RABL3_HUMAN	26.4	99.8%	2	2	3	0.00%	8.1%	YLAAGSSNAVK	99.7%	48.2	25	27.4	2	0	0	1080.57	185	195
Rac GTPase-activating protein 1	RACGAP1	RGAP1_HUMAN	71.0	100.0%	3	3	4	0.00%	4.0%	LHDFVSK	99.1%	34.7	25	18.2	1	0	0	845.45	286	292
Rac GTPase-activating protein 1	RACGAP1	RGAP1_HUMAN	71.0	100.0%	3	3	4	0.00%	4.0%	NLFEQLVR	97.9%	31.4	25	21.6	1	0	0	1018.57	10	17
Rac GTPase-activating protein 1	RACGAP1	RGAP1_HUMAN	71.0	100.0%	3	3	4	0.00%	4.0%	TPSSSSLSQR	99.7%	41.6	25	40.3	2	0	0	1049.52	588	597
RAC-alpha serine/threonine-protein kinase	AKT1	AKT1_HUMAN	55.7	100.0%	3	3	3	0.00%	5.0%	ITDFGLCK	98.8%	33.7	25	0	1	0	0	953.48	290	297
RAC-alpha serine/threonine-protein kinase	AKT1	AKT1_HUMAN	55.7	100.0%	3	3	3	0.00%	5.0%	LENLMLDK	96.9%	29.8	25	1.33	1	0	0	975.52	277	284
RAC-alpha serine/threonine-protein kinase	AKT1	AKT1_HUMAN	55.7	100.0%	3	3	3	0.00%	5.0%	YSFQTHDR	94.7%	27.8	25	18.1	1	0	0	1053.47	215	222
Ragulator complex protein LAMTOR1	LAMTOR1	LTOR1_HUMAN	17.7	100.0%	3	3	5	0.00%	23.6%	IAAYAYSALSQIR	99.7%	74	25	68.6	2	0	0	1426.77	135	147
Ragulator complex protein LAMTOR1	LAMTOR1	LTOR1_HUMAN	17.7	100.0%	3	3	5	0.00%	23.6%	LAVLSSSLTHWK	99.7%	44	25	35.6	1	0	0	1341.75	92	103
Ragulator complex protein LAMTOR1	LAMTOR1	LTOR1_HUMAN	17.7	100.0%	3	3	5	0.00%	23.6%	TDEQALLSSILAK	99.7%	91	25	90	2	0	0	1388.76	48	60
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	19	34	0.03%	32.2%	AFNSSSFNSNTFLTR	99.7%	84	25	72.7	1	0	0	1692.80	501	515
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	19	34	0.03%	32.2%	GAVAIADAIR	99.7%	73.1	25	64.5	4	0	0	956.55	280	289
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	19	34	0.03%	32.2%	GAVAMAETLK	99.7%	50.4	25	23.5	3	0	0	990.53	252	261
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	19	34	0.03%	32.2%	HSLLQTLYKV	99.7%	52.3	25	50.8	2	0	0	1201.69	578	587

Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	19	34	0.03%	32.2%	ILAAALTECHR	99.7%	60.7	25	60.7	2	0	0	1254.66	161	171
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	19	34	0.03%	32.2%	LEGNTVGVEAAR	99.7%	102	25	88.9	2	0	0	1215.63	56	67
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	19	34	0.03%	32.2%	LLVHMGLLK	99.6%	38.2	25	38.2	1	0	0	1023.64	516	524
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	19	34	0.03%	32.2%	LNNCGMGIGGGK	99.7%	47.6	25	47.1	2	0	0	1177.55	149	160
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	19	34	0.03%	32.2%	LNTAEDAKDVIK	99.7%	48.5	25	39.8	1	0	0	1316.71	32	43
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	19	34	0.03%	32.2%	MAVQDAVDALMQK	99.7%	69.3	25	61.9	3	0	0	1419.70	488	500
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	19	34	0.03%	32.2%	QVEVINFGDCLVR	99.7%	91.1	25	87.3	2	0	0	1548.78	265	277
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	19	34	0.03%	32.2%	SSACFTLQELK	99.2%	35.4	25	28.2	1	0	0	1283.63	138	148
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	19	34	0.03%	32.2%	SSVLIAQQTDTSDPEK	99.7%	114	25	109	2	0	0	1718.84	453	468
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	19	34	0.03%	32.2%	TQVAGGQLSFK	99.7%	63.6	25	52	2	0	0	1135.61	16	26
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	19	34	0.03%	32.2%	VINLNDNTFTEK	99.7%	61.8	25	54.2	3	0	0	1407.71	240	251
Ran GTPase-activating protein 1	RANGAP1	RAGP1_HUMAN	63.5	100.0%	16	19	34	0.03%	32.2%	VSSVFKDEATVR	99.7%	67.4	25	54.9	2	1	0	1337.71	476	487
Ran-specific GTPase-activating protein	RANBP1	RANG_HUMAN	23.3	99.8%	2	2	4	0.00%	10.0%	FLNAENAQK	99.7%	40	25	22	2	0	0	1034.53	142	150
Ran-specific GTPase-activating protein	RANBP1	RANG_HUMAN	23.3	99.8%	2	2	4	0.00%	10.0%	TLEEDEEELFK	99.7%	58.8	25	54	2	0	0	1381.64	40	50
Ras GTPase-activating protein-binding protein 1	G3BP1	G3BP1_HUMAN	52.2	100.0%	4	4	8	0.01%	11.8%	EAGEQGDIEPR	99.7%	60.7	25	54.9	2	0	0	1200.55	321	331
Ras GTPase-activating protein-binding protein 1	G3BP1	G3BP1_HUMAN	52.2	100.0%	4	4	8	0.01%	11.8%	FMQTFVLAPEGSVANK	99.7%	70.2	25	67.4	2	0	0	1738.88	108	123
Ras GTPase-activating protein-binding protein 1	G3BP1	G3BP1_HUMAN	52.2	100.0%	4	4	8	0.01%	11.8%	SSSPAPADIAQTVQEDLR	99.7%	98.6	25	93.9	2	0	0	1884.93	230	247
Ras GTPase-activating protein-binding protein 1	G3BP1	G3BP1_HUMAN	52.2	100.0%	4	4	8	0.01%	11.8%	TFSWASVTSK	99.7%	51.7	25	45.1	2	0	0	1113.56	248	257
Ras GTPase-activating protein-binding protein 2	G3BP2	G3BP2_HUMAN	54.1	100.0%	3	4	7	0.01%	8.5%	LPNFGFVVFDDSEPVQR	99.7%	76.3	25	76.3	2	0	0	1965.97	371	387
Ras GTPase-activating protein-binding protein 2	G3BP2	G3BP2_HUMAN	54.1	100.0%	3	4	7	0.01%	8.5%	TEELKPQVEEK	99.7%	52.6	25	38	2	0	0	1329.69	206	216
Ras GTPase-activating protein-binding protein 2	G3BP2	G3BP2_HUMAN	54.1	100.0%	3	4	7	0.01%	8.5%	VEAKPEVQSQPPR	99.7%	48.9	25	48.9	2	1	0	1464.78	278	290
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	16	16	30	0.03%	12.0%	ALESGDVNTVWK	99.7%	69.9	25	64.8	2	0	0	1318.66	466	477
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	16	16	30	0.03%	12.0%	ALQSPALGLR	99.7%	39.5	25	33	2	0	0	1025.61	327	336
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	16	16	30	0.03%	12.0%	ATFYGEQVDYYK	99.7%	61.3	25	61.3	2	0	0	1483.67	1517	1528
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	16	16	30	0.03%	12.0%	EEIQSSISGVTAAYNR	99.7%	81.7	25	81.7	1	0	0	1724.84	723	738
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	16	16	30	0.03%	12.0%	GLQQQNSDWYLK	99.7%	55.5	25	51.1	2	0	0	1479.72	337	348
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	16	16	30	0.03%	12.0%	GVLLEIEDLQVNQFK	99.7%	55.8	25	55.8	2	0	0	1744.95	1572	1586
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	16	16	30	0.03%	12.0%	ILAIGLINEALDEGDAQK	99.7%	93.5	25	93.5	2	0	0	1883.01	539	556
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	16	16	30	0.03%	12.0%	LAAVALINAAIQK	99.7%	67.6	25	52.1	2	0	0	1295.80	389	401
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	16	16	30	0.03%	12.0%	LGNFFSPK	99.7%	54.6	25	48.9	2	0	0	909.48	81	88
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	16	16	30	0.03%	12.0%	LIFQMPQNK	99.2%	35.5	25	26.6	2	0	0	1118.60	989	997
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	16	16	30	0.03%	12.0%	LIVDVIR	99.4%	36.7	25	6.9	2	0	0	827.54	1391	1397
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	16	16	30	0.03%	12.0%	LPYDVTPEQALAHEEVK	99.7%	55.7	25	47.6	0	2	0	1938.98	1112	1128
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	16	16	30	0.03%	12.0%	LQQTYAALNSK	99.7%	73.8	25	62.5	2	0	0	1236.66	1506	1516
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	16	16	30	0.03%	12.0%	NVIFEISPTEEVGDFEVK	99.7%	69	25	67.1	2	0	0	2052.02	1587	1604
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	16	16	30	0.03%	12.0%	TLQALQIPAAK	99.7%	76.7	25	69.4	2	0	0	1153.69	557	567
Ras GTPase-activating-like protein IQGAP1	IQGAP1	IQGA1_HUMAN	189.3	100.0%	16	16	30	0.03%	12.0%	YQELINDIAR	99.7%	45.1	25	45.1	1	0	0	1234.64	1478	1487
Ras GTPase-activating-like protein IQGAP2	IQGAP2	IQGA2_HUMAN	180.6	99.9%	2	2	2	0.00%	2.3%	ENIWSASEELLLR	99.7%	58.8	25	53.5	1	0	0	1559.81	654	666
Ras GTPase-activating-like protein IQGAP2	IQGAP2	IQGA2_HUMAN	180.6	99.9%	2	2	2	0.00%	2.3%	LIFQMPQNK	99.2%	35.5	25	26.6	2	0	0	1118.60	902	910
Ras GTPase-activating-like protein IQGAP2	IQGAP2	IQGA2_HUMAN	180.6	99.9%	2	2	2	0.00%	2.3%	TLVGSENPPLTVIR	99.7%	58	25	50.8	1	0	0	1495.85	772	785
Ras suppressor protein 1	RSU1	RSU1_HUMAN	31.5	100.0%	3	3	3	0.00%	12.3%	ALYLSDNDFEILPPDIGK	95.9%	28.8	25	28.8	1	0	0	2020.03	138	155
Ras suppressor protein 1	RSU1	RSU1_HUMAN	31.5	100.0%	3	3	3	0.00%	12.3%	EIGELTQLK	99.7%	39.9	25	28.9	1	0	0	1030.58	175	183
Ras suppressor protein 1	RSU1	RSU1_HUMAN	31.5	100.0%	3	3	3	0.00%	12.3%	LQILSLR	99.2%	35.3	25	22.3	1	0	0	842.55	159	165
Ras-related protein Rab-10	RAB10	RAB10_HUMAN	22.5	99.9%	2	2	4	0.00%	17.0%	AFLTLAEDILR	99.7%	78.1	25	68.9	2	0	0	1261.72	162	172
Ras-related protein Rab-10	RAB10	RAB10_HUMAN	22.5	99.9%	2	2	4	0.00%	17.0%	LQIWDTAGQER	99.7%	75.6	25	0	5	0	0	1316.66	60	70
Ras-related protein Rab-10	RAB10	RAB10_HUMAN	22.5	99.9%	2	2	4	0.00%	17.0%	NIDEHANEDVER	99.7%	49.1	25	47.4	2	0	0	1440.64	106	117
Ras-related protein Rab-13	RAB13	RAB13_HUMAN	22.8	100.0%	4	5	10	0.01%	26.1%	FAEDNFNNTYISTIGIDFK	99.7%	61	25	61	2	0	0	2209.04	28	46
Ras-related protein Rab-13	RAB13	RAB13_HUMAN	22.8	100.0%	4	5	10	0.01%	26.1%	SIKENASAGVER	99.7%	61.6	25	47.6	2	0	0	1260.65	105	116
Ras-related protein Rab-13	RAB13	RAB13_HUMAN	22.8	100.0%	4	5	10	0.01%	26.1%	SSMNVDEAFSSLAR	99.7%	98.2	25	94.7	4	0	0	1513.70	154	167
Ras-related protein Rab-13	RAB13	RAB13_HUMAN	22.8	100.0%	4	5	10	0.01%	26.1%	TITTAYYR	97.7%	31	25	20.7	2	0	0	988.51	72	79
Ras-related protein Rab-18	RAB18	RAB18_HUMAN	23.0	100.0%	4	4	7	0.01%	24.3%	GAQGVILVYDVTR	99.7%	41.3	25	41.3	1	0	0	1390.77	80	92

Ras-related protein Rab-18	RAB18	RAB18_HUMAN	23.0	100.0%	4	4	7	0.01%	24.3%	IIQTPGLWESENQNK	99.7%	60.3	25	60.3	2	0	0	1756.89	169	183
Ras-related protein Rab-18	RAB18	RAB18_HUMAN	23.0	100.0%	4	4	7	0.01%	24.3%	ILIIGESGVGK	99.7%	52.9	25	19.8	2	0	0	1085.66	11	21
Ras-related protein Rab-18	RAB18	RAB18_HUMAN	23.0	100.0%	4	4	7	0.01%	24.3%	LAIWDTAGQER	99.7%	47.5	25	45	2	0	0	1259.64	59	69
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	4	4	9	0.01%	24.9%	EFADSLGIPFLETSAK	99.5%	37.9	25	30.5	2	0	0	1724.87	138	153
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	4	4	9	0.01%	24.9%	LQIWDTAGQER	99.7%	75.6	25	0	5	0	0	1316.66	59	69
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	4	4	9	0.01%	24.9%	MGPGAASGGERPNLK	99.7%	52.6	25	48.4	1	0	0	1457.72	173	187
Ras-related protein Rab-1B	RAB1B	RAB1B_HUMAN	22.2	100.0%	4	4	9	0.01%	24.9%	QWLQEIDR	99.7%	42.7	25	22.6	1	0	0	1087.55	101	108
Ras-related protein Rab-2A	RAB2A	RAB2A_HUMAN	23.5	99.8%	2	2	3	0.00%	12.7%	LQIWDTAGQESFR	99.7%	72.2	25	68.9	1	0	0	1550.76	57	69
Ras-related protein Rab-2A	RAB2A	RAB2A_HUMAN	23.5	99.8%	2	2	3	0.00%	12.7%	TASNVEEAFINTAK	99.7%	72.4	25	61.7	2	0	0	1494.74	152	165
Ras-related protein Rab-32	RAB32	RAB32_HUMAN	25.0	99.8%	2	2	3	0.00%	9.3%	DNINIEEAAR	99.7%	53	25	43.8	1	0	0	1144.56	177	186
Ras-related protein Rab-32	RAB32	RAB32_HUMAN	25.0	99.8%	2	2	3	0.00%	9.3%	LQLWDIAGQER	99.7%	65.9	25	53	2	0	0	1328.70	77	87
Ras-related protein Rab-5C	RAB5C	RAB5C_HUMAN	23.5	100.0%	3	3	3	0.00%	17.1%	LVLLGESAVGK	99.7%	69.9	25	46.8	1	0	0	1085.66	24	34
Ras-related protein Rab-5C	RAB5C	RAB5C_HUMAN	23.5	100.0%	3	3	3	0.00%	17.1%	NEPQNATGAPGR	98.9%	34	25	29.9	1	0	0	1211.58	185	196
Ras-related protein Rab-5C	RAB5C	RAB5C_HUMAN	23.5	100.0%	3	3	3	0.00%	17.1%	QASPNIVIALAGNK	99.7%	39.6	25	36.9	1	0	0	1395.80	122	135
Ras-related protein Rab-9A	RAB9A	RAB9A_HUMAN	22.8	99.8%	2	2	3	0.00%	12.9%	DATNVAAAFEEAVRR	95.4%	28.3	25	23.8	1	0	0	1619.81	157	171
Ras-related protein Rab-9A	RAB9A	RAB9A_HUMAN	22.8	99.8%	2	2	3	0.00%	12.9%	VILLGDGGVGK	99.7%	62.5	25	36.2	2	0	0	1027.61	10	20
Ras-related protein Rap-2c	RAP2C	RAP2C_HUMAN	20.7	100.0%	3	3	6	0.01%	28.4%	ALAQEWGCPFMETSAK	97.0%	29.9	25	29.9	1	0	0	1825.82	133	148
Ras-related protein Rap-2c	RAP2C	RAP2C_HUMAN	20.7	100.0%	3	3	6	0.01%	28.4%	SALTVQFVTGTFIEK	99.7%	81.9	25	78.6	3	0	0	1640.89	17	31
Ras-related protein Rap-2c	RAP2C	RAP2C_HUMAN	20.7	100.0%	3	3	6	0.01%	28.4%	SMVDELFAEIVR	99.7%	58.7	25	58.7	2	0	0	1424.71	151	162
Ras-related protein Rap-2c	RAP2C	RAP2C_HUMAN	20.7	100.0%	3	3	6	0.01%	28.4%	VPLILVGNK	99.5%	37.2	25	0	1	0	0	952.62	109	117
Ras-related protein R-Ras2	RRAS2	RRAS2_HUMAN	23.4	100.0%	3	3	4	0.00%	17.2%	LVVVGGGGVGK	98.2%	32	25	32	1	0	0	941.58	17	27
Ras-related protein R-Ras2	RRAS2	RRAS2_HUMAN	23.4	100.0%	3	3	4	0.00%	17.2%	MNVDQAFHELVR	99.7%	53.9	25	42.9	1	0	0	1458.72	162	173
Ras-related protein R-Ras2	RRAS2	RRAS2_HUMAN	23.4	100.0%	3	3	4	0.00%	17.2%	QVTQEEGQQLAR	99.7%	49.5	25	37.2	2	0	0	1386.70	136	147
Regulation of nuclear pre-mRNA domain-containing protein 1A	RPRD1A	RPR1A_HUMAN	35.7	100.0%	5	5	8	0.01%	23.1%	ALQDLENAASGDAAVHQR	99.7%	83.6	25	78.8	1	0	0	1865.91	169	186
Regulation of nuclear pre-mRNA domain-containing protein 1A	RPRD1A	RPR1A_HUMAN	35.7	100.0%	5	5	8	0.01%	23.1%	DFAPVIVEAFK	99.7%	48.4	25	44.6	2	0	0	1235.67	80	90
Regulation of nuclear pre-mRNA domain-containing protein 1A	RPRD1A	RPR1A_HUMAN	35.7	100.0%	5	5	8	0.01%	23.1%	IASLPVEVQEVSLLDK	99.7%	50.8	25	49.8	2	0	0	1739.98	187	202
Regulation of nuclear pre-mRNA domain-containing protein 1A	RPRD1A	RPR1A_HUMAN	35.7	100.0%	5	5	8	0.01%	23.1%	LTFLYLANDVIQNSK	99.7%	86.7	25	86.7	2	0	0	1738.94	57	71
Regulation of nuclear pre-mRNA domain-containing protein 1A	RPRD1A	RPR1A_HUMAN	35.7	100.0%	5	5	8	0.01%	23.1%	SVYENDVLEQLK	99.7%	59.7	25	53.1	1	0	0	1436.73	115	126
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	ADSVVVLLCR	99.7%	58.2	25	52.9	2	0	0	1131.62	201	210
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	AGAKPDQIGIITPYEGQR	99.7%	38.2	25	34	0	2	0	1914.01	794	811
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	AGLSQSLFER	99.7%	90.2	25	65.7	2	0	0	1107.58	689	698
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	AYQHGGVTGLSQY	99.7%	45.4	25	45.4	2	0	0	1380.65	1117	1129
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	DETGELSSADEKR	99.5%	37.2	25	37.2	1	0	0	1436.65	593	605
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	DGPLGETVLECYNCGCR	99.7%	82.3	25	82.3	2	0	0	1999.83	173	189
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	EAIIPGSVYDR	99.7%	40.6	25	32.1	2	0	0	1219.63	950	960
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	EKDFIILSCVR	99.7%	45.9	25	39.8	2	0	0	1379.74	844	854
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	ESLMQFSKPR	95.5%	23.3	25	19.3	0	1	0	1238.62	919	928
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	ESQTQDNITVR	99.7%	40.5	25	34	2	0	0	1290.63	322	332
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	FMTTAMYDAR	99.7%	64.3	25	62.5	3	0	0	1206.53	940	949
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	FTAQGLPDLNHSQVYAVK	99.5%	31.5	25	31.5	0	1	0	1988.02	474	491
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	GNTSGSHIVNHLVR	95.5%	23.2	25	23.2	0	1	0	1490.78	149	162
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	IAYFTLPK	99.7%	45.4	25	41.3	2	0	0	952.55	342	349
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	IPSEQEQLR	99.7%	45.4	25	31.6	2	0	0	1099.57	245	253
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	KLVNTINPGAR	99.7%	71.6	25	64.8	2	0	0	1182.70	929	939
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	LKESQTQDNITVR	98.4%	27	25	21.4	0	1	0	1531.81	320	332
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	LLGHEVEDVIIK	99.7%	74.3	25	71.3	2	0	0	1364.78	456	467
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	LMQGDEICLR	99.7%	49.5	25	37.3	2	0	0	1234.59	367	376
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	LQVQYR	98.3%	32.3	25	0	3	0	0	806.45	709	714
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	LVNTINPGAR	99.7%	39.5	25	32.4	2	0	0	1054.60	930	939
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	SQIDVALSQDSTYQGER	99.7%	99.7	25	90.6	2	0	0	1896.89	1100	1116
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	TVLQRPLSLIQGPPGTGK	99.7%	44.8	25	44.8	0	2	0	1862.09	492	509

Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	TVTSATIVYHLAR	99.7%	111	25	102	2	0	0	1431.80	510	522
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	VLVEGPLNNLR	99.7%	57.2	25	50.7	2	0	0	1223.71	908	918
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	VPDNYGDEIAIELR	99.7%	92.4	25	92.4	2	0	0	1603.80	394	407
Regulator of nonsense transcripts 1	UPF1	RENT1_HUMAN	124.3	100.0%	27	28	52	0.05%	27.7%	YEDAYQYQNIFGPLVK	99.7%	91.8	25	90.9	3	0	0	1947.95	296	311
Regulator of nonsense transcripts 3B	UPF3B	REN3B_HUMAN	57.8	100.0%	5	7	10	0.01%	12.4%	FLESYATDNEK	98.8%	33.7	25	33.7	1	0	0	1316.60	163	173
Regulator of nonsense transcripts 3B	UPF3B	REN3B_HUMAN	57.8	100.0%	5	7	10	0.01%	12.4%	KAESTESIGSSEK	99.7%	59.5	25	56.5	2	0	0	1352.65	406	418
Regulator of nonsense transcripts 3B	UPF3B	REN3B_HUMAN	57.8	100.0%	5	7	10	0.01%	12.4%	MTSTPETLLEEIEAK	99.7%	66.6	25	65	3	0	0	1691.84	174	188
Regulator of nonsense transcripts 3B	UPF3B	REN3B_HUMAN	57.8	100.0%	5	7	10	0.01%	12.4%	NQEDIILFR	99.7%	61.6	25	50.3	2	0	0	1147.61	103	111
Regulator of nonsense transcripts 3B	UPF3B	REN3B_HUMAN	57.8	100.0%	5	7	10	0.01%	12.4%	VGTIDDDPEYRK	99.7%	37.4	25	37.3	1	1	0	1407.68	151	162
Regulatory-associated protein of mTOR	RPTOR	RPTOR_HUMAN	149.0	100.0%	4	4	4	0.00%	3.2%	LDDQIFLNR	99.0%	34.7	25	24.3	1	0	0	1133.60	1013	1021
Regulatory-associated protein of mTOR	RPTOR	RPTOR_HUMAN	149.0	100.0%	4	4	4	0.00%	3.2%	MPESVNVLQIVK	99.7%	41.5	25	24.2	1	0	0	1356.76	1243	1254
Regulatory-associated protein of mTOR	RPTOR	RPTOR_HUMAN	149.0	100.0%	4	4	4	0.00%	3.2%	SLIVAGLGDGSIR	99.7%	63.2	25	53	1	0	0	1257.72	1179	1191
Regulatory-associated protein of mTOR	RPTOR	RPTOR_HUMAN	149.0	100.0%	4	4	4	0.00%	3.2%	SVSSYGNIR	97.6%	30.9	25	28	1	0	0	982.50	719	727
Replication factor C subunit 1	RFC1	RFC1_HUMAN	128.3	100.0%	5	5	8	0.01%	5.8%	AALLSGPPGVGK	99.7%	50.9	25	43.1	2	0	0	1066.63	646	657
Replication factor C subunit 1	RFC1	RFC1_HUMAN	128.3	100.0%	5	5	8	0.01%	5.8%	AIVAESLNNTSIK	99.7%	68.5	25	56.7	2	0	0	1359.75	688	700
Replication factor C subunit 1	RFC1	RFC1_HUMAN	128.3	100.0%	5	5	8	0.01%	5.8%	ELSQNTDESGLNDEAIAK	99.7%	64.8	25	64.8	2	0	0	1933.90	188	205
Replication factor C subunit 1	RFC1	RFC1_HUMAN	128.3	100.0%	5	5	8	0.01%	5.8%	GGIQELIGLIK	98.7%	33.3	25	31.7	1	0	0	1140.70	732	742
Replication factor C subunit 1	RFC1	RFC1_HUMAN	128.3	100.0%	5	5	8	0.01%	5.8%	IIDEDGLLNLIR	99.7%	48.2	25	39.3	1	0	0	1383.78	469	480
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	6	6	14	0.01%	22.0%	DAMLELNASNDR	99.7%	57.6	25	51.4	2	0	0	1348.62	100	111
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	6	6	14	0.01%	22.0%	EGNVPNIIIAGPPGTGK	99.7%	57.4	25	56	4	0	0	1633.89	66	82
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	6	6	14	0.01%	22.0%	IIEPIQSR	99.0%	34.7	25	12.7	1	0	0	955.56	177	184
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	6	6	14	0.01%	22.0%	IIILDEADSMTDGAQQALR	99.7%	81.2	25	75.3	2	0	0	2076.03	137	155
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	6	6	14	0.01%	22.0%	LNEIVGNEDTVSR	99.7%	88	25	88	2	0	0	1445.72	47	59
Replication factor C subunit 2	RFC2	RFC2_HUMAN	39.2	100.0%	6	6	14	0.01%	22.0%	LTDAQILTR	99.7%	48.5	25	40.4	3	0	0	1030.59	193	201
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	3	4	6	0.01%	10.4%	ALLMCEACR	98.5%	32.7	25	32.7	2	0	0	1123.51	226	234
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	3	4	6	0.01%	10.4%	ETANAIVSQQTPQR	99.7%	92.3	25	84.1	2	0	0	1542.79	257	270
Replication factor C subunit 3	RFC3	RFC3_HUMAN	40.6	100.0%	3	4	6	0.01%	10.4%	TVAQSQQLETNSQR	99.7%	108	25	93.8	2	0	0	1589.79	114	127
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	6	6	9	0.01%	17.4%	AITFLQSATR	99.7%	48.9	25	43.6	2	0	0	1107.62	241	250
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	6	6	9	0.01%	17.4%	IIEPLTSR	99.3%	36	25	11.2	1	0	0	928.55	186	193
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	6	6	9	0.01%	17.4%	ISDEGIAYLVK	99.7%	69	25	63.6	2	0	0	1207.66	222	232
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	6	6	9	0.01%	17.4%	NFAQLTVSGSR	99.7%	41.1	25	16.7	1	0	0	1179.61	125	135
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	6	6	9	0.01%	17.4%	VITDIAGVIPAEK	99.7%	62.7	25	54.5	1	0	0	1325.77	261	273
Replication factor C subunit 4	RFC4	RFC4_HUMAN	39.7	100.0%	6	6	9	0.01%	17.4%	VLELNASDER	99.7%	47	25	42.7	2	0	0	1145.58	105	114
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	15	28	0.03%	35.9%	ALNILQSTNMAFGK	99.7%	93.9	25	73.1	4	0	0	1507.79	216	229
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	15	28	0.03%	35.9%	ALVTLSSGDMR	99.7%	76.9	25	65.3	4	0	0	1149.59	204	214
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	15	28	0.03%	35.9%	FCLICNYLSK	99.7%	51.6	25	51.6	2	0	0	1317.63	151	160
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	15	28	0.03%	35.9%	FGPLTPELMVPR	99.7%	49.2	25	42	5	0	0	1356.73	174	185
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	15	28	0.03%	35.9%	GPILSFASTR	99.7%	63.5	25	60.7	2	0	0	1048.58	103	112
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	15	28	0.03%	35.9%	IQLSSLIAAFQVTR	99.7%	117	25	117	2	0	0	1546.90	320	333
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	15	28	0.03%	35.9%	LSVGTNEK	97.8%	31.2	25	22.9	1	0	0	847.45	312	319
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	15	28	0.03%	35.9%	LVILDEADAMTQDAQNALR	99.7%	103	25	103	4	0	0	2103.04	121	139
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	15	28	0.03%	35.9%	MADIEYR	99.7%	45.2	25	35.1	2	0	0	897.41	305	311
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	15	28	0.03%	35.9%	TSTILACAK	98.0%	31.5	25	23.5	1	0	0	964.51	67	75
Replication factor C subunit 5	RFC5	RFC5_HUMAN	38.5	100.0%	11	15	28	0.03%	35.9%	VDFPSSVR	99.7%	42.5	25	34.2	1	0	0	906.47	291	298
Required for meiotic nuclear division protein 1 homolog	RMND1	RMND1_HUMAN	51.6	100.0%	4	4	6	0.01%	10.5%	DAANILVMGVENSAK	99.7%	88.7	25	88.7	2	0	0	1531.78	205	219
Required for meiotic nuclear division protein 1 homolog	RMND1	RMND1_HUMAN	51.6	100.0%	4	4	6	0.01%	10.5%	EGAAVFWNVK	98.7%	33.3	25	33.3	1	0	0	1120.58	231	240
Required for meiotic nuclear division protein 1 homolog	RMND1	RMND1_HUMAN	51.6	100.0%	4	4	6	0.01%	10.5%	IGELFALR	99.7%	70.5	25	51.9	2	0	0	918.54	353	360
Required for meiotic nuclear division protein 1 homolog	RMND1	RMND1_HUMAN	51.6	100.0%	4	4	6	0.01%	10.5%	LNSELDLDDAILEK	99.7%	43	25	40.2	1	0	0	1587.81	289	302
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	6	12	0.01%	23.3%	AEELHYPLGER	99.3%	36.4	25	29.6	2	0	0	1313.65	25	35
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	6	12	0.01%	23.3%	EALLGVQEDVDEYVK	99.7%	103	25	103	2	0	0	1706.85	42	56
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	6	12	0.01%	23.3%	QLHDDYFYHDEL	99.5%	37.8	25	36.8	2	0	0	1594.68	306	317

Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	6	12	0.01%	23.3%	VIDFDENTALDDAEEESFR	99.7%	133	25	133	2	0	0	2214.97	130	148
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	6	12	0.01%	23.3%	VIDFDENTALDDAEEESFRK	99.7%	34.9	25	30.9	0	2	0	2343.06	130	149
Reticulocalbin-2	RCN2	RCN2_HUMAN	36.9	100.0%	6	6	12	0.01%	23.3%	WDPTANEDPEWILVEK	99.7%	74.1	25	74.1	2	0	0	1941.92	217	232
Retinoid-inducible serine carboxypeptidase	SCPEP1	RISC_HUMAN	50.8	100.0%	5	5	8	0.01%	11.5%	DALSQLMNGPIR	99.7%	48.5	25	41.8	2	0	0	1314.68	307	318
Retinoid-inducible serine carboxypeptidase	SCPEP1	RISC_HUMAN	50.8	100.0%	5	5	8	0.01%	11.5%	MAAGIGLELYK	99.1%	35	25	29.7	1	0	0	1165.63	172	182
Retinoid-inducible serine carboxypeptidase	SCPEP1	RISC_HUMAN	50.8	100.0%	5	5	8	0.01%	11.5%	NLAFYWILK	99.7%	40.8	25	31.4	2	0	0	1167.66	420	428
Retinoid-inducible serine carboxypeptidase	SCPEP1	RISC_HUMAN	50.8	100.0%	5	5	8	0.01%	11.5%	SLETSAFVK	99.7%	45.6	25	37	2	0	0	981.53	408	416
Retinoid-inducible serine carboxypeptidase	SCPEP1	RISC_HUMAN	50.8	100.0%	5	5	8	0.01%	11.5%	VAEQVLNAVNK	99.7%	83.2	25	77.2	1	0	0	1184.66	233	243
Rho-related GTP-binding protein RhoC	RHOC	RHOC_HUMAN	22.0	99.8%	2	2	3	0.00%	10.4%	EVFEMATR	98.2%	31.9	25	28.3	1	0	0	982.47	169	176
Rho-related GTP-binding protein RhoC	RHOC	RHOC_HUMAN	22.0	99.8%	2	2	3	0.00%	10.4%	ISAFGYLECSAK	99.7%	64.1	25	57.7	2	0	0	1345.65	151	162
Rho-related GTP-binding protein RhoG	RHOG	RHOG_HUMAN	21.3	100.0%	5	5	5	0.00%	39.3%	AVLNPTPIKR	98.5%	32.8	25	20.9	1	0	0	1108.68	175	184
Rho-related GTP-binding protein RhoG	RHOG	RHOG_HUMAN	21.3	100.0%	5	5	5	0.00%	39.3%	EYIPTVFDNYSAQSAVDGR	99.7%	60.7	25	60.7	1	0	0	2131.99	31	49
Rho-related GTP-binding protein RhoG	RHOG	RHOG_HUMAN	21.3	100.0%	5	5	5	0.00%	39.3%	LKEQGQAPITPQQGQALAK	94.5%	22.6	25	22.6	0	1	0	2006.10	129	147
Rho-related GTP-binding protein RhoG	RHOG	RHOG_HUMAN	21.3	100.0%	5	5	5	0.00%	39.3%	TCLLICYTTNAFPK	99.7%	53.2	25	45.9	1	0	0	1701.83	17	30
Rho-related GTP-binding protein RhoG	RHOG	RHOG_HUMAN	21.3	100.0%	5	5	5	0.00%	39.3%	YLECSALQQDGVK	99.7%	55.9	25	53.1	1	0	0	1510.72	154	166
Ribonuclease P protein subunit p14	RPP14	RPP14_HUMAN	13.7	99.8%	2	2	4	0.00%	20.2%	PAPAATYER	99.7%	45.7	25	37.6	2	0	0	975.49	2	10
Ribonuclease P protein subunit p14	RPP14	RPP14_HUMAN	13.7	99.8%	2	2	4	0.00%	20.2%	VIQVSPFLLALSGNSR	99.7%	74.1	25	62.7	2	0	0	1700.97	104	119
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	6	6	11	0.01%	32.3%	ADLHGAIISVTK	98.6%	33	25	25.1	1	0	0	1224.69	133	144
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	6	6	11	0.01%	32.3%	AVVLEYFTR	99.7%	53.5	25	46.1	2	0	0	1097.60	55	63
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	6	6	11	0.01%	32.3%	CPSYVGITGILLQETK	99.7%	60.6	25	60.6	2	0	0	1778.94	147	162
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	6	6	11	0.01%	32.3%	EANDSDVQPSGAQR	99.7%	78.4	25	70.6	2	0	0	1473.66	13	26
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	6	6	11	0.01%	32.3%	LFDIKPEQQR	99.7%	40.9	25	32	2	0	0	1273.69	86	95
Ribonuclease P protein subunit p29	POP4	RPP29_HUMAN	25.4	100.0%	6	6	11	0.01%	32.3%	SVIYHALSQK	99.7%	65.2	25	59.5	2	0	0	1145.63	3	12
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	8	9	17	0.02%	38.1%	AALLHGETR	99.7%	51.4	25	39	2	0	0	967.53	227	235
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	8	9	17	0.02%	38.1%	GLAFELVYSPAIK	99.7%	91.5	25	86.3	2	0	0	1407.79	149	161
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	8	9	17	0.02%	38.1%	GPYDVANLGLLFGLSESDAK	99.7%	43.5	25	43.5	1	0	0	2066.04	199	218
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	8	9	17	0.02%	38.1%	KTAFGIISTVK	99.7%	53.9	25	53.9	2	0	0	1164.70	236	246
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	8	9	17	0.02%	38.1%	LYDVVAVFPK	99.7%	67	25	67	3	0	0	1150.65	99	108
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	8	9	17	0.02%	38.1%	NVIISSAAERPLEIR	99.7%	44	25	34.3	2	0	0	1667.94	184	198
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	8	9	17	0.02%	38.1%	RPPINVAIDR	97.3%	30.4	25	9.61	2	0	0	1150.67	139	148
Ribonuclease P protein subunit p30	RPP30	RPP30_HUMAN	29.3	100.0%	8	9	17	0.02%	38.1%	YTISSALNLMQICK	99.7%	72.8	25	72.8	3	0	0	1641.83	168	181
Ribonuclease P protein subunit p38	RPP38	RPP38_HUMAN	31.8	100.0%	3	3	4	0.00%	11.0%	NTTDFVDEVR	99.7%	54.2	25	44.5	2	0	0	1195.56	185	194
Ribonuclease P protein subunit p38	RPP38	RPP38_HUMAN	31.8	100.0%	3	3	4	0.00%	11.0%	QLAIGVNEVTR	99.7%	45.7	25	28.9	1	0	0	1199.67	112	122
Ribonuclease P protein subunit p38	RPP38	RPP38_HUMAN	31.8	100.0%	3	3	4	0.00%	11.0%	TSLNNPYIIR	98.8%	33.6	25	30.1	1	0	0	1190.65	23	32
Ribonuclease P/MRP protein subunit POP5	POP5	POP5_HUMAN	18.8	100.0%	5	5	7	0.01%	36.2%	FLIQYNR	99.7%	48.3	25	39	1	0	0	953.52	113	119
Ribonuclease P/MRP protein subunit POP5	POP5	POP5_HUMAN	18.8	100.0%	5	5	7	0.01%	36.2%	LSLDDRVLSSLVR	97.2%	25	25	24.1	0	1	0	1472.84	22	34
Ribonuclease P/MRP protein subunit POP5	POP5	POP5_HUMAN	18.8	100.0%	5	5	7	0.01%	36.2%	QLLILLQNCTDEGER	99.7%	56.3	25	56.3	1	0	0	1801.91	121	135
Ribonuclease P/MRP protein subunit POP5	POP5	POP5_HUMAN	18.8	100.0%	5	5	7	0.01%	36.2%	YLLCELVSDDPR	99.7%	51.1	25	46.1	2	0	0	1479.72	8	19
Ribonuclease P/MRP protein subunit POP5	POP5	POP5_HUMAN	18.8	100.0%	5	5	7	0.01%	36.2%	YLNAYTGIVLLR	99.7%	70.6	25	64.1	2	0	0	1395.80	57	68
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	4	4	8	0.01%	5.0%	AGPEGTSQEIPK	99.7%	59.5	25	50.9	2	0	0	1213.61	89	100
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	4	4	8	0.01%	5.0%	NQPTNVTLSSGFVADR	99.7%	111	25	111	2	0	0	1705.85	15	30
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	4	4	8	0.01%	5.0%	SSNSLVFQTLPR	99.7%	60.7	25	43.3	2	0	0	1348.72	126	137
Ribonucleases P/MRP protein subunit POP1	POP1	POP1_HUMAN	114.7	100.0%	4	4	8	0.01%	5.0%	YITASTFAQAR	99.7%	47.9	25	39.9	2	0	0	1228.63	101	111
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	11	14	29	0.03%	39.6%	ENISEWR	96.9%	29.8	25	23.2	1	0	0	933.44	157	163
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	11	14	29	0.03%	39.6%	IFSGSSHQDLSQK	99.7%	77.2	25	71.6	2	0	0	1433.70	6	18
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	11	14	29	0.03%	39.6%	IQVIDISMILAEAIR	98.9%	34.2	25	34.2	1	0	0	1700.96	287	301
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	11	14	29	0.03%	39.6%	LNVDFALIHK	99.7%	43.8	25	30.2	2	0	0	1169.67	185	194
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	11	14	29	0.03%	39.6%	MVLVGDVK	99.1%	34.9	25	22.1	2	0	0	876.49	205	212
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	11	14	29	0.03%	39.6%	MVLVGDVKDR	99.7%	70.2	25	57.7	3	0	0	1147.61	205	214
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	11	14	29	0.03%	39.6%	NCTIVSPDAGGAK	99.7%	58.5	25	45.2	2	0	0	1289.62	164	176
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	11	14	29	0.03%	39.6%	RVTSIADR	96.3%	29.1	25	15.6	1	0	0	917.52	177	184

Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	11	14	29	0.03%	39.6%	VAILVDDMADTCGTICHAADK	99.7%	39.7	25	39.7	0	4	0	2276.04	215	235
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	11	14	29	0.03%	39.6%	VTAVIPCFPYAR	99.7%	52.4	25	49.4	4	0	0	1393.73	85	96
Ribose-phosphate pyrophosphokinase 1	PRPS1	PRPS1_HUMAN	34.8	100.0%	11	14	29	0.03%	39.6%	VYAILTHGIFSGPAISR	99.7%	70.3	25	65.2	4	3	0	1802.00	244	260
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	3	3	4	0.00%	40.3%	FSNQETSVEIGESVR	99.7%	100	25	98.3	2	0	0	1681.80	35	49
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	3	3	4	0.00%	40.3%	IQVIDISMILAEAIR	98.9%	34.2	25	34.2	1	0	0	1700.96	287	301
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	3	3	4	0.00%	40.3%	MVLVGDVK	99.1%	34.9	25	22.1	2	0	0	876.49	205	212
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	3	3	4	0.00%	40.3%	MVLVGDVKDR	99.7%	70.2	25	57.7	3	0	0	1147.61	205	214
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	3	3	4	0.00%	40.3%	NCIIVSPDAGGAK	99.7%	39.7	25	39.7	1	0	0	1301.65	164	176
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	3	3	4	0.00%	40.3%	PNIVLFSGSSHQDLSQR	98.2%	26.7	25	26.7	0	1	0	1884.96	2	18
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	3	3	4	0.00%	40.3%	RVTSIADR	96.3%	29.1	25	15.6	1	0	0	917.52	177	184
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	3	3	4	0.00%	40.3%	VAILVDDMADTCGTICHAADK	99.7%	39.7	25	39.7	0	4	0	2276.04	215	235
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	3	3	4	0.00%	40.3%	VTAVIPCFPYAR	99.7%	52.4	25	49.4	4	0	0	1393.73	85	96
Ribose-phosphate pyrophosphokinase 2	PRPS2	PRPS2_HUMAN	34.8	100.0%	3	3	4	0.00%	40.3%	VYAILTHGIFSGPAISR	99.7%	70.3	25	65.2	4	3	0	1802.00	244	260
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	4	4	7	0.01%	6.8%	FVNLISER	99.7%	49.3	25	31.4	2	0	0	977.54	122	129
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	4	4	7	0.01%	6.8%	GCYFVLDWLQK	99.7%	80.7	25	73.9	2	0	0	1428.70	172	182
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	4	4	7	0.01%	6.8%	LLDVTGGLGTDELR	99.7%	92.4	25	87.2	1	0	0	1458.78	99	112
Ribosomal biogenesis protein LAS1L	LAS1L	LAS1L_HUMAN	83.1	100.0%	4	4	7	0.01%	6.8%	SGNELPLAVASTADLIR	99.7%	102	25	97.9	2	0	0	1726.93	80	96
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	16	16	27	0.03%	32.9%	AAESETPGKSPEK	99.7%	48.4	25	45.3	2	0	0	1330.65	418	430
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	16	16	27	0.03%	32.9%	ATNESEDEIPQLVPIGK	99.7%	42.6	25	35.3	1	0	0	1839.93	357	373
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	16	16	27	0.03%	32.9%	DDVAPESGDTTVK	99.2%	35.6	25	35.6	1	0	0	1333.61	319	331
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	16	16	27	0.03%	32.9%	EINDCIGGTVLNISK	99.7%	92.2	25	89.1	2	0	0	1632.83	193	207
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	16	16	27	0.03%	32.9%	KALPASETPK	99.7%	53.3	25	43.8	2	0	0	1041.59	408	417
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	16	16	27	0.03%	32.9%	KVPVSVNLLSK	99.7%	40.6	25	40.6	1	0	0	1183.74	178	188
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	16	16	27	0.03%	32.9%	LLPSLIGR	99.6%	38.5	25	26.3	2	0	0	868.56	164	171
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	16	16	27	0.03%	32.9%	LLSSFDFFLTDAR	99.7%	94.9	25	89.1	2	0	0	1531.78	148	160
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	16	16	27	0.03%	32.9%	LPEKWESVK	96.5%	29.3	25	11.6	1	0	0	1115.61	241	249
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	16	16	27	0.03%	32.9%	LTLPHSIR	99.7%	41	25	41	2	0	0	936.56	82	89
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	16	16	27	0.03%	32.9%	RLLPSLIGR	99.7%	39.4	25	33.1	2	0	0	1024.66	163	171
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	16	16	27	0.03%	32.9%	SAALPIFSSFVSNWDEATK	99.7%	93	25	92.7	1	0	0	2070.02	258	276
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	16	16	27	0.03%	32.9%	TPANEKVEIQK	99.7%	46.1	25	38.7	2	0	0	1256.68	375	385
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	16	16	27	0.03%	32.9%	TVSQIISLQTLK	99.7%	69	25	69	2	0	0	1330.79	125	136
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	16	16	27	0.03%	32.9%	TVSQIISLQTLKK	99.7%	57.2	25	57.2	2	0	0	1458.89	125	137
Ribosomal L1 domain-containing protein 1	RSL1D1	RL1D1_HUMAN	55.0	100.0%	16	16	27	0.03%	32.9%	VPVSVNLLSK	99.7%	60.4	25	54	2	0	0	1055.65	179	188
Ribosomal protein S6 kinase alpha-1	RPS6KA1	KS6A1_HUMAN	82.7	100.0%	3	3	3	0.00%	8.0%	DLKPENILLDEEGHIK	99.7%	53.5	25	51.1	0	2	0	1862.99	187	202
Ribosomal protein S6 kinase alpha-1	RPS6KA1	KS6A1_HUMAN	82.7	100.0%	3	3	3	0.00%	8.0%	EASFVLHTIGK	99.7%	56.4	25	54.4	1	0	0	1201.66	511	521
Ribosomal protein S6 kinase alpha-1	RPS6KA1	KS6A1_HUMAN	82.7	100.0%	3	3	3	0.00%	8.0%	ICDFGFAK	99.7%	52.3	25	0	2	0	0	957.45	555	562
Ribosomal protein S6 kinase alpha-1	RPS6KA1	KS6A1_HUMAN	82.7	100.0%	3	3	3	0.00%	8.0%	LGSGPDGAEEIKR	99.7%	53.3	25	48.6	1	0	0	1328.68	305	317
Ribosomal protein S6 kinase alpha-1	RPS6KA1	KS6A1_HUMAN	82.7	100.0%	3	3	3	0.00%	8.0%	NLVFSDGYVVK	98.1%	31.8	25	12.2	1	0	0	1240.66	411	421
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	7	7	9	0.01%	12.0%	DLKPENILLDEEGHIK	99.7%	53.5	25	51.1	0	2	0	1862.99	193	208
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	7	7	9	0.01%	12.0%	EASAVLFTITK	99.7%	53.2	25	49.3	1	0	0	1179.66	515	525
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	7	7	9	0.01%	12.0%	FSLSGGYWNSVSDTAK	99.7%	70.6	25	70.6	1	0	0	1718.80	638	653
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	7	7	9	0.01%	12.0%	ICDFGFAK	99.7%	52.3	25	0	2	0	0	957.45	559	566
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	7	7	9	0.01%	12.0%	LGMPQFLSPEAQSLLR	98.9%	34.1	25	34.1	1	0	0	1786.95	285	300
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	7	7	9	0.01%	12.0%	NQSPVLEPVGR	99.7%	43.4	25	33.3	1	0	0	1195.64	713	723
Ribosomal protein S6 kinase alpha-3	RPS6KA3	KS6A3_HUMAN	83.7	100.0%	7	7	9	0.01%	12.0%	PLAQLADPWQK	98.1%	31.9	25	27.8	1	0	0	1266.68	2	12
Ribosomal RNA processing protein 1 homolog A	RRP1	RRP1_HUMAN	52.8	100.0%	3	3	5	0.00%	7.4%	LAGNEQVTR	99.7%	75.6	25	59.8	2	0	0	987.52	17	25
Ribosomal RNA processing protein 1 homolog A	RRP1	RRP1_HUMAN	52.8	100.0%	3	3	5	0.00%	7.4%	TKDSLVLNNITR	99.7%	64.9	25	59.6	1	0	0	1373.77	204	215
Ribosomal RNA processing protein 1 homolog A	RRP1	RRP1_HUMAN	52.8	100.0%	3	3	5	0.00%	7.4%	VGAEELTADQNLK	99.7%	68.2	25	50.6	2	0	0	1387.71	180	192
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	10	11	18	0.02%	18.3%	ELLADQNLK	99.3%	36.2	25	30.5	2	0	0	1043.57	183	191
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	10	11	18	0.02%	18.3%	ETGGFSQEELLK	99.7%	66.2	25	52.9	2	0	0	1337.66	42	53
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	10	11	18	0.02%	18.3%	GSPTGGAQLLK	97.8%	31.1	25	17.9	1	0	0	1028.57	512	522

Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	10	11	18	0.02%	18.3%	GVFEAIVDQSPFVPEETMEEQK	99.7%	47.7	25	47.7	0	3	0	2525.18	215	236
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	10	11	18	0.02%	18.3%	HHLQPENPGPGGAAPSLEQNR	99.7%	34.4	25	31.8	0	1	0	2206.08	407	427
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	10	11	18	0.02%	18.3%	SILVSPTGPSR	97.1%	30.1	25	23.2	2	0	0	1113.63	702	712
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	10	11	18	0.02%	18.3%	SSTATHPPGPAVQLNK	99.7%	44.8	25	44.2	2	0	0	1604.84	661	676
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	10	11	18	0.02%	18.3%	TPTSSPASSPLVAK	99.7%	60.3	25	60.2	2	0	0	1342.72	728	741
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	10	11	18	0.02%	18.3%	VFCVEEEDSESSLQK	99.7%	98.1	25	84	2	0	0	1785.78	384	398
Ribosomal RNA processing protein 1 homolog B	RRP1B	RRP1B_HUMAN	84.4	100.0%	10	11	18	0.02%	18.3%	VFLDVLMK	94.5%	27.6	25	21.4	1	0	0	980.55	144	151
Ribosome biogenesis protein BMS1 homolog	BMS1	BMS1_HUMAN	145.8	100.0%	3	3	5	0.00%	2.3%	AFAVQSAVR	99.7%	47.4	25	34.1	1	0	0	948.53	44	52
Ribosome biogenesis protein BMS1 homolog	BMS1	BMS1_HUMAN	145.8	100.0%	3	3	5	0.00%	2.3%	IAATGVVLDLDK	99.7%	92.2	25	84.4	2	0	0	1214.70	1008	1019
Ribosome biogenesis protein BMS1 homolog	BMS1	BMS1_HUMAN	145.8	100.0%	3	3	5	0.00%	2.3%	STLIQCLIR	99.7%	43.4	25	25.6	2	0	0	1103.62	96	104
Ribosome biogenesis protein BRX1 homolog	BRIX1	BRX1_HUMAN	41.4	100.0%	3	3	7	0.01%	8.8%	ELLIQIFSTPR	99.7%	56	25	56	4	0	0	1316.76	183	193
Ribosome biogenesis protein BRX1 homolog	BRIX1	BRX1_HUMAN	41.4	100.0%	3	3	7	0.01%	8.8%	FLVQNIHTLAELK	99.7%	91.5	25	86.9	2	0	0	1525.87	141	153
Ribosome biogenesis protein BRX1 homolog	BRIX1	BRX1_HUMAN	41.4	100.0%	3	3	7	0.01%	8.8%	FVLNLIK	97.8%	31.1	25	28.2	1	0	0	846.54	236	242
Ribosome production factor 2 homolog	RPF2	RPF2_HUMAN	35.6	100.0%	3	3	4	0.00%	8.5%	GPTVSNIR	98.8%	33.8	25	23.8	2	0	0	843.47	169	176
Ribosome production factor 2 homolog	RPF2	RPF2_HUMAN	35.6	100.0%	3	3	4	0.00%	8.5%	KPYGVLYK	95.8%	28.7	25	12.4	1	0	0	967.56	57	64
Ribosome production factor 2 homolog	RPF2	RPF2_HUMAN	35.6	100.0%	3	3	4	0.00%	8.5%	THLASDDLYK	99.7%	44	25	37.6	1	0	0	1162.57	228	237
Ribosome-binding protein 1	RRBP1	RRBP1_HUMAN	152.5	100.0%	4	4	6	0.01%	3.5%	EQEITAVQAR	99.7%	46	25	39	2	0	0	1144.60	752	761
Ribosome-binding protein 1	RRBP1	RRBP1_HUMAN	152.5	100.0%	4	4	6	0.01%	3.5%	LQSSEAEVR	99.3%	36.2	25	29.5	1	0	0	1018.52	922	930
Ribosome-binding protein 1	RRBP1	RRBP1_HUMAN	152.5	100.0%	4	4	6	0.01%	3.5%	NTDVAQSPEAPK	99.7%	64.4	25	48	1	0	0	1256.61	609	620
Ribosome-binding protein 1	RRBP1	RRBP1_HUMAN	152.5	100.0%	4	4	6	0.01%	3.5%	VEPAVSSVVNSIQVLTSK	99.7%	55.4	25	55.4	2	0	0	1857.03	149	166
RNA 3'-terminal phosphate cyclase	RTCA	RTCA_HUMAN	39.3	100.0%	4	4	7	0.01%	13.1%	AFVAGVLPFK	99.7%	51.9	25	47	2	0	0	1048.62	196	205
RNA 3'-terminal phosphate cyclase	RTCA	RTCA_HUMAN	39.3	100.0%	4	4	7	0.01%	13.1%	FGFIFNCDIK	99.7%	52.4	25	46.5	2	0	0	1260.61	147	156
RNA 3'-terminal phosphate cyclase	RTCA	RTCA_HUMAN	39.3	100.0%	4	4	7	0.01%	13.1%	VGIEAAEMLLANLR	99.7%	51.7	25	46.2	1	0	0	1499.83	273	286
RNA 3'-terminal phosphate cyclase	RTCA	RTCA_HUMAN	39.3	100.0%	4	4	7	0.01%	13.1%	VSTALSCLLGLPLR	99.7%	64.4	25	64.4	2	0	0	1499.86	22	35
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	3	0.00%	41.8%	ALETVFGK	96.0%	28.8	25	15.7	1	0	0	864.48	23	30
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	3	0.00%	41.8%	DRDYSDHPSGGSYR	99.7%	65.5	25	65.5	2	1	0	1611.68	269	282
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	3	0.00%	41.8%	DSYESYGNSR	99.7%	73.2	25	69.8	4	0	0	1177.48	283	292
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	3	0.00%	41.8%	DSYGGPPR	99.2%	35.2	25	21.6	2	0	0	848.39	188	195
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	3	0.00%	41.8%	DVYLSPR	95.3%	28.2	25	24.8	1	0	0	849.45	204	210
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	3	0.00%	41.8%	DYAPPPRDYTYR	95.3%	28.2	25	28.2	1	0	0	1513.71	233	244
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	3	0.00%	41.8%	DYGHSSSRDDYPSR	99.7%	45.5	25	44.4	2	2	0	1641.69	245	258
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	3	0.00%	41.8%	DYSDHPSGGSYR	99.7%	61.3	25	60.9	2	0	0	1340.55	271	282
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	3	0.00%	41.8%	GFAFVTFESPADAK	99.7%	106	25	70.9	12	0	0	1486.72	50	63
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	3	0.00%	41.8%	GFAFVTFESPADAKDAAR	99.7%	93.3	25	93.3	2	2	0	1899.92	50	67
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	3	0.00%	41.8%	GGHMDDGGYSMNFNMSSSR	99.7%	73.9	25	73.9	2	10	0	2097.77	126	144
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	3	0.00%	41.8%	GPPPSYGGSSR	99.7%	62.6	25	55.7	3	0	0	1061.50	299	309
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	3	0.00%	41.8%	GRDSYGGPPR	99.7%	47.3	25	6.68	2	0	0	1061.51	186	195
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	3	0.00%	41.8%	LFIGGLNTETNEK	99.7%	89.9	25	82.4	9	0	0	1435.74	10	22
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	3	0.00%	41.8%	RDVYLSPR	99.5%	37.5	25	25.9	1	0	0	1005.55	203	210
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	3	0.00%	41.8%	REPLPSR	98.1%	31.8	25	16.4	1	0	0	854.48	196	202
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	3	0.00%	41.8%	VEQATKPSFER	99.7%	41.9	25	36.8	2	0	0	1291.66	81	91
RNA binding motif protein, X-linked-like-1	RBMXL1	RMXL1_HUMAN	42.1	99.8%	2	2	3	0.00%	41.8%	YDDYSSSR	99.7%	44.9	25	44.9	2	0	0	992.40	310	317
RNA binding protein fox-1 homolog 1	RBFOX1	RFOX1_HUMAN,RFOX2_HUMAN	42.8	100.0%	2	2	3	0.00%	6.3%	GFGFVTFENSADADR	99.7%	78.3	25	78.3	1	0	0	1632.73	157	171
RNA binding protein fox-1 homolog 1	RBFOX1	RFOX1_HUMAN,RFOX2_HUMAN	42.8	100.0%	2	2	3	0.00%	6.3%	KIEVNNATAR	99.7%	44.9	25	34.2	2	0	0	1115.62	185	194
RNA methyltransferase-like protein 1	RNMTL1	RMTL1_HUMAN	47.0	100.0%	3	3	5	0.00%	8.3%	EKQPLEESASR	99.4%	36.7	25	34	1	0	0	1273.64	72	82
RNA methyltransferase-like protein 1	RNMTL1	RMTL1_HUMAN	47.0	100.0%	3	3	5	0.00%	8.3%	KAPSEASAQEQR	99.7%	62.4	25	55.6	2	0	0	1301.64	60	71
RNA methyltransferase-like protein 1	RNMTL1	RMTL1_HUMAN	47.0	100.0%	3	3	5	0.00%	8.3%	VVFPSGEVVEQK	99.7%	52.5	25	41.2	2	0	0	1317.70	40	51
RNA polymerase II-associated factor 1 homolog	PAF1	PAF1_HUMAN	60.0	100.0%	3	3	6	0.01%	7.3%	AGVQSGTNALLVVK	99.7%	89.3	25	80.5	2	0	0	1356.78	339	352
RNA polymerase II-associated factor 1 homolog	PAF1	PAF1_HUMAN	60.0	100.0%	3	3	6	0.01%	7.3%	GYEENYFFIFR	99.7%	57	25	55.5	2	0	0	1484.68	306	316
RNA polymerase II-associated factor 1 homolog	PAF1	PAF1_HUMAN	60.0	100.0%	3	3	6	0.01%	7.3%	VTPVEVMPVFPDFK	99.7%	63.2	25	54	2	0	0	1604.84	199	212
RNA pseudouridylate synthase domain-containing protein 3	RPUSD3	RUSD3_HUMAN	38.5	100.0%	3	3	4	0.00%	9.1%	QVLDEALLR	95.5%	28.4	25	15.6	1	0	0	1056.60	288	296

RNA pseudouridylate synthase domain-containing protein 3	RPUSD3	RUSD3_HUMAN	38.5	100.0%	3	3	4	0.00%	9.1%	SGPLGDQPFAGLLPK	99.7%	50.3	25	50.3	2	0	0	1496.81	54	68
RNA pseudouridylate synthase domain-containing protein 3	RPUSD3	RUSD3_HUMAN	38.5	100.0%	3	3	4	0.00%	9.1%	TLQCLGLR	99.1%	35	25	13.6	1	0	0	960.53	342	349
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	101	0.09%	47.6%	AIKVEQATKPSFESGR	99.7%	84.9	25	84.9	2	4	0	1747.93	78	93
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	101	0.09%	47.6%	ALEAVFGK	99.7%	54.5	25	42.8	2	0	0	834.47	23	30
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	101	0.09%	47.6%	DRDYSDHPSGGSYR	99.7%	65.5	25	65.5	2	1	0	1611.68	269	282
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	101	0.09%	47.6%	DSYESYGNSR	99.7%	73.2	25	69.8	4	0	0	1177.48	283	292
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	101	0.09%	47.6%	DSYGGPPR	99.2%	35.2	25	21.6	2	0	0	848.39	188	195
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	101	0.09%	47.6%	DVYLSPR	95.3%	28.2	25	24.8	1	0	0	849.45	204	210
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	101	0.09%	47.6%	DYAPPPRDYTYR	95.3%	28.2	25	28.2	1	0	0	1513.71	233	244
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	101	0.09%	47.6%	DYGHSSSRDDYPSR	99.7%	45.5	25	44.4	2	2	0	1641.69	245	258
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	101	0.09%	47.6%	DYSDHPSGGSYR	99.7%	61.3	25	60.9	2	0	0	1340.55	271	282
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	101	0.09%	47.6%	GFAFVTFESPADAK	99.7%	106	25	70.9	12	0	0	1486.72	50	63
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	101	0.09%	47.6%	GFAFVTFESPADAKDAAR	99.7%	93.3	25	93.3	2	2	0	1899.92	50	67
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	101	0.09%	47.6%	GGHMDDGGYSMNFNMSSSR	99.7%	73.9	25	73.9	2	10	0	2097.77	126	144
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	101	0.09%	47.6%	GPPPSYGGSSR	99.7%	62.6	25	55.7	3	0	0	1061.50	299	309
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	101	0.09%	47.6%	GRDSYGGPPR	99.7%	47.3	25	6.68	2	0	0	1061.51	186	195
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	101	0.09%	47.6%	IVEVLLMK	99.7%	66.7	25	43.2	6	0	0	960.58	34	41
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	101	0.09%	47.6%	IVEVLLMKDR	99.7%	67.6	25	63.7	2	0	0	1231.71	34	43
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	101	0.09%	47.6%	LFIGGLNTETNEK	99.7%	89.9	25	82.4	9	0	0	1435.74	10	22
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	101	0.09%	47.6%	RDVYLSPR	99.5%	37.5	25	25.9	1	0	0	1005.55	203	210
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	101	0.09%	47.6%	REPLPSR	98.1%	31.8	25	16.4	1	0	0	854.48	196	202
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	101	0.09%	47.6%	RGPPPPPR	99.7%	55.9	25	47.5	12	0	0	873.51	94	101
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	101	0.09%	47.6%	VEQATKPSFESGR	99.7%	65.4	25	56	6	4	0	1435.72	81	93
RNA-binding motif protein, X chromosome	RBMX	RBMX_HUMAN	42.3	100.0%	22	30	101	0.09%	47.6%	YDDYSSSR	99.7%	44.9	25	44.9	2	0	0	992.40	310	317
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	20	23	57	0.05%	25.8%	ASNIVMLR	99.7%	60.6	25	49.4	2	0	0	903.51	127	134
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	20	23	57	0.05%	25.8%	DGLGSDNIGSR	99.7%	46.6	25	38.9	2	0	0	1090.51	854	864
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	20	23	57	0.05%	25.8%	EKYGIPEPPEPK	99.6%	39.2	25	31.2	2	0	0	1383.72	823	834
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	20	23	57	0.05%	25.8%	ESATADAGYAILEK	99.7%	129	25	120	4	0	0	1438.71	686	699
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	20	23	57	0.05%	25.8%	GDPTGAGPEASLEPGADSVSMQAFSR	99.7%	63	25	63	1	2	0	2550.14	473	498
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	20	23	57	0.05%	25.8%	GFAFVEFSHLQDATR	99.7%	87.7	25	80.1	1	1	0	1724.84	172	186
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	20	23	57	0.05%	25.8%	GLVAAYSGESDSEEEQER	99.7%	158	25	149	2	0	0	1955.85	727	744
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	20	23	57	0.05%	25.8%	GQLQSHGVQAR	99.7%	67.2	25	47.5	9	0	0	1180.62	147	157
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	20	23	57	0.05%	25.8%	GSSYGVTSTESYK	99.7%	49	25	49	1	0	0	1365.62	903	915
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	20	23	57	0.05%	25.8%	INEDWLCNK	99.7%	62.9	25	45.2	3	0	0	1191.55	213	221
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	20	23	57	0.05%	25.8%	KYGGISTASVDFEQPTR	98.3%	26.8	25	26.8	0	1	0	1855.92	837	853
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	20	23	57	0.05%	25.8%	LACLLCR	99.7%	46.7	25	34.5	2	0	0	905.47	759	765
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	20	23	57	0.05%	25.8%	LDQQTLPLGGR	99.7%	82.1	25	71.4	6	0	0	1197.66	253	263
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	20	23	57	0.05%	25.8%	MLPQAATEDDIR	99.7%	63.6	25	57	4	0	0	1359.66	135	146
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	20	23	57	0.05%	25.8%	NSFQPISSLR	99.7%	47.8	25	22.3	4	0	0	1148.61	671	680
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	20	23	57	0.05%	25.8%	QGIVTPIEAQTR	99.7%	55.9	25	43.8	2	0	0	1312.72	882	893
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	20	23	57	0.05%	25.8%	SEAEQKLPLGTR	99.7%	61.6	25	45.3	2	0	0	1328.72	241	252
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	20	23	57	0.05%	25.8%	TINVEFAK	99.7%	39.6	25	29.3	2	0	0	921.50	376	383
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	20	23	57	0.05%	25.8%	TYVPALEQSADGHK	99.7%	61	25	58.5	2	0	0	1515.74	614	627
RNA-binding protein 10	RBM10	RBM10_HUMAN	103.5	100.0%	20	23	57	0.05%	25.8%	YGGISTASVDFEQPTR	99.7%	90.2	25	90.2	2	0	0	1727.82	838	853
RNA-binding protein 12B	RBM12B	RB12B_HUMAN	118.1	99.8%	2	2	3	0.00%	2.0%	DSSVELFLSSK	99.7%	45	25	45	1	0	0	1211.62	66	76
RNA-binding protein 12B	RBM12B	RB12B_HUMAN	118.1	99.8%	2	2	3	0.00%	2.0%	FLGTEVLLR	99.7%	54	25	42.3	2	0	0	1047.62	465	473
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	10	21	0.02%	20.2%	AIEALHGHELRPGR	98.5%	27.3	25	26.1	0	1	0	1555.85	51	64
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	10	21	0.02%	20.2%	AQPSASLGVGYR	99.7%	55.8	25	48.8	2	0	0	1205.63	251	262
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	10	21	0.02%	20.2%	AQPSVSLGAAYR	97.1%	30.1	25	30	1	0	0	1219.64	239	250
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	10	21	0.02%	20.2%	AQPSVSLGAPYR	98.3%	32.1	25	25.7	2	0	0	1245.66	275	286
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	10	21	0.02%	20.2%	ASYVAPLTAQPATYR	99.7%	90	25	79.4	2	0	0	1608.84	224	238

RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	10	21	0.02%	20.2%	IFVGNVSAACTSQELR	99.7%	114	25	114	5	0	0	1751.87	81	96
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	10	21	0.02%	20.2%	INVELSTK	99.0%	34.3	25	25.6	2	0	0	903.51	142	149
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	10	21	0.02%	20.2%	KGPGLAVQSGDK	99.7%	55.3	25	48.5	2	0	0	1156.63	153	164
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	10	21	0.02%	20.2%	TQSSASLAASYAAQQHPQAAASYR	99.7%	80.2	25	80.2	0	2	0	2465.18	518	541
RNA-binding protein 14	RBM14	RBM14_HUMAN	69.5	100.0%	10	10	21	0.02%	20.2%	YSGSYNDYLR	99.7%	69.1	25	62.5	2	0	0	1237.55	648	657
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	9	15	0.01%	12.0%	EDINAIEMEEDKR	98.4%	32.4	25	32.4	1	0	0	1591.73	262	274
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	9	15	0.01%	12.0%	EKEELEEIR	99.6%	39.2	25	23.6	2	0	0	1174.60	539	547
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	9	15	0.01%	12.0%	EYSSELNAPSQESDSHPR	99.7%	35.9	25	35.9	0	1	0	2032.88	217	234
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	9	15	0.01%	12.0%	FPVAPLIPYPLITK	99.7%	43.2	25	43.2	2	0	0	1568.95	248	261
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	9	15	0.01%	12.0%	GAIEVLIR	99.7%	54.2	25	41.8	2	0	0	870.54	209	216
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	9	15	0.01%	12.0%	LGASNSPGQPNSVK	99.7%	52.1	25	52	2	0	0	1355.69	672	685
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	9	15	0.01%	12.0%	LLAEGHPDPDAELQR	99.7%	51.1	25	47.5	2	2	0	1660.83	550	564
RNA-binding protein 25	RBM25	RBM25_HUMAN	100.2	100.0%	8	9	15	0.01%	12.0%	LLHDLQIGEK	99.0%	34.4	25	27.9	1	0	0	1165.66	146	155
RNA-binding protein 26	RBM26	RBM26_HUMAN	113.6	100.0%	3	3	4	0.00%	3.7%	AEAEAAAVHGAR	99.7%	72	25	64	2	0	0	1152.58	936	947
RNA-binding protein 26	RBM26	RBM26_HUMAN	113.6	100.0%	3	3	4	0.00%	3.7%	AISSTEAVLNNR	99.7%	63.8	25	53.7	1	0	0	1274.67	586	597
RNA-binding protein 26	RBM26	RBM26_HUMAN	113.6	100.0%	3	3	4	0.00%	3.7%	EGSTQQLQTTSPK	99.7%	65.3	25	54	1	0	0	1404.70	606	618
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	5	6	9	0.01%	8.3%	AAEGVSAADMAK	99.7%	72.4	25	71.2	3	0	0	1136.53	454	465
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	5	6	9	0.01%	8.3%	AEVEQVELPDGK	99.7%	52.9	25	51.9	1	0	0	1313.66	654	665
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	5	6	9	0.01%	8.3%	IVLHPDTEHSK	99.7%	34.1	25	31.2	0	1	0	1275.67	366	376
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	5	6	9	0.01%	8.3%	LINNNPEIFGPLK	99.7%	49.6	25	45.6	2	0	0	1468.82	559	571
RNA-binding protein 28	RBM28	RBM28_HUMAN	85.7	100.0%	5	6	9	0.01%	8.3%	SEQLEELFSQVGPVK	99.7%	58.4	25	52.1	2	0	0	1689.87	17	31
RNA-binding protein 39	RBM39	RBM39_HUMAN	59.4	100.0%	5	5	14	0.01%	11.9%	AAAMANNLQK	95.3%	28.2	25	12	1	0	0	1031.53	235	244
RNA-binding protein 39	RBM39	RBM39_HUMAN	59.4	100.0%	5	5	14	0.01%	11.9%	DLEEFFSTVGK	99.7%	69	25	59.1	4	0	0	1271.62	168	178
RNA-binding protein 39	RBM39	RBM39_HUMAN	59.4	100.0%	5	5	14	0.01%	11.9%	TDASSASSFLDSDELER	99.7%	111	25	111	2	0	0	1829.80	330	346
RNA-binding protein 39	RBM39	RBM39_HUMAN	59.4	100.0%	5	5	14	0.01%	11.9%	TGIDLGTTGR	99.7%	54.2	25	48.6	3	0	0	990.52	347	356
RNA-binding protein 39	RBM39	RBM39_HUMAN	59.4	100.0%	5	5	14	0.01%	11.9%	VLGVPIIVQASQAEK	99.7%	105	25	105	4	0	0	1551.91	218	232
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	5	5	8	0.01%	14.0%	AEDAVEAIR	99.7%	42.4	25	25.4	2	0	0	973.49	121	129
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	5	5	8	0.01%	14.0%	GLDNTEFQGK	99.7%	45.6	25	44.5	2	0	0	1108.53	130	139
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	5	5	8	0.01%	14.0%	TAAEDAIR	98.4%	32.5	25	26.6	1	0	0	846.43	46	53
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	5	5	8	0.01%	14.0%	VADLTEQYNEQYGAVR	99.7%	96.3	25	91	2	0	0	1855.88	183	198
RNA-binding protein 4	RBM4	RBM4_HUMAN	40.3	100.0%	5	5	8	0.01%	14.0%	VLECDIIK	95.5%	28.4	25	11.5	1	0	0	989.53	28	35
RNA-binding protein FUS	FUS	FUS_HUMAN	53.4	100.0%	3	4	7	0.01%	6.3%	AAIDWFDGKEFSGNPIK	99.7%	68	25	67.8	1	2	0	1894.93	349	365
RNA-binding protein FUS	FUS	FUS_HUMAN	53.4	100.0%	3	4	7	0.01%	6.3%	GEATVSFDDPPSAK	99.7%	88.3	25	80.9	2	0	0	1420.66	335	348
RNA-binding protein FUS	FUS	FUS_HUMAN	53.4	100.0%	3	4	7	0.01%	6.3%	LKGEATVSFDDPPSAK	99.7%	43.8	25	43.8	0	2	0	1661.84	333	348
RNA-binding protein Musashi homolog 2	MSI2	MSI2H_HUMAN	35.2	100.0%	3	3	13	0.01%	14.0%	GFGFVTFADPASVDK	99.7%	83	25	82.9	6	0	0	1557.76	63	77
RNA-binding protein Musashi homolog 2	MSI2	MSI2H_HUMAN	35.2	100.0%	3	3	13	0.01%	14.0%	GFGFVTFENEDVVEK	99.7%	62.1	25	53.5	3	0	0	1716.81	152	166
RNA-binding protein Musashi homolog 2	MSI2	MSI2H_HUMAN	35.2	100.0%	3	3	13	0.01%	14.0%	IFVGGLSANTVVEDVK	99.7%	89.2	25	84.9	4	0	0	1647.90	112	127
RNA-binding protein PNO1	PNO1	PNO1_HUMAN	27.9	99.9%	2	2	4	0.00%	7.9%	AEEGFTQVTR	99.7%	61.2	25	51.5	2	0	0	1137.55	12	21
RNA-binding protein PNO1	PNO1	PNO1_HUMAN	27.9	99.9%	2	2	4	0.00%	7.9%	MDTEEARPAK	96.9%	29.8	25	27	2	0	0	1147.54	47	56
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	10	10	63	0.06%	30.4%	GYAFVQYSNER	99.7%	73.2	25	65.4	6	0	0	1333.62	56	66
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	10	10	63	0.06%	30.4%	KSDVETIFSK	99.7%	68.2	25	52.8	8	0	0	1153.61	35	44
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	10	10	63	0.06%	30.4%	LEQIAAEQK	99.7%	54.8	25	44.2	5	0	0	1029.56	208	216
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	10	10	63	0.06%	30.4%	LQASNVTNK	99.7%	40.3	25	30.3	2	0	0	974.53	5	13
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	10	10	63	0.06%	30.4%	LQASNVTNKNDPK	99.6%	38.5	25	34.2	1	0	0	1428.74	5	17
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	10	10	63	0.06%	30.4%	SDVETIFSK	99.7%	47.7	25	37.1	4	0	0	1025.52	36	44
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	10	10	63	0.06%	30.4%	SNIDALLSR	99.7%	91.8	25	57.7	12	0	0	988.54	199	207
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	10	10	63	0.06%	30.4%	SSELQAIK	99.7%	52.8	25	24.8	6	0	0	875.48	184	191
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	10	10	63	0.06%	30.4%	VFIGNLNTALVK	99.7%	87	25	0	17	0	0	1288.76	23	34
RNA-binding protein Raly	RALY	RALY_HUMAN	32.5	100.0%	10	10	63	0.06%	30.4%	VLAGQTLDINMAGEPKPDRPK	99.7%	54.5	25	54.5	0	2	0	2266.19	79	99
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	11	12	21	0.02%	39.3%	ANCIDSTASAEAVFASEVK	99.7%	116	25	116	2	0	0	1969.92	266	284
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	11	12	21	0.02%	39.3%	ANCIDSTASAEAVFASEVKK	99.3%	30.3	25	30	0	2	0	2098.01	266	285

rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	11	12	21	0.02%	39.3%	DHAVVVGVYRPPPK	99.7%	80.3	25	79.8	2	1	0	1533.85	305	318
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	11	12	21	0.02%	39.3%	GKEDALVTK	99.7%	41.2	25	31	1	0	0	960.54	101	109
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	11	12	21	0.02%	39.3%	HEGVFICR	97.3%	30.4	25	30.4	2	0	0	1017.49	93	100
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	11	12	21	0.02%	39.3%	IVALNAHTFLR	99.7%	59.3	25	56.4	3	0	0	1254.73	245	255
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	11	12	21	0.02%	39.3%	MQQENMKPQEQLTLEPYER	99.6%	33	25	33	0	1	0	2424.12	286	304
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	11	12	21	0.02%	39.3%	NLVPGESVYGEKR	99.7%	50.5	25	46.8	2	0	0	1447.75	110	122
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	11	12	21	0.02%	39.3%	NVMVEPHR	96.5%	29.4	25	27.1	1	0	0	997.49	85	92
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	11	12	21	0.02%	39.3%	TNIIPVIEDAR	99.7%	62.5	25	0	2	0	0	1240.69	208	218
rRNA 2'-O-methyltransferase fibrillarin	FBL	FBRL_HUMAN	33.8	100.0%	11	12	21	0.02%	39.3%	VSISEGDDKIEYR	99.7%	79.1	25	75.3	2	0	0	1510.74	123	135
RRP12-like protein	RRP12	RRP12_HUMAN	143.7	100.0%	5	5	7	0.01%	4.3%	APAHHPAAISTAK	96.9%	29.8	25	29.8	1	0	0	1271.69	274	286
RRP12-like protein	RRP12	RRP12_HUMAN	143.7	100.0%	5	5	7	0.01%	4.3%	RAVLETIR	98.3%	32.1	25	16.1	1	0	0	957.58	711	718
RRP12-like protein	RRP12	RRP12_HUMAN	143.7	100.0%	5	5	7	0.01%	4.3%	SWLLPVIR	99.5%	38	25	11.2	2	0	0	983.60	567	574
RRP12-like protein	RRP12	RRP12_HUMAN	143.7	100.0%	5	5	7	0.01%	4.3%	TYLTITDTQLVNSLLEK	99.7%	58	25	58	1	0	0	1952.06	719	735
RRP12-like protein	RRP12	RRP12_HUMAN	143.7	100.0%	5	5	7	0.01%	4.3%	VLATQPGPGR	99.7%	49.2	25	43.2	2	0	0	995.56	1129	1138
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	15	0.01%	19.3%	ALESSIAPIVIFASNR	99.7%	80.7	25	80.7	2	2	0	1687.94	318	333
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	15	0.01%	19.3%	AVLLAGPPGTGK	99.7%	44.2	25	39.3	2	0	0	1080.64	65	76
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	15	0.01%	19.3%	EACGVIVELIK	99.7%	56	25	39.5	2	0	0	1230.68	47	57
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	15	0.01%	19.3%	GLGLDESGLAK	99.7%	42	25	36.5	2	0	0	1059.57	23	33
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	15	0.01%	19.3%	LDPSIFESLQK	99.1%	35	25	25	1	0	0	1276.68	172	182
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	15	0.01%	19.3%	QAASGLVGQENAR	99.7%	82.4	25	71.8	2	0	0	1300.66	34	46
RuvB-like 1	RUVBL1	RUVB1_HUMAN	50.2	100.0%	7	8	15	0.01%	19.3%	TALALAIAQELGSK	99.7%	103	25	99	2	0	0	1385.80	77	90
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	11	20	0.02%	30.2%	ALESDMAPVLIMATNR	99.7%	65.8	25	59.2	2	0	0	1731.88	315	330
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	11	20	0.02%	30.2%	AVLIAGQPGTGK	99.7%	68.2	25	54.2	2	0	0	1111.65	72	83
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	11	20	0.02%	30.2%	DKVQAGDVITIDK	99.7%	78.1	25	64.2	2	0	0	1401.76	185	197
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	11	20	0.02%	30.2%	EVVHTVSLHEIDVINSR	99.7%	45.9	25	45.9	0	2	0	1947.03	237	253
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	11	20	0.02%	30.2%	FVQCPDGELQK	98.4%	32.5	25	28.6	1	0	0	1320.63	224	234
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	11	20	0.02%	30.2%	GTEVQVDDIKR	99.7%	57.5	25	40.8	2	0	0	1259.66	418	428
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	11	20	0.02%	30.2%	LLIVSTTPYSEK	99.7%	60.6	25	49.9	2	0	0	1350.75	354	365
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	11	20	0.02%	30.2%	TEALTQAFR	99.7%	50.4	25	41.5	1	0	0	1036.54	116	124
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	11	20	0.02%	30.2%	TQGFLALFSGDTGEIK	99.7%	127	25	122	2	0	0	1683.86	254	269
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	11	20	0.02%	30.2%	TTEMETIYDLGTK	99.7%	60.3	25	60.3	2	0	0	1517.70	165	177
RuvB-like 2	RUVBL2	RUVB2_HUMAN	51.2	100.0%	11	11	20	0.02%	30.2%	VYSLFLDESR	99.7%	65.4	25	54.7	2	0	0	1228.62	429	438
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	3	5	10	0.01%	10.9%	FVIGGPQGDAGLTGR	99.7%	110	25	103	2	0	0	1444.75	250	264
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	3	5	10	0.01%	10.9%	TGMILLAGEITSR	99.7%	79.9	25	74.3	4	0	0	1361.75	62	74
S-adenosylmethionine synthase isoform type-2	MAT2A	METK2_HUMAN	43.7	100.0%	3	5	10	0.01%	10.9%	YLDEDTIYHLQPSGR	99.7%	55.5	25	55.5	2	2	0	1806.87	235	249
SAFB-like transcription modulator	SLTM	SLTM_HUMAN	117.2	99.9%	2	2	4	0.00%	2.1%	ELLSAEENKR	99.7%	49.3	25	35.1	2	0	0	1188.62	141	150
SAFB-like transcription modulator	SLTM	SLTM_HUMAN	117.2	99.9%	2	2	4	0.00%	2.1%	TELHGQLISVEK	99.7%	47.2	25	46.6	2	0	0	1353.74	448	459
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	AEIGIAMGSGTAVAK	99.7%	70.8	25	65.4	3	0	0	1391.72	713	727
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	AMGVVVATGVNTEIGK	99.7%	86.5	25	68.7	2	0	0	1561.83	219	234
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	CLALATHDNPLR	99.7%	48.3	25	45	1	0	0	1380.71	560	571
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	CLALATHDNPLRR	98.6%	27.7	25	18.9	0	1	0	1536.81	560	572
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	DIVPGDIVEIAVGDK	99.7%	42.1	25	40.5	1	0	0	1539.83	144	158
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	EEMHLEDSANFIK	99.2%	35.6	25	30.7	1	0	0	1562.72	573	585
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	EFDELNPSAQR	99.7%	63.4	25	57.8	3	0	0	1305.61	656	666
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	EFTLEFSR	99.7%	50.4	25	41	3	0	0	1028.50	482	489
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	EWGSGSDTLR	99.7%	49.7	25	43.6	2	0	0	1107.51	550	559
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	GAPEGVIDR	99.7%	47.2	25	39.7	2	0	0	913.47	515	523
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	GTAVAICR	97.1%	30	25	8.81	2	0	0	847.45	629	636
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	IGIFGQDEDVTSK	99.7%	83.3	25	74.8	3	0	0	1408.70	638	650
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	IRDEMVATEQER	99.7%	54.5	25	46.2	4	1	0	1476.71	235	246
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	ISLPVILMDETLK	99.7%	99.1	25	92.7	4	0	0	1471.84	972	984

Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	KAEIGIAMGSGTAVAK	99.7%	84.4	25	81.2	3	1	0	1503.82	712	727
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	KSMSVYCTPNKPSR	96.1%	23.8	25	23.8	0	1	0	1670.80	492	505
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	LDEFGEQLSK	99.7%	60.7	25	43.3	3	0	0	1165.57	253	262
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	MNVFDTELK	99.7%	41.3	25	23.6	3	0	0	1112.53	452	460
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	NMLFSGTNIAAGK	99.7%	80.3	25	73.4	5	0	0	1323.67	206	218
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	NYLEPGKECVQPATK	99.3%	36.1	25	28.7	1	0	0	1733.85	989	1003
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	RIGIFGQDEDVTSK	99.7%	37.3	25	37.3	0	2	0	1564.80	637	650
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	SLPSVETLGCTSVICSDK	99.7%	101	25	99.6	2	0	0	1952.93	335	352
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	SMSVYCTPNKPSR	99.7%	51.9	25	51.9	3	0	0	1526.71	493	505
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	TGTLTTNQMSVCR	99.7%	62.6	25	59.2	4	0	0	1468.69	353	365
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	VDQSILTGESVSVIK	99.7%	75	25	70.2	5	0	0	1574.86	175	189
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	VGEATETALTCLVEK	99.7%	125	25	116	4	0	0	1620.82	437	451
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	AT2A2_HUMAN	114.8	100.0%	27	37	71	0.07%	27.7%	VIMITGDNK	98.1%	31.7	25	24.9	1	0	0	990.53	620	628
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	12	14	44	0.04%	16.5%	ADSLLAVVK	99.7%	71.9	25	51.8	4	0	0	915.55	286	294
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	12	14	44	0.04%	16.5%	AIEDEGGNPDEIEITSEGNKK	99.7%	86.3	25	86.3	2	4	0	2245.05	64	84
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	12	14	44	0.04%	16.5%	CYGFVTMSTAEEATK	99.7%	83	25	83	4	0	0	1694.74	448	462
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	12	14	44	0.04%	16.5%	DGWGGYGSDKR	99.7%	40.6	25	31.4	1	0	0	1197.53	796	806
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	12	14	44	0.04%	16.5%	ILDILGETCK	99.7%	79.7	25	68.8	6	0	0	1161.62	217	226
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	12	14	44	0.04%	16.5%	KFDFDACNEVPPAPK	99.0%	28.9	25	28.9	0	2	0	1734.82	356	370
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	12	14	44	0.04%	16.5%	MSSPEDDSDTKR	99.7%	58.4	25	55.8	2	1	0	1367.57	382	393
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	12	14	44	0.04%	16.5%	NFWVSGLSSTTR	99.7%	75.7	25	65.6	8	0	0	1354.67	407	418
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	12	14	44	0.04%	16.5%	REPAEQPGDGER	99.6%	38.1	25	37.5	3	0	0	1340.62	295	306
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	12	14	44	0.04%	16.5%	RPYDLDR	99.1%	34.7	25	17.1	2	0	0	934.47	712	718
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	12	14	44	0.04%	16.5%	RPYDLDRR	98.9%	34.2	25	16	1	0	0	1090.58	712	719
Scaffold attachment factor B1	SAFB	SAFB1_HUMAN	102.6	100.0%	12	14	44	0.04%	16.5%	SEPVKEESSELEQPFAQDTSSVGPDR	99.7%	74.3	25	74.3	0	4	0	2848.31	227	252
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	30	0.03%	19.8%	ADSLLAVVK	99.7%	71.9	25	51.8	4	0	0	915.55	285	293
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	30	0.03%	19.8%	AWQGAMDAGAASR	99.7%	72.7	25	61.8	1	0	0	1291.58	861	873
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	30	0.03%	19.8%	DGWGGYGSDKR	99.7%	40.6	25	31.4	1	0	0	1197.53	820	830
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	30	0.03%	19.8%	DIKPIIKDEK	99.6%	39	25	29.2	3	1	0	1198.70	389	398
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	30	0.03%	19.8%	EYVAAQLR	99.7%	41.9	25	15.4	4	0	0	949.51	164	171
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	30	0.03%	19.8%	GQYQDHAIDRR	95.3%	23.1	25	22.1	0	1	0	1358.66	774	784
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	30	0.03%	19.8%	ILDILGETCK	99.7%	79.7	25	68.8	6	0	0	1161.62	216	225
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	30	0.03%	19.8%	KFDFDACNEVPPAPK	99.0%	28.9	25	28.9	0	2	0	1734.82	355	369
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	30	0.03%	19.8%	LEAFHER	99.7%	47.8	25	38.7	4	0	0	901.45	651	657
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	30	0.03%	19.8%	NLWVSGLSSTTR	99.7%	75.6	25	70	4	0	0	1320.69	408	419
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	30	0.03%	19.8%	NTLETSSLNFK	99.7%	78.7	25	72.7	4	0	0	1253.64	189	199
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	30	0.03%	19.8%	REPAEQPGDGER	99.6%	38.1	25	37.5	3	0	0	1340.62	294	305
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	30	0.03%	19.8%	RPYDLDR	99.1%	34.7	25	17.1	2	0	0	934.47	730	736
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	30	0.03%	19.8%	RPYDLDRR	98.9%	34.2	25	16	1	0	0	1090.58	730	737
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	30	0.03%	19.8%	SEPVKEESSELEQPFAQDTSSVGPDR	99.7%	74.3	25	74.3	0	4	0	2848.31	226	251
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	30	0.03%	19.8%	SKGEPVISVK	98.7%	33.2	25	28.1	4	0	0	1043.61	577	586
Scaffold attachment factor B2	SAFB2	SAFB2_HUMAN	107.5	100.0%	9	10	30	0.03%	19.8%	VTPDIEESLLEPENEK	99.7%	79.6	25	76	4	0	0	1841.90	200	215
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	10	10	24	0.02%	13.5%	EPAVLMGILGIYK	99.7%	70.9	25	70.9	2	0	0	1403.80	539	551
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	10	10	24	0.02%	13.5%	LGSSSLTNIPEEVR	99.7%	62.4	25	49.7	2	0	0	1501.79	288	301
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	10	10	24	0.02%	13.5%	LILPELGPVFK	99.7%	54.7	25	36.6	4	0	0	1225.76	408	418
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	10	10	24	0.02%	13.5%	LLTVQHPLEESR	99.7%	46.8	25	41.2	3	0	0	1421.77	101	112
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	10	10	24	0.02%	13.5%	LYDVETK	99.2%	35.5	25	26.4	1	0	0	867.45	149	155
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	10	10	24	0.02%	13.5%	MVHGNITPENIILNK	95.2%	23.1	25	23.1	0	1	0	1692.91	174	188
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	10	10	24	0.02%	13.5%	NACLQTSSLAVR	99.7%	77.2	25	68.3	3	0	0	1319.67	494	505
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	10	10	24	0.02%	13.5%	QQEPIQILLIFLQK	99.7%	41.2	25	41.2	2	0	0	1711.02	419	432
SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	10	10	24	0.02%	13.5%	VTADVTSAVMGNPVTR	99.7%	103	25	91.5	2	0	0	1633.82	15	30

SCY1-like protein 2	SCYL2	SCYL2_HUMAN	103.7	100.0%	10	10	24	0.02%	13.5%	VTNIGNQQIDK	99.7%	60.6	25	47.1	4	0	0	1229.65	637	647
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	6	6	9	0.01%	13.4%	FGQDIISPLLSVK	99.7%	79.8	25	79.8	3	0	0	1416.81	51	63
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	6	6	9	0.01%	13.4%	GSPFPEVAESVQQELESYR	99.7%	62.7	25	62.7	1	0	0	2152.02	331	349
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	6	6	9	0.01%	13.4%	LTSAVSSLPELLEK	99.7%	83.9	25	59.2	2	0	0	1486.84	382	395
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	6	6	9	0.01%	13.4%	QQNLPVTR	95.7%	28.5	25	26	1	0	0	955.53	542	549
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	6	6	9	0.01%	13.4%	SYDLTPVDKFWQK	99.7%	39.7	25	39.7	1	0	0	1626.82	316	328
Sec1 family domain-containing protein 1	SCFD1	SCFD1_HUMAN	72.4	100.0%	6	6	9	0.01%	13.4%	VNLEESSGVENSPAGARPK	99.7%	94.8	25	94.1	1	0	0	1940.97	292	310
Sentrin-specific protease 3	SENP3	SENP3_HUMAN	65.0	100.0%	3	3	5	0.00%	6.1%	GLVLQLIQSYQR	99.7%	55.7	25	47.3	1	0	0	1417.82	358	369
Sentrin-specific protease 3	SENP3	SENP3_HUMAN	65.0	100.0%	3	3	5	0.00%	6.1%	LGLLGALMAEDGVR	99.7%	98.3	25	97	3	0	0	1414.77	197	210
Sentrin-specific protease 3	SENP3	SENP3_HUMAN	65.0	100.0%	3	3	5	0.00%	6.1%	YLQAEAVKK	97.9%	31.4	25	21.8	1	0	0	1049.60	498	506
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	7	7	14	0.01%	13.5%	FINDQYEK	95.6%	28.5	25	18.1	1	0	0	1056.50	382	389
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	7	7	14	0.01%	13.5%	LEPKPQPPVAEATPR	99.7%	49.1	25	49	0	2	0	1629.90	223	237
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	7	7	14	0.01%	13.5%	QVENAGAIGPSR	99.7%	59.8	25	46.1	2	0	0	1198.62	118	129
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	7	7	14	0.01%	13.5%	STLINTLFK	99.5%	37.5	25	19.4	2	0	0	1036.60	312	320
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	7	7	14	0.01%	13.5%	VPEVPTAPATDAAPK	99.7%	59.8	25	51.8	3	0	0	1463.77	172	186
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	7	7	14	0.01%	13.5%	VVNIVPVIAK	99.7%	46.1	25	46.1	2	0	0	1051.69	436	445
Septin-9	9-Sep	SEPT9_HUMAN	65.4	100.0%	7	7	14	0.01%	13.5%	YLQEEVNINR	99.7%	48.7	25	33.3	2	0	0	1277.65	390	399
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	9	9	15	0.01%	25.2%	AACFAIQK	99.7%	49.3	25	36.9	2	0	0	908.47	190	197
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	9	9	15	0.01%	25.2%	DHPALNYNIVSGPPSHK	99.7%	40	25	40	0	1	0	1845.92	76	92
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	9	9	15	0.01%	25.2%	ECINFASFNFLGLLDNPR	99.7%	96.7	25	96.7	2	0	0	2127.03	99	116
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	9	9	15	0.01%	25.2%	EQEIEDQKNPR	99.7%	63.4	25	48.8	2	0	0	1385.67	223	233
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	9	9	15	0.01%	25.2%	LLQEIVDQCMNR	99.7%	77.7	25	77.7	2	0	0	1518.74	411	422
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	9	9	15	0.01%	25.2%	RGDIVFVDR	99.5%	37.7	25	16.7	1	0	0	1076.58	181	189
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	9	9	15	0.01%	25.2%	VVGESLSPAFHLQLEESTGSR	99.2%	29.9	25	29.9	0	1	0	2243.13	385	405
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	9	9	15	0.01%	25.2%	VVVTVEQTEEELER	99.7%	110	25	104	2	0	0	1659.84	446	459
Serine palmitoyltransferase 1	SPTLC1	SPTC1_HUMAN	52.7	100.0%	9	9	15	0.01%	25.2%	YGVGTCGPR	99.2%	35.6	25	29.6	2	0	0	966.45	128	136
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	13	57	0.05%	40.7%	DAEDAVYGR	99.7%	54.7	25	52.7	2	0	0	995.44	66	74
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	13	57	0.05%	40.7%	DGTGVVEFVR	99.7%	68	25	58.8	7	0	0	1078.55	155	164
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	13	57	0.05%	40.7%	DGYDYDGYR	99.7%	54.6	25	54.6	7	0	0	1123.43	75	83
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	13	57	0.05%	40.7%	DIEDVFYK	99.3%	36	25	28.2	1	0	0	1028.49	31	38
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	13	57	0.05%	40.7%	EAGDVCYADVYR	99.7%	68.8	25	68.8	8	0	0	1417.61	143	154
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	13	57	0.05%	40.7%	GGPPFAFVEFEDPR	99.7%	52.9	25	52.9	2	0	0	1564.74	52	65
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	13	57	0.05%	40.7%	GGPPFAFVEFEDPRDAEDAVYGR	99.7%	44.6	25	44.6	0	2	0	2541.17	52	74
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	13	57	0.05%	40.7%	IYVGNLPPDIR	99.7%	57.9	25	46.5	7	0	0	1256.70	18	28
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	13	57	0.05%	40.7%	KEDMTYAVR	99.7%	64.1	25	54.4	7	0	0	1112.54	165	173
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	13	57	0.05%	40.7%	LRVEFPR	99.4%	36.6	25	22.8	12	0	0	916.54	84	90
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	13	57	0.05%	40.7%	SHEGETAYIR	99.7%	57.2	25	51.8	7	0	0	1162.55	182	191
Serine/arginine-rich splicing factor 1	SRSF1	SRSF1_HUMAN	27.7	100.0%	11	13	57	0.05%	40.7%	TKDIEDVFYK	99.7%	65.4	25	63.2	5	2	0	1257.64	29	38
Serine/arginine-rich splicing factor 10	SRSF10	SRS10_HUMAN	31.3	100.0%	6	7	19	0.02%	23.7%	DAEDALHNLDR	99.7%	65.4	25	65.4	2	0	0	1268.59	63	73
Serine/arginine-rich splicing factor 10	SRSF10	SRS10_HUMAN	31.3	100.0%	6	7	19	0.02%	23.7%	GFAYVQFEDVR	99.7%	62.5	25	56	4	0	0	1330.64	52	62
Serine/arginine-rich splicing factor 10	SRSF10	SRS10_HUMAN	31.3	100.0%	6	7	19	0.02%	23.7%	QIEIQFAQGDR	99.7%	76.2	25	70.1	4	0	0	1304.66	80	90
Serine/arginine-rich splicing factor 10	SRSF10	SRS10_HUMAN	31.3	100.0%	6	7	19	0.02%	23.7%	QIEIQFAQGDRK	99.7%	67.5	25	43.2	2	2	0	1432.75	80	91
Serine/arginine-rich splicing factor 10	SRSF10	SRS10_HUMAN	31.3	100.0%	6	7	19	0.02%	23.7%	YGPIVDVYVPLDFYTR	99.7%	56.6	25	56.6	3	0	0	1916.98	33	48
Serine/arginine-rich splicing factor 10	SRSF10	SRS10_HUMAN	31.3	100.0%	6	7	19	0.02%	23.7%	YLRPPNTSLFVR	99.7%	40.3	25	40.3	0	2	0	1462.82	4	15
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	10	12	42	0.04%	46.3%	AFGYYGPLR	99.7%	57.5	25	51.8	8	0	0	1043.53	29	37
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	10	12	42	0.04%	46.3%	DSCPLDCK	97.0%	29.9	25	29.9	3	0	0	994.40	4	11
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	10	12	42	0.04%	46.3%	GPPPSWGR	94.6%	27.7	25	23.9	1	0	0	853.43	91	98
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	10	12	42	0.04%	46.3%	NPPGFAFVEFEDPR	99.7%	73.3	25	73.3	6	0	0	1621.76	44	57
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	10	12	42	0.04%	46.3%	NPPGFAFVEFEDPRDAADAVR	99.7%	44.2	25	44.2	1	3	0	2320.10	44	64
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	10	12	42	0.04%	46.3%	NRGPPPSWGR	99.7%	43.4	25	41.3	4	0	0	1123.58	89	98
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	10	12	42	0.04%	46.3%	VELSNGEKR	97.5%	30.7	25	23.5	1	0	0	1031.55	78	86

Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	10	12	42	0.04%	46.3%	VRVELSNGEK	99.7%	61.8	25	47.8	4	0	0	1130.62	76	85
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	10	12	42	0.04%	46.3%	VYVGNLGNNGNK	99.7%	74.1	25	64.8	4	0	0	1248.63	12	23
Serine/arginine-rich splicing factor 3	SRSF3	SRSF3_HUMAN	19.3	100.0%	10	12	42	0.04%	46.3%	VYVGNLGNNGNKTELER	99.7%	91.6	25	75.9	3	4	0	1876.95	12	28
Serine/arginine-rich splicing factor 5	SRSF5	SRSF5_HUMAN	31.3	99.9%	2	2	6	0.01%	8.8%	LIVENLSSR	99.7%	51.3	25	46.6	3	0	0	1030.59	110	118
Serine/arginine-rich splicing factor 5	SRSF5	SRSF5_HUMAN	31.3	99.9%	2	2	6	0.01%	8.8%	LNEGVVEFASYGDLK	99.7%	110	25	105	3	0	0	1640.82	144	158
Serine/arginine-rich splicing factor 7	SRSF7	SRSF7_HUMAN	27.4	100.0%	6	6	13	0.01%	26.1%	AFSYYGPLR	99.7%	42.8	25	32.2	2	0	0	1073.54	30	38
Serine/arginine-rich splicing factor 7	SRSF7	SRSF7_HUMAN	27.4	100.0%	6	6	13	0.01%	26.1%	GHYAYDCHR	96.1%	28.9	25	28.9	1	0	0	1178.48	113	121
Serine/arginine-rich splicing factor 7	SRSF7	SRSF7_HUMAN	27.4	100.0%	6	6	13	0.01%	26.1%	NPPGFAFVEFEDPR	99.7%	73.3	25	73.3	6	0	0	1621.76	45	58
Serine/arginine-rich splicing factor 7	SRSF7	SRSF7_HUMAN	27.4	100.0%	6	6	13	0.01%	26.1%	NPPGFAFVEFEDPRDAEDAVR	99.7%	45.6	25	45.6	0	2	0	2378.10	45	65
Serine/arginine-rich splicing factor 7	SRSF7	SRSF7_HUMAN	27.4	100.0%	6	6	13	0.01%	26.1%	VELSTGMPR	96.4%	29.2	25	23.9	1	0	0	989.51	79	87
Serine/arginine-rich splicing factor 7	SRSF7	SRSF7_HUMAN	27.4	100.0%	6	6	13	0.01%	26.1%	VRVELSTGMPR	99.7%	45	25	45	2	0	0	1244.68	77	87
Serine/arginine-rich splicing factor 7	SRSF7	SRSF7_HUMAN	27.4	100.0%	6	6	13	0.01%	26.1%	VYVGNLGTGAGK	99.7%	75.7	25	74	5	0	0	1135.61	13	24
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	13	18	59	0.06%	51.6%	DAEDAIYGR	98.7%	33.2	25	23.1	2	0	0	1009.46	64	72
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	13	18	59	0.06%	51.6%	DGVGMVEYLR	99.7%	74	25	50.8	6	0	0	1138.56	145	154
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	13	18	59	0.06%	51.6%	EAGDVCYADVQK	99.7%	73.6	25	68.9	4	0	0	1354.59	133	144
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	13	18	59	0.06%	51.6%	EDMEYALR	99.7%	41.5	25	32.9	2	0	0	1026.46	156	163
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	13	18	59	0.06%	51.6%	EKDLEDLFYK	99.7%	62.1	25	51.2	2	2	0	1299.65	27	36
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	13	18	59	0.06%	51.6%	FEDPRDAEDAIYGR	99.7%	35.7	25	35.7	2	3	0	1653.75	59	72
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	13	18	59	0.06%	51.6%	GSPHYFSPFRPY	99.7%	55.4	25	54	3	2	0	1454.69	210	221
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	13	18	59	0.06%	51.6%	HGLVPFAFVR	99.7%	43.3	25	42.7	5	0	0	1142.65	49	58
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	13	18	59	0.06%	51.6%	IYVGNLPTDVR	99.7%	58.2	25	39	2	0	0	1246.68	16	26
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	13	18	59	0.06%	51.6%	KEDMEYALR	99.7%	54.9	25	53	5	0	0	1154.55	155	163
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	13	18	59	0.06%	51.6%	LRVEFPR	99.4%	36.6	25	22.8	12	0	0	916.54	82	88
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	13	18	59	0.06%	51.6%	NGYDYGQCR	99.7%	52.5	25	48.6	3	0	0	1132.45	73	81
Serine/arginine-rich splicing factor 9	SRSF9	SRSF9_HUMAN	25.5	100.0%	13	18	59	0.06%	51.6%	SHEGETSYIR	99.7%	43.2	25	43.2	4	0	0	1178.54	172	181
Serine/threonine-protein kinase 3	STK3	STK3_HUMAN	56.3	100.0%	2	2	3	0.00%	5.1%	AGNILLNTEGHAK	99.7%	49.2	25	49.2	1	0	0	1337.72	149	161
Serine/threonine-protein kinase 3	STK3	STK3_HUMAN	56.3	100.0%	2	2	3	0.00%	5.1%	TLIEDEIATILK	99.7%	82.3	25	81.8	2	0	0	1358.78	117	128
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	14	24	0.02%	46.7%	AKDLILR	97.9%	31.4	25	20.8	2	0	0	828.53	353	359
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	14	24	0.02%	46.7%	DIKPDNLLLDSK	99.7%	41.2	25	41.1	2	0	0	1370.75	212	223
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	14	24	0.02%	46.7%	DILVEADSLWVVK	99.7%	69	25	63.3	3	0	0	1486.82	139	151
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	14	24	0.02%	46.7%	DTGHVYAMK	99.5%	37.4	25	31.5	2	0	0	1021.48	110	118
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	14	24	0.02%	46.7%	DWVFINYTYK	99.7%	54.9	25	0	4	0	0	1348.66	437	446
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	14	24	0.02%	46.7%	FCCEWEHR	99.7%	47.3	25	47.3	1	0	0	1223.47	360	367
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	14	24	0.02%	46.7%	IGAPGVEEIK	99.7%	56.8	25	41.2	2	0	0	1012.57	368	377
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	14	24	0.02%	46.7%	LGLEDFESLK	99.7%	65.9	25	62	2	0	0	1150.60	84	93
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	14	24	0.02%	46.7%	LSDFGLCTGLK	99.7%	77.7	25	73.6	4	0	0	1210.61	228	238
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	14	24	0.02%	46.7%	LSDFGLCTGLKK	99.7%	69.9	25	62.5	3	0	0	1338.71	228	239
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	14	24	0.02%	46.7%	NLNHSLPSDFTFQNMNSK	99.7%	61.3	25	61.3	0	2	0	2093.97	248	265
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	14	24	0.02%	46.7%	QLAFSTVGTPDYIAPEVFMQTGYNK	99.7%	49.7	25	49.7	0	2	0	2777.35	277	301
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	14	24	0.02%	46.7%	RFEGLTAR	99.7%	42.7	25	32.8	2	0	0	949.52	447	454
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	14	24	0.02%	46.7%	SIDDTSNFDEFPESDILKPTVATSNHPETDYK	99.7%	78.1	25	77.4	0	2	0	3612.65	403	434
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	14	24	0.02%	46.7%	SNSFFEGVDWEHIR	99.7%	65.2	25	65.2	1	1	0	1722.79	378	391
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	14	24	0.02%	46.7%	VMEEEGLKDEEK	99.7%	49.5	25	33.6	1	0	0	1435.66	51	62
Serine/threonine-protein kinase 38	STK38	STK38_HUMAN	54.2	100.0%	13	14	24	0.02%	46.7%	VTLENFYSNLIAQHEER	99.7%	80.1	25	76.1	1	0	0	2063.02	25	41
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	16	43	0.04%	31.2%	AKDLILR	97.9%	31.4	25	20.8	2	0	0	828.53	354	360
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	16	43	0.04%	31.2%	DIKPDNLLLDAK	99.7%	48.7	25	47	4	0	0	1354.76	213	224
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	16	43	0.04%	31.2%	DTGHIYAMK	99.7%	40.4	25	34.1	3	0	0	1035.49	111	119
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	16	43	0.04%	31.2%	DWVFLNYTYK	99.7%	54.9	25	0	4	0	0	1348.66	435	444
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	16	43	0.04%	31.2%	ERPAAIPIEIK	99.7%	48.4	25	40	4	0	0	1236.73	393	403
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	16	43	0.04%	31.2%	FCIDSENR	99.7%	50.1	25	45	4	0	0	1040.45	361	368
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	16	43	0.04%	31.2%	FEGLTQR	99.4%	36.8	25	18.8	2	0	0	850.44	446	452

Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	16	43	0.04%	31.2%	GHPFFEGVDWEHIR	99.7%	44.1	25	44.1	0	2	0	1725.81	379	392
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	16	43	0.04%	31.2%	LGLDDFESLK	99.7%	56.8	25	53.2	3	0	0	1136.58	85	94
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	16	43	0.04%	31.2%	LSDFGLCTGLK	99.7%	77.7	25	73.6	4	0	0	1210.61	229	239
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	16	43	0.04%	31.2%	LSDFGLCTGLKK	99.7%	69.9	25	62.5	3	0	0	1338.71	229	240
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	16	43	0.04%	31.2%	LTLENFYSNLILQHEER	99.7%	78.7	25	78.7	1	2	0	2119.08	26	42
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	16	43	0.04%	31.2%	MFYSFQDKR	99.5%	37.6	25	32.8	1	0	0	1221.57	153	161
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	16	43	0.04%	31.2%	NLTHNPPSDFSFQNMNSK	99.7%	43.3	25	43.3	0	2	0	2093.93	249	266
Serine/threonine-protein kinase 38-like	STK38L	ST38L_HUMAN	54.0	100.0%	15	16	43	0.04%	31.2%	RFEGLTQR	98.8%	33.7	25	18.3	2	0	0	1006.54	445	452
Serine/threonine-protein kinase D2	PRKD2	KPCD2_HUMAN	96.8	99.8%	2	2	3	0.00%	3.6%	FLITQILVALR	99.7%	57.8	25	57.8	2	0	0	1286.82	653	663
Serine/threonine-protein kinase D2	PRKD2	KPCD2_HUMAN	96.8	99.8%	2	2	3	0.00%	3.6%	SVVGTPAYLAPEVLLNQGYNR	99.7%	52.6	25	52.6	1	0	0	2261.19	710	730
Serine/threonine-protein kinase MST4	MST4	MST4_HUMAN	46.5	100.0%	5	5	10	0.01%	15.4%	AANVLLSEQGDVK	99.7%	69.4	25	67.1	3	0	0	1343.72	147	159
Serine/threonine-protein kinase MST4	MST4	MST4_HUMAN	46.5	100.0%	5	5	10	0.01%	15.4%	ADIWSLGITAIELAK	99.7%	68.8	25	28.4	2	0	0	1600.89	200	214
Serine/threonine-protein kinase MST4	MST4	MST4_HUMAN	46.5	100.0%	5	5	10	0.01%	15.4%	AGPFDEFQIATMLK	99.7%	53.4	25	52.3	2	0	0	1567.78	113	126
Serine/threonine-protein kinase MST4	MST4	MST4_HUMAN	46.5	100.0%	5	5	10	0.01%	15.4%	SIAVAEAACPGITDK	99.7%	72.3	25	67.6	1	0	0	1502.75	384	398
Serine/threonine-protein kinase MST4	MST4	MST4_HUMAN	46.5	100.0%	5	5	10	0.01%	15.4%	VLFLIPK	97.4%	30.5	25	30.5	2	0	0	829.55	227	233
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	3	3	5	0.00%	1.3%	LFDAPEAPLPSR	99.4%	36.6	25	29.3	1	0	0	1312.69	1121	1132
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	3	3	5	0.00%	1.3%	TLDQSPELR	98.0%	31.5	25	23.5	2	0	0	1058.55	1162	1170
Serine/threonine-protein kinase mTOR	MTOR	MTOR_HUMAN	288.9	100.0%	3	3	5	0.00%	1.3%	VLGLLGALDPYK	99.7%	51.6	25	51.6	2	0	0	1258.74	887	898
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	8	8	14	0.01%	20.5%	DLVIVAANLQK	99.7%	79.6	25	65.1	2	0	0	1183.70	478	488
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	8	8	14	0.01%	20.5%	DTAEGVSQELISAGLVDGR	99.7%	73.5	25	66	2	0	0	1916.96	459	477
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	8	8	14	0.01%	20.5%	EVLEGLEYLHK	99.7%	58	25	43	1	0	0	1329.71	129	139
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	8	8	14	0.01%	20.5%	IPISLVLR	99.7%	64.2	25	64.2	2	0	0	910.61	432	439
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	8	8	14	0.01%	20.5%	LLSGGSVLDIIK	99.7%	90.4	25	67.8	2	0	0	1214.74	94	105
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	8	8	14	0.01%	20.5%	SGVLDESTIATILR	99.7%	78.6	25	78.6	2	0	0	1474.81	115	128
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	8	8	14	0.01%	20.5%	TAQALSSGSGSQETK	99.7%	95.1	25	84.9	2	0	0	1451.70	417	431
Serine/threonine-protein kinase OSR1	OXSR1	OXSR1_HUMAN	58.0	100.0%	8	8	14	0.01%	20.5%	TFVGTPCWMAPEVMEQVR	99.7%	39.4	25	39.4	1	0	0	2137.99	185	202
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	23	88	0.08%	38.2%	AMEIASQR	99.7%	39.8	25	25.7	4	0	0	905.45	402	409
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	23	88	0.08%	38.2%	ATVEQVLDPR	99.7%	64.4	25	53	7	0	0	1127.61	156	165
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	23	88	0.08%	38.2%	DCANVNDFFMR	99.7%	73	25	73	6	0	0	1388.57	360	370
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	23	88	0.08%	38.2%	EANVYHASTANGESR	99.7%	85.7	25	85.7	5	0	0	1605.73	191	205
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	23	88	0.08%	38.2%	ELFEFVTDPSITHENMDAYLSK	99.7%	36.2	25	35.9	0	6	0	2586.21	380	401
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	23	88	0.08%	38.2%	ELYLQVIQYMR	99.7%	89.1	25	80.9	8	0	0	1455.77	302	312
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	23	88	0.08%	38.2%	GIITEINGCISTGK	99.7%	71.1	25	66.7	2	0	0	1462.76	177	190
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	23	88	0.08%	38.2%	GYVWNGGSNPQANR	99.7%	65.8	25	65.8	2	0	0	1519.70	82	95
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	23	88	0.08%	38.2%	HSVAVMTVR	99.7%	47.7	25	31.8	8	0	0	999.54	371	379
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	23	88	0.08%	38.2%	INLDKLNVTDSVINK	99.7%	91.8	25	88.4	4	5	0	1685.94	120	134
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	23	88	0.08%	38.2%	LKEEDMAMNAQQDNILYQTVTGLK	99.7%	47.1	25	47.1	0	1	0	2785.34	450	473
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	23	88	0.08%	38.2%	LNTAEIPCPEPIMLR	99.7%	62	25	44.5	6	0	0	1753.90	257	271
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	23	88	0.08%	38.2%	LNVTDSVINK	99.7%	82.6	25	65.1	6	0	0	1102.61	125	134
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	23	88	0.08%	38.2%	SSQDHVDEEVFKR	99.7%	60	25	58.3	2	4	0	1575.74	415	427
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	23	88	0.08%	38.2%	TSILVFK	99.1%	35.1	25	33.5	4	0	0	807.50	212	218
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	23	88	0.08%	38.2%	VPALLENQVEER	99.7%	82.7	25	82.7	6	0	0	1396.74	482	493
Serine/threonine-protein kinase RIO1	RIOK1	RIOK1_HUMAN	65.6	100.0%	17	23	88	0.08%	38.2%	VVPGQFDDADSSDSENR	99.7%	100	25	100	2	0	0	1837.78	11	27
Serine/threonine-protein kinase VRK1	VRK1	VRK1_HUMAN	45.5	100.0%	3	3	4	0.00%	9.6%	ASNLLLNYK	99.7%	62	25	51.8	1	0	0	1035.58	180	188
Serine/threonine-protein kinase VRK1	VRK1	VRK1_HUMAN	45.5	100.0%	3	3	4	0.00%	9.6%	NPDQVYLVDYGLAYR	99.7%	104	25	98.5	1	0	0	1785.88	189	203
Serine/threonine-protein kinase VRK1	VRK1	VRK1_HUMAN	45.5	100.0%	3	3	4	0.00%	9.6%	VEPSDNGPLFTELK	99.7%	48.5	25	40.8	2	0	0	1545.78	72	85
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	6	6	10	0.01%	12.1%	ESSLTEPVIVGLLK	99.7%	54.5	25	54.5	3	0	0	1484.86	354	367
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	6	6	10	0.01%	12.1%	FLESPDFQPNIAK	99.7%	63.2	25	53.3	1	0	0	1505.76	220	232
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	6	6	10	0.01%	12.1%	FVLALLDLFDSEDPR	99.2%	35.5	25	30.6	1	0	0	1749.91	239	253
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	6	6	10	0.01%	12.1%	TVETEAVQMLK	99.7%	46.6	25	37.6	2	0	0	1248.65	550	560
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	6	6	10	0.01%	12.1%	VLPIMFPALYR	99.7%	57.2	25	57.2	2	0	0	1319.75	442	452

Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	2A5D_HUMAN	70.0	100.0%	6	6	10	0.01%	12.1%	YSGGPQIVK	98.0%	31.6	25	21.5	1	0	0	948.52	74	82
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	7	7	12	0.01%	15.1%	ELVSDANQHVK	99.7%	41.2	25	30.6	2	0	0	1239.63	332	342
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	7	7	12	0.01%	15.1%	LAGGDWFTSR	98.1%	31.8	25	16.6	2	0	0	1109.54	135	144
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	7	7	12	0.01%	15.1%	LNIISNLDCVNEVIGIR	99.7%	66.1	25	66.1	1	0	0	1942.04	382	398
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	7	7	12	0.01%	15.1%	LSTIALALGVER	99.7%	60.6	25	58.8	2	0	0	1242.74	35	46
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	7	7	12	0.01%	15.1%	LTQDQDVDVK	99.7%	53	25	41.6	2	0	0	1160.58	567	576
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	7	7	12	0.01%	15.1%	MAGDPVANVR	99.7%	46.9	25	41.5	1	0	0	1029.51	528	537
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	2AAA_HUMAN	65.3	100.0%	7	7	12	0.01%	15.1%	SEIIPMFSNLASDEQDSVR	99.7%	65	25	65	2	0	0	2138.01	203	221
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	PPP2R1B	2AAB_HUMAN	66.2	100.0%	3	3	5	0.00%	13.1%	ELVSDTNQHVK	99.7%	42.4	25	28.1	1	0	0	1269.64	344	354
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	PPP2R1B	2AAB_HUMAN	66.2	100.0%	3	3	5	0.00%	13.1%	IGPILDTNALQGEVKPVLQK	99.7%	43.8	25	35	0	2	0	2133.23	559	578
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	PPP2R1B	2AAB_HUMAN	66.2	100.0%	3	3	5	0.00%	13.1%	LNIISNLDCVNEVIGIR	99.7%	66.1	25	66.1	1	0	0	1942.04	394	410
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	PPP2R1B	2AAB_HUMAN	66.2	100.0%	3	3	5	0.00%	13.1%	LSTIALALGVER	99.7%	60.6	25	58.8	2	0	0	1242.74	47	58
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	PPP2R1B	2AAB_HUMAN	66.2	100.0%	3	3	5	0.00%	13.1%	SEIVPLFTSLASDEQDSVR	99.7%	62	25	62	2	0	0	2093.04	215	233
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	6	7	18	0.02%	24.9%	AHQLVHEGYK	99.7%	57.3	25	57.3	1	0	0	1181.61	236	245
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	6	7	18	0.02%	24.9%	APLDLDKYVEIAR	99.7%	84.7	25	77.1	4	3	0	1502.82	2	14
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	6	7	18	0.02%	24.9%	GAGWLFGAK	99.7%	47.1	25	32.8	2	0	0	906.48	211	219
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	6	7	18	0.02%	24.9%	LVTVWSAPNYCYR	99.7%	49.7	25	49.7	2	0	0	1628.79	252	264
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	6	7	18	0.02%	24.9%	TGGQVPDTNYIFMGDFVDR	99.7%	78.4	25	78.4	4	0	0	2131.98	67	85
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	PPP6_HUMAN	35.1	100.0%	6	7	18	0.02%	24.9%	VTNEFVHINNLK	99.7%	50.5	25	50.5	2	0	0	1427.76	220	231
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	10	11	29	0.03%	35.3%	AIETTDIISR	99.7%	75.4	25	56.7	5	0	0	1118.61	153	162
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	10	11	29	0.03%	35.3%	ALQFPPEGWLR	95.5%	28.4	25	23.1	1	0	0	1313.70	241	251
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	10	11	29	0.03%	35.3%	EPLSLINVR	99.7%	54.7	25	51.2	2	0	0	1040.61	66	74
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	10	11	29	0.03%	35.3%	EQAELTGLR	99.7%	62.5	25	41.8	4	0	0	1016.54	126	134
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	10	11	29	0.03%	35.3%	HSQYHVDGSLEKDR	99.7%	38.8	25	35.8	0	2	0	1670.79	105	118
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	10	11	29	0.03%	35.3%	NVESGEEELASK	99.7%	77.3	25	69.9	5	0	0	1291.60	77	88
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	10	11	29	0.03%	35.3%	QEEDSYEIFICHANVIR	99.7%	39.1	25	39.1	0	2	0	2122.99	219	235
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	10	11	29	0.03%	35.3%	REPLSLINVR	98.9%	34.3	25	29.4	2	0	0	1196.71	65	74
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	10	11	29	0.03%	35.3%	TLGDTGFMPPDK	99.7%	66.3	25	60.3	4	0	0	1278.60	274	285
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	PGAM5_HUMAN	32.0	100.0%	10	11	29	0.03%	35.3%	VSTDLLR	99.5%	37.2	25	19	2	0	0	803.46	170	176
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	PP1G_HUMAN	37.0	100.0%	3	3	6	0.01%	13.9%	EIFLSQPILLELEAPLK	99.7%	53.9	25	53.9	2	0	0	1953.13	44	60
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	PP1G_HUMAN	37.0	100.0%	3	3	6	0.01%	13.9%	NVQLQENEIR	99.7%	45.7	25	40.4	2	0	0	1242.64	27	36
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	PP1G_HUMAN	37.0	100.0%	3	3	6	0.01%	13.9%	TFTDCFNCLPIAAIVDEK	99.7%	42.6	25	42.4	2	0	0	2113.99	151	168
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	3	3	5	0.00%	14.0%	FSPDGELYASGSEDGTLR	99.7%	59.1	25	51.3	1	0	0	1900.86	273	290
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	3	3	5	0.00%	14.0%	TVDFTQDSNYLLTGGQDK	99.7%	72.4	25	72.4	2	0	0	2001.94	105	122
Serine-threonine kinase receptor-associated protein	STRAP	STRAP_HUMAN	38.4	100.0%	3	3	5	0.00%	14.0%	YDYNSGEELESYK	99.7%	73.7	25	73.7	2	0	0	1596.67	250	262
Serine--tRNA ligase, cytoplasmic	SARS	SYSC_HUMAN	58.8	99.8%	2	2	2	0.00%	4.1%	GYIPIYTPFFMR	99.0%	34.4	25	32.9	1	0	0	1504.77	219	230
Serine--tRNA ligase, cytoplasmic	SARS	SYSC_HUMAN	58.8	99.8%	2	2	2	0.00%	4.1%	LLIDEAILK	96.7%	29.6	25	16.3	1	0	0	1027.64	108	116
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	13	24	0.02%	38.3%	DQAVENILVSPVVVASSLGLVSLGGK	99.7%	67.3	25	67.3	0	2	0	2551.43	61	86
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	13	24	0.02%	38.3%	DTQSGSLLFIGR	99.7%	102	25	86.6	3	0	0	1293.68	394	405
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	13	24	0.02%	38.3%	GVVEVTHDLQK	99.7%	52.1	25	33.6	2	0	0	1224.66	309	319
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	13	24	0.02%	38.3%	HLAGLGLTEAIDKNK	99.7%	67.4	25	67.4	0	2	0	1579.88	320	334
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	13	24	0.02%	38.3%	KPAAAAAPGTAEK	99.7%	51.2	25	39.5	2	0	0	1182.65	23	35
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	13	24	0.02%	38.3%	LFYADHPFIFLVR	99.7%	52.8	25	52.8	2	1	0	1637.88	381	393
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	13	24	0.02%	38.3%	LQIVEMPLAHK	99.7%	48.3	25	37.6	2	0	0	1294.72	253	263
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	13	24	0.02%	38.3%	LSSLIILMPHHVEPLER	99.7%	52.2	25	50.8	0	3	0	1984.11	264	280
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	13	24	0.02%	38.3%	LYGPSSVSFADDFVR	99.7%	90.6	25	85.7	2	0	0	1659.80	134	148
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	13	24	0.02%	38.3%	SAGLAFSLYQAMAK	99.7%	84.2	25	80.2	2	0	0	1457.75	47	60
Serpin H1	SERPINH1	SERPH_HUMAN	46.4	100.0%	11	13	24	0.02%	38.3%	TGLYNYYDDEKEK	99.4%	31.4	25	31.4	0	1	0	1637.73	240	252
Serrate RNA effector molecule homolog	SRRT	SRRT_HUMAN	100.7	99.8%	2	2	2	0.00%	2.3%	ESLSEEEAQK	99.7%	41.4	25	37.1	1	0	0	1149.53	678	687
Serrate RNA effector molecule homolog	SRRT	SRRT_HUMAN	100.7	99.8%	2	2	2	0.00%	2.3%	VALSEPQPER	99.7%	44	25	34.8	1	0	0	1125.59	450	459
Serum albumin	ALB	ALBU_HUMAN	69.4	100.0%	3	4	9	0.01%	4.4%	AVMDDFAAFVEK	98.5%	32.8	25	31.7	1	0	0	1342.63	570	581

Serum albumin	ALB	ALBU_HUMAN	69.4	100.0%	3	4	9	0.01%	4.4%	KVPQVSTPTLVEVSR	99.7%	93.8	25	93.8	2	4	0	1639.94	438	452
Serum albumin	ALB	ALBU_HUMAN	69.4	100.0%	3	4	9	0.01%	4.4%	VPQVSTPTLVEVSR	99.7%	48.4	25	48.4	2	0	0	1511.84	439	452
Sestrin-2	SESN2	SESN2_HUMAN	54.5	99.8%	2	2	4	0.00%	6.0%	FAPGGVGDSGPGEEQR	99.7%	78.3	25	74.9	2	0	0	1559.71	18	33
Sestrin-2	SESN2	SESN2_HUMAN	54.5	99.8%	2	2	4	0.00%	6.0%	GPSAFIPVEEVLR	99.7%	64.7	25	57.1	2	0	0	1413.77	43	55
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	6	6	11	0.01%	19.2%	ASSTCPLTFENVK	99.7%	57.2	25	46.7	2	0	0	1453.70	257	269
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	6	6	11	0.01%	19.2%	ATYLPQLTTEK	95.7%	28.5	25	28.5	1	0	0	1264.68	160	170
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	6	6	11	0.01%	19.2%	FAQEQIAPLVSTMDENSK	99.7%	59.1	25	59.1	2	0	0	2023.96	71	88
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	6	6	11	0.01%	19.2%	IGTIYEGASNIQLNTIAK	99.7%	71.7	25	69	2	0	0	1906.03	409	426
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	6	6	11	0.01%	19.2%	YAIGSLNEGR	99.7%	53.3	25	42.2	2	0	0	1079.55	285	294
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	ACDSB_HUMAN	47.5	100.0%	6	6	11	0.01%	19.2%	YYASEIAGQTTSK	99.7%	102	25	96.6	2	0	0	1418.68	372	384
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	13	18	28	0.03%	42.9%	ANHFFTVTDPR	99.7%	56.5	25	53.9	2	2	0	1304.64	25	35
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	13	18	28	0.03%	42.9%	HVSPLIGR	97.7%	31	25	28.7	1	0	0	878.52	171	178
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	13	18	28	0.03%	42.9%	ILMAAPGMAIPPFIMNTLEK	99.4%	36.8	25	18.4	3	0	0	2174.14	234	253
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	13	18	28	0.03%	42.9%	IQESHPELR	99.7%	54.1	25	40.8	2	0	0	1108.57	306	314
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	13	18	28	0.03%	42.9%	IQESHPELRR	99.6%	32.6	25	27.3	1	1	0	1264.68	306	315
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	13	18	28	0.03%	42.9%	NILLTNEQLESAR	99.7%	97.7	25	94.8	2	0	0	1500.80	36	48
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	13	18	28	0.03%	42.9%	NILLTNEQLESARK	99.7%	69.9	25	66.1	1	0	0	1628.90	36	49
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	13	18	28	0.03%	42.9%	QAITQVVVSR	99.7%	72.6	25	60	1	0	0	1100.64	224	233
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	13	18	28	0.03%	42.9%	QGIVPPGLTENELWR	98.7%	33.4	25	31.4	2	0	0	1708.90	56	70
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	13	18	28	0.03%	42.9%	SSMSVTSLEAELQAK	99.7%	89.3	25	89.2	3	0	0	1596.78	291	305
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	13	18	28	0.03%	42.9%	VGIPVTDENGNR	99.7%	57.5	25	53.8	2	0	0	1270.64	203	214
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	13	18	28	0.03%	42.9%	WDQSTFIGR	99.7%	59.5	25	0	2	0	0	1109.54	16	24
Sideroflexin-1	SFXN1	SFXN1_HUMAN	35.6	100.0%	13	18	28	0.03%	42.9%	YIYDSAFHPDTGEK	99.7%	81.5	25	78.1	2	1	0	1642.74	73	86
Sideroflexin-2	SFXN2	SFXN2_HUMAN	36.2	100.0%	2	2	7	0.01%	7.8%	AAAIGITQVVISR	99.7%	58.4	25	46.5	3	0	0	1298.78	220	232
Sideroflexin-2	SFXN2	SFXN2_HUMAN	36.2	100.0%	2	2	7	0.01%	7.8%	YGELEPYVYFNK	99.7%	55.9	25	47.4	4	0	0	1521.73	309	320
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	100.0%	5	6	8	0.01%	19.3%	DAVPAFIEPNVR	99.7%	42.2	25	35.4	2	0	0	1327.70	19	30
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	100.0%	5	6	8	0.01%	19.3%	FWITER	97.9%	31.3	25	16.8	1	0	0	851.44	31	36
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	100.0%	5	6	8	0.01%	19.3%	IQSPTEETEIFYHR	99.7%	50.6	25	49	1	2	0	1749.84	322	335
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	100.0%	5	6	8	0.01%	19.3%	QLLCTNEDVSSPASADQR	99.7%	83.9	25	81.1	1	0	0	1990.91	67	84
Sideroflexin-4	SFXN4	SFXN4_HUMAN	38.0	100.0%	5	6	8	0.01%	19.3%	SLATVHPDSSNLIPK	99.7%	53.2	25	47	1	0	0	1578.85	92	106
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	5	7	18	0.02%	26.8%	GDLLFLTNR	99.7%	69.6	25	51.8	4	0	0	1048.58	64	72
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	5	7	18	0.02%	26.8%	GDLLFLTNRVEDPIR	99.3%	30.5	25	29.7	0	2	0	1757.95	64	78
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	5	7	18	0.02%	26.8%	GDNNAVDDRGLYK	99.7%	47.8	25	47.8	4	0	0	1436.68	115	127
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	5	7	18	0.02%	26.8%	MLSLDFLDDVRR	99.7%	37.8	25	34.8	1	3	0	1495.76	1	12
Signal peptidase complex catalytic subunit SEC11A	SEC11A	SC11A_HUMAN	20.6	100.0%	5	7	18	0.02%	26.8%	VGEIVVFR	99.7%	71.9	25	66.9	4	0	0	918.54	79	86
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	10	20	0.02%	40.3%	DPTGMDPDDIWQLSSSLK	99.7%	53.6	25	53.6	2	0	0	2004.92	147	164
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	10	20	0.02%	40.3%	FDDKYTLK	99.7%	39.7	25	30.7	2	0	0	1029.53	166	173
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	10	20	0.02%	40.3%	FFDHSGTLVMDAYEPEISR	99.7%	59.9	25	59.9	1	4	0	2214.02	196	214
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	10	20	0.02%	40.3%	IDKWDGSAVK	99.7%	45	25	23.9	2	0	0	1118.58	48	57
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	10	20	0.02%	40.3%	LHDSLAIER	99.7%	42	25	36.9	3	0	0	1053.57	215	223
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	10	20	0.02%	40.3%	SGLLDKWK	99.7%	49.9	25	33.9	2	0	0	946.54	33	40
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	10	20	0.02%	40.3%	SIFLVAHR	99.7%	40.2	25	31.5	2	0	0	942.55	138	145
Signal peptidase complex subunit 2	SPCS2	SPCS2_HUMAN	25.0	100.0%	8	10	20	0.02%	40.3%	YVENFGLIDGR	99.7%	94.3	25	85.2	2	0	0	1282.64	74	84
Signal peptidase complex subunit 3	SPCS3	SPCS3_HUMAN	20.3	100.0%	5	5	10	0.01%	23.3%	MNTVLSR	99.7%	46.7	25	18.9	2	0	0	820.43	1	7
Signal peptidase complex subunit 3	SPCS3	SPCS3_HUMAN	20.3	100.0%	5	5	10	0.01%	23.3%	NNALNQVVLWDK	99.7%	76.9	25	58	2	0	0	1413.75	97	108
Signal peptidase complex subunit 3	SPCS3	SPCS3_HUMAN	20.3	100.0%	5	5	10	0.01%	23.3%	NVEDFTGPR	99.7%	50.9	25	43.1	2	0	0	1034.49	50	58
Signal peptidase complex subunit 3	SPCS3	SPCS3_HUMAN	20.3	100.0%	5	5	10	0.01%	23.3%	YFFFDDGNGLK	99.7%	52.8	25	37.1	2	0	0	1322.61	127	137
Signal peptidase complex subunit 3	SPCS3	SPCS3_HUMAN	20.3	100.0%	5	5	10	0.01%	23.3%	YFFFDDGNGLKGNR	99.7%	46.2	25	46.2	2	0	0	1649.77	127	140
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	7	11	31	0.03%	44.9%	EVNKFQMAYSNLLR	99.7%	68.4	25	61.7	4	4	0	1712.88	75	88
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	7	11	31	0.03%	44.9%	FQMAYSNLLR	99.7%	56.4	25	46.2	6	0	0	1242.63	79	88
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	7	11	31	0.03%	44.9%	GTVEGFEPADNK	99.7%	67.3	25	67.3	2	0	0	1263.59	44	55

Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	7	11	31	0.03%	44.9%	KGTVEGFEPADNK	99.7%	45	25	40.3	4	0	0	1391.68	43	55
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	7	11	31	0.03%	44.9%	KISTVVSSK	99.7%	43.3	25	35.6	2	0	0	948.57	66	74
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	7	11	31	0.03%	44.9%	TSGSVYITLKK	99.7%	63.3	25	63.3	3	0	0	1196.69	22	32
Signal recognition particle 14 kDa protein	SRP14	SRP14_HUMAN	14.6	100.0%	7	11	31	0.03%	44.9%	VLLESEQFLTELTR	99.7%	93.5	25	93.5	6	0	0	1677.91	2	15
Signal recognition particle 19 kDa protein	SRP19	SRP19_HUMAN	16.2	99.9%	2	3	6	0.01%	18.8%	SVMLYAAEMIPK	99.7%	65.6	25	53.8	4	0	0	1384.69	103	114
Signal recognition particle 19 kDa protein	SRP19	SRP19_HUMAN	16.2	99.9%	2	3	6	0.01%	18.8%	TGGADQSLQQGEGSK	99.7%	83.5	25	76.6	2	0	0	1462.68	122	136
Signal recognition particle 9 kDa protein	SRP9	SRP09_HUMAN	10.1	99.8%	2	3	9	0.01%	22.1%	LYLADPMK	99.5%	37.7	25	18.5	5	0	0	966.50	17	24
Signal recognition particle 9 kDa protein	SRP9	SRP09_HUMAN	10.1	99.8%	2	3	9	0.01%	22.1%	VTDDLVCLVYK	99.7%	79.1	25	60.6	4	0	0	1324.68	42	52
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	4	5	8	0.01%	7.8%	AGAVEQLR	99.7%	44.7	25	24.6	2	0	0	843.47	459	466
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	4	5	8	0.01%	7.8%	DAAGIAMEAIAFAR	99.7%	106	25	91.3	2	0	0	1406.71	497	510
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	4	5	8	0.01%	7.8%	KEGSDGPLATSKPVPAEK	98.4%	27	25	23.4	0	1	0	1810.95	174	191
Signal recognition particle receptor subunit alpha	SRPR	SRPR_HUMAN	69.8	100.0%	4	5	8	0.01%	7.8%	MLDFFTIFSK	99.7%	56.9	25	50.4	3	0	0	1264.63	1	10
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	27	0.03%	50.9%	AIVFVVDSAAFQR	99.7%	81.2	25	80.1	4	0	0	1422.77	138	150
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	27	0.03%	50.9%	AVLLVGLCDSGK	99.7%	72.7	25	72.2	2	0	0	1231.67	66	77
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	27	0.03%	50.9%	DTQTSITDSCAVYR	99.7%	73.8	25	73.8	3	0	0	1616.72	91	104
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	27	0.03%	50.9%	GDVGSADIQDLEK	99.7%	86.4	25	77.2	4	0	0	1346.64	253	265
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	27	0.03%	50.9%	GNSLTLIDLPGHESLR	99.7%	48.1	25	48.1	2	2	0	1721.92	110	125
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	27	0.03%	50.9%	LIQQQLEK	99.7%	39.5	25	19.1	2	0	0	999.58	192	199
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	27	0.03%	50.9%	LLTGLYR	99.7%	42.8	25	4.93	1	0	0	835.50	84	90
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	27	0.03%	50.9%	LQFLER	99.4%	36.7	25	0	2	0	0	805.46	126	131
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	27	0.03%	50.9%	NTPSFLIACNK	99.7%	66.2	25	56.5	2	0	0	1264.64	171	181
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	27	0.03%	50.9%	SAAPSTLDSSSTAPAQLGK	99.7%	107	25	107	1	0	0	1788.90	209	227
Signal recognition particle receptor subunit beta	SRPRB	SRPRB_HUMAN	29.7	100.0%	11	12	27	0.03%	50.9%	VADGGGAGGTFQPYLDTLR	99.7%	90.4	25	90.4	2	0	0	1894.93	9	27
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	13	13	30	0.03%	25.2%	ALLQQQPEDDSKR	99.7%	39.1	25	35.8	0	1	0	1527.78	405	417
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	13	13	30	0.03%	25.2%	DLPDVQELITQVR	99.7%	56.8	25	53.1	4	0	0	1525.82	509	521
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	13	13	30	0.03%	25.2%	EFGDSLSLEILQIIK	99.7%	49.5	25	44.2	1	0	0	1704.94	53	67
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	13	13	30	0.03%	25.2%	FETFCLDPSLVTK	99.7%	76.5	25	73.2	2	0	0	1556.77	558	570
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	13	13	30	0.03%	25.2%	LASAFTEEQAVLYNQR	99.7%	89.2	25	80.2	4	0	0	1839.92	221	236
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	13	13	30	0.03%	25.2%	LEALITQTR	99.4%	36.5	25	29.1	1	0	0	1044.60	278	286
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	13	13	30	0.03%	25.2%	LFESMLSECR	99.7%	48.8	25	42.4	2	0	0	1271.58	336	345
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	13	13	30	0.03%	25.2%	QAATMSEVEWR	99.7%	41.1	25	39.4	1	0	0	1307.60	289	299
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	13	13	30	0.03%	25.2%	SGGTEGLLAEKLEALITQTR	99.4%	31.3	25	31.3	0	1	0	2087.13	267	286
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	13	13	30	0.03%	25.2%	VEEISPNIR	99.7%	45.9	25	41.5	4	0	0	1056.57	237	245
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	13	13	30	0.03%	25.2%	VSNLQYLHSYLTYIK	99.4%	31.1	25	31.1	0	2	0	1841.98	373	387
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	13	13	30	0.03%	25.2%	VTEELLTDNR	99.7%	76.5	25	64.3	4	0	0	1189.61	113	122
Signal recognition particle subunit SRP68	SRP68	SRP68_HUMAN	70.7	100.0%	13	13	30	0.03%	25.2%	YANEVNSDAGAFK	99.7%	78	25	63.8	3	0	0	1385.63	492	504
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	9	9	15	0.01%	16.7%	AIELLQEFSDQHPENAAEIK	99.7%	41.5	25	41.5	0	2	0	2282.13	357	376
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	9	9	15	0.01%	16.7%	EALNVINTHTK	94.8%	27.8	25	20	1	0	0	1239.67	63	73
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	9	9	15	0.01%	16.7%	GTQGATAGASSELDASK	99.7%	97.1	25	94	1	0	0	1550.73	601	617
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	9	9	15	0.01%	16.7%	SPAHLSLIR	99.7%	55.2	25	45.7	2	0	0	993.58	443	451
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	9	9	15	0.01%	16.7%	TEEALQLYNQIIK	99.7%	81.8	25	73.7	2	0	0	1562.84	242	254
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	9	9	15	0.01%	16.7%	TIESANQQTDKLK	99.7%	77.4	25	65.1	2	0	0	1475.77	100	112
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	9	9	15	0.01%	16.7%	VLANNSLSFEK	99.7%	72.8	25	62.8	2	0	0	1221.65	74	84
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	9	9	15	0.01%	16.7%	YDECLAVYR	99.7%	51.1	25	42.4	1	0	0	1188.54	125	133
Signal recognition particle subunit SRP72	SRP72	SRP72_HUMAN	74.6	100.0%	9	9	15	0.01%	16.7%	YGQNGDFTR	99.7%	40.5	25	34.1	2	0	0	1057.47	21	29
Signal transducer and activator of transcription 1-alpha/beta	STAT1	STAT1_HUMAN	87.3	100.0%	3	3	3	0.00%	4.7%	LQELNYNLK	95.8%	28.6	25	13.2	1	0	0	1134.62	351	359
Signal transducer and activator of transcription 1-alpha/beta	STAT1	STAT1_HUMAN	87.3	100.0%	3	3	3	0.00%	4.7%	TELISVSEVHPSR	99.7%	55.2	25	51	1	0	0	1453.76	704	716
Signal transducer and activator of transcription 1-alpha/beta	STAT1	STAT1_HUMAN	87.3	100.0%	3	3	3	0.00%	4.7%	VMAAENIPENPLK	99.7%	42.1	25	39	1	0	0	1425.74	653	665
Signal transducer and activator of transcription 3	STAT3	STAT3_HUMAN	88.1	100.0%	3	3	5	0.00%	6.9%	FLQESNVLYQHNLR	99.7%	66	25	60.2	1	0	0	1760.91	71	84
Signal transducer and activator of transcription 3	STAT3	STAT3_HUMAN	88.1	100.0%	3	3	5	0.00%	6.9%	GLSIEQLTTLAEK	99.7%	73.4	25	60.3	2	0	0	1402.78	519	531
Signal transducer and activator of transcription 3	STAT3	STAT3_HUMAN	88.1	100.0%	3	3	5	0.00%	6.9%	LLQTAATAAQQGGQANHPTAAVVTEK	99.7%	93.2	25	93.2	0	2	0	2576.34	115	140

Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	6	6	12	0.01%	48.0%	DVAYQYVK	99.7%	44.2	25	38.3	2	0	0	985.50	96	103
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	6	6	12	0.01%	48.0%	IDYGEYMDKNNVR	99.5%	38.1	25	38.1	2	0	0	1632.73	114	126
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	6	6	12	0.01%	48.0%	ISVFRPGLR	97.0%	29.9	25	22.6	2	0	0	1044.63	87	95
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	6	6	12	0.01%	48.0%	QATTIIADNIIFLSDQTK	99.7%	85.6	25	85.6	2	0	0	1992.07	128	145
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	6	6	12	0.01%	48.0%	SGDSEVYQLGDVSQK	99.7%	102	25	102	2	0	0	1611.75	67	81
Single-stranded DNA-binding protein, mitochondrial	SSBP1	SSBP_HUMAN	17.3	100.0%	6	6	12	0.01%	48.0%	VGQDPVLR	99.7%	53.7	25	46.8	2	0	0	883.50	39	46
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	10	10	15	0.01%	9.3%	DLALVNDQLLGFVR	99.7%	74.1	25	73.9	2	0	0	1572.87	391	404
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	10	10	15	0.01%	9.3%	EINSDQATQGNISSDR	99.7%	79.8	25	79.8	1	0	0	1734.79	1220	1235
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	10	10	15	0.01%	9.3%	EVQLAQIFEPLSR	99.7%	62.5	25	60.7	2	0	0	1529.83	751	763
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	10	10	15	0.01%	9.3%	IETDLPQIR	99.7%	48.8	25	38.5	2	0	0	1084.60	709	717
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	10	10	15	0.01%	9.3%	LLVACCLADIFR	99.7%	61.2	25	52.1	2	0	0	1450.75	88	99
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	10	10	15	0.01%	9.3%	SHDPEEAIR	99.3%	35.8	25	30.5	1	0	0	1053.50	369	377
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	10	10	15	0.01%	9.3%	SIEGTADDEEEGVSPDTAIR	99.7%	120	25	107	2	0	0	2090.94	638	657
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	10	10	15	0.01%	9.3%	SQDVDQLR	99.6%	38.2	25	25.9	1	0	0	960.47	1018	1025
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	10	10	15	0.01%	9.3%	STLIPILHQK	99.7%	48.5	25	16.5	1	0	0	1149.70	718	727
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	PDS5A_HUMAN	150.8	100.0%	10	10	15	0.01%	9.3%	TVTAAGAENIQQK	99.7%	67	25	57.8	1	0	0	1330.70	1240	1252
Small nuclear ribonucleoprotein E	SNRPE	RUXE_HUMAN	10.8	99.8%	2	2	5	0.00%	25.0%	GDNITLLQSVSN	99.7%	92.9	25	83.9	3	0	0	1260.64	81	92
Small nuclear ribonucleoprotein E	SNRPE	RUXE_HUMAN	10.8	99.8%	2	2	5	0.00%	25.0%	VMVQPINLIFR	99.6%	38.2	25	37.9	2	0	0	1345.77	13	23
Small nuclear ribonucleoprotein F	SNRPF	RUXF_HUMAN	9.7	99.8%	2	3	7	0.01%	24.4%	CNNVLYIR	99.7%	56.5	25	36.6	4	0	0	1051.54	66	73
Small nuclear ribonucleoprotein F	SNRPF	RUXF_HUMAN	9.7	99.8%	2	3	7	0.01%	24.4%	GVEEEEEDGEMRE	99.7%	59.5	25	59.5	3	0	0	1553.59	74	86
Small nuclear ribonucleoprotein Sm D1	SNRPD1	SMD1_HUMAN	13.3	100.0%	4	7	23	0.02%	37.8%	EPVQLETLSIR	99.7%	42.7	25	22.5	4	0	0	1284.72	51	61
Small nuclear ribonucleoprotein Sm D1	SNRPD1	SMD1_HUMAN	13.3	100.0%	4	7	23	0.02%	37.8%	LSHETVTIELK	99.7%	67	25	53.8	7	2	0	1269.71	10	20
Small nuclear ribonucleoprotein Sm D1	SNRPD1	SMD1_HUMAN	13.3	100.0%	4	7	23	0.02%	37.8%	NGTQVHGTITGVDVSMNTHLK	99.7%	55	25	55	0	4	0	2209.10	21	41
Small nuclear ribonucleoprotein Sm D1	SNRPD1	SMD1_HUMAN	13.3	100.0%	4	7	23	0.02%	37.8%	NREPVQLETLSIR	99.7%	68.8	25	67.8	4	2	0	1554.86	49	61
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	6	9	26	0.02%	49.2%	EEEEFNTGPLSVLTQSVK	99.7%	95.1	25	95.1	4	0	0	2006.99	20	37
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	6	9	26	0.02%	49.2%	GDSVIVVLR	99.7%	76.8	25	62.8	6	0	0	957.57	103	111
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	6	9	26	0.02%	49.2%	HCNMVLENVK	99.7%	60.9	25	60.9	3	0	0	1243.59	62	71
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	6	9	26	0.02%	49.2%	NNTQVLINCR	99.7%	69.7	25	61	4	0	0	1231.62	38	47
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	6	9	26	0.02%	49.2%	REEEEFNTGPLSVLTQSVK	99.7%	53.3	25	53.3	2	2	0	2163.09	19	37
Small nuclear ribonucleoprotein Sm D2	SNRPD2	SMD2_HUMAN	13.5	100.0%	6	9	26	0.02%	49.2%	SEMTPEELQK	99.7%	53.3	25	42	5	0	0	1191.56	9	18
Small nuclear ribonucleoprotein Sm D3	SNRPD3	SMD3_HUMAN	13.9	100.0%	4	5	14	0.01%	47.6%	FLILPDMLK	99.7%	46.9	25	27.7	8	0	0	1105.63	70	78
Small nuclear ribonucleoprotein Sm D3	SNRPD3	SMD3_HUMAN	13.9	100.0%	4	5	14	0.01%	47.6%	LIEAEDNMNCQMSNITVTYR	99.7%	53.5	25	53.5	2	0	0	2402.08	32	51
Small nuclear ribonucleoprotein Sm D3	SNRPD3	SMD3_HUMAN	13.9	100.0%	4	5	14	0.01%	47.6%	VAQLEQVYIR	99.7%	79.8	25	69.4	2	0	0	1218.68	55	64
Small nuclear ribonucleoprotein Sm D3	SNRPD3	SMD3_HUMAN	13.9	100.0%	4	5	14	0.01%	47.6%	VLHEAEGHIVTCETNTGEVYR	99.7%	66.1	25	62	0	2	0	2414.14	9	29
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN,RSMN_HUMAN	24.6	100.0%	5	6	16	0.02%	18.3%	GENLVSMTVEGPPPK	99.7%	52.3	25	44.5	4	0	0	1554.78	74	88
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN,RSMN_HUMAN	24.6	100.0%	5	6	16	0.02%	18.3%	GENLVSMTVEGPPPKDTGIAR	99.7%	56.7	25	56.7	0	2	0	2184.10	74	94
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN,RSMN_HUMAN	24.6	100.0%	5	6	16	0.02%	18.3%	IFIGTFK	99.4%	36.7	25	22.7	2	0	0	825.49	26	32
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN,RSMN_HUMAN	24.6	100.0%	5	6	16	0.02%	18.3%	MLQHIDYR	99.0%	34.5	25	27.5	1	0	0	1091.53	9	16
Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	RSMB_HUMAN,RSMN_HUMAN	24.6	100.0%	5	6	16	0.02%	18.3%	VLGLVLLR	99.7%	62.3	25	62.3	7	0	0	882.61	66	73
SNW domain-containing protein 1	SNW1	SNW1_HUMAN	61.5	100.0%	6	6	11	0.01%	11.6%	GLQTVHINENFAK	99.7%	74.4	25	72.8	2	0	0	1470.77	274	286
SNW domain-containing protein 1	SNW1	SNW1_HUMAN	61.5	100.0%	6	6	11	0.01%	11.6%	IKYDAIAR	99.3%	35.8	25	29.5	2	0	0	949.55	96	103
SNW domain-containing protein 1	SNW1	SNW1_HUMAN	61.5	100.0%	6	6	11	0.01%	11.6%	LAEALYIADR	99.7%	78.6	25	75.5	2	0	0	1134.62	287	296
SNW domain-containing protein 1	SNW1	SNW1_HUMAN	61.5	100.0%	6	6	11	0.01%	11.6%	LAPAQYIR	98.3%	32.3	25	9.68	2	0	0	931.54	171	178
SNW domain-containing protein 1	SNW1	SNW1_HUMAN	61.5	100.0%	6	6	11	0.01%	11.6%	VAAAMPVR	99.4%	36.9	25	33.2	2	0	0	814.46	159	166
SNW domain-containing protein 1	SNW1	SNW1_HUMAN	61.5	100.0%	6	6	11	0.01%	11.6%	YTPSQQGVAFNSGAK	99.7%	68.6	25	65.4	1	0	0	1554.75	179	193
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.07%	29.9%	ADIGVAMGIAGSDVSK	99.7%	111	25	110	5	0	0	1490.75	728	743
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.07%	29.9%	AVAGDASESALLK	99.7%	105	25	97.7	6	0	0	1231.65	446	458
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.07%	29.9%	AVFQANQENLPILK	99.7%	90.1	25	76.3	4	0	0	1584.87	431	444
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.07%	29.9%	CIELCCGSVK	99.7%	50.8	25	35.2	2	0	0	1225.54	459	468
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.07%	29.9%	DGPNALTPPPTTPEWIK	99.7%	46.3	25	44.9	2	0	0	1833.94	75	91
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.07%	29.9%	GIVVYTGDR	99.7%	57.4	25	55.3	3	0	0	979.52	256	264

Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.07%	29.9%	GVGIISEGNETVEDIAAR	99.7%	110	25	105	2	0	0	1829.92	630	647
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.07%	29.9%	IVEIPFNSTNK	99.7%	47.2	25	45.9	2	0	0	1261.68	477	487
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.07%	29.9%	LIFDNLKK	99.5%	37.3	25	26.5	1	0	0	990.60	767	774
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.07%	29.9%	LIIVEGCQR	99.7%	55.3	25	48.2	5	0	0	1087.59	699	707
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.07%	29.9%	LNIPVSQVNPR	99.7%	57.1	25	50.7	5	0	0	1236.71	648	658
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.07%	29.9%	LSLDELHR	99.7%	55	25	48.6	2	0	0	982.53	46	53
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.07%	29.9%	MSINAEEVVVGDLVEVK	99.7%	75.5	25	70.1	2	0	0	1846.95	178	194
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.07%	29.9%	NIAFFSTNCVEGTAR	99.7%	95	25	94	2	0	0	1686.79	241	255
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.07%	29.9%	NLEAVETLGSTSTICSDK	99.7%	82.4	25	82.4	2	0	0	1924.92	360	377
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.07%	29.9%	NMVPQQALVIR	99.7%	41.9	25	41.9	4	0	0	1268.71	163	173
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.07%	29.9%	NPNTSEPQHLLVMK	99.7%	69.2	25	59.8	4	0	0	1607.82	495	508
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.07%	29.9%	QGAIVAVTGDGVNDSPALK	99.7%	111	25	109	2	0	0	1811.95	708	726
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.07%	29.9%	QGAIVAVTGDGVNDSPALKK	99.7%	57.3	25	57.3	0	1	0	1940.05	708	727
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.07%	29.9%	SPDFTNENPLETR	99.7%	96.1	25	89.7	4	0	0	1519.70	228	240
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.07%	29.9%	TSATWLALSR	99.7%	83.7	25	70.3	2	0	0	1105.60	414	423
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.07%	29.9%	VDNSSLTGESEPQTR	99.7%	85.4	25	74.1	3	0	0	1619.75	213	227
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.07%	29.9%	VIMVTGDHPITAK	99.7%	78.6	25	76.9	5	1	0	1381.75	613	625
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.07%	29.9%	YGTDLSR	99.3%	35.9	25	23.5	2	0	0	811.39	55	61
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	AT1A1_HUMAN	112.9	100.0%	25	31	75	0.07%	29.9%	YHTEIVFAR	99.7%	45.5	25	33.4	2	0	0	1135.59	684	692
Solute carrier family 2, facilitated glucose transporter member 1	SLC2A1	GTR1_HUMAN	54.1	99.8%	2	2	3	0.00%	3.7%	TFDEIASGFR	99.7%	58.9	25	46.9	1	0	0	1142.55	459	468
Solute carrier family 2, facilitated glucose transporter member 1	SLC2A1	GTR1_HUMAN	54.1	99.8%	2	2	3	0.00%	3.7%	VTILELFR	99.7%	50.2	25	42.3	2	0	0	990.60	257	264
Sorting and assembly machinery component 50 homolog	SAMM50	SAM50_HUMAN	52.0	100.0%	6	6	10	0.01%	14.9%	ICDGVQFGAGIR	99.7%	62.3	25	58.4	2	0	0	1292.64	456	467
Sorting and assembly machinery component 50 homolog	SAMM50	SAM50_HUMAN	52.0	100.0%	6	6	10	0.01%	14.9%	SSLSHAMVIDSR	99.7%	56.4	25	44	2	0	0	1302.65	256	267
Sorting and assembly machinery component 50 homolog	SAMM50	SAM50_HUMAN	52.0	100.0%	6	6	10	0.01%	14.9%	TKDDIIICEIGDVFK	99.7%	98.5	25	92.8	2	0	0	1765.90	58	72
Sorting and assembly machinery component 50 homolog	SAMM50	SAM50_HUMAN	52.0	100.0%	6	6	10	0.01%	14.9%	VTFQFSYGTK	99.3%	36.4	25	36.4	1	0	0	1177.59	159	168
Sorting and assembly machinery component 50 homolog	SAMM50	SAM50_HUMAN	52.0	100.0%	6	6	10	0.01%	14.9%	VTGQFPWSSLR	99.6%	38.5	25	34.8	2	0	0	1277.66	195	205
Sorting and assembly machinery component 50 homolog	SAMM50	SAM50_HUMAN	52.0	100.0%	6	6	10	0.01%	14.9%	WSYGAGIVLR	99.5%	38.1	25	25.7	1	0	0	1121.61	424	433
Sorting nexin-2	SNX2	SNX2_HUMAN	58.5	100.0%	3	3	5	0.00%	6.7%	AVNTQALSGAGILR	99.5%	38	25	25.1	1	0	0	1370.78	270	283
Sorting nexin-2	SNX2	SNX2_HUMAN	58.5	100.0%	3	3	5	0.00%	6.7%	ELSANTAAFAK	99.7%	65.6	25	55.5	2	0	0	1122.58	336	346
Sorting nexin-2	SNX2	SNX2_HUMAN	58.5	100.0%	3	3	5	0.00%	6.7%	QFLESSELPR	99.7%	44.8	25	22.6	2	0	0	1205.62	260	269
Sorting nexin-9	SNX9	SNX9_HUMAN	66.6	99.8%	2	2	2	0.00%	3.7%	FGSAIPIPSLPDK	98.0%	31.5	25	23.1	1	0	0	1341.74	301	313
Sorting nexin-9	SNX9	SNX9_HUMAN	66.6	99.8%	2	2	2	0.00%	3.7%	IYDYNSVIR	99.7%	40.7	25	35.9	1	0	0	1142.58	560	568
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	4	4	4	0.00%	2.5%	ALVADSHPESER	99.0%	34.4	25	33.5	1	0	0	1310.63	1657	1668
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	4	4	4	0.00%	2.5%	GNLEVLLFTIQSK	99.7%	44.3	25	44.3	1	0	0	1461.83	360	372
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	4	4	4	0.00%	2.5%	LQQFLR	97.6%	30.8	25	0	1	0	0	804.47	1064	1069
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	4	4	4	0.00%	2.5%	LVSQDNFGFDLPAVEAATK	99.5%	38.1	25	38.1	1	0	0	2022.02	444	462
Spectrin beta chain, non-erythrocytic 1	SPTBN1	SPTB2_HUMAN	274.6	100.0%	4	4	4	0.00%	2.5%	VLDNAIETEK	99.0%	34.5	25	31	1	0	0	1131.59	293	302
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	15	17	27	0.03%	32.0%	AIDLMNALMR	99.7%	60.3	25	56.2	3	0	0	1179.59	385	394
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	15	17	27	0.03%	32.0%	ASAALAALEK	99.7%	79.8	25	59.1	2	0	0	944.54	564	573
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	15	17	27	0.03%	32.0%	DKPTETLLNTVK	99.7%	43.6	25	34.6	1	0	0	1358.75	111	122
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	15	17	27	0.03%	32.0%	DNLPIQIQK	99.7%	42.7	25	36.7	2	0	0	1068.61	123	131
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	15	17	27	0.03%	32.0%	FPTYPVPHYSFF	99.7%	53.1	25	53.1	2	0	0	1501.72	661	672
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	15	17	27	0.03%	32.0%	FVMEVEVDGQK	99.7%	69.9	25	68.9	12	0	0	1296.61	541	551
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	15	17	27	0.03%	32.0%	GWPLELICEK	99.7%	70.1	25	0	11	0	0	1244.63	240	249
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	15	17	27	0.03%	32.0%	HVSDWLDETNKGTK	99.6%	33	25	33	0	1	0	1629.79	44	57
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	15	17	27	0.03%	32.0%	LFSGPNAANNK	99.7%	60.4	25	41.9	2	0	0	1132.57	574	584
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	15	17	27	0.03%	32.0%	LFSGPNAANNKK	98.7%	33.2	25	19.1	1	0	0	1260.67	574	585
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	15	17	27	0.03%	32.0%	LNQIRPGLQYK	99.7%	45	25	45	2	2	0	1329.76	395	405
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	15	17	27	0.03%	32.0%	LSAFGQIYK	99.7%	45.9	25	41.5	2	0	0	1026.56	316	324
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	15	17	27	0.03%	32.0%	NPVMELNEK	99.7%	50.3	25	43.9	10	0	0	1073.53	513	521
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	15	17	27	0.03%	32.0%	NPVMELNEKR	99.7%	54	25	43	3	0	0	1229.63	513	522

Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	15	17	27	0.03%	32.0%	NTKEPTLTLK	99.0%	34.5	25	20.8	2	0	0	1144.66	152	161
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	15	17	27	0.03%	32.0%	SCVIVLR	99.7%	46.9	25	0	2	0	0	846.49	217	223
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	15	17	27	0.03%	32.0%	SFANDDRHVMVK	98.5%	27.4	25	24.8	0	1	0	1418.68	6	17
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	15	17	27	0.03%	32.0%	SIGTCNRPLGAGEALR	98.9%	28.7	25	26	0	1	0	1671.86	250	265
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	15	17	27	0.03%	32.0%	TQGPILTASGK	99.1%	35.2	25	30.2	2	0	0	1072.60	502	512
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	15	17	27	0.03%	32.0%	VLEMDPLPSSKPFQK	99.7%	33.4	25	32	0	1	0	1731.90	325	339
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	15	17	27	0.03%	32.0%	YELISETGGSHDK	99.7%	67.8	25	51.9	2	0	0	1435.67	527	539
Spermatid perinuclear RNA-binding protein	STRBP	STRBP_HUMAN	73.7	100.0%	15	17	27	0.03%	32.0%	YELISETGGSHDKR	99.7%	72.6	25	68.8	6	2	0	1591.77	527	540
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	6	6	10	0.01%	17.5%	AAFVLPEFAR	99.5%	37.2	25	32.3	2	0	0	1120.61	286	295
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	6	6	10	0.01%	17.5%	FLPGMAIGYSSSK	99.7%	52.9	25	31.6	1	0	0	1357.68	136	148
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	6	6	10	0.01%	17.5%	KVLIIGGGDGGVLR	99.7%	39.3	25	39.3	0	1	0	1353.82	96	109
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	6	6	10	0.01%	17.5%	VLIIGGGDGGVLR	99.7%	51.8	25	48.6	2	0	0	1225.73	97	109
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	6	6	10	0.01%	17.5%	YQDILVFR	99.7%	59.9	25	53.7	2	0	0	1053.57	48	55
Spermidine synthase	SRM	SPEE_HUMAN	33.8	100.0%	6	6	10	0.01%	17.5%	YYNSDVHR	99.3%	36.2	25	36.2	2	0	0	1053.47	278	285
S-phase kinase-associated protein 1	SKP1	SKP1_HUMAN	18.7	99.9%	2	2	3	0.00%	12.9%	GLLDVTCK	99.1%	35.2	25	31.1	2	0	0	905.48	114	121
S-phase kinase-associated protein 1	SKP1	SKP1_HUMAN	18.7	99.9%	2	2	3	0.00%	12.9%	TDDIPVWDQEFLK	97.3%	30.3	25	28.5	1	0	0	1605.78	82	94
Sphingosine-1-phosphate lyase 1	SGPL1	SGPL1_HUMAN	63.5	100.0%	3	3	3	0.00%	7.2%	AFEPYLEILEVYSTK	99.7%	76.1	25	71.8	1	0	0	1801.93	11	25
Sphingosine-1-phosphate lyase 1	SGPL1	SGPL1_HUMAN	63.5	100.0%	3	3	3	0.00%	7.2%	GIFVFGNPQLSVIALGSR	99.7%	64.9	25	64.9	1	0	0	1875.05	439	456
Sphingosine-1-phosphate lyase 1	SGPL1	SGPL1_HUMAN	63.5	100.0%	3	3	3	0.00%	7.2%	KIEAEIVR	98.6%	33	25	16.2	1	0	0	957.57	183	190
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	3	4	13	0.01%	15.3%	GTVLDQVPVNPSLYLIK	99.7%	58.8	25	47.2	4	0	0	1856.05	74	90
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	3	4	13	0.01%	15.3%	SSVGPSKPVSQPR	99.7%	37.7	25	30.3	3	4	0	1325.72	38	50
Spindlin-1	SPIN1	SPIN1_HUMAN	29.6	100.0%	3	4	13	0.01%	15.3%	VSALEVLPDR	99.7%	82.8	25	69.8	2	0	0	1098.62	108	117
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	19	22	43	0.04%	16.7%	AIVNVIGMHK	99.7%	42.4	25	42.4	4	0	0	1097.61	999	1008
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	19	22	43	0.04%	16.7%	ATVNTFGYIAK	99.7%	78.6	25	73.7	2	0	0	1184.63	1076	1086
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	19	22	43	0.04%	16.7%	EIISNLAK	99.7%	42	25	21.2	2	0	0	887.52	595	602
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	19	22	43	0.04%	16.7%	EVMLILIR	99.7%	57.8	25	37.2	3	0	0	986.61	768	775
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	19	22	43	0.04%	16.7%	GDTPGHATPGHGGATSSAR	99.7%	60.8	25	60.8	0	2	0	1733.80	271	289
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	19	22	43	0.04%	16.7%	GGDSIGETPTPGASK	99.7%	65.6	25	65.1	2	0	0	1373.65	319	333
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	19	22	43	0.04%	16.7%	ICFELLELLK	97.3%	30.3	25	20.1	1	0	0	1277.72	1058	1067
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	19	22	43	0.04%	16.7%	IYNDDKNTYIR	99.7%	55	25	50.9	2	2	0	1414.70	1287	1297
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	19	22	43	0.04%	16.7%	LLVDVDESTLSPEEQKER	99.7%	54.4	25	47.6	0	2	0	2087.05	478	495
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	19	22	43	0.04%	16.7%	QLVDTTVELANK	99.7%	93.4	25	90.9	2	0	0	1330.72	832	843
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	19	22	43	0.04%	16.7%	QQAADLISR	99.6%	38.7	25	24.7	2	0	0	1001.54	949	957
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	19	22	43	0.04%	16.7%	TEILPPFFK	99.1%	35.2	25	25	3	0	0	1091.61	808	816
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	19	22	43	0.04%	16.7%	THEDIEAQIR	99.7%	50.7	25	44.7	2	0	0	1211.60	7	16
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	19	22	43	0.04%	16.7%	TMIISPER	99.7%	45.8	25	33.2	2	0	0	962.50	125	132
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	19	22	43	0.04%	16.7%	VGAAEIISR	99.7%	81.3	25	42.4	2	0	0	915.53	844	852
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	19	22	43	0.04%	16.7%	VPELNVQNGVLK	99.7%	74.8	25	68.7	2	0	0	1309.75	1138	1149
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	19	22	43	0.04%	16.7%	VQENCIDLVGR	99.7%	61.9	25	56.5	2	0	0	1302.65	1031	1041
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	19	22	43	0.04%	16.7%	VVNGAAASQPPSKR	99.7%	45	25	39.1	2	0	0	1381.75	183	196
Splicing factor 3B subunit 1	SF3B1	SF3B1_HUMAN	145.8	100.0%	19	22	43	0.04%	16.7%	WDQTADQTPGATPK	99.7%	58.5	25	51.6	2	0	0	1515.71	200	213
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	10	11	16	0.02%	12.1%	AAVLLEQER	99.7%	53.4	25	46.2	2	0	0	1028.57	184	192
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	10	11	16	0.02%	12.1%	FTVAELK	97.7%	31	25	19.7	1	0	0	807.46	460	466
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	10	11	16	0.02%	12.1%	GPPPPPGDENR	97.0%	29.9	25	29.1	1	0	0	1132.54	248	258
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	10	11	16	0.02%	12.1%	ISLGMPVGPNAHK	99.7%	45.6	25	33.6	2	1	0	1320.71	615	627
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	10	11	16	0.02%	12.1%	KPGDLSDELR	99.7%	54.2	25	41.9	2	0	0	1129.59	605	614
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	10	11	16	0.02%	12.1%	LAEIGAPIQGNR	99.7%	49.5	25	47.6	2	0	0	1238.69	36	47
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	10	11	16	0.02%	12.1%	LAQQQAALLMQQEER	99.7%	100	25	99.4	1	0	0	1756.90	149	163
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	10	11	16	0.02%	12.1%	TEEEEIDR	94.9%	27.9	25	16.3	1	0	0	1020.45	698	705
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	10	11	16	0.02%	12.1%	VGEPVALSEEER	99.7%	76	25	67.1	2	0	0	1314.65	135	146
Splicing factor 3B subunit 2	SF3B2	SF3B2_HUMAN	100.2	100.0%	10	11	16	0.02%	12.1%	YGPPPSYPNLK	95.2%	28.1	25	25.4	1	0	0	1232.63	639	649

Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	15	15	32	0.03%	15.4%	DYIVVGSDSGR	99.7%	61.7	25	53.7	1	0	0	1167.56	76	86
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	15	15	32	0.03%	15.4%	FGNICVVR	99.7%	56.7	25	47	2	0	0	964.50	1050	1057
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	15	15	32	0.03%	15.4%	FLAVGLVDNTVR	99.7%	73.2	25	61.9	3	0	0	1303.74	604	615
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	15	15	32	0.03%	15.4%	FSNTGEDWYVLVGVAK	99.7%	70.9	25	63	2	0	0	1784.89	896	911
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	15	15	32	0.03%	15.4%	IVILEYQPSK	99.7%	60.9	25	56.1	4	0	0	1189.68	87	96
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	15	15	32	0.03%	15.4%	LGAVFNQVAFPLQYTPR	99.7%	83.6	25	83.6	4	0	0	1921.03	770	786
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	15	15	32	0.03%	15.4%	MFLYNLTLQR	99.7%	61.1	25	59.1	2	0	0	1298.69	1	10
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	15	15	32	0.03%	15.4%	MQGQEAVLAMSSR	99.7%	74.5	25	74.5	1	0	0	1407.67	706	718
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	15	15	32	0.03%	15.4%	NENQLIIFADDTYPR	99.7%	52	25	52	1	0	0	1808.88	1017	1031
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	15	15	32	0.03%	15.4%	NFGDQPDIR	99.7%	49.9	25	41.4	2	0	0	1061.50	260	268
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	15	15	32	0.03%	15.4%	SVAGGFVYTYK	99.7%	68.6	25	58.5	3	0	0	1191.60	919	929
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	15	15	32	0.03%	15.4%	SWLSYSYQSR	99.7%	40.6	25	37.5	1	0	0	1276.60	719	728
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	15	15	32	0.03%	15.4%	TPVEEVPAAIAPFQGR	99.7%	75.3	25	67.3	2	0	0	1681.89	943	958
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	15	15	32	0.03%	15.4%	TVLDPVTGDLSDTR	99.7%	89.7	25	84.8	3	0	0	1488.75	677	690
Splicing factor 3B subunit 3	SF3B3	SF3B3_HUMAN	135.6	100.0%	15	15	32	0.03%	15.4%	YFDTVPVAAAMCVLK	99.7%	46.9	25	46.9	1	0	0	1684.84	329	343
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	6	6	11	0.01%	31.7%	AVIDLNNR	99.7%	52.6	25	35.3	2	0	0	914.51	126	133
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	6	6	11	0.01%	31.7%	GGFCNFMHLKPISR	97.1%	24.9	25	24.9	0	1	0	1679.81	166	179
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	6	6	11	0.01%	31.7%	NPQNSSQSADGLR	99.7%	83.2	25	83.2	2	0	0	1373.64	54	66
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	6	6	11	0.01%	31.7%	QYEMGECTR	99.7%	47.5	25	35.5	2	0	0	1173.47	157	165
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	6	6	11	0.01%	31.7%	VNCSFYFK	99.7%	53	25	53	2	0	0	1064.49	16	23
Splicing factor U2AF 35 kDa subunit	U2AF1	U2AF1_HUMAN	27.9	100.0%	6	6	11	0.01%	31.7%	YGEVEEMNVCDNLGDHLVGNVYVK	99.7%	59.5	25	59.5	0	2	0	2769.25	93	116
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	10	16	32	0.03%	28.6%	AMQGLTGR	99.7%	61.9	25	44	2	0	0	833.43	445	452
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	10	16	32	0.03%	28.6%	ELLTSFGPLK	99.7%	47.1	25	38	2	0	0	1104.63	277	286
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	10	16	32	0.03%	28.6%	GAKEEHGGLIR	99.7%	62.1	25	48.8	2	0	0	1166.63	68	78
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	10	16	32	0.03%	28.6%	IFVEFTSVFDCQK	99.7%	96	25	96	2	0	0	1619.78	432	444
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	10	16	32	0.03%	28.6%	LFIGGLPNYLNDDQVK	99.7%	78.6	25	60	2	0	0	1805.94	261	276
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	10	16	32	0.03%	28.6%	LGGLTQAPGNPVLAVQINQDK	99.7%	70.2	25	70	2	2	0	2133.17	175	195
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	10	16	32	0.03%	28.6%	NFAFLEFR	99.7%	52.6	25	44.7	2	0	0	1043.53	196	203
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	10	16	32	0.03%	28.6%	SIEIPRPVDGVEVPGCGK	99.7%	58	25	58	2	2	0	1908.99	414	431
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	10	16	32	0.03%	28.6%	SVDETTQAMAFDGIIFQGQSLK	99.7%	121	25	114	4	4	0	2386.16	204	225
Splicing factor U2AF 65 kDa subunit	U2AF2	U2AF2_HUMAN	53.5	100.0%	10	16	32	0.03%	28.6%	YCDPDSYHR	99.7%	48.7	25	48.7	2	2	0	1212.47	463	471
Splicing factor, arginine/serine-rich 15	SCAF4	SFR15_HUMAN	125.9	100.0%	3	3	5	0.00%	4.2%	DLSIGNPIPTVVSGAR	99.7%	44.4	25	44.4	2	0	0	1595.88	778	793
Splicing factor, arginine/serine-rich 15	SCAF4	SFR15_HUMAN	125.9	100.0%	3	3	5	0.00%	4.2%	TVEPPISQVGNVDTASELEK	99.7%	61.7	25	56.1	1	0	0	2113.07	1092	1111
Splicing factor, arginine/serine-rich 15	SCAF4	SFR15_HUMAN	125.9	100.0%	3	3	5	0.00%	4.2%	VPGLYVIDSIVR	99.7%	58.8	25	50.3	2	0	0	1330.77	60	71
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	5	5	7	0.01%	10.7%	AVVIVDDR	99.7%	39.8	25	28.1	4	0	0	886.50	400	407
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	5	5	7	0.01%	10.7%	FAQHGTFEYEYSQR	99.0%	29.1	25	29.1	0	1	0	1762.78	480	493
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	5	5	7	0.01%	10.7%	FATHAAALSVR	99.7%	68.6	25	59.9	1	0	0	1143.63	366	376
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	5	5	7	0.01%	10.7%	FGQGGAGPVGGQGPR	99.7%	61.3	25	60	2	0	0	1341.67	667	681
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	5	5	7	0.01%	10.7%	LFVGNLPADITEDEFKR	99.7%	64.6	25	62.1	0	2	0	1964.01	299	315
Splicing factor, proline- and glutamine-rich	SFPQ	SFPQ_HUMAN	76.1	100.0%	5	5	7	0.01%	10.7%	YGEPGEVFINK	97.9%	31.4	25	28.7	1	0	0	1252.62	320	330
SRA stem-loop-interacting RNA-binding protein, mitochondrial	SLIRP	SLIRP_HUMAN	12.3	99.8%	2	2	3	0.00%	25.7%	GLGWVQFSSEEGLR	99.1%	35.1	25	35.1	1	0	0	1564.78	61	74
SRA stem-loop-interacting RNA-binding protein, mitochondrial	SLIRP	SLIRP_HUMAN	12.3	99.8%	2	2	3	0.00%	25.7%	NALQQENHIIDGVK	99.7%	61.3	25	55.3	2	0	0	1578.82	75	88
SRSF protein kinase 1	SRPK1	SRPK1_HUMAN	74.3	100.0%	5	5	10	0.01%	8.9%	EMVVQLLDDFK	99.7%	53	25	47.5	2	0	0	1336.68	142	152
SRSF protein kinase 1	SRPK1	SRPK1_HUMAN	74.3	100.0%	5	5	10	0.01%	8.9%	HFTEDIQTR	99.3%	36.3	25	24	3	0	0	1146.55	507	515
SRSF protein kinase 1	SRPK1	SRPK1_HUMAN	74.3	100.0%	5	5	10	0.01%	8.9%	LAAEATEWQR	99.7%	72.9	25	60.3	2	0	0	1174.59	231	240
SRSF protein kinase 1	SRPK1	SRPK1_HUMAN	74.3	100.0%	5	5	10	0.01%	8.9%	SAEHYTETALDEIR	99.7%	55.9	25	48.8	1	0	0	1634.77	113	126
SRSF protein kinase 1	SRPK1	SRPK1_HUMAN	74.3	100.0%	5	5	10	0.01%	8.9%	STAGNFLVNPLEPK	99.7%	44.7	25	37.8	2	0	0	1486.79	473	486
SRSF protein kinase 2	SRPK2	SRPK2_HUMAN	77.5	99.8%	2	2	3	0.00%	4.8%	AADLLVNPLDPR	99.7%	45	25	43.3	2	0	0	1293.72	508	519
SRSF protein kinase 2	SRPK2	SRPK2_HUMAN	77.5	99.8%	2	2	3	0.00%	4.8%	HFTEDIQTR	99.3%	36.3	25	24	3	0	0	1146.55	540	548
SRSF protein kinase 2	SRPK2	SRPK2_HUMAN	77.5	99.8%	2	2	3	0.00%	4.8%	TVSASSTGDLPK	99.7%	48.6	25	36.8	1	0	0	1162.60	492	503
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	4	4	8	0.01%	16.3%	AEQINQAAGEASAVLAK	99.7%	97.8	25	95.7	2	0	0	1670.87	234	250

Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	4	4	8	0.01%	16.3%	APVPGTPDSLSSGSSR	99.7%	52.5	25	49.8	2	0	0	1514.74	322	337
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	4	4	8	0.01%	16.3%	ATVLESEGTR	99.7%	67.5	25	47.9	2	0	0	1062.54	202	211
Stomatin-like protein 2, mitochondrial	STOML2	STML2_HUMAN	38.5	100.0%	4	4	8	0.01%	16.3%	DVQGTDASLDEELDR	99.7%	48.4	25	44.4	2	0	0	1662.75	338	352
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	19	23	50	0.05%	39.3%	AQFEGIVTDLIR	99.7%	86.6	25	85.7	4	0	0	1361.74	349	360
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	19	23	50	0.05%	39.3%	ASNGDAWVEAHGK	99.7%	67.2	25	67.2	2	0	0	1341.62	147	159
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	19	23	50	0.05%	39.3%	DAGQISGLNVLR	99.7%	81.8	25	67.3	3	0	0	1242.68	207	218
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	19	23	50	0.05%	39.3%	EQQIVIQSSGGLSKDDIENMVK	99.7%	58.1	25	58.1	0	2	0	2418.22	542	563
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	19	23	50	0.05%	39.3%	ETGVDLTKDNMALQR	99.7%	47.8	25	46	1	0	0	1706.84	293	307
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	19	23	50	0.05%	39.3%	LLGQFTLIGIPPAPR	99.7%	61.5	25	61.5	4	0	0	1592.95	499	513
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	19	23	50	0.05%	39.3%	LYSPSQIGAFVLMK	99.7%	64.2	25	64.2	2	1	0	1569.83	160	173
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	19	23	50	0.05%	39.3%	MKETAENYLGHTAK	99.7%	78.2	25	67.8	1	1	0	1592.77	174	187
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	19	23	50	0.05%	39.3%	NAVITVPAYFNDSQR	99.7%	67.5	25	67.5	2	0	0	1694.85	188	202
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	19	23	50	0.05%	39.3%	QAASSLQQASLK	99.7%	72.5	25	66.9	4	0	0	1231.66	635	646
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	19	23	50	0.05%	39.3%	QAVTNPNNTFYATK	99.7%	90.3	25	83.3	2	0	0	1568.77	108	121
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	19	23	50	0.05%	39.3%	RYDDPEVQK	99.7%	45.3	25	33.2	2	0	0	1149.55	127	135
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	19	23	50	0.05%	39.3%	SDIGEVILVGGMTR	99.7%	77.9	25	74.2	4	0	0	1446.76	378	391
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	19	23	50	0.05%	39.3%	SQVFSTAADGQTQVEIK	99.7%	117	25	115	2	0	0	1808.90	469	485
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	19	23	50	0.05%	39.3%	STNGDTFLGGEDFDQALLR	99.7%	115	25	111	2	0	0	2055.96	266	284
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	19	23	50	0.05%	39.3%	TTPSVVAFTADGER	99.7%	105	25	104	4	0	0	1450.72	86	99
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	19	23	50	0.05%	39.3%	VINEPTAAALAYGLDK	99.7%	106	25	103	3	0	0	1645.88	219	234
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	19	23	50	0.05%	39.3%	VLENAEGAR	99.7%	64.7	25	45.8	2	0	0	958.50	77	85
Stress-70 protein, mitochondrial	HSPA9	GRP75_HUMAN	73.7	100.0%	19	23	50	0.05%	39.3%	VQQTVQDLFGR	99.7%	74.9	25	67.5	2	0	0	1290.68	395	405
Striatin-interacting protein 1	STRIP1	STRP1_HUMAN	95.6	100.0%	5	5	6	0.01%	6.8%	EVFSKPISWEELLQ	97.4%	30.5	25	26.4	1	0	0	1704.88	824	837
Striatin-interacting protein 1	STRIP1	STRP1_HUMAN	95.6	100.0%	5	5	6	0.01%	6.8%	FFNQNIMSYITAK	99.7%	65	25	65	1	0	0	1576.78	616	628
Striatin-interacting protein 1	STRIP1	STRP1_HUMAN	95.6	100.0%	5	5	6	0.01%	6.8%	ILLAAAPTSK	99.7%	49.5	25	39	2	0	0	984.61	527	536
Striatin-interacting protein 1	STRIP1	STRP1_HUMAN	95.6	100.0%	5	5	6	0.01%	6.8%	LLDGLEVTAR	99.7%	72.4	25	56	1	0	0	1086.62	129	138
Striatin-interacting protein 1	STRIP1	STRP1_HUMAN	95.6	100.0%	5	5	6	0.01%	6.8%	NLFSCINLLR	94.8%	27.8	25	18.2	1	0	0	1249.67	664	673
Stromal cell-derived factor 2-like protein 1	SDF2L1	SDF2L_HUMAN	23.6	99.9%	2	2	2	0.00%	16.7%	TGAELVTCGSVLK	99.7%	50.3	25	36.6	1	0	0	1334.70	31	43
Stromal cell-derived factor 2-like protein 1	SDF2L1	SDF2L_HUMAN	23.6	99.9%	2	2	2	0.00%	16.7%	YGSGSGQQSVTGVEASDDANSYWR	99.7%	87.7	25	87.7	1	0	0	2521.09	60	83
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	AATLAQELEK	99.7%	45.2	25	25.4	1	0	0	1073.58	386	395
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	ADQDRLDLEER	99.0%	34.5	25	27.5	2	1	0	1359.65	402	412
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	AEEDTQFNYHR	99.7%	56.4	25	48	1	0	0	1409.61	178	188
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	AFVSMVYSEEGAEDR	99.7%	99.6	25	91.8	2	0	0	1689.74	78	92
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	DCIQYIK	99.0%	34.3	25	0.09	1	0	0	939.46	555	561
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	DKFQETSDEFEAAR	99.7%	66	25	66	1	1	0	1672.75	1036	1049
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	DLIHGAPVGKPAANR	99.6%	33.2	25	33.2	0	2	0	1515.84	63	77
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	DLTLEENQVK	99.7%	71.2	25	51.1	2	0	0	1188.61	364	373
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	DLTLEENQVKK	97.3%	30.4	25	24.1	1	0	0	1316.71	364	374
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	ELNQVMEQLGDAR	99.7%	67.2	25	67.2	2	0	0	1502.73	476	488
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	HLALNLQEK	99.1%	34.8	25	28.7	2	0	0	1065.61	726	734
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	IIDETMAQLQDLK	99.7%	84	25	75.4	4	0	0	1533.78	862	874
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	LEEYITTSK	99.7%	41.9	25	41.1	2	0	0	1083.56	438	446
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	LGIQLDFEK	99.7%	46.9	25	36.3	2	0	0	1062.58	817	825
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	LIEIENFK	96.6%	29.5	25	7.67	1	0	0	1005.56	6	13
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	LNEQQSVLQR	99.7%	73.8	25	54.4	2	0	0	1214.65	1010	1019
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	LTEELKEQMK	99.7%	44.4	25	37.4	2	0	0	1248.65	681	690
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	LYHNEVEIEK	99.7%	49	25	42.7	2	1	0	1273.64	228	237
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	NMDAIIVDSEK	99.7%	50.5	25	41.8	2	0	0	1250.59	541	551
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	QIIGPFQR	98.2%	31.9	25	10.4	2	0	0	958.55	19	26
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	SGELAQEYDKR	99.7%	56.8	25	50.5	2	0	0	1295.62	161	171
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	SGVISGGASDLK	99.7%	53.9	25	33.4	2	0	0	1090.57	649	660

Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	SNLMDAISFVLGEK	99.7%	68.1	25	68.1	2	0	0	1539.77	39	52
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	TALFEEISR	99.7%	66.5	25	60.6	2	0	0	1065.56	152	160
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	TVALDGTLFQK	99.7%	56.3	25	31.1	2	0	0	1192.66	638	648
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	VLTFDLTKYPDANPNPNEQ	99.7%	45.5	25	45.2	2	0	0	2176.06	1215	1233
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	VVQLHEYSEELEK	99.7%	68.2	25	68.2	1	0	0	1602.80	111	123
Structural maintenance of chromosomes protein 1A	SMC1A	SMC1A_HUMAN	143.2	100.0%	28	32	54	0.05%	24.6%	YSQSDLEQTK	99.7%	66.2	25	58.7	2	0	0	1198.56	714	723
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	ALEEELAGLK	99.7%	63.3	27.2	53.1	1	0	0	1072.59	697	706
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	ALNHEIEELEK	99.7%	45.2	25	39.9	2	1	0	1324.67	276	286
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	AMNVLTEAEER	99.7%	54.9	25	42.8	3	0	0	1278.60	987	997
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	ASNLQDLVYK	99.7%	40.2	25	33	1	0	0	1150.61	59	68
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	ASVSITFDNSDKK	99.7%	44.1	25	33.2	2	0	0	1411.71	77	89
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	DQEALEAVKR	99.0%	34.6	25	24.7	2	0	0	1158.61	447	456
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	DTSATTALELVAGER	99.7%	102	25	89.1	2	0	0	1533.78	534	548
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	ENLTELSGGQR	99.7%	82	25	71.7	2	0	0	1203.60	1080	1090
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	EVITAQDTVIK	99.7%	52.8	25	49.2	2	0	0	1216.68	880	890
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	FQELKDVQDELR	99.7%	49.8	25	38.7	2	0	0	1519.78	678	689
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	FVDGVSTVAR	99.7%	84.2	25	71.2	2	0	0	1050.56	1161	1170
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	GLVASLISVK	99.7%	61.8	25	59.2	2	0	0	986.62	524	533
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	HLFGQPNSAYDFK	99.7%	55.3	25	53.2	2	0	0	1523.73	946	958
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	IKELDHNISK	99.7%	40	25	27.4	2	0	0	1196.66	910	919
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	ILTTIEDLDQKK	99.7%	60.1	25	39.9	2	0	0	1416.79	1015	1026
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	LKETYEALLAR	99.7%	60.6	25	52.2	2	0	0	1306.74	492	502
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	LQEELSENDKK	99.7%	51	25	40.8	2	0	0	1332.66	263	273
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	LYNVVVDTEVTGK	99.7%	97.6	25	89.1	2	0	0	1436.76	549	561
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	QQLEAVNEAIK	99.0%	34.5	25	32.6	2	0	0	1242.67	838	848
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	SAEELKEMQDK	99.7%	42.9	25	37.6	2	0	0	1307.61	249	259
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	SIILEGFK	99.7%	44.3	25	44.3	2	0	0	906.53	5	12
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	SLEDALAEAQR	99.7%	84.6	25	72.9	2	0	0	1202.60	298	308
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	SQAASILTK	99.6%	39.1	25	26.4	2	0	0	918.53	669	677
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	SQSAFDLKK	96.0%	28.8	25	20.4	1	0	0	1023.55	313	321
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	SSYLEYQK	97.9%	31.3	25	28	1	0	0	1017.49	215	222
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	SYESQIEVMAAEVAK	99.7%	54.8	25	48.7	1	0	0	1670.79	849	863
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	TEEADLLQTK	99.7%	43.7	25	35.4	1	0	0	1147.58	723	732
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	TIEESEETLK	99.7%	50.5	25	36.3	2	0	0	1178.58	751	760
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	TILEEEITPTIQK	99.7%	71.6	25	62.7	2	0	0	1514.83	197	209
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	TVTLGGDVFDPHGTLSGGAR	99.7%	37.8	25	37.8	0	2	0	1956.98	649	668
Structural maintenance of chromosomes protein 2	SMC2	SMC2_HUMAN	135.7	100.0%	31	33	57	0.05%	29.3%	YLINGVNANNTR	99.7%	49.6	25	39.5	1	0	0	1348.70	115	126
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	AELGTDLLSQLSLEDQK	99.7%	66.5	25	64	2	0	0	1859.96	779	795
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	AILNGIDSINK	99.7%	39.8	25	37.6	2	0	0	1157.65	504	514
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	AKLDELSAK	98.6%	33	25	19.8	1	0	0	974.55	237	245
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	ALDQFVNFSEQK	99.7%	72.7	25	72.7	2	0	0	1425.70	986	997
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	ALEYTIYNQELNETR	99.7%	74.3	25	56	2	0	0	1856.90	222	236
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	DLEDTEANKEK	99.7%	55.1	25	50.1	2	0	0	1291.60	419	429
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	DQTIVDPFSSK	99.7%	50.9	25	21.4	2	0	0	1236.61	16	26
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	DTAYPETNDAIPMISK	99.7%	57	25	54.7	3	0	0	1765.83	597	612
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	EENAEQQALAAK	99.7%	77.6	25	70.6	2	0	0	1301.63	475	486
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	ELGSLPQEAFEK	99.7%	50.6	25	40.6	2	0	0	1347.68	945	956
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	GALTGGYYDTR	99.7%	54.2	25	48.2	2	0	0	1173.55	662	672
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	IKLEGIITR	96.5%	29.3	25	13.5	1	0	0	1042.66	819	827
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	ILMEFNK	98.0%	31.5	25	13.2	1	0	0	910.47	572	578
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	INQMATAPDSQR	99.7%	67.1	25	61.2	3	0	0	1331.64	144	155

Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	KAEEELGELEAK	99.7%	81.6	25	70.3	2	0	0	1345.68	684	695
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	KEESISLMK	99.0%	34.7	25	21.7	1	0	0	1064.57	172	180
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	KYEAIQLTFK	99.1%	34.8	25	30.6	1	0	0	1240.69	1025	1034
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	LALLHEGTGPR	99.7%	48.1	25	39.8	2	0	0	1163.65	62	72
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	MNLPGEVTFLPLNK	99.7%	73.6	25	65.7	4	0	0	1588.84	579	592
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	NDVMNLLESAGFSR	99.7%	96.9	25	96	4	0	0	1552.74	119	132
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	NFSEVFQK	98.8%	33.7	25	18.4	1	0	0	998.49	1039	1046
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	QVIIQGFR	99.7%	40.4	25	25.8	2	0	0	960.56	5	12
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	SEDLDNSIDKTEAGIK	99.7%	84.4	25	75.4	1	0	0	1734.84	880	895
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	SLDQAINDK	99.7%	40.7	25	30.8	2	0	0	1003.51	401	409
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	SMEVSTQLAR	99.7%	55.9	25	47.1	4	0	0	1121.56	635	644
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	VDALNDEIR	99.7%	54.2	25	28.6	1	0	0	1044.53	797	805
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	VETYLNENLR	99.7%	56.4	25	29.6	2	0	0	1250.64	828	837
Structural maintenance of chromosomes protein 3	SMC3	SMC3_HUMAN	141.5	100.0%	28	33	55	0.05%	26.1%	VSHIDVITAEMAK	99.7%	49.4	25	43.1	1	0	0	1413.74	1195	1207
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	AKEALIAASETLK	99.7%	64.2	25	60.8	1	0	0	1344.77	523	535
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	DNTSVYHISGK	99.1%	34.9	25	30.5	1	0	0	1220.59	192	202
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	DTLVADNLDQATR	99.7%	73.1	25	66.3	2	0	0	1431.71	714	726
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	ELEANVLATAPDK	99.7%	64.6	25	62.6	2	0	0	1370.72	841	853
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	FTASIQR	97.1%	30	25	20.2	2	0	0	822.45	821	827
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	FTQLDLEDVQVR	99.7%	96.8	25	83.8	2	0	0	1462.75	390	401
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	HNTAVSQLTK	99.7%	54.7	25	49.8	2	0	0	1098.59	513	522
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	IAEMETQKEK	99.7%	45.3	25	33	2	0	0	1206.60	334	343
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	IFNLSGGEK	99.7%	48	25	32.3	1	0	0	964.51	1188	1196
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	IHEDTKEINEK	99.7%	69.8	25	64.6	2	0	0	1355.68	344	354
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	LGDLGAIDEK	99.3%	36.2	25	29	1	0	0	1030.54	619	628
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	LHNTIVEINNHK	99.0%	28.8	25	28.8	0	1	0	1431.77	887	898
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	LLEENVSAFK	99.7%	61.8	25	50.3	2	0	0	1149.62	858	867
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	LMITHIVNQNFK	99.7%	52.8	25	38.5	1	0	0	1457.79	82	93
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	LTQEETNFK	99.7%	50.7	25	43.9	2	0	0	1109.55	565	573
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	NAQFIIISLR	99.7%	76.8	25	69.8	2	0	0	1174.69	1243	1252
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	NNMFEISDR	99.3%	35.8	25	27.5	1	0	0	1141.49	1253	1261
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	NTNAAEESLPEIQK	99.7%	92.2	25	88.8	2	0	0	1543.76	975	988
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	QAFYFALR	97.1%	30	25	14.9	2	0	0	1015.54	706	713
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	QLDECASAITK	99.7%	67.8	25	65.7	2	0	0	1235.59	912	922
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	QNIGVATFIGLDK	99.7%	64.3	25	54.7	2	0	0	1375.76	661	673
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	SLVHDLFQK	97.9%	31.4	25	20.7	1	0	0	1086.59	574	582
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	SNNIINETTTR	99.7%	65.9	25	58	3	0	0	1262.63	435	445
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	SNVIDSMLFVFGYR	99.7%	71.9	25	71.9	3	0	0	1647.82	120	133
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	TEYDAVAEK	94.8%	27.8	25	25.2	1	0	0	1025.48	868	876
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	VAELDKITYER	99.7%	55.5	25	50.7	1	0	0	1336.71	1107	1117
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	VIQENEHALQK	99.7%	80.1	25	78.1	2	0	0	1308.69	999	1009
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	VLDAIIQEK	99.7%	47.2	25	36.6	2	0	0	1028.60	599	607
Structural maintenance of chromosomes protein 4	SMC4	SMC4_HUMAN	147.2	100.0%	29	31	50	0.05%	25.0%	VVTLQGQIIEQSGTMTGGGSK	99.7%	129	25	129	2	0	0	2107.07	737	757
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	SDHB	SDHB_HUMAN	31.6	100.0%	2	2	2	0.00%	8.6%	IKNEVDSTLTFR	99.7%	58.4	25	58.4	1	0	0	1422.76	79	90
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	SDHB	SDHB_HUMAN	31.6	100.0%	2	2	2	0.00%	8.6%	YLGPAVLMQAYR	99.4%	36.8	25	35	1	0	0	1381.73	206	217
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	7	9	16	0.02%	28.9%	GGQTHLGLPVFNTVK	99.7%	56.3	25	56.3	1	1	0	1567.86	91	105
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	7	9	16	0.02%	28.9%	IICQGFTGK	99.6%	38.7	25	32	2	0	0	1023.53	58	66
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	7	9	16	0.02%	28.9%	ISALQSAGVVVSMSPAQLGTTIYK	99.7%	61	25	61	0	2	0	2437.30	315	338
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	7	9	16	0.02%	28.9%	LIGPNCPGVINPGECK	99.7%	68.3	25	61.5	2	0	0	1724.85	167	182
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	7	9	16	0.02%	28.9%	LVGGTTPGK	99.7%	44.1	25	34.6	2	0	0	829.48	82	90
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	7	9	16	0.02%	28.9%	MGHAGAIIAGGK	99.7%	59.5	25	59.5	4	0	0	1098.57	297	308

Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	SUCA_HUMAN	36.3	100.0%	7	9	16	0.02%	28.9%	QGTFHSQQALEYGTK	99.7%	47.9	25	44.2	0	2	0	1694.81	67	81
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	12	12	19	0.02%	30.5%	DLEIKIPVVVR	99.7%	42.2	25	42.2	1	0	0	1280.79	397	407
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	12	12	19	0.02%	30.5%	EPIDIEEGIKK	99.5%	37.3	25	33.4	1	0	0	1270.69	206	216
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	12	12	19	0.02%	30.5%	EQALQLAQK	99.7%	58.5	25	51.4	1	0	0	1028.57	217	225
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	12	12	19	0.02%	30.5%	ICNQVLVCER	99.7%	54.5	25	50.7	2	0	0	1290.63	151	160
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	12	12	19	0.02%	30.5%	ILACDDLDEAAR	99.7%	83.3	25	73	2	0	0	1361.64	427	438
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	12	12	19	0.02%	30.5%	INFDSNSAYR	99.7%	66.3	25	62.9	2	0	0	1186.55	275	284
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	12	12	19	0.02%	30.5%	IVFSPEEAK	97.4%	30.5	25	24.3	1	0	0	1019.54	121	129
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	12	12	19	0.02%	30.5%	LHGGTPANFLDVGGGATVHQVTEAFK	99.7%	36.2	25	36.2	0	1	0	2623.33	337	362
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	12	12	19	0.02%	30.5%	LSEIVTLAK	99.7%	50.3	25	31.7	2	0	0	973.59	443	451
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	12	12	19	0.02%	30.5%	LYSLFLK	99.6%	39.3	25	24.9	2	0	0	883.53	243	249
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	12	12	19	0.02%	30.5%	MGFPPNIVESAAENMVK	99.7%	55.3	25	50.7	2	0	0	1833.89	226	242
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	SUCB1_HUMAN	50.3	100.0%	12	12	19	0.02%	30.5%	SPDEAYAIAK	99.7%	58.9	25	58.9	2	0	0	1064.53	79	88
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	9	11	20	0.02%	24.3%	DPNVVGQLAK	97.5%	30.6	25	24.7	1	0	0	1040.57	109	118
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	9	11	20	0.02%	24.3%	EAQVYQAFK	99.7%	42.4	25	35.9	2	0	0	1083.55	339	347
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	9	11	20	0.02%	24.3%	ETYLAILMDR	99.7%	50.1	25	44.8	3	0	0	1240.62	151	160
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	9	11	20	0.02%	24.3%	FFVADTANEALEAAK	99.7%	115	25	115	2	0	0	1596.79	59	73
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	9	11	20	0.02%	24.3%	ILNNSGLPITSAIDLEDAAK	99.7%	86	25	86	2	0	0	2055.10	404	423
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	9	11	20	0.02%	24.3%	LEGTNVQEAQK	99.7%	74.3	25	60.5	2	0	0	1216.62	393	403
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	9	11	20	0.02%	24.3%	LYNLFLK	99.7%	44.4	25	23.7	2	0	0	910.54	228	234
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	9	11	20	0.02%	24.3%	MAENLGFVGPLK	99.7%	81	25	71.5	4	0	0	1275.68	207	218
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SUCB2_HUMAN	46.5	100.0%	9	11	20	0.02%	24.3%	VMVAEALDISR	99.7%	93.6	25	83.1	2	0	0	1203.64	140	150
SUMO-activating enzyme subunit 2	UBA2	SAE2_HUMAN	71.2	100.0%	3	3	4	0.00%	5.8%	ELAEAVAGGR	99.7%	56.5	25	38.9	1	0	0	972.51	10	19
SUMO-activating enzyme subunit 2	UBA2	SAE2_HUMAN	71.2	100.0%	3	3	4	0.00%	5.8%	QFILVMNALDNR	99.7%	56.3	25	46.7	1	0	0	1433.76	108	119
SUMO-activating enzyme subunit 2	UBA2	SAE2_HUMAN	71.2	100.0%	3	3	4	0.00%	5.8%	VLVVGAGGIGCELLK	99.7%	107	25	107	2	0	0	1484.85	20	34
SUN domain-containing protein 2	SUN2	SUN2_HUMAN	80.3	100.0%	3	3	6	0.01%	6.3%	DSSPHFQAEQR	99.7%	44.4	25	38.9	2	0	0	1301.59	265	275
SUN domain-containing protein 2	SUN2	SUN2_HUMAN	80.3	100.0%	3	3	6	0.01%	6.3%	IGLADYALESGGASVISTR	99.7%	142	25	138	2	0	0	1879.98	544	562
SUN domain-containing protein 2	SUN2	SUN2_HUMAN	80.3	100.0%	3	3	6	0.01%	6.3%	LTTAASLLDVFVLTR	99.7%	63.3	25	57.2	2	0	0	1619.94	191	205
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	32	0.03%	17.6%	AIGNTELENK	99.7%	45.1	25	37.6	1	0	0	1088.56	1013	1022
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	32	0.03%	17.6%	DVDFEGTDEPIFGK	99.7%	80	25	80	2	0	0	1568.71	65	78
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	32	0.03%	17.6%	EAIQCVDNNQSVLVSAHTSAGK	96.2%	23.9	25	23.9	0	1	0	2328.12	146	167
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	32	0.03%	17.6%	EYPFILDAFQR	99.7%	51.7	25	42.1	4	0	0	1398.71	135	145
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	32	0.03%	17.6%	IVIPNEESVVIYYK	97.3%	30.3	25	29.2	2	0	0	1665.91	615	628
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	32	0.03%	17.6%	KAQIAIDIK	99.7%	49.3	25	32.3	1	0	0	999.62	825	833
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	32	0.03%	17.6%	LDFNTDEEKK	96.1%	28.9	25	22.5	1	0	0	1238.59	409	418
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	32	0.03%	17.6%	LGFATSSDVIEMK	99.7%	83.9	25	61.9	2	0	0	1397.70	861	873
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	32	0.03%	17.6%	LTEQLAGPLR	99.7%	77.8	25	67.9	2	0	0	1097.63	924	933
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	32	0.03%	17.6%	MTDVFEGSIIR	99.7%	78.5	25	69.8	3	0	0	1267.64	985	995
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	32	0.03%	17.6%	NFQPVIIFSFSK	99.7%	48.8	25	48.8	4	0	0	1426.77	385	396
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	32	0.03%	17.6%	RLEELLR	96.2%	29	25	11.2	1	0	0	928.56	999	1005
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	32	0.03%	17.6%	SFYQFQHYR	99.2%	35.8	25	34.4	2	0	0	1275.59	588	596
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	32	0.03%	17.6%	TVLQMDELK	97.3%	30.4	25	23.2	2	0	0	1076.57	844	852
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	32	0.03%	17.6%	VEEINPEYMLEK	99.7%	41.8	25	37	2	0	0	1493.72	576	587
Superkiller viralicidic activity 2-like 2	SKIV2L2	SK2L2_HUMAN	117.8	100.0%	16	17	32	0.03%	17.6%	YCLPFLQPGR	96.5%	29.4	25	19.8	2	0	0	1250.64	649	658
Suppressor of SWI4 1 homolog	PPAN	SSF1_HUMAN	53.2	100.0%	7	7	10	0.01%	18.4%	CLLIDYNPDSQELDFR	99.7%	50.3	25	46	1	0	0	1997.93	180	195
Suppressor of SWI4 1 homolog	PPAN	SSF1_HUMAN	53.2	100.0%	7	7	10	0.01%	18.4%	DCVAVAGPLGVTHFLILSK	99.2%	35.6	25	35.6	1	0	0	1997.09	72	90
Suppressor of SWI4 1 homolog	PPAN	SSF1_HUMAN	53.2	100.0%	7	7	10	0.01%	18.4%	LPGGPTLTFQVK	99.7%	81.4	25	80	2	0	0	1257.72	102	113
Suppressor of SWI4 1 homolog	PPAN	SSF1_HUMAN	53.2	100.0%	7	7	10	0.01%	18.4%	MTLQLIK	99.5%	37.9	25	12.8	1	0	0	846.51	279	285
Suppressor of SWI4 1 homolog	PPAN	SSF1_HUMAN	53.2	100.0%	7	7	10	0.01%	18.4%	QLSLDVR	97.7%	31.1	25	15.4	1	0	0	830.47	45	51
Suppressor of SWI4 1 homolog	PPAN	SSF1_HUMAN	53.2	100.0%	7	7	10	0.01%	18.4%	TEEELQAILEAK	99.7%	86	25	72.7	2	0	0	1373.72	304	315
Suppressor of SWI4 1 homolog	PPAN	SSF1_HUMAN	53.2	100.0%	7	7	10	0.01%	18.4%	VGGSDEEASGIPSR	99.7%	85.9	25	72.1	2	0	0	1360.63	356	369

Surfeit locus protein 4	SURF4	SURF4_HUMAN	30.4	100.0%	4	5	11	0.01%	21.2%	GQNDLMGTAEDFADQFLR	99.7%	95.7	25	95.7	3	0	0	2043.91	2	19
Surfeit locus protein 4	SURF4	SURF4_HUMAN	30.4	100.0%	4	5	11	0.01%	21.2%	LCLISTFLEDGIR	99.7%	97.7	25	90.2	4	0	0	1536.81	31	43
Surfeit locus protein 4	SURF4	SURF4_HUMAN	30.4	100.0%	4	5	11	0.01%	21.2%	NLALGGGLLLLLAESR	99.7%	66.2	25	62.5	1	0	0	1609.96	120	135
Surfeit locus protein 4	SURF4	SURF4_HUMAN	30.4	100.0%	4	5	11	0.01%	21.2%	SMFAGVPTMR	99.7%	46.7	25	41.2	3	0	0	1128.52	140	149
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	3	3	4	0.00%	3.6%	ALNIVDQEGSLLGK	99.7%	71.1	25	69.2	2	0	0	1456.80	215	228
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	3	3	4	0.00%	3.6%	GADQKPTSADCAVR	99.2%	35.4	25	33.4	1	0	0	1475.69	646	659
SURP and G-patch domain-containing protein 2	SUGP2	SUGP2_HUMAN	120.2	100.0%	3	3	4	0.00%	3.6%	YSLSGSVAHSR	99.7%	61.5	25	55.2	1	0	0	1163.58	63	73
Survival motor neuron protein	SMN1	SMN_HUMAN	31.8	100.0%	3	3	6	0.01%	13.9%	ETCVVVYTGYGNR	99.7%	81.8	25	81.2	2	0	0	1517.71	121	133
Survival motor neuron protein	SMN1	SMN_HUMAN	31.8	100.0%	3	3	6	0.01%	13.9%	GTGQSDDSDIWDDTALIK	99.7%	102	25	102	2	0	0	1936.88	24	41
Survival motor neuron protein	SMN1	SMN_HUMAN	31.8	100.0%	3	3	6	0.01%	13.9%	NTAASLQQWK	99.7%	47.9	25	38.3	2	0	0	1146.59	84	93
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	19	29	0.03%	16.1%	CNELQDIEK	99.7%	43.4	25	25.8	1	0	0	1148.53	891	899
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	19	29	0.03%	16.1%	CNTLITLIER	99.7%	39.8	25	31.2	1	0	0	1232.67	1001	1010
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	19	29	0.03%	16.1%	DFNQFIK	98.3%	32.2	25	10.7	1	0	0	911.46	849	855
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	19	29	0.03%	16.1%	DIDILNSAGK	99.7%	61.3	25	38.6	2	0	0	1045.55	431	440
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	19	29	0.03%	16.1%	EIQEPDPTYEEK	99.7%	46.7	25	38	1	0	0	1477.67	72	83
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	19	29	0.03%	16.1%	ESEITDEDIDGILER	99.7%	99.8	25	99.8	2	0	0	1733.81	666	680
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	19	29	0.03%	16.1%	FITDNTVEER	99.7%	53.1	25	43.3	2	0	0	1223.59	607	616
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	19	29	0.03%	16.1%	LDGQTPHDER	99.6%	38.6	25	31.8	1	0	0	1167.54	529	538
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	19	29	0.03%	16.1%	LDSIVIQQGR	99.7%	89.4	25	74.4	2	0	0	1128.64	627	636
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	19	29	0.03%	16.1%	LLNILMQLR	99.7%	42.5	25	42.1	3	0	0	1113.68	446	454
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	19	29	0.03%	16.1%	NPELPNAAQAQK	99.7%	53.9	25	47.6	1	0	0	1280.66	803	814
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	19	29	0.03%	16.1%	QNLLSVGDYR	99.7%	52.2	25	39.2	2	0	0	1164.60	133	142
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	19	29	0.03%	16.1%	RTEQEEDEELLTESSK	99.5%	31.8	25	31.8	0	1	0	1922.88	145	160
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	19	29	0.03%	16.1%	SVCLIGDKEQR	99.7%	53.8	25	25.6	1	0	0	1304.66	257	267
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	19	29	0.03%	16.1%	TEQEEDEELLTESSK	99.7%	99.1	25	99.1	2	0	0	1766.78	146	160
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	19	29	0.03%	16.1%	VLIFSQMTR	99.7%	58.5	25	51.9	4	0	0	1094.60	502	510
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	SMCA5_HUMAN	121.9	100.0%	17	19	29	0.03%	16.1%	YLVIDEAHR	99.7%	39.4	25	35.5	2	0	0	1115.58	304	312
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	SMARCD2	SMRD2_HUMAN	58.9	100.0%	4	4	4	0.00%	9.6%	AEGDSAGTAGTPGGTPAGDK	99.7%	59.4	25	59.4	1	0	0	1716.77	207	226
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	SMARCD2	SMRD2_HUMAN	58.9	100.0%	4	4	4	0.00%	9.6%	IITDVIGNPEEERR	97.5%	25.4	25	24.8	0	1	0	1640.86	481	494
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	SMARCD2	SMRD2_HUMAN	58.9	100.0%	4	4	4	0.00%	9.6%	KLDQTIAR	99.0%	34.3	25	24.3	1	0	0	944.55	168	175
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	SMARCD2	SMRD2_HUMAN	58.9	100.0%	4	4	4	0.00%	9.6%	LLGVHTQTR	98.5%	32.8	25	15.5	1	0	0	1024.59	320	328
Symplekin	SYMPK	SYMPK_HUMAN	141.2	99.9%	2	2	5	0.00%	2.3%	LLSGLQEKPDQK	98.5%	32.8	25	21	1	0	0	1355.75	649	660
Symplekin	SYMPK	SYMPK_HUMAN	141.2	99.9%	2	2	5	0.00%	2.3%	VVLEAPLITESALEVVR	99.7%	67.4	25	67.4	4	0	0	1838.06	667	683
Synembryn-A	RIC8A	RIC8A_HUMAN	59.7	100.0%	3	3	4	0.00%	5.8%	LLFLLTALR	99.7%	60.2	25	60.2	2	0	0	1059.69	167	175
Synembryn-A	RIC8A	RIC8A_HUMAN	59.7	100.0%	3	3	4	0.00%	5.8%	VIWLQSVR	99.7%	42	25	35.3	1	0	0	1000.59	64	71
Synembryn-A	RIC8A	RIC8A_HUMAN	59.7	100.0%	3	3	4	0.00%	5.8%	YTGYGNAAGLLAAR	99.7%	90.7	25	87.6	1	0	0	1397.72	410	423
Syntaxin-binding protein 2	STXBP2	STXB2_HUMAN	66.5	100.0%	3	3	4	0.00%	7.1%	EPIPSLEAIYLLSPTEK	99.7%	46	25	46	1	0	0	1900.03	66	82
Syntaxin-binding protein 2	STXBP2	STXB2_HUMAN	66.5	100.0%	3	3	4	0.00%	7.1%	LIVPVLLDAAVPAYDK	99.7%	105	25	105	2	0	0	1696.99	388	403
Syntaxin-binding protein 2	STXBP2	STXB2_HUMAN	66.5	100.0%	3	3	4	0.00%	7.1%	VLLLYILLR	99.7%	41.7	25	41.7	1	0	0	1115.76	406	414
Tail-anchored protein insertion receptor WRB	WRB	WRB_HUMAN	19.8	99.8%	2	2	2	0.00%	10.9%	ILLPSFSSFMSR	99.3%	36.3	25	24.1	1	0	0	1400.72	26	37
Tail-anchored protein insertion receptor WRB	WRB	WRB_HUMAN	19.8	99.8%	2	2	2	0.00%	10.9%	LVAFPTR	97.2%	30.2	25	27	1	0	0	803.48	142	148
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	5	5	12	0.01%	12.3%	FGGNPGGFGNQGGFGNSR	99.7%	112	25	106	2	0	0	1726.77	276	293
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	5	5	12	0.01%	12.3%	FTEYETQVK	99.7%	44.8	25	24.7	5	0	0	1144.55	152	160
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	5	5	12	0.01%	12.3%	KMDETDASSAVK	99.7%	40	25	31	2	0	0	1297.59	84	95
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	5	5	12	0.01%	12.3%	MDETDASSAVK	94.5%	27.6	25	27.6	1	0	0	1153.50	85	95
TAR DNA-binding protein 43	TARDBP	TADBP_HUMAN	44.7	100.0%	5	5	12	0.01%	12.3%	TSDLIVLGLPWK	99.7%	64.3	25	50.2	2	0	0	1341.78	103	114
Target of EGR1 protein 1	TOE1	TOE1_HUMAN	56.5	100.0%	5	5	9	0.01%	10.4%	ALLNLPGTQTSGEAK	99.7%	55.1	25	52.5	2	0	0	1499.81	348	362
Target of EGR1 protein 1	TOE1	TOE1_HUMAN	56.5	100.0%	5	5	9	0.01%	10.4%	EMWPSLLLAIK	99.7%	42.7	25	24.6	1	0	0	1300.73	46	56
Target of EGR1 protein 1	TOE1	TOE1_HUMAN	56.5	100.0%	5	5	9	0.01%	10.4%	SILSLGLACFK	99.7%	63.7	25	48.1	2	0	0	1208.67	96	106
Target of EGR1 protein 1	TOE1	TOE1_HUMAN	56.5	100.0%	5	5	9	0.01%	10.4%	TLFLELIR	96.5%	29.3	25	18.5	2	0	0	1004.61	175	182
Target of EGR1 protein 1	TOE1	TOE1_HUMAN	56.5	100.0%	5	5	9	0.01%	10.4%	YAAEFHAR	99.7%	41.9	25	34.5	2	0	0	964.46	231	238

TATA box-binding protein-like protein 1	TBPL1	TBPL1_HUMAN	20.9	99.8%	2	2	2	0.00%	11.3%	ITATIWSSGK	99.5%	37.6	25	37.4	1	0	0	1063.58	56	65
TATA box-binding protein-like protein 1	TBPL1	TBPL1_HUMAN	20.9	99.8%	2	2	2	0.00%	11.3%	LGFQVIFTDFK	97.8%	31.2	25	31.2	1	0	0	1314.71	91	101
TATA-binding protein-associated factor 172	BTAF1	BTAF1_HUMAN	206.9	100.0%	4	4	6	0.01%	2.4%	AVTLAVQPR	97.7%	31.1	25	20.4	1	0	0	954.57	745	753
TATA-binding protein-associated factor 172	BTAF1	BTAF1_HUMAN	206.9	100.0%	4	4	6	0.01%	2.4%	FGDFVSDEVVAPVR	99.7%	45.4	25	45.4	1	0	0	1536.77	355	368
TATA-binding protein-associated factor 172	BTAF1	BTAF1_HUMAN	206.9	100.0%	4	4	6	0.01%	2.4%	QVLPFLLR	99.7%	40.2	25	23.6	2	0	0	985.62	1495	1502
TATA-binding protein-associated factor 172	BTAF1	BTAF1_HUMAN	206.9	100.0%	4	4	6	0.01%	2.4%	YQQDGVNWLAFLNK	99.7%	53.1	25	40.3	2	0	0	1695.85	1269	1282
TBC1 domain family member 15	TBC1D15	TBC15_HUMAN	79.5	100.0%	3	3	4	0.00%	4.3%	EFSFLDILR	99.7%	53.8	25	34	1	0	0	1139.61	539	547
TBC1 domain family member 15	TBC1D15	TBC15_HUMAN	79.5	100.0%	3	3	4	0.00%	4.3%	TQLIQLSTLLR	99.7%	68.8	25	64.3	2	0	0	1285.78	497	507
TBC1 domain family member 15	TBC1D15	TBC15_HUMAN	79.5	100.0%	3	3	4	0.00%	4.3%	VTNYIFDSLR	99.7%	60.4	25	38.2	1	0	0	1227.64	253	262
TBC1 domain family member 4	TBC1D4	TBCD4_HUMAN	146.6	100.0%	5	5	7	0.01%	5.3%	ATDPSQVPDVISSIR	99.7%	56	25	52.1	1	0	0	1584.82	161	175
TBC1 domain family member 4	TBC1D4	TBCD4_HUMAN	146.6	100.0%	5	5	7	0.01%	5.3%	IQALESNLENLLTR	99.7%	98.4	25	94.9	2	0	0	1613.89	1227	1240
TBC1 domain family member 4	TBC1D4	TBCD4_HUMAN	146.6	100.0%	5	5	7	0.01%	5.3%	LLPADALVNCDLLLR	99.7%	49.6	25	43.8	2	0	0	1695.95	1268	1282
TBC1 domain family member 4	TBC1D4	TBCD4_HUMAN	146.6	100.0%	5	5	7	0.01%	5.3%	QAFSTAAALQSAK	99.7%	55.9	25	54.7	1	0	0	1293.68	435	447
TBC1 domain family member 4	TBC1D4	TBCD4_HUMAN	146.6	100.0%	5	5	7	0.01%	5.3%	SLTSSLENIFSR	99.7%	74.2	25	69	1	0	0	1353.70	566	577
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	AFHNEAQVNPER	99.7%	71.4	25	67.4	4	4	0	1411.67	469	480
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	AFHNEAQVNPERK	99.7%	53	25	43.5	3	4	0	1539.77	469	481
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	DCLINAAK	99.7%	47.2	25	27.4	3	0	0	904.46	146	153
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	DDKHGSYEDAVHSGALND	99.7%	81.2	25	81.2	2	3	0	1929.82	539	556
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	EQLAIAEFAR	99.7%	68.8	25	58.5	10	0	0	1147.61	434	443
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	EVGDGTTSVVIIAAELLK	99.7%	112	25	105	3	0	0	1815.01	85	102
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	FATEAAITILR	99.7%	91.9	25	71.2	9	0	0	1205.69	516	526
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	GANDFMCDEMER	99.7%	73.3	25	73.3	9	0	0	1474.54	379	390
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	HGSYEDAVHSGALND	99.7%	89.7	25	85.9	2	1	0	1571.67	542	556
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	IACLDFSLQK	99.7%	69.8	25	66.3	4	0	0	1194.62	234	243
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	ICDDELILIK	99.7%	64.3	25	53.9	4	0	0	1231.66	356	365
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	IHPTSVISGYR	99.7%	39.8	25	37.6	2	0	0	1229.66	112	122
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	IIGINGDFFANMVVDAVLAIK	99.7%	56.3	25	56.3	1	0	0	2236.20	160	180
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	ILATGANVILTTGGIDDMCLK	99.7%	97.8	25	97.3	4	2	0	2192.13	278	298
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	LGVQVVITDPEK	99.7%	85.1	25	81.5	2	0	0	1297.74	248	259
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	LGVQVVITDPEKLDQIR	99.7%	76.4	25	76.4	4	4	0	1923.09	248	264
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	LLEVEHPAAK	99.7%	70.8	25	60.9	9	0	0	1106.62	64	73
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	MLVDDIGDVTITNDGATILK	99.7%	137	25	131	4	1	0	2104.08	44	63
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	QAGVFEPTIVK	99.7%	51.7	25	41.3	2	0	0	1188.66	500	510
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	QKIHPTSVISGYR	99.7%	46.2	25	46.2	0	1	0	1485.82	110	122
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	SLHDALCVVK	99.7%	45	25	31.9	3	0	0	1141.60	391	400
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	SLHDALCVVKR	99.7%	46.1	25	44.5	2	2	0	1297.70	391	401
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	SLLVIPNTLAVNAAQDSTDLVAK	99.7%	104	25	104	15	3	0	2353.30	444	466
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	SQMESMLISGYALNCVVGSQGMPK	99.7%	33.3	25	33.3	0	5	0	2603.20	204	227
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	SQNVMAAASIANIVK	99.7%	133	25	127	6	0	0	1532.81	19	33
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	SSLGPVGLDK	99.7%	61.6	25	38.2	4	0	0	972.54	34	43
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	SVVPGGGAVEAALSIYLENYATSMGSR	99.7%	110	25	110	1	1	0	2699.33	407	433
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	TSASIILR	99.7%	66.8	25	48.3	2	0	0	860.52	371	378
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	VLCELADLQDK	99.7%	88.1	25	78.2	2	0	0	1303.66	74	84
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	VLCELADLQDKEVGDGTTSVVIIAAELLK	99.7%	61.2	25	61	0	1	0	3099.65	74	102
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	WIGLDLSNGKPR	99.7%	56.1	25	47.7	2	2	0	1355.74	485	496
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	YFVEAGAMAVR	99.7%	81	25	71.9	6	0	0	1213.60	299	309
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	YINENLIVNTDELGRDCLINAAK	99.7%	41.3	25	32.8	0	2	0	2648.34	131	153
T-complex protein 1 subunit alpha	TCP1	TCPA_HUMAN	60.3	100.0%	34	50	162	0.15%	71.9%	YPVNSVNILK	99.7%	51.2	25	32.8	2	0	0	1146.65	190	199
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	17	22	37	0.03%	43.7%	AAHSEGNTTAGLDMR	99.7%	74.2	25	74.2	1	2	0	1530.70	467	481
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	17	22	37	0.03%	43.7%	DASLMVTNDGATILK	99.7%	74.6	25	68.7	2	0	0	1548.79	58	72
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	17	22	37	0.03%	43.7%	EALLSSAVDHGSDEVK	99.7%	91.9	25	90.9	2	1	0	1656.81	139	154

T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	17	22	37	0.03%	43.7%	EAVAMESYAK	99.7%	41.3	25	41.3	2	0	0	1098.51	432	441
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	17	22	37	0.03%	43.7%	EGTIGDMAILGITESFQVK	99.7%	103	25	103	2	0	0	2009.03	482	500
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	17	22	37	0.03%	43.7%	GATQQILDEAER	99.7%	83.9	25	78.8	2	0	0	1330.66	377	388
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	17	22	37	0.03%	43.7%	HGINCFINR	99.7%	54.8	25	48.4	2	0	0	1130.55	285	293
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	17	22	37	0.03%	43.7%	ILIANTGMDTDKIK	99.7%	99.9	25	87.3	3	0	0	1532.84	237	250
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	17	22	37	0.03%	43.7%	KIHPQTIIAGWR	99.2%	29.8	25	29.8	0	1	0	1419.82	120	131
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	17	22	37	0.03%	43.7%	LALVTGGEIASTFDHPELVK	99.7%	69.4	25	69.4	1	2	0	2097.12	323	342
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	17	22	37	0.03%	43.7%	LAVEAVLR	99.7%	66.1	25	19.9	2	0	0	870.54	182	189
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	17	22	37	0.03%	43.7%	LKGSGNLEAIHIIK	99.7%	41.8	25	26.7	0	2	0	1492.88	190	203
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	17	22	37	0.03%	43.7%	LTSFIGAIAIGDLVK	99.7%	104	25	104	1	0	0	1517.89	26	40
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	17	22	37	0.03%	43.7%	MLPTIIADNAGYDSADLVAQLR	99.7%	112	25	112	2	2	0	2347.20	445	466
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	17	22	37	0.03%	43.7%	VAEIEHAEK	99.7%	42.7	25	42.7	1	0	0	1025.53	264	272
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	17	22	37	0.03%	43.7%	VAEIEHAEKEK	99.7%	66	25	54.3	2	0	0	1282.66	264	274
T-complex protein 1 subunit beta	CCT2	TCPB_HUMAN	57.5	100.0%	17	22	37	0.03%	43.7%	VQDDEVGDGTTSVTVLAAELLR	99.7%	150	25	150	2	0	0	2288.16	90	111
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	34	116	0.11%	62.0%	AFADAMEVIPSTLAENAGLNPISTVTELR	98.5%	27.2	25	23.1	0	1	0	3030.55	453	481
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	34	116	0.11%	62.0%	ALIAGGGAPEIELALR	99.7%	102	25	101	11	0	0	1550.89	420	435
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	34	116	0.11%	62.0%	AQDIEAGDGTTSVVIIAGSLLDSCTK	99.7%	124	25	124	2	2	0	2621.30	97	122
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	34	116	0.11%	62.0%	AYILNLVK	99.7%	44	25	36	2	0	0	933.58	281	288
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	34	116	0.11%	62.0%	DALSDLALHFLNK	99.7%	94.1	25	75.7	9	2	0	1456.78	307	319
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	34	116	0.11%	62.0%	DIEREDIEFICK	99.7%	54.8	25	51.7	3	1	0	1566.75	327	338
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	34	116	0.11%	62.0%	FSNISAAK	99.7%	43	25	26.9	2	0	0	837.45	35	42
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	34	116	0.11%	62.0%	GAYQDRDKPAQIR	99.7%	35.9	25	35.9	0	2	0	1517.78	22	34
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	34	116	0.11%	62.0%	GDVTITNDGATILK	99.7%	63.8	25	61	1	0	0	1417.75	66	79
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	34	116	0.11%	62.0%	GIEILTDMSRPVELSDRETLLNSATTSLNSK	99.7%	52	25	51.8	0	4	0	3390.74	144	174
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	34	116	0.11%	62.0%	GIHPTIISESFQK	99.7%	38.7	25	37.1	3	2	0	1456.78	127	139
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	34	116	0.11%	62.0%	IDDVVNTR	99.7%	59.4	25	53	2	0	0	931.48	532	539
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	34	116	0.11%	62.0%	IGLIQFCLSAPK	99.7%	67.9	25	67.9	12	0	0	1346.75	246	257
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	34	116	0.11%	62.0%	KTGCNVLLIQK	99.7%	52.5	25	32	2	0	0	1273.73	292	302
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	34	116	0.11%	62.0%	LGGTIDDCELVEGLVLTQK	99.7%	106	25	106	2	2	0	2060.06	214	232
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	34	116	0.11%	62.0%	LVIEEAER	99.7%	59.2	25	45.2	6	0	0	958.52	396	403
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	34	116	0.11%	62.0%	MIQDGKGDVTITNDGATILK	99.7%	86.7	25	83.7	1	7	0	2106.08	60	79
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	34	116	0.11%	62.0%	MLVELSK	98.2%	31.9	25	6.69	2	0	0	835.46	90	96
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	34	116	0.11%	62.0%	QMQVLHPAAR	99.7%	54.2	25	47.6	3	0	0	1150.62	80	89
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	34	116	0.11%	62.0%	SIHDALCVIR	99.7%	61.7	25	0	4	0	0	1183.63	404	413
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	34	116	0.11%	62.0%	TDMDNQIVVSDYAQMDR	99.7%	104	25	101	6	0	0	2016.86	258	274
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	34	116	0.11%	62.0%	TGCNVLLIQK	99.7%	51.8	25	37.7	4	0	0	1145.63	293	302
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	34	116	0.11%	62.0%	TLSGMESYCVR	99.7%	69.4	25	64.2	8	0	0	1318.58	442	452
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	34	116	0.11%	62.0%	VIDPATATSVDLR	99.7%	102	25	92	8	0	0	1357.73	194	206
T-complex protein 1 subunit delta	CCT4	TCPD_HUMAN	57.9	100.0%	24	34	116	0.11%	62.0%	VVSQYSSLLSPMSVNAVMK	99.7%	102	25	80.1	4	0	0	2056.05	175	193
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	AVTIFIR	99.7%	51.8	25	30.8	3	0	0	819.51	382	388
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	CPTLEQYAMR	99.7%	52.5	25	52.5	3	0	0	1268.58	440	449
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	DKMLVIEQCK	99.7%	45.2	25	36	1	0	0	1279.64	369	378
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	DTEPLIQTAK	99.6%	38.4	25	37.7	2	0	0	1115.59	161	170
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	DVDFELIK	99.3%	36.2	25	15.5	2	0	0	978.51	203	210
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	DVDFELIKVEGK	99.7%	70.4	25	59.9	2	0	0	1391.74	203	214
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	EKFEEMIQQIK	99.7%	35.8	25	17.8	2	2	0	1438.72	283	293
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	EMNPALGIDCLHK	99.7%	75.7	25	69.2	4	4	0	1513.71	484	496
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	FEEMIQQIK	99.7%	51.4	25	30.2	4	0	0	1165.59	285	293
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	FSELTAEK	99.7%	52.8	25	42.1	2	0	0	924.47	345	352
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	GVIVDKDFSHPQMPK	99.7%	81.8	25	79.9	4	4	0	1697.87	227	241
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	HKLDVTSVEDYK	99.7%	42.6	25	37.3	2	2	0	1433.73	264	275

T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	IADGYEQAAR	99.7%	82.5	25	77.4	6	0	0	1093.53	133	142
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	IAILTCPFEPPKPK	99.7%	48.6	25	48.6	2	2	0	1610.90	248	261
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	IDDIRKPGESEE	99.7%	50.8	25	41.8	2	0	0	1387.67	530	541
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	ISDSVLVDIKDTEPLIQTAK	99.7%	74.5	25	74.5	1	2	0	2185.20	151	170
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	KQQISLATQMVR	99.7%	68.9	25	63.5	4	2	0	1402.78	514	525
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	LDVTSVEDYK	99.7%	65.4	25	57.9	2	0	0	1168.57	266	275
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	LGFAGLVQEISFGTTK	99.7%	128	25	121	8	0	0	1667.90	353	368
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	LMGLEALK	99.7%	44.1	25	25.8	3	0	0	874.51	28	35
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	LMVELSK	99.7%	41.5	25	12.2	4	0	0	835.46	90	96
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	MIIEEAKR	99.7%	59.4	25	36.9	3	0	0	989.54	393	400
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	MLVIEQCK	99.7%	44.3	25	31.5	2	0	0	1036.52	371	378
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	QQHVIETLIGK	99.5%	31.4	25	30.7	2	2	0	1265.72	503	513
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	QQHVIETLIGKK	95.0%	28	25	15.5	1	0	0	1393.82	503	514
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	QQISLATQMVR	99.7%	63.1	25	52.6	4	0	0	1274.69	515	525
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	RDVDFELIK	99.7%	48	25	18.9	2	0	0	1134.62	202	210
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	SLHDALCVIR	99.7%	61.7	25	0	4	0	0	1183.63	401	410
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	TSLGPNGLDK	99.7%	63.8	25	51.9	2	0	0	1001.53	50	59
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	VAIEHLDK	99.7%	52.3	25	33.6	2	0	0	924.52	143	150
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	VVYGGGAAEISCALAVSQEADK	98.8%	28.3	25	24.1	0	1	0	2195.07	418	439
T-complex protein 1 subunit epsilon	CCT5	TCPE_HUMAN	59.7	100.0%	32	51	109	0.10%	52.5%	WVGGPEIELIAIATGGR	99.7%	120	25	113	3	0	0	1738.95	324	340
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	25	32	80	0.07%	57.8%	ALEIIPR	99.7%	43.4	25	37.9	4	0	0	811.50	441	447
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	25	32	80	0.07%	57.8%	ATISNDGATILK	99.7%	62.4	25	46.9	3	0	0	1203.66	56	67
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	25	32	80	0.07%	57.8%	CQVFEETQIGGER	99.7%	93.5	25	82.9	4	0	0	1552.71	345	357
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	25	32	80	0.07%	57.8%	GGAEQFMEETER	99.7%	89.9	25	89.9	7	0	0	1383.58	376	387
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	25	32	80	0.07%	57.8%	IALLNVELELK	99.7%	52.6	25	46.2	2	0	0	1254.77	237	247
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	25	32	80	0.07%	57.8%	IKEIAVTVK	99.6%	38.9	25	35.8	2	0	0	1000.64	136	144
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	25	32	80	0.07%	57.8%	INALTAASEAACLIVSVDETIK	99.7%	106	25	106	2	3	0	2289.20	500	521
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	25	32	80	0.07%	57.8%	INALTAASEAACLIVSVDETIKNPR	99.7%	69	25	67.4	0	2	0	2656.40	500	524
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	25	32	80	0.07%	57.8%	LLDVVHPAAK	99.7%	48.3	25	39.7	4	0	0	1062.63	68	77
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	25	32	80	0.07%	57.8%	LPIGDVATQYFADR	99.7%	97.7	25	95.3	4	0	0	1565.80	293	306
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	25	32	80	0.07%	57.8%	LPIGDVATQYFADRDMFCAGR	99.6%	33.3	25	33.3	0	1	0	2403.12	293	313
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	25	32	80	0.07%	57.8%	MVVDAVMMLDDLLQLK	99.7%	84	25	44.6	2	0	0	1849.95	178	193
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	25	32	80	0.07%	57.8%	NDSVVAGGGAIEMELSK	99.7%	91.5	25	90.1	1	0	0	1692.81	402	418
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	25	32	80	0.07%	57.8%	QLCDNAGFDATNILNK	99.7%	148	25	133	2	0	0	1793.85	448	463
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	25	32	80	0.07%	57.8%	QQLLIGAYAK	99.7%	48.2	25	44	2	0	0	1104.64	431	440
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	25	32	80	0.07%	57.8%	QVKPYVEEGLHPQIIIR	99.4%	31.3	25	31.3	0	1	0	2019.14	107	123
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	25	32	80	0.07%	57.8%	SLHDAIMIVR	99.7%	47.5	25	38.7	5	0	0	1154.64	388	397
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	25	32	80	0.07%	57.8%	SQDAEVGDGTTSVTLLAAEFLK	99.7%	154	25	154	5	2	0	2252.13	85	106
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	25	32	80	0.07%	57.8%	TATQLAVNK	99.7%	67.9	25	59	3	0	0	945.54	127	135
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	25	32	80	0.07%	57.8%	TCTFILR	99.7%	45.3	25	19.4	4	0	0	910.48	369	375
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	25	32	80	0.07%	57.8%	TFSYAGFEMQPK	99.7%	92.9	25	92.9	3	0	0	1421.64	219	230
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	25	32	80	0.07%	57.8%	TMMACGGSIQTSVNALSADVLGR	99.7%	62.1	25	62.1	1	1	0	2339.12	322	344
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	25	32	80	0.07%	57.8%	VPEEDLKR	99.7%	62.5	25	52.5	4	0	0	985.53	314	321
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	25	32	80	0.07%	57.8%	VQGGALEDSQLVAGVAFK	99.7%	117	25	117	2	0	0	1788.95	200	217
T-complex protein 1 subunit eta	CCT7	TCPH_HUMAN	59.4	100.0%	25	32	80	0.07%	57.8%	YNFFTGCPK	99.7%	58.3	25	46	4	0	0	1133.51	358	366
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	ACTILLR	99.7%	47.2	25	28.9	4	0	0	846.49	371	377
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	ALDDMISTLK	99.7%	78.2	25	70.3	6	0	0	1106.58	129	138
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	ALDDMISTLKK	99.7%	67.1	25	57.1	3	1	0	1234.67	129	139
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	AMTGVEQWPYR	99.7%	57.8	25	52.1	6	0	0	1337.63	428	438
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	AVAQALEVIPR	99.7%	92.3	25	67.5	12	0	0	1166.69	439	449
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	EILSEVER	99.7%	60.3	25	16.6	8	0	0	974.52	382	389

T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	EIQVQHPAAK	99.7%	59.1	25	47.6	10	0	0	1120.61	69	78
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	ELGIWEPLAVK	99.7%	69.1	25	63.3	4	0	0	1254.71	492	502
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	GISDLAQHYLMR	99.7%	79.8	25	79.8	11	4	0	1403.71	295	306
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	HTQENCETWGVNGETGTLVDMK	99.7%	57.2	25	57.2	0	2	0	2506.10	470	491
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	IDDIVSGHK	99.7%	65	25	50.1	8	0	0	983.52	519	527
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	IDDIVSGHKK	98.6%	33.1	25	25.4	2	0	0	1111.61	519	528
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	IGDEYFTFITDCK	99.7%	85.3	25	80.1	2	0	0	1608.73	355	367
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	IGDEYFTFITDCKDPK	99.7%	51.2	25	49.9	4	3	0	1948.90	355	370
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	IPGGIIEDSCVLR	99.7%	102	25	92.7	6	0	0	1428.75	204	216
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	ISIPVDISDSDMMLNIINSSITTK	99.5%	37.2	25	37.2	2	0	0	2639.32	140	163
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	IVLLDSSLEYK	99.7%	75.2	25	60.1	7	0	0	1279.71	238	248
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	IVLLDSSLEYKK	99.7%	69.1	25	65.2	4	2	0	1407.81	238	249
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	IVSRPEELREDDVGTGAGLLEIK	99.7%	55.6	25	55.6	0	2	0	2496.33	331	353
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	KGESQTDIEITR	99.7%	89.2	25	58.4	2	2	0	1376.70	249	260
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	MLLDPMGGIVMTNDGNAILR	99.7%	117	25	117	16	5	0	2131.07	49	68
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	MVQFEENGR	99.7%	52	25	39.6	2	0	0	1109.50	182	190
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	MVQFEENGRK	99.7%	40.1	25	27.6	2	0	0	1237.60	182	191
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	NLQDAMQVCR	99.7%	65.8	25	52.2	10	0	0	1234.57	390	399
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	NVLLDPQLVPGGGASEMAVAHALTEK	99.7%	36.3	25	30.9	0	8	0	2617.37	400	425
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	SMIEISR	99.7%	45.9	25	28.6	1	0	0	835.43	79	85
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	TAVETAVLLLR	99.7%	103	25	88.7	7	0	0	1185.72	508	518
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	TLIQNCGASTIR	99.7%	70.4	25	57.2	2	0	0	1333.69	450	461
T-complex protein 1 subunit gamma	CCT3	TCPG_HUMAN	60.5	100.0%	29	45	175	0.16%	59.1%	WSSLACNIALDAVK	99.7%	101	25	95.5	5	0	0	1547.79	168	181
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	16	0.02%	18.2%	AIADTGANVVVTGGK	99.7%	88.8	25	81.2	2	0	0	1372.74	282	296
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	16	0.02%	18.2%	APGFAQMLK	95.2%	28.1	25	20.1	1	0	0	978.51	8	16
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	16	0.02%	18.2%	AVDDGVNTFK	99.7%	80.1	25	70.2	2	0	0	1065.52	391	400
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	16	0.02%	18.2%	DIDEVSSLLR	99.7%	71.3	25	59.9	2	0	0	1146.60	156	165
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	16	0.02%	18.2%	DMLEAGILDTYLGK	99.7%	87.7	25	87.7	1	0	0	1538.78	491	504
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	16	0.02%	18.2%	ETEGDVTSVK	99.7%	47.5	25	43.3	2	0	0	1064.51	226	235
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	16	0.02%	18.2%	FAEAFEAIPR	99.7%	74.7	25	59.3	2	0	0	1150.59	441	450
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	16	0.02%	18.2%	LFVTNDAATILR	99.7%	96.5	25	85.8	2	0	0	1333.75	63	74
T-complex protein 1 subunit theta	CCT8	TCPQ_HUMAN	59.6	100.0%	9	9	16	0.02%	18.2%	LYAVHQEGNK	99.5%	38.1	25	35.1	2	0	0	1158.59	467	476
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	21	33	107	0.10%	45.8%	ALQFLEEVK	99.7%	50.7	25	44.3	2	0	0	1076.60	130	138
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	21	33	107	0.10%	45.8%	AQAALAVNISAAR	99.7%	100	25	94.2	8	0	0	1255.71	16	28
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	21	33	107	0.10%	45.8%	AQLGVQAFADALLIIPK	99.7%	95.6	25	93.8	7	2	0	1768.04	433	449
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	21	33	107	0.10%	45.8%	DGNVLLHEMQIQHPTASLIAK	99.7%	49.3	25	49.3	0	7	0	2315.22	59	79
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	21	33	107	0.10%	45.8%	EGIVALRR	96.1%	28.9	25	11.6	2	0	0	913.56	308	315
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	21	33	107	0.10%	45.8%	EMDRETLIDVAR	99.7%	48.6	25	40.3	4	4	0	1447.72	142	153
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	21	33	107	0.10%	45.8%	ETLIDVAR	99.7%	56.3	25	46.5	2	0	0	916.51	146	153
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	21	33	107	0.10%	45.8%	GFVVINQK	99.7%	42.1	25	27.4	2	0	0	904.53	288	295
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	21	33	107	0.10%	45.8%	GIDPFSLDALSK	99.7%	84.7	25	34	8	0	0	1262.66	296	307
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	21	33	107	0.10%	45.8%	GLQDVLR	99.7%	41.1	25	14	2	0	0	800.46	29	35
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	21	33	107	0.10%	45.8%	GLVLDHGAR	99.7%	54.4	25	43.3	8	0	0	937.52	209	217
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	21	33	107	0.10%	45.8%	HKSETDTSLIR	99.7%	37	25	25.5	2	2	0	1286.67	198	208
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	21	33	107	0.10%	45.8%	IITEGFEAAK	99.7%	67.4	25	29.6	4	0	0	1078.58	118	127
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	21	33	107	0.10%	45.8%	MLVSGAGDIK	99.7%	64.4	25	39.1	6	0	0	990.53	46	55
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	21	33	107	0.10%	45.8%	NAIDDGCVVPGAGAVEVAMAEALIK	99.7%	42.2	25	34.4	2	2	0	2470.23	400	424
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	21	33	107	0.10%	45.8%	QADLYISEGLHPR	99.7%	108	25	98.5	4	3	0	1498.77	105	117
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	21	33	107	0.10%	45.8%	SETDTSLIR	99.7%	62.7	25	50.6	5	0	0	1021.52	200	208
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	21	33	107	0.10%	45.8%	TEVNSGFFYK	99.7%	61.5	25	58.2	2	0	0	1191.57	242	251
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	21	33	107	0.10%	45.8%	VATAQDDITGDGTTSNVLIIGELLK	99.7%	112	25	112	3	3	0	2544.34	80	104

T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	21	33	107	0.10%	45.8%	VCGDSDKGFVVINQK	99.7%	76	25	73.8	2	2	0	1665.83	281	295
T-complex protein 1 subunit zeta	CCT6A	TCPZ_HUMAN	58.0	100.0%	21	33	107	0.10%	45.8%	VLAQNSGFDLQETLVK	99.7%	112	25	112	7	0	0	1761.94	450	465
Telomere length regulation protein TEL2 homolog	TELO2	TELO2_HUMAN	91.7	99.8%	2	2	3	0.00%	3.7%	AVLICLAQLGEPELR	99.7%	47.8	25	43.5	2	0	0	1681.93	363	377
Telomere length regulation protein TEL2 homolog	TELO2	TELO2_HUMAN	91.7	99.8%	2	2	3	0.00%	3.7%	LQQENLAEFFPQNYFR	99.7%	70.9	25	70	1	0	0	2043.99	171	186
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	10	10	15	0.01%	6.0%	DAPDVVVSAIWK	98.0%	31.5	25	26.5	1	0	0	1299.69	492	503
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	10	10	15	0.01%	6.0%	GLEEIPVFDISEK	96.9%	29.9	25	26.6	1	0	0	1475.76	2370	2382
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	10	10	15	0.01%	6.0%	IGISDISSLSEK	99.7%	72.7	25	63	2	0	0	1248.67	1700	1711
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	10	10	15	0.01%	6.0%	ITSELSEANALELLSK	99.7%	68.3	25	67.9	1	0	0	1717.92	88	103
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	10	10	15	0.01%	6.0%	LIAEQTLQENLIEK	99.7%	92	25	88.1	2	0	0	1641.91	1468	1481
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	10	10	15	0.01%	6.0%	LVSDIIDPVALEIPLSK	99.7%	66.4	25	66.4	2	0	0	1822.06	2399	2415
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	10	10	15	0.01%	6.0%	SLIDNFALNPDILCSAK	99.7%	60.4	25	60.4	2	0	0	1890.96	299	315
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	10	10	15	0.01%	6.0%	SNESVDIQDQEEK	99.7%	43	25	43	1	0	0	1520.67	1576	1588
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	10	10	15	0.01%	6.0%	TLGETSANAETEQNKK	99.7%	59.9	25	55.8	2	0	0	1720.83	1489	1504
Telomere-associated protein RIF1	RIF1	RIF1_HUMAN	274.5	100.0%	10	10	15	0.01%	6.0%	YAEYSFTSLPVPESNLR	99.7%	46	25	46	1	0	0	1972.97	1659	1675
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	7	7	11	0.01%	9.9%	AVYTLYQQR	99.7%	50.6	25	40.5	2	0	0	1141.60	505	513
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	7	7	11	0.01%	9.9%	LAAVQLLQFLAPK	99.7%	64.1	25	62	2	0	0	1411.87	116	128
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	7	7	11	0.01%	9.9%	LLLQHAPLR	99.7%	49.4	25	46.3	1	0	0	1060.66	866	874
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	7	7	11	0.01%	9.9%	NPELSTQLIDIIHTAAAR	98.5%	32.8	25	26.2	1	0	0	1963.06	566	583
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	7	7	11	0.01%	9.9%	SQNFDILQSAISK	99.7%	96.1	25	90	2	0	0	1450.75	747	759
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	7	7	11	0.01%	9.9%	VGPEELPVVGQLLR	99.7%	45.2	25	45.2	2	0	0	1505.87	852	865
Testis-expressed sequence 10 protein	TEX10	TEX10_HUMAN	105.7	100.0%	7	7	11	0.01%	9.9%	VLDILLEQYPALITGR	99.7%	75.3	25	75.3	1	0	0	1814.04	163	178
Tetratricopeptide repeat protein 19, mitochondrial	TTC19	TTC19_HUMAN	42.5	99.8%	2	2	3	0.00%	5.8%	ALQISEEIQGER	99.4%	37	25	36	2	0	0	1372.71	263	274
Tetratricopeptide repeat protein 19, mitochondrial	TTC19	TTC19_HUMAN	42.5	99.8%	2	2	3	0.00%	5.8%	LASIYAAQNR	99.6%	39.2	25	31.1	1	0	0	1106.60	185	194
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	7	7	12	0.01%	5.5%	AALVDYLDGK	99.5%	37.6	25	37.6	2	0	0	1064.56	682	691
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	7	7	12	0.01%	5.5%	ASELNPESIYSVFK	99.7%	47.5	25	47.5	2	0	0	1583.80	624	637
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	7	7	12	0.01%	5.5%	LSDYDSSEEAIR	99.7%	82.5	25	82.5	1	0	0	1384.62	363	374
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	7	7	12	0.01%	5.5%	SGPGLIGLGIK	99.7%	68.8	25	49.5	2	0	0	1011.62	271	281
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	7	7	12	0.01%	5.5%	SNPDQPAVILLLR	99.1%	34.9	25	34.9	2	0	0	1435.83	1355	1367
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	7	7	12	0.01%	5.5%	TLDQISDADNIPGLLVLK	99.7%	48.7	25	48.7	1	0	0	1925.06	375	392
Tetratricopeptide repeat protein 37	TTC37	TTC37_HUMAN	175.5	100.0%	7	7	12	0.01%	5.5%	VVAQYAQR	99.7%	49.5	25	35.6	2	0	0	934.51	1202	1209
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	9	9	16	0.02%	25.0%	IHSDTFASGGER	99.7%	47	25	33	2	0	0	1276.59	337	348
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	9	9	16	0.02%	25.0%	LSQLGLDAGK	99.7%	64.1	25	48.5	2	0	0	1001.56	218	227
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	9	9	16	0.02%	25.0%	QTSLDAVAQAVVDR	99.7%	113	25	103	2	0	0	1472.77	320	333
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	9	9	16	0.02%	25.0%	QVGIICGQESTR	99.7%	41.4	25	34.8	1	0	0	1347.67	230	241
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	9	9	16	0.02%	25.0%	SFLESIDDALAEK	99.7%	97.5	25	89.5	2	0	0	1437.71	116	128
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	9	9	16	0.02%	25.0%	STVDGLQVTQLNVDHTTENEDELFR	99.0%	28.9	25	28.9	0	1	0	2860.36	193	217
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	9	9	16	0.02%	25.0%	VLLQAFDVVER	99.7%	81.7	25	71.9	3	0	0	1288.73	105	115
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	9	9	16	0.02%	25.0%	VYPVSVPYSSAQSTSK	99.6%	39.1	25	38.4	1	0	0	1699.85	387	402
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	TAB1_HUMAN	54.6	100.0%	9	9	16	0.02%	25.0%	YGYTDIDLLSAAK	99.7%	88.8	25	88.8	2	0	0	1429.72	250	262
Thioredoxin	TXN	THIO_HUMAN	11.7	100.0%	3	3	5	0.00%	19.0%	EKLEATINELV	99.7%	49.8	25	45.8	1	0	0	1258.69	95	105
Thioredoxin	TXN	THIO_HUMAN	11.7	100.0%	3	3	5	0.00%	19.0%	VGEFSGANK	99.7%	55.8	25	47.1	2	0	0	908.45	86	94
Thioredoxin	TXN	THIO_HUMAN	11.7	100.0%	3	3	5	0.00%	19.0%	VGEFSGANKEK	99.3%	36.3	25	28.1	2	0	0	1165.58	86	96
Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3	PRDX3_HUMAN	27.7	99.8%	2	2	3	0.00%	9.0%	GLFIIDPNGVIK	99.7%	51.7	25	42	2	0	0	1285.75	185	196
Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3	PRDX3_HUMAN	27.7	99.8%	2	2	3	0.00%	9.0%	HLSVNDLPVGR	99.7%	48.9	25	36	1	0	0	1206.66	197	207
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	11.2%	ADQLDYENFR	99.7%	50.9	25	50.9	1	0	0	1270.57	1085	1094
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	11.2%	AEGGYFGQIR	99.7%	53.7	25	48.5	2	0	0	1097.54	711	720
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	11.2%	ATGFDGGNKADQLDYENFR	99.7%	36.1	25	36.1	0	1	0	2117.95	1076	1094
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	11.2%	CIFSAIDAVYCAR	99.7%	106	25	106	2	0	0	1545.72	986	998
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	11.2%	ECGNYPGFLTILR	99.7%	42.6	25	36.3	2	0	0	1539.76	1063	1075
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	11.2%	FLCCMLETVTR	99.7%	62.1	25	58.8	2	0	0	1429.66	1042	1052
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	11.2%	FLQLCIFPR	99.7%	51.7	25	35.4	2	0	0	1193.65	977	985

THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	11.2%	FVELVHQQK	99.7%	41.5	25	37.9	2	0	0	1127.62	999	1007
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	11.2%	GEFLHLCR	99.7%	49.2	25	39.1	2	0	0	1031.51	22	29
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	11.2%	LDPETLESLGLIK	99.7%	85.4	25	75	2	0	0	1427.80	127	139
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	11.2%	LGLLEALLK	99.7%	61.5	25	50.6	2	0	0	969.63	346	354
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	11.2%	LIALAICK	99.2%	35.5	25	22.9	1	0	0	901.55	378	385
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	11.2%	NILIVLTK	98.9%	34.2	25	30.3	2	0	0	913.61	1122	1129
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	11.2%	SFDLLILK	99.7%	42.2	25	38.9	2	0	0	948.58	673	680
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	11.2%	TPNFSTLLCYDR	99.7%	84.9	25	79.8	2	0	0	1486.70	1008	1019
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	11.2%	VFSDIIYTVASCTENEASR	99.7%	88.3	25	86.4	2	0	0	2162.01	1020	1038
THO complex subunit 2	THOC2	THOC2_HUMAN	182.8	100.0%	17	17	32	0.03%	11.2%	VLNLGQALER	99.7%	59.1	25	49.2	3	0	0	1112.64	1137	1146
THO complex subunit 4	ALYREF	THOC4_HUMAN	26.9	100.0%	4	6	14	0.01%	24.9%	MDMSLDDIIK	99.7%	47.9	25	41.2	2	0	0	1180.56	5	14
THO complex subunit 4	ALYREF	THOC4_HUMAN	26.9	100.0%	4	6	14	0.01%	24.9%	QQLSAEELDAQLDAYNAR	99.7%	109	25	108	2	1	0	2034.97	236	253
THO complex subunit 4	ALYREF	THOC4_HUMAN	26.9	100.0%	4	6	14	0.01%	24.9%	QYNGVPLDGRPMNIQLVTSQIDAQR	99.7%	43.3	25	39.1	0	1	0	2829.43	165	189
THO complex subunit 4	ALYREF	THOC4_HUMAN	26.9	100.0%	4	6	14	0.01%	24.9%	SLGTADVHFER	99.7%	84	25	72.4	6	2	0	1231.61	145	155
THO complex subunit 6 homolog	THOC6	THOC6_HUMAN	37.5	99.8%	2	2	4	0.00%	7.6%	TSLEVPEINALLLVPK	99.7%	39.4	25	38.7	2	0	0	1736.02	122	137
THO complex subunit 6 homolog	THOC6	THOC6_HUMAN	37.5	99.8%	2	2	4	0.00%	7.6%	VDVFTNLGYR	99.7%	64.3	25	55	2	0	0	1183.61	326	335
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	5	5	9	0.01%	8.2%	GAYIYNALIEFIR	99.7%	84.6	25	76.3	2	0	0	1542.83	349	361
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	5	5	9	0.01%	8.2%	GFQEVVTPNIFNSR	99.7%	63	25	55.5	1	0	0	1607.82	368	381
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	5	5	9	0.01%	8.2%	LADFGVLHR	99.7%	51.9	25	38.9	2	0	0	1027.57	434	442
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	5	5	9	0.01%	8.2%	NELSGALTGLTR	99.7%	77.8	25	61.3	2	0	0	1231.66	443	454
Threonine--tRNA ligase, cytoplasmic	TARS	SYTC_HUMAN	83.4	100.0%	5	5	9	0.01%	8.2%	TVYSVFGFSFK	99.7%	41	25	41	2	0	0	1281.65	485	495
Threonine--tRNA ligase, mitochondrial	TARS2	SYTM_HUMAN	81.0	100.0%	3	3	5	0.00%	4.5%	LADFGALHR	99.7%	58.5	25	46.5	2	0	0	999.54	430	438
Threonine--tRNA ligase, mitochondrial	TARS2	SYTM_HUMAN	81.0	100.0%	3	3	5	0.00%	4.5%	VSGISFPTTELLR	99.7%	40.6	25	40.6	1	0	0	1419.78	276	288
Threonine--tRNA ligase, mitochondrial	TARS2	SYTM_HUMAN	81.0	100.0%	3	3	5	0.00%	4.5%	VYNALVAFIR	99.7%	77.7	25	71.1	2	0	0	1165.67	331	340
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	5	5	8	0.01%	12.0%	AANNIASLLTK	99.7%	55.7	25	45.5	2	0	0	1115.64	359	369
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	5	5	8	0.01%	12.0%	AVLLTQDTK	98.2%	32	25	23.3	1	0	0	988.57	441	449
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	5	5	8	0.01%	12.0%	NITHFGPTTLR	98.9%	34	25	34	1	0	0	1256.67	294	304
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	5	5	8	0.01%	12.0%	TGSVDIIVTDLPFGK	99.7%	68	25	64.4	2	0	0	1561.85	397	411
THUMP domain-containing protein 3	THUMPD3	THUM3_HUMAN	57.0	100.0%	5	5	8	0.01%	12.0%	TPQAFVHPSEQDGER	99.7%	40	25	40	0	2	0	1697.79	485	499
Thymidine kinase, cytosolic	TK1	KITH_HUMAN	25.5	100.0%	3	3	4	0.00%	15.8%	GQIQVILGPMFSGK	99.7%	41.5	25	41.5	1	0	0	1474.81	19	32
Thymidine kinase, cytosolic	TK1	KITH_HUMAN	25.5	100.0%	3	3	4	0.00%	15.8%	TVIVAALDGTFQR	99.7%	90.8	25	84.6	2	0	0	1390.77	118	130
Thymidine kinase, cytosolic	TK1	KITH_HUMAN	25.5	100.0%	3	3	4	0.00%	15.8%	YSSSFCTHDR	99.7%	44.1	25	39.5	1	0	0	1259.51	61	70
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	13	14	41	0.04%	14.2%	ASAVSELSPR	99.7%	72.5	25	64.3	5	0	0	1016.54	236	245
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	13	14	41	0.04%	14.2%	DSRPSQAAGDNQGDEAK	99.4%	30.8	25	30.8	0	1	0	1745.77	186	202
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	13	14	41	0.04%	14.2%	EESAASGGAAYTK	99.7%	71.3	25	67.7	4	0	0	1241.56	334	346
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	13	14	41	0.04%	14.2%	EQTFSGGTSQDTK	99.7%	74.3	25	68.9	2	0	0	1385.62	203	215
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	13	14	41	0.04%	14.2%	GSFSDTGLGDGK	99.7%	62.3	25	58.9	6	0	0	1140.52	376	387
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	13	14	41	0.04%	14.2%	KTEELEEESFPER	99.7%	34.7	25	30.5	0	1	0	1622.75	486	498
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	13	14	41	0.04%	14.2%	NREEEWDPEYTPK	96.4%	29.2	25	29.2	1	0	0	1692.75	864	876
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	13	14	41	0.04%	14.2%	SIFQHIQSAQSQR	99.7%	66.4	25	49.9	5	4	0	1529.78	609	621
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	13	14	41	0.04%	14.2%	SPLQSVVVR	99.7%	56.9	25	44.5	4	0	0	984.58	253	261
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	13	14	41	0.04%	14.2%	SPPSTGSTYGSSQK	99.7%	72	25	72	2	0	0	1383.64	320	333
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	13	14	41	0.04%	14.2%	SPPSTGSTYGSSQKEESAASGGAAYTK	99.1%	29.4	25	29.4	0	1	0	2606.19	320	346
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	13	14	41	0.04%	14.2%	TEELEEESFPER	99.7%	63.1	25	50.1	2	0	0	1494.66	487	498
Thyroid hormone receptor-associated protein 3	THRAP3	TR150_HUMAN	108.7	100.0%	13	14	41	0.04%	14.2%	YKDDPVDLR	99.7%	42.6	25	30.3	3	0	0	1120.56	710	718
Tight junction protein ZO-1	TJP1	ZO1_HUMAN	195.5	99.9%	2	2	3	0.00%	1.2%	MSARAAAAK	98.2%	32	25	0.85	1	0	0	876.47	1	9
Tight junction protein ZO-1	TJP1	ZO1_HUMAN	195.5	99.9%	2	2	3	0.00%	1.2%	SVASSQPAKPTK	99.7%	39.7	25	22.8	2	0	0	1200.66	175	186
Tight junction protein ZO-2	TJP2	ZO2_HUMAN	134.0	99.8%	2	2	3	0.00%	2.4%	EDAVLYLLEIPK	99.7%	46.8	25	46.8	2	0	0	1402.78	569	580
Tight junction protein ZO-2	TJP2	ZO2_HUMAN	134.0	99.8%	2	2	3	0.00%	2.4%	SNPSAVAGNETPGASTK	95.1%	28.1	25	28.1	1	0	0	1587.76	1017	1033
Torsin-1A-interacting protein 1	TOR1AIP1	TOIP1_HUMAN	66.2	99.8%	2	2	3	0.00%	4.5%	FESFPAGSTLIFYK	99.7%	44.1	25	44.1	1	0	0	1606.82	481	494
Torsin-1A-interacting protein 1	TOR1AIP1	TOIP1_HUMAN	66.2	99.8%	2	2	3	0.00%	4.5%	SQPAILLLTAAR	99.7%	60.3	25	58.6	2	0	0	1253.76	405	416

TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	5	6	9	0.01%	26.1%	AFLSTHPNTETVFEAFLK	95.8%	28.7	25	28.7	1	0	0	2052.04	206	223
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	5	6	9	0.01%	26.1%	ATTPADGEEPAPEAEALAAAR	99.7%	102	25	102	2	1	0	2037.97	6	26
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	5	6	9	0.01%	26.1%	FLSGLELVK	99.7%	53	25	42	2	0	0	1005.60	32	40
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	5	6	9	0.01%	26.1%	TIGQVLAR	97.8%	31.1	25	8.98	1	0	0	857.52	145	152
TP53-regulating kinase	TP53RK	PRPK_HUMAN	28.2	100.0%	5	6	9	0.01%	26.1%	TPQGLSNLAK	99.7%	56.7	25	46.5	2	0	0	1028.57	135	144
Trafficking protein particle complex subunit 1	TRAPPC1	TPPC1_HUMAN	16.8	100.0%	5	6	12	0.01%	37.9%	DGFLAFQTSR	99.7%	51.8	25	41.8	2	0	0	1141.56	59	68
Trafficking protein particle complex subunit 1	TRAPPC1	TPPC1_HUMAN	16.8	100.0%	5	6	12	0.01%	37.9%	LHYYETPTGIK	99.3%	35.8	25	25	2	0	0	1321.68	71	81
Trafficking protein particle complex subunit 1	TRAPPC1	TPPC1_HUMAN	16.8	100.0%	5	6	12	0.01%	37.9%	NPLCPLGQTVQSELFR	99.7%	51.4	25	51.4	2	0	0	1858.95	112	127
Trafficking protein particle complex subunit 1	TRAPPC1	TPPC1_HUMAN	16.8	100.0%	5	6	12	0.01%	37.9%	SRLDSYVR	99.7%	46.6	25	36.9	2	0	0	995.53	128	135
Trafficking protein particle complex subunit 1	TRAPPC1	TPPC1_HUMAN	16.8	100.0%	5	6	12	0.01%	37.9%	TVHNLYLFDR	99.7%	47.2	25	36.1	2	2	0	1277.66	2	11
Trafficking protein particle complex subunit 6B	TRAPPC6B	TPC6B_HUMAN	18.0	99.8%	2	2	3	0.00%	11.4%	VGQGLIER	99.7%	53.9	25	35.9	2	0	0	871.50	43	50
Trafficking protein particle complex subunit 6B	TRAPPC6B	TPC6B_HUMAN	18.0	99.8%	2	2	3	0.00%	11.4%	YLAFTCGLIR	99.2%	35.7	25	33.7	1	0	0	1213.64	118	127
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	8	8	14	0.01%	5.5%	AVATYHANTER	99.7%	47.3	25	42.5	2	0	0	1232.60	503	513
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	8	8	14	0.01%	5.5%	DTALETALNAK	99.7%	75.4	25	66.7	2	0	0	1146.60	427	437
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	8	8	14	0.01%	5.5%	ELPEYYELIR	99.7%	51.5	25	48.6	2	0	0	1324.68	1493	1502
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	8	8	14	0.01%	5.5%	GLDPVEILQER	99.7%	75.2	25	66.3	2	0	0	1268.68	360	370
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	8	8	14	0.01%	5.5%	IQELENLPGSLAGDLR	99.7%	59.6	25	50.1	1	0	0	1724.92	382	397
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	8	8	14	0.01%	5.5%	LCTVNSVEEK	99.3%	36.1	25	25.2	2	0	0	1178.57	1204	1213
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	8	8	14	0.01%	5.5%	QLSEVFIQLPSR	99.2%	35.3	25	27.3	1	0	0	1416.78	1480	1491
Transcription activator BRG1	SMARCA4	SMCA4_HUMAN	184.6	100.0%	8	8	14	0.01%	5.5%	VIQAGMFDQK	99.7%	40.1	25	34.3	2	0	0	1136.58	1228	1237
Transcription elongation factor B polypeptide 1	TCEB1	ELOC_HUMAN	12.5	99.8%	2	2	3	0.00%	28.6%	AMLSGPGQFAENETNEVNFR	99.7%	70.2	25	70.2	1	0	0	2227.01	44	63
Transcription elongation factor B polypeptide 1	TCEB1	ELOC_HUMAN	12.5	99.8%	2	2	3	0.00%	28.6%	LISSDGHEFIVK	99.7%	42.4	25	38.5	2	0	0	1344.72	21	32
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	5	6	11	0.01%	22.0%	AEWQVYKEEISR	99.7%	56.7	25	56.7	2	2	0	1537.76	105	116
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	5	6	11	0.01%	22.0%	FSKEQLPIFK	99.0%	34.5	25	24.9	2	0	0	1236.70	60	69
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	5	6	11	0.01%	22.0%	IYQDAYR	99.7%	41.8	25	33.2	1	0	0	928.45	98	104
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	5	6	11	0.01%	22.0%	NLSDSEKELYIQHAK	99.7%	43	25	39.8	0	2	0	1774.90	191	205
Transcription factor A, mitochondrial	TFAM	TFAM_HUMAN	29.1	100.0%	5	6	11	0.01%	22.0%	SAYNVYVAER	99.7%	65.5	25	58.5	2	0	0	1171.57	160	169
Transcriptional activator protein Pur-alpha	PURA	PURA_HUMAN	34.9	99.9%	2	2	3	0.00%	15.2%	GPGLGSTQGQTIALPAQGLIEFR	99.7%	101	25	101	2	0	0	2311.24	177	199
Transcriptional activator protein Pur-alpha	PURA	PURA_HUMAN	34.9	99.9%	2	2	3	0.00%	15.2%	LIDDYGVEEEPAELPEGTSLTVDNKR	99.7%	55.6	25	55.6	0	1	0	2889.40	205	230
Transducin beta-like protein 3	TBL3	TBL3_HUMAN	89.0	100.0%	5	5	9	0.01%	8.5%	ALLLAQWAWQEGSVTR	99.7%	79.3	25	79.3	2	0	0	1828.97	87	102
Transducin beta-like protein 3	TBL3	TBL3_HUMAN	89.0	100.0%	5	5	9	0.01%	8.5%	LLLFSSATDAAIR	97.2%	30.2	25	25.2	1	0	0	1377.77	166	178
Transducin beta-like protein 3	TBL3	TBL3_HUMAN	89.0	100.0%	5	5	9	0.01%	8.5%	LWALQDFSCLK	96.8%	29.7	25	26.4	1	0	0	1380.70	547	557
Transducin beta-like protein 3	TBL3	TBL3_HUMAN	89.0	100.0%	5	5	9	0.01%	8.5%	SPGLYFLTAGDQGTLR	99.7%	43.3	25	43.3	1	0	0	1695.87	257	272
Transducin beta-like protein 3	TBL3	TBL3_HUMAN	89.0	100.0%	5	5	9	0.01%	8.5%	VNILEVASGAVLR	99.7%	100	25	92.2	4	0	0	1340.79	47	59
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	20	21	35	0.03%	31.4%	AVLGTSNFK	99.7%	41.6	25	35.3	1	0	0	936.51	487	495
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	20	21	35	0.03%	31.4%	DENLALYVENQFR	99.7%	41.2	25	37.4	1	0	0	1610.78	162	174
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	20	21	35	0.03%	31.4%	DSAQNSVIIVDK	99.7%	92.6	25	82.1	2	0	0	1288.67	194	205
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	20	21	35	0.03%	31.4%	EMGLSLQWLYSAR	99.7%	59.1	25	49.5	2	0	0	1553.78	634	646
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	20	21	35	0.03%	31.4%	GFVEPDHYVVVGAQR	99.7%	43.3	25	39.5	0	2	0	1672.84	395	409
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	20	21	35	0.03%	31.4%	ILNIFGVIK	99.7%	53.2	25	38.6	2	0	0	1016.65	386	394
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	20	21	35	0.03%	31.4%	LAQMFSDMVLK	99.7%	46.7	25	41.4	1	0	0	1282.65	429	439
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	20	21	35	0.03%	31.4%	LAVDEEENADNNTK	99.7%	85.5	25	44.1	2	0	0	1561.70	40	53
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	20	21	35	0.03%	31.4%	LDSTDFTGTIK	96.0%	28.8	25	20.5	1	0	0	1197.60	135	145
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	20	21	35	0.03%	31.4%	LLNENSYVPR	99.7%	62.5	25	50.6	2	0	0	1204.63	146	155
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	20	21	35	0.03%	31.4%	LTTDFGNAEK	99.7%	52.1	25	32	2	0	0	1095.53	656	665
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	20	21	35	0.03%	31.4%	LTVSNVLK	99.7%	43.6	25	23.2	1	0	0	873.54	375	382
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	20	21	35	0.03%	31.4%	LVYLVENPGGYVAYSK	99.7%	97.8	25	97.8	2	0	0	1771.93	209	224
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	20	21	35	0.03%	31.4%	QVDGDNSHVEMK	99.4%	37	25	30.5	1	0	0	1358.60	28	39
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	20	21	35	0.03%	31.4%	SAFSNLFGGEPLSYTR	99.7%	97.7	25	97.7	2	0	0	1745.85	7	22
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	20	21	35	0.03%	31.4%	SGVGTALLLK	99.7%	56	25	37.2	2	0	0	958.59	419	428
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	20	21	35	0.03%	31.4%	SSGLPNIPVQTISR	99.7%	59.7	25	46.2	2	0	0	1468.81	326	339

Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	20	21	35	0.03%	31.4%	VEYHFLSPYVSPK	99.7%	50.5	25	50.5	1	2	0	1565.80	681	693
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	20	21	35	0.03%	31.4%	VSASPLLYTLIEK	99.7%	105	25	104	2	0	0	1433.83	496	508
Transferrin receptor protein 1	TFRC	TFR1_HUMAN	84.9	100.0%	20	21	35	0.03%	31.4%	YNSQLLSFVR	99.7%	64	25	58	2	0	0	1226.65	614	623
Transformation/transcription domain-associated protein	TRRAP	TRRAP_HUMAN	437.6	99.8%	2	2	3	0.00%	0.6%	ACQLPLFSYIVER	97.4%	30.5	25	20.3	2	0	0	1595.83	1132	1144
Transformation/transcription domain-associated protein	TRRAP	TRRAP_HUMAN	437.6	99.8%	2	2	3	0.00%	0.6%	LGFTPSVTIEQR	95.1%	28	25	21.2	1	0	0	1347.73	1992	2003
Transformer-2 protein homolog alpha	TRA2A	TRA2A_HUMAN	32.7	100.0%	4	4	17	0.02%	18.1%	GFAFVYFER	99.7%	67.2	25	44.8	7	0	0	1135.56	161	169
Transformer-2 protein homolog alpha	TRA2A	TRA2A_HUMAN	32.7	100.0%	4	4	17	0.02%	18.1%	IDDSKEAMER	99.7%	50	25	39.4	2	0	0	1193.55	170	179
Transformer-2 protein homolog alpha	TRA2A	TRA2A_HUMAN	32.7	100.0%	4	4	17	0.02%	18.1%	IRVDYSITK	99.7%	45.5	25	26.8	2	0	0	1094.62	190	198
Transformer-2 protein homolog alpha	TRA2A	TRA2A_HUMAN	32.7	100.0%	4	4	17	0.02%	18.1%	RSPSPYYSR	99.2%	35.2	25	25.2	2	0	0	1112.55	259	267
Transformer-2 protein homolog alpha	TRA2A	TRA2A_HUMAN	32.7	100.0%	4	4	17	0.02%	18.1%	YGPLSGVNVVYDQR	99.7%	65.1	25	57.2	6	0	0	1566.79	142	155
Transformer-2 protein homolog beta	TRA2B	TRA2B_HUMAN	33.7	100.0%	3	3	11	0.01%	13.5%	GFAFVYFENVDDAK	99.7%	79.1	25	65.6	5	0	0	1621.75	160	173
Transformer-2 protein homolog beta	TRA2B	TRA2B_HUMAN	33.7	100.0%	3	3	11	0.01%	13.5%	RSPSPYYSR	99.2%	35.2	25	25.2	2	0	0	1112.55	263	271
Transformer-2 protein homolog beta	TRA2B	TRA2B_HUMAN	33.7	100.0%	3	3	11	0.01%	13.5%	YGPIADVSIVYDQQSR	99.7%	94	25	91.8	4	0	0	1810.90	141	156
Transgelin-2	TAGLN2	TAGL2_HUMAN	22.4	99.9%	2	2	2	0.00%	9.6%	GPAYGLSR	98.6%	33.1	25	24.9	1	0	0	820.43	5	12
Transgelin-2	TAGLN2	TAGL2_HUMAN	22.4	99.9%	2	2	2	0.00%	9.6%	NFSDNQLQEGK	99.3%	35.8	25	35.8	1	0	0	1279.59	161	171
Transitional endoplasmic reticulum ATPase	VCP	TERA_HUMAN	89.3	100.0%	2	2	3	0.00%	3.7%	LDQLIYIPLPDEK	97.3%	30.4	25	30.4	1	0	0	1556.86	639	651
Transitional endoplasmic reticulum ATPase	VCP	TERA_HUMAN	89.3	100.0%	2	2	3	0.00%	3.7%	NAPAIIFIDELDAIAPK	99.7%	96.1	25	91	2	0	0	1811.00	296	312
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	3	3	6	0.01%	11.8%	DGATILTHAYSR	99.7%	71.9	25	70.9	2	0	0	1304.66	121	132
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	3	3	6	0.01%	11.8%	DKGETIQGLR	99.3%	36	25	27.1	2	0	0	1116.60	37	46
Translation initiation factor eIF-2B subunit alpha	EIF2B1	EI2BA_HUMAN	33.7	100.0%	3	3	6	0.01%	11.8%	FISLASLEYSDYSK	99.7%	88.1	25	82.3	2	0	0	1622.79	75	88
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	99.8%	2	3	6	0.01%	8.0%	MTAAQPSETTVGNMVR	99.7%	73.8	25	67.5	4	0	0	1724.79	68	83
Translation initiation factor eIF-2B subunit beta	EIF2B2	EI2BB_HUMAN	39.0	99.8%	2	3	6	0.01%	8.0%	SDESDQQESLHK	99.7%	47.4	25	47.4	2	0	0	1402.61	100	111
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	10	11	21	0.02%	25.2%	AHNVPVLVCCETYK	99.7%	39.6	25	39.4	0	1	0	1689.81	429	442
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	10	11	21	0.02%	25.2%	ALQQVIQDYTTPPNEELSR	99.7%	40.3	25	37.1	2	0	0	2202.10	232	250
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	10	11	21	0.02%	25.2%	ASPSTAGETPSGVK	99.7%	73.7	25	67.9	2	0	0	1288.64	129	142
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	10	11	21	0.02%	25.2%	ILQEAWTEGR	99.7%	82.7	25	66.8	2	0	0	1202.62	345	354
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	10	11	21	0.02%	25.2%	IVLAAQAISR	99.7%	74	25	43	2	0	0	1041.64	312	321
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	10	11	21	0.02%	25.2%	LGLQYSQGLVSGSNAR	99.7%	96.5	25	95.1	2	0	0	1649.86	210	225
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	10	11	21	0.02%	25.2%	LPEYPQVDDLLLR	99.7%	62.3	25	62.3	2	0	0	1570.85	144	156
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	10	11	21	0.02%	25.2%	VGTAQLALVAR	99.7%	98.2	25	79.3	2	0	0	1098.66	418	428
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	10	11	21	0.02%	25.2%	VSLFSHLPQYSR	99.7%	57.2	25	51.3	2	2	0	1433.75	177	188
Translation initiation factor eIF-2B subunit delta	EIF2B4	EI2BD_HUMAN	57.6	100.0%	10	11	21	0.02%	25.2%	VVVVDSRPWLEGR	99.7%	45.2	25	32.7	2	0	0	1511.83	358	370
Translation initiation factor eIF-2B subunit epsilon	EIF2B5	EI2BE_HUMAN	80.4	100.0%	3	3	5	0.00%	4.2%	GYNPAEVGAAGK	99.2%	35.5	25	29.3	1	0	0	1133.56	482	493
Translation initiation factor eIF-2B subunit epsilon	EIF2B5	EI2BE_HUMAN	80.4	100.0%	3	3	5	0.00%	4.2%	IITSELYR	99.6%	38.4	25	24.8	1	0	0	994.56	122	129
Translation initiation factor eIF-2B subunit epsilon	EIF2B5	EI2BE_HUMAN	80.4	100.0%	3	3	5	0.00%	4.2%	YCALLLPLLK	99.7%	39.5	25	39.5	3	0	0	1203.72	617	626
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	6	6	10	0.01%	17.0%	AYDASLAMLMR	99.7%	68.9	25	63.1	1	0	0	1241.60	123	133
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	6	6	10	0.01%	17.0%	DFIGVDSTGKR	95.1%	28	25	18.8	1	0	0	1194.61	156	166
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	6	6	10	0.01%	17.0%	KGQDSIEPVPGQK	99.7%	64.1	25	63.2	2	0	0	1382.73	134	146
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	6	6	10	0.01%	17.0%	LLSALCPEEPPVHSSAQIVSK	99.5%	31.8	25	31.8	0	2	0	2262.18	329	349
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	6	6	10	0.01%	17.0%	SELIPYLVR	99.2%	35.6	25	20.7	2	0	0	1089.63	226	234
Translation initiation factor eIF-2B subunit gamma	EIF2B3	EI2BG_HUMAN	50.2	100.0%	6	6	10	0.01%	17.0%	VGFEEVIVVTTR	99.7%	82.8	25	69.6	2	0	0	1348.75	46	57
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	AALLETLSLLLAK	99.7%	84.7	25	84.7	4	0	0	1355.85	2324	2336
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	ADYTSHLR	99.7%	48.5	25	35.5	2	0	0	962.47	2184	2191
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	AGSVELLGAMAYCAPK	99.7%	94	25	91.2	2	0	0	1637.80	1515	1530
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	AIITALGVER	99.7%	66.7	25	39.2	2	0	0	1042.63	1872	1881
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	ALADENEFVR	99.7%	71	25	64.3	2	0	0	1163.57	1785	1794
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	ALGTLVSHVTLR	99.7%	72.7	25	59.4	2	0	0	1266.75	915	926
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	ALVAVLLSR	99.7%	76.2	25	65.5	4	0	0	941.61	568	576
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	AVMSNLSAHGVK	99.7%	47.8	25	40.4	3	0	0	1213.64	1485	1496
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	AYSDQAIVNLLK	99.7%	95.3	25	68.9	2	0	0	1334.73	2610	2621
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	CLQNPSSDIR	97.5%	30.6	25	17.2	1	0	0	1189.56	2558	2567

Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	CLQTLLDTK	99.4%	36.6	25	25.8	2	0	0	1091.58	1595	1603
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	EDAGGMIQR	99.6%	38.6	25	14.9	2	0	0	976.45	1372	1380
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	EEFAIMQTPAGELYDK	99.7%	62.1	25	62.1	2	0	0	1841.86	761	776
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	ENVNSLLPVFEEFLK	99.7%	55.8	25	52.5	1	0	0	1777.94	1290	1304
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	FDKEEEIR	95.9%	28.7	25	18.1	1	0	0	1065.52	1135	1142
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	FTPYVGPIIPCILK	99.7%	40.6	25	40.2	1	0	0	1617.91	1771	1784
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	GAAYGLAGLVK	99.7%	70.1	25	56.9	2	0	0	1019.59	1396	1406
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	GEPGAAPLSAPAFSLVFPFLK	99.7%	45.3	25	45.3	1	0	0	2116.15	966	986
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	GIKEEVQLTSK	99.7%	42.3	25	27.4	2	0	0	1231.69	819	829
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	GLGILSLK	99.7%	44.5	25	13.9	2	0	0	800.52	1407	1414
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	GVTSILPVLR	99.7%	47.4	25	47.4	2	0	0	1054.66	2260	2269
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	HHIETGGGQLPAK	99.7%	50.4	25	44.6	1	2	0	1344.70	2538	2550
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	HLDQIIPR	99.7%	40.7	25	33.8	2	0	0	991.57	705	712
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	HLFAILGGSEGK	99.7%	43.3	25	39.9	2	0	0	1228.67	341	352
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	IDPEAFITR	99.7%	43.9	25	33.9	2	0	0	1061.56	696	704
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	ILPEIIPILEEGLR	99.7%	70.1	25	70.1	2	0	0	1604.96	1960	1973
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	IVVSNTPR	98.6%	33.2	25	25.6	2	0	0	885.52	1910	1917
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	KGVTSILPVLR	99.7%	42.9	25	39.5	2	0	0	1182.76	2259	2269
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	LAHGLLEELK	95.5%	28.4	25	12	1	0	0	1122.65	600	609
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	LFCLTLHR	94.7%	27.8	25	19.1	1	0	0	1059.58	53	60
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	LMDEAVLALR	99.7%	62.5	25	50.3	4	0	0	1130.62	314	323
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	LMEIYQEK	99.7%	41.1	25	38.4	2	0	0	1053.53	1201	1208
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	LMQQLLESDKYAER	98.9%	28.7	25	23.4	0	1	0	1723.87	1381	1394
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	LSSFWQLIVDEK	99.7%	53.7	25	53.7	1	0	0	1464.77	510	521
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	LTEVLTDSHVK	99.7%	66	25	56.5	2	0	0	1241.67	1543	1553
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	LTSADALRPSVVSITGPLIR	99.6%	33.2	25	33.2	0	2	0	2066.20	2293	2312
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	LYRPPPVLDALGR	99.7%	58.2	25	58.1	2	2	0	1466.85	1209	1221
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	NAPNDASYDAVR	99.7%	69.9	25	69.9	2	0	0	1292.59	1305	1316
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	NLLHSLQSSGIGSK	99.7%	65.1	25	54.8	2	2	0	1440.78	88	101
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	QAAAIILNIYCSR	99.7%	71.2	25	59.8	1	0	0	1492.79	2169	2181
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	QAGAEALSQAVAR	99.7%	72.4	25	58.8	2	0	0	1271.67	1177	1189
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	QGEEVFQSLSK	99.7%	48.4	25	38.9	2	0	0	1251.62	2624	2634
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	QLSSCLPNIVPK	99.7%	45.1	25	40.4	1	0	0	1355.74	1531	1542
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	SALLDFYMK	99.7%	47.6	25	38.4	3	0	0	1087.55	221	229
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	SDTQLVVR	99.7%	39.7	25	8.78	2	0	0	917.51	1894	1901
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	SGAAQGLAEVMAGLGVEK	99.7%	101	25	91.4	2	0	0	1687.87	1714	1731
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	SIIQSAQQDSIK	99.7%	41.9	25	37.5	1	0	0	1317.70	777	788
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	SIIQSAQQDSIKK	99.7%	64.7	25	52.7	2	0	0	1445.80	777	789
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	SLVSGLIR	99.7%	49.8	25	22.5	2	0	0	844.53	2192	2199
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	SWCQEELSVAVK	99.7%	56.5	25	44.8	2	0	0	1435.69	937	948
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	VDENGPELLPR	99.7%	73.3	25	65	2	0	0	1238.64	1027	1037
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	VDIAPHVR	99.4%	36.9	25	35.5	1	0	0	906.52	1746	1753
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	VDPLFTELLNGIR	99.0%	34.4	25	32	1	0	0	1486.83	2381	2393
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	VISESPPDQWEAR	99.7%	55.3	25	53.3	2	0	0	1513.73	1222	1234
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	VLAFLSSVAGDALTR	99.7%	79.3	25	79.3	4	0	0	1519.85	2093	2107
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	VLAGLYMGR	99.7%	44.8	25	38.4	1	0	0	979.54	1885	1893
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	VLPLEALVTDAGEVTEAGK	99.7%	72.6	25	72.6	2	2	0	1912.03	617	635
Translational activator GCN1	GCN1L1	GCN1L_HUMAN	292.8	100.0%	58	65	118	0.11%	24.6%	YLLDSCAPLLR	99.7%	69.4	25	68.6	2	0	0	1320.70	241	251
Translocation protein SEC63 homolog	SEC63	SEC63_HUMAN	88.0	100.0%	4	4	6	0.01%	6.1%	AYAALTDEESR	99.7%	57.5	25	42.7	2	0	0	1225.57	148	158
Translocation protein SEC63 homolog	SEC63	SEC63_HUMAN	88.0	100.0%	4	4	6	0.01%	6.1%	DATSRPTDNILIPQLIR	98.3%	26.9	25	17.2	0	1	0	1923.07	263	279
Translocation protein SEC63 homolog	SEC63	SEC63_HUMAN	88.0	100.0%	4	4	6	0.01%	6.1%	VLLLSHLAR	99.7%	49.4	25	49.4	1	0	0	1021.65	303	311

Translocation protein SEC63 homolog	SEC63	SEC63_HUMAN	88.0	100.0%	4	4	6	0.01%	6.1%	YSGDQILIR	99.7%	44.4	25	32.4	2	0	0	1064.57	218	226
Translocator protein	TSPO	TSPOA_HUMAN	18.8	99.8%	2	2	3	0.00%	9.5%	ELGGFTEK	99.7%	64.3	25	26.1	2	0	0	880.44	70	77
Translocator protein	TSPO	TSPOA_HUMAN	18.8	99.8%	2	2	3	0.00%	9.5%	FVHGEGLR	99.0%	34.7	25	27.1	1	0	0	914.48	25	32
Translocon-associated protein subunit alpha	SSR1	SSRA_HUMAN	32.2	99.8%	2	2	4	0.00%	9.1%	GEDFPANNIVK	99.7%	60.9	25	52.7	2	0	0	1203.60	92	102
Translocon-associated protein subunit alpha	SSR1	SSRA_HUMAN	32.2	99.8%	2	2	4	0.00%	9.1%	GTEDFIVESLDASFR	99.7%	61.9	25	56.6	2	0	0	1685.80	111	125
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	6	8	26	0.02%	37.0%	FFDEESYSLLR	99.7%	75.9	25	75.1	8	0	0	1405.66	106	116
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	6	8	26	0.02%	37.0%	FFDEESYSLLRK	99.7%	65	25	58.8	2	0	0	1533.76	106	117
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	6	8	26	0.02%	37.0%	NNEDISIIPPLFTVSVDHR	99.7%	34.2	25	34.2	1	2	0	2166.12	121	139
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	6	8	26	0.02%	37.0%	SAHAGTYEVR	99.7%	42.3	25	36.6	3	0	0	1090.53	96	105
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	6	8	26	0.02%	37.0%	VQNMALYADVGGK	99.7%	93.6	25	87.1	7	0	0	1365.68	61	73
Translocon-associated protein subunit delta	SSR4	SSRD_HUMAN	19.0	100.0%	6	8	26	0.02%	37.0%	YQVSWSLDHK	99.7%	48.2	25	37	3	0	0	1262.62	86	95
Transmembrane 9 superfamily member 3	TM9SF3	TM9S3_HUMAN	67.9	100.0%	3	4	10	0.01%	5.4%	NLSGQPNFPCR	99.7%	46.9	25	46.3	2	0	0	1289.61	419	429
Transmembrane 9 superfamily member 3	TM9SF3	TM9S3_HUMAN	67.9	100.0%	3	4	10	0.01%	5.4%	YFSLPFCVGSK	99.7%	52.9	25	43	4	0	0	1304.63	60	70
Transmembrane 9 superfamily member 3	TM9SF3	TM9S3_HUMAN	67.9	100.0%	3	4	10	0.01%	5.4%	YLDPSFFQHR	99.7%	55.2	25	43.3	3	1	0	1309.63	211	220
Transmembrane and coiled-coil domain-containing protein 1	TMCO1	TMCO1_HUMAN	21.2	100.0%	3	3	5	0.00%	16.5%	ETITESAGR	99.3%	36.3	25	21.7	2	0	0	963.47	55	63
Transmembrane and coiled-coil domain-containing protein 1	TMCO1	TMCO1_HUMAN	21.2	100.0%	3	3	5	0.00%	16.5%	ILGLAPSR	98.7%	33.3	25	29.5	2	0	0	826.51	161	168
Transmembrane and coiled-coil domain-containing protein 1	TMCO1	TMCO1_HUMAN	21.2	100.0%	3	3	5	0.00%	16.5%	QAGGFLGPPPPSGK	99.7%	43.7	25	40.1	1	0	0	1309.69	173	186
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	7	10	23	0.02%	31.1%	DLLVTGAYEISDQSGGAGGLR	99.7%	97.4	25	95.2	2	0	0	2079.04	51	71
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	7	10	23	0.02%	31.1%	IPDQLVILDMK	99.7%	67.8	25	45.4	8	0	0	1284.72	117	127
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	7	10	23	0.02%	31.1%	ITDSAGHILYSK	99.7%	76.9	25	66.8	2	2	0	1304.68	76	87
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	7	10	23	0.02%	31.1%	ITDSAGHILYSKEDATK	99.7%	45.8	25	43.5	1	3	0	1848.93	76	92
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	7	10	23	0.02%	31.1%	LKPLEVELR	99.7%	40.8	25	34.2	2	0	0	1096.67	144	152
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	7	10	23	0.02%	31.1%	NYEEIAK	99.5%	37.8	25	30.8	1	0	0	866.43	134	140
Transmembrane emp24 domain-containing protein 10	TMED10	TMEDA_HUMAN	25.0	100.0%	7	10	23	0.02%	31.1%	NYEEIAKVEK	99.7%	56	25	45.4	2	0	0	1222.63	134	143
Transmembrane emp24 domain-containing protein 2	TMED2	TMED2_HUMAN	22.8	100.0%	2	4	11	0.01%	12.4%	IVMFTIDIGEAPK	99.7%	92.6	25	92.6	7	0	0	1433.77	105	117
Transmembrane emp24 domain-containing protein 2	TMED2	TMED2_HUMAN	22.8	100.0%	2	4	11	0.01%	12.4%	YTFAAHMDGTYK	99.7%	49.3	25	49.3	4	0	0	1404.63	80	91
Transmembrane protein 11, mitochondrial	TMEM11	TMM11_HUMAN	21.5	100.0%	5	6	18	0.02%	27.1%	KIYELYAV	97.9%	31.4	25	31.4	2	0	0	998.56	185	192
Transmembrane protein 11, mitochondrial	TMEM11	TMM11_HUMAN	21.5	100.0%	5	6	18	0.02%	27.1%	LGPGSSGGSAR	99.7%	42.9	25	35.5	1	0	0	945.47	9	19
Transmembrane protein 11, mitochondrial	TMEM11	TMM11_HUMAN	21.5	100.0%	5	6	18	0.02%	27.1%	LPLHTLTSSTPVVLVR	99.7%	66.5	25	66.5	4	4	0	1733.03	146	161
Transmembrane protein 11, mitochondrial	TMEM11	TMM11_HUMAN	21.5	100.0%	5	6	18	0.02%	27.1%	YIVIEPTR	99.7%	51.9	25	48.8	3	0	0	990.56	59	66
Transmembrane protein 11, mitochondrial	TMEM11	TMM11_HUMAN	21.5	100.0%	5	6	18	0.02%	27.1%	YQVEYDAYK	99.7%	42	25	35.5	4	0	0	1178.54	134	142
Transmembrane protein 126A	TMEM126A	T126A_HUMAN	21.5	100.0%	6	7	14	0.01%	37.9%	ALQLSEPGKEIH	99.4%	36.6	25	36.6	2	0	0	1321.71	184	195
Transmembrane protein 126A	TMEM126A	T126A_HUMAN	21.5	100.0%	6	7	14	0.01%	37.9%	GNILSYWIR	99.4%	36.6	25	30.9	2	0	0	1121.61	142	150
Transmembrane protein 126A	TMEM126A	T126A_HUMAN	21.5	100.0%	6	7	14	0.01%	37.9%	IAAGLPMAGIPFLTTDLTYR	99.7%	72.4	25	71.2	3	0	0	2137.14	65	84
Transmembrane protein 126A	TMEM126A	T126A_HUMAN	21.5	100.0%	6	7	14	0.01%	37.9%	KINQLPEAER	99.4%	36.8	25	25.4	2	0	0	1197.66	20	29
Transmembrane protein 126A	TMEM126A	T126A_HUMAN	21.5	100.0%	6	7	14	0.01%	37.9%	SNNKENITIVDISR	99.3%	36.2	25	30.9	2	0	0	1602.84	6	19
Transmembrane protein 126A	TMEM126A	T126A_HUMAN	21.5	100.0%	6	7	14	0.01%	37.9%	YQSALLPHK	99.7%	41.9	25	37.6	3	0	0	1056.58	133	141
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	6	6	10	0.01%	25.5%	ALLANALTSALR	99.7%	99.3	25	93.4	4	0	0	1213.73	58	69
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	6	6	10	0.01%	25.5%	GSNSLPLLR	98.1%	31.7	25	21.6	1	0	0	956.55	135	143
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	6	6	10	0.01%	25.5%	LCLQSIAFISR	99.7%	63	25	58.8	2	0	0	1307.71	231	241
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	6	6	10	0.01%	25.5%	LDTAMWLSR	99.6%	38.9	25	27.9	1	0	0	1092.55	23	31
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	6	6	10	0.01%	25.5%	SVLDKLSANQQNILK	99.6%	32.7	25	30.1	0	1	0	1670.94	144	158
Transmembrane protein 33	TMEM33	TMM33_HUMAN	28.0	100.0%	6	6	10	0.01%	25.5%	TLFNELR	95.0%	27.9	25	11.5	1	0	0	892.49	206	212
Transmembrane protein 97	TMEM97	TMM97_HUMAN	20.8	99.8%	2	2	4	0.00%	13.1%	EFKDPLLQEPPAWFK	99.2%	35.6	25	32.6	2	0	0	1844.96	53	67
Transmembrane protein 97	TMEM97	TMM97_HUMAN	20.8	99.8%	2	2	4	0.00%	13.1%	ELYPVEFR	99.7%	41.2	25	31.2	2	0	0	1052.54	37	44
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	23	0.02%	16.3%	ALVMLLEVR	99.7%	66.2	25	61.1	3	0	0	1059.62	246	254
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	23	0.02%	16.3%	ATVGILITTIASK	99.7%	102	25	102	2	0	0	1287.79	116	128
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	23	0.02%	16.3%	ESQSPDTTIQR	99.7%	54.9	25	44.9	2	0	0	1261.60	29	39
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	23	0.02%	16.3%	FSDQFPLPLK	99.7%	49.7	25	48.4	1	0	0	1191.64	880	889
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	23	0.02%	16.3%	GDVEEDETIPDSEQDIRPR	99.7%	41.5	25	41.3	0	1	0	2200.00	328	346
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	23	0.02%	16.3%	GELQNWPDLLPK	99.7%	71.6	25	56.8	2	0	0	1409.74	129	140

Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	23	0.02%	16.3%	QSSFALLGDLTK	99.7%	90.9	25	82	2	0	0	1279.69	693	704
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	23	0.02%	16.3%	SECLNNIGDSSPLIR	99.7%	70	25	70	2	0	0	1674.81	101	115
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	23	0.02%	16.3%	SITCWTLSR	99.7%	41	25	22	2	0	0	1123.56	464	472
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	23	0.02%	16.3%	SNILTLMYQCMQDK	99.7%	98	25	93	2	0	0	1744.81	674	687
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	23	0.02%	16.3%	TLLENTAITIGR	99.7%	70.1	25	55.2	2	0	0	1301.74	774	785
Transportin-1	TNPO1	TNPO1_HUMAN	102.4	100.0%	12	13	23	0.02%	16.3%	YSDIDIILLK	99.7%	54.1	25	51.1	2	0	0	1192.68	318	327
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	16	0.02%	14.1%	ASFWLGELQR	99.7%	46.9	25	22.8	2	0	0	1206.63	30	39
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	16	0.02%	14.1%	ETTVGAVTVTHK	99.7%	59.6	25	43.9	2	0	0	1242.67	882	893
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	16	0.02%	14.1%	GTALVLAR	99.7%	56.6	25	31.8	2	0	0	800.50	564	571
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	16	0.02%	14.1%	IFTELCETFLEK	99.7%	59.4	25	49.3	1	0	0	1529.76	298	309
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	16	0.02%	14.1%	IVCTPGQGLGDLR	99.7%	60.5	25	56.5	2	0	0	1385.72	310	322
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	16	0.02%	14.1%	LLALLFEVLQQDK	99.7%	56.3	25	54.5	1	0	0	1529.89	224	236
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	16	0.02%	14.1%	SLDSFLLSPEAAVGLLK	99.7%	75.7	25	75.7	2	0	0	1759.98	547	563
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	16	0.02%	14.1%	SVDPENNPTLVEVLEGVVR	99.7%	77.3	25	77.3	1	0	0	2066.08	450	468
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	16	0.02%	14.1%	TNDEVIHGIFK	97.4%	30.6	25	5.9	1	0	0	1272.66	356	366
Transportin-3	TNPO3	TNPO3_HUMAN	104.2	100.0%	10	10	16	0.02%	14.1%	VIQEIWPVLSETLNK	99.7%	43.8	25	43.8	2	0	0	1768.98	637	651
Treacle protein	TCOF1	TCOF_HUMAN	152.1	100.0%	5	5	6	0.01%	4.3%	AGPVAVQVK	99.5%	37.3	25	23.9	1	0	0	868.53	592	600
Treacle protein	TCOF1	TCOF_HUMAN	152.1	100.0%	5	5	6	0.01%	4.3%	GSLGQGTAPVLPGK	99.7%	68.8	25	60.3	1	0	0	1281.72	733	746
Treacle protein	TCOF1	TCOF_HUMAN	152.1	100.0%	5	5	6	0.01%	4.3%	SPAGPAATPAQAQAASTPR	99.7%	70.3	25	70.3	1	0	0	1749.89	967	985
Treacle protein	TCOF1	TCOF_HUMAN	152.1	100.0%	5	5	6	0.01%	4.3%	TSQVGAASAPAK	99.7%	41.8	25	37.2	1	0	0	1087.57	368	379
Treacle protein	TCOF1	TCOF_HUMAN	152.1	100.0%	5	5	6	0.01%	4.3%	VLTELLEQER	99.7%	44.4	25	28.5	2	0	0	1229.67	1318	1327
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	7	9	27	0.03%	22.8%	FFVMTSLR	99.7%	50.5	25	32.5	8	0	0	1000.53	199	206
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	7	9	27	0.03%	22.8%	FIHDQTSPNPK	99.7%	49.3	25	49.1	3	3	0	1283.64	150	160
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	7	9	27	0.03%	22.8%	GLSSLLYGSIPK	99.7%	54.7	25	34.5	2	0	0	1234.70	86	97
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	7	9	27	0.03%	22.8%	GTYQGLTATVLK	99.7%	68	25	60.2	4	0	0	1251.69	179	190
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	7	9	27	0.03%	22.8%	NTWDCGLQILK	99.7%	50.2	25	40.8	2	0	0	1347.67	258	268
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	7	9	27	0.03%	22.8%	SHGVLGLYR	99.7%	40.4	25	38.2	1	0	0	1001.55	77	85
Tricarboxylate transport protein, mitochondrial	SLC25A1	TXTP_HUMAN	34.0	100.0%	7	9	27	0.03%	22.8%	TQLQLDER	99.7%	52.5	25	30.3	4	0	0	1002.52	51	58
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	32	62	0.06%	43.0%	ADMVIEAVFEDLSLK	99.7%	100	25	99.2	4	0	0	1695.85	441	455
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	32	62	0.06%	43.0%	ALMGLYHGQVLCK	99.7%	49.8	25	48.3	2	0	0	1489.77	338	350
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	32	62	0.06%	43.0%	ALTSFER	99.3%	35.9	25	20.4	2	0	0	823.43	416	422
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	32	62	0.06%	43.0%	CLAPMMSEVIR	99.7%	40.3	25	34.1	2	0	0	1306.63	550	560
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	32	62	0.06%	43.0%	DATLTALDR	99.7%	65.6	25	25.9	2	0	0	975.51	391	399
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	32	62	0.06%	43.0%	DGPGFYTTR	99.7%	59	25	47	2	0	0	1013.47	541	549
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	32	62	0.06%	43.0%	DLNSDMDSILASLK	99.7%	111	25	105	2	0	0	1521.75	647	660
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	32	62	0.06%	43.0%	DSIFSNLTGQLDYQGFEK	99.7%	111	25	111	2	0	0	2061.98	423	440
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	32	62	0.06%	43.0%	DTSASAVAVGLK	99.7%	78.1	25	57.9	2	0	0	1118.61	520	531
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	32	62	0.06%	43.0%	EVEAVIPDHCIFASNTSALPISEIAAVSK	99.7%	42.2	25	42.2	0	2	0	3068.56	461	489
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	32	62	0.06%	43.0%	FGELVMTK	99.7%	46	25	25.1	1	0	0	940.48	327	334
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	32	62	0.06%	43.0%	FGGGNPELLTQMVSK	99.7%	84.6	25	74.9	4	0	0	1577.80	611	625
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	32	62	0.06%	43.0%	FVDLYGAQK	99.5%	37.6	25	34.5	2	0	0	1040.54	720	728
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	32	62	0.06%	43.0%	GFYIYQEGVK	99.7%	74.3	25	62.5	2	0	0	1203.60	635	644
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	32	62	0.06%	43.0%	LTAYAMTIPFVR	99.7%	91	25	85.1	6	0	0	1382.75	268	279
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	32	62	0.06%	43.0%	MGLVDQLVEPLGPGLKPPEER	99.7%	50.7	25	50.7	0	4	0	2290.21	215	235
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	32	62	0.06%	43.0%	MQLLEIITTEK	99.7%	82.1	25	75.1	3	0	0	1318.73	506	516
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	32	62	0.06%	43.0%	MVGVPAALDMMLTGR	99.7%	106	25	106	3	0	0	1561.79	191	205
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	32	62	0.06%	43.0%	SEVSSDEDIQFR	99.7%	75.2	25	74.8	2	0	0	1411.63	665	676
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	32	62	0.06%	43.0%	TGIEQGSDAGYLCESQK	99.7%	110	25	110	2	0	0	1842.82	310	326
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	32	62	0.06%	43.0%	TIEYLEEVAITFAK	99.7%	77.8	25	69	1	0	0	1626.86	236	249
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	32	62	0.06%	43.0%	TLQEVTQLSQEAQR	99.7%	105	25	95.4	2	1	0	1630.84	112	125
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	32	62	0.06%	43.0%	TVLGTPEVLLGALPGAGGTQR	99.7%	96.4	25	95.8	3	2	0	2007.12	167	187

Trifunctional enzyme subunit alpha, mitochondrial	HADHA	ECHA_HUMAN	83.0	100.0%	24	32	62	0.06%	43.0%	VIGMHYFSPVDK	99.7%	41.9	25	35.2	2	0	0	1392.70	494	505
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	15	18	32	0.03%	34.0%	AALTGLLHR	99.7%	45.4	25	34.9	1	0	0	951.57	82	90
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	15	18	32	0.03%	34.0%	ALAMGYKPK	99.6%	38.8	25	32.5	4	0	0	978.54	326	334
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	15	18	32	0.03%	34.0%	DLMPHDLAR	99.7%	42	25	39	1	0	0	1083.53	73	81
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	15	18	32	0.03%	34.0%	DNGIRPSSLEQMAK	99.7%	55.6	25	25.8	2	0	0	1545.77	278	291
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	15	18	32	0.03%	34.0%	DQLLLGPTYATPK	99.7%	68.6	25	64.8	2	0	0	1416.77	349	361
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	15	18	32	0.03%	34.0%	EAALGAGFSDK	99.7%	61.8	25	54.4	2	0	0	1065.52	118	128
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	15	18	32	0.03%	34.0%	EGGQYGLVAACAAGGQGHAMIVEAYPK	99.7%	78.8	25	78.8	0	3	0	2705.28	448	474
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	15	18	32	0.03%	34.0%	EVVDYIIFGTVIQEVK	99.7%	106	25	105	1	0	0	1852.01	96	111
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	15	18	32	0.03%	34.0%	KLMLDLNK	99.7%	39.8	25	7.33	2	0	0	990.57	181	188
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	15	18	32	0.03%	34.0%	LAAAFAVSR	99.7%	75.3	25	57.1	2	0	0	905.52	230	238
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	15	18	32	0.03%	34.0%	LVMAAANR	99.7%	59.8	25.3	51	2	0	0	845.47	437	444
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	15	18	32	0.03%	34.0%	NVVVVDGVR	99.7%	57.9	25	52.1	2	0	0	956.55	53	61
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	15	18	32	0.03%	34.0%	TPFLLSGTSYK	99.7%	56.7	25	52	2	0	0	1213.65	62	72
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	15	18	32	0.03%	34.0%	TPFLLSGTSYKDLMPHDLAR	99.7%	44.9	25	44.9	0	4	0	2262.16	62	81
Trifunctional enzyme subunit beta, mitochondrial	HADHB	ECHB_HUMAN	51.3	100.0%	15	18	32	0.03%	34.0%	VGLPPLEK	98.2%	32	25	30.2	2	0	0	852.52	409	416
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	59	0.06%	32.8%	AAGFKDPLLASGTDGVGTK	99.7%	41.2	25	41.2	0	2	0	1804.94	481	499
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	59	0.06%	32.8%	AFAHITGGGLLENIPR	99.7%	77.4	25	68.7	2	2	0	1665.91	677	692
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	59	0.06%	32.8%	AIAFLQQPR	99.7%	44.7	25	30.3	2	0	0	1043.60	425	433
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	59	0.06%	32.8%	AVQEIMQEK	99.7%	45.5	25	36.9	2	0	0	1091.54	170	178
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	59	0.06%	32.8%	ENLISALEEAKK	99.7%	55.3	25	38.9	2	0	0	1344.74	394	405
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	59	0.06%	32.8%	EQTEQILR	96.7%	29.5	25	20.6	2	0	0	1016.54	744	751
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	59	0.06%	32.8%	ESGVDIAAGNMLVK	99.7%	64.8	25	59.1	2	0	0	1403.72	439	452
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	59	0.06%	32.8%	FGDPECQVILPLLK	99.7%	73.7	25	66.4	4	0	0	1628.87	293	306
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	59	0.06%	32.8%	GDTVATLSER	99.7%	54.2	25	23	2	0	0	1048.53	966	975
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	59	0.06%	32.8%	IKDTVLQR	99.7%	46.1	25	25.3	3	0	0	972.58	250	257
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	59	0.06%	32.8%	ISNTAISISDHTALAQFCK	99.7%	54.2	25	54.2	0	4	0	2077.04	45	63
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	59	0.06%	32.8%	ITEGDVVVGIASSGLHSNGFSLVR	99.7%	50.2	25	50.2	0	1	0	2414.27	605	628
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	59	0.06%	32.8%	IYSHSLLPVLR	99.7%	42.4	25	41.5	2	2	0	1297.76	661	671
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	59	0.06%	32.8%	KIEFVVVGPEAPLAAGIVGNLR	99.3%	30.6	25	30.6	0	2	0	2249.30	66	87
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	59	0.06%	32.8%	LDLSVTEAVVAGIAK	99.7%	53.3	25	43.2	2	0	0	1485.85	543	557
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	59	0.06%	32.8%	LGVDLDAQTWR	99.3%	35.8	25	28.9	1	0	0	1273.65	698	708
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	59	0.06%	32.8%	MLNIHPSLLPSFK	99.7%	51.4	25	49.9	3	1	0	1496.83	911	923
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	59	0.06%	32.8%	QVLVAPGNAGTACSEK	99.7%	60.2	25	60.2	1	0	0	1601.80	29	44
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	59	0.06%	32.8%	SAGVQCFGPTAEAAQLESSKR	99.3%	30.5	25	30.5	0	2	0	2194.06	88	108
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	59	0.06%	32.8%	TFNCGVGAVLVVSK	99.7%	110	25	104	2	0	0	1450.77	730	743
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	59	0.06%	32.8%	VDLGGFAGLFDLK	99.7%	93.2	25	83.5	3	0	0	1351.73	468	480
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	59	0.06%	32.8%	VFSWLQQEGHLSEEEMAR	99.7%	55	25	51.8	0	1	0	2176.01	712	729
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	59	0.06%	32.8%	VLAVTAIR	99.7%	52.8	25	28.5	4	0	0	842.55	386	393
Trifunctional purine biosynthetic protein adenosine-3	GART	PUR2_HUMAN	107.8	100.0%	24	28	59	0.06%	32.8%	VLEFNCR	99.3%	36.1	25	36.1	3	0	0	937.46	286	292
Triosephosphate isomerase	TPI1	TPIS_HUMAN	30.8	99.8%	2	2	7	0.01%	9.8%	TATPQQAQEVHEK	99.7%	43.9	25	42.5	3	0	0	1466.72	213	225
Triosephosphate isomerase	TPI1	TPIS_HUMAN	30.8	99.8%	2	2	7	0.01%	9.8%	VVLAYEPVWAIGTGK	99.7%	79.8	25	69.8	4	0	0	1602.89	198	212
TRMT1-like protein	TRMT1L	TRM1L_HUMAN	81.7	100.0%	3	3	4	0.00%	6.1%	NLGIVSVTSTDISSLYAK	99.7%	103	25	103	2	0	0	1868.00	391	408
TRMT1-like protein	TRMT1L	TRM1L_HUMAN	81.7	100.0%	3	3	4	0.00%	6.1%	QLIFCTLAALAEER	99.7%	60.7	25	60.7	1	0	0	1634.86	261	274
TRMT1-like protein	TRMT1L	TRM1L_HUMAN	81.7	100.0%	3	3	4	0.00%	6.1%	SSYIAASTAKPPK	99.7%	49	25	44.8	1	0	0	1320.72	214	226
tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6	TRMT6	TRM6_HUMAN	55.8	100.0%	3	3	6	0.01%	8.5%	MGGFGSIIQLYPGGGPVR	99.7%	64.9	25	64.9	2	0	0	1805.94	221	238
tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6	TRMT6	TRM6_HUMAN	55.8	100.0%	3	3	6	0.01%	8.5%	NADGLIVASR	99.7%	75.7	25	70.6	2	0	0	1015.55	368	377
tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6	TRMT6	TRM6_HUMAN	55.8	100.0%	3	3	6	0.01%	8.5%	YDTLAQMLTLGNIR	99.7%	73.2	25	63.6	2	0	0	1608.84	185	198
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	21	43	0.04%	32.6%	DGQWFTDWDAVPHSR	99.6%	33.2	25	33.2	0	2	0	1816.80	370	384
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	21	43	0.04%	32.6%	EDPFVFIPEDDPLFPPIEK	99.7%	46.5	25	44.4	1	0	0	2244.11	517	535
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	21	43	0.04%	32.6%	EGVILTNESAASTGQPDNDVTEGQR	99.1%	29.2	25	29.2	0	1	0	2588.21	713	737

tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	21	43	0.04%	32.6%	FHQFLVSETESGNISR	99.7%	36.5	25	32.1	0	1	0	1850.90	145	160
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	21	43	0.04%	32.6%	GAEQLAEGGR	99.7%	83.3	25	71.2	2	0	0	987.49	306	315
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	21	43	0.04%	32.6%	IITVSMEDVK	99.7%	49.2	25	40.5	4	0	0	1134.61	619	628
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	21	43	0.04%	32.6%	ILCDVPCSGDGTMR	99.7%	48.8	25	48.8	2	0	0	1580.69	265	278
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	21	43	0.04%	32.6%	ILLTQENPFFR	99.7%	85.6	25	79.9	6	0	0	1377.75	629	639
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	21	43	0.04%	32.6%	IVPEGEWGQFMDALR	98.8%	33.8	25	33.8	1	0	0	1747.85	57	71
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	21	43	0.04%	32.6%	KLSSETYSQAK	99.7%	58.3	25	57.5	3	0	0	1241.64	640	650
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	21	43	0.04%	32.6%	LAQEGIYTLYPFINSR	99.7%	82.6	25	82.3	2	2	0	1884.99	603	618
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	21	43	0.04%	32.6%	LQIDVDGR	99.2%	35.3	25	27.8	2	0	0	915.49	249	256
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	21	43	0.04%	32.6%	LQQQQRPEDAEDGAEGGGK	99.7%	41.4	25	41.4	0	2	0	2012.93	10	28
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	21	43	0.04%	32.6%	LSSETYSQAK	99.7%	63.7	25	61.5	2	0	0	1113.54	641	650
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	21	43	0.04%	32.6%	MMGLEVLGEK	99.7%	41.3	25	34	2	0	0	1106.56	701	710
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	21	43	0.04%	32.6%	NNSGEEFDCAFR	99.7%	72.4	25	72.4	2	0	0	1445.58	591	602
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	21	43	0.04%	32.6%	SEGALELADVSNELPGLK	99.7%	120	25	115	4	0	0	1841.95	339	356
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	NSUN2_HUMAN	86.5	100.0%	18	21	43	0.04%	32.6%	YEPDSANPDALQCPIVLCGWR	99.7%	75.6	25	75.6	1	1	0	2461.13	661	681
tRNA methyltransferase 112 homolog	TRMT112	TR112_HUMAN	14.2	99.9%	2	2	3	0.00%	21.6%	GPVEGYEENEEFLR	99.7%	71.5	25	71.5	2	0	0	1667.75	69	82
tRNA methyltransferase 112 homolog	TRMT112	TR112_HUMAN	14.2	99.9%	2	2	3	0.00%	21.6%	ICPVEFNPNFVAR	97.8%	31.1	25	29.4	1	0	0	1562.78	32	44
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	16	18	24	0.02%	41.4%	DLEEALEMGVDWSLR	99.7%	52.2	25	49.2	1	0	0	1778.83	167	181
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	16	18	24	0.02%	41.4%	EGYAWAEDKEHCEEYGR	96.8%	24.5	25	24.5	0	1	0	2128.87	182	198
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	16	18	24	0.02%	41.4%	GFVPNMQVEGVFYVNDALEK	99.7%	49.5	25	49.5	1	0	0	2256.10	25	44
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	16	18	24	0.02%	41.4%	GGGVGGFLPAMK	99.7%	45.4	25	28.2	2	0	0	1090.57	56	67
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	16	18	24	0.02%	41.4%	GMAAAGNYAWVNR	99.7%	73.7	25	60.9	2	0	0	1380.65	309	321
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	16	18	24	0.02%	41.4%	GQVCVMIHSGSR	99.7%	67	25	67	1	0	0	1330.64	252	263
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	16	18	24	0.02%	41.4%	LADMGIAIR	99.7%	68.1	25	56.3	1	0	0	959.53	452	460
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	16	18	24	0.02%	41.4%	LMFEELR	99.6%	38.7	25	33.7	2	0	0	937.48	45	51
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	16	18	24	0.02%	41.4%	LVMEEAPESYK	99.7%	42.8	25	23.6	2	0	0	1311.61	466	476
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	16	18	24	0.02%	41.4%	NLDFQDVLDKLADMGIAIR	99.7%	47.2	25	46.4	0	1	0	2163.11	442	460
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	16	18	24	0.02%	41.4%	NVTDVVNTCHDAGISK	99.7%	49.7	25	49.7	1	0	0	1729.82	477	492
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	16	18	24	0.02%	41.4%	QIGNVAALPGIVHR	99.7%	41.1	25	40.1	0	2	0	1444.84	68	81
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	16	18	24	0.02%	41.4%	SSMTFLTR	99.7%	59.5	25	44.2	1	0	0	942.47	322	329
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	16	18	24	0.02%	41.4%	SYNDELQFLEK	99.7%	70.1	25	34.9	2	0	0	1385.66	4	14
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	16	18	24	0.02%	41.4%	VEQHVVDGKER	99.6%	33.2	25	30.4	1	2	0	1295.67	358	368
tRNA-splicing ligase RtcB homolog	RTCB	RTCB_HUMAN	55.2	100.0%	16	18	24	0.02%	41.4%	VFNTTPDDLDLHVIYDVSHNIAK	99.4%	31.3	25	30.4	0	1	0	2626.32	335	357
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	14	0.01%	66.7%	AFVHWYVGEGMEEGEFSEAR	99.7%	78.3	25	78.3	4	10	0	2330.02	403	422
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	14	0.01%	66.7%	AFVHWYVGEGMEEGEFSEAREDMAALEK	99.7%	66.7	25	66.7	0	4	0	3217.42	403	430
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	14	0.01%	66.7%	AVCMLSNTTAIAEAWAR	99.7%	113	25	99.9	19	7	0	1880.90	374	390
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	14	0.01%	66.7%	AVFVDLEPTVIDEVR	99.7%	109	25	108	42	4	0	1701.91	65	79
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	14	0.01%	66.7%	AYHEQLSVAEITNACFEPANQMVK	99.7%	130	25	130	3	9	0	2750.29	281	304
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	14	0.01%	66.7%	DVNAAIATIK	99.7%	78.4	25	61.2	15	0	0	1015.58	327	336
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	14	0.01%	66.7%	EDMAALEK	99.7%	48.8	25	31.7	4	0	0	906.42	423	430
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	14	0.01%	66.7%	EIIDLVLDR	99.7%	94.8	25	87.5	43	0	0	1085.62	113	121
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	14	0.01%	66.7%	FDGALNVDLTEFQTNLVPYPR	99.7%	124	25	124	10	2	0	2409.21	244	264
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	14	0.01%	66.7%	FDLMYAK	99.7%	44.6	25	30.1	7	0	0	903.43	395	401
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	14	0.01%	66.7%	IHFPLATYAPVISAEK	99.7%	84.5	25	81	10	12	0	1756.96	265	280
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	14	0.01%	66.7%	LADQCTGLQGFLVFHSFGGGTGSGFTSLLMER	99.7%	122	25	122	0	13	0	3406.62	125	156
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	14	0.01%	66.7%	LDHKFDLMYAK	99.7%	52.6	25	36.8	10	10	0	1380.70	391	401
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	14	0.01%	66.7%	LIGQIVSSITASLR	99.7%	91	25	91	3	0	0	1457.87	230	243
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	14	0.01%	66.7%	LSVDYGKK	99.7%	51.3	25	41.8	10	0	0	909.50	157	164
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	14	0.01%	66.7%	NLDIERPTYTNLNR	99.7%	63.4	25	58	10	12	0	1718.88	216	229
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	14	0.01%	66.7%	QLFHPEQLITGK	99.7%	50.9	25	0	5	3	0	1410.77	85	96
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	14	0.01%	66.7%	QLFHPEQLITGKEDAANNYAR	99.7%	85.3	25	85.3	2	7	0	2415.21	85	105

Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	14	0.01%	66.7%	RNLDIERPTYTNLNR	97.4%	25.2	25	25.2	0	2	0	1874.98	215	229
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	14	0.01%	66.7%	TIGGGDDSFNTFFSETGAGK	99.7%	108	25	108	25	0	0	2007.89	41	60
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	14	0.01%	66.7%	TIQFVDWCPTGFK	99.7%	85.2	25	83.3	11	0	0	1598.77	340	352
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	14	0.01%	66.7%	VGINYQPPTVVPGGDLAK	99.7%	64.3	25	64.3	24	0	0	1824.99	353	370
Tubulin alpha-1A chain	TUBA1A	TBA1A_HUMAN	50.1	99.8%	2	2	14	0.01%	66.7%	YMACCLLYR	99.7%	45.6	25	45.6	26	0	0	1249.55	312	320
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	47	403	0.38%	66.7%	AFVHWYVGEGMEEGEFSEAR	99.7%	78.3	25	78.3	4	10	0	2330.02	403	422
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	47	403	0.38%	66.7%	AFVHWYVGEGMEEGEFSEAREDMAALEK	99.7%	66.7	25	66.7	0	4	0	3217.42	403	430
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	47	403	0.38%	66.7%	AVCMLSNTTAIAEAWAR	99.7%	113	25	99.9	19	7	0	1880.90	374	390
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	47	403	0.38%	66.7%	AVFVDLEPTVIDEVR	99.7%	109	25	108	42	4	0	1701.91	65	79
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	47	403	0.38%	66.7%	AYHEQLSVAEITNACFEPANQMVK	99.7%	130	25	130	3	9	0	2750.29	281	304
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	47	403	0.38%	66.7%	DVNAAIATIK	99.7%	78.4	25	61.2	15	0	0	1015.58	327	336
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	47	403	0.38%	66.7%	EDMAALEK	99.7%	48.8	25	31.7	4	0	0	906.42	423	430
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	47	403	0.38%	66.7%	EIIDLVLDR	99.7%	94.8	25	87.5	43	0	0	1085.62	113	121
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	47	403	0.38%	66.7%	FDGALNVDLTEFQTNLVPYPR	99.7%	124	25	124	10	2	0	2409.21	244	264
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	47	403	0.38%	66.7%	FDLMYAK	99.7%	44.6	25	30.1	7	0	0	903.43	395	401
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	47	403	0.38%	66.7%	IHFPLATYAPVISAEK	99.7%	84.5	25	81	10	12	0	1756.96	265	280
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	47	403	0.38%	66.7%	LADQCTGLQGFLVFHSFGGGTGSGFTSLLMER	99.7%	122	25	122	0	13	0	3406.62	125	156
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	47	403	0.38%	66.7%	LDHKFDLMYAK	99.7%	52.6	25	36.8	10	10	0	1380.70	391	401
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	47	403	0.38%	66.7%	LISQIVSSITASLR	99.7%	105	25	105	15	3	0	1487.88	230	243
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	47	403	0.38%	66.7%	LSVDYGKK	99.7%	51.3	25	41.8	10	0	0	909.50	157	164
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	47	403	0.38%	66.7%	NLDIERPTYTNLNR	99.7%	63.4	25	58	10	12	0	1718.88	216	229
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	47	403	0.38%	66.7%	QLFHPEQLITGK	99.7%	50.9	25	0	5	3	0	1410.77	85	96
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	47	403	0.38%	66.7%	QLFHPEQLITGKEDAANNYAR	99.7%	85.3	25	85.3	2	7	0	2415.21	85	105
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	47	403	0.38%	66.7%	RNLDIERPTYTNLNR	97.4%	25.2	25	25.2	0	2	0	1874.98	215	229
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	47	403	0.38%	66.7%	SIQFVDWCPTGFK	99.7%	92.8	25	91.5	19	0	0	1584.75	340	352
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	47	403	0.38%	66.7%	SIQFVDWCPTGFKVGINYQPPTVVPGGDLAK	99.7%	41.1	25	41.1	0	2	0	3390.72	340	370
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	47	403	0.38%	66.7%	TIGGGDDSFNTFFSETGAGK	99.7%	108	25	108	25	0	0	2007.89	41	60
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	47	403	0.38%	66.7%	VGINYQPPTVVPGGDLAK	99.7%	64.3	25	64.3	24	0	0	1824.99	353	370
Tubulin alpha-1B chain	TUBA1B	TBA1B_HUMAN	50.2	100.0%	24	47	403	0.38%	66.7%	YMACCLLYR	99.7%	45.6	25	45.6	26	0	0	1249.55	312	320
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	8	0.01%	67.0%	AFVHWYVGEGMEEGEFSEAR	99.7%	78.3	25	78.3	4	10	0	2330.02	403	422
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	8	0.01%	67.0%	AFVHWYVGEGMEEGEFSEAREDMAALEK	99.7%	66.7	25	66.7	0	4	0	3217.42	403	430
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	8	0.01%	67.0%	AVCMLSNTTAVAEAWAR	99.7%	74.7	25	69	1	2	0	1866.88	374	390
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	8	0.01%	67.0%	AVFVDLEPTVIDEVR	99.7%	109	25	108	42	4	0	1701.91	65	79
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	8	0.01%	67.0%	AYHEQLTVAEITNACFEPANQMVK	99.7%	56.4	25	56.4	1	4	0	2764.31	281	304
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	8	0.01%	67.0%	DVNAAIATIK	99.7%	78.4	25	61.2	15	0	0	1015.58	327	336
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	8	0.01%	67.0%	EDMAALEK	99.7%	48.8	25	31.7	4	0	0	906.42	423	430
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	8	0.01%	67.0%	EIIDLVLDR	99.7%	94.8	25	87.5	43	0	0	1085.62	113	121
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	8	0.01%	67.0%	FDGALNVDLTEFQTNLVPYPR	99.7%	124	25	124	10	2	0	2409.21	244	264
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	8	0.01%	67.0%	FDLMYAK	99.7%	44.6	25	30.1	7	0	0	903.43	395	401
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	8	0.01%	67.0%	IHFPLATYAPVISAEK	99.7%	84.5	25	81	10	12	0	1756.96	265	280
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	8	0.01%	67.0%	LADQCTGLQGFLVFHSFGGGTGSGFTSLLMER	99.7%	122	25	122	0	13	0	3406.62	125	156
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	8	0.01%	67.0%	LDHKFDLMYAK	99.7%	52.6	25	36.8	10	10	0	1380.70	391	401
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	8	0.01%	67.0%	LISQIVSSITASLR	99.7%	105	25	105	15	3	0	1487.88	230	243
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	8	0.01%	67.0%	LSVDYGKK	99.7%	51.3	25	41.8	10	0	0	909.50	157	164
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	8	0.01%	67.0%	NLDIERPTYTNLNR	99.7%	63.4	25	58	10	12	0	1718.88	216	229
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	8	0.01%	67.0%	QLFHPEQLITGK	99.7%	50.9	25	0	5	3	0	1410.77	85	96
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	8	0.01%	67.0%	QLFHPEQLITGKEDAANNYAR	99.7%	85.3	25	85.3	2	7	0	2415.21	85	105
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	8	0.01%	67.0%	RNLDIERPTYTNLNR	97.4%	25.2	25	25.2	0	2	0	1874.98	215	229
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	8	0.01%	67.0%	TIGGGDDSFNTFFSETGAGK	99.7%	108	25	108	25	0	0	2007.89	41	60
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	8	0.01%	67.0%	TIQFVDWCPTGFK	99.7%	85.2	25	83.3	11	0	0	1598.77	340	352
Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	8	0.01%	67.0%	VGINYQPPTVVPGGDLAK	99.7%	64.3	25	64.3	24	0	0	1824.99	353	370

Tubulin alpha-1C chain	TUBA1C	TBA1C_HUMAN	49.9	99.8%	2	5	8	0.01%	67.0%	YMACCLLYR	99.7%	45.6	25	45.6	26	0	0	1249.55	312	320
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	AILVDLEPGTMDSVR	99.7%	98.3	25	87.8	34	0	0	1631.83	63	77
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	ALTVPELTQQVFDAK	99.7%	85.9	25	85.9	20	4	0	1659.90	283	297
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	98.8	25	0	0	8	0	3327.53	123	154
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	EIVHIQAGQCGNQIGAK	99.7%	94.1	25	0	4	4	0	1822.92	3	19
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	EVDEQMLNVQNK	99.7%	86.3	25	74	19	0	0	1446.69	325	336
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	FPGQLNADLR	99.7%	60.9	25	49.1	17	0	0	1130.60	242	251
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	FPGQLNADLRK	99.7%	44	25	31.6	9	4	0	1258.69	242	252
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	FWEVISDEHGIDPTGTYHGDSDLQLDR	99.7%	75	25	31.5	0	5	0	3102.41	20	46
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	GHYTEGAELVDSVLDVVR	99.7%	151	25	145	7	15	0	1958.98	104	121
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	GHYTEGAELVDSVLDVVRK	99.7%	94.6	25	84.1	4	5	0	2087.08	104	122
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	IMNTFSVVPSPK	99.7%	97.8	25	87.8	35	0	0	1319.70	163	174
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	IREEYPDR	99.6%	39.1	25	24.6	5	0	0	1077.53	155	162
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	ISEQFTAMFR	99.7%	80.1	25	71.8	25	0	0	1229.60	381	390
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	ISVYYNEATGGK	99.7%	82.4	25	79	28	0	0	1301.64	47	58
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	KEAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	81	25	0	0	3	0	3455.62	122	154
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	KLAVNMVPFPR	99.7%	78.1	25	77.3	6	3	0	1271.73	252	262
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	LAVNMVPFPR	99.7%	81.7	25	65	37	0	0	1143.63	253	262
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	LHFFMPGFAPLTSR	99.7%	65	25	49	21	19	0	1620.84	263	276
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	LTTPTYGDLNHLVSATMSGVTTCLR	99.7%	140	25	140	5	15	0	2708.34	217	241
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	LTTPTYGDLNHLVSATMSGVTTCLRFPGQLNADLR	99.7%	42.4	25	42.4	0	1	0	3819.92	217	251
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	MAVTFIGNSTAIQELFK	99.7%	136	25	133	25	4	0	1869.98	363	379
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	MAVTFIGNSTAIQELFKR	99.7%	110	25	110	8	8	0	2026.08	363	380
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	MREIVHIQAGQCGNQIGAK	99.7%	70.8	25	0	1	8	0	2110.06	1	19
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	MSMKEVDEQMLNVQNK	99.7%	52.8	25	51.5	4	18	0	1971.88	321	336
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	NMMAACDPR	99.7%	50.3	25	14.5	16	0	0	1081.42	298	306
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	NSSYFVEWIPNNVK	99.7%	84.2	25	72.5	17	0	0	1696.83	337	350
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	RISEQFTAMFR	99.7%	55.4	25	51.5	2	0	0	1385.70	380	390
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	SGPFGQIFRPDNFVFGQSGAGNNWAK	99.7%	93.1	25	93.1	2	12	0	2798.34	78	103
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	TAVCDIPPR	99.7%	59.8	25	44.9	30	0	0	1028.52	351	359
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	99.7%	49.1	25	49.1	0	3	0	4593.11	175	213
Tubulin beta chain	TUBB	TBB5_HUMAN	49.7	100.0%	31	64	531	0.50%	83.1%	YLTVAAVFR	99.7%	84	25	75.6	11	0	0	1039.59	310	318
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	AILVDLEPGTMDSVR	99.7%	98.3	25	87.8	34	0	0	1631.83	63	77
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	ALTVPELTQQMFDSK	99.7%	104	25	29.7	8	0	0	1707.86	283	297
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	EIVHIQAGQCGNQIGAK	99.7%	94.1	25	0	4	4	0	1822.92	3	19
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	ESESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	69.9	25	69.9	0	2	0	3343.52	123	154
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	EVDEQMLNVQNK	99.7%	86.3	25	74	19	0	0	1446.69	325	336
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	FPGQLNADLR	99.7%	60.9	25	49.1	17	0	0	1130.60	242	251
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	FPGQLNADLRK	99.7%	44	25	31.6	9	4	0	1258.69	242	252
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	GHYTEGAELVDSVLDVVR	99.7%	151	25	145	7	15	0	1958.98	104	121
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	GHYTEGAELVDSVLDVVRK	99.7%	94.6	25	84.1	4	5	0	2087.08	104	122
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	IMNTFSVMPSPK	99.7%	97.5	25	82.2	12	0	0	1351.67	163	174
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	INVYYNEATGNK	99.7%	79.4	25	74.3	4	0	0	1385.67	47	58
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	IREEYPDR	99.6%	39.1	25	24.6	5	0	0	1077.53	155	162
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	ISEQFTAMFR	99.7%	80.1	25	71.8	25	0	0	1229.60	381	390
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	KLAVNMVPFPR	99.7%	78.1	25	77.3	6	3	0	1271.73	252	262
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	LAVNMVPFPR	99.7%	81.7	25	65	37	0	0	1143.63	253	262
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	LHFFMPGFAPLTSR	99.7%	65	25	49	21	19	0	1620.84	263	276
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	LTTPTYGDLNHLVSATMSGVTTCLR	99.7%	140	25	140	5	15	0	2708.34	217	241
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	LTTPTYGDLNHLVSATMSGVTTCLRFPGQLNADLR	99.7%	42.4	25	42.4	0	1	0	3819.92	217	251
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	MREIVHIQAGQCGNQIGAK	99.7%	70.8	25	0	1	8	0	2110.06	1	19

Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	MSATFIGNSTAIQELFK	99.7%	119	25	0	11	0	0	1873.94	363	379
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	MSATFIGNSTAIQELFKR	99.7%	71.7	25	0	2	7	0	2014.04	363	380
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	MSMKEVDEQMLNVQNK	99.7%	52.8	25	51.5	4	18	0	1971.88	321	336
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	NMMAACDPR	99.7%	50.3	25	14.5	16	0	0	1081.42	298	306
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	NSSYFVEWIPNNVK	99.7%	84.2	25	72.5	17	0	0	1696.83	337	350
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	RISEQFTAMFR	99.7%	55.4	25	51.5	2	0	0	1385.70	380	390
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	SGPFGQIFRPDNFVFGQSGAGNNWAK	99.7%	93.1	25	93.1	2	12	0	2798.34	78	103
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	TAVCDIPPR	99.7%	59.8	25	44.9	30	0	0	1028.52	351	359
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	99.7%	49.1	25	49.1	0	3	0	4593.11	175	213
Tubulin beta-2B chain	TUBB2B	TBB2B_HUMAN	50.0	100.0%	5	7	32	0.03%	76.9%	YLTVAAIFR	99.7%	78.9	25	66.6	6	0	0	1053.61	310	318
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	7	0.01%	42.0%	AILVDLEPGTMDSVR	99.7%	98.3	25	87.8	34	0	0	1631.83	63	77
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	7	0.01%	42.0%	ALTVPELTQQMFDAK	99.7%	96.8	25	95.3	11	1	0	1691.87	283	297
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	7	0.01%	42.0%	EIVHIQAGQCGNQIGAK	99.7%	94.1	25	0	4	4	0	1822.92	3	19
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	7	0.01%	42.0%	EVDEQMLAIQSK	99.7%	67.4	25	56.7	1	0	0	1390.69	325	336
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	7	0.01%	42.0%	FPGQLNADLR	99.7%	60.9	25	49.1	17	0	0	1130.60	242	251
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	7	0.01%	42.0%	FPGQLNADLRK	99.7%	44	25	31.6	9	4	0	1258.69	242	252
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	7	0.01%	42.0%	GHYTEGAELVDSVLDVVR	99.7%	151	25	145	7	15	0	1958.98	104	121
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	7	0.01%	42.0%	GHYTEGAELVDSVLDVVRK	99.7%	94.6	25	84.1	4	5	0	2087.08	104	122
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	7	0.01%	42.0%	IMNTFSVVPSPK	99.7%	97.8	25	87.8	35	0	0	1319.70	163	174
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	7	0.01%	42.0%	ISEQFTAMFR	99.7%	80.1	25	71.8	25	0	0	1229.60	381	390
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	7	0.01%	42.0%	KLAVNMVPFPR	99.7%	78.1	25	77.3	6	3	0	1271.73	252	262
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	7	0.01%	42.0%	LATPTYGDLNHLVSATMSGVTTSLR	99.7%	44.6	25	44.6	0	1	0	2605.33	217	241
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	7	0.01%	42.0%	LAVNMVPFPR	99.7%	81.7	25	65	37	0	0	1143.63	253	262
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	7	0.01%	42.0%	MREIVHIQAGQCGNQIGAK	99.7%	70.8	25	0	1	8	0	2110.06	1	19
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	7	0.01%	42.0%	MSSTFIGNSTAIQELFK	99.7%	119	25	0	5	0	0	1873.94	363	379
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	7	0.01%	42.0%	NMMAACDPR	99.7%	50.3	25	14.5	16	0	0	1081.42	298	306
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	7	0.01%	42.0%	NSSYFVEWIPNNVK	99.7%	84.2	25	72.5	17	0	0	1696.83	337	350
Tubulin beta-3 chain	TUBB3	TBB3_HUMAN	50.4	100.0%	3	3	7	0.01%	42.0%	RISEQFTAMFR	99.7%	55.4	25	51.5	2	0	0	1385.70	380	390
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	ALTVPELTQQMFDAK	99.7%	96.8	25	95.3	11	1	0	1691.87	283	297
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	AVLVDLEPGTMDSVR	99.7%	97.2	25	77	16	0	0	1617.82	63	77
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	98.8	25	0	0	8	0	3327.53	123	154
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	EIVHLQAGQCGNQIGAK	99.7%	94.1	25	0	4	4	0	1822.92	3	19
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	EVDEQMLSVQSK	99.7%	78.6	25	71.7	1	0	0	1392.67	325	336
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	FPGQLNADLR	99.7%	60.9	25	49.1	17	0	0	1130.60	242	251
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	FPGQLNADLRK	99.7%	44	25	31.6	9	4	0	1258.69	242	252
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	FWEVISDEHGIDPTGTYHGDSDLQLER	99.7%	77	25	75	0	2	0	3116.42	20	46
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	GHYTEGAELVDAVLDVVR	99.7%	48.5	25	45	0	3	0	1942.99	104	121
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	IMNTFSVVPSPK	99.7%	97.8	25	87.8	35	0	0	1319.70	163	174
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	INVYYNEATGGNYVPR	99.7%	105	25	105	2	0	0	1829.88	47	62
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	IREEFPDR	98.7%	33.5	25	18.7	4	0	0	1061.54	155	162
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	ISEQFTAMFR	99.7%	80.1	25	71.8	25	0	0	1229.60	381	390
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	KEAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	81	25	0	0	3	0	3455.62	122	154
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	KLAVNMVPFPR	99.7%	78.1	25	77.3	6	3	0	1271.73	252	262
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	LAVNMVPFPR	99.7%	81.7	25	65	37	0	0	1143.63	253	262
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	LHFFMPGFAPLTSR	99.7%	65	25	49	21	19	0	1620.84	263	276
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	LTTPTYGDLNHLVSATMSGVTTCLR	99.7%	140	25	140	5	15	0	2708.34	217	241
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	LTTPTYGDLNHLVSATMSGVTTCLRFPGQLNADLR	99.7%	42.4	25	42.4	0	1	0	3819.92	217	251
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	MAATFIGNSTAIQELFK	99.7%	89.2	25	3.83	11	0	0	1857.94	363	379
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	MAATFIGNSTAIQELFKR	99.7%	75.4	25	2.78	4	0	0	2014.04	363	380
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	MREIVHLQAGQCGNQIGAK	99.7%	70.8	25	0	1	8	0	2110.06	1	19
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	NMMAACDPR	99.7%	50.3	25	14.5	16	0	0	1081.42	298	306

Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	NSSYFVEWIPNNVK	99.7%	84.2	25	72.5	17	0	0	1696.83	337	350
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	RISEQFTAMFR	99.7%	55.4	25	51.5	2	0	0	1385.70	380	390
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	SGPFGQIFRPDNFVFGQSGAGNNWAK	99.7%	93.1	25	93.1	2	12	0	2798.34	78	103
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	TAVCDIPPR	99.7%	59.8	25	44.9	30	0	0	1028.52	351	359
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	99.7%	49.1	25	49.1	0	3	0	4593.11	175	213
Tubulin beta-4A chain	TUBB4A	TBB4A_HUMAN	49.6	100.0%	6	6	25	0.02%	83.1%	YLTVAAVFR	99.7%	84	25	75.6	11	0	0	1039.59	310	318
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	ALTVPELTQQMFDAK	99.7%	96.8	25	95.3	11	1	0	1691.87	283	297
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	AVLVDLEPGTMDSVR	99.7%	97.2	25	77	16	0	0	1617.82	63	77
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	98.8	25	0	0	8	0	3327.53	123	154
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	EIVHLQAGQCGNQIGAK	99.7%	94.1	25	0	4	4	0	1822.92	3	19
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	EVDEQMLNVQNK	99.7%	86.3	25	74	19	0	0	1446.69	325	336
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	FPGQLNADLR	99.7%	60.9	25	49.1	17	0	0	1130.60	242	251
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	FPGQLNADLRK	99.7%	44	25	31.6	9	4	0	1258.69	242	252
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	FWEVISDEHGIDPTGTYHGDSDLQLER	99.7%	77	25	75	0	2	0	3116.42	20	46
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	GHYTEGAELVDSVLDVVR	99.7%	151	25	145	7	15	0	1958.98	104	121
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	GHYTEGAELVDSVLDVVRK	99.7%	94.6	25	84.1	4	5	0	2087.08	104	122
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	IMNTFSVVPSPK	99.7%	97.8	25	87.8	35	0	0	1319.70	163	174
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	INVYYNEATGGK	99.7%	78	25	64	12	0	0	1328.65	47	58
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	IREEYPDR	99.6%	39.1	25	24.6	5	0	0	1077.53	155	162
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	ISEQFTAMFR	99.7%	80.1	25	71.8	25	0	0	1229.60	381	390
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	KEAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	99.7%	81	25	0	0	3	0	3455.62	122	154
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	KLAVNMVPFPR	99.7%	78.1	25	77.3	6	3	0	1271.73	252	262
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	LAVNMVPFPR	99.7%	81.7	25	65	37	0	0	1143.63	253	262
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	LHFFMPGFAPLTSR	99.7%	65	25	49	21	19	0	1620.84	263	276
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	LTTPTYGDLNHLVSATMSGVTTCLR	99.7%	140	25	140	5	15	0	2708.34	217	241
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	LTTPTYGDLNHLVSATMSGVTTCLRFPGQLNADLR	99.7%	42.4	25	42.4	0	1	0	3819.92	217	251
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	MREIVHLQAGQCGNQIGAK	99.7%	70.8	25	0	1	8	0	2110.06	1	19
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	MSATFIGNSTAIQELFK	99.7%	119	25	0	11	0	0	1873.94	363	379
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	MSATFIGNSTAIQELFKR	99.7%	71.7	25	0	2	7	0	2014.04	363	380
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	MSMKEVDEQMLNVQNK	99.7%	52.8	25	51.5	4	18	0	1971.88	321	336
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	NMMAACDPR	99.7%	50.3	25	14.5	16	0	0	1081.42	298	306
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	NSSYFVEWIPNNVK	99.7%	84.2	25	72.5	17	0	0	1696.83	337	350
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	RISEQFTAMFR	99.7%	55.4	25	51.5	2	0	0	1385.70	380	390
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	SGPFGQIFRPDNFVFGQSGAGNNWAK	99.7%	93.1	25	93.1	2	12	0	2798.34	78	103
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	TAVCDIPPR	99.7%	59.8	25	44.9	30	0	0	1028.52	351	359
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	99.7%	49.1	25	49.1	0	3	0	4593.11	175	213
Tubulin beta-4B chain	TUBB4B	TBB4B_HUMAN	49.8	100.0%	6	12	62	0.06%	82.9%	YLTVAAVFR	99.7%	84	25	75.6	11	0	0	1039.59	310	318
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	3	6	0.01%	43.7%	AALVDLEPGTMDSVR	99.5%	37.8	25	31.5	1	0	0	1589.78	63	77
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	3	6	0.01%	43.7%	ALTVPELTQQMFDAR	99.7%	58.5	25	55.5	3	0	0	1719.87	283	297
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	3	6	0.01%	43.7%	EVDEQMLAIQSK	99.7%	67.4	25	56.7	1	0	0	1390.69	325	336
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	3	6	0.01%	43.7%	FPGQLNADLR	99.7%	60.9	25	49.1	17	0	0	1130.60	242	251
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	3	6	0.01%	43.7%	FPGQLNADLRK	99.7%	44	25	31.6	9	4	0	1258.69	242	252
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	3	6	0.01%	43.7%	GHYTEGAELVDAVLDVVR	99.7%	48.5	25	45	0	3	0	1942.99	104	121
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	3	6	0.01%	43.7%	IMNTFSVMPSPK	99.7%	97.5	25	82.2	12	0	0	1351.67	163	174
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	3	6	0.01%	43.7%	IREEFPDR	98.7%	33.5	25	18.7	4	0	0	1061.54	155	162
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	3	6	0.01%	43.7%	KLAVNMVPFPR	99.7%	78.1	25	77.3	6	3	0	1271.73	252	262
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	3	6	0.01%	43.7%	LAVNMVPFPR	99.7%	81.7	25	65	37	0	0	1143.63	253	262
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	3	6	0.01%	43.7%	LHFFMPGFAPLTSR	99.7%	65	25	49	21	19	0	1620.84	263	276
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	3	6	0.01%	43.7%	MASTFIGNSTAIQELFK	99.7%	119	25	0	8	0	0	1873.94	363	379
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	3	6	0.01%	43.7%	MASTFIGNSTAIQELFKR	99.7%	71.7	25	0	2	0	0	2014.04	363	380
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	3	6	0.01%	43.7%	NMMAACDPR	99.7%	50.3	25	14.5	16	0	0	1081.42	298	306

Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	3	6	0.01%	43.7%	NSSYFVEWIPNNVK	99.7%	84.2	25	72.5	17	0	0	1696.83	337	350
Tubulin beta-6 chain	TUBB6	TBB6_HUMAN	49.9	100.0%	3	3	6	0.01%	43.7%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	99.7%	49.1	25	49.1	0	3	0	4593.11	175	213
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	6	7	11	0.01%	13.7%	AVLLDLEPR	99.7%	44.5	25	35.8	2	0	0	1025.60	64	72
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	6	7	11	0.01%	13.7%	DVFFYQADDEHYIPR	99.7%	83.6	25	83.5	1	0	0	1914.87	49	63
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	6	7	11	0.01%	13.7%	EAFLEQFR	99.5%	37.7	25	18.9	2	0	0	1039.52	402	409
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	6	7	11	0.01%	13.7%	KTTVLDVMR	99.7%	63.7	25	55.2	2	0	0	1062.60	287	295
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	6	7	11	0.01%	13.7%	SPYLPSAHR	95.7%	28.5	25	28.5	1	0	0	1027.53	364	372
Tubulin gamma-1 chain	TUBG1	TBG1_HUMAN	51.2	100.0%	6	7	11	0.01%	13.7%	VIHSILNSPYAK	99.7%	57.3	25	47	2	1	0	1341.75	73	84
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	7	7	12	0.01%	6.5%	AVTHTSPEDVSFAESR	98.9%	28.6	25	21.6	0	1	0	1732.81	800	815
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	7	7	12	0.01%	6.5%	DAAAVLVSR	99.7%	57.4	25	42.8	2	0	0	901.51	205	213
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	7	7	12	0.01%	6.5%	GACSVGTNVR	99.1%	34.7	25	21.4	1	0	0	1020.49	455	464
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	7	7	12	0.01%	6.5%	ITQLLGLPTYR	99.7%	40.3	25	40.3	2	0	0	1274.75	969	979
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	7	7	12	0.01%	6.5%	LDGNLLTQPGQAR	99.7%	45.4	25	38.6	2	0	0	1382.74	170	182
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	7	7	12	0.01%	6.5%	LQQVLTGLR	99.7%	59.1	25	39.5	2	0	0	1027.63	791	799
Tubulin-specific chaperone D	TBCD	TBCD_HUMAN	132.6	100.0%	7	7	12	0.01%	6.5%	VIEQLLVGLK	99.7%	72.2	25	69.3	2	0	0	1111.71	361	370
Tuftelin-interacting protein 11	TFIP11	TFP11_HUMAN	96.8	99.8%	2	2	2	0.00%	2.9%	DVFTPGSWEAFMVK	97.3%	30.4	25	21.5	1	0	0	1613.77	597	610
Tuftelin-interacting protein 11	TFIP11	TFP11_HUMAN	96.8	99.8%	2	2	2	0.00%	2.9%	GAVGAYGSER	98.7%	33.5	25	15	1	0	0	966.46	188	197
Tyrosine-protein kinase CSK	CSK	CSK_HUMAN	50.7	100.0%	2	2	2	0.00%	4.9%	GDVLTIVAVTK	99.7%	48	25	37.1	1	0	0	1115.67	33	43
Tyrosine-protein kinase CSK	CSK	CSK_HUMAN	50.7	100.0%	2	2	2	0.00%	4.9%	NVLVSEDNVAK	99.1%	35.1	25	23.5	1	0	0	1187.63	319	329
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	AFCEPGNVENNGVLSFIK	99.7%	90.8	25	79.7	2	0	0	1994.96	248	265
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	AMLESIGVPLEK	99.7%	75.4	25	62.1	4	0	0	1302.70	103	114
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	APWELLELR	99.7%	57.4	25	40.1	2	0	0	1126.63	85	93
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	DFAAEVVHPGDLK	99.7%	75.7	25	57.1	2	0	0	1397.71	298	310
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	EYTLDVYR	99.7%	53.5	25	48.2	2	0	0	1058.52	128	135
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	GQPDEELKPK	99.7%	48.4	25	38.1	2	0	0	1140.59	475	484
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	GTDYQLSK	98.9%	34	25	18.6	2	0	0	911.45	120	127
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	GVESQGMLLCASIEGINR	99.7%	118	25	109	4	0	0	1933.95	433	450
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	HPDADSLYVEK	99.7%	49.6	25	40.5	2	0	0	1273.61	381	391
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	HVLFPLK	99.2%	35.5	25	27.1	2	0	0	853.53	266	272
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	IDVGEAEPR	99.7%	71.7	25	57.6	2	0	0	985.50	392	400
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	IITVEKHPDADSLYVEK	99.7%	70.8	25	70.8	2	2	0	1957.03	375	391
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	ISEECIAQWK	99.7%	78.9	25	72.4	2	0	0	1263.60	497	506
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	IYWGTATTGKPHVAYFVPMSK	99.7%	35.2	25	35.2	0	2	0	2370.20	38	58
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	KIFTFAEK	99.7%	42	25	26.9	2	0	0	983.56	190	197
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	KLASAAYPDPSK	99.7%	62.7	25	54.6	2	0	0	1247.66	335	346
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	LASAAYPDPSK	99.7%	69.8	25	59.5	2	0	0	1119.57	336	346
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	LLDPIREK	99.7%	44.2	25	32.5	2	0	0	983.59	320	327
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	LSSVVTQHDSK	99.7%	70.3	25	63.1	2	0	0	1200.62	136	146
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	LSSVVTQHDSKK	99.7%	58.7	25	47.9	2	1	0	1328.72	136	147
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	LVVVLCNLKPQK	99.7%	55.1	25	54.7	2	1	0	1410.85	419	430
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	MSSSEEESKIDLLDR	99.7%	65.9	25	58.7	3	4	0	1738.82	223	237
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	NLQEVLGEEK	99.7%	65.6	25	56.3	2	0	0	1158.60	17	26
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	NSEPEEVIPSR	99.7%	61	25	48.2	2	0	0	1256.61	357	367
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	NSVEVALNK	99.7%	75.6	25	58.3	2	0	0	973.53	311	319
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	QTNFMTK	98.3%	32.3	25	25.5	1	0	0	869.42	507	513
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	QVEPLDPPAGSAPGEHVFVK	99.7%	54.3	25	54.3	2	2	0	2074.06	451	470
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	SEFVILR	99.7%	49	25	44.1	2	0	0	863.50	273	279
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	SEFVILRDEK	99.7%	47	25	30.3	2	0	0	1235.66	273	282
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	TVVSGLVQFVPK	99.7%	94	25	82.6	2	0	0	1273.75	401	412
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	TVVSGLVQFVPKEELQDR	99.7%	64.9	25	64.9	1	2	0	2044.11	401	418
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	TYTAYVDLEK	99.7%	53	25	46.4	2	0	0	1202.59	288	297

Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	VDAQFGGIDQR	99.7%	72.9	25	59.5	2	0	0	1205.59	179	189
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	VHLMNPMVPGLTGSK	99.7%	69.3	25	33.9	4	1	0	1596.82	208	222
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	VSYYENVIK	99.7%	40.1	25	37.9	3	0	0	1114.58	94	102
Tyrosine--tRNA ligase, cytoplasmic	YARS	SYYC_HUMAN	59.1	100.0%	36	48	91	0.09%	69.3%	YLPALGYSK	99.7%	49.4	25	27.7	2	0	0	1011.55	198	206
U1 small nuclear ribonucleoprotein 70 kDa	SNRNP70	RU17_HUMAN	51.6	100.0%	5	5	6	0.01%	12.4%	DPIPYLPPLEK	99.5%	37.8	25	21.6	2	0	0	1281.71	17	27
U1 small nuclear ribonucleoprotein 70 kDa	SNRNP70	RU17_HUMAN	51.6	100.0%	5	5	6	0.01%	12.4%	EFEVYGPIKR	96.3%	29.1	25	23.2	1	0	0	1237.66	122	131
U1 small nuclear ribonucleoprotein 70 kDa	SNRNP70	RU17_HUMAN	51.6	100.0%	5	5	6	0.01%	12.4%	MWDPHNDPNAQGDAFK	98.1%	26.4	25	26.2	0	1	0	1842.79	88	103
U1 small nuclear ribonucleoprotein 70 kDa	SNRNP70	RU17_HUMAN	51.6	100.0%	5	5	6	0.01%	12.4%	RQQEVETELK	95.5%	28.4	25	19.1	1	0	0	1259.66	78	87
U1 small nuclear ribonucleoprotein 70 kDa	SNRNP70	RU17_HUMAN	51.6	100.0%	5	5	6	0.01%	12.4%	VLVDVER	97.2%	30.3	25	11.3	1	0	0	829.48	174	180
U1 small nuclear ribonucleoprotein A	SNRPA	SNRPA_HUMAN	31.3	100.0%	5	5	8	0.01%	19.9%	AVQGGGATPVVGAVQGPVPGMPPMTQAPR	99.4%	31.1	25	29.9	0	2	0	2759.40	124	152
U1 small nuclear ribonucleoprotein A	SNRPA	SNRPA_HUMAN	31.3	100.0%	5	5	8	0.01%	19.9%	EVSSATNALR	99.7%	72.6	25	48	2	0	0	1047.54	61	70
U1 small nuclear ribonucleoprotein A	SNRPA	SNRPA_HUMAN	31.3	100.0%	5	5	8	0.01%	19.9%	GQAFVIFK	99.6%	39.1	25	30.9	2	0	0	909.52	53	60
U1 small nuclear ribonucleoprotein A	SNRPA	SNRPA_HUMAN	31.3	100.0%	5	5	8	0.01%	19.9%	KAVQGGGATPVVGAVQGPVPGMPPMTQAPR	99.7%	44.8	25	44.8	0	1	0	2887.49	123	152
U1 small nuclear ribonucleoprotein A	SNRPA	SNRPA_HUMAN	31.3	100.0%	5	5	8	0.01%	19.9%	TDSDIIAK	97.6%	30.8	25	12.9	1	0	0	862.45	89	96
U1 small nuclear ribonucleoprotein C	SNRPC	RU1C_HUMAN	17.4	99.8%	2	2	3	0.00%	18.9%	FYCDYCDTYLTHDSPSVR	99.7%	37.8	25	37.8	0	1	0	2298.94	4	21
U1 small nuclear ribonucleoprotein C	SNRPC	RU1C_HUMAN	17.4	99.8%	2	2	3	0.00%	18.9%	WMEEQAQSLIDK	99.7%	95.6	25	87.7	2	0	0	1477.70	41	52
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	6	6	13	0.01%	21.6%	GLLQSGQIPGR	99.7%	75.2	25	31.8	3	0	0	1125.64	222	232
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	6	6	13	0.01%	21.6%	KLDGFPLLR	99.0%	34.4	25	20.6	2	0	0	1058.64	56	64
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	6	6	13	0.01%	21.6%	LDGFPLLR	99.6%	38.9	25	25.1	2	0	0	930.54	57	64
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	6	6	13	0.01%	21.6%	NAIANASTLAEVER	99.7%	98.9	25	93.3	2	0	0	1458.75	206	219
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	6	6	13	0.01%	21.6%	SLTYLSILR	99.7%	56.1	25	49.7	2	0	0	1065.63	114	122
U2 small nuclear ribonucleoprotein A'	SNRPA1	RU2A_HUMAN	28.4	100.0%	6	6	13	0.01%	21.6%	TFNPGAGLPTDK	99.7%	49.4	25	46	2	0	0	1217.62	180	191
U2 snRNP-associated SURP motif-containing protein	U2SURP	SR140_HUMAN	118.3	99.8%	2	2	3	0.00%	2.5%	LYLVSDVLYNSSAK	99.7%	69.6	25	69.6	1	0	0	1571.83	595	608
U2 snRNP-associated SURP motif-containing protein	U2SURP	SR140_HUMAN	118.3	99.8%	2	2	3	0.00%	2.5%	LYSILQGDSPTK	99.7%	74.2	25	62.6	2	0	0	1321.70	477	488
U3 small nucleolar RNA-interacting protein 2	RRP9	U3IP2_HUMAN	51.8	99.8%	2	2	3	0.00%	3.4%	LKEDVLEQR	99.7%	55.8	25	45.2	1	0	0	1129.62	112	120
U3 small nucleolar RNA-interacting protein 2	RRP9	U3IP2_HUMAN	51.8	99.8%	2	2	3	0.00%	3.4%	LYLEQLR	99.4%	36.9	25	26.5	2	0	0	934.54	85	91
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	20	28	68	0.06%	48.1%	ASEVMGPVEAAPEYR	99.7%	92.5	25	91.8	6	0	0	1605.76	77	91
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	20	28	68	0.06%	48.1%	FPELESLVPNALDYIR	99.7%	50.8	25	50.8	1	0	0	1875.99	122	137
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	20	28	68	0.06%	48.1%	IEEYISK	99.7%	43.6	25	28.8	2	0	0	881.46	67	73
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	20	28	68	0.06%	48.1%	IMGVAGGLTNLSK	99.7%	95.1	25	79	5	0	0	1260.70	231	243
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	20	28	68	0.06%	48.1%	IYEYVESR	99.7%	66.3	25	56.7	4	0	0	1058.52	204	211
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	20	28	68	0.06%	48.1%	LEEACDMALELNASK	99.7%	82.4	25	82.4	2	0	0	1693.78	187	201
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	20	28	68	0.06%	48.1%	LGLTEIR	99.7%	53.7	25	15.9	2	0	0	801.48	366	372
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	20	28	68	0.06%	48.1%	LGLTEIRK	99.7%	62	25	49	4	0	0	929.58	366	373
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	20	28	68	0.06%	48.1%	MFAEIMMK	99.3%	36.3	25	7.95	5	0	0	1016.46	59	66
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	20	28	68	0.06%	48.1%	MPACNIMLLGAQR	99.7%	82.4	25	72.3	6	0	0	1490.73	244	256
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	20	28	68	0.06%	48.1%	MSFGEIEEDAYQEDLGFSLGHLGK	99.7%	51.5	25	51.5	0	2	0	2672.22	378	401
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	20	28	68	0.06%	48.1%	MSFIAPNLSIIIGASTAAK	99.7%	70.3	25	70.3	3	0	0	1905.05	212	230
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	20	28	68	0.06%	48.1%	QVKPLPAPLDGQR	99.5%	31.7	25	31.7	2	2	0	1418.81	339	351
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	20	28	68	0.06%	48.1%	RFPELESLVPNALDYIR	99.6%	32.2	25	29.5	0	1	0	2032.09	121	137
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	20	28	68	0.06%	48.1%	SSGTASSVAFTPLQGLEIVNPQAAEK	99.7%	92.6	25	92.6	2	4	0	2602.34	445	470
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	20	28	68	0.06%	48.1%	SSGTASSVAFTPLQGLEIVNPQAAEKK	99.1%	29.4	25	29.4	0	1	0	2730.43	445	471
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	20	28	68	0.06%	48.1%	VDSFHESTEGK	99.7%	62.2	25	60.7	4	0	0	1235.55	305	315
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	20	28	68	0.06%	48.1%	VGYELKDEIER	99.7%	78.3	25	54.1	3	2	0	1350.69	316	326
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	20	28	68	0.06%	48.1%	VIVDANNLTVEIENELNIIHK	99.7%	43.4	25	40.4	0	1	0	2390.29	92	112
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	PRP31_HUMAN	55.5	100.0%	20	28	68	0.06%	48.1%	YFSSMAEFLK	99.7%	59.7	25	53	4	0	0	1238.58	479	488
U4/U6 small nuclear ribonucleoprotein Prp4	PRPF4	PRP4_HUMAN	58.5	100.0%	3	3	3	0.00%	7.9%	ALGEPITLFGEGPAER	99.7%	83.1	25	83.1	1	0	0	1656.86	114	129
U4/U6 small nuclear ribonucleoprotein Prp4	PRPF4	PRP4_HUMAN	58.5	100.0%	3	3	3	0.00%	7.9%	NILSVVGTDALKK	99.5%	37.5	25	36.4	1	0	0	1357.81	135	147
U4/U6 small nuclear ribonucleoprotein Prp4	PRPF4	PRP4_HUMAN	58.5	100.0%	3	3	3	0.00%	7.9%	QINVSTDDSEVK	96.6%	29.5	25	21.2	1	0	0	1334.64	98	109
U4/U6.U5 tri-snRNP-associated protein 1	SART1	SNUT1_HUMAN	90.3	100.0%	4	4	6	0.01%	7.6%	EAAGTTAAAGTGGATEQPPR	99.7%	80	25	77.4	1	0	0	1813.87	12	31
U4/U6.U5 tri-snRNP-associated protein 1	SART1	SNUT1_HUMAN	90.3	100.0%	4	4	6	0.01%	7.6%	LEQGGTADGLR	99.7%	67.2	25	51.3	2	0	0	1116.56	351	361

U4/U6.U5 tri-snRNP-associated protein 1	SART1	SNUT1_HUMAN	90.3	100.0%	4	4	6	0.01%	7.6%	LQAQSLSTVGPR	99.7%	69.9	25	67	2	0	0	1256.70	374	385
U4/U6.U5 tri-snRNP-associated protein 1	SART1	SNUT1_HUMAN	90.3	100.0%	4	4	6	0.01%	7.6%	TLGEDDPWLDDTAAWIER	99.7%	76.3	25	76.3	1	0	0	2102.97	189	206
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	AALETDENLLLCAPTGAGK	99.7%	101	25	92.3	2	0	0	1943.97	491	509
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	ANSNLVLQADR	99.7%	84.5	25	66.9	2	0	0	1200.63	15	25
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	DEPTGEVLSLVGK	99.7%	77.5	25	62.3	2	0	0	1343.71	34	46
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	DIDAFWLQR	99.7%	64.5	25	42.9	2	0	0	1163.58	262	270
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	DILCGAADEVLAVLK	99.7%	95	25	80.7	2	0	0	1586.85	130	144
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	DMCLEKDTLGLFLR	96.5%	24.2	25	19.6	0	1	0	1710.86	740	753
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	DTLGLFLR	99.7%	54.7	25	30.3	2	0	0	934.54	746	753
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	EEEKLELQK	99.5%	37.3	25	21.4	2	0	0	1145.61	1031	1039
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	EEGWWVVIGDAK	99.7%	74	25	52.2	2	0	0	1388.68	2061	2072
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	EGSASTEVLR	99.7%	48.3	25	36.6	2	0	0	1048.53	754	763
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	ESIEEPSAK	97.6%	30.8	25	24.4	1	0	0	989.48	1050	1058
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	FQIMNEIVYEK	99.7%	71.9	25	59.5	3	0	0	1429.70	701	711
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	FYDDAIVSQK	99.7%	63.7	25	55.3	2	0	0	1185.58	275	284
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	GLIEIISNAAEYENIPIR	99.3%	35.8	25	31.3	1	0	0	2015.08	1844	1861
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	GNIIISTPEKWDILSR	99.7%	37.8	25	37.8	2	2	0	1842.01	1422	1437
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	GTQVYSPEK	99.3%	36.3	25	29.2	1	0	0	1008.50	830	838
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	GWAQLTDK	98.9%	34.1	25	20.3	1	0	0	918.47	1103	1110
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	HINMDGTINVDDFK	99.7%	51	25	47.7	1	0	0	1634.75	524	537
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	HLILPEK	99.2%	35.5	25	17.5	1	0	0	849.52	1288	1294
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	IIYIAPMR	99.3%	36.1	25	22	4	0	0	992.56	538	545
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	IVALSSSLSNAK	99.7%	105	25	97.5	4	0	0	1189.68	1487	1498
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	KADEVLEILK	99.7%	75.8	25	59.7	2	0	0	1157.68	285	294
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	KPVIVFVPSR	99.7%	55.4	25	54.2	2	0	0	1141.71	1557	1566
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	LIGLSATLPNYEDVATFLR	99.7%	77.8	25	77.8	2	0	0	2093.13	648	666
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	LTAIDILTTCAADIQR	99.7%	111	25	103	2	0	0	1774.94	1571	1586
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	LYDLNHNEIGELIR	99.7%	67.4	25	62.1	2	2	0	1698.88	1153	1166
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	MEADPELSK	96.5%	29.3	25	23.5	2	0	0	1019.47	350	358
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	MLLQSSEGR	98.4%	32.4	25	22.1	1	0	0	1036.51	1367	1375
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	MQLSAELQSDTEEILSK	99.7%	101	25	93.1	2	0	0	1937.94	1902	1918
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	MTQNPNYYNLQGISHR	99.4%	31.3	25	31.3	0	3	0	1935.91	1764	1779
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	NALLQLTDSQIADVAR	99.7%	130	25	125	2	0	0	1727.93	1994	2009
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	NIEMTQEDVR	99.7%	53.3	25	51.4	3	0	0	1250.57	638	647
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	NQVLVFVHSR	99.7%	60.2	25	56.7	2	0	0	1198.67	719	728
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	SLVQEMVGSFGK	99.7%	102	25	97.7	5	0	0	1281.65	546	557
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	SNSLISIKR	99.7%	39.3	25	24.6	1	0	0	1017.61	2073	2081
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	SPTLYGISHDDLK	99.7%	48.4	25	45.3	2	0	0	1445.73	932	944
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	SPTLYGISHDDLKGDPLLDQR	94.5%	22.6	25	22.6	0	1	0	2340.18	932	952
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	TGNFQVTELGR	99.7%	69.8	25	65.1	2	0	0	1221.62	976	986
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	TNLLLQAHLSR	99.7%	74.9	25	70.3	2	0	0	1265.73	1891	1901
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	TYTQLVR	99.7%	41.5	25	18.7	2	0	0	880.49	604	610
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	VELTITPDFQWDEK	99.7%	66.7	25	63.6	2	0	0	1720.84	1200	1213
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	VFSLSSEFK	99.7%	40.2	25	31.9	2	0	0	1043.54	1017	1025
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	VPIPVKESIEEPSAK	99.6%	32.8	25	31.7	0	1	0	1622.90	1044	1058
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	VVLLTGETSTDLK	99.7%	101	25	94.7	2	0	0	1375.77	1405	1417
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	WLSCETQLPVSFR	99.7%	62.8	25	56.7	2	0	0	1622.80	1275	1287
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	U520_HUMAN	244.5	100.0%	46	53	95	0.09%	24.6%	YAQAGFEGFK	99.7%	57.4	25	57.2	2	0	0	1117.53	470	479
U5 small nuclear ribonucleoprotein 40 kDa protein	SNRNP40	SNR40_HUMAN	39.3	100.0%	3	3	8	0.01%	10.4%	FVYVWDTTSR	99.7%	54.7	25	54.7	2	0	0	1273.62	308	317
U5 small nuclear ribonucleoprotein 40 kDa protein	SNRNP40	SNR40_HUMAN	39.3	100.0%	3	3	8	0.01%	10.4%	GPQLVCTGSDDGTVK	99.7%	58	25	58	2	0	0	1533.72	163	177
U5 small nuclear ribonucleoprotein 40 kDa protein	SNRNP40	SNR40_HUMAN	39.3	100.0%	3	3	8	0.01%	10.4%	TVAVWDSETGER	99.7%	46.8	25	40	4	0	0	1349.63	132	143

UAP56-interacting factor	FYTTD1	UIF_HUMAN	35.8	100.0%	2	2	4	0.00%	9.4%	GVPLQFDINSVGK	99.7%	43.2	25	41.1	2	0	0	1373.74	273	285
UAP56-interacting factor	FYTTD1	UIF_HUMAN	35.8	100.0%	2	2	4	0.00%	9.4%	VQAQLNTEQLLDDVVAK	99.7%	111	25	111	2	0	0	1884.01	199	215
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	4	4	7	0.01%	2.3%	LEAASSALGGPTLTHAVTR	99.2%	29.8	25	29.8	0	2	0	1851.99	877	895
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	4	4	7	0.01%	2.3%	SSQLNNPQFVWVVPALR	99.7%	56.3	25	52.1	2	0	0	1955.05	621	637
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	4	4	7	0.01%	2.3%	VLYNLEVLSSK	99.7%	67.8	25	67.8	1	0	0	1264.71	1174	1184
Ubiquitin carboxyl-terminal hydrolase 24	USP24	UBP24_HUMAN	294.4	100.0%	4	4	7	0.01%	2.3%	YVITIEDFYSVPR	99.7%	52	25	52	2	0	0	1601.82	934	946
Ubiquitin carboxyl-terminal hydrolase 34	USP34	UBP34_HUMAN	404.2	99.8%	2	2	3	0.00%	0.7%	AAAYDLLVEMVK	99.7%	57.9	25	48.7	1	0	0	1322.70	1842	1853
Ubiquitin carboxyl-terminal hydrolase 34	USP34	UBP34_HUMAN	404.2	99.8%	2	2	3	0.00%	0.7%	SFLLLAASTLLK	99.7%	59.5	25	59.5	2	0	0	1276.79	1694	1705
Ubiquitin conjugation factor E4 A	UBE4A	UBE4A_HUMAN	122.6	99.8%	2	2	2	0.00%	2.6%	DAQQSSSPAADNLR	99.7%	59.2	25	58.7	1	0	0	1459.68	545	558
Ubiquitin conjugation factor E4 A	UBE4A	UBE4A_HUMAN	122.6	99.8%	2	2	2	0.00%	2.6%	IFLITLDNSDPSLK	99.7%	63.8	25	54.3	1	0	0	1575.86	91	104
Ubiquitin conjugation factor E4 B	UBE4B	UBE4B_HUMAN	146.2	99.8%	2	2	3	0.00%	1.7%	ELFEEVISK	99.1%	35	25	26.6	2	0	0	1093.58	1181	1189
Ubiquitin conjugation factor E4 B	UBE4B	UBE4B_HUMAN	146.2	99.8%	2	2	3	0.00%	1.7%	YFSGPAITLENTR	99.1%	35	25	35	1	0	0	1468.74	611	623
Ubiquitin thioesterase OTUB1	OTUB1	OTUB1_HUMAN	31.3	100.0%	4	4	8	0.01%	17.0%	EYAEDDNIYQQK	99.7%	59.3	25	55.9	2	0	0	1515.66	60	71
Ubiquitin thioesterase OTUB1	OTUB1	OTUB1_HUMAN	31.3	100.0%	4	4	8	0.01%	17.0%	FFEHFIEGGR	99.7%	57.1	25	48.8	2	0	0	1238.60	189	198
Ubiquitin thioesterase OTUB1	OTUB1	OTUB1_HUMAN	31.3	100.0%	4	4	8	0.01%	17.0%	IQQEIAVQNPLVSER	99.7%	107	25	95	2	0	0	1723.93	37	51
Ubiquitin thioesterase OTUB1	OTUB1	OTUB1_HUMAN	31.3	100.0%	4	4	8	0.01%	17.0%	LLTSGYLQR	99.7%	66.2	25	57.2	2	0	0	1050.59	177	185
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	9	70	0.07%	56.4%	CCLTYCFNKPEDK	99.7%	66.5	25	66.2	3	0	0	1734.73	144	156
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	9	70	0.07%	56.4%	ECPSDECGAGVFMASHFDR	99.7%	69.8	25	69.8	3	1	0	2187.85	120	138
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	9	70	0.07%	56.4%	ESTLHLVLR	99.7%	62.9	25	49.3	11	0	0	1067.62	64	72
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	9	70	0.07%	56.4%	IQDKEGIPPDQQR	99.7%	55.8	25	55.8	10	0	0	1523.78	30	42
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	9	70	0.07%	56.4%	TITLEVEPSDTIENVK	99.7%	109	25	99.4	23	0	0	1787.93	12	27
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	9	70	0.07%	56.4%	TLSDYNIQK	99.7%	61.5	25	46.4	15	0	0	1081.55	55	63
Ubiquitin-40S ribosomal protein S27a	RPS27A	RS27A_HUMAN	18.0	100.0%	7	9	70	0.07%	56.4%	YYKVDENGK	99.7%	39.4	25	32	4	0	0	1115.54	105	113
Ubiquitin-conjugating enzyme E2 N	UBE2N	UBE2N_HUMAN	17.1	99.8%	2	2	3	0.00%	11.8%	ICLDILK	97.8%	31.3	25	20.4	1	0	0	874.51	86	92
Ubiquitin-conjugating enzyme E2 N	UBE2N	UBE2N_HUMAN	17.1	99.8%	2	2	3	0.00%	11.8%	TNEAQAIETAR	99.7%	68.2	25	58.9	2	0	0	1203.60	131	141
Ubiquitin-like modifier-activating enzyme 1	UBA1	UBA1_HUMAN	117.9	100.0%	4	4	6	0.01%	6.0%	AAVATFLQSVQVPEFTPK	99.2%	35.3	25	35.3	2	0	0	1933.04	785	802
Ubiquitin-like modifier-activating enzyme 1	UBA1	UBA1_HUMAN	117.9	100.0%	4	4	6	0.01%	6.0%	LAGTQPLEVLEAVQR	99.7%	67.3	25	67.3	1	0	0	1623.91	679	693
Ubiquitin-like modifier-activating enzyme 1	UBA1	UBA1_HUMAN	117.9	100.0%	4	4	6	0.01%	6.0%	LQTSSVLVSGLR	99.7%	45.6	25	40.9	1	0	0	1259.73	70	81
Ubiquitin-like modifier-activating enzyme 1	UBA1	UBA1_HUMAN	117.9	100.0%	4	4	6	0.01%	6.0%	SLVASLAEPDFVVTDFAK	99.7%	62.7	25	62.7	2	0	0	1909.00	305	322
Ubiquitin-protein ligase E3A	UBE3A	UBE3A_HUMAN	100.7	100.0%	3	3	4	0.00%	4.5%	EFVNLYSDYILNK	99.7%	56.8	25	42.9	1	0	0	1617.82	712	724
Ubiquitin-protein ligase E3A	UBE3A	UBE3A_HUMAN	100.7	100.0%	3	3	4	0.00%	4.5%	IGDSSQGDNNLQK	99.7%	49.9	25	46.1	1	0	0	1375.65	214	226
Ubiquitin-protein ligase E3A	UBE3A	UBE3A_HUMAN	100.7	100.0%	3	3	4	0.00%	4.5%	VFSSAEALVQSFR	99.7%	70	25	64.4	2	0	0	1440.75	156	168
Ubiquitin-protein ligase E3C	UBE3C	UBE3C_HUMAN	123.9	100.0%	6	6	9	0.01%	5.6%	LPEFYDETLLR	99.7%	47.9	25	47.7	2	0	0	1395.72	1057	1067
Ubiquitin-protein ligase E3C	UBE3C	UBE3C_HUMAN	123.9	100.0%	6	6	9	0.01%	5.6%	NAIIIQSFIR	99.7%	42.9	25	32.5	2	0	0	1174.69	48	57
Ubiquitin-protein ligase E3C	UBE3C	UBE3C_HUMAN	123.9	100.0%	6	6	9	0.01%	5.6%	SGFNPNQGFFK	98.1%	31.9	25	30.2	1	0	0	1242.59	783	793
Ubiquitin-protein ligase E3C	UBE3C	UBE3C_HUMAN	123.9	100.0%	6	6	9	0.01%	5.6%	SLYLLINSK	98.8%	33.7	25	33.7	1	0	0	1050.62	210	218
Ubiquitin-protein ligase E3C	UBE3C	UBE3C_HUMAN	123.9	100.0%	6	6	9	0.01%	5.6%	VTQLYVPASR	99.7%	39.6	25	28.8	2	0	0	1133.63	639	648
Ubiquitin-protein ligase E3C	UBE3C	UBE3C_HUMAN	123.9	100.0%	6	6	9	0.01%	5.6%	VVEGFTDEEK	95.6%	28.5	25	28.5	1	0	0	1152.54	999	1008
UDP-glucose 6-dehydrogenase	UGDH	UGDH_HUMAN	55.0	100.0%	5	5	6	0.01%	13.0%	DVLNLVYLCEALNLPEVAR	99.7%	61.9	25	60.8	1	0	0	2201.16	280	298
UDP-glucose 6-dehydrogenase	UGDH	UGDH_HUMAN	55.0	100.0%	5	5	6	0.01%	13.0%	IAILGFAFK	99.7%	49.7	25	49.7	2	0	0	979.60	331	339
UDP-glucose 6-dehydrogenase	UGDH	UGDH_HUMAN	55.0	100.0%	5	5	6	0.01%	13.0%	IIDSLFNTVTDKK	99.7%	45.3	25	44.3	1	0	0	1493.82	318	330
UDP-glucose 6-dehydrogenase	UGDH	UGDH_HUMAN	55.0	100.0%	5	5	6	0.01%	13.0%	VLIGGDETPEGQR	99.3%	36.1	25	34	1	0	0	1370.69	178	190
UDP-glucose 6-dehydrogenase	UGDH	UGDH_HUMAN	55.0	100.0%	5	5	6	0.01%	13.0%	VTVVDVNESR	99.7%	46.4	25	38.4	1	0	0	1117.58	32	41
UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	OGT	OGT1_HUMAN	116.9	100.0%	3	3	4	0.00%	2.9%	AATGEEVPR	99.3%	35.8	25	17.4	1	0	0	929.47	817	825
UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	OGT	OGT1_HUMAN	116.9	100.0%	3	3	4	0.00%	2.9%	LVSIVADQLEK	99.7%	79.5	25	51.9	1	0	0	1214.70	489	499
UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	OGT	OGT1_HUMAN	116.9	100.0%	3	3	4	0.00%	2.9%	VPNSVLWLLR	99.7%	55.6	25	48.6	2	0	0	1196.72	868	877
Uncharacterized protein C11orf84	C11orf84	CK084_HUMAN	41.0	100.0%	4	4	5	0.00%	13.4%	AESPSPAPPPGLR	95.0%	28	25	15.9	1	0	0	1275.67	306	318
Uncharacterized protein C11orf84	C11orf84	CK084_HUMAN	41.0	100.0%	4	4	5	0.00%	13.4%	DREVAEGGLPR	99.7%	49.9	25	38.4	1	0	0	1198.62	295	305
Uncharacterized protein C11orf84	C11orf84	CK084_HUMAN	41.0	100.0%	4	4	5	0.00%	13.4%	GTLDLQVIR	99.7%	42.2	25	28	2	0	0	1014.59	319	327
Uncharacterized protein C11orf84	C11orf84	CK084_HUMAN	41.0	100.0%	4	4	5	0.00%	13.4%	SNILEAWSEGVALLQDVR	99.7%	84.5	25	50.1	1	0	0	2000.04	126	143
Uncharacterized protein C17orf85	C17orf85	CQ085_HUMAN	70.6	100.0%	3	3	3	0.00%	5.7%	AFSSNPVVR	99.4%	36.7	25	30.5	1	0	0	976.52	504	512

Uncharacterized protein C17orf85	C17orf85	CQ085_HUMAN	70.6	100.0%	3	3	3	0.00%	5.7%	AGSFITGIDVTSK	99.7%	52.4	25	39	1	0	0	1295.68	71	83
Uncharacterized protein C17orf85	C17orf85	CQ085_HUMAN	70.6	100.0%	3	3	3	0.00%	5.7%	ALIGDDVGLTSYK	99.7%	53.6	25	46.9	1	0	0	1351.71	317	329
Uncharacterized protein C2orf47, mitochondrial	C2orf47	CB047_HUMAN	32.5	100.0%	3	4	11	0.01%	13.1%	EFTQGVKPDWTIAR	98.9%	34	25	32.1	1	0	0	1647.85	270	283
Uncharacterized protein C2orf47, mitochondrial	C2orf47	CB047_HUMAN	32.5	100.0%	3	4	11	0.01%	13.1%	FDLLEELVAK	99.7%	54.8	25	43.1	3	0	0	1176.65	164	173
Uncharacterized protein C2orf47, mitochondrial	C2orf47	CB047_HUMAN	32.5	100.0%	3	4	11	0.01%	13.1%	MIVLGFSNPINWVR	99.7%	82.5	25	82.5	7	0	0	1661.88	110	123
Uncharacterized protein C7orf50	C7orf50	CG050_HUMAN	22.1	100.0%	3	3	5	0.00%	28.4%	ASAEGPLLGPEAAPSGEGAGSK	95.1%	28.1	25	28.1	1	0	0	1952.96	22	43
Uncharacterized protein C7orf50	C7orf50	CG050_HUMAN	22.1	100.0%	3	3	5	0.00%	28.4%	GEAVLRPGLDAEPELSPEEQR	99.7%	39.8	25	39.8	0	2	0	2292.15	44	64
Uncharacterized protein C7orf50	C7orf50	CG050_HUMAN	22.1	100.0%	3	3	5	0.00%	28.4%	SGAELALDYLCR	99.7%	53.2	25	49.8	2	0	0	1367.66	97	108
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	8	8	12	0.01%	8.5%	EQLLQSNPVLEAFGNAK	99.7%	85.4	25	85.4	2	0	0	1857.97	140	156
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	8	8	12	0.01%	8.5%	IFLLTNNNLLLADQK	99.7%	68.9	25	68.9	2	0	0	1729.98	1007	1021
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	8	8	12	0.01%	8.5%	IIIAEVVNK	99.7%	54.3	25	43.8	2	0	0	998.62	987	995
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	8	8	12	0.01%	8.5%	LEASELFK	98.0%	31.6	25	23.8	1	0	0	936.50	942	949
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	8	8	12	0.01%	8.5%	LVMSYVAAVCGK	97.5%	30.6	25	30.6	1	0	0	1297.66	120	131
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	8	8	12	0.01%	8.5%	SEVPLVDVTK	95.9%	28.7	25	26.5	1	0	0	1086.60	1027	1036
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	8	8	12	0.01%	8.5%	SSALVIQSYIR	99.7%	81.2	25	66.6	2	0	0	1236.69	752	762
Unconventional myosin-Ib	MYO1B	MYO1B_HUMAN	132.0	100.0%	8	8	12	0.01%	8.5%	VSTTLNVAQAYYAR	99.7%	71.6	25	63.4	1	0	0	1556.81	336	349
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	8	8	15	0.01%	10.0%	DGTIDFTPGSELLITK	99.7%	80.9	25	80.9	2	0	0	1706.89	1032	1047
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	8	8	15	0.01%	10.0%	GEELLSPLNLEQAAYAR	99.7%	66.9	25	66.9	1	0	0	1873.97	362	378
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	8	8	15	0.01%	10.0%	LGTDEISPR	99.7%	87.3	25	66.5	2	0	0	987.51	901	909
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	8	8	15	0.01%	10.0%	LLQFYAETCPAPER	99.7%	63.5	25	54.3	2	0	0	1694.82	153	166
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	8	8	15	0.01%	10.0%	LLQSNPVLEAFGNAK	99.7%	79.7	25	79.7	2	0	0	1600.87	174	188
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	8	8	15	0.01%	10.0%	TSFLLNLR	99.7%	71	25	68.2	2	0	0	963.56	814	821
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	8	8	15	0.01%	10.0%	VLQALGSEPIQYAVPVVK	99.7%	65.3	25	61	2	0	0	1911.10	910	927
Unconventional myosin-Ic	MYO1C	MYO1C_HUMAN	121.7	100.0%	8	8	15	0.01%	10.0%	YLGLLENLR	99.7%	47.5	25	47.5	2	0	0	1090.63	648	656
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	4	4	6	0.01%	4.4%	IGELVGVLVNHFK	99.7%	50	25	47.8	2	0	0	1424.83	942	954
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	4	4	6	0.01%	4.4%	NYDTTIHGK	95.6%	28.4	25	23.7	1	0	0	1048.51	367	375
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	4	4	6	0.01%	4.4%	TLFTLEELR	99.7%	46.5	25	36.7	1	0	0	1121.62	686	694
Unconventional myosin-Id	MYO1D	MYO1D_HUMAN	116.2	100.0%	4	4	6	0.01%	4.4%	VTDEMFLEALNSK	99.7%	42.5	25	35.1	2	0	0	1496.73	466	478
Unconventional myosin-Vb	MYO5B	MYO5B_HUMAN	213.7	99.8%	2	2	2	0.00%	1.2%	ILNLYTPLNEFEER	99.7%	61	25	60.7	1	0	0	1750.90	1775	1788
Unconventional myosin-Vb	MYO5B	MYO5B_HUMAN	213.7	99.8%	2	2	2	0.00%	1.2%	TIQAQLQER	96.5%	29.3	25	23.3	1	0	0	1086.59	1796	1804
Unhealthy ribosome biogenesis protein 2 homolog	URB2	URB2_HUMAN	170.5	99.8%	2	2	2	0.00%	1.7%	ADVQAVVSAVTLLR	99.5%	37.6	25	15.8	1	0	0	1441.84	1262	1275
Unhealthy ribosome biogenesis protein 2 homolog	URB2	URB2_HUMAN	170.5	99.8%	2	2	2	0.00%	1.7%	SLDSSTPLPIVR	99.7%	41.8	25	34	1	0	0	1284.72	555	566
UPF0444 transmembrane protein C12orf23	C12orf23	CL023_HUMAN	11.7	99.8%	2	2	2	0.00%	30.2%	GGVSAVAGGVTAVGSAVVNK	99.7%	70.3	25	63.4	1	0	0	1699.93	85	104
UPF0444 transmembrane protein C12orf23	C12orf23	CL023_HUMAN	11.7	99.8%	2	2	2	0.00%	30.2%	TAVTTVPSMGIGLVK	99.7%	40.3	25	35.4	1	0	0	1489.83	70	84
UPF0488 protein C8orf33	C8orf33	CH033_HUMAN	25.0	100.0%	4	4	5	0.00%	21.8%	AAAYSAQVQPVDGATR	99.7%	67.1	25	58	1	0	0	1604.80	183	198
UPF0488 protein C8orf33	C8orf33	CH033_HUMAN	25.0	100.0%	4	4	5	0.00%	21.8%	ATLDMPDEEFRFNFF	99.4%	37	25	37	1	0	0	1894.83	215	229
UPF0488 protein C8orf33	C8orf33	CH033_HUMAN	25.0	100.0%	4	4	5	0.00%	21.8%	LPGPVSSAR	99.7%	44.5	25	19.2	2	0	0	883.50	28	36
UPF0488 protein C8orf33	C8orf33	CH033_HUMAN	25.0	100.0%	4	4	5	0.00%	21.8%	QKEQAIGAIR	94.8%	27.8	25	20.5	1	0	0	1113.64	134	143
UPF0505 protein C16orf62	C16orf62	CP062_HUMAN	109.6	99.8%	2	2	2	0.00%	2.4%	FLPFLDMFQK	98.5%	32.8	25	22.8	1	0	0	1285.67	569	578
UPF0505 protein C16orf62	C16orf62	CP062_HUMAN	109.6	99.8%	2	2	2	0.00%	2.4%	FVLITDILDTFGK	99.7%	74.2	25	74.2	1	0	0	1481.83	231	243
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	17	0.02%	19.6%	AALGPLVTGLYDVQAFK	99.7%	93	25	93	2	0	0	1762.97	6	22
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	17	0.02%	19.6%	FADIGNTVK	99.7%	45.8	25	33.1	2	0	0	964.51	315	323
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	17	0.02%	19.6%	FGDFVLK	99.7%	42.3	25	31.2	2	0	0	825.45	23	29
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	17	0.02%	19.6%	IASWADLVNAHVVPGSGVVK	99.7%	51.7	25	51.7	0	2	0	2019.10	333	352
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	17	0.02%	19.6%	KFADIGNTVK	99.7%	64	25	54.1	1	0	0	1092.60	314	323
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	17	0.02%	19.6%	KVDAETVGR	99.7%	59.1	25	47.4	2	0	0	974.53	188	196
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	17	0.02%	19.6%	MLEILEQQK	99.7%	44.9	25	34.5	2	0	0	1131.61	179	187
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	17	0.02%	19.6%	SGLSSPIYIDLR	99.7%	57.8	25	43.9	2	0	0	1320.72	30	41
Uridine 5'-monophosphate synthase	UMPS	UMPS_HUMAN	52.2	100.0%	9	9	17	0.02%	19.6%	VTDAIVLLDR	99.7%	101	25	68.5	2	0	0	1114.65	146	155
Uridine-cytidine kinase 2	UCK2	UCK2_HUMAN	29.3	100.0%	3	3	4	0.00%	11.5%	IVQLLGQNEVDYR	99.7%	57.8	25	57.8	1	0	0	1546.82	40	52
Uridine-cytidine kinase 2	UCK2	UCK2_HUMAN	29.3	100.0%	3	3	4	0.00%	11.5%	TLKEITEGK	95.6%	28.5	25	23.5	1	0	0	1018.58	97	105

Uridine-cytidine kinase 2	UCK2	UCK2_HUMAN	29.3	100.0%	3	3	4	0.00%	11.5%	YADVIIPR	99.7%	42.2	25	42.2	2	0	0	946.54	203	210
Uridine-cytidine kinase-like 1	UCKL1	UCKL1_HUMAN	61.1	99.8%	2	2	4	0.00%	4.2%	EAFAIGLGGGSASGK	99.7%	83.1	25	75.9	2	0	0	1321.67	97	111
Uridine-cytidine kinase-like 1	UCKL1	UCKL1_HUMAN	61.1	99.8%	2	2	4	0.00%	4.2%	LADIVVPR	99.7%	55.5	25	51.8	2	0	0	882.54	274	281
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	4	4	8	0.01%	17.7%	EITGIGPSTTTETETIAK	99.7%	51.5	25	51.5	2	0	0	1848.94	215	232
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	4	4	8	0.01%	17.7%	ELALPGELTQSR	99.7%	55.2	25	50.5	2	0	0	1313.71	94	105
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	4	4	8	0.01%	17.7%	FESPESQASAEQPEM	99.7%	66.9	25	66.9	2	0	0	1682.69	313	327
Vacuolar protein sorting-associated protein 26A	VPS26A	VP26A_HUMAN	38.2	100.0%	4	4	8	0.01%	17.7%	LFLAGYDPTPTMR	99.7%	55.8	25	55.3	2	0	0	1497.74	250	262
Vacuolar protein sorting-associated protein 29	VPS29	VPS29_HUMAN	20.5	99.8%	2	2	3	0.00%	12.6%	GDFDENLNYPEQK	99.7%	47.3	25	47.3	1	0	0	1568.69	61	73
Vacuolar protein sorting-associated protein 29	VPS29	VPS29_HUMAN	20.5	99.8%	2	2	3	0.00%	12.6%	TLAGDVHIVR	99.7%	69.9	25	53.1	2	0	0	1080.62	51	60
Vacuolar protein sorting-associated protein 33B	VPS33B	VP33B_HUMAN	70.6	99.8%	2	2	4	0.00%	3.4%	FIFLTTAVTNSAR	99.7%	75	25	68.2	2	0	0	1440.78	595	607
Vacuolar protein sorting-associated protein 33B	VPS33B	VP33B_HUMAN	70.6	99.8%	2	2	4	0.00%	3.4%	IIEQVLER	98.9%	34	25	15.5	2	0	0	999.58	524	531
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	12	22	0.02%	17.0%	AQLAAITLIIGTFER	99.3%	36.3	25	36.3	2	0	0	1616.94	623	637
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	12	22	0.02%	17.0%	ENDAVTIQVLNQLIQK	99.7%	85.2	25	73.3	1	0	0	1826.00	734	749
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	12	22	0.02%	17.0%	ESPESEGPIYEGLIL	98.7%	33.3	25	23.3	1	0	0	1632.80	782	796
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	12	22	0.02%	17.0%	HASNMLGELR	94.7%	27.8	25	17	1	0	0	1143.56	45	54
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	12	22	0.02%	17.0%	ILVGTNLVR	99.7%	63.8	25	47.8	2	0	0	984.62	218	226
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	12	22	0.02%	17.0%	IPVDTYNNILTVLK	99.7%	78.1	25	72.5	4	0	0	1602.91	404	417
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	12	22	0.02%	17.0%	LFDIFSQQVATVIQSR	99.7%	100	25	83.7	2	2	0	1852.00	324	339
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	12	22	0.02%	17.0%	LNLEHIATSSAVSK	99.7%	81.9	25	79.8	2	2	0	1469.80	383	396
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	12	22	0.02%	17.0%	LSQLEGVNVER	99.7%	76.6	25	67	2	0	0	1243.66	227	237
Vacuolar protein sorting-associated protein 35	VPS35	VPS35_HUMAN	91.7	100.0%	10	12	22	0.02%	17.0%	SEDPDQQYLILNTAR	99.7%	81.4	25	81	1	0	0	1762.86	500	514
Vacuolar protein-sorting-associated protein 25	VPS25	VPS25_HUMAN	20.7	100.0%	3	3	5	0.00%	14.8%	AEIITVSDGR	99.7%	45.8	25	23.6	1	0	0	1060.56	162	171
Vacuolar protein-sorting-associated protein 25	VPS25	VPS25_HUMAN	20.7	100.0%	3	3	5	0.00%	14.8%	LIYQWVSR	99.7%	41.9	25	34	2	0	0	1064.59	110	117
Vacuolar protein-sorting-associated protein 25	VPS25	VPS25_HUMAN	20.7	100.0%	3	3	5	0.00%	14.8%	SSFLIMWR	97.5%	30.6	25	14.8	2	0	0	1055.53	95	102
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	10	10	14	0.01%	8.9%	ADYNLTR	99.5%	37.5	25	8.61	1	0	0	852.42	1123	1129
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	10	10	14	0.01%	8.9%	DINLDVNR	97.8%	31.2	25	13.3	1	0	0	958.50	935	942
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	10	10	14	0.01%	8.9%	DPGVITYDLPTPPGEK	99.7%	69.6	25	64.5	1	0	0	1698.86	274	289
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	10	10	14	0.01%	8.9%	ITPAHDQNDYEVGQR	98.9%	28.5	25	27.9	0	1	0	1742.81	592	606
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	10	10	14	0.01%	8.9%	KVDEAIALFQK	99.7%	61.2	25	52.1	1	0	0	1261.72	1252	1262
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	10	10	14	0.01%	8.9%	LHEEGIIYR	99.0%	34.6	25	25.9	2	0	0	1129.60	462	470
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	10	10	14	0.01%	8.9%	LQQTEAELR	99.7%	53.4	25	38.5	1	0	0	1087.57	1243	1251
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	10	10	14	0.01%	8.9%	LSAAVTEAFVR	99.7%	111	25	103	2	0	0	1163.64	451	461
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	10	10	14	0.01%	8.9%	SSAQDPQAVLGALGR	99.7%	85.7	25	82.1	2	0	0	1469.77	123	137
Valine--tRNA ligase	VARS	SYVC_HUMAN	140.5	100.0%	10	10	14	0.01%	8.9%	VPLEVQEADEAK	99.7%	68.4	25	63.2	2	0	0	1327.67	1231	1242
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	7	8	16	0.02%	20.2%	FSFTLPYPVK	99.7%	43.2	25	38.8	1	0	0	1198.65	310	319
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	7	8	16	0.02%	20.2%	LESEGSPETLTNLR	99.7%	126	25	116	3	0	0	1545.78	133	146
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	7	8	16	0.02%	20.2%	LRLESEGSPETLTNLR	99.7%	75.8	25	75.5	2	2	0	1814.96	131	146
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	7	8	16	0.02%	20.2%	QVNITVQK	99.7%	61.4	25	36.7	2	0	0	929.54	77	84
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	7	8	16	0.02%	20.2%	RPLFLAPDFDR	99.1%	34.9	25	26	2	0	0	1346.72	99	109
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	7	8	16	0.02%	20.2%	VELSDVQNPAISITENVLHFK	98.4%	27.2	25	27.2	0	2	0	2353.24	23	43
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	PTPLAD1	HACD3_HUMAN	43.2	100.0%	7	8	16	0.02%	20.2%	VSQWWER	99.7%	46.3	25	31.2	2	0	0	990.48	86	92
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	5	5	17	0.02%	15.6%	HYEVEILDAK	99.7%	57.5	25	50	1	0	0	1216.62	3	12
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	5	5	17	0.02%	15.6%	LLETLFVHR	99.7%	63.3	25	40.3	4	0	0	1127.66	142	150
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	5	5	17	0.02%	15.6%	LPVGTTATLYFR	99.7%	73	25	71.3	4	0	0	1338.74	68	79
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	5	5	17	0.02%	15.6%	SLKDEDVLQK	99.7%	49.7	25	39.6	4	0	0	1174.63	58	67
Very-long-chain enoyl-CoA reductase	TECR	TECR_HUMAN	36.0	100.0%	5	5	17	0.02%	15.6%	YDFTSSR	99.5%	37.6	25	25.5	4	0	0	875.39	117	123
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	35	0.03%	25.9%	AENSSLNLIGK	99.7%	79.7	25	59.5	2	0	0	1145.62	188	198
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	35	0.03%	25.9%	DFQSGQHVIVR	99.6%	39.2	25	34.4	1	0	0	1285.66	28	38
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	35	0.03%	25.9%	DIEAMDPSILK	98.9%	34.1	25	23.6	1	0	0	1247.62	151	161
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	35	0.03%	25.9%	GILLYGPPGCGK	99.5%	37.9	25	26.5	2	0	0	1231.65	255	266
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	35	0.03%	25.9%	GSMAGSTGVHDTVVNQLLSK	99.7%	47.7	25	43.8	0	2	0	2001.01	338	357

Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	35	0.03%	25.9%	IAEESNFPFIK	99.7%	56.1	25	42.3	2	0	0	1294.67	556	566
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	35	0.03%	25.9%	KLLIIGTTSR	99.7%	47.7	25	37.8	2	0	0	1101.70	639	648
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	35	0.03%	25.9%	LLDYVPIGPR	99.7%	53.7	25	47.1	2	0	0	1142.66	608	617
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	35	0.03%	25.9%	LLIIGTTSR	99.7%	58.1	25	48.1	2	0	0	973.60	640	648
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	35	0.03%	25.9%	NFSGAELEGLVR	99.7%	82.6	25	66.2	2	0	0	1291.66	435	446
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	35	0.03%	25.9%	QSIINPDWNFEK	99.7%	66.4	25	63.7	2	0	0	1490.73	206	217
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	35	0.03%	25.9%	SIDSNPYDTDK	98.8%	33.7	25	33.7	2	0	0	1254.55	106	116
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	35	0.03%	25.9%	SQLSCVVVDDIER	99.7%	94.5	25	91.6	2	0	0	1519.74	595	607
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	35	0.03%	25.9%	TPLVSVLLEGPPHSGK	99.7%	67	25	64.6	2	2	0	1630.92	534	549
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	35	0.03%	25.9%	VLDDGELLVQQTK	99.7%	84.9	25	84.9	3	0	0	1457.78	517	529
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	35	0.03%	25.9%	VVNGPEILNK	99.7%	53.5	25	43.5	2	0	0	1082.62	284	293
Vesicle-fusing ATPase	NSF	NSF_HUMAN	82.6	100.0%	17	18	35	0.03%	25.9%	YVGESEANIR	99.7%	51.6	25	44.1	2	0	0	1137.55	294	303
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	DGQVINETSQHHDDLE	99.7%	62.5	25	62.5	5	2	0	1836.80	451	466
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	DNLAEDIMR	99.7%	60	25	52.3	4	0	0	1076.50	176	184
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	EEAENTLQSFR	99.7%	69	25	57.2	4	0	0	1323.62	197	207
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	EEAENTLQSFRQDVDNASLAR	99.7%	35.8	25	35.8	0	1	0	2393.13	197	217
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	EKLQEEMLQR	99.7%	55.7	25	47.3	4	0	0	1319.66	187	196
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	EMEENFAVEAANYQDTIGR	99.7%	113	25	113	5	1	0	2186.97	346	364
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	ETNLDSLPLVDTHSK	99.7%	74.9	25	66.2	3	1	0	1668.84	425	439
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	ETNLDSLPLVDTHSKR	99.7%	62.1	25	58.8	2	2	0	1824.95	425	440
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	EYQDLLNVK	99.7%	55.2	25	43.9	6	0	0	1121.58	382	390
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	FADLSEAANR	99.7%	63.1	25	47.7	5	0	0	1093.53	295	304
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	FANYIDK	99.7%	48.6	25	40.3	2	0	0	870.44	114	120
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	FANYIDKVR	99.7%	65.4	25	57.9	4	0	0	1125.61	114	122
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	FLEQQNK	99.1%	35.1	25	11.2	1	0	0	906.47	123	129
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	ILLAELEQLK	99.7%	68.1	25	60.3	4	0	0	1169.71	130	139
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	ILLAELEQLKGQGK	99.7%	71.8	25	71.8	4	4	0	1539.91	130	143
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	ISLPLPNFSSLNLR	99.7%	86.8	25	76.7	5	2	0	1570.90	411	424
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	KLLEGEESR	99.7%	53.7	25	32.4	2	0	0	1060.56	402	410
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	KVESLQEEIAFLK	99.7%	108	25	101	4	1	0	1533.85	223	235
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	LGDLYEEEMR	99.7%	65.7	25	65.6	6	0	0	1270.56	146	155
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	LLEGEESR	99.7%	48.4	25	40.5	3	0	0	932.47	403	410
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	LLQDSVDFSLADAINTEFK	99.7%	128	25	123	9	2	0	2126.07	79	97
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	LQDEIQNMK	99.7%	43.6	25	35.5	4	0	0	1118.55	365	373
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	LQDEIQNMKEEMAR	99.7%	81.5	25	68.5	7	6	0	1734.82	365	378
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	LQEEMLQR	99.7%	42.3	25	27.1	4	0	0	1062.53	189	196
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	LQEEMLQREEAENTLQSFR	99.7%	60.7	25	60.7	0	4	0	2351.13	189	207
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	MALDIEIATYR	99.7%	82.4	25	37.1	4	0	0	1295.67	391	401
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	MFGGPGTASRPSSSR	99.7%	35.3	25	33.5	2	3	0	1510.71	14	28
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	NLQEAEEWYK	99.7%	50.9	25	50.7	2	0	0	1309.61	283	292
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	QDVDNASLAR	99.7%	67.5	25	56.7	6	0	0	1088.53	208	217
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	QQYESVAAK	99.7%	48.7	25	35	2	0	0	1023.51	274	282
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	QVDQLTNDK	99.7%	56.1	25	41.3	2	0	0	1060.53	160	168
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	QVDQLTNDKAR	99.7%	52.6	25	36.7	2	2	0	1287.67	160	170
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	QVQSLTCEVDALK	99.7%	70.6	25	60.8	2	0	0	1490.75	322	334
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	QVQSLTCEVDALKGTNESLER	99.7%	75.8	25	75.8	2	2	0	2377.17	322	342
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	RQVDQLTNDK	99.7%	60.4	25	50	2	0	0	1216.63	159	168
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	SLYASSPGGVYATR	99.7%	98.3	25	98.3	6	0	0	1428.71	51	64
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	SYVTTSTR	99.7%	46.7	25	36.7	2	0	0	914.46	29	36
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	TNEKVELQELNDR	99.7%	69	25	66.4	4	4	0	1587.80	101	113
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	TYSLGSALRPSTSR	99.7%	51.7	25	51.6	3	2	0	1495.79	37	50

Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	VELQELNDR	99.7%	60.7	25	56.3	2	0	0	1115.57	105	113
Vimentin	VIM	VIME_HUMAN	53.7	100.0%	41	69	190	0.18%	75.3%	VEVERDNLAEDIMR	99.7%	48.8	25	48.2	5	6	0	1688.83	171	184
Vitamin K epoxide reductase complex subunit 1-like protein 1	VKORC1L1	VKORL_HUMAN	19.8	100.0%	3	3	3	0.00%	17.0%	ALCDLGPWVK	99.7%	47.4	25	26.6	1	0	0	1158.60	48	57
Vitamin K epoxide reductase complex subunit 1-like protein 1	VKORC1L1	VKORL_HUMAN	19.8	100.0%	3	3	3	0.00%	17.0%	GFGLLGSIFGK	99.7%	40.3	25	37.5	1	0	0	1095.62	69	79
Vitamin K epoxide reductase complex subunit 1-like protein 1	VKORC1L1	VKORL_HUMAN	19.8	100.0%	3	3	3	0.00%	17.0%	LVYLNEAWK	98.2%	32.1	25	20.3	1	0	0	1135.61	160	168
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	8	8	14	0.01%	36.7%	GYGFGLIK	98.0%	31.5	25	24.2	1	0	0	854.48	21	28
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	8	8	14	0.01%	36.7%	KLETAVNLAWTAGNSNTR	98.0%	26.3	25	26.3	0	1	0	1946.01	201	218
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	8	8	14	0.01%	36.7%	LTFDSSFSPNTGK	99.7%	64.9	25	56	2	0	0	1400.67	97	109
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	8	8	14	0.01%	36.7%	LTFDSSFSPNTGKK	99.7%	91.4	25	91.4	2	0	0	1528.76	97	110
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	8	8	14	0.01%	36.7%	LTLSALLDGK	99.7%	81.7	25	0	10	0	0	1030.61	257	266
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	8	8	14	0.01%	36.7%	VNNSSLIGLGYTQTLKPGIK	99.6%	32.6	25	32.6	0	2	0	2103.18	237	256
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	8	8	14	0.01%	36.7%	VTQSNFAVGYK	99.7%	54.6	25	42	2	0	0	1213.62	164	174
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	8	8	14	0.01%	36.7%	WTEYGLTFTEK	99.7%	55.4	25	55.4	2	0	0	1374.66	64	74
Voltage-dependent anion-selective channel protein 1	VDAC1	VDAC1_HUMAN	30.8	100.0%	8	8	14	0.01%	36.7%	YQIDPDACFSAK	99.7%	55.4	25	54.5	2	0	0	1414.63	225	236
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	12	31	0.03%	50.0%	GFGFGLVK	98.9%	34	25	26.6	2	0	0	824.47	32	39
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	12	31	0.03%	50.0%	LTFDTTFSPNTGK	99.7%	101	25	90.8	2	0	0	1428.70	108	120
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	12	31	0.03%	50.0%	LTFDTTFSPNTGKK	99.7%	71.5	25	71.5	2	0	0	1556.80	108	121
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	12	31	0.03%	50.0%	LTLSALVDGK	99.7%	88.5	25	79.4	5	0	0	1016.60	268	277
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	12	31	0.03%	50.0%	NNFAVGYR	99.7%	47.6	25	39.5	4	0	0	940.46	178	185
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	12	31	0.03%	50.0%	SCSGVEFSTSGSSNTDTGK	99.7%	117	25	117	2	0	0	1907.79	46	64
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	12	31	0.03%	50.0%	TGDFQLHTNVNDGTEFGGSIYQK	99.7%	67.9	25	67.9	0	3	0	2528.17	186	208
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	12	31	0.03%	50.0%	VNNSSLIGVGYTQTLRPGVK	99.7%	82.6	25	82.6	2	2	0	2103.16	248	267
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	12	31	0.03%	50.0%	WCEYGLTFTEK	99.7%	50	25	50	2	0	0	1433.64	75	85
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	12	31	0.03%	50.0%	WNTDNTLGTEIAIEDQICQGLK	99.7%	55.2	25	55.2	1	0	0	2519.21	86	107
Voltage-dependent anion-selective channel protein 2	VDAC2	VDAC2_HUMAN	31.6	100.0%	11	12	31	0.03%	50.0%	YQLDPTASISAK	99.7%	66.2	25	57.4	4	0	0	1293.67	236	247
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	13	16	53	0.05%	48.1%	GYGFGMVK	99.7%	42.5	25	32.6	5	0	0	874.41	21	28
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	13	16	53	0.05%	48.1%	IETSINLAWTAGSNNTR	99.7%	84.9	25	84.9	1	0	0	1847.92	202	218
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	13	16	53	0.05%	48.1%	LSQNNFALGYK	99.7%	69.8	25	56.6	6	0	0	1254.65	164	174
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	13	16	53	0.05%	48.1%	LTLDTIFVPNTGK	99.7%	93.3	25	93.3	5	0	0	1418.79	97	109
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	13	16	53	0.05%	48.1%	LTLDTIFVPNTGKK	99.7%	48.8	25	45.3	4	3	0	1546.88	97	110
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	13	16	53	0.05%	48.1%	LTLSALIDGK	99.7%	81.7	25	0	10	0	0	1030.61	257	266
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	13	16	53	0.05%	48.1%	SCSGVEFSTSGHAYTDTGK	99.7%	85.7	25	85.7	1	0	0	1990.84	35	53
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	13	16	53	0.05%	48.1%	SKLSQNNFALGYK	99.7%	48.7	25	45.2	2	0	0	1469.77	162	174
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	13	16	53	0.05%	48.1%	VCNYGLTFTQK	99.7%	70.7	25	63.5	4	0	0	1330.65	64	74
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	13	16	53	0.05%	48.1%	VNNASLIGLGYTQTLRPGVK	99.7%	86.1	25	82.4	2	4	0	2101.18	237	256
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	13	16	53	0.05%	48.1%	WNTDNTLGTEISWENK	99.7%	90.4	25	85.9	2	0	0	1907.88	75	90
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	13	16	53	0.05%	48.1%	YKVCNYGLTFTQK	99.7%	53.2	25	52.2	2	0	0	1621.80	62	74
Voltage-dependent anion-selective channel protein 3	VDAC3	VDAC3_HUMAN	30.7	100.0%	13	16	53	0.05%	48.1%	YMLDCR	99.2%	35.3	25	35.3	2	0	0	873.36	225	230
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	7	8	12	0.01%	15.6%	ALDEYYDKHFTEFVPLR	99.7%	41.8	25	41.8	0	2	0	2143.05	460	476
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	7	8	12	0.01%	15.6%	FTMVQVWPVR	99.7%	46.2	25	39.6	2	0	0	1262.67	203	212
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	7	8	12	0.01%	15.6%	GVNVSALSR	99.7%	75.7	25	60.7	2	0	0	902.51	121	129
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	7	8	12	0.01%	15.6%	LPANHPLLTGQR	99.5%	31.9	25	30.9	0	1	0	1316.74	221	232
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	7	8	12	0.01%	15.6%	TALVANTSNMPVAAR	99.7%	71.4	25	63.9	1	0	0	1515.79	309	323
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	7	8	12	0.01%	15.6%	VGHSELVGEIIR	99.7%	54.5	25	46.8	1	1	0	1308.73	45	56
V-type proton ATPase catalytic subunit A	ATP6V1A	VATA_HUMAN	68.3	100.0%	7	8	12	0.01%	15.6%	VGSHITGGDIYGIVSENSLIK	99.7%	56.1	25	48.4	0	2	0	2159.13	143	163
V-type proton ATPase subunit H	ATP6V1H	VATH_HUMAN	55.9	100.0%	4	4	9	0.01%	12.6%	LLEVSDDPQVLAVAAHDVGEYVR	99.7%	34.8	25	34.5	0	2	0	2495.28	397	419
V-type proton ATPase subunit H	ATP6V1H	VATH_HUMAN	55.9	100.0%	4	4	9	0.01%	12.6%	QLQSEQPQTAAAR	99.7%	59	25	52.3	2	0	0	1427.72	470	482
V-type proton ATPase subunit H	ATP6V1H	VATH_HUMAN	55.9	100.0%	4	4	9	0.01%	12.6%	VSIFFDYAR	99.7%	57.2	25	46.2	2	0	0	1117.57	108	116
V-type proton ATPase subunit H	ATP6V1H	VATH_HUMAN	55.9	100.0%	4	4	9	0.01%	12.6%	YNIIPVLSDILQESVK	99.7%	57.9	25	54.2	3	0	0	1831.02	263	278
WASH complex subunit 7	KIAA1033	WASH7_HUMAN	136.4	99.8%	2	2	4	0.00%	1.8%	LGEPSEIDQR	99.7%	54.7	25	48.1	2	0	0	1143.56	303	312
WASH complex subunit 7	KIAA1033	WASH7_HUMAN	136.4	99.8%	2	2	4	0.00%	1.8%	MLVDVFAPEFR	99.7%	43	25	41	2	0	0	1323.68	993	1003

WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	20	0.02%	22.4%	DYSGQGVVK	97.2%	30.2	25	17.3	1	0	0	952.47	397	405
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	20	0.02%	22.4%	GPVTDVAYSHDGAFLAVCDASK	99.7%	49.3	25	49.3	0	2	0	2280.06	490	511
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	20	0.02%	22.4%	IAVVGEGR	99.3%	36	25	23.6	2	0	0	800.46	117	124
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	20	0.02%	22.4%	LATGSDDNCAAFFEGPPFK	99.7%	91.2	25	87.6	2	0	0	2043.91	162	180
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	20	0.02%	22.4%	LYSILGTTLKDEGK	99.7%	96.7	25	77.9	2	2	0	1537.85	471	484
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	20	0.02%	22.4%	NIDNPALADIYTEHAHQVVVAK	99.7%	39.6	25	36.5	0	2	0	2418.24	44	65
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	20	0.02%	22.4%	VFASLPQVER	99.7%	49.2	25	38.3	2	0	0	1145.63	8	17
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	20	0.02%	22.4%	YAPSGFYIASGDVSGK	99.7%	119	25	113	2	0	0	1618.77	66	81
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	20	0.02%	22.4%	YEYQPFAGK	96.5%	29.3	25	29.3	2	0	0	1102.52	96	104
WD repeat-containing protein 1	WDR1	WDR1_HUMAN	66.2	100.0%	10	11	20	0.02%	22.4%	YTSLMLR	98.1%	31.7	25	20.8	1	0	0	883.47	390	396
WD repeat-containing protein 37	WDR37	WDR37_HUMAN	54.7	99.8%	2	2	2	0.00%	5.5%	LAAEGQAIDGAELSK	99.7%	84.7	25	76.7	1	0	0	1472.76	90	104
WD repeat-containing protein 37	WDR37	WDR37_HUMAN	54.7	99.8%	2	2	2	0.00%	5.5%	STLLELFGQIER	99.7%	69.5	25	63.4	1	0	0	1405.77	56	67
WD repeat-containing protein 5	WDR5	WDR5_HUMAN	36.6	100.0%	3	3	5	0.00%	10.5%	FTLAGHTK	98.6%	32.9	25	13.8	1	0	0	874.48	39	46
WD repeat-containing protein 5	WDR5	WDR5_HUMAN	36.6	100.0%	3	3	5	0.00%	10.5%	IWDTASGQCLK	99.7%	46	25	41.2	2	0	0	1278.61	197	207
WD repeat-containing protein 5	WDR5	WDR5_HUMAN	36.6	100.0%	3	3	5	0.00%	10.5%	TLPAHSDPVSAVHFNR	99.7%	34.6	25	32.9	0	2	0	1747.89	166	181
WD repeat-containing protein 6	WDR6	WDR6_HUMAN	121.7	100.0%	5	5	7	0.01%	5.9%	ATSELILLPVTGLECVGDR	96.1%	28.9	25	28.4	1	0	0	2043.08	12	30
WD repeat-containing protein 6	WDR6	WDR6_HUMAN	121.7	100.0%	5	5	7	0.01%	5.9%	DGQLQPVLR	98.8%	33.8	25	21.5	2	0	0	1025.57	598	606
WD repeat-containing protein 6	WDR6	WDR6_HUMAN	121.7	100.0%	5	5	7	0.01%	5.9%	GLGVSALCFK	99.6%	38.9	25	34	2	0	0	1051.56	334	343
WD repeat-containing protein 6	WDR6	WDR6_HUMAN	121.7	100.0%	5	5	7	0.01%	5.9%	LFLLQDSGR	99.7%	56.6	25	44.7	1	0	0	1048.58	890	898
WD repeat-containing protein 6	WDR6	WDR6_HUMAN	121.7	100.0%	5	5	7	0.01%	5.9%	VVPINTPTAAVDQTLFPGK	99.7%	60.7	25	60.7	1	0	0	1968.08	419	437
WD repeat-containing protein 82	WDR82	WDR82_HUMAN	35.1	100.0%	4	5	13	0.01%	18.2%	LILISTNGSFIR	99.7%	74.4	25	60.2	2	0	0	1333.78	208	219
WD repeat-containing protein 82	WDR82	WDR82_HUMAN	35.1	100.0%	4	5	13	0.01%	18.2%	SFDKGPFATFK	99.7%	42.5	25	34.1	2	0	0	1244.63	178	188
WD repeat-containing protein 82	WDR82	WDR82_HUMAN	35.1	100.0%	4	5	13	0.01%	18.2%	VVALSMSPVDDTFISGSLDK	99.7%	108	25	103	5	0	0	2097.04	110	129
WD repeat-containing protein 82	WDR82	WDR82_HUMAN	35.1	100.0%	4	5	13	0.01%	18.2%	YTHAANTVVYSSNK	99.7%	78.5	25	78.5	4	0	0	1554.75	71	84
WD40 repeat-containing protein SMU1	SMU1	SMU1_HUMAN	57.5	99.8%	2	2	3	0.00%	3.5%	IQSGQCLR	97.5%	30.7	25	15.7	1	0	0	961.49	293	300
WD40 repeat-containing protein SMU1	SMU1	SMU1_HUMAN	57.5	99.8%	2	2	3	0.00%	3.5%	LMALLGQALK	99.7%	68.5	25	59	2	0	0	1057.64	161	170
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	19	21	54	0.05%	25.3%	AFREEAIK	97.4%	30.4	25	1.83	1	0	0	963.53	641	648
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	19	21	54	0.05%	25.3%	ALQEKVEIK	97.6%	30.8	25	10.8	1	0	0	1057.63	661	669
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	19	21	54	0.05%	25.3%	CFSVLGFCK	99.7%	54.9	25	50.6	2	0	0	1117.52	339	347
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	19	21	54	0.05%	25.3%	EDGSGDRGDGPFR	98.7%	33.5	25	26.2	2	0	0	1364.58	172	184
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	19	21	54	0.05%	25.3%	EEASGSSVTAEEAK	99.7%	116	25	116	4	0	0	1394.63	689	702
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	19	21	54	0.05%	25.3%	EEASGSSVTAEEAKK	99.7%	101	25	88.1	4	0	0	1522.72	689	703
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	19	21	54	0.05%	25.3%	EPLPPIQQHIWNMLNPPAEVTTK	99.7%	34.6	25	34.6	0	2	0	2669.38	503	525
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	19	21	54	0.05%	25.3%	FFMGNQVLK	99.7%	45.9	25	39.3	2	0	0	1083.57	355	363
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	19	21	54	0.05%	25.3%	HIEIFTDLSSR	99.7%	67.7	25	54.7	4	0	0	1317.68	131	141
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	19	21	54	0.05%	25.3%	LFQCLLHR	99.7%	40.9	25	26.2	4	0	0	1086.59	490	497
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	19	21	54	0.05%	25.3%	LGGHGPSFPLK	99.7%	44.1	25	33.6	3	0	0	1109.61	185	195
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	19	21	54	0.05%	25.3%	LTIGSNLSIR	99.7%	69.1	25	55.5	2	0	0	1073.63	251	260
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	19	21	54	0.05%	25.3%	QYMFSSLK	99.7%	57.5	25	39.9	2	0	0	1003.49	432	439
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	19	21	54	0.05%	25.3%	RFFMGNQVLK	97.3%	30.3	25	9.6	1	0	0	1239.67	354	363
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	19	21	54	0.05%	25.3%	SQLDIIIHSLK	99.7%	58.7	25	47.5	2	0	0	1266.74	145	155
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	19	21	54	0.05%	25.3%	TDTLEDLFPTTK	99.7%	72.8	25	67.3	4	0	0	1380.69	470	481
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	19	21	54	0.05%	25.3%	TLFPLIEAK	99.7%	43.1	25	23.5	4	0	0	1031.61	535	543
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	19	21	54	0.05%	25.3%	VITMFVQR	99.7%	62.5	25	42.8	6	0	0	993.56	37	44
X-ray repair cross-complementing protein 5	XRCC5	XRCC5_HUMAN	82.7	100.0%	19	21	54	0.05%	25.3%	YGSDIVPFSK	99.7%	55.9	25	45.8	4	0	0	1112.56	316	325
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	21	28	52	0.05%	43.3%	DSLIFLVDASK	99.7%	85.2	25	76.2	5	0	0	1207.66	36	46
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	21	28	52	0.05%	43.3%	DTGIFLDLMHLK	99.7%	64.3	25	60.7	5	0	0	1402.74	195	206
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	21	28	52	0.05%	43.3%	EVAALCR	99.1%	35.2	25	17.8	1	0	0	818.42	393	399
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	21	28	52	0.05%	43.3%	FDDPGLMLMGFKPLVLLK	98.6%	27.6	25	22.5	0	2	0	2034.12	340	357
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	21	28	52	0.05%	43.3%	FTVPMLK	96.9%	29.8	25	21.4	1	0	0	835.47	576	582
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	21	28	52	0.05%	43.3%	IISSDRDLLAVVFYGTEK	99.7%	54.2	25	49.3	2	2	0	2026.09	75	92

X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	21	28	52	0.05%	43.3%	ILELDQFK	99.7%	47.7	25	15.2	2	0	0	1005.56	116	123
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	21	28	52	0.05%	43.3%	ILELDQFKGQQGQK	99.7%	75.5	25	62.3	2	0	0	1631.88	116	129
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	21	28	52	0.05%	43.3%	IMATPEQVGK	99.7%	54.2	25	41	4	0	0	1089.56	452	461
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	21	28	52	0.05%	43.3%	IMLFTNEDNPHGNDSAK	99.7%	85.3	25	85.3	1	2	0	1902.87	166	182
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	21	28	52	0.05%	43.3%	IQVTPPGFQLVFLPFADDK	99.7%	62.5	25	60.7	1	0	0	2132.14	425	443
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	21	28	52	0.05%	43.3%	KPGGFDISLFYR	99.7%	49.3	25	39.5	2	2	0	1399.74	207	218
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	21	28	52	0.05%	43.3%	KQELLEALTK	99.7%	54	25	43.5	2	0	0	1172.69	596	605
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	21	28	52	0.05%	43.3%	LGSLVDEFK	99.7%	53.7	25	37.6	2	0	0	1007.54	518	526
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	21	28	52	0.05%	43.3%	LGSLVDEFKELVYPPDYNPEGK	99.7%	38.6	25	36.2	0	2	0	2509.25	518	539
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	21	28	52	0.05%	43.3%	NIPPYFVALVPQEEELDDQK	99.7%	55.1	25	54.2	2	0	0	2344.17	405	424
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	21	28	52	0.05%	43.3%	NIYVLQELDNPGAK	99.7%	125	25	120	2	0	0	1573.82	101	114
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	21	28	52	0.05%	43.3%	NLEALALDLMEPEQAVDLTLPK	99.7%	74.2	25	74.2	2	0	0	2439.27	489	510
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	21	28	52	0.05%	43.3%	QELLEALTK	99.7%	53.9	25	37.8	2	0	0	1044.59	597	605
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	21	28	52	0.05%	43.3%	SDSFENPVLQQHFR	99.7%	55.3	25	50.6	0	2	0	1703.81	475	488
X-ray repair cross-complementing protein 6	XRCC6	XRCC6_HUMAN	69.8	100.0%	21	28	52	0.05%	43.3%	TFNTSTGGLLLPSDTKR	99.7%	98.6	25	96.2	2	0	0	1807.96	302	318
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	7	7	15	0.01%	33.3%	AGEAPTENPAPPTQQSSAE	99.7%	49.1	25	49.1	2	0	0	1881.85	354	372
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	7	7	15	0.01%	33.3%	DGVPEGAQLQGPVHR	99.7%	78.6	25	69.1	2	0	0	1559.79	269	283
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	7	7	15	0.01%	33.3%	EDVFVHQTAIK	99.7%	57	25	51.8	2	0	0	1286.67	114	124
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	7	7	15	0.01%	33.3%	EDVFVHQTAIKK	99.7%	42	25	34	1	0	0	1414.77	114	125
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	7	7	15	0.01%	33.3%	GAEAANVTGPDGVPVEGSR	99.7%	77.1	25	74.4	3	0	0	1782.86	151	169
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	7	7	15	0.01%	33.3%	IQAGEIGEMK	99.7%	39.7	25	30.3	2	0	0	1091.54	259	268
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	7	7	15	0.01%	33.3%	IQAGEIGEMKDGVPEGAQLQGPVHR	99.7%	63	25	63	0	4	0	2632.32	259	283
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	7	7	15	0.01%	33.3%	NDTKEDVFVHQTAIK	99.7%	75.9	25	70.6	2	5	0	1744.89	110	124
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	7	7	15	0.01%	33.3%	NGYGFINR	99.7%	51.4	25	43.7	4	0	0	940.46	102	109
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	7	7	15	0.01%	33.3%	RPRPPNAPSQDGK	97.8%	25.8	25	19.3	0	1	0	1419.75	338	350
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	7	7	15	0.01%	33.3%	SVGDGETVEFDVVEGEK	99.7%	111	25	103	7	0	0	1795.82	134	150
Y-box-binding protein 3	YBX3	YBOX3_HUMAN	40.1	100.0%	7	7	15	0.01%	33.3%	VLPHPNR	94.7%	27.8	25	8.45	1	0	0	832.48	252	258
YTH domain-containing family protein 2	YTHDF2	YTHD2_HUMAN	62.3	100.0%	3	3	10	0.01%	5.9%	LENNENKPVTNSR	99.7%	36.3	25	31.4	0	4	0	1514.76	515	527
YTH domain-containing family protein 2	YTHDF2	YTHD2_HUMAN	62.3	100.0%	3	3	10	0.01%	5.9%	LGSTEVASNVPK	99.7%	84.1	25	73.2	4	0	0	1201.64	194	205
YTH domain-containing family protein 2	YTHDF2	YTHD2_HUMAN	62.3	100.0%	3	3	10	0.01%	5.9%	SYSEDDIHR	99.7%	48.5	25	48.5	2	0	0	1121.49	417	425
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	13	14	25	0.02%	18.6%	DVFLNGSYNDYVR	99.7%	49.2	25	45.8	1	0	0	1561.73	582	594
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	13	14	25	0.02%	18.6%	GISPIVFDR	99.7%	46.7	25	36	2	0	0	1003.56	306	314
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	13	14	25	0.02%	18.6%	GVWSTLPVNEK	99.7%	66.9	25	54.7	2	0	0	1229.65	375	385
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	13	14	25	0.02%	18.6%	IDWICR	95.5%	28.4	25	11.4	2	0	0	862.42	445	450
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	13	14	25	0.02%	18.6%	IGLEVDR	99.7%	43.7	25	25.2	1	0	0	801.45	155	161
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	13	14	25	0.02%	18.6%	IGLEVDRR	98.7%	33.2	25	13.3	1	0	0	957.55	155	162
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	13	14	25	0.02%	18.6%	QLVSKPLSSSVSNNKR	99.7%	36.9	25	36.9	0	1	0	1743.97	68	83
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	13	14	25	0.02%	18.6%	SATEYKNEEYQR	99.7%	59.9	25	54.7	2	0	0	1517.69	91	102
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	13	14	25	0.02%	18.6%	SEASDSGSESVSFTDGSVR	99.7%	168	25	166	2	0	0	1903.82	268	286
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	13	14	25	0.02%	18.6%	SGSSASESYAGSEK	99.7%	73.1	25	71.9	2	0	0	1346.57	315	328
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	13	14	25	0.02%	18.6%	SNNHENVSLAK	99.7%	56.2	25	56.1	3	1	0	1212.60	362	372
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	13	14	25	0.02%	18.6%	SVILIFSVR	99.7%	66.6	25	62.7	2	0	0	1033.64	396	404
YTH domain-containing protein 1	YTHDC1	YTDC1_HUMAN	84.7	100.0%	13	14	25	0.02%	18.6%	YVLQDAR	99.7%	44.3	25	28.5	3	0	0	864.46	350	356
Zinc finger CCCH domain-containing protein 11A	ZC3H11A	ZC11A_HUMAN	89.1	100.0%	3	3	5	0.00%	5.4%	AAVAVVPLVSEDK	99.7%	41	25	39.7	1	0	0	1297.74	700	712
Zinc finger CCCH domain-containing protein 11A	ZC3H11A	ZC11A_HUMAN	89.1	100.0%	3	3	5	0.00%	5.4%	TLEEILLER	99.7%	49.2	25	36.2	2	0	0	1115.63	360	368
Zinc finger CCCH domain-containing protein 11A	ZC3H11A	ZC11A_HUMAN	89.1	100.0%	3	3	5	0.00%	5.4%	VQQSSESSTSSPSQHEATPGAR	99.7%	44	25	44	0	2	0	2258.03	485	506
Zinc finger CCCH domain-containing protein 18	ZC3H18	ZCH18_HUMAN	106.4	100.0%	5	5	6	0.01%	8.4%	AGVQSVGEKESLEAAK	99.7%	68.7	25	65.3	1	0	0	1602.83	169	184
Zinc finger CCCH domain-containing protein 18	ZC3H18	ZCH18_HUMAN	106.4	100.0%	5	5	6	0.01%	8.4%	ASDLEDEESAAR	99.7%	68.3	25	63.6	1	0	0	1292.56	45	56
Zinc finger CCCH domain-containing protein 18	ZC3H18	ZCH18_HUMAN	106.4	100.0%	5	5	6	0.01%	8.4%	GGQYENFR	99.5%	37.7	25	24.3	1	0	0	970.44	382	389
Zinc finger CCCH domain-containing protein 18	ZC3H18	ZCH18_HUMAN	106.4	100.0%	5	5	6	0.01%	8.4%	SSQQPSTPQQAPPGQPQQGTFVAHK	99.7%	36.5	25	36.5	0	1	0	2631.29	790	814
Zinc finger CCCH domain-containing protein 18	ZC3H18	ZCH18_HUMAN	106.4	100.0%	5	5	6	0.01%	8.4%	TLSGSGSGSGSSYSGSSSR	99.7%	127	25	123	2	0	0	1707.74	683	701

Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	100.0%	7	7	11	0.01%	22.0%	AVHNSVAAQLTGVAGH	95.4%	23.2	25	23.1	0	1	0	1531.80	389	404
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	100.0%	7	7	11	0.01%	22.0%	DFVVGALILR	99.7%	69	25	65.1	2	0	0	1102.66	183	192
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	100.0%	7	7	11	0.01%	22.0%	DPAGEAVDPR	97.3%	30.4	25	27.6	1	0	0	1026.49	103	112
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	100.0%	7	7	11	0.01%	22.0%	ICFQGDEGACPTR	99.7%	68.7	25	62.9	2	0	0	1510.64	170	182
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	100.0%	7	7	11	0.01%	22.0%	NETVDVEDIVTWLK	99.7%	65.2	25	57.8	1	0	0	1660.84	262	275
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	100.0%	7	7	11	0.01%	22.0%	SIGMDPSDIYAVIQIPGSR	99.7%	74.6	25	67	2	0	0	2035.02	193	211
Zinc finger CCHC domain-containing protein 3	ZCCHC3	ZCHC3_HUMAN	43.6	100.0%	7	7	11	0.01%	22.0%	TLFILFR	99.6%	38.6	25	38.6	2	0	0	909.56	255	261
Zinc finger CCHC domain-containing protein 9	ZCCHC9	ZCHC9_HUMAN	30.5	99.8%	2	2	3	0.00%	8.9%	GSFEGTSQNLPK	99.7%	41.7	25	35.1	1	0	0	1264.62	27	38
Zinc finger CCHC domain-containing protein 9	ZCCHC9	ZCHC9_HUMAN	30.5	99.8%	2	2	3	0.00%	8.9%	VDPALGEFPFAK	99.6%	38.6	25	36.7	2	0	0	1290.67	174	185
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	6	9	15	0.01%	25.5%	EEVEHMIQK	99.7%	48.9	25	37.4	3	0	0	1142.55	57	65
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	6	9	15	0.01%	25.5%	IVLNSIEQYQAHVSGFK	99.7%	64.1	25	64.1	1	1	0	1933.02	246	262
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	6	9	15	0.01%	25.5%	LADPAVTDFPAGK	99.7%	67.1	25	59.2	2	0	0	1301.67	225	237
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	6	9	15	0.01%	25.5%	NQCLFTNTQCK	99.7%	62	25	59.4	2	0	0	1413.63	66	76
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	6	9	15	0.01%	25.5%	TVASSLGQIPMQR	99.7%	93.2	25	73.5	4	0	0	1387.74	270	282
Zinc finger protein 346	ZNF346	ZN346_HUMAN	32.9	100.0%	6	9	15	0.01%	25.5%	VCCALLISESQK	99.7%	85.4	25	75.5	2	0	0	1407.70	77	88
Zinc finger protein 512	ZNF512	ZN512_HUMAN	64.7	99.8%	2	2	3	0.00%	3.2%	AGLAYHLR	99.7%	48.2	25	32.5	2	0	0	900.51	300	307
Zinc finger protein 512	ZNF512	ZN512_HUMAN	64.7	99.8%	2	2	3	0.00%	3.2%	VLQDLVPDDR	98.7%	33.4	25	33.4	1	0	0	1169.62	367	376
Zinc finger protein 768	ZNF768	ZN768_HUMAN	60.2	100.0%	4	4	6	0.01%	7.8%	AFADSSYLLR	99.7%	61.3	25	52.2	2	0	0	1142.58	325	334
Zinc finger protein 768	ZNF768	ZN768_HUMAN	60.2	100.0%	4	4	6	0.01%	7.8%	AFGDSSYLLR	99.4%	36.9	25	26.8	1	0	0	1128.57	353	362
Zinc finger protein 768	ZNF768	ZN768_HUMAN	60.2	100.0%	4	4	6	0.01%	7.8%	AFSQSSDLIR	99.3%	36.2	25	15.6	1	0	0	1123.57	521	530
Zinc finger protein 768	ZNF768	ZN768_HUMAN	60.2	100.0%	4	4	6	0.01%	7.8%	FGQSSVLAIHAR	99.7%	76.1	25	62.8	2	0	0	1285.70	438	449
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	12	12	32	0.03%	14.6%	AGYSQGATQYTQAQQTR	99.7%	98.3	25	97.6	1	0	0	1858.87	192	208
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	12	12	32	0.03%	14.6%	AISSASSPQSPGDALR	99.7%	90.4	25	80	4	0	0	1543.77	954	969
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	12	12	32	0.03%	14.6%	EDITSSAQFALR	99.7%	95.6	25	89.6	5	0	0	1337.67	1008	1019
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	12	12	32	0.03%	14.6%	FNIHNNR	96.2%	29	25	13.3	2	0	0	914.46	1042	1048
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	12	12	32	0.03%	14.6%	GLTTTGNSSLNSTSNTK	99.7%	118	25	118	4	0	0	1682.82	468	484
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	12	12	32	0.03%	14.6%	INFVGGNK	99.0%	34.6	25	23.8	2	0	0	848.46	502	509
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	12	12	32	0.03%	14.6%	IVSITER	95.2%	28.1	25	17.7	1	0	0	817.48	747	753
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	12	12	32	0.03%	14.6%	KVNPDLQVEVKPSIR	99.7%	54.9	25	54.9	0	1	0	1721.99	613	627
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	12	12	32	0.03%	14.6%	LVSDSLSEHEK	99.7%	50.6	25	46.2	4	0	0	1243.62	757	767
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	12	12	32	0.03%	14.6%	QAAAAAAAAAATAAWTGTTFTK	99.7%	44.8	25	44.8	0	2	0	2023.02	289	310
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	12	12	32	0.03%	14.6%	STAPAVAYDSK	99.7%	84.2	25	70.8	2	0	0	1109.55	148	158
Zinc finger RNA-binding protein	ZFR	ZFR_HUMAN	117.0	100.0%	12	12	32	0.03%	14.6%	STPVTSAVQIPEVK	99.7%	86.3	25	78.5	4	0	0	1455.81	528	541

Table S-2. Spectral counting-based identification of proteins co-immunoprecipitating with H7N9 NS1

Protein name	Accession number	Gene name	Spectral counts (SCs)						Ratio of NS1/VC[a]
			Vector control (VC)			H7N9 NS1 (NS1)			
			Rep 1	Rep 2	Rep 3	Rep 1	Rep 2	Rep 3	
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA_HUMAN	PRKRA	0	0	0	71	65	55	65.023
Scaffold attachment factor B1	SAFB1_HUMAN	SAFB	0	0	0	63	54	44	54.772
Phosphatidylinositol 3-kinase regulatory subunit beta	P85B_HUMAN	PIK3R2	0	0	0	35	37	34	36.141
Scaffold attachment factor B2	SAFB2_HUMAN	SAFB2	0	0	0	29	29	30	30.010
Insulin-like growth factor 2 mRNA-binding protein 2	IF2B2_HUMAN	IGF2BP2	0	2	0	39	37	45	28.951
Heterogeneous nuclear ribonucleoprotein D-like	HNRDL_HUMAN	HNRNPDL	0	0	0	31	31	23	28.938
Pre-mRNA-splicing factor	SYF1_HUMAN	XAB2	0	0	0	32	27	25	28.592
Spermatid perinuclear RNA-binding protein	STRBP_HUMAN	STRBP	0	0	0	27	25	27	26.932
YTH domain-containing	YTDC1_HUMAN	YTHDC1	0	0	0	26	24	25	25.562
Putative helicase MOV-10	MOV10_HUMAN	MOV10	0	2	5	75	75	73	24.294
Polyadenylate-binding protein	PABP2_HUMAN	PABPN1	0	0	0	27	22	22	24.170
ELAV-like protein 2	ELAV2_HUMAN	ELAVL2	0	0	0	23	22	15	20.412
Zinc finger RNA-binding	ZFR_HUMAN	ZFR	0	3	2	38	46	32	17.287
Crooked neck-like protein 1	CRNL1_HUMAN	CRNKL1	0	2	0	24	20	27	16.981
Serine/arginine-rich splicing	SRSF7_HUMAN	SRSF7	0	0	0	19	16	13	16.327
Cleavage and polyadenylation specificity factor subunit 2	CPSF2_HUMAN	CPSF2	0	0	0	14	13	20	16.056
Serine/arginine-rich splicing factor 10	SRS10_HUMAN	SRSF10	0	0	0	12	15	19	15.729
ATP-dependent RNA helicase DHX8	DHX8_HUMAN	DHX8	0	0	0	16	17	11	14.977
Double-stranded RNA-binding protein Staufen homolog 2	STAU2_HUMAN	STAU2	0	0	0	18	13	13	14.964
Y-box-binding protein 3	YBOX3_HUMAN	YBX3	0	0	0	11	11	15	12.638
RNA-binding protein Musashi homolog 2	MSI2H_HUMAN	MSI2	0	0	0	12	12	13	12.621
SNW domain-containing	SNW1_HUMAN	SNW1	0	0	0	14	10	11	11.909
U5 small nuclear ribonucleoprotein 40 kDa	SNR40_HUMAN	SNRNP40	0	0	0	11	15	8	11.585
Putative RNA-binding protein Luc7-like 2	LC7L2_HUMAN	LUC7L2	2	2	0	25	20	17	11.399
Peptidyl-prolyl cis-trans isomerase-like 1	PPIL1_HUMAN	PPIL1	0	0	0	10	14	7	10.562
Double-stranded RNA-binding protein Staufen homolog 1	STAU1_HUMAN	STAU1	4	3	2	35	38	29	10.021
Protein BUD31 homolog	BUD31_HUMAN	BUD31	0	0	0	7	10	11	9.575
Protein PRRC2A	PRC2A_HUMAN	PRRC2A	0	0	0	8	13	7	9.552
Transformer-2 protein homolog beta	TRA2B_HUMAN	TRA2B	3	0	0	21	18	11	9.425
Cleavage and polyadenylation specificity factor subunit 7	CPSF7_HUMAN	CPSF7	0	0	0	9	9	8	8.860
Myosin regulatory light chain	ML12A_HUMAN	MYL12A	0	0	0	10	8	8	8.850
Ribosome-binding protein 1	RRBP1_HUMAN	RRBP1	0	0	0	10	9	6	8.500

Transformer-2 protein homolog alpha	TRA2A_HUMAN	TRA2A	5	0	0	22	21	17	7.982
KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDR1_HUMAN	KHDRBS1	0	0	0	7	8	8	7.850
Heterogeneous nuclear ribonucleoproteins A2/B1	ROA2_HUMAN	HNRNPA2B1	25	31	22	229	225	231	7.735
Zinc finger CCHC domain-containing protein 3	ZCHC3_HUMAN	ZCCHC3	0	3	2	20	21	11	7.732
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRPC_HUMAN	HNRNPC	30	28	27	256	216	267	7.638
Pre-mRNA-processing factor	PRP17_HUMAN	CDC40	0	0	0	6	3	13	7.533
Activated RNA polymerase II transcriptional coactivator p15	TCP4_HUMAN	SUB1	0	0	0	9	6	6	7.137
DNA-directed RNA polymerase II subunit RPB3	RPB3_HUMAN	POLR2C	0	0	0	5	8	6	6.490
Nuclear receptor coactivator 5	NCOA5_HUMAN	NCOA5	0	0	0	6	8	5	6.477
Probable ATP-dependent RNA helicase DDX23	DDX23_HUMAN	DDX23	0	0	3	16	13	7	6.470
39S ribosomal protein L49, mitochondrial	RM49_HUMAN	MRPL49	0	0	0	7	7	5	6.467
Actin, alpha cardiac muscle 1	ACTC_HUMAN	ACTC1	0	0	0	7	11	0	6.441
Chromodomain-helicase-DNA-binding protein 4	CHD4_HUMAN	CHD4	0	3	0	7	16	10	6.251
Protein SON	SON_HUMAN	SON	0	0	0	5	7	6	6.147
Dolichol-phosphate mannosyltransferase subunit 3	DPM3_HUMAN	DPM3	0	0	0	6	6	6	6.137
U1 small nuclear ribonucleoprotein 70 kDa	RU17_HUMAN	SNRNP70	0	0	0	8	4	6	6.118
Polyadenylate-binding protein	PABP4_HUMAN	PABPC4	9	14	7	64	65	73	5.955
RNA-binding protein Raly	RALY_HUMAN	RALY	8	7	9	48	52	63	5.952
Heterogeneous nuclear ribonucleoprotein A3	ROA3_HUMAN	HNRNPA3	18	16	9	100	99	88	5.907
Zinc finger CCCH domain-containing protein 11A	ZC11A_HUMAN	ZC3H11A	0	0	0	5	7	5	5.801
Pre-mRNA-processing factor 40 homolog A	PR40A_HUMAN	PRPF40A	2	0	0	7	8	9	5.757
RNA-binding motif protein, X chromosome	RBMX_HUMAN	RBMX	21	16	18	126	121	101	5.549
UAP56-interacting factor	UIF_HUMAN	FYTTD1	0	0	0	6	6	4	5.444
Insulin receptor substrate 4	IRS4_HUMAN	IRS4	0	2	3	13	18	6	5.438
Zinc finger protein 346	ZN346_HUMAN	ZNF346	0	4	6	27	24	15	5.221
Heterogeneous nuclear ribonucleoprotein L	HNRPL_HUMAN	HNRNPL	22	24	23	133	130	147	5.217
Probable ATP-dependent RNA helicase YTHDC2	YTDC2_HUMAN	YTHDC2	5	0	0	16	13	10	5.180
Pleiotropic regulator 1	PLRG1_HUMAN	PLRG1	5	3	4	22	22	26	5.125
Heterogeneous nuclear ribonucleoprotein Q	HNRPQ_HUMAN	SYNCRIP	29	33	28	164	172	182	5.062
NTF2-related export protein 1	NXT1_HUMAN	NXT1	0	0	0	9	5	0	5.049
Heterogeneous nuclear ribonucleoprotein H3	HNRH3_HUMAN	HNRNPH3	9	7	8	41	47	45	4.868
Centrin-2	CETN2_HUMAN	CETN2	0	0	0	4	4	6	4.784

Splicing factor, arginine/serine-rich 15	SFR15_HUMAN	SCAF4	0	0	0	5	4	5	4.771
Heterogeneous nuclear ribonucleoprotein A1	ROA1_HUMAN	HNRNPA1	25	34	22	149	147	139	4.732
Protein lin-28 homolog B	LN28B_HUMAN	LIN28B	4	0	0	12	12	6	4.675
Heterogeneous nuclear ribonucleoprotein R	HNRPR_HUMAN	HNRNPR	32	32	22	152	148	144	4.555
60S ribosomal protein L26-like	RL26L_HUMAN	RPL26L1	0	0	0	0	6	6	4.471
Interleukin enhancer-binding factor 3	ILF3_HUMAN	ILF3	56	53	53	276	281	261	4.432
Mitotic spindle-associated MMXD complex subunit	MIP18_HUMAN	FAM96B	0	0	0	5	4	4	4.425
Pre-mRNA-splicing factor CWC22 homolog	CWC22_HUMAN	CWC22	0	0	0	5	4	4	4.425
Protein LYRIC	LYRIC_HUMAN	MTDH	0	0	0	5	4	4	4.425
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase	STT3B_HUMAN	STT3B	3	0	0	10	7	6	4.335
DBIRD complex subunit	ZN326_HUMAN	ZNF326	3	4	3	17	16	16	4.308
Far upstream element-binding protein 3	FUBP3_HUMAN	FUBP3	7	10	7	34	37	46	4.298
Ras GTPase-activating protein-binding protein 2	G3BP2_HUMAN	G3BP2	3	0	0	8	7	7	4.158
26S proteasome non-ATPase regulatory subunit 9	PSMD9_HUMAN	PSMD9	0	0	0	5	4	3	4.078
U1 small nuclear ribonucleoprotein C	RU1C_HUMAN	SNRPC	0	0	0	5	4	3	4.078
Cleavage and polyadenylation specificity factor subunit 4	CPSF4_HUMAN	CPSF4	0	0	0	6	3	3	4.069
RNA-binding protein 34	RBM34_HUMAN	RBM34	0	0	0	6	5	0	4.049
Heterogeneous nuclear ribonucleoprotein D0	HNRPD_HUMAN	HNRNPD	21	20	24	101	104	91	3.984
Apoptotic chromatin condensation inducer in the	ACINU_HUMAN	ACIN1	7	4	6	25	25	25	3.867
Zinc finger CCCH domain-containing protein 18	ZCH18_HUMAN	ZC3H18	0	2	0	4	6	6	3.836
Protein disulfide-isomerase	PDIA1_HUMAN	P4HB	0	0	0	2	6	3	3.765
ATP-dependent RNA helicase DDX24	DDX24_HUMAN	DDX24	0	0	0	4	2	5	3.752
Protein YIPF5	YIPF5_HUMAN	YIPF5	0	0	0	4	3	4	3.748
tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6	TRM6_HUMAN	TRMT6	0	0	0	4	0	6	3.745
Clathrin light chain A	CLCA_HUMAN	CLTA	0	0	0	4	4	3	3.745
Heat shock protein beta-1	HSPB1_HUMAN	HSPB1	0	0	0	4	4	3	3.745
Nuclear cap-binding protein subunit 2	NCBP2_HUMAN	NCBP2	0	0	0	4	4	3	3.745
Pre-mRNA-splicing factor ISY1 homolog	ISY1_HUMAN	ISY1	0	0	0	6	4	0	3.706
Histone H1.0	H10_HUMAN	H1F0	0	0	0	9	0	0	3.667
Heterogeneous nuclear ribonucleoprotein U-like	HNRL1_HUMAN	HNRNPUL1	6	11	13	46	42	37	3.624

RNA binding protein fox-1 homolog 1	RFOX1_HUMAN	RBFOX1	2	0	0	6	6	3	3.581
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1_HUMAN	PLOD1	4	2	3	13	11	12	3.509
Polypyrimidine tract-binding protein 3	PTBP3_HUMAN	PTBP3	0	0	0	0	3	6	3.441
Mitochondrial import inner membrane translocase subunit Tim21	TIM21_HUMAN	TIMM21	0	0	0	3	3	4	3.415
Sestrin-2	SESN2_HUMAN	SESN2	0	0	0	3	3	4	3.415
2'-deoxynucleoside 5'-phosphate N-hydrolase 1	DNPH1_HUMAN	DNPH1	0	0	0	3	0	6	3.412
RNA binding motif protein, X-linked-like-1	RMXL1_HUMAN	RBMXL1	0	0	0	3	4	3	3.412
Mitochondrial translocator assembly and maintenance protein 41 homolog	TAM41_HUMAN	TAMM41	0	0	0	4	3	3	3.402
Tight junction protein ZO-2	ZO2_HUMAN	TJP2	0	0	0	4	3	3	3.402
Sterol-4-alpha-carboxylate 3-dehydrogenase,	NSDHL_HUMAN	NSDHL	0	0	0	4	5	0	3.382
Pinin	PININ_HUMAN	PNN	0	0	0	5	4	0	3.372
60S ribosome subunit biogenesis protein NIP7	NIP7_HUMAN	NIP7	0	0	0	6	3	0	3.363
Renin receptor	RENR_HUMAN	ATP6AP2	0	0	0	6	3	0	3.363
Serine/arginine-rich splicing	SRSF3_HUMAN	SRSF3	16	13	7	45	47	42	3.299
Interferon-induced, double-stranded RNA-activated protein kinase	E2AK2_HUMAN	EIF2AK2	4	4	4	17	16	12	3.285
39S ribosomal protein L17, mitochondrial	RM17_HUMAN	MRPL17	0	0	3	7	6	5	3.243
Pre-mRNA-splicing factor	SPF27_HUMAN	BCAS2	0	4	3	12	11	6	3.205
Matrin-3	MATR3_HUMAN	MATR3	44	46	38	157	163	143	3.181
Polypyrimidine tract-binding protein 1	PTBP1_HUMAN	PTBP1	12	11	12	36	40	49	3.138
G-rich sequence factor 1	GRSF1_HUMAN	GRSF1	0	0	0	0	4	4	3.092
39S ribosomal protein L45, mitochondrial	RM45_HUMAN	MRPL45	2	0	0	8	4	0	3.071
Ras-related protein Rab-2A	RAB2A_HUMAN	RAB2A	0	0	0	3	3	3	3.069
U2 snRNP-associated SURP motif-containing protein	SR140_HUMAN	U2SURP	0	0	0	3	3	3	3.069
ELAV-like protein 1	ELAV1_HUMAN	ELAVL1	23	19	14	67	65	62	3.058
Treacle protein	TCOF_HUMAN	TCOF1	2	3	0	7	7	6	3.056
Mediator of DNA damage checkpoint protein 1	MDC1_HUMAN	MDC1	0	5	0	9	7	7	3.051
Transcription elongation	TCRG1_HUMAN	TCERG1	0	0	0	3	5	0	3.049
Keratin-associated protein 24-1	KR241_HUMAN	KRTAP24-1	0	0	0	4	4	0	3.039
Spliceosome RNA helicase DDX39B	DX39B_HUMAN	DDX39B	0	0	0	4	4	0	3.039
Histone H3.1t	H31T_HUMAN	HIST3H3	4	5	6	15	16	21	3.033
V-set and immunoglobulin domain-containing protein 8	VSIG8_HUMAN	VSIG8	0	0	0	5	3	0	3.029
Interleukin enhancer-binding factor 2	ILF2_HUMAN	ILF2	31	33	35	110	125	105	3.010

Heterogeneous nuclear ribonucleoprotein A0	ROA0_HUMAN	HNRNPA0	11	10	8	33	28	36	2.948
Pre-mRNA 3'-end-processing factor FIP1	FIP1_HUMAN	FIP1L1	3	0	3	10	7	6	2.904
Heterogeneous nuclear ribonucleoprotein A/B	ROAA_HUMAN	HNRNPAB	10	9	12	36	36	31	2.902
Huntingtin	HD_HUMAN	HTT	0	2	0	4	5	3	2.867
Fragile X mental retardation syndrome-related protein 2	FXR2_HUMAN	FXR2	4	7	7	20	19	20	2.864
DnaJ homolog subfamily C member 9	DNJC9_HUMAN	DNAJC9	0	2	2	6	7	3	2.853
Ribose-phosphate pyrophosphokinase 2	PRPS2_HUMAN	PRPS2	0	3	2	7	8	4	2.826
Serine/arginine-rich splicing	SRSF9_HUMAN	SRSF9	17	20	21	64	63	59	2.807
Cyclin-dependent kinase inhibitor 2A, isoforms 1/2/3	CD2A1_HUMAN	CDKN2A	0	0	0	0	3	4	2.748
Beta-casein	CASB_HUMAN	CSN2	0	0	0	0	0	6	2.745
pre-rRNA processing protein FTSJ3	SPB1_HUMAN	FTSJ3	0	0	0	0	0	6	2.745
Prolyl 4-hydroxylase subunit alpha-2	P4HA2_HUMAN	P4HA2	0	0	0	0	0	6	2.745
Zinc finger protein 512	ZN512_HUMAN	ZNF512	0	0	0	0	4	3	2.745
Regulator of nonsense transcripts 3B	REN3B_HUMAN	UPF3B	6	3	0	9	11	10	2.735
FACT complex subunit SPT16	SP16H_HUMAN	SUPT16H	4	3	0	10	7	7	2.732
Eukaryotic translation initiation factor 5B	IF2P_HUMAN	EIF5B	0	0	0	2	4	2	2.732
Glutamate--cysteine ligase regulatory subunit	GSH0_HUMAN	GCLM	0	0	0	3	2	3	2.726
UPF0444 transmembrane protein C12orf23	CL023_HUMAN	C12orf23	0	0	0	3	3	2	2.722
E3 ubiquitin-protein ligase	TRIPC_HUMAN	TRIP12	0	0	0	3	0	4	2.719
Desmoglein-4	DSG4_HUMAN	DSG4	0	0	0	3	4	0	2.706
Myotrophin	MTPN_HUMAN	MTPN	0	0	0	3	4	0	2.706
Serine/threonine-protein kinase Chk1	CHK1_HUMAN	CHEK1	0	0	0	3	4	0	2.706
FACT complex subunit SSRP1	SSRP1_HUMAN	SSRP1	0	0	3	6	4	5	2.703
Peptidyl-prolyl cis-trans isomerase-like 3	PPIL3_HUMAN	PPIL3	0	0	0	4	3	0	2.696
Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	PP2AA_HUMAN	PPP2CA	0	0	0	4	3	0	2.696
Vesicle-trafficking protein	SC22B_HUMAN	SEC22B	0	0	0	4	3	0	2.696
Vitamin K epoxide reductase complex subunit 1	VKOR1_HUMAN	VKORC1	0	0	0	6	0	0	2.667
Cell division cycle 5-like	CDC5L_HUMAN	CDC5L	11	15	11	37	39	34	2.615
Heterogeneous nuclear ribonucleoprotein U-like	HNRL2_HUMAN	HNRNPUL2	15	16	12	38	42	46	2.585
AP-3 complex subunit delta-1	AP3D1_HUMAN	AP3D1	5	7	0	12	12	13	2.584
Glyoxylate reductase/hydroxypyruvate reductase	GRHPR_HUMAN	GRHPR	7	0	0	11	8	6	2.560
Protein mago nashi homolog 2	MGN2_HUMAN	MAGOHB	4	0	2	7	8	5	2.558

H/ACA ribonucleoprotein complex subunit 2	NHP2_HUMAN	NHP2	5	6	0	10	11	12	2.501
PHD finger protein 6	PHF6_HUMAN	PHF6	0	4	0	6	6	4	2.491
La-related protein 1	LARP1_HUMAN	LARP1	19	17	7	44	42	34	2.476
39S ribosomal protein L1, mitochondrial	RM01_HUMAN	MRPL1	3	0	0	5	5	3	2.453
NHP2-like protein 1	NH2L1_HUMAN	NHP2L1	3	0	0	5	5	3	2.453
Polyadenylate-binding protein	PABP1_HUMAN	PABPC1	107	104	95	282	293	276	2.445
Eukaryotic translation initiation factor 4 gamma 1	IF4G1_HUMAN	EIF4G1	0	0	0	0	2	4	2.405
SAFB-like transcription	SLTM_HUMAN	SLTM	0	0	0	0	2	4	2.405
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 3, mitochondrial	PDK3_HUMAN	PDK3	0	0	0	0	3	3	2.402
Histidine triad nucleotide-binding protein 2,	HINT2_HUMAN	HINT2	0	0	0	0	3	3	2.402
Trafficking protein particle complex subunit 6B	TPC6B_HUMAN	TRAPPC6B	0	0	0	0	3	3	2.402
tRNA methyltransferase 112 homolog	TR112_HUMAN	TRMT112	0	0	0	0	3	3	2.402
ER lumen protein retaining receptor 1	ERD21_HUMAN	KDELR1	0	0	0	0	0	5	2.399
Histone H2A.V	H2AV_HUMAN	H2AFV	0	0	0	0	0	5	2.399
Fragile X mental retardation protein 1	FMR1_HUMAN	FMR1	4	3	0	7	7	7	2.397
Serine hydroxymethyltransferase,	GLYM_HUMAN	SHMT2	0	2	0	3	6	0	2.379
RNA-binding protein 12B	RB12B_HUMAN	RBM12B	0	0	0	3	0	3	2.373
U3 small nucleolar RNA-interacting protein 2	U3IP2_HUMAN	RRP9	0	0	0	3	0	3	2.373
Ubiquitin-conjugating enzyme	UBE2N_HUMAN	UBE2N	0	0	0	3	0	3	2.373
Zinc finger CCHC domain-containing protein 9	ZCHC9_HUMAN	ZCCHC9	0	0	0	3	0	3	2.373
Calmodulin-like protein 5	CALL5_HUMAN	CALML5	0	0	0	2	4	0	2.372
Active regulator of SIRT1	AROS_HUMAN	RPS19BP1	0	0	0	3	3	0	2.363
ATP synthase subunit delta, mitochondrial	ATPD_HUMAN	ATP5D	0	0	0	3	3	0	2.363
Intraflagellar transport protein 27 homolog	IFT27_HUMAN	IFT27	0	0	0	3	3	0	2.363
Keratin-associated protein 19-5	KR195_HUMAN	KRTAP19-5	0	0	0	3	3	0	2.363
Putative ataxin-7-like protein	A7L3B_HUMAN	ATXN7L3B	0	0	0	3	3	0	2.363
RISC-loading complex subunit TARBP2	TRBP2_HUMAN	TARBP2	0	0	0	3	3	0	2.363
Stathmin	STMN1_HUMAN	STMN1	0	0	0	3	3	0	2.363
Transmembrane protein 109	TM109_HUMAN	TMEM109	0	0	0	3	3	0	2.363
Pre-mRNA-processing-splicing factor 8	PRP8_HUMAN	PRPF8	45	47	55	123	128	144	2.353
Cleavage and polyadenylation specificity factor subunit 1	CPSF1_HUMAN	CPSF1	13	11	8	26	30	29	2.348
28S ribosomal protein S18a, mitochondrial	RT18A_HUMAN	MRPS18A	4	4	4	10	13	9	2.340
Splicing factor 3B subunit 5	SF3B5_HUMAN	SF3B5	0	0	0	5	0	0	2.333

Signal recognition particle 14 kDa protein	SRP14_HUMAN	SRP14	14	14	11	38	33	31	2.301
Cold-inducible RNA-binding protein	CIRBP_HUMAN	CIRBP	3	0	0	4	4	4	2.270
Histone deacetylase complex subunit SAP18	SAP18_HUMAN	SAP18	9	4	3	19	10	12	2.265
H/ACA ribonucleoprotein complex subunit 3	NOP10_HUMAN	NOP10	5	0	0	7	5	5	2.259
Protein RRP5 homolog	RRP5_HUMAN	PDCD11	13	18	9	39	32	31	2.251
Eukaryotic translation initiation factor 3 subunit M	EIF3M_HUMAN	EIF3M	3	0	0	6	5	0	2.247
Cleavage and polyadenylation specificity factor subunit 5	CPSF5_HUMAN	NUDT21	6	6	4	12	18	10	2.208
39S ribosomal protein L4, mitochondrial	RM04_HUMAN	MRPL4	7	2	0	7	10	7	2.188
Dolichyldiphosphatase 1	DOPP1_HUMAN	DOLPP1	2	0	0	0	0	7	2.172
Rab-like protein 3	RABL3_HUMAN	RABL3	0	4	0	8	3	3	2.167
Insulin-like growth factor 2 mRNA-binding protein 3	IF2B3_HUMAN	IGF2BP3	19	26	22	50	51	64	2.165
Nucleoside diphosphate kinase, mitochondrial	NDKM_HUMAN	NME4	5	4	4	11	12	9	2.163
PC4 and SFRS1-interacting	PSIP1_HUMAN	PSIP1	0	0	3	5	3	4	2.161
Vacuolar protein-sorting-associated protein 25	VPS25_HUMAN	VPS25	2	0	0	3	0	5	2.153
Telomere length regulation protein TEL2 homolog	TELO2_HUMAN	TELO2	0	2	0	4	2	3	2.145
Endoplasmic reticulum-Golgi intermediate compartment	ERGI1_HUMAN	ERGIC1	2	0	0	4	4	0	2.135
DNA polymerase epsilon catalytic subunit A	DPOE1_HUMAN	POLE	0	6	5	7	10	12	2.135
Regulator of nonsense	RENT1_HUMAN	UPF1	19	35	18	61	61	52	2.131
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PP1G_HUMAN	PPP1CC	8	5	0	15	12	6	2.128
HCLS1-associated protein X-1	HAX1_HUMAN	HAX1	6	4	3	11	12	8	2.106
Derlin-1	DERL1_HUMAN	DERL1	0	0	2	0	0	7	2.087
Cellular nucleic acid-binding	CNBP_HUMAN	CNBP	3	0	0	4	4	3	2.078
Coiled-coil-helix-coiled-coil-helix domain-containing protein 6, mitochondrial	CHCH6_HUMAN	CHCHD6	3	0	0	4	4	3	2.078
NADH-ubiquinone oxidoreductase chain 1	NU1M_HUMAN	MT-ND1	0	3	0	4	4	3	2.074
Sphingosine-1-phosphate lyase	SGPL1_HUMAN	SGPL1	0	3	0	5	3	3	2.069
39S ribosomal protein L3, mitochondrial	RM03_HUMAN	MRPL3	3	0	0	6	0	4	2.064
Elongation factor Ts,	EFTS_HUMAN	TSFM	3	4	0	5	7	6	2.057
Golgi phosphoprotein 3	GOLP3_HUMAN	GOLPH3	0	0	0	0	3	2	2.056
Microtubule-associated protein	MAP1S_HUMAN	MAP1S	0	0	0	0	3	2	2.056
Protein LLP homolog	LLPH_HUMAN	LLPH	0	0	0	0	0	4	2.052
Protein PBDC1	PBDC1_HUMAN	PBDC1	0	0	0	2	0	3	2.039
Inorganic pyrophosphatase	IPYR_HUMAN	PPA1	0	0	0	0	4	0	2.039
Nesprin-1	SYNE1_HUMAN	SYNE1	0	0	0	0	4	0	2.039
Pre-mRNA-splicing factor	RBM22_HUMAN	RBM22	0	0	0	0	4	0	2.039

Proteasome activator complex subunit 4	PSME4_HUMAN	PSME4	0	0	0	0	4	0	2.039
Serine/threonine-protein phosphatase 4 catalytic subunit	PP4C_HUMAN	PPP4C	0	0	0	0	4	0	2.039
Splicing factor U2AF 35 kDa subunit	U2AF1_HUMAN	U2AF1	10	6	6	20	20	11	2.038
Mitochondrial thiamine pyrophosphate carrier	TPC_HUMAN	SLC25A19	4	0	0	4	6	3	2.032
39S ribosomal protein L32, mitochondrial	RM32_HUMAN	MRPL32	0	0	0	2	3	0	2.029
tRNA-splicing endonuclease subunit Sen34	SEN34_HUMAN	TSEN34	0	0	0	2	3	0	2.029
2-oxoisovalerate dehydrogenase subunit beta,	ODBB_HUMAN	BCKDHB	5	3	0	6	8	6	2.028
Conserved oligomeric Golgi complex subunit 2	COG2_HUMAN	COG2	0	0	0	3	2	0	2.020
Probable ATP-dependent RNA helicase DHX37	DHX37_HUMAN	DHX37	0	0	0	3	2	0	2.020
Transmembrane protein 11, mitochondrial	TMM11_HUMAN	TMEM11	9	7	3	14	11	18	2.014
Thyroid hormone receptor-associated protein 3	TR150_HUMAN	THRAP3	20	20	17	45	44	41	2.006
Eukaryotic translation initiation factor 1A, X-	IF1AX_HUMAN	EIF1AX	0	0	0	4	0	0	2.000
Fatty acyl-CoA reductase 1	FACR1_HUMAN	FAR1	0	0	0	4	0	0	2.000
Keratin-associated protein 11-1	KR111_HUMAN	KRTAP11-1	0	0	0	4	0	0	2.000
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3	NDUF3_HUMAN	NDUFAF3	0	0	0	4	0	0	2.000
Translocon-associated protein subunit gamma	SSRG_HUMAN	SSR3	0	0	0	4	0	0	2.000
U2 small nuclear ribonucleoprotein B"	RU2B_HUMAN	SNRPB2	0	0	0	4	0	0	2.000
DNA-directed RNA polymerase II subunit RPB1	RPB1_HUMAN	POLR2A	0	0	3	3	4	4	1.990
U1 small nuclear ribonucleoprotein A	SNRPA_HUMAN	SNRPA	4	4	4	10	9	8	1.972
Nuclease-sensitive element-binding protein 1	YBOX1_HUMAN	YBX1	17	23	18	46	41	43	1.969
Protein timeless homolog	TIM_HUMAN	TIMELESS	0	2	0	0	4	3	1.925
HEAT repeat-containing	HEAT1_HUMAN	HEATR1	4	4	3	8	6	10	1.925
Putative ATP-dependent RNA helicase DHX57	DHX57_HUMAN	DHX57	0	3	2	7	3	3	1.925
Ubiquitin thioesterase OTUB1	OTUB1_HUMAN	OTUB1	6	3	3	8	10	8	1.915
Coiled-coil domain-containing protein 137	CC137_HUMAN	CCDC137	2	0	0	0	6	0	1.914
H/ACA ribonucleoprotein complex subunit 4	DKC1_HUMAN	DKC1	11	11	9	19	18	30	1.908
Bcl-2-associated transcription factor 1	BCLF1_HUMAN	BCLAF1	9	9	4	16	15	16	1.895
Serine/arginine-rich splicing	SRSF1_HUMAN	SRSF1	32	22	27	63	55	57	1.895
Heterogeneous nuclear ribonucleoprotein F	HNRPF_HUMAN	HNRNPF	11	13	13	28	31	21	1.893

WD40 repeat-containing protein SMU1	SMU1_HUMAN	SMU1	0	3	0	3	4	3	1.889
Translocon-associated protein subunit alpha	SSRA_HUMAN	SSR1	4	0	0	4	4	4	1.876
Small nuclear ribonucleoprotein Sm D3	SMD3_HUMAN	SNRPD3	5	0	8	8	8	14	1.871
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1_HUMAN	GBF1	6	7	6	15	16	9	1.846
Phosphatidylserine decarboxylase proenzyme	PISD_HUMAN	PISD	3	2	0	3	4	5	1.842
Nucleolar transcription factor 1	UBF1_HUMAN	UBTF	2	3	0	4	4	4	1.835
Splicing factor 3B subunit 2	SF3B2_HUMAN	SF3B2	9	12	6	20	20	16	1.833
ATP-dependent RNA helicase	DHX9_HUMAN	DHX9	130	156	123	279	278	294	1.831
Histone-binding protein	RBBP4_HUMAN	RBBP4	3	2	0	5	4	3	1.830
Small nuclear	RUXF_HUMAN	SNRPF	0	3	6	7	7	7	1.828
39S ribosomal protein L44, mitochondrial	RM44_HUMAN	MRPL44	10	5	5	16	14	11	1.807
THO complex subunit 6	THOC6_HUMAN	THOC6	5	0	2	6	6	4	1.791
Ribonuclease P/MRP protein subunit POP5	POP5_HUMAN	POP5	0	5	3	5	6	7	1.781
DNA-directed RNA polymerases I, II, and III	RPAB1_HUMAN	POLR2E	3	0	2	6	5	0	1.773
39S ribosomal protein L13, mitochondrial	RM13_HUMAN	MRPL13	10	13	0	17	15	15	1.768
Translocator protein	TSPOA_HUMAN	TSPO	3	0	3	6	5	3	1.767
Bystin	BYST_HUMAN	BYSL	0	3	3	6	5	3	1.765
Poly [ADP-ribose] polymerase	PARP1_HUMAN	PARP1	17	18	25	44	41	36	1.757
ER membrane protein complex subunit 4	EMC4_HUMAN	EMC4	7	7	0	9	10	10	1.754
SRSF protein kinase 1	SRPK1_HUMAN	SRPK1	6	7	0	9	8	10	1.750
Insulin-like growth factor 2 mRNA-binding protein 1	IF2B1_HUMAN	IGF2BP1	74	70	65	142	137	136	1.745
NF-kappa-B-repressing factor	NKRF_HUMAN	NKRF	8	8	11	20	16	18	1.744
Signal recognition particle subunit SRP72	SRP72_HUMAN	SRP72	9	12	6	20	18	15	1.733
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15_HUMAN	DHX15	22	20	23	48	35	45	1.724
Transcription factor A, mitochondrial	TFAM_HUMAN	TFAM	8	10	6	21	15	11	1.722
3-keto-steroid reductase	DHB7_HUMAN	HSD17B7	4	0	0	4	4	3	1.717
Endonuclease III-like protein 1	NTH_HUMAN	NTHL1	4	0	0	4	4	3	1.717
Protein RFT1 homolog	RFT1_HUMAN	RFT1	0	0	0	0	2	2	1.712
Rho-related GTP-binding protein RhoG	RHOG_HUMAN	RHOG	4	3	0	6	4	5	1.709
Protein THEM6	THEM6_HUMAN	THEM6	0	3	0	2	3	4	1.707
39S ribosomal protein L50, mitochondrial	RM50_HUMAN	MRPL50	0	0	0	0	0	3	1.706
ATP-dependent DNA helicase	RECQ1_HUMAN	RECQL	0	0	0	0	0	3	1.706
Autophagy protein 5	ATG5_HUMAN	ATG5	0	0	0	0	0	3	1.706
BAG family molecular chaperone regulator 2	BAG2_HUMAN	BAG2	0	0	0	0	0	3	1.706

DNA dC->dU-editing enzyme APOBEC-3C	ABC3C_HUMAN	APOBEC3C	0	0	0	0	0	3	1.706
Glycylpeptide N-tetradecanoyltransferase 1	NMT1_HUMAN	NMT1	0	0	0	0	0	3	1.706
Golgin subfamily A member 7	GOGA7_HUMAN	GOLGA7	0	0	0	0	0	3	1.706
Interferon-related developmental regulator 2	IFRD2_HUMAN	IFRD2	0	0	0	0	0	3	1.706
La-related protein 4B	LAR4B_HUMAN	LARP4B	0	0	0	0	0	3	1.706
Leydig cell tumor 10 kDa protein homolog	L10K_HUMAN	C19orf53	0	0	0	0	0	3	1.706
Multidrug resistance-associated protein 4	MRP4_HUMAN	ABCC4	0	0	0	0	0	3	1.706
Nuclear export mediator factor NEMF	NEMF_HUMAN	NEMF	0	0	0	0	0	3	1.706
Nuclear pore glycoprotein p62	NUP62_HUMAN	NUP62	0	0	0	0	0	3	1.706
Phosphatidylinositol 4-kinase	PI4KA_HUMAN	PI4KA	0	0	0	0	0	3	1.706
Probable ATP-dependent RNA helicase DDX56	DDX56_HUMAN	DDX56	0	0	0	0	0	3	1.706
RAC-alpha serine/threonine-protein kinase	AKT1_HUMAN	AKT1	0	0	0	0	0	3	1.706
Serine/threonine-protein kinase	STK3_HUMAN	STK3	0	0	0	0	0	3	1.706
Solute carrier family 2, facilitated glucose transporter	GTR1_HUMAN	SLC2A1	0	0	0	0	0	3	1.706
S-phase kinase-associated protein 1	SKP1_HUMAN	SKP1	0	0	0	0	0	3	1.706
Ubiquitin carboxyl-terminal hydrolase 34	UBP34_HUMAN	USP34	0	0	0	0	0	3	1.706
Uncharacterized protein	CQ085_HUMAN	C17orf85	0	0	0	0	0	3	1.706
Vitamin K epoxide reductase complex subunit 1-like protein	VKORL_HUMAN	VKORC1L1	0	0	0	0	0	3	1.706
Melanoma-associated antigen	MAGG1_HUMAN	NDNL2	3	0	0	3	3	3	1.703
39S ribosomal protein L18, mitochondrial	RM18_HUMAN	MRPL18	8	7	0	10	10	10	1.699
Heterochromatin protein 1-binding protein 3	HP1B3_HUMAN	HP1BP3	10	10	8	18	17	19	1.699
CDGSH iron-sulfur domain-containing protein 3,	CISD3_HUMAN	CISD3	0	0	0	0	3	0	1.696
Decaprenyl-diphosphate synthase subunit 2	DLP1_HUMAN	PDSS2	0	0	0	0	3	0	1.696
Dual specificity mitogen-activated protein kinase kinase	MP2K1_HUMAN	MAP2K1	0	0	0	0	3	0	1.696
Isobutyryl-CoA dehydrogenase, mitochondrial	ACAD8_HUMAN	ACAD8	0	0	0	0	3	0	1.696
Leucine-rich repeat-containing protein 59	LRC59_HUMAN	LRRC59	0	0	0	0	3	0	1.696
Mitochondrial import inner membrane translocase subunit Tim17-B	TI17B_HUMAN	TIMM17B	0	0	0	0	3	0	1.696
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	NDUBA_HUMAN	NDUFB10	0	0	0	0	3	0	1.696
Nucleoporin-like protein 2	NUPL2_HUMAN	NUPL2	0	0	0	0	3	0	1.696
Proteasome inhibitor PI31	PSMF1_HUMAN	PSMF1	0	0	0	0	3	0	1.696

Protein kinase C delta type	KPCD_HUMAN	PRKCD	0	0	0	0	3	0	1.696
Protein misato homolog 1	MSTO1_HUMAN	MSTO1	0	0	0	0	3	0	1.696
Spliceosome-associated protein CWC15 homolog	CWC15_HUMAN	CWC15	0	0	0	0	3	0	1.696
Ubiquitin-conjugating enzyme	UBE2O_HUMAN	UBE2O	0	0	0	0	3	0	1.696
UPF0553 protein C9orf64	CI064_HUMAN	C9orf64	0	0	0	0	3	0	1.696
Transcription elongation factor B polypeptide 1	ELOC_HUMAN	TCEB1	2	4	0	5	5	3	1.695
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit	GBB2_HUMAN	GNB2	5	5	4	11	8	8	1.694
Histone H4	H4_HUMAN	HIST1H4A	25	26	26	57	56	36	1.694
Adenylosuccinate synthetase isozyme 2	PURA2_HUMAN	ADSS	5	4	4	8	10	7	1.691
39S ribosomal protein L43, mitochondrial	RM43_HUMAN	MRPL43	5	4	4	9	8	8	1.690
Peroxisomal multifunctional enzyme type 2	DHB4_HUMAN	HSD17B4	2	0	0	0	2	4	1.689
Septin-2	SEPT2_HUMAN	SEPT2	0	0	0	2	2	0	1.686
Retinoid-inducible serine carboxypeptidase	RISC_HUMAN	SCPEP1	4	4	3	6	7	8	1.686
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta	2AAB_HUMAN	PPP2R1B	2	0	0	0	0	5	1.685
Mitochondrial import inner membrane translocase subunit Tim13	TIM13_HUMAN	TIMM13	0	3	0	4	4	0	1.683
Transmembrane emp24 domain-containing protein 10	TMEDA_HUMAN	TMED10	16	14	4	24	17	23	1.677
Adenosine 3'-phospho 5'-phosphosulfate transporter 1	S35B2_HUMAN	SLC35B2	0	2	0	0	5	0	1.671
WD repeat-containing protein	WDR6_HUMAN	WDR6	0	4	4	5	5	7	1.668
39S ribosomal protein L23, mitochondrial	RM23_HUMAN	MRPL23	0	0	0	3	0	0	1.667
Casein kinase I isoform epsilon	KC1E_HUMAN	CSNK1E	0	0	0	3	0	0	1.667
Lipase maturation factor 2	LMF2_HUMAN	LMF2	0	0	0	3	0	0	1.667
Lysozyme C	LYSC_HUMAN	LYZ	0	0	0	3	0	0	1.667
Methylsterol monooxygenase 1	MSMO1_HUMAN	MSMO1	0	0	0	3	0	0	1.667
Mitochondrial folate transporter/carrier	MFTC_HUMAN	SLC25A32	0	0	0	3	0	0	1.667
Myeloid leukemia factor 2	MLF2_HUMAN	MLF2	0	0	0	3	0	0	1.667
NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	NDUV2_HUMAN	NDUFV2	0	0	0	3	0	0	1.667
Peroxisomal membrane protein PEX16	PEX16_HUMAN	PEX16	0	0	0	3	0	0	1.667
Protein PRRC2C	PRC2C_HUMAN	PRRC2C	0	0	0	3	0	0	1.667
Putative RNA-binding protein	RBM3_HUMAN	RBM3	0	0	0	3	0	0	1.667
Ribonuclease P protein subunit	POP7_HUMAN	POP7	0	0	0	3	0	0	1.667
Ribosome maturation protein SBDS	SBDS_HUMAN	SBDS	0	0	0	3	0	0	1.667
Serine/arginine-rich splicing	SRSF2_HUMAN	SRSF2	0	0	0	3	0	0	1.667

Serine/threonine-protein phosphatase 4 regulatory subunit 3A	P4R3A_HUMAN	SMEK1	0	0	0	3	0	0	1.667
Small nuclear ribonucleoprotein G-like	RUXGL_HUMAN	SNRPGP15	0	0	0	3	0	0	1.667
Testis-expressed sequence 264 protein	TX264_HUMAN	TEX264	0	0	0	3	0	0	1.667
Thymidylate kinase	KTHY_HUMAN	DTYMK	0	0	0	3	0	0	1.667
Transcription and mRNA export factor ENY2	ENY2_HUMAN	ENY2	0	0	0	3	0	0	1.667
Transcription elongation factor, mitochondrial	TEFM_HUMAN	TEFM	0	0	0	3	0	0	1.667
WW domain-binding protein	WBP11_HUMAN	WBP11	0	0	0	3	0	0	1.667
Zinc finger protein 622	ZN622_HUMAN	ZNF622	0	0	0	3	0	0	1.667
Centromere protein V	CENPV_HUMAN	CENPV	12	7	10	16	19	20	1.666
Putative RNA-binding protein	RBM15_HUMAN	RBM15	7	6	5	14	10	10	1.660
Cytochrome c oxidase assembly factor 3 homolog,	COA3_HUMAN	COA3	2	0	0	3	3	0	1.659
Cytochrome c oxidase assembly protein COX15	COX15_HUMAN	COX15	2	0	0	3	3	0	1.659
Splicing factor 45	SPF45_HUMAN	RBM17	2	0	0	3	3	0	1.659
Sideroflexin-4	SFXN4_HUMAN	SFXN4	8	5	3	12	10	8	1.659
Small nuclear ribonucleoprotein-associated	RSMB_HUMAN	SNRPB	14	11	12	27	27	16	1.657
ATP-dependent RNA helicase DDX54	DDX54_HUMAN	DDX54	3	0	4	4	5	6	1.655
60S ribosomal protein L30	RL30_HUMAN	RPL30	27	22	32	51	49	52	1.640
General transcription factor 3C polypeptide 2	TF3C2_HUMAN	GTF3C2	0	0	4	3	4	4	1.637
Protein AAR2 homolog	AAR2_HUMAN	AAR2	0	2	0	5	0	0	1.636
Sorting and assembly machinery component 50	SAM50_HUMAN	SAMM50	6	3	6	8	10	10	1.633
28S ribosomal protein S10, mitochondrial	RT10_HUMAN	MRPS10	5	10	3	10	9	14	1.631
Putative ribonuclease	YBEY_HUMAN	YBEY	0	0	3	3	3	3	1.625
Ribose-phosphate pyrophosphokinase 1	PRPS1_HUMAN	PRPS1	16	16	10	25	23	29	1.621
Ribosomal RNA processing protein 1 homolog A	RRP1_HUMAN	RRP1	6	3	3	10	7	5	1.612
General transcription factor 3C polypeptide 1	TF3C1_HUMAN	GTF3C1	6	7	4	10	12	9	1.611
Mitochondrial fission process protein 1	MTFP1_HUMAN	MTFP1	9	8	5	13	15	12	1.608
Coatomer subunit epsilon	COPE_HUMAN	COPE	17	8	8	24	20	16	1.603
Probable ATP-dependent RNA helicase DDX49	DDX49_HUMAN	DDX49	0	2	3	6	4	0	1.601
Chromobox protein homolog 3	CBX3_HUMAN	CBX3	0	5	0	4	3	5	1.596
Heterogeneous nuclear ribonucleoprotein H2	HNRH2_HUMAN	HNRNPH2	12	11	10	24	19	17	1.595
Hornerin	HORN_HUMAN	HRNR	11	8	24	25	22	32	1.588
Eukaryotic translation initiation factor 2 subunit 3	IF2G_HUMAN	EIF2S3	7	5	2	11	7	7	1.584

NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	NDUB4_HUMAN	NDUFB4	7	6	8	13	11	14	1.583
Leukotriene A-4 hydrolase	LKHA4_HUMAN	LTA4H	3	3	0	3	6	3	1.571
14-3-3 protein beta/alpha	1433B_HUMAN	YWHAB	4	0	0	2	5	3	1.569
Mitotic spindle assembly checkpoint protein MAD2A	MD2L1_HUMAN	MAD2L1	4	0	0	3	5	2	1.563
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9,	NDUA9_HUMAN	NDUFA9	19	16	13	32	30	23	1.558
ADP-ribosylation factor 1	ARF1_HUMAN	ARF1	6	7	4	11	10	9	1.558
Transmembrane protein 126A	T126A_HUMAN	TMEM126A	9	11	0	11	11	14	1.553
AP-2 complex subunit sigma	AP2S1_HUMAN	AP2S1	3	2	4	5	5	6	1.549
Histone H2A type 1-B/E	H2A1B_HUMAN	HIST1H2AB	16	15	21	31	31	30	1.545
Heterogeneous nuclear ribonucleoprotein K	HNRPK_HUMAN	HNRNPK	50	53	56	83	89	106	1.535
ADP-ribosylation factor-like protein 2	ARL2_HUMAN	ARL2	10	12	0	13	12	14	1.533
ATP-dependent RNA helicase DDX1	DDX1_HUMAN	DDX1	4	4	4	8	7	6	1.533
THO complex subunit 4	THOC4_HUMAN	ALYREF	11	7	10	18	17	14	1.531
Regulation of nuclear pre-mRNA domain-containing	RPR1A_HUMAN	RPRD1A	10	0	2	6	8	8	1.524
Pyridoxal phosphate	PLPP_HUMAN	PDXP	3	0	0	0	4	3	1.523
Tight junction protein ZO-1	ZO1_HUMAN	TJP1	0	3	0	0	4	3	1.520
NAD(P)H-hydrate epimerase	NNRE_HUMAN	APOA1BP	3	0	3	5	4	3	1.516
Protein DEK	DEK_HUMAN	DEK	7	10	9	18	15	12	1.513
Guanine nucleotide-binding protein-like 3	GNL3_HUMAN	GNL3	9	11	13	16	17	24	1.513
Ubiquitin-protein ligase E3C	UBE3C_HUMAN	UBE3C	0	2	9	5	7	9	1.510
Alpha-aminoadipic semialdehyde dehydrogenase	AL7A1_HUMAN	ALDH7A1	5	5	4	9	8	7	1.507
La-related protein 7	LARP7_HUMAN	LARP7	5	3	7	10	11	5	1.503
DNA polymerase alpha catalytic subunit	DPOLA_HUMAN	POLA1	3	0	0	3	4	0	1.501
Importin subunit alpha-4	IMA4_HUMAN	KPNA3	3	0	0	4	3	0	1.496
TATA-binding protein-associated factor 172	BTAF1_HUMAN	BTAF1	5	5	0	3	9	6	1.495
39S ribosomal protein L20, mitochondrial	RM20_HUMAN	MRPL20	3	3	4	4	8	5	1.488
LINE-1 retrotransposable element ORF1 protein	LORF1_HUMAN	L1RE1	0	3	2	4	4	2	1.486
Probable ATP-dependent RNA helicase DDX27	DDX27_HUMAN	DDX27	5	5	7	12	8	9	1.485
28S ribosomal protein S25, mitochondrial	RT25_HUMAN	MRPS25	15	18	0	21	17	18	1.484
tRNA-splicing ligase RtcB	RTCB_HUMAN	RTCB	15	11	12	20	20	24	1.482
Calcium uniporter protein, mitochondrial	MCU_HUMAN	MCU	2	0	3	2	4	4	1.481
Actin-related protein 2/3 complex subunit 3	ARPC3_HUMAN	ARPC3	5	5	0	9	3	6	1.481
Transformation/transcription domain-associated protein	TRRAP_HUMAN	TRRAP	0	2	3	2	5	3	1.478

NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUAC_HUMAN	NDUFA12	10	10	7	17	14	14	1.468
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5_HUMAN	PGAM5	20	25	19	40	38	29	1.468
Peptidyl-prolyl cis-trans isomerase H	PPIH_HUMAN	PPIH	4	4	4	6	6	8	1.465
Acetyl-CoA carboxylase 1	ACACA_HUMAN	ACACA	11	14	10	18	20	20	1.460
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6_HUMAN	PPP6C	15	11	8	18	20	18	1.456
60S ribosomal protein L7-like	RL7L_HUMAN	RPL7L1	0	4	3	0	5	7	1.455
5'-3' exoribonuclease 2	XRN2_HUMAN	XRN2	9	11	9	18	16	14	1.453
Trafficking protein particle complex subunit 1	TPPC1_HUMAN	TRAPPC1	5	5	8	10	8	12	1.452
E3 ubiquitin-protein ligase	UBR4_HUMAN	UBR4	0	4	3	2	6	5	1.450
28S ribosomal protein S34, mitochondrial	RT34_HUMAN	MRPS34	11	8	10	18	17	13	1.449
Phenylalanine--tRNA ligase alpha subunit	SYFA_HUMAN	FARSA	17	18	19	29	28	32	1.445
Histone H2B type 1-C/E/F/G/I	H2B1C_HUMAN	HIST1H2BC	16	23	24	35	37	32	1.443
Signal recognition particle subunit SRP68	SRP68_HUMAN	SRP68	18	16	16	24	28	30	1.443
Methylcrotonoyl-CoA carboxylase subunit alpha,	MCCA_HUMAN	MCCC1	2	0	0	0	0	4	1.442
A-kinase anchor protein 8-like	AKP8L_HUMAN	AKAP8L	0	0	3	3	3	2	1.441
Ubiquitin-40S ribosomal protein S27a	RS27A_HUMAN	RPS27A	50	44	44	76	79	70	1.432
Plasma membrane calcium-transporting ATPase 1	AT2B1_HUMAN	ATP2B1	0	3	4	4	4	5	1.431
Putative deoxyribose-phosphate aldolase	DEOC_HUMAN	DERA	11	5	0	13	10	4	1.431
Pre-mRNA-processing factor	PRP19_HUMAN	PRPF19	22	20	23	34	33	39	1.430
39S ribosomal protein L22, mitochondrial	RM22_HUMAN	MRPL22	11	12	0	14	12	12	1.429
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1_HUMAN	AIMP1	24	16	8	30	25	22	1.422
Melanoma-associated antigen	MAGD2_HUMAN	MAGED2	6	6	3	8	7	9	1.418
Protein jagunal homolog 1	JAGN1_HUMAN	JAGN1	7	8	0	8	8	9	1.417
Paired amphipathic helix protein Sin3a	SIN3A_HUMAN	SIN3A	2	3	3	6	3	4	1.416
DNA topoisomerase 2-alpha	TOP2A_HUMAN	TOP2A	23	35	25	43	44	46	1.410
WD repeat-containing protein	WDR82_HUMAN	WDR82	15	6	6	15	15	13	1.409
Signal recognition particle 9 kDa protein	SRP09_HUMAN	SRP9	8	6	6	12	11	9	1.405
Activating signal cointegrator 1 complex subunit 3	ASCC3_HUMAN	ASCC3	8	7	4	9	10	11	1.400
Myosin light polypeptide 6	MYL6_HUMAN	MYL6	9	9	6	12	13	13	1.399
28S ribosomal protein S24, mitochondrial	RT24_HUMAN	MRPS24	4	5	6	9	6	9	1.396
60S ribosomal protein L6	RL6_HUMAN	RPL6	50	48	41	88	73	60	1.396

DNA-directed RNA polymerase III subunit RPC2	RPC2_HUMAN	POLR3B	0	3	3	3	4	4	1.395
Transmembrane protein 97	TMM97_HUMAN	TMEM97	0	3	3	3	4	4	1.395
Ras GTPase-activating protein-binding protein 1	G3BP1_HUMAN	G3BP1	5	3	4	5	6	8	1.394
Nicalin	NCLN_HUMAN	NCLN	12	10	12	19	20	15	1.390
Chromodomain-helicase-DNA-binding protein 1-like	CHD1L_HUMAN	CHD1L	6	5	3	8	6	8	1.390
DNA topoisomerase 1	TOP1_HUMAN	TOP1	31	26	31	51	44	44	1.383
Nucleosome assembly protein 1-like 1	NP1L1_HUMAN	NAP1L1	11	11	13	15	18	22	1.379
Gamma-tubulin complex component 2	GCP2_HUMAN	TUBGCP2	4	7	8	10	8	12	1.377
Unhealthy ribosome biogenesis protein 2 homolog	URB2_HUMAN	URB2	0	2	4	4	5	2	1.375
Programmed cell death protein	PDCD6_HUMAN	PDCD6	11	13	0	14	12	12	1.372
Cofilin-1	COF1_HUMAN	CFL1	8	9	10	14	11	17	1.362
Anaphase-promoting complex subunit 1	APC1_HUMAN	ANAPC1	3	5	3	6	4	7	1.362
Signal recognition particle 19 kDa protein	SRP19_HUMAN	SRP19	4	4	3	6	5	6	1.362
28S ribosomal protein S23, mitochondrial	RT23_HUMAN	MRPS23	10	10	9	17	15	13	1.362
Translation initiation factor eIF-2B subunit delta	EI2BD_HUMAN	EIF2B4	10	12	11	13	17	21	1.360
ATP-dependent RNA helicase DDX55	DDX55_HUMAN	DDX55	0	0	0	0	0	2	1.360
Calmodulin	CALM_HUMAN	CALM1	0	0	0	0	0	2	1.360
Etoposide-induced protein 2.4 homolog	EI24_HUMAN	EI24	0	0	0	0	0	2	1.360
High mobility group protein	HMGB1_HUMAN	HMGB1	0	0	0	0	0	2	1.360
Lysine-rich nucleolar protein 1	KNOP1_HUMAN	KNOP1	0	0	0	0	0	2	1.360
Methylcrotonoyl-CoA carboxylase beta chain,	MCCB_HUMAN	MCCC2	0	0	0	0	0	2	1.360
Ras GTPase-activating-like protein IQGAP2	IQGA2_HUMAN	IQGAP2	0	0	0	0	0	2	1.360
Serine--tRNA ligase,	SYSC_HUMAN	SARS	0	0	0	0	0	2	1.360
Tail-anchored protein insertion receptor WRB	WRB_HUMAN	WRB	0	0	0	0	0	2	1.360
Tuftelin-interacting protein 11	TFP11_HUMAN	TFIP11	0	0	0	0	0	2	1.360
WD repeat-containing protein	WDR37_HUMAN	WDR37	0	0	0	0	0	2	1.360
Anaphase-promoting complex subunit 10	APC10_HUMAN	ANAPC10	0	0	0	0	2	0	1.353
Atlastin-3	ATLA3_HUMAN	ATL3	0	0	0	0	2	0	1.353
ATPase family AAA domain-containing protein 1	ATAD1_HUMAN	ATAD1	0	0	0	0	2	0	1.353
Cytochrome c oxidase protein 20 homolog	COX20_HUMAN	COX20	0	0	0	0	2	0	1.353
Dedicator of cytokinesis	DOC11_HUMAN	DOCK11	0	0	0	0	2	0	1.353
Exosome complex component RRP40	EXOS3_HUMAN	EXOSC3	0	0	0	0	2	0	1.353
Glycerol kinase	GLPK_HUMAN	GK	0	0	0	0	2	0	1.353
Integral membrane protein	GP180_HUMAN	GPR180	0	0	0	0	2	0	1.353

Low density lipoprotein receptor adapter protein 1	ARH_HUMAN	LDLRAP1	0	0	0	0	2	0	1.353
Multiple myeloma tumor-associated protein 2	MMTA2_HUMAN	MMTAG2	0	0	0	0	2	0	1.353
Propionyl-CoA carboxylase beta chain, mitochondrial	PCCB_HUMAN	PCCB	0	0	0	0	2	0	1.353
Unconventional myosin-IXb	MYO9B_HUMAN	MYO9B	0	0	0	0	2	0	1.353
Zinc finger HIT domain-containing protein 2	ZNHI2_HUMAN	ZNHIT2	0	0	0	0	2	0	1.353
40S ribosomal protein S21	RS21_HUMAN	RPS21	4	3	4	6	6	5	1.352
Basic leucine zipper and W2 domain-containing protein 1	BZW1_HUMAN	BZW1	4	3	4	7	6	4	1.349
RNA-binding protein 39	RBM39_HUMAN	RBM39	9	10	9	15	14	14	1.348
Ribonuclease P protein subunit	RPP38_HUMAN	RPP38	4	7	4	9	10	4	1.347
Nucleolar protein 16	NOP16_HUMAN	NOP16	8	8	5	11	12	9	1.346
GTP-binding protein 10	GTPBA_HUMAN	GTPBP10	0	4	6	8	4	5	1.343
Structural maintenance of chromosomes protein 4	SMC4_HUMAN	SMC4	24	36	32	51	40	50	1.343
26S proteasome non-ATPase regulatory subunit 14	PSDE_HUMAN	PSMD14	8	11	6	13	16	9	1.341
Ribosome biogenesis protein BMS1 homolog	BMS1_HUMAN	BMS1	0	5	0	2	3	5	1.336
Acyl-CoA dehydrogenase family member 11	ACD11_HUMAN	ACAD11	0	0	0	2	0	0	1.333
Ataxin-2-like protein	ATX2L_HUMAN	ATXN2L	0	0	0	2	0	0	1.333
FAD-dependent oxidoreductase domain-	FXRD1_HUMAN	FOXRED1	0	0	0	2	0	0	1.333
G2/mitotic-specific cyclin-B1	CCNB1_HUMAN	CCNB1	0	0	0	2	0	0	1.333
Glutathione S-transferase P	GSTP1_HUMAN	GSTP1	0	0	0	2	0	0	1.333
GPI transamidase component PIG-S	PIGS_HUMAN	PIGS	0	0	0	2	0	0	1.333
Integrator complex subunit 1	INT1_HUMAN	INTS1	0	0	0	2	0	0	1.333
Msx2-interacting protein	MINT_HUMAN	SPEN	0	0	0	2	0	0	1.333
NF-kappa-B inhibitor-interacting Ras-like protein 2	KBRS2_HUMAN	NKIRAS2	0	0	0	2	0	0	1.333
Protein argonaute-2	AGO2_HUMAN	AGO2	0	0	0	2	0	0	1.333
Protein O-linked-mannose beta-1,4-N-acetylglucosaminyltransferase	PMGT2_HUMAN	POMGNT2	0	0	0	2	0	0	1.333
Rho guanine nucleotide exchange factor 7	ARHG7_HUMAN	ARHGEF7	0	0	0	2	0	0	1.333
Serine racemase	SRR_HUMAN	SRR	0	0	0	2	0	0	1.333
Serine/arginine-rich splicing	SRSF6_HUMAN	SRSF6	0	0	0	2	0	0	1.333
Sister chromatid cohesion protein PDS5 homolog B	PDS5B_HUMAN	PDS5B	0	0	0	2	0	0	1.333
Splicing factor 3B subunit 4	SF3B4_HUMAN	SF3B4	0	0	0	2	0	0	1.333
Transducin beta-like protein 2	TBL2_HUMAN	TBL2	0	0	0	2	0	0	1.333
Importin subunit alpha-1	IMA1_HUMAN	KPNA2	6	11	15	15	13	21	1.333
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase	STT3A_HUMAN	STT3A	8	8	9	12	14	12	1.332
Nucleolar complex protein 3 homolog	NOC3L_HUMAN	NOC3L	13	12	12	18	19	19	1.330

CDP-diacylglycerol--inositol 3-phosphatidyltransferase	CDIPT_HUMAN	CDIPT	14	16	3	15	12	22	1.329
DNA-directed RNA polymerase I subunit RPA49	RPA49_HUMAN	POLR1E	0	5	0	3	5	2	1.329
Tubulin beta-3 chain	TBB3_HUMAN	TUBB3	0	0	6	0	4	7	1.328
ADP-ribosylation factor 4	ARF4_HUMAN	ARF4	20	20	7	22	20	28	1.326
COP9 signalosome complex subunit 8	CSN8_HUMAN	COPS8	3	0	0	2	0	4	1.324
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X_HUMAN	USP9X	23	26	17	34	33	32	1.323
Nucleoporin NUP188 homolog	NU188_HUMAN	NUP188	2	10	6	9	7	11	1.316
39S ribosomal protein L16, mitochondrial	RM16_HUMAN	MRPL16	5	6	5	9	10	5	1.315
Acyl-coenzyme A thioesterase	ACOT8_HUMAN	ACOT8	4	4	0	5	4	4	1.314
Serine/threonine-protein kinase VRK1	VRK1_HUMAN	VRK1	4	4	4	7	7	4	1.313
Coronin-1C	COR1C_HUMAN	CORO1C	3	0	0	3	3	0	1.311
Lysophospholipid	MBOA7_HUMAN	MBOAT7	0	3	0	3	3	0	1.308
60S ribosomal protein L13a	RL13A_HUMAN	RPL13A	17	14	16	22	21	27	1.308
39S ribosomal protein L48, mitochondrial	RM48_HUMAN	MRPL48	10	7	0	9	8	9	1.308
39S ribosomal protein L28, mitochondrial	RM28_HUMAN	MRPL28	3	0	0	4	2	0	1.306
Cytoskeleton-associated	CKAP5_HUMAN	CKAP5	10	7	4	13	11	7	1.305
40S ribosomal protein S25	RS25_HUMAN	RPS25	30	26	23	41	40	36	1.303
116 kDa U5 small nuclear ribonucleoprotein component	U5S1_HUMAN	EFTUD2	59	65	66	95	95	92	1.301
40S ribosomal protein S15a	RS15A_HUMAN	RPS15A	31	26	41	46	50	50	1.300
Chromatin target of PRMT1 protein	CHTOP_HUMAN	CHTOP	18	16	18	26	25	26	1.298
39S ribosomal protein L47, mitochondrial	RM47_HUMAN	MRPL47	6	7	6	8	11	9	1.296
Sideroflexin-2	SFXN2_HUMAN	SFXN2	7	4	4	6	9	7	1.296
40S ribosomal protein S7	RS7_HUMAN	RPS7	22	28	27	33	33	47	1.289
AP-3 complex subunit sigma-2	AP3S2_HUMAN	AP3S2	6	5	0	5	7	5	1.288
Cleavage and polyadenylation specificity factor subunit 6	CPSF6_HUMAN	CPSF6	13	10	10	12	14	22	1.284
Zinc finger protein 768	ZN768_HUMAN	ZNF768	4	5	4	7	6	6	1.283
Protein CMSS1	CMS1_HUMAN	CMSS1	10	0	3	6	8	6	1.278
Angio-associated migratory cell protein	AAMP_HUMAN	AAMP	4	3	2	5	4	4	1.276
60S ribosomal protein L3	RL3_HUMAN	RPL3	62	64	64	89	95	92	1.275
Nuclear mitotic apparatus	NUMA1_HUMAN	NUMA1	11	17	14	20	19	22	1.275
60S ribosomal protein L35a	RL35A_HUMAN	RPL35A	22	18	24	31	27	35	1.272
Malate dehydrogenase,	MDHC_HUMAN	MDH1	0	0	3	0	3	3	1.272
Replication factor C subunit 5	RFC5_HUMAN	RFC5	26	23	13	31	30	28	1.271
SRSF protein kinase 2	SRPK2_HUMAN	SRPK2	3	0	3	3	4	3	1.268
Magnesium transporter protein	MAGT1_HUMAN	MAGT1	7	5	6	8	12	6	1.268
ADP-ribosylation factor 5	ARF5_HUMAN	ARF5	9	8	2	10	8	9	1.267
28S ribosomal protein S35, mitochondrial	RT35_HUMAN	MRPS35	5	8	5	12	10	4	1.266
Serine/arginine-rich splicing	SRSF5_HUMAN	SRSF5	7	5	4	10	7	6	1.265

Single-stranded DNA-binding protein, mitochondrial	SSBP_HUMAN	SSBP1	8	5	13	16	10	12	1.264
N-alpha-acetyltransferase 10	NAA10_HUMAN	NAA10	15	15	14	19	22	22	1.259
AP-1 complex subunit sigma-	AP1S1_HUMAN	AP1S1	9	11	8	13	13	14	1.258
Methyltransferase-like protein	MET13_HUMAN	METTL13	0	2	4	3	3	4	1.255
60S acidic ribosomal protein	RLA2_HUMAN	RPLP2	8	6	11	12	12	12	1.254
39S ribosomal protein L40, mitochondrial	RM40_HUMAN	MRPL40	4	3	0	4	0	6	1.254
Geranylgeranyl transferase type-2 subunit alpha	PGTA_HUMAN	RABGGTA	4	0	0	2	0	5	1.253
40S ribosomal protein S26	RS26_HUMAN	RPS26	27	20	17	33	30	28	1.253
FAST kinase domain-containing protein 5	FAKD5_HUMAN	FASTKD5	0	0	3	3	3	0	1.251
Plakophilin-1	PKP1_HUMAN	PKP1	0	0	3	3	3	0	1.251
40S ribosomal protein S4, X isoform	RS4X_HUMAN	RPS4X	93	85	91	129	126	128	1.249
Insulin-degrading enzyme	IDE_HUMAN	IDE	0	2	2	0	5	0	1.249
Conserved oligomeric Golgi complex subunit 4	COG4_HUMAN	COG4	4	0	0	3	3	2	1.248
60S acidic ribosomal protein	RLA0_HUMAN	RPLP0	52	62	42	79	67	75	1.248
Putative ATP-dependent RNA helicase DHX30	DHX30_HUMAN	DHX30	61	68	65	93	99	84	1.248
RNA-binding protein PNO1	PNO1_HUMAN	PNO1	6	3	3	7	6	4	1.247
DnaJ homolog subfamily B member 6	DNJB6_HUMAN	DNAJB6	7	6	8	11	13	6	1.247
HEAT repeat-containing	HEAT3_HUMAN	HEATR3	2	0	2	3	0	3	1.245
Protein QIL1	QIL1_HUMAN	QIL1	0	2	4	4	5	0	1.243
Ras-related protein Rab-5A	RAB5A_HUMAN	RAB5A	0	0	3	5	0	0	1.235
60S ribosomal protein L23a	RL23A_HUMAN	RPL23A	63	50	49	72	70	85	1.234
Heterogeneous nuclear ribonucleoprotein H	HNRH1_HUMAN	HNRNPH1	76	75	82	110	113	105	1.234
40S ribosomal protein S14	RS14_HUMAN	RPS14	51	45	44	67	70	59	1.230
Hydroxysteroid dehydrogenase-like protein 2	HSDL2_HUMAN	HSDL2	7	6	7	8	9	11	1.230
60S ribosomal protein L29	RL29_HUMAN	RPL29	18	22	18	28	31	22	1.226
Nuclear pore complex protein Nup205	NU205_HUMAN	NUP205	27	34	29	37	38	50	1.222
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP_HUMAN	OSGEP	10	6	7	12	11	9	1.222
Protein tyrosine phosphatase type IVA 1	TP4A1_HUMAN	PTP4A1	4	4	0	3	4	5	1.219
60S ribosomal protein L5	RL5_HUMAN	RPL5	63	61	44	78	74	80	1.218
Prolyl 4-hydroxylase subunit alpha-1	P4HA1_HUMAN	P4HA1	11	13	10	15	12	20	1.218
Probable serine carboxypeptidase CPVL	CPVL_HUMAN	CPVL	8	7	6	10	10	9	1.216
40S ribosomal protein S3a	RS3A_HUMAN	RPS3A	92	97	68	121	118	115	1.214
Enhancer of rudimentary	ERH_HUMAN	ERH	9	11	11	16	14	13	1.214
Lupus La protein	LA_HUMAN	SSB	18	16	16	22	21	26	1.213
Myb-binding protein 1A	MBB1A_HUMAN	MYBBP1A	36	49	43	61	59	57	1.213
Cancer-related nucleoside-triphosphatase	NTPCR_HUMAN	NTPCR	10	16	9	15	16	17	1.211
TRMT1-like protein	TRM1L_HUMAN	TRMT1L	2	0	7	5	5	4	1.210

40S ribosomal protein S23	RS23_HUMAN	RPS23	17	14	14	24	21	17	1.209
Nucleoside diphosphate kinase	NDK6_HUMAN	NME6	4	7	0	6	6	4	1.208
14-3-3 protein gamma	1433G_HUMAN	YWHAG	6	0	4	5	5	5	1.208
Nucleophosmin	NPM_HUMAN	NPM1	51	53	48	72	74	63	1.207
Coatomer subunit beta'	COPB2_HUMAN	COPB2	7	8	9	9	12	12	1.205
E3 ubiquitin-protein ligase MYCBP2	MYCB2_HUMAN	MYCBP2	0	5	0	0	4	4	1.205
40S ribosomal protein S17-like	RS17L_HUMAN	RPS17L	26	29	26	35	42	34	1.204
Nucleolar GTP-binding protein	NOG1_HUMAN	GTPBP4	9	9	9	12	12	13	1.203
AP-2 complex subunit mu	AP2M1_HUMAN	AP2M1	14	12	14	23	15	17	1.202
Nucleolar protein 56	NOP56_HUMAN	NOP56	14	13	16	19	18	22	1.202
DNA topoisomerase 2-beta	TOP2B_HUMAN	TOP2B	12	19	15	22	21	20	1.202
40S ribosomal protein S19	RS19_HUMAN	RPS19	19	7	24	21	22	26	1.200
Ras suppressor protein 1	RSU1_HUMAN	RSU1	3	0	2	2	3	3	1.198
Dynamin-2	DYN2_HUMAN	DNM2	25	23	28	35	38	31	1.197
AP-2 complex subunit alpha-1	AP2A1_HUMAN	AP2A1	17	19	19	23	25	27	1.197
COUP transcription factor 2	COT2_HUMAN	NR2F2	0	2	0	0	3	0	1.189
Probable global transcription activator SNF2L1	SMCA1_HUMAN	SMARCA1	0	2	0	0	3	0	1.189
Ubiquitin carboxyl-terminal hydrolase 24	UBP24_HUMAN	USP24	3	9	5	10	6	7	1.186
ATP-dependent RNA helicase DDX50	DDX50_HUMAN	DDX50	8	8	7	10	10	11	1.186
40S ribosomal protein S24	RS24_HUMAN	RPS24	40	42	34	52	49	55	1.184
Prohibitin-2	PHB2_HUMAN	PHB2	78	94	65	102	108	108	1.183
Small nuclear	RUXE_HUMAN	SNRPE	4	10	13	17	15	5	1.183
SUMO-conjugating enzyme	UBC9_HUMAN	UBE2I	0	2	0	2	2	0	1.182
N-acetyltransferase 14	NAT14_HUMAN	NAT14	5	4	0	5	4	4	1.182
Fanconi anemia group D2	FACD2_HUMAN	FANCD2	5	4	0	6	5	2	1.177
Protein KRI1 homolog	KRI1_HUMAN	KRI1	3	4	7	6	7	6	1.177
E3 ubiquitin-protein ligase	HUWE1_HUMAN	HUWE1	28	37	38	45	45	48	1.173
Phosphatidylserine synthase 1	PTSS1_HUMAN	PTDSS1	4	4	4	5	5	6	1.171
Transcription activator BRG1	SMCA4_HUMAN	SMARCA4	14	17	9	19	20	14	1.170
Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L_HUMAN	GPD1L	4	6	5	7	7	6	1.169
rRNA 2'-O-methyltransferase fibrillarin	FBRL_HUMAN	FBL	27	19	13	27	30	21	1.169
Ras-related protein Rab-13	RAB13_HUMAN	RAB13	6	7	3	5	6	10	1.169
Aldehyde dehydrogenase, mitochondrial	ALDH2_HUMAN	ALDH2	3	4	5	4	6	6	1.166
60S ribosomal protein L11	RL11_HUMAN	RPL11	36	35	25	48	40	39	1.165
Transferrin receptor protein 1	TFR1_HUMAN	TFRC	28	25	29	37	37	35	1.165
Probable dimethyladenosine transferase	DIM1_HUMAN	DIMT1	12	8	8	12	13	12	1.164
Probable ATP-dependent RNA helicase DDX28	DDX28_HUMAN	DDX28	9	6	7	8	8	13	1.162
5'-nucleotidase domain-containing protein 2	NT5D2_HUMAN	NT5DC2	5	3	4	9	4	3	1.161
Heterogeneous nuclear ribonucleoprotein M	HNRPM_HUMAN	HNRNPM	167	161	155	222	210	206	1.160
Splicing factor U2AF 65 kDa subunit	U2AF2_HUMAN	U2AF2	20	22	26	29	29	32	1.158
60S ribosomal protein L18a	RL18A_HUMAN	RPL18A	45	48	32	53	60	51	1.158

Dolichyl-diphosphooligosaccharide--protein glycosyltransferase	RPN2_HUMAN	RPN2	14	21	16	19	18	30	1.157
39S ribosomal protein L12, mitochondrial	RM12_HUMAN	MRPL12	6	4	0	5	4	5	1.157
Ribonuclease P protein subunit	RPP29_HUMAN	POP4	8	6	8	9	9	11	1.156
Ribosome biogenesis protein BRX1 homolog	BRX1_HUMAN	BRIX1	5	3	2	4	2	7	1.156
Poly(U)-binding-splicing factor PUF60	PUF60_HUMAN	PUF60	17	18	19	21	20	30	1.155
ATP-dependent RNA helicase DDX18	DDX18_HUMAN	DDX18	14	12	7	15	10	18	1.154
Pentatricopeptide repeat domain-containing protein 3,	PTCD3_HUMAN	PTCD3	12	13	11	10	15	22	1.154
Mitochondrial import receptor subunit TOM22 homolog	TOM22_HUMAN	TOMM22	13	11	3	14	12	9	1.153
39S ribosomal protein L39, mitochondrial	RM39_HUMAN	MRPL39	6	5	5	8	6	7	1.152
Acyl-CoA dehydrogenase family member 10	ACD10_HUMAN	ACAD10	0	0	2	0	0	3	1.152
Exosome complex component CSL4	EXOS1_HUMAN	EXOSC1	4	6	3	8	6	3	1.150
60S ribosomal protein L35	RL35_HUMAN	RPL35	20	19	14	21	23	25	1.150
Ribosomal RNA processing protein 1 homolog B	RRP1B_HUMAN	RRP1B	10	13	15	17	15	18	1.150
Probable ATP-dependent RNA helicase DDX20	DDX20_HUMAN	DDX20	3	0	3	0	4	4	1.149
Nucleolar MIF4G domain-containing protein 1	NOM1_HUMAN	NOM1	2	3	7	6	4	6	1.148
Replication factor C subunit 1	RFC1_HUMAN	RFC1	3	9	7	11	6	8	1.148
Hypoxanthine-guanine phosphoribosyltransferase	HPRT_HUMAN	HPRT1	9	8	6	12	11	7	1.147
Ribosomal L1 domain-containing protein 1	RL1D1_HUMAN	RSL1D1	20	26	17	28	27	27	1.147
Ras GTPase-activating-like protein IQGAP1	IQGA1_HUMAN	IQGAP1	24	23	22	30	30	30	1.146
T-complex protein 1 subunit	TCPD_HUMAN	CCT4	98	92	103	135	132	116	1.145
60S ribosomal protein L27	RL27_HUMAN	RPL27	39	40	26	46	43	47	1.144
Histone deacetylase 2	HDAC2_HUMAN	HDAC2	4	3	0	3	0	6	1.142
60S ribosomal protein L21	RL21_HUMAN	RPL21	33	36	23	38	46	35	1.142
28S ribosomal protein S18b, mitochondrial	RT18B_HUMAN	MRPS18B	10	11	9	15	12	12	1.142
AP-2 complex subunit alpha-2	AP2A2_HUMAN	AP2A2	14	13	13	20	18	14	1.139
Peptidyl-prolyl cis-trans isomerase B	PPIB_HUMAN	PPIB	3	0	0	0	0	4	1.139
Multidrug resistance-associated protein 1	MRP1_HUMAN	ABCC1	0	3	0	0	0	4	1.137
Peptidyl-tRNA hydrolase ICT1, mitochondrial	ICT1_HUMAN	ICT1	3	4	0	5	0	4	1.133
60S ribosomal protein L36a-	RL36L_HUMAN	RPL36AL	15	11	12	18	17	14	1.132
40S ribosomal protein S15	RS15_HUMAN	RPS15	19	17	16	25	21	21	1.131
Probable ATP-dependent RNA helicase DDX17	DDX17_HUMAN	DDX17	19	21	22	25	28	27	1.131

YTH domain-containing family protein 2	YTHD2_HUMAN	YTHDF2	7	7	7	9	8	10	1.129
TAR DNA-binding protein 43	TADBP_HUMAN	TARDBP	12	12	11	17	16	12	1.128
Small nuclear ribonucleoprotein Sm D1	SMD1_HUMAN	SNRPD1	18	14	20	21	23	23	1.127
Transducin beta-like protein 3	TBL3_HUMAN	TBL3	3	4	7	0	8	9	1.125
60S ribosomal protein L32	RL32_HUMAN	RPL32	39	33	26	43	39	43	1.125
40S ribosomal protein S30	RS30_HUMAN	FAU	4	6	4	7	10	0	1.125
ATP synthase F(0) complex subunit B1, mitochondrial	AT5F1_HUMAN	ATP5F1	21	11	20	26	24	17	1.124
Ragulator complex protein LAMTOR1	LTOR1_HUMAN	LAMTOR1	4	4	3	4	5	5	1.124
Glutamine--tRNA ligase	SYQ_HUMAN	QARS	19	22	26	30	29	27	1.121
Activating signal cointegrator 1 complex subunit 1	ASCC1_HUMAN	ASCC1	3	0	0	3	2	0	1.121
Transcriptional activator protein Pur-alpha	PURA_HUMAN	PURA	4	4	6	6	9	3	1.119
60S ribosomal protein L19	RL19_HUMAN	RPL19	23	17	19	25	26	24	1.117
Serine/threonine-protein kinase OSR1	OXSR1_HUMAN	OXSR1	9	8	9	9	10	14	1.116
26S proteasome non-ATPase regulatory subunit 2	PSMD2_HUMAN	PSMD2	73	70	60	76	92	89	1.115
Deoxyuridine 5'-triphosphate nucleotidohydrolase,	DUT_HUMAN	DUT	4	4	0	3	5	3	1.115
AP-1 complex subunit gamma-	AP1G1_HUMAN	AP1G1	24	19	17	26	27	23	1.115
28S ribosomal protein S33, mitochondrial	RT33_HUMAN	MRPS33	5	3	0	4	3	4	1.114
Eukaryotic initiation factor 4A-	IF4A3_HUMAN	EIF4A3	21	21	21	28	26	26	1.114
Clathrin heavy chain 1	CLH1_HUMAN	CLTC	47	63	54	69	64	75	1.114
60S ribosomal protein L26	RL26_HUMAN	RPL26	41	44	24	52	45	40	1.110
U2 small nuclear ribonucleoprotein A'	RU2A_HUMAN	SNRPA1	11	8	11	13	12	13	1.109
Protein unc-45 homolog A	UN45A_HUMAN	UNC45A	15	13	14	18	18	17	1.107
40S ribosomal protein S27	RS27_HUMAN	RPS27	21	22	28	31	33	26	1.107
60S ribosomal protein L23	RL23_HUMAN	RPL23	62	47	69	82	61	82	1.104
DNA-directed RNA polymerases I, II, and III	RPAB3_HUMAN	POLR2H	11	10	10	15	13	11	1.103
5'-AMP-activated protein kinase catalytic subunit alpha-2	AAPK2_HUMAN	PRKAA2	6	5	5	6	2	12	1.103
Small nuclear ribonucleoprotein Sm D2	SMD2_HUMAN	SNRPD2	17	19	28	30	25	26	1.101
RNA-binding protein 26	RBM26_HUMAN	RBM26	5	4	3	6	5	4	1.101
DNA mismatch repair protein Msh6	MSH6_HUMAN	MSH6	26	31	20	30	34	32	1.101
TP53-regulating kinase	PRPK_HUMAN	TP53RK	9	8	10	13	12	9	1.100
39S ribosomal protein L9, mitochondrial	RM09_HUMAN	MRPL9	9	8	7	11	12	7	1.098
Oligosaccharyltransferase complex subunit OSTC	OSTC_HUMAN	OSTC	7	6	7	7	8	10	1.098
Cytochrome c oxidase assembly protein COX11,	COX11_HUMAN	COX11	0	4	0	0	0	5	1.098
Lymphoid-specific helicase	HELLS_HUMAN	HELLS	4	0	0	2	2	3	1.097
Tubulin beta-4A chain	TBB4A_HUMAN	TUBB4A	17	13	15	14	17	25	1.096

UPF0488 protein C8orf33	CH033_HUMAN	C8orf33	7	4	5	9	6	5	1.094
NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	NDUS6_HUMAN	NDUFS6	4	4	4	6	5	4	1.094
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3	HACD3_HUMAN	PTPLAD1	9	13	14	14	15	16	1.093
Tricarboxylate transport protein, mitochondrial	TXTP_HUMAN	SLC25A1	27	21	22	30	30	27	1.092
Argininosuccinate synthase	ASSY_HUMAN	ASS1	6	4	6	8	6	6	1.091
60S ribosomal protein L10	RL10_HUMAN	RPL10	45	39	39	56	54	43	1.091
Apoptosis regulator BAX	BAX_HUMAN	BAX	4	0	0	3	0	3	1.088
Dual specificity mitogen-activated protein kinase kinase	MP2K2_HUMAN	MAP2K2	17	11	14	18	17	17	1.086
Heterogeneous nuclear ribonucleoprotein U	HNRPU_HUMAN	HNRNPU	171	173	142	209	187	204	1.086
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4	NDUF4_HUMAN	NDUFAF4	0	4	0	3	0	3	1.086
H/ACA ribonucleoprotein complex subunit 1	GAR1_HUMAN	GAR1	5	4	4	5	5	6	1.083
Histone H1x	H1X_HUMAN	H1FX	21	18	17	24	24	21	1.083
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA_HUMAN	LRBA	8	10	8	10	11	11	1.083
39S ribosomal protein L19, mitochondrial	RM19_HUMAN	MRPL19	8	5	8	9	9	8	1.082
Histone deacetylase 1	HDAC1_HUMAN	HDAC1	13	15	15	16	16	21	1.082
28S ribosomal protein S12, mitochondrial	RT12_HUMAN	MRPS12	6	5	6	8	6	7	1.081
40S ribosomal protein S18	RS18_HUMAN	RPS18	71	54	54	75	77	68	1.081
Condensin complex subunit 1	CND1_HUMAN	NCAPD2	17	21	15	22	22	21	1.080
Coiled-coil domain-containing protein 47	CCD47_HUMAN	CCDC47	19	19	19	21	21	28	1.079
Translational activator GCN1	GCN1L_HUMAN	GCN1L1	83	92	84	104	96	118	1.079
Polymerase delta-interacting protein 2	PDIP2_HUMAN	POLDIP2	8	7	7	8	12	7	1.079
Calpain-2 catalytic subunit	CAN2_HUMAN	CAPN2	3	5	5	5	4	7	1.078
ATP-binding cassette sub-family F member 1	ABCF1_HUMAN	ABCF1	10	11	17	15	15	17	1.077
Coatomer subunit gamma-1	COPG1_HUMAN	COPG1	39	43	45	51	55	50	1.076
MKI67 FHA domain-interacting nucleolar	MK67I_HUMAN	NIFK	5	4	4	6	9	0	1.075
39S ribosomal protein L21, mitochondrial	RM21_HUMAN	MRPL21	8	7	0	7	6	6	1.075
ADP-ribosylation factor-like protein 1	ARL1_HUMAN	ARL1	7	8	4	7	7	9	1.073
DNA replication licensing factor MCM6	MCM6_HUMAN	MCM6	33	30	24	38	33	35	1.073
39S ribosomal protein L46, mitochondrial	RM46_HUMAN	MRPL46	9	7	7	8	9	11	1.073
60S ribosomal protein L31	RL31_HUMAN	RPL31	44	42	37	50	50	50	1.073
CAD protein	PYR1_HUMAN	CAD	54	68	71	75	81	80	1.071
Importin subunit alpha-5	IMA5_HUMAN	KPNA1	7	5	6	9	5	8	1.071

Importin-11	IPO11_HUMAN	IPO11	8	11	15	20	11	11	1.070
28S ribosomal protein S6, mitochondrial	RT06_HUMAN	MRPS6	5	5	0	6	4	3	1.070
Structural maintenance of chromosomes protein 1A	SMC1A_HUMAN	SMC1A	42	66	34	61	57	54	1.069
Nucleoside diphosphate kinase	NDKA_HUMAN	NME1	33	32	17	38	29	32	1.068
Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	MTDC_HUMAN	MTHFD2	5	4	5	4	7	6	1.067
40S ribosomal protein S11	RS11_HUMAN	RPS11	51	42	31	56	46	48	1.067
14-3-3 protein zeta/delta	1433Z_HUMAN	YWHAZ	12	9	15	15	13	16	1.066
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2_HUMAN	NSUN2	31	30	39	42	37	43	1.066
Testis-expressed sequence 10 protein	TEX10_HUMAN	TEX10	9	10	9	12	11	11	1.066
Conserved oligomeric Golgi complex subunit 5	COG5_HUMAN	COG5	2	0	2	2	3	0	1.065
Importin-8	IPO8_HUMAN	IPO8	4	6	8	7	6	9	1.065
Translocon-associated protein subunit delta	SSRD_HUMAN	SSR4	21	21	16	21	23	26	1.065
Putative GTP-binding protein	GTPB6_HUMAN	GTPBP6	3	2	0	2	4	0	1.065
60S ribosomal protein L12	RL12_HUMAN	RPL12	26	28	22	33	31	28	1.065
Double-stranded RNA-specific adenosine deaminase	DSRAD_HUMAN	ADAR	9	8	7	9	10	10	1.065
Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACAM_HUMAN	NACA	6	4	4	8	6	3	1.064
Mitochondrial 10-formyltetrahydrofolate dehydrogenase	AL1L2_HUMAN	ALDH1L2	12	17	21	22	22	17	1.062
TBC1 domain family member	TBCD4_HUMAN	TBC1D4	2	7	5	7	3	7	1.062
Alcohol dehydrogenase class-3	ADHX_HUMAN	ADH5	5	5	4	8	8	0	1.060
Protein diaphanous homolog 1	DIAP1_HUMAN	DIAPH1	7	9	4	10	8	6	1.060
60S ribosomal protein L7	RL7_HUMAN	RPL7	42	41	50	56	55	50	1.058
Cytoplasmic aconitate	ACOC_HUMAN	ACO1	9	11	10	8	16	12	1.056
Required for meiotic nuclear division protein 1 homolog	RMND1_HUMAN	RMND1	7	7	6	7	11	6	1.056
28S ribosomal protein S28, mitochondrial	RT28_HUMAN	MRPS28	13	13	6	12	13	13	1.054
3-hydroxyacyl-CoA dehydrogenase type-2	HCD2_HUMAN	HSD17B10	12	11	15	19	18	9	1.054
Translation initiation factor eIF-2B subunit beta	EI2BB_HUMAN	EIF2B2	10	7	8	10	14	6	1.053
26S protease regulatory	PRS4_HUMAN	PSMC1	39	32	36	42	39	47	1.050
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUS7_HUMAN	NDUFS7	19	16	12	21	18	17	1.050
DnaJ homolog subfamily C member 13	DJC13_HUMAN	DNAJC13	7	11	8	9	10	12	1.050
Emerin	EMD_HUMAN	EMD	15	10	11	17	13	13	1.048
Protein SAAL1	SAAL1_HUMAN	SAAL1	8	6	3	6	5	9	1.047

Actin-related protein 2/3 complex subunit 4	ARPC4_HUMAN	ARPC4	5	7	4	7	7	5	1.047
Serpin H1	SERPH_HUMAN	SERPINH1	19	18	24	23	26	24	1.046
Protein virilizer homolog	VIR_HUMAN	KIAA1429	4	4	3	3	4	6	1.046
Calcium-binding mitochondrial carrier protein SCaMC-1	SCMC1_HUMAN	SLC25A24	22	15	16	22	19	22	1.045
60S ribosomal protein L17	RL17_HUMAN	RPL17	40	44	34	47	43	50	1.045
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta	2A5D_HUMAN	PPP2R5D	9	7	6	8	8	10	1.043
Nucleosome assembly protein 1-like 4	NP1L4_HUMAN	NAP1L4	15	14	18	18	19	19	1.042
Cytochrome c oxidase subunit	COX2_HUMAN	MT-CO2	19	23	10	18	17	26	1.042
Cytoplasmic dynein 1 light intermediate chain 1	DC1L1_HUMAN	DYNC1LI1	8	10	9	9	11	12	1.042
60S ribosomal protein L18	RL18_HUMAN	RPL18	55	53	57	67	72	57	1.041
Lysophosphatidylcholine acyltransferase 1	PCAT1_HUMAN	LPCAT1	6	4	6	6	7	6	1.040
Target of EGR1 protein 1	TOE1_HUMAN	TOE1	6	6	5	5	6	9	1.039
DNA mismatch repair protein Msh2	MSH2_HUMAN	MSH2	20	20	20	24	20	27	1.039
60S ribosomal protein L24	RL24_HUMAN	RPL24	80	77	72	99	93	79	1.039
Suppressor of SWI4 1	SSF1_HUMAN	PPAN	5	7	5	6	4	10	1.038
Pyrroline-5-carboxylate reductase 2	P5CR2_HUMAN	PYCR2	36	29	29	39	37	35	1.038
Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCH3_HUMAN	CHCHD3	12	8	12	15	12	11	1.037
ATP synthase subunit O, mitochondrial	ATPO_HUMAN	ATP5O	21	19	21	22	24	26	1.036
60S ribosomal protein L8	RL8_HUMAN	RPL8	28	28	29	29	37	34	1.033
Bromodomain adjacent to zinc finger domain protein 1A	BAZ1A_HUMAN	BAZ1A	0	7	0	0	5	4	1.033
Putative mitochondrial import inner membrane translocase subunit Tim23B	TI23B_HUMAN	TIMM23B	6	7	0	7	5	4	1.033
Tubulin gamma-1 chain	TBG1_HUMAN	TUBG1	10	8	10	11	11	11	1.033
Protein TBRG4	TBRG4_HUMAN	TBRG4	12	11	12	11	11	19	1.031
40S ribosomal protein S5	RS5_HUMAN	RPS5	18	16	17	25	12	23	1.031
Coatomer subunit delta	COPD_HUMAN	ARCN1	29	33	31	33	34	42	1.030
Transmembrane and coiled-coil domain-containing protein	TMCO1_HUMAN	TMCO1	4	5	3	5	4	5	1.030
Histone H2B type 1-B	H2B1B_HUMAN	HIST1H2BB	0	0	4	3	3	0	1.029
28S ribosomal protein S17, mitochondrial	RT17_HUMAN	MRPS17	3	6	3	5	5	4	1.029
Galactokinase	GALK1_HUMAN	GALK1	17	14	15	23	18	13	1.027
40S ribosomal protein S12	RS12_HUMAN	RPS12	28	28	35	39	33	35	1.027
Dynein light chain 1,	DYL1_HUMAN	DYNLL1	10	9	10	13	11	10	1.026
Coatomer subunit alpha	COPA_HUMAN	COPA	57	66	47	73	62	63	1.025
60S ribosomal protein L36	RL36_HUMAN	RPL36	21	20	28	27	27	27	1.025
Probable ATP-dependent RNA helicase DDX47	DDX47_HUMAN	DDX47	10	8	11	12	13	9	1.024

U5 small nuclear ribonucleoprotein 200 kDa	U520_HUMAN	SNRNP200	66	79	76	88	75	95	1.024
40S ribosomal protein S20	RS20_HUMAN	RPS20	15	15	18	17	20	19	1.022
Probable ATP-dependent RNA helicase DDX5	DDX5_HUMAN	DDX5	61	61	61	71	67	75	1.022
X-ray repair cross-complementing protein 6	XRCC6_HUMAN	XRCC6	36	37	33	38	33	52	1.022
Exosome complex exonuclease RRP44	RRP44_HUMAN	DIS3	17	16	25	23	23	22	1.021
Protein transport protein	SC23A_HUMAN	SEC23A	4	0	2	3	0	4	1.021
6-phosphogluconate dehydrogenase,	6PGD_HUMAN	PGD	14	12	11	17	13	13	1.021
Glycogen phosphorylase, liver	PYGL_HUMAN	PYGL	60	59	61	72	69	68	1.018
Protein pelota homolog	PELO_HUMAN	PELO	9	5	5	9	10	3	1.018
Peroxisomal biogenesis factor	PEX3_HUMAN	PEX3	3	4	0	4	4	0	1.017
RNA-binding protein 4	RBM4_HUMAN	RBM4	14	11	12	18	17	8	1.017
Monocarboxylate transporter 1	MOT1_HUMAN	SLC16A1	10	16	12	16	14	14	1.016
Proteasome-associated protein ECM29 homolog	ECM29_HUMAN	ECM29	31	38	29	35	40	38	1.015
Hexokinase-1	HXK1_HUMAN	HK1	19	17	26	22	27	23	1.014
Lysosomal protective protein	PPGB_HUMAN	CTSA	3	5	0	3	0	6	1.013
Poly(rC)-binding protein 1	PCBP1_HUMAN	PCBP1	17	17	22	24	21	20	1.013
60S ribosomal protein L10a	RL10A_HUMAN	RPL10A	33	41	43	44	48	43	1.010
Ubiquitin-protein ligase E3A	UBE3A_HUMAN	UBE3A	0	3	8	4	6	4	1.010
Tyrosine--tRNA ligase, cytoplasmic	SYYC_HUMAN	YARS	74	73	75	88	76	91	1.008
Eukaryotic translation elongation factor 1 epsilon-1	MCA3_HUMAN	EEF1E1	11	12	11	13	12	14	1.008
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCA_HUMAN	SUCLG1	20	19	16	22	25	16	1.007
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUAD_HUMAN	NDUFA13	11	9	8	11	10	11	1.006
Exosome complex component RRP4	EXOS2_HUMAN	EXOSC2	7	3	9	8	8	6	1.005
GTP-binding protein Rheb	RHEB_HUMAN	RHEB	13	17	13	15	17	17	1.003
HEAT repeat-containing	HEAT2_HUMAN	HEATR2	18	18	20	19	21	24	1.003
Ribosomal protein S6 kinase alpha-1	KS6A1_HUMAN	RPS6KA1	2	2	3	0	4	3	1.002
Translocation protein SEC63 homolog	SEC63_HUMAN	SEC63	4	5	5	5	5	6	1.002
Phosphoglycolate phosphatase	PGP_HUMAN	PGP	19	10	8	17	15	10	1.002
Voltage-dependent anion-selective channel protein 1	VDAC1_HUMAN	VDAC1	15	13	14	17	17	14	1.002
Signal transducer and activator of transcription 1-alpha/beta	STAT1_HUMAN	STAT1	0	2	4	3	2	3	1.001
40S ribosomal protein S13	RS13_HUMAN	RPS13	29	32	31	37	33	35	1.001
28S ribosomal protein S16, mitochondrial	RT16_HUMAN	MRPS16	8	5	8	8	8	8	1.000
D-3-phosphoglycerate dehydrogenase	SERA_HUMAN	PHGDH	107	99	101	113	115	121	0.998
Tubulin beta chain	TBB5_HUMAN	TUBB	482	480	479	538	570	531	0.998

Protein transport protein Sec61 subunit alpha isoform 1	S61A1_HUMAN	SEC61A1	15	18	17	22	20	15	0.998
RNA methyltransferase-like protein 1	RMTL1_HUMAN	RNMTL1	8	0	6	6	6	5	0.997
Triosephosphate isomerase	TPIS_HUMAN	TPI1	7	3	5	5	5	7	0.997
NAD(P) transhydrogenase, mitochondrial	NNTM_HUMAN	NNT	9	9	6	6	11	10	0.997
Cell growth-regulating nucleolar protein	LYAR_HUMAN	LYAR	8	10	5	11	10	5	0.996
L-lactate dehydrogenase A	LDHA_HUMAN	LDHA	148	153	113	159	153	156	0.996
40S ribosomal protein S6	RS6_HUMAN	RPS6	55	49	41	55	56	53	0.996
40S ribosomal protein S8	RS8_HUMAN	RPS8	58	57	56	64	70	60	0.996
ATP-dependent RNA helicase DDX19A	DD19A_HUMAN	DDX19A	29	26	28	32	25	37	0.994
Nucleolin	NUCL_HUMAN	NCL	167	175	150	182	189	185	0.994
Coatomer subunit beta	COPB_HUMAN	COPB1	64	65	62	70	69	77	0.994
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48	OST48_HUMAN	DDOST	15	14	16	18	17	16	0.992
Uridine 5'-monophosphate	UMPS_HUMAN	UMPS	18	13	15	19	16	17	0.992
DNA replication licensing factor MCM5	MCM5_HUMAN	MCM5	27	31	28	30	33	34	0.991
Exportin-T	XPOT_HUMAN	XPOT	39	41	37	45	45	42	0.991
28S ribosomal protein S14, mitochondrial	RT14_HUMAN	MRPS14	9	9	6	11	8	8	0.991
Tyrosine-protein kinase CSK	CSK_HUMAN	CSK	4	6	0	4	6	2	0.990
Replication factor C subunit 2	RFC2_HUMAN	RFC2	26	21	17	28	30	14	0.989
Probable ATP-dependent RNA helicase DDX52	DDX52_HUMAN	DDX52	8	7	3	6	5	9	0.989
60S ribosomal protein L15	RL15_HUMAN	RPL15	26	12	17	25	21	16	0.989
Ribosome production factor 2 homolog	RPF2_HUMAN	RPF2	7	3	5	9	4	4	0.988
Probable ATP-dependent RNA helicase DDX41	DDX41_HUMAN	DDX41	10	8	7	9	11	8	0.987
40S ribosomal protein S16	RS16_HUMAN	RPS16	73	88	75	93	89	83	0.986
Alpha-enolase	ENOA_HUMAN	ENO1	28	27	26	32	35	24	0.986
Transportin-3	TNPO3_HUMAN	TNPO3	16	17	16	19	20	16	0.985
Cyclin-dependent kinase 9	CDK9_HUMAN	CDK9	6	4	6	6	6	6	0.984
39S ribosomal protein L15, mitochondrial	RM15_HUMAN	MRPL15	14	12	9	13	12	14	0.984
N-alpha-acetyltransferase 20	NAA20_HUMAN	NAA20	9	7	9	9	8	11	0.982
ATP synthase subunit g, mitochondrial	ATP5L_HUMAN	ATP5L	29	27	28	32	37	25	0.981
RNA-binding protein Musashi homolog 1	MSI1H_HUMAN	MSI1	6	7	4	8	10	0	0.981
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	ODPB_HUMAN	PDHB	31	38	23	31	33	38	0.980
NEDD8-activating enzyme E1 regulatory subunit	ULA1_HUMAN	NAE1	12	11	12	12	9	18	0.979
Probable glutamate--tRNA ligase, mitochondrial	SYEM_HUMAN	EARS2	5	4	7	7	6	5	0.978
Adenylate kinase 4,	KAD4_HUMAN	AK4	14	13	16	17	16	15	0.976

Cytoplasmic dynein 1 heavy	DYHC1_HUMAN	DYNC1H1	158	188	228	210	193	237	0.974
26S protease regulatory	PRS8_HUMAN	PSMC5	56	50	51	59	55	60	0.973
40S ribosomal protein S3	RS3_HUMAN	RPS3	120	108	101	123	119	122	0.973
Transmembrane 9 superfamily member 3	TM9S3_HUMAN	TM9SF3	7	6	6	7	4	10	0.973
Dermcidin	DCD_HUMAN	DCD	53	44	50	59	48	56	0.972
Dihydropyrimidinase-related protein 4	DPYL4_HUMAN	DPYSL4	10	10	10	6	8	19	0.972
Heat shock protein HSP 90-	HS90B_HUMAN	HSP90AB1	261	300	266	304	313	298	0.972
Alpha-centractin	ACTZ_HUMAN	ACTR1A	29	26	28	33	32	27	0.971
Ataxin-10	ATX10_HUMAN	ATXN10	17	20	18	23	25	13	0.971
Armadillo repeat-containing protein 6	ARMC6_HUMAN	ARMC6	8	4	6	9	8	3	0.970
Aldehyde dehydrogenase X, mitochondrial	AL1B1_HUMAN	ALDH1B1	17	19	14	19	17	19	0.969
Signal peptidase complex	SPCS2_HUMAN	SPCS2	15	20	15	17	18	20	0.969
Tubulin alpha-1B chain	TBA1B_HUMAN	TUBA1B	404	389	380	449	442	403	0.968
ATP-binding cassette sub-family F member 2	ABCF2_HUMAN	ABCF2	27	24	19	30	24	23	0.968
Proteasomal ubiquitin receptor ADRM1	ADRM1_HUMAN	ADRM1	4	0	5	3	4	4	0.968
Adenine	APT_HUMAN	APRT	22	22	12	17	16	28	0.967
COP9 signalosome complex subunit 1	CSN1_HUMAN	GPS1	10	8	12	10	11	12	0.962
40S ribosomal protein S9	RS9_HUMAN	RPS9	68	67	63	79	71	67	0.962
28S ribosomal protein S7, mitochondrial	RT07_HUMAN	MRPS7	9	9	11	13	13	6	0.962
Bifunctional glutamate/proline--tRNA ligase	SYEP_HUMAN	EPRS	83	84	85	88	90	98	0.961
Prolactin-inducible protein	PIP_HUMAN	PIP	12	8	18	14	11	17	0.961
AP-1 complex subunit beta-1	AP1B1_HUMAN	AP1B1	29	26	29	30	30	32	0.961
Tubulin beta-2B chain	TBB2B_HUMAN	TUBB2B	31	28	27	32	30	32	0.961
GTPase-activating protein and VPS9 domain-containing	GAPD1_HUMAN	GAPVD1	2	5	4	2	6	4	0.959
Inosine triphosphate pyrophosphatase	ITPA_HUMAN	ITPA	8	8	7	7	8	10	0.958
Phosphatidylethanolamine-binding protein 1	PEBP1_HUMAN	PEBP1	2	0	0	0	0	2	0.955
Surfeit locus protein 4	SURF4_HUMAN	SURF4	7	8	8	8	6	11	0.954
60S ribosomal protein L9	RL9_HUMAN	RPL9	40	38	32	35	36	48	0.954
Lanosterol synthase	ERG7_HUMAN	LSS	0	2	0	0	0	2	0.953
Very-long-chain enoyl-CoA reductase	TECR_HUMAN	TECR	17	16	15	16	19	17	0.953
mRNA turnover protein 4	MRT4_HUMAN	MRTO4	15	11	17	19	17	11	0.952
60S ribosomal protein L38	RL38_HUMAN	RPL38	20	22	24	29	29	14	0.952
Creatine kinase B-type	KCRB_HUMAN	CKB	8	9	7	10	8	8	0.952
Thioredoxin	THIO_HUMAN	TXN	6	4	10	9	8	5	0.951
Gem-associated protein 5	GEMI5_HUMAN	GEMIN5	16	13	11	11	15	17	0.950
Adenylosuccinate lyase	PUR8_HUMAN	ADSL	12	11	13	12	13	14	0.950
40S ribosomal protein S10	RS10_HUMAN	RPS10	25	26	16	25	21	26	0.949
CCAAT/enhancer-binding protein zeta	CEBPZ_HUMAN	CEBPZ	4	5	4	3	8	3	0.949

ER membrane protein complex subunit 1	EMC1_HUMAN	EMC1	7	14	7	8	10	12	0.948
Guanine nucleotide-binding protein subunit alpha-11	GNA11_HUMAN	GNA11	4	4	4	5	6	2	0.948
Kinesin-like protein KIF22	KIF22_HUMAN	KIF22	0	3	7	4	3	5	0.947
Puromycin-sensitive aminopeptidase	PSA_HUMAN	NPEPPS	70	70	65	74	76	71	0.947
KRR1 small subunit processome component	KRR1_HUMAN	KRR1	8	7	9	9	10	7	0.947
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15_HUMAN	NAA15	52	51	49	59	53	52	0.947
BRCA1-associated ATM activator 1	BRAT1_HUMAN	BRAT1	3	0	0	0	0	3	0.947
Nucleoporin NDC1	NDC1_HUMAN	NDC1	3	0	0	0	0	3	0.947
Cell division control protein 45 homolog	CDC45_HUMAN	CDC45	8	9	9	8	8	12	0.946
Aladin	AAAS_HUMAN	AAAS	10	8	9	7	9	13	0.946
Acetolactate synthase-like	ILVBL_HUMAN	ILVBL	0	3	0	0	0	3	0.945
COBW domain-containing protein 1	CBWD1_HUMAN	CBWD1	0	3	0	0	0	3	0.945
Periodic tryptophan protein 2 homolog	PWP2_HUMAN	PWP2	0	3	0	0	0	3	0.945
Protein zwilch homolog	ZWILC_HUMAN	ZWILCH	0	3	0	0	0	3	0.945
Apoptosis-inducing factor 1, mitochondrial	AIFM1_HUMAN	AIFM1	47	45	42	47	49	48	0.945
Acyl-CoA dehydrogenase family member 9,	ACAD9_HUMAN	ACAD9	40	43	38	43	39	48	0.945
MMS19 nucleotide excision repair protein homolog	MMS19_HUMAN	MMS19	10	14	14	15	10	16	0.944
Delta-1-pyrroline-5-carboxylate dehydrogenase,	AL4A1_HUMAN	ALDH4A1	7	11	9	9	9	11	0.943
Methionine--tRNA ligase, cytoplasmic	SYMC_HUMAN	MARS	61	59	49	62	57	62	0.943
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	AT2A2_HUMAN	ATP2A2	67	73	59	70	72	71	0.942
39S ribosomal protein L24, mitochondrial	RM24_HUMAN	MRPL24	7	0	6	5	7	3	0.941
Synembryn-A	RIC8A_HUMAN	RIC8A	4	0	0	0	0	4	0.941
NADH-cytochrome b5	NB5R3_HUMAN	CYB5R3	3	0	0	0	3	0	0.941
Protein LSM12 homolog	LSM12_HUMAN	LSM12	3	0	0	0	3	0	0.941
Glyceraldehyde-3-phosphate dehydrogenase	G3P_HUMAN	GAPDH	36	34	21	40	32	25	0.940
Cytoplasmic dynein 2 light intermediate chain 1	DC2L1_HUMAN	DYNC2LI1	0	3	0	0	3	0	0.939
Probable cation-transporting ATPase 13A1	AT131_HUMAN	ATP13A1	11	11	8	12	11	9	0.939
Importin subunit beta-1	IMB1_HUMAN	KPNB1	42	47	42	48	49	43	0.938
Threonine--tRNA ligase, mitochondrial	SYTM_HUMAN	TARS2	8	4	4	6	6	5	0.938
T-complex protein 1 subunit	TCPZ_HUMAN	CCT6A	108	91	98	105	105	107	0.937
Signal recognition particle receptor subunit beta	SRPRB_HUMAN	SRPRB	26	26	24	26	28	27	0.937

Glucose-6-phosphate 1-dehydrogenase	G6PD_HUMAN	G6PD	2	0	0	2	0	0	0.936
Aspartate--tRNA ligase, cytoplasmic	SYDC_HUMAN	DARS	56	49	55	61	58	52	0.936
RNA-binding protein 25	RBM25_HUMAN	RBM25	16	16	14	18	16	15	0.936
Reticulocalbin-2	RCN2_HUMAN	RCN2	13	12	9	10	14	12	0.935
DNA-directed RNA polymerases I, II, and III	RPAB5_HUMAN	POLR2L	0	5	0	0	0	5	0.935
Cullin-4B	CUL4B_HUMAN	CUL4B	5	4	5	7	3	5	0.935
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUS3_HUMAN	NDUFS3	15	13	16	16	16	15	0.935
T-complex protein 1 subunit gamma	TCPG_HUMAN	CCT3	155	150	155	161	153	175	0.933
RNA pseudouridylate synthase domain-containing protein 3	RUSD3_HUMAN	RPUSD3	7	4	5	6	7	4	0.933
Heat shock protein HSP 90-	HS90A_HUMAN	HSP90AA1	62	59	49	61	61	58	0.932
THO complex subunit 2	THOC2_HUMAN	THOC2	22	32	21	25	22	32	0.929
Carbamoyl-phosphate synthase [ammonia], mitochondrial	CPSM_HUMAN	CPS1	0	5	0	0	5	0	0.929
60 kDa heat shock protein, mitochondrial	CH60_HUMAN	HSPD1	48	51	53	55	46	60	0.929
DNA-dependent protein kinase catalytic subunit	PRKDC_HUMAN	PRKDC	294	336	341	343	319	366	0.928
Constitutive coactivator of PPAR-gamma-like protein 1	F120A_HUMAN	FAM120A	15	15	10	13	16	13	0.928
39S ribosomal protein L11, mitochondrial	RM11_HUMAN	MRPL11	20	24	6	17	19	16	0.927
Eukaryotic translation initiation factor 2 subunit 1	IF2A_HUMAN	EIF2S1	19	20	16	21	22	15	0.927
ADP-ribosylation factor 6	ARF6_HUMAN	ARF6	13	10	12	13	12	12	0.927
DNA-directed RNA polymerase III subunit RPC10	RPC10_HUMAN	POLR3K	3	0	0	3	0	0	0.925
Acetyl-CoA acetyltransferase, mitochondrial	THIL_HUMAN	ACAT1	43	39	43	50	47	35	0.924
Origin recognition complex subunit 5	ORC5_HUMAN	ORC5	11	6	5	9	7	7	0.923
Exocyst complex component 2	EXOC2_HUMAN	EXOC2	5	6	7	7	5	7	0.922
60S ribosomal protein L28	RL28_HUMAN	RPL28	46	40	30	43	42	36	0.920
Ras-related protein Rap-2c	RAP2C_HUMAN	RAP2C	4	3	0	0	0	6	0.919
Growth arrest and DNA damage-inducible proteins-interacting protein 1	G45IP_HUMAN	GADD45GIP1	4	4	0	0	4	4	0.918
Arginine--tRNA ligase,	SYRC_HUMAN	RARS	66	64	66	65	65	75	0.918
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUV1_HUMAN	NDUFV1	10	9	5	11	11	3	0.918
Sorting nexin-9	SNX9_HUMAN	SNX9	0	0	2	0	0	2	0.918
TATA box-binding protein-like protein 1	TBPL1_HUMAN	TBPL1	0	0	2	0	0	2	0.918
Glycogen phosphorylase, brain form	PYGB_HUMAN	PYGB	12	16	16	15	16	15	0.915

RNA polymerase-associated protein CTR9 homolog	CTR9_HUMAN	CTR9	0	0	2	0	2	0	0.913
Nicotinamide phosphoribosyltransferase	NAMPT_HUMAN	NAMPT	28	30	26	27	27	33	0.911
L-lactate dehydrogenase B	LDHB_HUMAN	LDHB	125	135	94	126	119	121	0.911
26S proteasome non-ATPase regulatory subunit 3	PSMD3_HUMAN	PSMD3	55	67	52	53	64	63	0.911
Tubulin alpha-1A chain	TBA1A_HUMAN	TUBA1A	19	19	16	21	21	14	0.911
Pre-mRNA-processing factor 6	PRP6_HUMAN	PRPF6	38	41	36	36	41	42	0.910
DnaJ homolog subfamily A member 1	DNJA1_HUMAN	DNAJA1	12	7	8	13	10	5	0.908
CCR4-NOT transcription complex subunit 1	CNOT1_HUMAN	CNOT1	22	19	21	19	19	26	0.907
78 kDa glucose-regulated	GRP78_HUMAN	HSPA5	34	36	31	34	33	37	0.906
Calcium-binding mitochondrial carrier protein Aralar2	CMC2_HUMAN	SLC25A13	43	45	43	44	41	50	0.905
Proteasome subunit alpha type-	PSA7_HUMAN	PSMA7	13	10	11	11	13	11	0.904
Trifunctional enzyme subunit beta, mitochondrial	ECHB_HUMAN	HADHB	29	38	33	33	38	32	0.904
28S ribosomal protein S11, mitochondrial	RT11_HUMAN	MRPS11	7	9	11	10	10	8	0.904
Bifunctional UDP-N-acetylglucosamine 2-epimerase/N-	GLCNE_HUMAN	GNE	0	0	3	0	0	3	0.903
60 kDa SS-A/Ro	RO60_HUMAN	TROVE2	20	20	25	19	21	27	0.903
6-phosphofructokinase type C	K6PP_HUMAN	PFKP	12	15	12	12	13	15	0.903
Probable ATP-dependent RNA helicase DHX36	DHX36_HUMAN	DHX36	6	8	0	7	4	4	0.902
T-complex protein 1 subunit	TCPA_HUMAN	TCP1	144	134	151	144	135	162	0.901
Exportin-1	XPO1_HUMAN	XPO1	88	100	78	86	88	98	0.901
Actin, cytoplasmic 1	ACTB_HUMAN	ACTB	269	255	271	287	286	241	0.897
Nucleolar protein 58	NOP58_HUMAN	NOP58	16	16	17	14	17	19	0.896
28S ribosomal protein S29, mitochondrial	RT29_HUMAN	DAP3	18	19	16	19	19	16	0.895
Pyruvate kinase PKM	KPYM_HUMAN	PKM	211	201	220	207	205	233	0.895
Exportin-7	XPO7_HUMAN	XPO7	30	28	33	31	31	31	0.895
Importin-7	IPO7_HUMAN	IPO7	61	63	52	62	58	59	0.895
Microsomal glutathione S-transferase 1	MGST1_HUMAN	MGST1	14	14	17	16	14	16	0.894
Probable leucine--tRNA ligase, mitochondrial	SYLM_HUMAN	LARS2	18	19	18	20	16	20	0.894
DnaJ homolog subfamily A member 2	DNJA2_HUMAN	DNAJA2	20	16	17	21	17	16	0.893
60S ribosomal protein L4	RL4_HUMAN	RPL4	126	120	119	123	121	127	0.893
E3 UFM1-protein ligase 1	UFL1_HUMAN	UFL1	23	20	23	21	22	24	0.891
Elongation factor 1-alpha 1	EF1A1_HUMAN	EEF1A1	231	244	216	225	243	232	0.891
ATP-dependent RNA helicase DDX39A	DX39A_HUMAN	DDX39A	23	22	25	21	23	27	0.890
Anaphase-promoting complex subunit 7	APC7_HUMAN	ANAPC7	29	29	29	25	26	37	0.890
ATP synthase subunit beta, mitochondrial	ATPB_HUMAN	ATP5B	217	206	207	217	211	210	0.889

Pachytene checkpoint protein 2 homolog	PCH2_HUMAN	TRIP13	25	27	25	28	25	25	0.889
Spermidine synthase	SPEE_HUMAN	SRM	10	8	6	7	7	10	0.885
Elongation factor 2	EF2_HUMAN	EEF2	53	51	47	52	50	50	0.885
60S ribosomal protein L14	RL14_HUMAN	RPL14	86	76	82	90	79	77	0.884
Tubulin beta-4B chain	TBB4B_HUMAN	TUBB4B	64	64	60	65	62	62	0.883
Carbonic anhydrase 2	CAH2_HUMAN	CA2	0	2	4	0	3	3	0.882
Acyl-coenzyme A thioesterase	ACO13_HUMAN	ACOT13	9	8	8	6	7	12	0.882
Uridine-cytidine kinase-like 1	UCKL1_HUMAN	UCKL1	3	2	3	0	3	4	0.882
Dihydropyrimidinase-related protein 1	DPYL1_HUMAN	CRMP1	14	11	11	11	8	17	0.881
Nuclear cap-binding protein subunit 1	NCBP1_HUMAN	NCBP1	17	16	13	15	15	16	0.881
Fanconi anemia group I protein	FANCI_HUMAN	FANCI	28	35	21	33	29	22	0.881
AFG3-like protein 2	AFG32_HUMAN	AFG3L2	12	15	12	11	14	14	0.881
Nucleolar pre-ribosomal-associated protein 1	NPA1P_HUMAN	URB1	3	3	2	3	0	4	0.880
RuvB-like 1	RUVB1_HUMAN	RUVBL1	16	14	14	13	16	15	0.880
40S ribosomal protein S2	RS2_HUMAN	RPS2	85	82	70	83	85	69	0.879
Leucine-rich repeat-containing protein 40	LRC40_HUMAN	LRRC40	13	14	16	10	13	20	0.879
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUA5_HUMAN	NDUFA5	9	10	8	10	9	8	0.879
Poly(rC)-binding protein 2	PCBP2_HUMAN	PCBP2	20	18	17	19	20	16	0.879
DNA primase small subunit	PRI1_HUMAN	PRIM1	5	4	6	3	4	8	0.878
Kidney mitochondrial carrier protein 1	KMCP1_HUMAN	SLC25A30	4	0	3	4	3	0	0.878
Condensin-2 complex subunit	CNDD3_HUMAN	NCAPD3	4	6	6	4	4	8	0.878
Translation initiation factor eIF-2B subunit gamma	EI2BG_HUMAN	EIF2B3	7	6	8	5	6	10	0.878
Origin recognition complex subunit 4	ORC4_HUMAN	ORC4	3	5	3	5	3	3	0.878
60S ribosomal protein L22-like	RL22L_HUMAN	RPL22L1	6	6	6	6	6	6	0.878
F-actin-capping protein subunit alpha-1	CAZA1_HUMAN	CAPZA1	4	4	4	4	4	4	0.878
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUS2_HUMAN	NDUFS2	5	11	6	10	6	6	0.878
Sodium/potassium-transporting ATPase subunit alpha-1	AT1A1_HUMAN	ATP1A1	71	75	73	75	69	75	0.877
Syntaxin-binding protein 2	STXB2_HUMAN	STXBP2	6	4	5	5	6	4	0.877
60S ribosomal protein L34	RL34_HUMAN	RPL34	32	30	25	37	32	18	0.877
Eukaryotic translation initiation factor 3 subunit F	EIF3F_HUMAN	EIF3F	16	15	17	15	17	16	0.877
Nucleolar RNA helicase 2	DDX21_HUMAN	DDX21	83	88	91	87	91	84	0.877
Glutamate-rich WD repeat-containing protein 1	GRWD1_HUMAN	GRWD1	12	11	13	12	11	13	0.876
28S ribosomal protein S22, mitochondrial	RT22_HUMAN	MRPS22	24	25	25	26	34	14	0.876
Protein NipSnap homolog 1	NIPS1_HUMAN	NIPSNAP1	9	7	9	9	7	9	0.876
Dynein light chain Tctex-type	DYLT1_HUMAN	DYNLT1	5	6	5	7	5	4	0.876
Proteasome subunit alpha type-	PSA1_HUMAN	PSMA1	0	2	2	3	0	0	0.874

Eukaryotic translation initiation factor 4 gamma 2	IF4G2_HUMAN	EIF4G2	11	11	15	12	12	13	0.873
Immunoglobulin-binding	IGBP1_HUMAN	IGBP1	0	3	3	4	2	0	0.873
Conserved oligomeric Golgi complex subunit 1	COG1_HUMAN	COG1	4	6	7	6	3	8	0.873
DNA replication licensing factor MCM3	MCM3_HUMAN	MCM3	56	51	51	52	51	54	0.873
60S ribosomal protein L27a	RL27A_HUMAN	RPL27A	34	36	26	32	32	31	0.872
Endoplasmin	ENPL_HUMAN	HSP90B1	3	7	8	6	4	8	0.871
39S ribosomal protein L37, mitochondrial	RM37_HUMAN	MRPL37	8	9	12	11	9	9	0.871
C-1-tetrahydrofolate synthase, cytoplasmic	C1TC_HUMAN	MTHFD1	88	95	91	96	93	83	0.871
Mitochondrial 2-oxoglutarate/malate carrier	M2OM_HUMAN	SLC25A11	37	33	39	34	36	38	0.869
26S proteasome non-ATPase regulatory subunit 1	PSMD1_HUMAN	PSMD1	49	58	47	49	50	53	0.868
Leucine-rich repeat-containing protein 47	LRC47_HUMAN	LRRC47	5	3	7	6	5	4	0.867
CTP synthase 1	PYRG1_HUMAN	CTPS1	44	47	41	39	43	48	0.867
Exportin-2	XPO2_HUMAN	CSE1L	95	103	95	93	100	96	0.866
RNA-binding protein 14	RBM14_HUMAN	RBM14	22	22	16	22	16	21	0.866
WASH complex subunit	STRUM_HUMAN	KIAA0196	0	2	5	3	4	0	0.865
Elongation factor 1-gamma	EF1G_HUMAN	EEF1G	31	26	32	34	28	26	0.865
Voltage-dependent anion-selective channel protein 3	VDAC3_HUMAN	VDAC3	50	51	47	50	42	53	0.861
26S protease regulatory	PRS6A_HUMAN	PSMC3	50	54	48	54	49	46	0.860
Tetratricopeptide repeat	TTC37_HUMAN	TTC37	13	13	6	10	9	12	0.860
60S ribosomal protein L22	RL22_HUMAN	RPL22	31	32	33	32	32	30	0.858
Serine palmitoyltransferase 1	SPTC1_HUMAN	SPTLC1	19	11	14	16	12	15	0.858
Pescadillo homolog	PESC_HUMAN	PES1	14	13	12	13	11	14	0.857
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP_HUMAN	C1QBP	13	13	12	12	14	11	0.856
Lamin-B receptor	LBR_HUMAN	LBR	23	25	21	20	20	27	0.855
Mitochondrial inner membrane protein	IMMT_HUMAN	IMMT	49	55	45	52	44	49	0.855
Mitochondrial dicarboxylate	DIC_HUMAN	SLC25A10	29	23	29	26	27	26	0.855
Phosphoacetylglucosamine	AGM1_HUMAN	PGM3	11	14	12	13	9	14	0.854
Signal peptidase complex catalytic subunit SEC11A	SC11A_HUMAN	SEC11A	17	25	11	17	16	18	0.852
DNA replication licensing factor MCM4	MCM4_HUMAN	MCM4	21	25	28	22	22	28	0.852
Origin recognition complex subunit 3	ORC3_HUMAN	ORC3	9	9	2	5	4	10	0.851
Transportin-1	TNPO1_HUMAN	TNPO1	22	23	25	24	21	23	0.851
Erlin-2	ERLN2_HUMAN	ERLIN2	35	29	31	30	32	30	0.851
EH domain-containing protein	EHD1_HUMAN	EHD1	20	18	25	15	17	29	0.849
26S proteasome non-ATPase regulatory subunit 6	PSMD6_HUMAN	PSMD6	40	41	36	39	42	32	0.848
Alanine--tRNA ligase, mitochondrial	SYAM_HUMAN	AARS2	21	20	24	22	20	21	0.848

28S ribosomal protein S9, mitochondrial	RT09_HUMAN	MRPS9	11	12	15	16	16	5	0.847
26S protease regulatory	PRS7_HUMAN	PSMC2	56	55	57	52	58	52	0.846
Heat shock cognate 71 kDa	HSP7C_HUMAN	HSPA8	73	87	71	68	75	79	0.846
Exosome component 10	EXOSX_HUMAN	EXOSC10	11	8	11	10	11	8	0.846
General vesicular transport factor p115	USO1_HUMAN	USO1	24	25	25	21	25	25	0.843
Long-chain-fatty-acid--CoA ligase 3	ACSL3_HUMAN	ACSL3	16	17	15	15	17	14	0.842
Dephospho-CoA kinase domain-containing protein	DCAKD_HUMAN	DCAKD	8	7	6	7	6	7	0.839
Ribosomal protein S6 kinase alpha-3	KS6A3_HUMAN	RPS6KA3	8	6	10	6	8	9	0.838
Vacuolar protein sorting-associated protein 35	VPS35_HUMAN	VPS35	22	21	15	17	16	22	0.838
Hypoxia up-regulated protein 1	HYOU1_HUMAN	HYOU1	34	41	34	38	36	30	0.837
Extended synaptotagmin-2	ESYT2_HUMAN	ESYT2	7	8	8	9	6	7	0.837
Heat shock 70 kDa protein	HSP71_HUMAN	HSPA1A	66	67	66	59	59	71	0.834
Proliferating cell nuclear	PCNA_HUMAN	PCNA	32	36	33	32	33	31	0.834
Putative ribosomal RNA methyltransferase NOP2	NOP2_HUMAN	NOP2	29	27	26	30	25	23	0.834
T-complex protein 1 subunit	TCPH_HUMAN	CCT7	66	63	73	56	56	80	0.834
DNA replication licensing factor MCM7	MCM7_HUMAN	MCM7	44	46	46	37	38	54	0.834
WD repeat-containing protein	WDR5_HUMAN	WDR5	8	6	4	7	5	5	0.834
Cytochrome b-c1 complex subunit 2, mitochondrial	QCR2_HUMAN	UQCRC2	44	46	44	42	44	41	0.832
GTP-binding nuclear protein	RAN_HUMAN	RAN	35	29	31	31	28	31	0.832
Queuine tRNA-ribosyltransferase subunit	QTRD1_HUMAN	QTRTD1	6	7	6	7	5	6	0.831
Phosphatidylinositide phosphatase SAC1	SAC1_HUMAN	SACM1L	6	6	6	5	4	8	0.831
ATP-binding cassette sub-family E member 1	ABCE1_HUMAN	ABCE1	12	13	14	13	14	10	0.830
Eukaryotic translation initiation factor 3 subunit E	EIF3E_HUMAN	EIF3E	62	65	53	62	63	45	0.830
Phenylalanine--tRNA ligase beta subunit	SYFB_HUMAN	FARSB	24	24	21	20	21	24	0.829
Large neutral amino acids transporter small subunit 1	LAT1_HUMAN	SLC7A5	7	7	5	9	8	0	0.828
Phosphoglycerate mutase 1	PGAM1_HUMAN	PGAM1	8	4	6	7	4	6	0.827
Eukaryotic translation initiation factor 3 subunit I	EIF3I_HUMAN	EIF3I	50	47	25	41	45	28	0.826
Isoleucine--tRNA ligase, mitochondrial	SYIM_HUMAN	IARS2	48	49	49	43	44	50	0.824
T-complex protein 1 subunit	TCPQ_HUMAN	CCT8	17	16	13	14	13	16	0.824
DnaJ homolog subfamily B member 12	DJB12_HUMAN	DNAJB12	6	5	6	6	6	4	0.823
Nucleolar complex protein 2 homolog	NOC2L_HUMAN	NOC2L	26	28	24	25	21	27	0.823
Phosphoribosyl pyrophosphate synthase-associated protein 1	KPRA_HUMAN	PRPSAP1	12	10	12	12	14	6	0.823

Estradiol 17-beta-dehydrogenase 12	DHB12_HUMAN	HSD17B12	36	28	31	30	30	29	0.823
DnaJ homolog subfamily C member 7	DNJC7_HUMAN	DNAJC7	6	5	4	5	5	4	0.822
DNA-directed RNA polymerase II subunit RPB7	RPB7_HUMAN	POLR2G	5	4	0	2	0	6	0.822
ADP/ATP translocase 3	ADT3_HUMAN	SLC25A6	41	43	42	38	41	39	0.822
26S protease regulatory	PRS6B_HUMAN	PSMC4	38	35	39	36	33	36	0.822
Survival motor neuron protein	SMN_HUMAN	SMN1	7	3	4	3	4	6	0.822
Calcium-binding mitochondrial carrier protein Aralar1	CMC1_HUMAN	SLC25A12	10	11	9	9	9	10	0.822
Nuclear pore membrane glycoprotein 210	PO210_HUMAN	NUP210	5	6	4	6	4	4	0.820
Torsin-1A-interacting protein 1	TOIP1_HUMAN	TOR1AIP1	4	7	4	6	5	3	0.820
Elongation factor Tu,	EFTU_HUMAN	TUFM	110	122	104	108	115	90	0.818
Thymidine kinase, cytosolic	KITH_HUMAN	TK1	5	5	6	6	5	4	0.818
Isocitrate dehydrogenase [NADP], mitochondrial	IDHP_HUMAN	IDH2	47	44	40	45	42	35	0.818
AP-1 complex subunit mu-1	AP1M1_HUMAN	AP1M1	18	23	16	20	19	14	0.817
Signal recognition particle receptor subunit alpha	SRPR_HUMAN	SRPR	11	8	13	11	11	8	0.817
Poly(A) RNA polymerase, mitochondrial	PAPD1_HUMAN	MTPAP	6	4	3	4	4	4	0.816
Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	ECSIT_HUMAN	ECSIT	5	5	5	6	5	3	0.816
Nucleolar and coiled-body phosphoprotein 1	NOLC1_HUMAN	NOLC1	6	5	3	6	6	0	0.815
AP-3 complex subunit beta-1	AP3B1_HUMAN	AP3B1	24	22	24	24	19	22	0.814
DNA methyltransferase 1-associated protein 1	DMAP1_HUMAN	DMAP1	5	3	6	3	3	7	0.813
Cyclin-dependent kinase 2	CDK2_HUMAN	CDK2	19	17	18	16	18	16	0.813
Long-chain fatty acid transport protein 4	S27A4_HUMAN	SLC27A4	6	4	5	6	7	0	0.813
39S ribosomal protein L53, mitochondrial	RM53_HUMAN	MRPL53	4	5	4	4	4	4	0.812
ATP synthase subunit alpha, mitochondrial	ATPA_HUMAN	ATP5A1	203	193	180	189	187	156	0.811
Succinyl-CoA ligase [ADP-forming] subunit beta,	SUCB1_HUMAN	SUCLA2	24	20	23	23	20	19	0.810
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	NDUA6_HUMAN	NDUFA6	8	9	9	9	7	8	0.808
Ras-related protein Rab-9A	RAB9A_HUMAN	RAB9A	5	4	3	4	4	3	0.808
Eukaryotic initiation factor 4A-	IF4A1_HUMAN	EIF4A1	48	47	42	46	42	38	0.808
Ran-specific GTPase-activating protein	RANG_HUMAN	RANBP1	5	3	5	4	4	4	0.807
Serine/threonine-protein kinase MST4	MST4_HUMAN	MST4	9	8	7	8	4	10	0.807
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	DHAK_HUMAN	DAK	11	13	13	11	11	12	0.806

Chaperone activity of bc1 complex-like, mitochondrial	ADCK3_HUMAN	ADCK3	4	3	0	0	2	4	0.805
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10,	NDUAA_HUMAN	NDUFA10	14	12	11	15	14	5	0.805
Eukaryotic translation initiation factor 3 subunit H	EIF3H_HUMAN	EIF3H	3	4	6	3	5	4	0.804
General transcription factor 3C polypeptide 4	TF3C4_HUMAN	GTF3C4	4	4	4	4	3	4	0.804
Motile sperm domain-containing protein 2	MSPD2_HUMAN	MOSPD2	8	8	7	7	5	9	0.804
RuvB-like 2	RUVB2_HUMAN	RUVBL2	24	23	22	23	20	20	0.801
6-phosphofructokinase, liver	K6PL_HUMAN	PFKL	34	35	26	21	27	38	0.801
Ribonucleases P/MRP protein subunit POP1	POP1_HUMAN	POP1	11	12	12	12	12	8	0.800
39S ribosomal protein L41, mitochondrial	RM41_HUMAN	MRPL41	7	8	9	9	6	7	0.800
Histone H1.4	H14_HUMAN	HIST1H1E	133	137	137	124	126	121	0.800
Non-POU domain-containing octamer-binding protein	NONO_HUMAN	NONO	61	58	61	53	55	56	0.800
Splicing factor, proline- and glutamine-rich	SFPQ_HUMAN	SFPQ	7	8	8	8	6	7	0.799
Catenin delta-1	CTND1_HUMAN	CTNND1	19	19	17	17	16	17	0.799
Mitochondrial glutamate	GHC1_HUMAN	SLC25A22	16	13	16	13	13	15	0.799
Cytochrome c oxidase subunit 7A2, mitochondrial	CX7A2_HUMAN	COX7A2	4	4	3	4	0	5	0.799
Eukaryotic translation initiation factor 3 subunit G	EIF3G_HUMAN	EIF3G	15	15	12	13	12	13	0.797
Diphosphoinositol polyphosphate	NUD11_HUMAN	NUDT11	4	3	0	3	2	2	0.797
Ras-related protein Rab-18	RAB18_HUMAN	RAB18	7	7	7	5	7	7	0.796
Eukaryotic translation initiation factor 3 subunit A	EIF3A_HUMAN	EIF3A	159	170	161	151	136	157	0.795
Trifunctional enzyme subunit alpha, mitochondrial	ECHA_HUMAN	HADHA	65	61	68	61	53	62	0.795
Cytochrome b-c1 complex subunit Rieske, mitochondrial	UCRI_HUMAN	UQCRFS1	9	6	5	6	6	6	0.795
Structural maintenance of chromosomes protein 2	SMC2_HUMAN	SMC2	56	64	55	51	50	57	0.794
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2_HUMAN	AIMP2	15	20	18	16	23	9	0.793
Cullin-associated NEDD8-dissociated protein 1	CAND1_HUMAN	CAND1	109	130	105	101	106	103	0.793
Protein flightless-1 homolog	FLII_HUMAN	FLII	21	16	11	14	17	12	0.792
Proteasome subunit alpha type-	PSA3_HUMAN	PSMA3	7	6	8	6	7	6	0.792
Coilin	COIL_HUMAN	COIL	4	3	0	3	3	0	0.791
Electron transfer flavoprotein subunit beta	ETFB_HUMAN	ETFB	18	21	22	16	20	19	0.791
T-complex protein 1 subunit	TCPE_HUMAN	CCT5	104	109	102	90	84	109	0.790
Coatomer subunit gamma-2	COPG2_HUMAN	COPG2	22	19	17	20	16	16	0.788
ATP synthase subunit d, mitochondrial	ATP5H_HUMAN	ATP5H	4	2	0	0	0	4	0.787

Nuclear pore complex protein Nup93	NUP93_HUMAN	NUP93	45	44	45	38	38	44	0.786
Methylthioribose-1-phosphate isomerase	MTNA_HUMAN	MRI1	17	17	15	19	17	8	0.786
Pyrroline-5-carboxylate reductase 1, mitochondrial	P5CR1_HUMAN	PYCR1	46	39	39	39	39	33	0.786
Leucine-rich PPR motif-containing protein,	LPPRC_HUMAN	LRPPRC	90	104	79	92	80	71	0.782
Isocitrate dehydrogenase [NAD] subunit beta,	IDH3B_HUMAN	IDH3B	31	32	29	30	30	22	0.782
26S proteasome non-ATPase regulatory subunit 11	PSD11_HUMAN	PSMD11	10	10	8	12	8	5	0.782
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase	RPN1_HUMAN	RPN1	39	43	30	26	28	45	0.782
Threonine--tRNA ligase, cytoplasmic	SYTC_HUMAN	TARS	12	7	7	7	7	9	0.781
Delta-1-pyrroline-5-carboxylate synthase	P5CS_HUMAN	ALDH18A1	77	89	75	68	64	82	0.781
Rho-related GTP-binding protein RhoC	RHOC_HUMAN	RHOC	0	4	0	0	0	3	0.781
Neutral amino acid transporter	AAAT_HUMAN	SLC1A5	36	42	39	34	31	39	0.780
Translation initiation factor eIF-2B subunit alpha	EI2BA_HUMAN	EIF2B1	10	8	10	10	9	6	0.780
Importin-4	IPO4_HUMAN	IPO4	50	55	46	47	42	45	0.780
Mitochondrial ribonuclease P protein 3	MRRP3_HUMAN	KIAA0391	9	9	8	7	8	8	0.779
Trifunctional purine biosynthetic protein adenosine-	PUR2_HUMAN	GART	71	64	69	62	60	59	0.778
C-terminal-binding protein 1	CTBP1_HUMAN	CTBP1	10	8	8	7	10	6	0.778
Parafibromin	CDC73_HUMAN	CDC73	4	2	3	3	0	4	0.778
TBC1 domain family member	TBC15_HUMAN	TBC1D15	3	3	3	3	0	4	0.778
60S ribosomal protein L37a	RL37A_HUMAN	RPL37A	26	24	20	25	24	13	0.778
N-acylneuraminate cytidylyltransferase	NEUA_HUMAN	CMAS	4	2	0	3	0	2	0.777
Protein Njmu-R1	NJMU_HUMAN	C17orf75	0	4	4	3	4	0	0.777
Dihydropyrimidinase-related protein 5	DPYL5_HUMAN	DPYSL5	5	7	5	5	4	6	0.777
Ribonuclease P protein subunit	RPP30_HUMAN	RPP30	23	16	23	17	21	17	0.777
Dynamin-1-like protein	DNM1L_HUMAN	DNM1L	14	16	10	7	12	16	0.776
Estradiol 17-beta-dehydrogenase 11	DHB11_HUMAN	HSD17B11	4	0	4	4	3	0	0.775
Serine/threonine-protein kinase mTOR	MTOR_HUMAN	MTOR	11	8	6	9	8	5	0.775
Exocyst complex component 4	EXOC4_HUMAN	EXOC4	7	10	8	6	7	9	0.775
Signal transducer and activator of transcription 3	STAT3_HUMAN	STAT3	6	5	7	7	4	5	0.775
General transcription factor 3C polypeptide 5	TF3C5_HUMAN	GTF3C5	18	21	20	16	15	21	0.774
X-ray repair cross-complementing protein 5	XRCC5_HUMAN	XRCC5	46	50	60	45	39	54	0.774
Nucleolar complex protein 4 homolog	NOC4L_HUMAN	NOC4L	7	10	7	5	5	11	0.774

DNA ligase 3	DNLI3_HUMAN	LIG3	6	4	8	6	4	6	0.773
ADP/ATP translocase 2	ADT2_HUMAN	SLC25A5	163	150	160	149	144	124	0.773
26S proteasome non-ATPase regulatory subunit 10	PSD10_HUMAN	PSMD10	6	5	6	6	6	3	0.771
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	C1TM_HUMAN	MTHFD1L	53	46	48	45	44	40	0.770
DNA-directed RNA polymerase III subunit RPC1	RPC1_HUMAN	POLR3A	16	14	8	10	11	12	0.770
Actin-related protein 3	ARP3_HUMAN	ACTR3	15	14	10	12	8	14	0.770
Bifunctional protein NCOAT	NCOAT_HUMAN	MGEA5	16	23	16	17	14	17	0.768
Eukaryotic translation initiation factor 3 subunit B	EIF3B_HUMAN	EIF3B	79	86	90	70	72	81	0.767
Peptidyl-prolyl cis-trans isomerase A	PPIA_HUMAN	PPIA	26	26	27	23	22	24	0.766
Protein phosphatase 1F	PPM1F_HUMAN	PPM1F	3	0	4	3	0	3	0.766
BRCA1-A complex subunit	BRE_HUMAN	BRE	3	2	0	0	0	3	0.766
Methylosome protein 50	MEP50_HUMAN	WDR77	222	237	197	180	182	208	0.765
60S ribosomal protein L7a	RL7A_HUMAN	RPL7A	69	61	65	58	56	56	0.765
Vesicle-fusing ATPase	NSF_HUMAN	NSF	38	41	37	34	32	35	0.765
Condensin complex subunit 2	CND2_HUMAN	NCAPH	10	9	14	11	10	8	0.765
Transmembrane emp24 domain-containing protein 2	TMED2_HUMAN	TMED2	9	8	0	0	3	11	0.763
Asparagine synthetase [glutamine-hydrolyzing]	ASNS_HUMAN	ASNS	38	39	37	33	29	37	0.763
Pumilio homolog 1	PUM1_HUMAN	PUM1	7	8	8	6	8	6	0.763
Stress-70 protein,	GRP75_HUMAN	HSPA9	46	57	47	41	39	50	0.762
T-complex protein 1 subunit	TCPB_HUMAN	CCT2	43	37	41	37	31	37	0.761
Importin-9	IPO9_HUMAN	IPO9	31	33	24	26	25	25	0.761
Vacuolar protein sorting-associated protein 26A	VP26A_HUMAN	VPS26A	14	12	12	14	11	8	0.760
Pre-mRNA branch site protein	PM14_HUMAN	SF3B14	23	19	16	16	15	19	0.760
ATP-citrate synthase	ACLY_HUMAN	ACLY	162	188	130	146	142	126	0.760
V-type proton ATPase subunit	VATH_HUMAN	ATP6V1H	7	7	7	0	8	9	0.759
ATP synthase subunit e, mitochondrial	ATP5I_HUMAN	ATP5I	5	4	7	6	5	3	0.759
BRCA2 and CDKN1A-interacting protein	BCCIP_HUMAN	BCCIP	0	0	5	0	0	4	0.759
ATP synthase subunit gamma, mitochondrial	ATPG_HUMAN	ATP5C1	43	38	36	34	33	34	0.759
Eukaryotic translation initiation factor 3 subunit L	EIF3L_HUMAN	EIF3L	56	64	56	52	47	53	0.759
Profilin-1	PROF1_HUMAN	PFN1	8	9	4	7	6	5	0.758
Isocitrate dehydrogenase [NAD] subunit alpha,	IDH3A_HUMAN	IDH3A	27	24	25	30	26	10	0.758
Phosphate carrier protein, mitochondrial	MPCP_HUMAN	SLC25A3	81	68	80	67	64	67	0.758
Unconventional myosin-Ic	MYO1C_HUMAN	MYO1C	18	20	22	19	18	15	0.758
Ornithine aminotransferase, mitochondrial	OAT_HUMAN	OAT	60	65	65	55	58	51	0.757
2-oxoisovalerate dehydrogenase subunit alpha,	ODBA_HUMAN	BCKDHA	3	2	0	2	2	0	0.757

Dehydrogenase/reductase SDR family member 7B	DRS7B_HUMAN	DHRS7B	25	23	25	22	21	20	0.756
Prohibitin	PHB_HUMAN	PHB	79	68	80	66	71	59	0.756
N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25_HUMAN	NAA25	29	30	27	24	26	24	0.756
Methylosome subunit pICln	ICLN_HUMAN	CLNS1A	37	45	31	34	31	32	0.756
Acylglycerol kinase,	AGK_HUMAN	AGK	12	12	12	10	12	9	0.756
N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	DDAH2_HUMAN	DDAH2	3	0	0	0	0	2	0.754
Stromal cell-derived factor 2-like protein 1	SDF2L_HUMAN	SDF2L1	3	0	0	0	0	2	0.754
Translation initiation factor eIF-2B subunit epsilon	EI2BE_HUMAN	EIF2B5	9	7	4	5	7	5	0.754
Basic leucine zipper and W2 domain-containing protein 2	BZW2_HUMAN	BZW2	5	4	5	3	4	5	0.753
Superkiller viralicidic activity 2-like 2	SK2L2_HUMAN	SKIV2L2	40	37	34	30	33	32	0.753
CDK5 regulatory subunit-associated protein 1	CK5P1_HUMAN	CDK5RAP1	0	3	0	0	0	2	0.753
Myosin-10	MYH10_HUMAN	MYH10	5	5	3	2	5	4	0.752
UPF0420 protein C16orf58	CP058_HUMAN	C16orf58	4	0	2	4	0	0	0.751
N-acetyltransferase 10	NAT10_HUMAN	NAT10	19	21	14	16	17	13	0.751
Probable histidine--tRNA ligase, mitochondrial	SYHM_HUMAN	HARS2	3	0	0	0	2	0	0.751
Flap endonuclease 1	FEN1_HUMAN	FEN1	7	7	7	7	7	4	0.750
Cystathionine beta-synthase	CBS_HUMAN	CBS	11	12	11	9	8	12	0.750
Ribosomal biogenesis protein LAS1L	LAS1L_HUMAN	LAS1L	10	9	8	9	7	7	0.748
Beta-galactosidase	BGAL_HUMAN	GLB1	20	21	19	16	14	21	0.748
60S ribosomal protein L13	RL13_HUMAN	RPL13	91	86	69	76	67	66	0.748
Dolichyl-phosphate beta-glucosyltransferase	ALG5_HUMAN	ALG5	6	4	3	4	4	3	0.747
Cytosolic non-specific	CNDP2_HUMAN	CNDP2	5	4	5	6	3	3	0.747
Phosphatidylglycerophosphatase and protein-tyrosine	PTPM1_HUMAN	PTPMT1	13	14	13	11	11	12	0.747
BolA-like protein 2	BOLA2_HUMAN	BOLA2	7	6	7	5	6	6	0.746
Phosphoribosyltransferase domain-containing protein 1	PRDC1_HUMAN	PRTFDC1	0	0	4	0	2	2	0.746
10 kDa heat shock protein, mitochondrial	CH10_HUMAN	HSPE1	6	7	7	6	6	5	0.744
Heat shock 70 kDa protein 4	HSP74_HUMAN	HSPA4	12	13	15	11	11	12	0.744
3-ketoacyl-CoA thiolase, mitochondrial	THIM_HUMAN	ACAA2	4	5	4	4	4	3	0.743
DNA-directed RNA polymerase II subunit RPB2	RPB2_HUMAN	POLR2B	11	12	9	9	11	7	0.743
Neurochondrin	NCDN_HUMAN	NCDN	0	3	3	4	0	0	0.742
Mitochondrial ribonuclease P protein 1	MRRP1_HUMAN	TRMT10C	44	29	39	37	33	25	0.742
Signal peptidase complex	SPCS3_HUMAN	SPCS3	12	12	6	6	9	10	0.741
Sideroflexin-1	SFXN1_HUMAN	SFXN1	42	39	33	34	34	28	0.741
4F2 cell-surface antigen heavy chain	4F2_HUMAN	SLC3A2	19	18	20	15	15	18	0.739

Ribosome biogenesis regulatory protein homolog	RRS1_HUMAN	RRS1	0	3	0	2	0	0	0.738
Kinetochore-associated protein	KNTC1_HUMAN	KNTC1	3	4	6	3	4	4	0.737
40S ribosomal protein S28	RS28_HUMAN	RPS28	6	4	0	4	4	0	0.737
39S ribosomal protein L14, mitochondrial	RM14_HUMAN	MRPL14	12	9	10	9	8	9	0.737
DNA primase large subunit	PRI2_HUMAN	PRIM2	7	6	5	4	6	5	0.736
Serum albumin	ALBU_HUMAN	ALB	6	4	10	7	0	9	0.736
Stomatin-like protein 2, mitochondrial	STML2_HUMAN	STOML2	18	16	16	17	17	8	0.735
Vacuolar protein sorting-associated protein 33B	VP33B_HUMAN	VPS33B	3	4	6	4	3	4	0.735
Nuclear pore complex protein Nup85	NUP85_HUMAN	NUP85	17	14	11	13	11	11	0.734
Nuclear pore complex protein Nup133	NU133_HUMAN	NUP133	32	37	28	30	26	25	0.734
Isoleucine--tRNA ligase, cytoplasmic	SYIC_HUMAN	IARS	67	76	65	64	60	50	0.734
Cyclin-dependent kinase 1	CDK1_HUMAN	CDK1	58	55	58	46	52	45	0.734
Eukaryotic translation initiation factor 3 subunit D	EIF3D_HUMAN	EIF3D	33	32	23	22	22	29	0.733
Importin-5	IPO5_HUMAN	IPO5	80	90	92	71	71	77	0.733
Structural maintenance of chromosomes protein 3	SMC3_HUMAN	SMC3	72	76	61	60	59	55	0.732
COP9 signalosome complex subunit 7a	CSN7A_HUMAN	COPS7A	6	2	4	3	4	3	0.732
GPI transamidase component PIG-T	PIGT_HUMAN	PIGT	7	6	4	3	5	6	0.731
RRP12-like protein	RRP12_HUMAN	RRP12	6	5	7	4	4	7	0.731
DDB1- and CUL4-associated factor 7	DCAF7_HUMAN	DCAF7	8	4	7	8	7	0	0.730
Erlin-1	ERLN1_HUMAN	ERLIN1	17	14	17	14	16	10	0.729
AP-1 complex subunit sigma-2	AP1S2_HUMAN	AP1S2	12	11	5	8	8	7	0.729
Nuclear pore complex protein Nup107	NU107_HUMAN	NUP107	18	18	17	16	14	14	0.728
ELMO domain-containing	ELMD2_HUMAN	ELMOD2	10	10	9	7	9	8	0.728
Enhancer of mRNA-decapping protein 3	EDC3_HUMAN	EDC3	6	8	10	6	5	9	0.728
WD repeat-containing protein	WDR1_HUMAN	WDR1	20	20	18	16	12	20	0.728
Helicase-like transcription	HLTF_HUMAN	HLTF	4	3	5	3	4	3	0.727
MOB kinase activator 2	MOB2_HUMAN	MOB2	20	18	19	14	16	17	0.725
Short/branched chain specific acyl-CoA dehydrogenase,	ACDSB_HUMAN	ACADSB	17	20	22	20	18	11	0.724
Eukaryotic translation initiation factor 3 subunit C	EIF3C_HUMAN	EIF3C	22	21	27	22	18	18	0.723
Septin-9	SEPT9_HUMAN	SEPT9	15	16	14	12	11	14	0.723
DnaJ homolog subfamily A member 3, mitochondrial	DNJA3_HUMAN	DNAJA3	14	17	14	13	12	12	0.722
CCR4-NOT transcription complex subunit 2	CNOT2_HUMAN	CNOT2	4	4	3	3	2	4	0.722
UDP-glucose 6-dehydrogenase	UGDH_HUMAN	UGDH	6	6	4	4	3	6	0.719

[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	PDK1_HUMAN	PDK1	5	7	4	4	5	4	0.718
ATP-binding cassette sub-family D member 3	ABCD3_HUMAN	ABCD3	14	11	12	10	7	13	0.713
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase	DAD1_HUMAN	DAD1	7	10	10	8	9	5	0.712
Sister chromatid cohesion protein PDS5 homolog A	PDS5A_HUMAN	PDS5A	19	28	22	22	19	15	0.711
Tubulin beta-6 chain	TBB6_HUMAN	TUBB6	8	11	7	9	6	6	0.710
Replication factor C subunit 4	RFC4_HUMAN	RFC4	18	17	18	17	17	9	0.710
Replication factor C subunit 3	RFC3_HUMAN	RFC3	23	20	21	24	22	6	0.709
Cyclin-dependent kinase 11B	CD11B_HUMAN	CDK11B	9	5	7	7	4	6	0.709
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMCA5_HUMAN	SMARCA5	40	50	33	35	35	29	0.709
ER membrane protein complex subunit 7	EMC7_HUMAN	EMC7	6	2	0	3	2	2	0.707
Lactoylglutathione lyase	LGUL_HUMAN	GLO1	11	11	8	7	9	8	0.706
Pyruvate dehydrogenase protein X component,	ODPX_HUMAN	PDHX	6	5	4	4	3	5	0.706
ATP-dependent RNA helicase DDX3X	DDX3X_HUMAN	DDX3X	45	41	42	37	32	34	0.706
Lon protease homolog, mitochondrial	LONM_HUMAN	LONP1	13	17	16	12	13	12	0.705
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CN37_HUMAN	CNP	12	8	5	10	7	3	0.704
Uncharacterized protein	CG050_HUMAN	C7orf50	6	6	0	0	4	5	0.704
26S proteasome non-ATPase regulatory subunit 7	PSMD7_HUMAN	PSMD7	2	0	0	0	0	0	0.702
ATPase WRNIP1	WRIP1_HUMAN	WRNIP1	2	0	0	0	0	0	0.702
Gamma-glutamyl hydrolase	GGH_HUMAN	GGH	2	0	0	0	0	0	0.702
Girdin	GRDN_HUMAN	CCDC88A	2	0	0	0	0	0	0.702
Glycosylphosphatidylinositol anchor attachment 1 protein	GPAA1_HUMAN	GPAA1	2	0	0	0	0	0	0.702
Hydroxyacylglutathione hydrolase, mitochondrial	GLO2_HUMAN	HAGH	2	0	0	0	0	0	0.702
NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	NDUS4_HUMAN	NDUFS4	2	0	0	0	0	0	0.702
Polycomb protein EED	EED_HUMAN	EED	2	0	0	0	0	0	0.702
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing	SMRCD_HUMAN	SMARCAD1	2	0	0	0	0	0	0.702
TGF-beta-activated kinase 1 and MAP3K7-binding protein	TAB2_HUMAN	TAB2	2	0	0	0	0	0	0.702
THO complex subunit 1	THOC1_HUMAN	THOC1	2	0	0	0	0	0	0.702
UPF0428 protein CXorf56	CX056_HUMAN	CXorf56	2	0	0	0	0	0	0.702
Dynactin subunit 1	DCTN1_HUMAN	DCTN1	60	66	53	51	49	43	0.702

Cleavage and polyadenylation specificity factor subunit 3	CPSF3_HUMAN	CPSF3	0	2	0	0	0	0	0.701
Diablo homolog,	DBLOH_HUMAN	DIABLO	0	2	0	0	0	0	0.701
Dimethylaniline monooxygenase [N-oxide-	FMO1_HUMAN	FMO1	0	2	0	0	0	0	0.701
ER membrane protein complex subunit 2	EMC2_HUMAN	EMC2	0	2	0	0	0	0	0.701
Histidine triad nucleotide-binding protein 1	HINT1_HUMAN	HINT1	0	2	0	0	0	0	0.701
Inositol 1,4,5-trisphosphate receptor type 2	ITPR2_HUMAN	ITPR2	0	2	0	0	0	0	0.701
Malignant T-cell-amplified sequence 1	MCTS1_HUMAN	MCTS1	0	2	0	0	0	0	0.701
Mitochondrial-processing peptidase subunit beta	MPPB_HUMAN	PMPCB	0	2	0	0	0	0	0.701
Nucleoporin NUP53	NUP53_HUMAN	NUP35	0	2	0	0	0	0	0.701
Periodic tryptophan protein 1 homolog	PWP1_HUMAN	PWP1	0	2	0	0	0	0	0.701
PHD finger-like domain-containing protein 5A	PHF5A_HUMAN	PHF5A	0	2	0	0	0	0	0.701
Phospholipase A-2-activating protein	PLAP_HUMAN	PLAA	0	2	0	0	0	0	0.701
Phosphoribosylformylglycinamidine synthase	PUR4_HUMAN	PFAS	0	2	0	0	0	0	0.701
Protein transport protein	SC23B_HUMAN	SEC23B	0	2	0	0	0	0	0.701
Stress-induced-phosphoprotein	STIP1_HUMAN	STIP1	0	2	0	0	0	0	0.701
Filamin-A	FLNA_HUMAN	FLNA	28	35	32	27	27	22	0.701
Lysine--tRNA ligase	SYK_HUMAN	KARS	11	15	14	11	11	10	0.701
RNA-binding protein 28	RBM28_HUMAN	RBM28	13	13	14	13	10	9	0.699
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX_HUMAN	CLPX	19	20	20	17	13	17	0.698
Protein CIP2A	CIP2A_HUMAN	KIAA1524	7	6	7	8	4	4	0.697
6-phosphofructokinase, muscle type	K6PF_HUMAN	PFKM	15	14	14	9	10	15	0.696
Cell differentiation protein RCD1 homolog	RCD1_HUMAN	RQCD1	10	9	10	7	8	8	0.696
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA_HUMAN	ETFA	45	35	40	32	32	31	0.695
Pyrroline-5-carboxylate reductase 3	P5CR3_HUMAN	PYCRL	18	13	17	12	16	10	0.694
Nucleolar protein 9	NOP9_HUMAN	NOP9	6	4	4	4	3	4	0.692
RNA-binding protein FUS	FUS_HUMAN	FUS	7	7	4	3	4	7	0.692
Probable arginine--tRNA ligase, mitochondrial	SYRM_HUMAN	RARS2	11	11	10	7	7	11	0.688
S-adenosylmethionine synthase isoform type-2	METK2_HUMAN	MAT2A	17	15	14	13	13	10	0.687
Rac GTPase-activating protein	RGAP1_HUMAN	RACGAP1	4	3	0	0	0	4	0.687
28S ribosomal protein S5, mitochondrial	RT05_HUMAN	MRPS5	18	16	17	17	15	8	0.686
Cell division cycle protein 23 homolog	CDC23_HUMAN	CDC23	13	15	7	8	6	13	0.685
Cytoplasmic dynein 2 heavy	DYHC2_HUMAN	DYNC2H1	5	7	6	4	5	5	0.684

Serine-threonine kinase receptor-associated protein	STRAP_HUMAN	STRAP	14	11	11	10	13	5	0.683
Nuclear RNA export factor 1	NXF1_HUMAN	NXF1	15	16	13	10	9	15	0.681
Mitochondrial import receptor subunit TOM40 homolog	TOM40_HUMAN	TOMM40	18	22	24	20	20	10	0.681
Uncharacterized protein C2orf47, mitochondrial	CB047_HUMAN	C2orf47	9	12	10	8	5	11	0.681
Tubulin-specific chaperone D	TBCD_HUMAN	TBCD	19	20	19	16	17	12	0.680
Centromere/kinetochore protein zw10 homolog	ZW10_HUMAN	ZW10	9	8	10	8	7	6	0.680
AP-3 complex subunit sigma-1	AP3S1_HUMAN	AP3S1	11	10	10	9	6	9	0.679
Ras-related protein R-Ras2	RRAS2_HUMAN	RRAS2	4	6	3	4	2	4	0.679
Proteasome subunit alpha type-	PSA5_HUMAN	PSMA5	12	12	11	8	9	10	0.679
Vimentin	VIME_HUMAN	VIM	263	224	250	194	186	190	0.678
39S ribosomal protein L10, mitochondrial	RM10_HUMAN	MRPL10	5	3	5	0	4	5	0.678
Mitochondrial carrier homolog	MTCH2_HUMAN	MTCH2	0	4	4	4	0	2	0.678
ATPase family AAA domain-containing protein 3A	ATD3A_HUMAN	ATAD3A	71	76	60	48	49	62	0.677
V-type proton ATPase subunit	VA0D1_HUMAN	ATP6V0D1	6	6	6	6	7	0	0.677
Voltage-dependent anion-selective channel protein 2	VDAC2_HUMAN	VDAC2	43	42	41	33	33	31	0.676
Casein kinase II subunit alpha'	CSK22_HUMAN	CSNK2A2	3	3	3	3	3	0	0.676
CDGSH iron-sulfur domain-containing protein 1	CISD1_HUMAN	CISD1	0	0	2	0	0	0	0.675
Membrane magnesium transporter 1	MMGT1_HUMAN	MMGT1	0	0	2	0	0	0	0.675
Phosphorylase b kinase regulatory subunit beta	KPBB_HUMAN	PHKB	0	0	2	0	0	0	0.675
Polynucleotide 5'-hydroxyl-kinase NOL9	NOL9_HUMAN	NOL9	0	0	2	0	0	0	0.675
Serpin B9	SPB9_HUMAN	SERPINB9	0	0	2	0	0	0	0.675
Syntaxin-binding protein 1	STXB1_HUMAN	STXBP1	0	0	2	0	0	0	0.675
Tropomyosin alpha-3 chain	TPM3_HUMAN	TPM3	0	0	2	0	0	0	0.675
Ubiquitin carboxyl-terminal hydrolase 7	UBP7_HUMAN	USP7	0	0	2	0	0	0	0.675
UPF0668 protein C10orf76	CJ076_HUMAN	C10orf76	0	0	2	0	0	0	0.675
Xanthine	XDH_HUMAN	XDH	0	0	2	0	0	0	0.675
Fatty acid synthase	FAS_HUMAN	FASN	44	42	49	36	34	34	0.674
ER membrane protein complex subunit 3	EMC3_HUMAN	EMC3	8	8	5	7	4	5	0.671
Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2_HUMAN	NUBP2	7	4	6	4	4	5	0.671
RNA 3'-terminal phosphate cyclase-like protein	RCL1_HUMAN	RCL1	0	4	4	5	0	0	0.670
Iron-sulfur protein NUBPL	NUBPL_HUMAN	NUBPL	7	4	6	5	4	4	0.669
Mannose-1-phosphate guanyltransferase beta	GMPPB_HUMAN	GMPPB	6	7	9	8	8	0	0.668
Programmed cell death 6-interacting protein	PDC6I_HUMAN	PDCD6IP	25	23	23	18	18	18	0.668
Tubulin alpha-1C chain	TBA1C_HUMAN	TUBA1C	9	11	9	7	7	8	0.667
Ancient ubiquitous protein 1	AUP1_HUMAN	AUP1	4	5	4	6	3	0	0.667

Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9_HUMAN	ACOT9	11	9	4	5	9	4	0.667
Mitochondrial import inner membrane translocase subunit TIM50	TIM50_HUMAN	TIMM50	24	23	19	21	20	9	0.664
ATPase family AAA domain-containing protein 3B	ATD3B_HUMAN	ATAD3B	13	16	11	9	9	12	0.662
39S ribosomal protein L27, mitochondrial	RM27_HUMAN	MRPL27	5	6	5	4	3	5	0.660
Chitobiosyldiphosphodolichol beta-mannosyltransferase	ALG1_HUMAN	ALG1	4	4	4	3	3	3	0.658
Protein NipSnap homolog 2	NIPS2_HUMAN	GBAS	6	8	6	6	5	4	0.658
Metaxin-2	MTX2_HUMAN	MTX2	8	7	5	8	4	3	0.658
ATP-binding cassette sub-family F member 3	ABCF3_HUMAN	ABCF3	4	4	4	3	0	5	0.658
V-type proton ATPase 116 kDa subunit a isoform 1	VPP1_HUMAN	ATP6V0A1	0	3	4	0	4	0	0.657
ER membrane protein complex subunit 6	EMC6_HUMAN	EMC6	5	4	3	4	4	0	0.656
Cell division cycle protein 16 homolog	CDC16_HUMAN	CDC16	0	3	4	3	2	0	0.651
Guanine nucleotide-binding protein G(k) subunit alpha	GNAI3_HUMAN	GNAI3	3	3	0	0	3	0	0.650
Transaldolase	TALDO_HUMAN	TALDO1	3	3	0	0	3	0	0.650
28S ribosomal protein S2, mitochondrial	RT02_HUMAN	MRPS2	14	11	14	12	7	10	0.650
cAMP-dependent protein kinase catalytic subunit beta	KAPCB_HUMAN	PRKACB	9	7	8	11	6	0	0.650
Splicing factor 3B subunit 3	SF3B3_HUMAN	SF3B3	38	53	39	32	32	32	0.650
Dolichol-phosphate mannosyltransferase subunit 1	DPM1_HUMAN	DPM1	23	19	19	16	13	16	0.648
Multifunctional protein ADE2	PUR6_HUMAN	PAICS	17	12	13	13	11	7	0.647
Probable C-mannosyltransferase DPY19L1	D19L1_HUMAN	DPY19L1	12	17	17	12	13	9	0.646
Adenylate kinase 2,	KAD2_HUMAN	AK2	4	4	3	0	3	4	0.646
NADH-ubiquinone oxidoreductase 75 kDa	NDUS1_HUMAN	NDUFS1	32	30	28	20	19	27	0.646
7-dehydrocholesterol reductase	DHCR7_HUMAN	DHCR7	24	23	25	18	18	17	0.645
Protein MON2 homolog	MON2_HUMAN	MON2	4	4	3	0	4	3	0.645
Enoyl-CoA hydratase, mitochondrial	ECHM_HUMAN	ECHS1	22	23	23	17	17	16	0.645
14-3-3 protein epsilon	1433E_HUMAN	YWHAE	15	12	15	13	10	8	0.645
Mediator of RNA polymerase II transcription subunit 23	MED23_HUMAN	MED23	9	11	6	8	5	6	0.644
Regulatory-associated protein of mTOR	RPTOR_HUMAN	RPTOR	5	7	7	5	5	4	0.644
U4/U6.U5 tri-snRNP-associated protein 1	SNUT1_HUMAN	SART1	6	6	11	4	7	6	0.644
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCKGM_HUMAN	PCK2	47	52	46	31	29	46	0.644
Putative methyltransferase	NSUN5_HUMAN	NSUN5	0	5	5	0	0	6	0.643

5'-AMP-activated protein kinase subunit gamma-1	AAKG1_HUMAN	PRKAG1	8	9	10	9	10	0	0.643
Vacuolar protein sorting-associated protein 29	VPS29_HUMAN	VPS29	6	4	5	4	4	3	0.643
Farnesyl pyrophosphate	FPPS_HUMAN	FDPS	23	21	20	20	20	7	0.643
Condensin complex subunit 3	CND3_HUMAN	NCAPG	23	24	20	19	14	16	0.642
DnaJ homolog subfamily B member 11	DJB11_HUMAN	DNAJB11	6	5	4	5	5	0	0.641
Peroxiredoxin-2	PRDX2_HUMAN	PRDX2	8	11	10	6	6	9	0.636
ATP-binding cassette sub-family B member 7,	ABCB7_HUMAN	ABCB7	6	8	8	6	4	6	0.636
Inactive hydroxysteroid dehydrogenase-like protein 1	HSDL1_HUMAN	HSDL1	7	8	7	7	7	2	0.636
Alkyldihydroxyacetonephosphate synthase, peroxisomal	ADAS_HUMAN	AGPS	7	10	8	4	5	9	0.635
26S proteasome non-ATPase regulatory subunit 8	PSMD8_HUMAN	PSMD8	11	12	9	6	9	8	0.635
Actin-related protein 2/3 complex subunit 2	ARPC2_HUMAN	ARPC2	4	3	4	4	2	2	0.633
Rab-like protein 2A	RBL2A_HUMAN	RABL2A	0	3	3	0	0	3	0.633
Elongation factor 1-delta	EF1D_HUMAN	EEF1D	8	4	6	5	4	4	0.633
Serine/threonine-protein kinase 38-like	ST38L_HUMAN	STK38L	51	54	57	41	33	43	0.633
Tetratricopeptide repeat protein 19, mitochondrial	TTC19_HUMAN	TTC19	3	4	4	4	0	3	0.632
Protein arginine N-methyltransferase 5	ANM5_HUMAN	PRMT5	369	402	379	266	259	300	0.630
U4/U6 small nuclear ribonucleoprotein Prp31	PRP31_HUMAN	PRPF31	82	80	86	57	53	68	0.630
Cytochrome b-c1 complex subunit 9	QCR9_HUMAN	UQCR10	5	5	4	3	0	6	0.629
Heat shock protein 105 kDa	HS105_HUMAN	HSPH1	31	29	44	23	25	27	0.629
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1_HUMAN	AHSA1	16	13	14	15	11	5	0.629
Striatin-interacting protein 1	STRP1_HUMAN	STRIP1	6	8	3	3	3	6	0.629
Splicing factor 3B subunit 1	SF3B1_HUMAN	SF3B1	72	89	63	58	59	43	0.628
Lethal(2) giant larvae protein homolog 1	L2GL1_HUMAN	LLGL1	5	6	3	5	0	4	0.628
ATP synthase mitochondrial F1 complex assembly factor 2	ATPF2_HUMAN	ATPAF2	3	0	3	2	2	0	0.627
Neutral alpha-glucosidase AB	GANAB_HUMAN	GANAB	0	0	5	2	0	2	0.626
Dual specificity mitogen-activated protein kinase kinase	MP2K3_HUMAN	MAP2K3	19	17	13	18	16	0	0.624
Mannose-1-phosphate guanyltransferase alpha	GMPPA_HUMAN	GMPPA	10	8	10	8	9	3	0.624
Proteasome subunit alpha type-	PSA4_HUMAN	PSMA4	29	23	35	21	23	18	0.622
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUS8_HUMAN	NDUFS8	11	13	10	8	6	10	0.622
Protein SET	SET_HUMAN	SET	7	7	7	7	7	0	0.621
V-type proton ATPase catalytic subunit A	VATA_HUMAN	ATP6V1A	17	12	11	6	10	12	0.620
Glutathione S-transferase	GSTK1_HUMAN	GSTK1	5	4	5	5	4	0	0.619

Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	ODPA_HUMAN	PDHA1	44	33	31	28	26	22	0.619
Phosphoribosyl pyrophosphate synthase-associated protein 2	KPRB_HUMAN	PRPSAP2	36	29	31	31	30	7	0.619
Leucine--tRNA ligase,	SYLC_HUMAN	LARS	48	47	40	34	33	28	0.619
Unconventional myosin-Id	MYO1D_HUMAN	MYO1D	12	8	7	9	4	6	0.618
Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	ODB2_HUMAN	DBT	4	6	3	0	4	4	0.617
Cytochrome b-c1 complex subunit 8	QCR8_HUMAN	UQCRQ	10	11	9	7	7	7	0.616
39S ribosomal protein L38, mitochondrial	RM38_HUMAN	MRPL38	8	10	9	8	10	0	0.613
Nuclear pore complex protein Nup98-Nup96	NUP98_HUMAN	NUP98	8	10	12	6	6	9	0.613
Ig kappa chain V-II region RPMI 6410	KV206_HUMAN	IGKV2-30	434	420	334	317	292	216	0.610
Ubiquitin-like modifier-activating enzyme 1	UBA1_HUMAN	UBA1	7	8	8	5	5	6	0.610
ATP-dependent zinc metalloprotease YME1L1	YMEL1_HUMAN	YME1L1	11	12	9	3	7	12	0.610
Eukaryotic translation initiation factor 3 subunit K	EIF3K_HUMAN	EIF3K	11	10	12	9	7	7	0.609
DNA polymerase delta subunit	DPOD2_HUMAN	POLD2	4	3	3	4	0	2	0.609
Kinesin-like protein KIF23	KIF23_HUMAN	KIF23	5	3	0	2	2	2	0.608
Mitochondrial Rho GTPase 2	MIRO2_HUMAN	RHOT2	9	9	8	7	5	6	0.608
Isocitrate dehydrogenase [NAD] subunit gamma,	IDH3G_HUMAN	IDH3G	9	7	7	8	7	0	0.606
26S proteasome non-ATPase regulatory subunit 13	PSD13_HUMAN	PSMD13	23	15	21	19	17	5	0.605
28S ribosomal protein S15, mitochondrial	RT15_HUMAN	MRPS15	14	8	10	7	8	7	0.605
Malate dehydrogenase, mitochondrial	MDHM_HUMAN	MDH2	12	13	10	8	9	7	0.604
Uncharacterized protein	CK084_HUMAN	C11orf84	6	7	6	4	4	5	0.602
Gem-associated protein 4	GEMI4_HUMAN	GEMIN4	4	9	6	5	3	5	0.600
Fermitin family homolog 2	FERM2_HUMAN	FERMT2	5	3	0	3	2	0	0.600
General transcription factor 3C polypeptide 3	TF3C3_HUMAN	GTF3C3	6	7	13	6	7	5	0.600
28S ribosomal protein S27, mitochondrial	RT27_HUMAN	MRPS27	28	23	21	15	17	17	0.600
Aspartate aminotransferase, mitochondrial	AATM_HUMAN	GOT2	13	12	13	9	13	4	0.599
FAS-associated factor 2	FAF2_HUMAN	FAF2	17	14	16	9	11	12	0.598
6-pyruvoyl tetrahydrobiopterin synthase	PTPS_HUMAN	PTS	8	4	7	5	4	4	0.598
Dihydrofolate reductase	DYR_HUMAN	DHFR	12	12	10	6	7	10	0.597
Cysteine desulfurase,	NFS1_HUMAN	NFS1	9	8	5	8	6	0	0.596
28S ribosomal protein S31, mitochondrial	RT31_HUMAN	MRPS31	13	11	14	12	9	5	0.596
Protein RCC2	RCC2_HUMAN	RCC2	3	0	2	0	0	2	0.595

Peroxiredoxin-6	PRDX6_HUMAN	PRDX6	22	23	26	14	19	15	0.592
DNA polymerase delta catalytic subunit	DPOD1_HUMAN	POLD1	42	46	36	25	28	30	0.590
Mitochondrial inner membrane protein OXA1L	OXA1L_HUMAN	OXA1L	13	8	10	10	10	0	0.590
39S ribosomal protein L2, mitochondrial	RM02_HUMAN	MRPL2	4	4	4	0	3	4	0.590
Protein YIF1A	YIF1A_HUMAN	YIF1A	4	4	4	0	3	4	0.590
Succinyl-CoA ligase [GDP-forming] subunit beta,	SUCB2_HUMAN	SUCLG2	40	31	32	24	25	20	0.588
Alpha-internexin	AINX_HUMAN	INA	31	31	25	17	17	24	0.588
Valine--tRNA ligase	SYVC_HUMAN	VARS	21	26	16	15	13	14	0.588
Exosome complex component RRP41	EXOS4_HUMAN	EXOSC4	6	7	5	4	4	4	0.587
SRA stem-loop-interacting RNA-binding protein,	SLIRP_HUMAN	SLIRP	5	6	4	4	3	3	0.587
Glucose-6-phosphate	G6PI_HUMAN	GPI	7	3	5	3	3	4	0.586
DNA repair protein RAD50	RAD50_HUMAN	RAD50	38	45	37	27	26	27	0.586
Filaggrin-2	FILA2_HUMAN	FLG2	24	14	12	9	6	18	0.586
Myosin-9	MYH9_HUMAN	MYH9	7	5	6	4	4	4	0.585
Cat eye syndrome critical region protein 5	CECR5_HUMAN	CECR5	24	24	25	23	22	4	0.585
EH domain-containing protein	EHD4_HUMAN	EHD4	7	7	7	5	5	4	0.584
26S protease regulatory subunit 10B	PRS10_HUMAN	PSMC6	41	37	46	33	29	21	0.584
Exocyst complex component 8	EXOC8_HUMAN	EXOC8	2	2	2	0	0	2	0.583
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMH1_HUMAN	SAMHD1	24	29	20	10	19	19	0.582
L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HDH_HUMAN	L2HGDH	17	16	8	12	10	5	0.581
S1 RNA-binding domain-containing protein 1	SRBD1_HUMAN	SRBD1	0	0	4	2	0	0	0.581
40S ribosomal protein SA	RSSA_HUMAN	RPSA	22	22	24	14	17	14	0.580
Glutaminyl-peptide cyclotransferase-like protein	QPCTL_HUMAN	QPCTL	24	27	26	20	21	10	0.579
Putative oxidoreductase	GLYR1_HUMAN	GLYR1	20	18	17	11	12	13	0.576
E3 SUMO-protein ligase	RBP2_HUMAN	RANBP2	21	23	29	14	17	17	0.575
Cartilage-associated protein	CRTAP_HUMAN	CRTAP	9	7	7	4	6	5	0.575
Proteasome subunit beta type-5	PSB5_HUMAN	PSMB5	8	7	5	4	5	4	0.574
Ran GTPase-activating protein	RAGP1_HUMAN	RANGAP1	47	38	32	23	19	34	0.574
E3 ubiquitin-protein ligase	RO52_HUMAN	TRIM21	29	29	28	23	20	13	0.570
Ethylmalonyl-CoA	ECHD1_HUMAN	ECHDC1	23	19	24	15	17	11	0.570
Mitotic checkpoint protein	BUB3_HUMAN	BUB3	6	10	7	7	7	0	0.568
Inosine-5'-monophosphate dehydrogenase 2	IMDH2_HUMAN	IMPDH2	8	4	8	5	3	5	0.567
Fructose-bisphosphate aldolase	ALDOA_HUMAN	ALDOA	13	13	14	12	9	5	0.567
Macrophage migration inhibitory factor	MIF_HUMAN	MIF	6	8	6	6	6	0	0.567
Ras-related protein Rab-32	RAB32_HUMAN	RAB32	6	5	6	4	4	3	0.566
Dihydrolipoyl dehydrogenase, mitochondrial	DLDH_HUMAN	DLD	47	39	46	26	29	30	0.565
Cellular tumor antigen p53	P53_HUMAN	TP53	9	11	11	8	6	6	0.564

UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	OGT1_HUMAN	OGT	6	3	5	3	2	4	0.564
Actin-related protein 2	ARP2_HUMAN	ACTR2	13	15	14	11	12	4	0.562
Peroxiredoxin-1	PRDX1_HUMAN	PRDX1	33	33	34	22	21	21	0.561
Probable proline--tRNA ligase, mitochondrial	SYPM_HUMAN	PARS2	6	4	4	4	4	0	0.561
Heat shock protein 75 kDa, mitochondrial	TRAP1_HUMAN	TRAP1	28	29	29	20	15	20	0.561
Ras-related protein Rab-5C	RAB5C_HUMAN	RAB5C	0	6	4	3	0	3	0.559
Elongation factor 1-beta	EF1B_HUMAN	EEF1B2	5	4	5	4	4	0	0.558
CTP synthase 2	PYRG2_HUMAN	CTPS2	11	8	8	4	4	9	0.557
39S ribosomal protein L34, mitochondrial	RM34_HUMAN	MRPL34	3	0	0	0	0	0	0.555
60S ribosomal export protein NMD3	NMD3_HUMAN	NMD3	3	0	0	0	0	0	0.555
ADP-ribosylation factor-like protein 10	ARL10_HUMAN	ARL10	3	0	0	0	0	0	0.555
Amidophosphoribosyltransfera	PUR1_HUMAN	PPAT	3	0	0	0	0	0	0.555
Aminopeptidase B	AMPB_HUMAN	RNPEP	3	0	0	0	0	0	0.555
Cytochrome P450 20A1	CP20A_HUMAN	CYP20A1	3	0	0	0	0	0	0.555
Histone H1.5	H15_HUMAN	HIST1H1B	3	0	0	0	0	0	0.555
Methionine synthase	METH_HUMAN	MTR	3	0	0	0	0	0	0.555
N-acetylserotonin O-methyltransferase-like protein	ASML_HUMAN	ASMTL	3	0	0	0	0	0	0.555
Peptidyl-prolyl cis-trans isomerase FKBP1A	FKB1A_HUMAN	FKBP1A	3	0	0	0	0	0	0.555
Peroxisomal membrane protein	PXMP2_HUMAN	PXMP2	3	0	0	0	0	0	0.555
Proteasome subunit alpha type-	PSA6_HUMAN	PSMA6	3	0	0	0	0	0	0.555
Protein FAM127A	F127A_HUMAN	FAM127A	3	0	0	0	0	0	0.555
Protein TFG	TFG_HUMAN	TFG	3	0	0	0	0	0	0.555
Ras-related protein Rab-39B	RB39B_HUMAN	RAB39B	3	0	0	0	0	0	0.555
Spindle and kinetochore-associated protein 1	SKA1_HUMAN	SKA1	3	0	0	0	0	0	0.555
Thyroid transcription factor 1-associated protein 26	TAP26_HUMAN	CCDC59	3	0	0	0	0	0	0.555
Vesicle-associated membrane protein-associated protein B/C	VAPB_HUMAN	VAPB	3	0	0	0	0	0	0.555
Zinc finger CCCH domain-containing protein 8	ZC3H8_HUMAN	ZC3H8	3	0	0	0	0	0	0.555
Fumarylacetoacetate hydrolase domain-containing protein 2A	FAH2A_HUMAN	FAHD2A	8	5	6	4	5	3	0.555
ADP-ribosylation factor-like protein 3	ARL3_HUMAN	ARL3	0	3	0	0	0	0	0.554
ADP-ribosylation factor-like protein 8B	ARL8B_HUMAN	ARL8B	0	3	0	0	0	0	0.554
Coordinator of PRMT5 and differentiation stimulator	COPRS_HUMAN	COPRS	0	3	0	0	0	0	0.554
DNA-directed RNA polymerase I subunit RPA2	RPA2_HUMAN	POLR1B	0	3	0	0	0	0	0.554
MAU2 chromatid cohesion factor homolog	SCC4_HUMAN	MAU2	0	3	0	0	0	0	0.554

Medium-chain specific acyl-CoA dehydrogenase,	ACADM_HUMAN	ACADM	0	3	0	0	0	0	0.554
Proteasome subunit beta type-2	PSB2_HUMAN	PSMB2	0	3	0	0	0	0	0.554
Ras-associating and dilute domain-containing protein	RADIL_HUMAN	RADIL	0	3	0	0	0	0	0.554
Ras-related protein Rap-2b	RAP2B_HUMAN	RAP2B	0	3	0	0	0	0	0.554
Torsin-1A-interacting protein 2	TOIP2_HUMAN	TOR1AIP2	0	3	0	0	0	0	0.554
Serine/threonine-protein kinase	STK38_HUMAN	STK38	31	26	35	16	18	24	0.553
Serine/threonine-protein kinase RIO1	RIOK1_HUMAN	RIOK1	122	138	128	80	76	88	0.552
Malonyl-CoA-acyl carrier protein transacylase,	FABD_HUMAN	MCAT	5	2	4	3	3	0	0.552
Programmed cell death protein	PDC10_HUMAN	PDCD10	9	9	6	5	7	3	0.551
Midasin	MDN1_HUMAN	MDN1	8	8	14	6	6	7	0.551
Sec1 family domain-containing protein 1	SCFD1_HUMAN	SCFD1	14	15	11	9	7	9	0.551
Chromosome transmission fidelity protein 18 homolog	CTF18_HUMAN	CHTF18	5	7	4	4	3	3	0.551
Kynurenine--oxoglutarate transaminase 3	KAT3_HUMAN	CCBL2	7	5	0	5	2	0	0.550
Exportin-4	XPO4_HUMAN	XPO4	3	6	0	0	2	3	0.549
Elongator complex protein 3	ELP3_HUMAN	ELP3	6	3	0	0	0	4	0.548
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	ODP2_HUMAN	DLAT	14	11	15	10	6	9	0.546
NADH dehydrogenase [ubiquinone] 1 subunit C2	NDUC2_HUMAN	NDUFC2	4	0	3	3	0	0	0.543
C-terminal-binding protein 2	CTBP2_HUMAN	CTBP2	10	8	11	6	6	6	0.543
PAX3- and PAX7-binding protein 1	PAXB1_HUMAN	PAXBP1	2	2	0	0	0	0	0.541
ATP-binding cassette sub-family B member 10,	ABCBA_HUMAN	ABCB10	13	13	10	5	8	9	0.541
mRNA export factor	RAE1L_HUMAN	RAE1	10	8	8	6	6	4	0.540
Nuclear pore complex protein Nup160	NU160_HUMAN	NUP160	18	26	21	15	12	13	0.540
Biliverdin reductase A	BIEA_HUMAN	BLVRA	5	4	0	3	2	0	0.539
RING finger protein 219	RN219_HUMAN	RNF219	6	3	7	5	4	0	0.539
ADP-ribosylation factor-like protein 6	ARL6_HUMAN	ARL6	9	8	3	2	3	7	0.538
14-3-3 protein theta	1433T_HUMAN	YWHAQ	8	8	10	7	4	5	0.536
Spindlin-1	SPIN1_HUMAN	SPIN1	25	19	23	15	13	13	0.536
Transmembrane protein 33	TMM33_HUMAN	TMEM33	15	15	16	8	10	10	0.534
Probable tRNA pseudouridine synthase 1	TRUB1_HUMAN	TRUB1	5	3	2	0	3	2	0.534
Exportin-5	XPO5_HUMAN	XPO5	45	48	47	31	31	23	0.532
Microtubule-associated protein	MAP1B_HUMAN	MAP1B	4	4	5	4	3	0	0.532
Unconventional myosin-Ib	MYO1B_HUMAN	MYO1B	17	21	12	9	9	12	0.531
Butyrophilin subfamily 1 member A1	BT1A1_HUMAN	BTN1A1	0	0	3	0	0	0	0.529
Centlein	CNTLN_HUMAN	CNTLN	0	0	3	0	0	0	0.529
COMM domain-containing protein 2	COMD2_HUMAN	COMMD2	0	0	3	0	0	0	0.529

Complement C3	CO3_HUMAN	C3	0	0	3	0	0	0	0.529
Dihydroxyacetone phosphate acyltransferase	GNPAT_HUMAN	GNPAT	0	0	3	0	0	0	0.529
Exocyst complex component 6	EXOC6_HUMAN	EXOC6	0	0	3	0	0	0	0.529
F-actin-capping protein subunit beta	CAPZB_HUMAN	CAPZB	0	0	3	0	0	0	0.529
Glutathione S-transferase Mu 3	GSTM3_HUMAN	GSTM3	0	0	3	0	0	0	0.529
HLA class I histocompatibility antigen, Cw-4 alpha chain	1C04_HUMAN	HLA-C	0	0	3	0	0	0	0.529
Isovaleryl-CoA dehydrogenase, mitochondrial	IVD_HUMAN	IVD	0	0	3	0	0	0	0.529
Mediator of RNA polymerase II transcription subunit 24	MED24_HUMAN	MED24	0	0	3	0	0	0	0.529
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	NDUA2_HUMAN	NDUFA2	0	0	3	0	0	0	0.529
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	NDUA7_HUMAN	NDUFA7	0	0	3	0	0	0	0.529
Neurofilament light	NFL_HUMAN	NEFL	0	0	3	0	0	0	0.529
Peflin	PEF1_HUMAN	PEF1	0	0	3	0	0	0	0.529
Proline-, glutamic acid- and leucine-rich protein 1	PELP1_HUMAN	PELP1	0	0	3	0	0	0	0.529
TATA-box-binding protein	TBP_HUMAN	TBP	0	0	3	0	0	0	0.529
Tetratricopeptide repeat	TTC27_HUMAN	TTC27	0	0	3	0	0	0	0.529
Transmembrane emp24 domain-containing protein 7	TMED7_HUMAN	TMED7	0	0	3	0	0	0	0.529
U3 small nucleolar RNA-associated protein 15 homolog	UTP15_HUMAN	UTP15	0	0	3	0	0	0	0.529
Guanine nucleotide-binding protein subunit beta-2-like 1	GBLP_HUMAN	GNB2L1	82	78	75	48	50	43	0.527
Transgelin-2	TAGL2_HUMAN	TAGLN2	4	7	4	4	3	2	0.527
39S ribosomal protein L33, mitochondrial	RM33_HUMAN	MRPL33	4	3	3	0	4	0	0.526
Cytochrome b-c1 complex subunit 1, mitochondrial	QCR1_HUMAN	UQCRC1	17	17	13	9	11	8	0.525
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3	NDUB3_HUMAN	NDUFB3	2	0	2	0	0	0	0.525
Serine/threonine-protein kinase Nek7	NEK7_HUMAN	NEK7	2	0	2	0	0	0	0.525
Serine/threonine-protein kinase ULK3	ULK3_HUMAN	ULK3	2	0	2	0	0	0	0.525
FAST kinase domain-containing protein 3	FAKD3_HUMAN	FASTKD3	0	2	2	0	0	0	0.524
Interferon-related developmental regulator 1	IFRD1_HUMAN	IFRD1	0	2	2	0	0	0	0.524
Serine/threonine-protein phosphatase 6 regulatory	PP6R1_HUMAN	PPP6R1	0	2	2	0	0	0	0.524
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	NDUA4_HUMAN	NDUFA4	3	6	6	3	0	5	0.523
AP-3 complex subunit mu-1	AP3M1_HUMAN	AP3M1	3	3	0	0	0	2	0.521

UPF0505 protein C16orf62	CP062_HUMAN	C16orf62	3	3	0	0	0	2	0.521
Probable cytosolic iron-sulfur protein assembly protein	CIAO1_HUMAN	CIAO1	7	5	8	5	6	0	0.520
Oxysterol-binding protein-related protein 8	OSBL8_HUMAN	OSBPL8	5	6	0	5	0	0	0.518
Sorting nexin-2	SNX2_HUMAN	SNX2	4	5	3	0	0	5	0.518
28S ribosomal protein S21, mitochondrial	RT21_HUMAN	MRPS21	16	12	11	12	0	10	0.517
Phosphoinositide 3-kinase regulatory subunit 4	PI3R4_HUMAN	PIK3R4	7	3	2	3	0	3	0.515
Pre-mRNA-splicing factor ATP-dependent RNA helicase	PRP16_HUMAN	DHX38	4	6	2	4	0	2	0.512
Proteasome activator complex subunit 3	PSME3_HUMAN	PSME3	8	8	8	5	5	4	0.511
THUMP domain-containing protein 3	THUM3_HUMAN	THUMPD3	10	11	10	5	5	8	0.511
Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial	CLPP_HUMAN	CLPP	8	9	7	6	6	2	0.511
Junction plakoglobin	PLAK_HUMAN	JUP	11	9	11	4	8	6	0.510
Thioredoxin-dependent peroxide reductase,	PRDX3_HUMAN	PRDX3	6	8	5	4	4	3	0.510
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha	2AAA_HUMAN	PPP2R1A	14	14	12	5	6	12	0.508
THO complex subunit 3	THOC3_HUMAN	THOC3	9	7	8	6	7	0	0.508
Exosome complex component MTR3	EXOS6_HUMAN	EXOSC6	15	11	12	9	7	6	0.507
Transcriptional activator protein Pur-beta	PURB_HUMAN	PURB	5	4	8	4	5	0	0.507
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	SMRD2_HUMAN	SMARCD2	5	7	2	3	0	4	0.507
ADP/ATP translocase 1	ADT1_HUMAN	SLC25A4	19	14	19	8	11	11	0.506
ATP synthase subunit f, mitochondrial	ATPK_HUMAN	ATP5J2	12	11	15	9	12	0	0.502
Acyl-coenzyme A thioesterase	ACOT1_HUMAN	ACOT1	5	6	3	4	0	3	0.502
Peroxiredoxin-4	PRDX4_HUMAN	PRDX4	3	3	6	3	3	0	0.501
Interferon-induced protein with tetratricopeptide repeats 5	IFIT5_HUMAN	IFIT5	2	0	4	0	0	2	0.500
Cullin-1	CUL1_HUMAN	CUL1	2	3	7	3	0	3	0.500
Integrator complex subunit 11	INT11_HUMAN	CPSF3L	5	6	5	0	2	6	0.499
Serine/threonine-protein phosphatase 6 regulatory	PP6R3_HUMAN	PPP6R3	4	4	0	3	0	0	0.495
Glomulin	GLMN_HUMAN	GLMN	9	4	10	4	0	8	0.493
Probable rRNA-processing protein EBP2	EBP2_HUMAN	EBNA1BP2	11	11	10	7	8	3	0.493
Cytoplasmic FMR1-interacting protein 1	CYFP1_HUMAN	CYFIP1	38	39	32	20	20	21	0.493
Syntaxin-18	STX18_HUMAN	STX18	5	0	3	2	2	0	0.489
DNA-directed RNA polymerase III subunit RPC3	RPC3_HUMAN	POLR3C	3	3	3	0	0	3	0.488

Telomere-associated protein	RIF1_HUMAN	RIF1	24	23	20	9	13	15	0.487
Plectin	PLEC_HUMAN	PLEC	45	56	59	27	31	31	0.487
Proteasome assembly	PSMG3_HUMAN	PSMG3	4	4	3	0	0	4	0.482
FAST kinase domain-containing protein 2	FAKD2_HUMAN	FASTKD2	23	26	16	9	6	20	0.478
Ubiquitin conjugation factor	UBE4B_HUMAN	UBE4B	4	6	3	2	2	3	0.477
Histone deacetylase 8	HDAC8_HUMAN	HDAC8	3	3	3	3	0	0	0.477
Ribonuclease P protein subunit	RPP14_HUMAN	RPP14	5	5	3	2	0	4	0.476
Ras-related protein Rab-10	RAB10_HUMAN	RAB10	5	4	4	2	0	4	0.473
Mitochondrial carnitine/acylcarnitine carrier	MCAT_HUMAN	SLC25A20	11	6	9	6	3	5	0.471
Glutamine--fructose-6-phosphate aminotransferase	GFPT1_HUMAN	GFPT1	15	15	11	10	7	5	0.471
Cohesin subunit SA-2	STAG2_HUMAN	STAG2	10	12	10	5	7	5	0.467
Carboxymethylenebutenolidase homolog	CMBL_HUMAN	CMBL	6	4	3	5	0	0	0.466
Exosome complex component RRP46	EXOS5_HUMAN	EXOSC5	6	6	7	3	3	4	0.461
Prolyl 3-hydroxylase 1	P3H1_HUMAN	LEPRE1	5	6	8	3	0	6	0.459
Annexin A2	ANXA2_HUMAN	ANXA2	4	0	0	0	0	0	0.459
Annexin A5	ANXA5_HUMAN	ANXA5	4	0	0	0	0	0	0.459
B-cell receptor-associated protein 31	BAP31_HUMAN	BCAP31	4	0	0	0	0	0	0.459
Extended synaptotagmin-1	ESYT1_HUMAN	ESYT1	4	0	0	0	0	0	0.459
Interleukin-1 receptor-associated kinase 1	IRAK1_HUMAN	IRAK1	4	0	0	0	0	0	0.459
Prostaglandin E synthase 3	TEBP_HUMAN	PTGES3	4	0	0	0	0	0	0.459
Protein FAM207A	F207A_HUMAN	FAM207A	4	0	0	0	0	0	0.459
SUMO-activating enzyme	SAE1_HUMAN	SAE1	4	0	0	0	0	0	0.459
Uridine-cytidine kinase 2	UCK2_HUMAN	UCK2	9	3	9	3	4	4	0.458
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5,	NDUB5_HUMAN	NDUFB5	0	4	0	0	0	0	0.458
Probable methyltransferase-like protein 15	MET15_HUMAN	METTL15	0	4	0	0	0	0	0.458
Proteasomal ATPase-associated factor 1	PAAF1_HUMAN	PAAF1	6	5	8	5	4	0	0.454
GDP-mannose 4,6 dehydratase	GMDS_HUMAN	GMDS	15	13	16	11	11	0	0.454
Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform	KPB1_HUMAN	PHKA1	4	3	0	0	2	0	0.453
RNA 3'-terminal phosphate	RTCA_HUMAN	RTCA	15	11	11	6	6	7	0.452
GTPase NRas	RASN_HUMAN	NRAS	3	2	0	0	0	0	0.449
Protein FRG1	FRG1_HUMAN	FRG1	3	2	0	0	0	0	0.449
Sterile alpha and TIR motif-containing protein 1	SARM1_HUMAN	SARM1	3	2	0	0	0	0	0.449
Thioredoxin domain-containing protein 5	TXND5_HUMAN	TXNDC5	3	2	0	0	0	0	0.449
LisH domain and HEAT repeat-containing protein	K1468_HUMAN	KIAA1468	2	3	0	0	0	0	0.449
Ras-related protein Rab-1B	RAB1B_HUMAN	RAB1B	19	25	17	11	11	9	0.447
Plasminogen activator inhibitor 1 RNA-binding protein	PAIRB_HUMAN	SERBP1	7	2	0	3	0	0	0.445

Lamin-B1	LMNB1_HUMAN	LMNB1	97	106	91	53	48	48	0.445
E3 ubiquitin-protein ligase	RING2_HUMAN	RNF2	5	0	2	0	2	0	0.445
DNA damage-binding protein	DDB1_HUMAN	DDB1	0	5	2	0	2	0	0.444
GMP synthase [glutamine-hydrolyzing]	GUAA_HUMAN	GMPS	6	5	3	3	0	3	0.440
DNA replication licensing factor MCM2	MCM2_HUMAN	MCM2	4	5	3	2	0	3	0.440
DnaJ homolog subfamily C member 11	DJC11_HUMAN	DNAJC11	16	13	11	8	5	7	0.440
Cyclin-dependent kinase 5	CDK5_HUMAN	CDK5	4	6	4	3	2	2	0.439
Methionine adenosyltransferase 2 subunit	MAT2B_HUMAN	MAT2B	3	0	2	0	0	0	0.438
Mitochondrial 2-oxodicarboxylate carrier	ODC_HUMAN	SLC25A21	0	3	2	0	0	0	0.437
Ras-related protein Rab-23	RAB23_HUMAN	RAB23	0	3	2	0	0	0	0.437
U4/U6 small nuclear ribonucleoprotein Prp4	PRP4_HUMAN	PRPF4	3	3	4	0	0	3	0.437
SURP and G-patch domain-containing protein 2	SUGP2_HUMAN	SUGP2	9	14	13	7	7	4	0.437
Profilin-2	PROF2_HUMAN	PFN2	7	5	6	4	0	4	0.437
2-amino-3-ketobutyrate coenzyme A ligase,	KBL_HUMAN	GCAT	8	8	8	6	3	3	0.436
Acidic leucine-rich nuclear phosphoprotein 32 family member B	AN32B_HUMAN	ANP32B	0	0	4	0	0	0	0.436
Fucose-1-phosphate guanylyltransferase	FPGT_HUMAN	FPGT	0	0	4	0	0	0	0.436
Glutaminyl-peptide	QPCT_HUMAN	QPCT	0	0	4	0	0	0	0.436
KATNB1-like protein 1	KTBL1_HUMAN	KATNBL1	0	0	4	0	0	0	0.436
Phosphoglycerate kinase 1	PGK1_HUMAN	PGK1	6	6	6	4	4	0	0.435
Transmembrane protein 209	TM209_HUMAN	TMEM209	2	0	3	0	0	0	0.432
Glycine--tRNA ligase	SYG_HUMAN	GARS	15	19	11	7	6	9	0.432
Unconventional myosin-Ie	MYO1E_HUMAN	MYO1E	0	2	3	0	0	0	0.432
Exocyst complex component 5	EXOC5_HUMAN	EXOC5	3	3	2	2	0	0	0.432
Translin-associated protein X	TSNAX_HUMAN	TSNAX	6	0	5	4	0	0	0.431
CCR4-NOT transcription complex subunit 8	CNOT8_HUMAN	CNOT8	3	0	4	2	0	0	0.430
Nck-associated protein 1	NCKP1_HUMAN	NCKAP1	14	23	26	11	9	11	0.429
GTP:AMP phosphotransferase AK3, mitochondrial	KAD3_HUMAN	AK3	2	6	4	4	0	0	0.429
Neurofilament medium	NFM_HUMAN	NEFM	10	13	8	5	4	6	0.427
Calmodulin-regulated spectrin-associated protein 3	CAMP3_HUMAN	CAMSAP3	10	11	8	5	4	5	0.425
Dedicator of cytokinesis	DOCK4_HUMAN	DOCK4	10	13	11	3	4	9	0.416
Exportin-6	XPO6_HUMAN	XPO6	6	9	10	7	4	0	0.414
RNA-binding protein 10	RBM10_HUMAN	RBM10	146	157	124	70	73	57	0.412
Transitional endoplasmic reticulum ATPase	TERA_HUMAN	VCP	5	5	9	3	3	3	0.412
Pyruvate carboxylase, mitochondrial	PYC_HUMAN	PC	13	13	11	4	7	6	0.405
Acidic fibroblast growth factor intracellular-binding protein	FIBP_HUMAN	FIBP	5	5	5	3	3	0	0.405
Ras-related protein Rab-7a	RAB7A_HUMAN	RAB7A	4	6	5	3	3	0	0.405

6-phosphogluconolactonase	6PGL_HUMAN	PGLS	4	5	4	2	0	3	0.404
Dimethyladenosine transferase 2, mitochondrial	TFB2M_HUMAN	TFB2M	5	4	8	4	3	0	0.404
Eukaryotic translation initiation factor 4B	IF4B_HUMAN	EIF4B	62	61	53	34	21	26	0.404
Calcium/calmodulin-dependent protein kinase type II subunit gamma	KCC2G_HUMAN	CAMK2G	4	3	4	0	0	3	0.398
RNA polymerase II-associated factor 1 homolog	PAF1_HUMAN	PAF1	8	6	6	2	0	6	0.397
Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL_HUMAN	HMGCL	8	4	8	2	2	5	0.395
DNA polymerase delta subunit	DPOD3_HUMAN	POLD3	7	6	7	3	4	2	0.394
Caspase-14	CASPE_HUMAN	CASP14	0	5	0	0	0	0	0.390
Protein VPRBP	VPRBP_HUMAN	VPRBP	0	5	0	0	0	0	0.390
Condensin-2 complex subunit	CNDG2_HUMAN	NCAPG2	3	4	4	3	0	0	0.389
Malectin	MLEC_HUMAN	MLEC	10	8	9	5	6	0	0.387
Cell division cycle protein 27 homolog	CDC27_HUMAN	CDC27	3	3	3	0	2	0	0.387
Tyrosine-protein kinase JAK1	JAK1_HUMAN	JAK1	4	2	0	0	0	0	0.384
Adenylate kinase isoenzyme 6	KAD6_HUMAN	AK6	3	3	0	0	0	0	0.383
Developmentally-regulated GTP-binding protein 2	DRG2_HUMAN	DRG2	3	3	0	0	0	0	0.383
DNA repair protein RAD51 homolog 3	RA51C_HUMAN	RAD51C	3	3	0	0	0	0	0.383
Integrator complex subunit 7	INT7_HUMAN	INTS7	3	3	0	0	0	0	0.383
Negative elongation factor B	NELFB_HUMAN	NELFB	3	3	0	0	0	0	0.383
Mitochondrial ornithine transporter 1	ORNT1_HUMAN	SLC25A15	8	8	5	0	3	5	0.382
Bifunctional purine biosynthesis protein PURH	PUR9_HUMAN	ATIC	12	11	5	3	3	6	0.382
SUMO-activating enzyme	SAE2_HUMAN	UBA2	4	6	4	0	0	4	0.379
Katanin p80 WD40 repeat-containing subunit B1	KTNB1_HUMAN	KATNB1	4	0	2	0	0	0	0.376
D-dopachrome decarboxylase	DOPD_HUMAN	DDT	0	4	2	0	0	0	0.375
Kinase D-interacting substrate of 220 kDa	KDIS_HUMAN	KIDINS220	0	4	2	0	0	0	0.375
All-trans-retinol 13,14-	RETST_HUMAN	RETSAT	3	0	3	0	0	0	0.372
Keratinocyte proline-rich	KPRP_HUMAN	KPRP	3	0	3	0	0	0	0.372
Complex I assembly factor TIMMDC1, mitochondrial	TIDC1_HUMAN	TIMMDC1	0	3	3	0	0	0	0.371
Protein SEC13 homolog	SEC13_HUMAN	SEC13	5	5	2	0	0	3	0.370
PCI domain-containing protein	PCID2_HUMAN	PCID2	11	10	12	7	4	3	0.369
Glutaryl-CoA dehydrogenase, mitochondrial	GCDH_HUMAN	GCDH	3	2	2	0	0	0	0.369
Cytochrome c	CYC_HUMAN	CYCS	6	3	3	0	0	3	0.368
TGF-beta-activated kinase 1 and MAP3K7-binding protein	TAB1_HUMAN	TAB1	30	26	30	10	10	16	0.368
Lamin-B2	LMNB2_HUMAN	LMNB2	53	46	43	18	17	24	0.366
Exosome complex component RRP43	EXOS8_HUMAN	EXOSC8	4	4	4	0	0	3	0.366
DnaJ homolog subfamily C member 10	DJC10_HUMAN	DNAJC10	28	30	31	11	13	13	0.365

Sentrin-specific protease 3	SENP3_HUMAN	SENP3	5	7	5	0	0	5	0.364
40S ribosomal protein S29	RS29_HUMAN	RPS29	3	6	0	0	2	0	0.361
Metaxin-1	MTX1_HUMAN	MTX1	4	5	6	2	3	0	0.347
Cell cycle and apoptosis regulator protein 2	CCAR2_HUMAN	CCAR2	17	24	15	8	8	6	0.346
Proteasome subunit beta type-6	PSB6_HUMAN	PSMB6	5	6	4	4	0	0	0.345
Dimethyladenosine transferase 1, mitochondrial	TFB1M_HUMAN	TFB1M	15	13	10	8	6	0	0.344
GTP-binding protein SAR1a	SAR1A_HUMAN	SAR1A	4	3	3	2	0	0	0.344
Protein S100-A8	S10A8_HUMAN	S100A8	8	7	15	8	0	3	0.342
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	SDHB_HUMAN	SDHB	6	6	6	2	3	2	0.342
SUN domain-containing	SUN2_HUMAN	SUN2	11	11	9	4	2	6	0.341
Mitochondrial pyruvate carrier	MPC2_HUMAN	MPC2	5	7	6	3	0	3	0.339
Spectrin beta chain, non-erythrocytic 1	SPTB2_HUMAN	SPTBN1	6	11	9	3	3	4	0.338
Katanin p60 ATPase-containing subunit A1	KTNA1_HUMAN	KATNA1	12	12	10	4	4	5	0.337
Aldehyde dehydrogenase family 16 member A1	A16A1_HUMAN	ALDH16A1	5	3	5	0	0	3	0.337
Protein SCO2 homolog, mitochondrial	SCO2_HUMAN	SCO2	5	4	4	2	0	2	0.336
Kinesin-like protein KIF11	KIF11_HUMAN	KIF11	9	7	5	3	0	4	0.336
Trafficking protein particle complex subunit 5	TPPC5_HUMAN	TRAPPC5	4	3	0	0	0	0	0.335
Hexokinase-2	HXK2_HUMAN	HK2	3	4	0	0	0	0	0.335
Lys-63-specific deubiquitinase BRCC36	BRCC3_HUMAN	BRCC3	5	4	4	3	0	0	0.331
SCY1-like protein 2	SCYL2_HUMAN	SCYL2	55	64	54	20	21	24	0.331
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	F263_HUMAN	PFKFB3	8	6	7	4	3	0	0.330
Sphingomyelin	NSMA3_HUMAN	SMPD4	4	3	6	3	0	0	0.327
Glycogen [starch] synthase,	GYS1_HUMAN	GYS1	4	0	3	0	0	0	0.326
Peroxisomal 2,4-dienoyl-CoA reductase	DECR2_HUMAN	DECR2	4	0	3	0	0	0	0.326
Protein KTI12 homolog	KTI12_HUMAN	KTI12	4	0	3	0	0	0	0.326
DNA-directed RNA polymerase, mitochondrial	RPOM_HUMAN	POLRMT	17	23	14	9	5	6	0.326
Ribonucleoside-diphosphate reductase subunit M2 B	RIR2B_HUMAN	RRM2B	0	4	3	0	0	0	0.325
GTPase Era, mitochondrial	ERAL1_HUMAN	ERAL1	10	11	11	7	4	0	0.325
Sodium/potassium-transporting ATPase subunit beta-3	AT1B3_HUMAN	ATP1B3	3	0	4	0	0	0	0.323
FH1/FH2 domain-containing protein 1	FHOD1_HUMAN	FHOD1	0	3	4	0	0	0	0.322
HHIP-like protein 2	HIPL2_HUMAN	HHIPL2	0	0	6	0	0	0	0.321
Lactoperoxidase	PERL_HUMAN	LPO	0	0	6	0	0	0	0.321
Protein YIF1B	YIF1B_HUMAN	YIF1B	0	0	6	0	0	0	0.321
CLIP-associating protein 2	CLAP2_HUMAN	CLASP2	4	4	3	0	2	0	0.318
Rab3 GTPase-activating protein non-catalytic subunit	RBGPR_HUMAN	RAB3GAP2	5	5	4	0	0	3	0.315

Desmoplakin	DESP_HUMAN	DSP	48	31	71	14	10	30	0.314
Symplekin	SYMPK_HUMAN	SYMPK	16	13	13	5	5	5	0.314
Eukaryotic translation initiation factor 6	IF6_HUMAN	EIF6	4	4	3	2	0	0	0.313
WASH complex subunit 7	WASH7_HUMAN	KIAA1033	12	15	7	3	5	4	0.313
GPI-anchor transamidase	GPI8_HUMAN	PIGK	7	5	5	3	0	2	0.308
Apolipoprotein O-like	APOOL_HUMAN	APOOL	5	5	7	2	0	3	0.307
Helicase SKI2W	SKIV2_HUMAN	SKIV2L	6	3	5	3	0	0	0.306
Cullin-associated NEDD8-dissociated protein 2	CAND2_HUMAN	CAND2	5	3	0	0	0	0	0.297
Protein transport protein Sec61 subunit beta	SC61B_HUMAN	SEC61B	5	3	0	0	0	0	0.297
Dual specificity protein phosphatase 3	DUS3_HUMAN	DUSP3	4	4	0	0	0	0	0.297
Eukaryotic translation initiation factor 4E type 2	IF4E2_HUMAN	EIF4E2	4	4	0	0	0	0	0.297
Heat shock 70 kDa protein	HS12A_HUMAN	HSPA12A	4	4	0	0	0	0	0.297
Nodal modulator 1	NOMO1_HUMAN	NOMO1	3	5	0	0	0	0	0.297
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	COQ5_HUMAN	COQ5	10	7	9	7	0	0	0.297
Carbonyl reductase [NADPH]	CBR1_HUMAN	CBR1	14	11	8	3	5	3	0.295
Elongator complex protein 1	ELP1_HUMAN	IKBKAP	13	12	8	5	5	0	0.292
28S ribosomal protein S26, mitochondrial	RT26_HUMAN	MRPS26	11	11	8	5	4	0	0.291
Microtubule-associated protein RP/EB family member 2	MARE2_HUMAN	MAPRE2	4	3	2	0	0	0	0.288
Protein disulfide-isomerase A6	PDIA6_HUMAN	PDIA6	4	3	2	0	0	0	0.288
Cytoplasmic FMR1-interacting protein 2	CYFP2_HUMAN	CYFIP2	3	4	2	0	0	0	0.288
Hsp70-binding protein 1	HPBP1_HUMAN	HSPBP1	0	4	4	0	0	0	0.287
RUN and FYVE domain-containing protein 1	RUFY1_HUMAN	RUFY1	3	3	3	0	0	0	0.286
Bloom syndrome protein	BLM_HUMAN	BLM	2	0	6	0	0	0	0.283
Adenosylhomocysteinase	SAHH_HUMAN	AHCY	8	9	8	3	4	0	0.279
Protein diaphanous homolog 3	DIAP3_HUMAN	DIAPH3	4	5	0	0	0	0	0.267
Ankyrin repeat and FYVE domain-containing protein 1	ANFY1_HUMAN	ANKFY1	10	13	7	2	4	3	0.266
MAX gene-associated protein	MGAP_HUMAN	MGA	6	10	4	3	2	0	0.262
Plastin-3	PLST_HUMAN	PLS3	6	2	2	0	0	0	0.260
Alpha-aminoadipic semialdehyde synthase,	AASS_HUMAN	AASS	4	4	2	0	0	0	0.260
Protein arginine N-methyltransferase 3	ANM3_HUMAN	PRMT3	4	4	2	0	0	0	0.260
Serpin B12	SPB12_HUMAN	SERPINB12	4	4	2	0	0	0	0.260
Neuroblastoma-amplified	NBAS_HUMAN	NBAS	4	3	3	0	0	0	0.258
Phosphomannomutase 2	PMM2_HUMAN	PMM2	4	3	3	0	0	0	0.258
Formin-like protein 2	FMNL2_HUMAN	FMNL2	3	4	3	0	0	0	0.258
Guanine nucleotide-binding protein G(s) subunit alpha	GNAS1_HUMAN	GNAS	6	5	9	4	0	0	0.255
Protein odr-4 homolog	ODR4_HUMAN	ODR4	7	8	6	0	0	4	0.252
Ubiquitin conjugation factor	UBE4A_HUMAN	UBE4A	5	6	3	0	0	2	0.252

5-methylcytosine rRNA methyltransferase NSUN4	NSUN4_HUMAN	NSUN4	5	5	4	0	2	0	0.250
Citrate synthase, mitochondrial	CISY_HUMAN	CS	6	4	0	0	0	0	0.243
Exosome complex component RRP45	EXOS9_HUMAN	EXOSC9	6	4	0	0	0	0	0.243
COMM domain-containing protein 3	COMD3_HUMAN	COMMD3	4	6	0	0	0	0	0.242
Cytosolic carboxypeptidase 1	CBPC1_HUMAN	AGTPBP1	4	6	0	0	0	0	0.242
Ras-related protein Rab-1A	RAB1A_HUMAN	RAB1A	4	6	0	0	0	0	0.242
Nuclear autoantigenic sperm protein	NASP_HUMAN	NASP	5	3	3	0	0	0	0.235
Serine/threonine-protein kinase	KPCD1_HUMAN	PRKD1	4	4	3	0	0	0	0.235
Serine/threonine-protein kinase	KPCD3_HUMAN	PRKD3	4	4	3	0	0	0	0.235
Chloride intracellular channel protein 1	CLIC1_HUMAN	CLIC1	5	0	5	0	0	0	0.235
ERO1-like protein alpha	ERO1A_HUMAN	ERO1L	4	3	4	0	0	0	0.234
Erythrocyte band 7 integral membrane protein	STOM_HUMAN	STOM	4	3	4	0	0	0	0.234
TraB domain-containing	TRABD_HUMAN	TRABD	4	3	4	0	0	0	0.234
Mitogen-activated protein kinase kinase kinase 7	M3K7_HUMAN	MAP3K7	2	5	4	0	0	0	0.233
Casein kinase II subunit alpha	CSK21_HUMAN	CSNK2A1	4	2	5	0	0	0	0.232
Structural maintenance of chromosomes protein 6	SMC6_HUMAN	SMC6	5	6	4	2	0	0	0.230
Chloride channel CLIC-like protein 1	CLCC1_HUMAN	CLCC1	9	5	5	3	0	0	0.227
General transcription factor II-I	GTF2I_HUMAN	GTF2I	8	11	8	3	0	3	0.227
26S proteasome non-ATPase regulatory subunit 4	PSMD4_HUMAN	PSMD4	25	19	18	7	5	4	0.226
Guanine nucleotide-binding protein subunit alpha-13	GNA13_HUMAN	GNA13	12	8	14	7	0	0	0.226
Far upstream element-binding protein 2	FUBP2_HUMAN	KHSRP	8	8	7	4	0	0	0.224
Enoyl-CoA delta isomerase 1, mitochondrial	ECI1_HUMAN	ECI1	5	6	0	0	0	0	0.222
Serine/threonine-protein kinase	KPCD2_HUMAN	PRKD2	5	5	10	0	0	3	0.217
Dual specificity protein phosphatase 9	DUS9_HUMAN	DUSP9	2	6	4	0	0	0	0.214
DNA mismatch repair protein Msh3	MSH3_HUMAN	MSH3	0	5	6	0	0	0	0.214
Microsomal glutathione S-transferase 3	MGST3_HUMAN	MGST3	4	3	5	0	0	0	0.213
Dynamin-like 120 kDa protein, mitochondrial	OPA1_HUMAN	OPA1	4	2	6	0	0	0	0.212
Phosphatidylinositol 4-phosphate 5-kinase type-1	PI51C_HUMAN	PIP5K1C	28	28	23	3	4	11	0.202
5'-AMP-activated protein kinase catalytic subunit alpha-1	AAPK1_HUMAN	PRKAA1	5	5	3	0	0	0	0.199
tRNA pseudouridine synthase A, mitochondrial	TRUA_HUMAN	PUS1	3	6	4	0	0	0	0.198
Desmoglein-1	DSG1_HUMAN	DSG1	10	6	25	0	0	7	0.190

Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	HEM6_HUMAN	CPOX	6	7	0	0	0	0	0.190
HEAT repeat-containing	HEAT6_HUMAN	HEATR6	5	8	0	0	0	0	0.190
Probable ATP-dependent RNA helicase DDX46	DDX46_HUMAN	DDX46	4	7	3	0	0	0	0.185
COP9 signalosome complex subunit 4	CSN4_HUMAN	COPS4	3	4	7	0	0	0	0.182
Lipoprotein lipase	LIPL_HUMAN	LPL	0	0	12	0	0	0	0.180
Uncharacterized protein	CS052_HUMAN	C19orf52	11	6	7	3	0	0	0.179
Serrate RNA effector molecule homolog	SRRT_HUMAN	SRRT	8	11	6	0	2	2	0.177
Protein DJ-1	PARK7_HUMAN	PARK7	7	9	9	0	0	3	0.175
Lamina-associated polypeptide 2, isoform alpha	LAP2A_HUMAN	TMPO	5	4	6	0	0	0	0.171
Ubiquinol-cytochrome-c reductase complex assembly	UQCC1_HUMAN	UQCC1	7	8	6	2	0	0	0.164
Spectrin alpha chain, non-erythrocytic 1	SPTN1_HUMAN	SPTAN1	10	12	5	0	3	0	0.163
14-3-3 protein eta	1433F_HUMAN	YWHAH	5	5	6	0	0	0	0.160
DNA-directed RNA polymerases I and III subunit	RPAC1_HUMAN	POLR1C	4	6	6	0	0	0	0.160
Peroxisomal membrane protein PMP34	PM34_HUMAN	SLC25A17	6	3	7	0	0	0	0.160
Unconventional myosin-Vb	MYO5B_HUMAN	MYO5B	8	11	4	0	0	2	0.154
Ubiquitin carboxyl-terminal hydrolase 15	UBP15_HUMAN	USP15	6	6	5	0	0	0	0.152
Transmembrane protein 201	TM201_HUMAN	TMEM201	5	6	6	0	0	0	0.151
YEATS domain-containing protein 4	YETS4_HUMAN	YEATS4	6	7	6	0	0	0	0.136
Protein arginine N-methyltransferase 1	ANM1_HUMAN	PRMT1	6	6	7	0	0	0	0.135
GrpE protein homolog 1, mitochondrial	GRPE1_HUMAN	GRPEL1	7	8	5	0	0	0	0.129
Pantothenate kinase 4	PANK4_HUMAN	PANK4	8	4	8	0	0	0	0.128
Phosphoserine	SERC_HUMAN	PSAT1	8	12	9	2	0	0	0.119
Ras-related protein Rab-6A	RAB6A_HUMAN	RAB6A	11	7	4	0	0	0	0.118
Ig kappa chain V-I region Lay	KV113_HUMAN	IGKV1-13	9	7	6	0	0	0	0.118
Protein phosphatase 1B	PPM1B_HUMAN	PPM1B	17	12	12	0	0	3	0.107
Transcription initiation factor TFIID subunit 4	TAF4_HUMAN	TAF4	8	10	7	0	0	0	0.103
Ig kappa chain V-IV region (Fragment)	KV401_HUMAN	IGKV4-1	22	21	20	0	0	0	0.041

[a] The value was obtained by the mean normalized SC of H7N9 NS1 vector (NS1) divided by that of control vector (VC). Proteins with ratios larger than the mean plus two SD (the ratios were above 7.728) and detected in more than two replicates of the NS1 group are defined as NS1 interacting partners.

Table S-3. List of the 67 proteins with the fold changes larger than the mean plus one SD

Protein name	Accession number	Gene name	Spectral counts (SCs)						Ratio of NS1/VC[a]
			Vector control (VC)			H7N9 NS1 (NS1)			
			Rep 1	Rep 2	Rep 3	Rep 1	Rep 2	Rep 3	
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA_HUMAN	PRKRA	0	0	0	71	65	55	65.023
Scaffold attachment factor B1	SAFB1_HUMAN	SAFB	0	0	0	63	54	44	54.772
Phosphatidylinositol 3-kinase regulatory subunit beta	P85B_HUMAN	PIK3R2	0	0	0	35	37	34	36.141
Scaffold attachment factor B2	SAFB2_HUMAN	SAFB2	0	0	0	29	29	30	30.010
Insulin-like growth factor 2 mRNA-binding protein 2	IF2B2_HUMAN	IGF2BP2	0	2	0	39	37	45	28.951
Heterogeneous nuclear ribonucleoprotein D-like	HNRDL_HUMAN	HNRNPDL	0	0	0	31	31	23	28.938
Pre-mRNA-splicing factor	SYF1_HUMAN	XAB2	0	0	0	32	27	25	28.592
Spermatid perinuclear RNA-binding protein	STRBP_HUMAN	STRBP	0	0	0	27	25	27	26.932
YTH domain-containing	YTDC1_HUMAN	YTHDC1	0	0	0	26	24	25	25.562
Putative helicase MOV-10	MOV10_HUMAN	MOV10	0	2	5	75	75	73	24.294
Polyadenylate-binding protein	PABP2_HUMAN	PABPN1	0	0	0	27	22	22	24.170
ELAV-like protein 2	ELAV2_HUMAN	ELAVL2	0	0	0	23	22	15	20.412
Zinc finger RNA-binding	ZFR_HUMAN	ZFR	0	3	2	38	46	32	17.287
Crooked neck-like protein 1	CRNL1_HUMAN	CRNKL1	0	2	0	24	20	27	16.981
Serine/arginine-rich splicing	SRSF7_HUMAN	SRSF7	0	0	0	19	16	13	16.327
Cleavage and polyadenylation specificity factor subunit 2	CPSF2_HUMAN	CPSF2	0	0	0	14	13	20	16.056
Serine/arginine-rich splicing factor 10	SRS10_HUMAN	SRSF10	0	0	0	12	15	19	15.729
ATP-dependent RNA helicase DHX8	DHX8_HUMAN	DHX8	0	0	0	16	17	11	14.977
Double-stranded RNA-binding protein Staufen homolog 2	STAU2_HUMAN	STAU2	0	0	0	18	13	13	14.964
Y-box-binding protein 3	YBOX3_HUMAN	YBX3	0	0	0	11	11	15	12.638
RNA-binding protein Musashi homolog 2	MSI2H_HUMAN	MSI2	0	0	0	12	12	13	12.621
SNW domain-containing	SNW1_HUMAN	SNW1	0	0	0	14	10	11	11.909
U5 small nuclear ribonucleoprotein 40 kDa	SNR40_HUMAN	SNRNP40	0	0	0	11	15	8	11.585
Putative RNA-binding protein Luc7-like 2	LC7L2_HUMAN	LUC7L2	2	2	0	25	20	17	11.399
Peptidyl-prolyl cis-trans isomerase-like 1	PPIL1_HUMAN	PPIL1	0	0	0	10	14	7	10.562
Double-stranded RNA-binding protein Staufen homolog 1	STAU1_HUMAN	STAU1	4	3	2	35	38	29	10.021
Protein BUD31 homolog	BUD31_HUMAN	BUD31	0	0	0	7	10	11	9.575
Protein PRRC2A	PRC2A_HUMAN	PRRC2A	0	0	0	8	13	7	9.552
Transformer-2 protein homolog beta	TRA2B_HUMAN	TRA2B	3	0	0	21	18	11	9.425
Cleavage and polyadenylation specificity factor subunit 7	CPSF7_HUMAN	CPSF7	0	0	0	9	9	8	8.860
Myosin regulatory light chain	ML12A_HUMAN	MYL12A	0	0	0	10	8	8	8.850

Ribosome-binding protein 1	RRBP1_HUMAN	RRBP1	0	0	0	10	9	6	8.500
Transformer-2 protein homolog alpha	TRA2A_HUMAN	TRA2A	5	0	0	22	21	17	7.982
KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDR1_HUMAN	KHDRBS1	0	0	0	7	8	8	7.850
Heterogeneous nuclear ribonucleoproteins A2/B1	ROA2_HUMAN	HNRNPA2B1	25	31	22	229	225	231	7.735
Zinc finger CCHC domain-containing protein 3	ZCHC3_HUMAN	ZCCHC3	0	3	2	20	21	11	7.732
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRPC_HUMAN	HNRNPC	30	28	27	256	216	267	7.638
Pre-mRNA-processing factor	PRP17_HUMAN	CDC40	0	0	0	6	3	13	7.533
Activated RNA polymerase II transcriptional coactivator p15	TCP4_HUMAN	SUB1	0	0	0	9	6	6	7.137
DNA-directed RNA polymerase II subunit RPB3	RPB3_HUMAN	POLR2C	0	0	0	5	8	6	6.490
Nuclear receptor coactivator 5	NCOA5_HUMAN	NCOA5	0	0	0	6	8	5	6.477
Probable ATP-dependent RNA helicase DDX23	DDX23_HUMAN	DDX23	0	0	3	16	13	7	6.470
39S ribosomal protein L49, mitochondrial	RM49_HUMAN	MRPL49	0	0	0	7	7	5	6.467
Actin, alpha cardiac muscle 1	ACTC_HUMAN	ACTC1	0	0	0	7	11	0	6.441
Chromodomain-helicase-DNA-binding protein 4	CHD4_HUMAN	CHD4	0	3	0	7	16	10	6.251
Protein SON	SON_HUMAN	SON	0	0	0	5	7	6	6.147
Dolichol-phosphate mannosyltransferase subunit 3	DPM3_HUMAN	DPM3	0	0	0	6	6	6	6.137
U1 small nuclear ribonucleoprotein 70 kDa	RU17_HUMAN	SNRNP70	0	0	0	8	4	6	6.118
Polyadenylate-binding protein	PABP4_HUMAN	PABPC4	9	14	7	64	65	73	5.955
RNA-binding protein Raly	RALY_HUMAN	RALY	8	7	9	48	52	63	5.952
Heterogeneous nuclear ribonucleoprotein A3	ROA3_HUMAN	HNRNPA3	18	16	9	100	99	88	5.907
Zinc finger CCCH domain-containing protein 11A	ZC11A_HUMAN	ZC3H11A	0	0	0	5	7	5	5.801
Pre-mRNA-processing factor 40 homolog A	PR40A_HUMAN	PRPF40A	2	0	0	7	8	9	5.757
RNA-binding motif protein, X chromosome	RBMX_HUMAN	RBMX	21	16	18	126	121	101	5.549
UAP56-interacting factor	UIF_HUMAN	FYTTD1	0	0	0	6	6	4	5.444
Insulin receptor substrate 4	IRS4_HUMAN	IRS4	0	2	3	13	18	6	5.438
Zinc finger protein 346	ZN346_HUMAN	ZNF346	0	4	6	27	24	15	5.221
Heterogeneous nuclear ribonucleoprotein L	HNRPL_HUMAN	HNRNPL	22	24	23	133	130	147	5.217
Probable ATP-dependent RNA helicase YTHDC2	YTDC2_HUMAN	YTHDC2	5	0	0	16	13	10	5.180
Pleiotropic regulator 1	PLRG1_HUMAN	PLRG1	5	3	4	22	22	26	5.125
Heterogeneous nuclear ribonucleoprotein Q	HNRPQ_HUMAN	SYNCRIP	29	33	28	164	172	182	5.062
NTF2-related export protein 1	NXT1_HUMAN	NXT1	0	0	0	9	5	0	5.049

Heterogeneous nuclear ribonucleoprotein H3	HNRH3_HUMAN	HNRNPH3	9	7	8	41	47	45	4.868
Centrin-2	CETN2_HUMAN	CETN2	0	0	0	4	4	6	4.784
Splicing factor, arginine/serine-rich 15	SFR15_HUMAN	SCAF4	0	0	0	5	4	5	4.771
Heterogeneous nuclear ribonucleoprotein A1	ROA1_HUMAN	HNRNPA1	25	34	22	149	147	139	4.732
Protein lin-28 homolog B	LN28B_HUMAN	LIN28B	4	0	0	12	12	6	4.675

[a] The value was obtained by the mean normalized SC of H7N9 NS1 vector (NS1) divided by that of control vector (VC). Proteins with ratios larger than the mean plus one SD (the ratios were above 4.611) and detected in more than two replicates of the NS1 group are defined as NS1 interacting partners.

Figure S-1

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                                        20                                  40                                  60
                                         |                                   |                                   |
NS1_PR_8_34_H1N1  MDPNTVSSFQ VDCFLWHVRK RVADQELGDA PFLDRLRRDQ KSLRGRGSTL GLDIETATRA 60
NS1_TW_1_2013_H7N9 ..S....... .......... .F....M... .......... ......S... ....R....E 60
                                        80                                 100                                 120
                                         |                                   |                                   |
NS1_PR_8_34_H1N1  GKQIVERILK EESDEALKMT MASVPASRYL TDMTLEEMSR EWSMLIPKQK VAGPLCIRMD 120
NS1_TW_1_2013_H7N9 ..H......E ......F..S I.....P... .......... D.L....... IT.S...... 120
                                       140                                 160                                 180
                                         |                                   |                                   |
NS1_PR_8_34_H1N1  QAIMDKNIIL KANFSVIFDR LETLILLRAF TEEGAIVGEI SPLPSLPGHT AEDVKNAVGV 180
NS1_TW_1_2013_H7N9 ...V....T. ........N. ..A....... .......... .......... DK.....IEI 180
                                       200                                 220
                                         |                                   |
NS1_PR_8_34_H1N1  LIGGLEWNDN TVRVSETLQR FAWRSSNENG RPPLTPKQKR EMAGTIRSEV 230
NS1_TW_1_2013_H7N9 ....F..... .......... ......D.D. .S..ST.--- ---------- 217
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Figure S-1. Sequence comparison of NS1 proteins encoded by influenza A virus Puerto Rico/8/34/H1N1 and Taiwan/1/2013/H7N9 strains.

Figure S-2

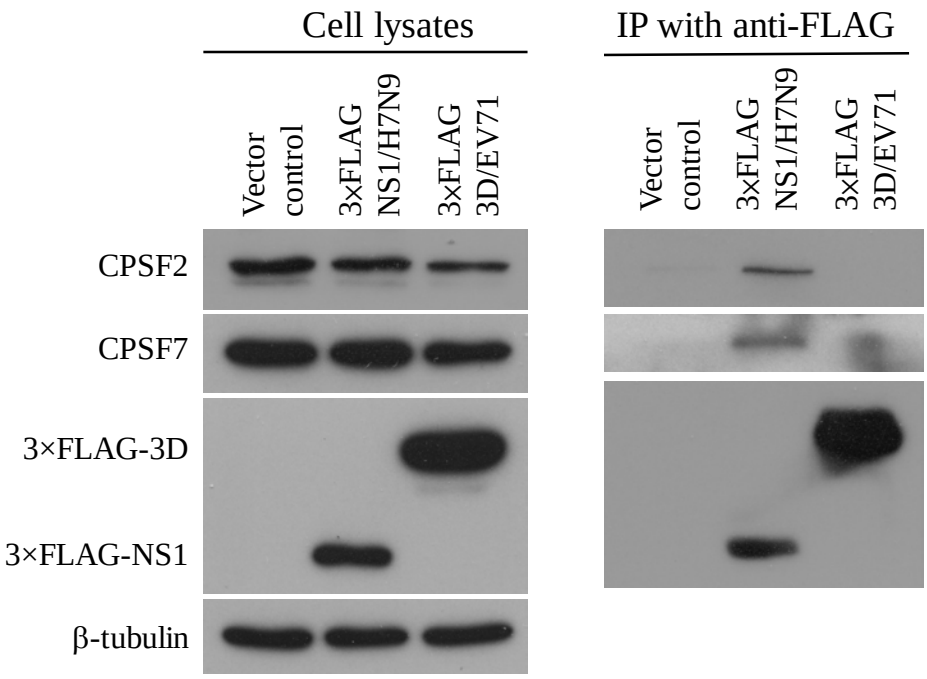

Figure S-2. Confirmation of the specificity for interactions of H7N9 NS1 with CPSF2 and CPSF7. Lysates of 293T cells that were transfected with a control vector and a plasmid that expresses either 3×FLAG-tagged H7N9 NS1 or 3×FLAG-tagged EV71 3D protein were collected and subjected to immunoprecipitation with anti-FLAG resin. The CPSF2 and CPSF7 in the lysates and IP precipitates were detected by western blot with anti-CPSF2 and anti-CPSF7 antibodies.